WCM2025

XXII World Congress of Malacology

ABSTRACT BOOK

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XXII WORLD CONGRESS OF MALACOLOGY

XXIX BRAZILIAN MEETING OF MALACOLOGY

"One Planet, One Health, One Challenge"

Molluscs and Global Health: Integrating Science for the Well-Being of One Planet

August 4th to 8 th 2025

São Paulo, SP, Brazil

https://wcm2025.com.br/

Organized by UNITAS Malacologica and the Brazilian Society of Malacology (SBMa)

ORGANIZATION

UNITAS MALACOLOGICA

SBMa - Sociedade Brasileira de Malacologia - 1969

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WCM 2025

XXII World Congress of Malacology

The logo design emerged from the work of MSc. Elisabete Tsukada and Dr. Lenita de Freitas Tallarico, highlighting the importance of understanding through knowledge the various groups of molluscs that are distributed across the planet and from the integration and connectivity between continents. The idea of using the shell of a pearl-bearing bivalve comes from the great importance of these animals in human culture, as well as the concept of the shell being the symbol of protection and care for our unique planet, the globe being represented by the pearl as a rare jewel that must be preserved and conserved in the best possible way. This is also in close connection to the WCM 2025 moto: One Planet, One Health, One Challenge.

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Welcome Remarks and Overview
Chairwoman of Unitas Malacologica

The XX World Congress of Malacology, concurrent with the XXIX Brazilian Meeting of Malacology, was held at the Butantan Institute in São Paulo, Brazil, from August 4 to 8, 2025. The congress is held in different countries every three years, and this edition is the first to be hosted in Latin America and in partnership with the Brazilian Society of Malacology (SBMa). We have a team of malacologists from different Brazilian and international institutions (Butantan Institute, UERJ, UFSCAR, UNICAMP, UNIRIO, USP, UFSCPA, UFJF, IFRR, UNAM, UVigo, Field Museum, University of Helsinki), and with the support of the malacological societies AMS (American Society of Malacology, SEM (Spanish Society of Malacology), ASAM (Argentine Association of Malacology), SMU (Malacological Society of Uruguay), SMMAC (Malacological Society of Mexico), and SMACH (Malacological Society of Chile). The congress was a multicultural event with the participation of diverse researchers and students from various parts of the world. The objective was to integrate education (bringing together students of all levels), research, technological activities, scientific and cultural outreach, promoting valuable international scientific exchanges in Malacology and related fields.

According to the World Health Organization, "One Health is an integrated and unifying approach to balancing and optimizing the health of people, animals, and ecosystems." This approach encourages the establishment of a global framework and an integrated system that involves collaboration across sectors and disciplines to improve global health. Environmental health is one of the issues addressed by One Health, and the main challenges associated with this field of knowledge are promoting a more comprehensive understanding of the drivers and effects of pollution and climate change. In this sense, the WCM2025 motto was "One Planet, One Health, One Challenge", and the theme is "Molluscs and Global Health: Integrating Science for the Well-Being of One Planet".

In this meeting we count on the participation of professionals and students of Biological Sciences and related areas, malacologists, representatives of public agencies, governmental and non-governmental institutions, promoting a valuable international scientific exchange, being a hub for extremely valuable institutional exchanges for global science, promoting the dissemination of knowledge, cooperation in research, appreciation of traditional knowledge, strengthening of sociocultural identities and the sustainable use of biodiversity, environmental health and public health, and the rescue of historical, cultural and natural heritage within the scope of Malacology.

During WCM 2025, productive scientific discussions were held, sharing and discussing ideas and perspectives on mollusks. The proposed program addressed current issues involving mollusks, evolutionary and developmental aspects, taxonomy, phylogeny, paleontology, genomics, functional morphology, ecology, biodiversity, conservation, exotic and endangered species, bioindicators, anthropogenic and climatic impacts, medical and applied malacology, and all methodological innovations related to malacology. The event aimed to encourage participants to reflect on the future through a critical look at scientific knowledge, including advances, challenges, and gaps, such as:

scientific-cultural references and legacy for future generations; biodiversity conservation; the impacts of invasive alien species/pests; the popularization of science; the pursuit of One Health; how to encourage and support the economy in traditional communities; among others. The entire conference was designed to integrate teaching at different levels of education. The traditional symposium of young taxonomists, an event held at national SBMa meetings, which this year allowed the inclusion of young researchers, providing great visibility to the work of all students. In return, they had the opportunity to exchange experiences with major established names in world malacology.

We had the participation of approximately 300 participants from 37 countries: Brazil (153), USA (29), Chile (13), Japan (9), Spain (8), Argentina (7), Germany (7), Mexico (7), Poland (6), Philippines (6), United Kingdom (6), Australia (5), India (5), France (4), Russia (4), Canada (3), Italy (3), Norway (3), Peru (2), South Africa (2), Uruguay (2), Belgium (1), Colombia (1), Costa Rica (1), Czech Republic (1), Egypt (1), El Salvador (1), Finland (1), Greece (1), Hong Kong (1), New Zealand (1), Nigeria (1), Paraguay (1), Portugal (1), Sweden (1), Switzerland (1) and Ukraine (1). With 165 students and 135 professionals in attendance, 178 poster presentations and 202 oral presentations were given. In total, there were four plenary lectures, 27 symposia, one working group, three scientific society assemblies (UNITAS Malacologica, SBMa, and AMS), a student fundraising auction, a cultural presentation (science slam), student awards from the societies Unitas Malacologica (six awards), the Brazilian Malacological Society (eight awards), the American Malacological Society (four awards), the Malacological Society of Japan (two awards), and the Malacological Society of London (two awards) for the best oral presentations and panels, and three more awards for the best malacophotographs, totaling 25 awards.

In this edition, we organized the exhibition "*Living Jewels – But Is That All*?" at the Professor Isaias Museum of Raw Microbiology. It opened on August 5, 2025, and will remain open to the public at the Butantan Institute's Science Park until the beginning of the next year, including schoolchildren and walk-ins. With a contemplative and educational approach, the exhibition articulates thematic content through collections, explanatory texts, panels, a collection of shells and ritualistic material, as well as two aquariums with gastropods that are the subject of research at the Butantan Institute's Parasitology Laboratory. Strengthening the relationship between science, society, and decision-makers is a complex and relevant challenge for enhancing critical awareness about the conservation of both aquatic and terrestrial ecosystems, the need to reduce social inequalities, food production and diversification, and the need to mitigate adverse environmental impacts and climate change.Thus, the exhibition's advantages include accessible scientific dissemination not only to professionals and students, but also to anyone interested in mollusk studies.

Lenita de Freitas Tallarico – Instituto Butantan (IB), Brazil
Chairwoman of Organizing Committee WCM2025

Exhibition Technical Sheet – "Living Jewels: But is that all?"

Exhibition Concept

The idea for this exhibition emerged from a conversation with Sandra Coccuzzo Sampaio Vessoni, Director of the *Centro de Desenvolvimento Científico* at the *Instituto Butantan*, during the planning of the World Congress of Malacology at the institution. She suggested that, in addition to the scientific event, an exhibition should be held at the Park of Science to raise awareness about the importance of mollusks and highlight the history of research on these organisms carried out at the institute.

A partnership with the team at the *Museu de Microbiologia Professor Isaias Raw* (MMB) was essential for the conception, organization, and setup of the exhibition. This collaboration made it possible to develop accessible and scientifically accurate content.

The exhibition's identity was initially developed by Lenita de Freitas Tallarico, a specialist from the *Laboratório de Parasitologia* and President of the World Congress of Malacology, in collaboration with the MMB team: cultural supervisor Adriano Dias de Oliveira, educational leader Cynthia Iszlaji, and cultural coordinator Glaucia Colli Inglez, with support from scientific researcher Paulo Henrique Nico Monteiro. They invited Renato Salgado from Zol Design to develop the exhibition's visual and spatial content.

Partnership with Conchologists

The collaboration with the *Conquiliologistas do Brasil* was essential to enrich the exhibition with stunning shells, fostering dialogue with experts, and expanding public knowledge and appreciation of mollusks.

Technical and Logistical Collaboration

The support of various departments of the Butantan Institute was vital to bring the exhibition to life, including teams from the *Centro de Desenvolvimento Cultural*, *Escola Superior do Instituto Butantan*, *Manutenção Predial* team, and other contributors who played a role in this project.

Curatorship and Execution

- **Parasitology Laboratory – Butantan Institute** Lenita de Freitas Tallarico
- **MMB – Butantan Institute** Adriano Dias de Oliveira, Cynthia Iszlaji, Glaucia Colli Inglez

Project Coordination

- **Scientific Development Center – Butantan Institute** Sandra Coccuzzo Sampaio Vessoni

Conchological Collection Production

- **Conquiliologistas do Brasil** Celso Luiz Rodrigues Esteves, Cristina Koprick Sodré, Eduardo Schirrmeister, José Roberto Heise, Maurício Sergio Uhle

Ritual Collection Production

- **University of São Paulo** Vagner Gonçalves da Silva

Exhibition Design and Visual Communication Zol Design

Text Editing

- **Laboratório de Ecologia e Evolução – IB** Paulo Henrique Nico Monteiro
- **Centro de Memória – IB** Audrea Santos De Santana, Bianca Silva Cruz, Henrique Sugahara Francisco, Juliana Cabral da Silva, Mariana Soares Popperl, Olga Fabergé Alves
- **Centro de Desenvolvimento Cultural – IB** Suzana Cesar Gouveia Fernandes
- **Universidade Federal de São Carlos** Eliane Pintor de Arruda
- **Universidade Federal do Estado do Rio de Janeiro** Igor Christo Miyahira

Text Revision

- **Escola Superior do Instituto Butantan** Andreia dos Santos Calegari, Leticia Ruiz Sueiro

Executive Production

- **Escola Superior do Instituto Butantan** Antonio Carlos Orlando Ribeiro da Costa, Carolina Julião Avancini, Maria Teresa Ghiuro Valentini Abdullatif

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Scenography Construction

- **Construção cenográfica** Daniel Prado da Silva, Douglas de Araruna Francisco, Ezequiel Saldanha Gilmar das Mercedes, Joaquin Rillo, José Roberto Ursulino, Leandro Lauro Cunha, Vinicyus de Jesus Lopes Galvão, Waldir Marques

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- **Instituto Butantan** Esper Georges Kallás, Lucio Gama, Rui Curi
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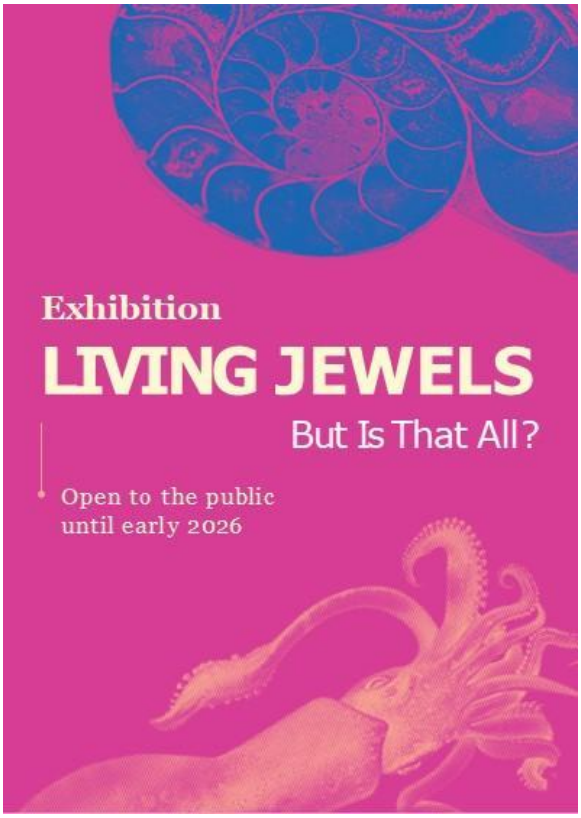

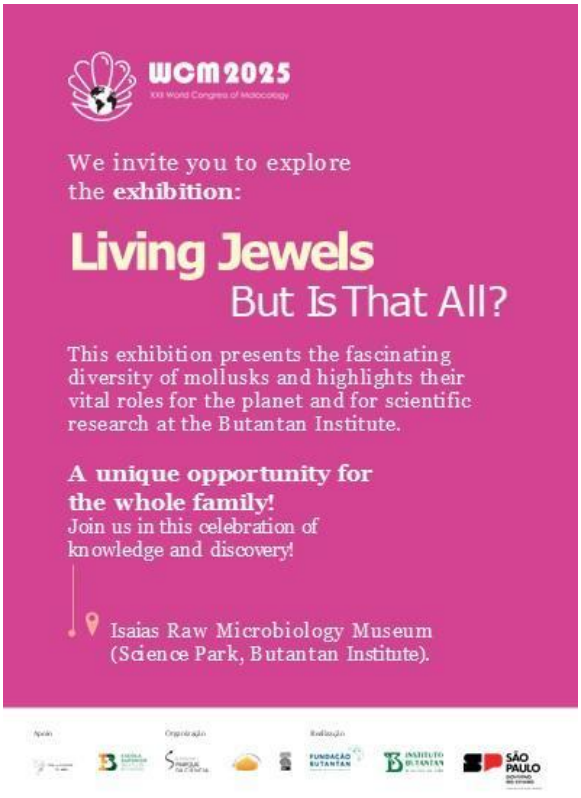

AWARDS

UNITAS Malacologica

- UM Best Poster: **Andrew Faner Torres** – University of Amsterdam, Netherlands.
  Title of the Abstract: CAPTURING REEF GASTROPOD DIVERSITY ALONG THE CENTRE OF THE CORAL TRIANGLE USING ARMS AND THE NOVEL GASTRO16 METABARCODING MARKER. *(p. 340)*
- UM 2nd Poster: **Antônia Ribeiro Cruz Silva** – Museu Nacional, Universidade Federal do Rio de Janeiro, Brazil.
  Title of the Abstract: ISOLATED BEAUTY: NUDIBRANCH DIVERSITY FROM GOUGH ISLAND, SOUTH ATLANTIC OCEAN. *(p. 418)*
- UM 3rd Poster: **Yuki Nagai** – Tohoku University, Japan.
  Title of the Abstract: INFESTATION OF FARMED AND WILD MOLLUSCS BY SHELL-BORING POLYDORID SPECIES (ANNELIDA, SPIONIDAE) ALONG THE COAST OF NORTHERN JAPAN. *(p. 330)*
- UM Best Oral: **Monisha Parameshwar Bharate** – University of Bergen, Norway.
  Title of the Abstract: UNRAVELING THE SECRETS OF *Smaragdinella* MARINE SNAILS: THE ONLY ROCK-DWELLING GENUS OF CEPHALASPIDS. *(p. 25)*
- UM 2nd Oral: **Yu Kai Tan** – University of Michigan, USA.
  Title of the Abstract: PEEK-A-BOO: CRYPTIC DIVERSITY IN CARRIER SNAILS REVEAL PHYLOGEOGRAPHIC BOUNDARIES. *(p. 236)*
- UM 3rd Oral: **Maria Fernanda Rosa da Silva** – Universidade Federal de São Carlos, Brazil.
  Title of the Abstract: ASSESSING MICROPLASTIC RETENTION AND BIOACCUMULATION IN *Anodontites trapesialis*: A FRESHWATER BIOINDICATOR STUDY. *(p. 173)*

BRAZILIAN SOCIETY OF MALACOLOGY (SBMa)

Maury Pinto de Oliveira Award

Undergraduate

- First Place, Poster: **Carolina Nascimento dos Santos** – Universidade Estadual de Campinas, Brazil.
  Title of the Abstract: THE ANATOMY OF THE EYES IN THE OPTIC SIPHONAL TENTACLES OF THE ANTARCTIC BIVALVE *Laternula elliptica* (P. P. KING, 1832) (LATERNULIDAE). *(p. 253)*
- Second Place, Poster: **Julia do Nascimento** – Universidade Estadual de Campinas, Brazil.
  Title of the Abstract: TAXONOMY, MORPHOLOGY, AND DISTRIBUTION OF THE CHITONS (MOLLUSCA: POLYPLACOPHORA) COLLECTED BY THE BRAZILIAN ANTARCTIC EXPEDITIONS. *(p. 409)*
- First Place, Oral: **Luca Castrezana** – Universidade Estadual de Campinas, Brazil.
  Title of the Abstract: LATITUDINAL DISTRIBUTION OF MOLLUSKS ASSOCIATED WITH MACROALGAE ALONG THE BRAZILIAN COAST, OCEANIC ISLANDS, AND THE CARIBBEAN. *(p. 209)*

- Second Place, Oral: **Juliana Soares Ferreira** – Universidade do Estado do Rio de Janeiro, Brazil.
  Title of the Abstract: FANTASTIC MOLLUSKS AND WHERE THEY LIVE: A PLAYFUL ACTIVITY ABOUT MALACOFAUNA OF COASTAL ECOSYSTEMS. *(p. 54)*

Postgraduate

- First Place, Poster: **Katarzyna Dorota Voncina** – Senckenberg Research Institute and Natural History Museum Frankfurt, Germany.
  Title of the Abstract: REDUCTION AND AESTHETE PATTERNS IN CRYPTOPLACOIDEA (POLYPLACOPHORA: CHITONIDA). *(p. 251)*
- Second Place, Poster: **Dina Mae Llido Ranises** – Université Libre de Bruxelles, Belgium.
  Title of the Abstract: GENETIC MIXING AMONG INVASIVE ANDROGENETIC *Corbicula* CLAMS IN WESTERN EUROPE. *(p. 390)*
- First Place, Oral: **Adriana Marie Halvonik-Sanchez** – University of S. Carolina, USA.
  Title of the Abstract: HOW FEEDING ECOLOGY AND PHYSIOLOGY CONTRIBUTE TO NICHE DIFFERENCES AMONG SYMPATRIC TROPICAL *Chiton*. *(p. 66)*
- Second Place, Oral: **Lisa Rouressol** – Carnegie-Caltech-Uvienna, USA-Austria.
  Title of the Abstract: SPATIO-TEMPORAL CHARACTERIZATION OF LIGHT ORGAN GENES AND PROTEINS DURING EMBRYOGENESIS: HOW THE SYMBIOTIC ORGAN SHAPES ITS INTERNAL ENVIRONMENT FOR SYMBIONT INTEGRATION. *(p. 138)*

American Malacological Society

Constance Boone Award for Best Student Presentation

- First Place, Poster: **Kokoro Holcomb** – Reed College, USA.
  Title of the Abstract: A STUDY OF PHENOTYPIC VARIATION IN *Phyllaplysia taylori* AND TRENDS IN SEAGRASS HABITAT ALONG THE NORTH AMERICAN WEST COAST. *(p. 252)*
- Second Place, Poster: **Andy Dick Yee Tan** – University of Colorado Boulder, USA.
  Title of the Abstract: INCREASING ROCKY MOUNTAIN AND GREAT PLAINS REGION INVERTEBRATE REPRESENTATION IN DIGITAL NATURAL HISTORY COLLECTION DATABASES. *(p. 260)*
- First Place, Oral: **Molly Hayne** – University of Colorado Boulder, USA.
  Title of the Abstract: EDUCATIONAL APPLICATIONS OF MALACOLOGICAL MUSEUM COLLECTIONS FOR UNDERREPRESENTED STUDENTS IN COLORADO. *(p. 164)*
- Second place, Oral: **Diana Carolina Vergara** – University of Michigan, USA.
  Title of the Abstract: DRIVERS OF MICROBIAL DIVERSITY IN VENOMOUS MARINE SNAILS. *(p. 134)*

MALACOLOGICAL SOCIETY OF JAPAN

- Best Poster: **Molly Lahn Rivers** – University of Aberdeen, United Kingdom.
  Title of the Abstract: ONTOLOGY OF SHELL MATRIX PROTEINS (SMPS) ACROSS MOLLUSCS. *(p. 326)*

- Best Oral: **Daya Lynn Hall-Stratton** – George Mason University, USA.
  Title of the Abstract: SPECIES CONFIRMATION AND DISTRIBUTION OF NON-NATIVE MYSTERY SNAILS *Cipangopaludina japonica* AND *C. chinensis* WITHIN NORTH AMERICA. *(p. 61)*

MALACOLOGICAL SOCIETY OF LONDON

- Best Poster: **Julia Mariana da Silva Carvalho** – Universidade Estadual de Campinas, Brazil.
  Title of the Abstract: A COMPARATIVE STUDY BETWEEN TWO SPECIES OF CAUDOFOVEATA (MOLLUSCA): DISCOVERING NEW ANATOMICAL PATTERNS THROUGH HISTOLOGY. *(p. 410)*
- Best Oral: **Rafael Masson Rosa** – Universidade de São Paulo, Brazil.
  Title of the Abstract: SNAILS FROM THE INSIDE OUT: EXPLORING THE SOFT ANATOMY OF GASTROPODS THROUGH CT. *(p. 139)*

PHOTO CONTEST WCM2025

First place: Lina Marie Raubold – American Museum of Natural History, USA.
Title of the work: *Translucent*.
Description: Translucent shows a sea slug, the Norwegian Polycera accompanied by lots of little snails and crustaceans that are perfectly hidden in the red seaweed. How many can you spot?— Rogaland, Norway. Translucent is part of "In The Weeds" — a larger photo series that revolves around marine invertebrates photographed in and around seaweeds along the North Atlantic coast. Originally developed for International House NYC's annual art exhibition, "In The Weeds" is meant to bring the beauty of marine taxa to the public eye. It highlights the immense and oftentimes hidden diversity of taxa that may benefit from aims to safeguard marine biodiversity.

First place: Lina Marie Raubold – American Museum of Natural History, USA.
Title of the work: *Feeling Blue*.
Description: Feeling Blue shows a group of blue mussels. Their feather-like and colorful mantle is revealed when they open to breathe and feed. White hydrozoans spread across the mussels and make them appear like a meadow of flowers underneath the surface of the Atlantic Ocean. — Øygarden, Norway. Feeling Blue is part of "In The Weeds" — a larger photo series that revolves around marine invertebrates photographed in and around seaweeds along the North Atlantic coast. Originally developed for International House NYC's annual art exhibition, "In The Weeds" is meant to bring the beauty of marine taxa to the public eye. It highlights the immense and oftentimes hidden diversity of taxa that may benefit from aims to safeguard marine biodiversity.

Second place: Larissa Teixeira – MATER NATURA, Instituto de estudos Ambientais, Brazil.
Title of the work: *Snail yoga*.
Description: An individual of *Simpulopsis* sp., a genus typical of the Atlantic Forest, cleaning and maintaining its shell with a beautiful stretch worthy of a yoga class. Photo taken with a Nikon D300S with 60 mm lens.

Third place: Laura Przybysz Paitch – Universidade Estadual de Ponta Grossa, Brazil.
Title of the work: *Villain or Anti-Hero?*
Description: Like many explorers, some mollusk species also possess the remarkable ability to disperse widely across the planet. Among them, we can highlight the exotic gastropod *Melanoides tuberculata*, observed in activity on the surface of an aquarium. Its expanded muscular foot, the texture of its tissue, the spiral of the shell, and the cephalic region in contact with the environment stand out. This contact is not random: it is part of a sensory and functional mapping. Its gliding reveals more than mere movement; it is a search for food, an exploration of space, and the construction of a territory where borders dissolve into mucus and traces. It is worth noting that exotic species (anti-heroes) are always intertwined with human uses of natural resources, e.g. aquarium keeping, making us (humans) the true villains of this contemporary story.

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PLENARY SPEAKERS

PLENARY SPEAKERS

SOUTH AMERICA FRESHWATER LIMPETS: WHAT DO WE KNOW AND WHAT REMAINS TO BE KNOWN?

SONIA BARBOSA DOS SANTOS – Brazil

The small freshwater limpet snails occurring in South America are distributed in eight genera which are differentiated by the shell sculpture and morphology of the soft tissues. In this lecture we will present the state-of-the-art about the group, point out the gaps in knowledge and present perspectives to refine the taxonomy, systematic and geographical distribution of the group.

AN INTEGRATIVE APPROACH TO GLOBAL MALACOLOGY: SPECIES, TREES, AND UNDISCOVERED FRONTIER

JULIA D. SIGWART – Germany

Studies of mollusc species shaped major advances in many areas of biology, in evolution, ecology, conservation, fisheries, human medicine and bioengineering. New advances in phylogenomics have recently solidified the backbone phylogeny for the phylum. Meanwhile, the vast disparity and species richness within the phylum has left many open questions, and generalised insights in biodiversity struggle to accommodate the true expanse of molluscan diversity. Our research agenda as a global community can put molluscs in their rightful place: centre stage.

FEEDING ON THE EARTH: DIVERSITY AND ADAPTATION OF MOLLUSCS FROM DEEP-SEA CHEMOSYNTHESIS-BASED ECOSYSTEMS

CHONG CHEN – Japan

‘There are shells! They’re big shells, they’re living!’ – exclaimed Jack Corliss on humanity’s first encounter with an active hydrothermal vent ecosystem dominated by the foot-long vesicomyid clam Turneroconcha magnifica in 1977, 2.5 km deep on the Galápagos Rift. Since then, over 600 hot vents have been discovered globally as well as numerous cold seeps and organic falls that host similar deep-sea chemosynthetic ecosystems. Here, I showcase an array unforgettable mollusc species endemic to these ‘extreme’ environments supported by microbes ‘feeding on Earth’ through chemosynthesis. Focusing on a few key taxa such as the ironclad snails Chrysomallon and Gigantopelta as well as abyssochrysoideans like Ifremeria and Rubyspira, I highlight their astounding adaptations that extend the known boundaries of how animals function – revealed by our integrative studies combining morphological and molecular analyses. Regrettably, these remarkable molluscs now face growing threats from deep-sea mining, particularly at vents. I present our collaborative efforts to advocate for their protection through the IUCN Red List, in order to ensure that these molluscs are seen by policymakers and included in conservation and management plans.

BLUE ONE HEALTH - THE OCEAN AND US AS ONE

ALEXANDER TURRA – Brazil

Blue One Health is an integrated approach that recognizes the vital interconnectedness among human, animal, and ecosystem health, explicitly including ocean health in the broader One Health framework. This perspective understands that oceans regulate the climate, store carbon, and support global biodiversity, directly affecting physical and mental well-being as well as the strength of the socioeconomic economy. Blue One Health broadens traditional health strategies by emphasizing collaboration across sectors, disciplines, and communities to address challenges such as climate change, zoonotic risks, pollution, and marine biodiversity loss. Examples of Blue One Health include initiatives that monitor ocean changes impacting disease transmission, promote sustainable fishing, and support marine ecosystem restoration to benefit both human health and livelihoods. The approach also covers bioprospecting for pharmaceuticals, early warning systems for marine toxins, and educational campaigns linking ocean health to well-being. In Brazil, projects linking scientific research with local knowledge demonstrate how involving coastal communities enhances resilience and sustainable resource management. Integrating Blue One Health into the blue economy can foster sustainable development by aligning economic interests with the goal of protecting health for people and the environment. By encouraging cross-disciplinary collaboration, investing in preventive health, and prioritizing conservation, the Blue One Health approach promotes innovation, equitable policymaking, and the development of new value chains in the blue economy, thereby contributing to sustainable development goals.

SYMPOSIA

SYMPOSIUM: PERSPECTIVES ON CONSERVATION OF FRESHWATER MUSSELS

PERSPECTIVES ON CONSERVATION OF FRESHWATER MUSSELS

Coordinators:

CRISTHIAN CLAVIJO – Vida Silvestre, Uruguay
IGOR CHRISTO MIYAHIRA – UNIRIO, Brazil

Freshwater mussels are one of the most incredible and threatened animals in the world. They have a unique life cycle and provide important ecosystem services. However, in recent years, they are also associated with a decrease in their populations due habitat modification and introduction of invasive species. Thus, measures to mitigate impact and improve conservation of mussels are urgently needed. The conservation strategies in Noth are by far better developed, and in this first World Congress of Malacology in South America, we have a unique opportunity in this symposium to establish a forum and a place for experience sharing, aiming a united effort for mussels conservation.

Perspectives on Conservation of Freshwater Mussels

Conservation

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AZA SAFE - HOW ZOOS AND AQUARIUMS ARE RAMPING UP FRESHWATER MUSSEL CONSERVATION

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Keywords: ex situ conservation, freshwater.

Stable freshwater mussel populations are crucial for healthy freshwater ecosystems through their important roles in water filtration, nutrient cycling, aquatic food webs, and habitat modification. At present, 92 of 209 valid North American freshwater mussel species (44%) assessed on the IUCN Red List are threatened with extinction. Knowing this, The Association of Zoos and Aquariums (AZA) has developed a Saving Animals From Extinction (SAFE) plan for North American freshwater mussels. The goal of the program is to assist and support ongoing efforts to reduce negative anthropogenic impacts on freshwater mussels and their ecosystems, while catalyzing the AZA community for effective freshwater mussel conservation, education, and advocacy. In its initial development phase, the program followed the steps for conservation planning set out by the IUCN SSC Conservation Planning Specialist Group (CPSG), from preparing to plan, defining success of the program (creating a vision) and gaining base-level understanding on the current involvement of AZA institutions and other stakeholders in mussel conservation, to an eventual two-day in-person planning workshop. The program's plan aims to encompass the conservation of 303 native freshwater mussel species in the United States and Canada. In the two-day planning workshop and through subsequent consultation with, for example, the Social Science Research and Evaluation Scientific Advisory Group, the following objectives were identified within the first 3-year plan, to assess capacity within AZA and align with priority targets of the National Strategy for the Conservation of Native Freshwater Mollusks developed by the Freshwater Mollusk Conservation Society: to understand both stakeholders and status of North American Freshwater Mussel conservation; build capacity of AZA partners in freshwater mussel assessment processes; grow a community of practice in freshwater health and freshwater mussel conservation; and advance the conservation education and communication about mussels and freshwaters across AZA. As a collection of highly recognized and visited zoos and aquariums, the participants of this program are in a key position to promote awareness and education on mussels, freshwater ecosystems, and their importance within their facilities. Initial outreach work from the program will help to build a better understanding of the network of stakeholders for these species in North America. In collaboration with the IUCN Mollusc Specialist Group, a top goal of the program is to produce the first Red List Assessment of North American Freshwater Mussels. By connecting the international community of mussel experts to AZA professionals, the program aims to bolster the scientific expertise of aquatic professionals in the zoo and aquarium community. We believe that by activating AZA organizations around these imperiled organisms, we can combine new voices and new audiences with efforts already underway by our many partners already working in freshwater mussel conservation. This will enable us to elevate the sense of urgency for a cascade of research, recovery and restoration, education, and advocacy on behalf of these amazing and underappreciated animals.

Funding Source: No.

Perspectives on Conservation of Freshwater Mussels

Conservation

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PRELIMINARY GREEN STATUS OF SPECIES ASSESSMENTS FOR EUROPEAN FRESHWATER MUSSELS

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Keywords: freshwater, green status of species, unionids.

Mussels are crucial for the health of freshwater ecosystems and are also one of the most endangered taxa of species on the planet. In Europe, freshwater mussels have been pushed towards extinction by a combination of well-documented threats. While protection currently exists for a limited number of highly threatened species, unionids have largely been underserved by conservation actions and policies. Preliminary Green Status of Species assessments were completed for twenty-three European unionids, following the Green Status of Species Standard and Guidelines. After completing preliminary assessments for all species, Green Status of Species metric categories were assigned collectively as an average for European unionids. Green Status of Species metrics were compared in a regional analysis between seven geographic areas. Appropriate statistical tests were used depending on test assumption conditions. If a test result was found to be significant, a post-hoc multiple comparison test was conducted. To assess the impact of past conservation actions for assessed species, the current and counterfactual Green Scores were also compared in a paired Wilcoxon signed-rank test. Initial results showed that the assessed species are 'Largely Depleted' with an average Species Recovery Score representing just 30% of a fully functional population. Preliminary assessments suggest that the Conservation Legacy for European unionids should be considered to be 'High.' Preliminary assessments suggest that European unionids have a 'Medium' Conservation Dependence. All assessed species (n=23) were found to have a Conservation Gain of 'Zero.'. Preliminary assessments also suggest that European unionids have a 'Medium' Recovery Potential. A paired Wilcoxon Test revealed that the difference between the median current Green Score and counterfactual Green Score was significant. A second paired Wilcoxon test supported this result even when considering uncertainty in Green Score under both scenarios. In the regional analysis of Green Status of Species metrics, A Kruskal-Wallis test detected a significant difference in SRS between the geographic regions. A post-Hoc Games-Howell comparison showed that the Scandinavia region has a significantly higher SRS than all of the other 6 regions. Kruskal-Wallis tests for Conservation Legacy and Conservation Dependence did not yield significant results. Gain for all assessed species (n=23) was determined to be 'Zero' and therefore no inferential statistical tests were conducted for the metric in the regional assessment. A one-way ANOVA detected a significant difference in the metric of Recovery Potential between geographical regions. A post-hoc Tukey-Kramer comparison showed that Iberia had a significantly smaller Recovery Potential than four other regions (the British Isles, Scandinavia, Central Europe, and the Balkans). Preliminary Green Status assessments of native European unionids supported a large depletion of the assessed species' populations. This work also showed differences in Species Recovery Score and Recovery Potential between geographic regions in Europe, thus creating a potentially important informational tool for priority setting at the European Union level. Investigation into an assessed lack of short-term Conservation Gain highlighted inadequacies in the taxonomic spread and robustness of ongoing conservation actions.

Funding Source: No.

Perspectives on Conservation of Freshwater Mussels

Ecology

Oral - 132

WITHIN-HOST ADAPTIVE SPECIATION OF COMMENSAL YOYO CLAMS LEADS TO ECOLOGICAL EXCLUSION, NOT CO-EXISTENCE

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Keywords: commensalism, speciation, community ecology, Galeommatoidea, *Divariscintilla*, *Lysiosquilla*.

Within-host speciation is prevalent among members of an extraordinary marine symbiosis in the Indian River Lagoon (IRL), Florida, composed of a host mantis shrimp, *Lysiosquilla scabricauda*, and seven host-specific commensal vasconiellinе "yoyo" clams (Galeommatoidea). Five of the seven form a host-specific clade with two well-supported sister relationships: one (composed of burrow-wall-attached commensals) a product of non-adaptive speciation, the other (containing a morphologically-differentiated, host-attached ectocommensal) a product of adaptive speciation. This within-host symbiont radiation provides a natural experiment to test how symbiont coexistence patterns are regulated in a common ancestral habitat. The competitive exclusion principle predicts that sister taxa produced by adaptive speciation (with distinct within-burrow niches) are most likely to coexist whereas the neutral theory predicts no difference among adaptive and non-adaptive sister taxa co-occurrence. To test these predictions, we engaged in 1) field-censusing commensal species assemblages; 2) trophic niche analyses; 3) laboratory behavioral observations. Although predicted by both models, the field census found no mixed-niche commensal assemblages: all observed cases of multi-species host burrow co-occurrence were exclusively composed of burrow-wall commensals. Co-occurrence of burrow-wall commensal species matched random assembly process expectations, but presence of the ectocommensal species had a highly significant negative effect on recruitment of burrow-wall commensal species ($P < 0.001$). A robustly negative recruitment effect was also apparent for the adaptive sister species pair: ectocommensal "*P.*" *squillina* and burrow-wall commensal *D. octotentaculata* ($P < 0.001$), a result explicitly incompatible with competitive exclusion principle expectations. Our stable isotope data indicated that commensals suspension feed on burrow water particulate organic matter and that co-occurring burrow-wall commensals may exhibit trophic niche differentiation. The artificial burrow behavioral experiment yielded no evidence of spatial segregation among burrow-wall commensals, but it was terminated by a sudden breakdown of the host-commensal relationship resulting in a mass mortality of all commensals unattached to the host. Our data indicate that this study system is composed of two distinct, superimposed patterns of commensal distribution: 1) all burrow-wall commensal species; 2) the ectocommensal species. Burrow-wall commensals represent the plesiomorphic condition in this radiation and they broadly adhere to neutral theory expectations of species assembly. In contrast, the adaptive evolution of ectocommensalism has apparently led to ecological exclusion rather than coexistence: an inverse outcome of theoretical expectations. Burrow-wall commensal/ectocommensal exclusion could result from differential recruitment to individual host burrows and/or differential survival in "mixed" burrow assemblages, the latter potentially due to changes in host predatory behavior. Both possibilities are addressable through further field and laboratory research. It would be particularly interesting to investigate southern Brazilian *L. scabricauda* commensal populations to establish if its ectocommensal, "*Parabornia*" *palliopillata*, also exhibits an ecological exclusion from regional burrow-wall commensals.

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Perspectives on Conservation of Freswater Mussels

Anatomy and Physiology

Oral - 335

COMPARED MORPHOLOGY AND BROODING PATTERN IN THE SOUTHAMERICAN FRESHWATER BIVALVE *Rheodreissena* GEDA ET AL. 2018, WITH ENPHASIS ON THE REVISION OF THE TYPE MATERIAL AND REDESCRIPTION OF *R. hoeblichi* (SCHÜTT, 1991) (DREISSENIDAE)

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Keywords: Dreissenidae, *Rheodreissena*, biphasic brooding, rio Orinoco.

Rheodreissena hoeblichi, from Orinoco River, was described as Congeria and later considered to be in the genus *Mytilopsis*. Based on analysis of genetic material from the Orinoco and Amazon rivers, this species was recently inserted in a new Neotropical genus, *Rheodreissena*. However, the scarcity of samples and the lack of morpho-ontological knowledge of the available material have led to doubts about the species taxonomic status. Holotype and paratypes of *R. hoeblichi* were examined, including specimens SBMF collection and recently samples from Orinoco River (VE and CO). Larvae from pallial cavity, details of the mesosculpture, ultrasculpture and internal microstructure of adult shells were photographed using a MEV-FEG Inspect F50-FEI and TESCAN -MIRA3, 10KV scanning microscope. Anatomy and comparative measurements of the shells, soft tissues, demibranchii and larvae were obtained under a stereomicroscope and the drawings with a camera lucida. Measurements and morfological data of *R. hoeblichi* were compared to other *Rheodreissena* known species. We also examined material from Amazon and Tocantis-Araguaia watersheds of *R. xinguana*, *R. lopesi*, and *R. cordinelata*. *R. hoeblichi* and all species examined are similar regarding brooding strategies. *R. hoeblichi* can be distinguished from others by its mytiloid to semicircular outline in lateral view. The anterior half is higher and recurved, with the top displaced forward. Posterior region descending in a gentle slope to the posterior margin, then truncate and slightly curved until it meets the ventral margin above the base. Slightly sinuous ventral margin, with shallow byssal notch and relative short pseudolunular fields. External mesosculpture with long parallel, perpendicular or gently curved bars over the entire external dorsal surface, frequently on the ventral one. Carina with bars forming one longitudinal row of imbricated “Vs” on each side of the shell. Narrow apophysis are associated to nymph. Large specimens, including type material, have a projecting, bowl-shaped apophysis. Periotracum ultrasculpture is present on the disc in form of rounded granules (1µm), forming longitudinal rows but not micro-roods. *R. hoeblichi* is closer to *R. cordilineata* regarding shell shape and microstructure, but is larger and never cordiform in dorsal view, meso- and periostracum ultrasculpture are unique. The external demibranch is reduced to around 1/2 height of the internal demibranch. Pr2 type larvae (400-500µm long) and post larvae in the juvenile stage, from pallial cavity, reached up to 1.2mm in length. The gills morphology and pallial cavity organs follows the pattern already described for the other species examined. Since the lower Miocene, these species were adapted to rheophilic environments, forming small clusters over rocks. However, are threatened due to river damming. Data of compared morphology and brooding pattern integrated *R. hoeblichi* in the genus. Interspecific differences are related to brood numbers and size of releasing dissoconches. Like other species of Rheodreissena, these data presumably represent adaptations to their rheophilic lifestyle, living fixed on rocks, forming small clusters, under running water. The shell size and contour, type of meso- and ultrasculpture of the shell are fundamental criteria for specific diagnosis

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Perspectives on Conservation of Freshwater Mussels

Ecology

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POLYMORPHISM IN THE AGGRESSIVE MIMICRY LURE OF THE FRESHWATER MUSSEL *Lampsilis fasciola*

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Keywords: Unionoida, parasitism, mantle lure, ddRADseq, captive brood, model species.

Gravid females of many North American unionoid freshwater mussel species utilize mimetic mantle lures to infect host fishes with their parasitic larvae. The mantle lure of Lampsilis fasciola is apparently polymorphic, with two distinct primary lure phenotypes. One, described as “darter-like”, has “eyespots”, a mottled body coloration, prominent marginal extensions, and a distinct “tail”. The other, described as “worm-like”, lacks those features and has an orange and black coloration. We investigated this phenomenon using a variety of approaches. They included phylogenomic (ddRAD-seq) analyses of multiple population as well as the captive rearing of the brood of a wild-mated gravid female. For our main study population, we determined past ratios of mantle lure phenotypes using museum specimens and current frequencies from field censuses. Lure displaying females were recorded using a Go Pro Hero 6 camera and the captured images were used to determine the main mantle lure variants and their display behaviors. These data were then used to identify putative models for the main mantle lure variants as well as to perform comparative analyses of their display behaviors. Within-brood lure variation and within-population phylogenomic analyses of individuals bearing different lures confirmed that this phenomenon is a true polymorphism. The relative abundance of the two morphs appears stable over ecological timeframes: the ratio of the two lure phenotypes in a River Raisin (MI) population in 2017 was consistent with that of museum samples collected at the same site six decades earlier. Within the River Raisin, four main “darter-like” lure motifs visually approximated four co-occurring darter species (*Etheostoma blennioides*, *E. exile*, *E. microperca*, and *Percina maculata*), and the “worm-like” lure resembled a widespread common leech, *Macrobdella decora*. Darters and leeches are typical prey of *Micropterus dolomieui* (smallmouth bass), the primary fish host of *L. fasciola*. In situ field recordings of the *L. fasciola* “darter” and “leech” lure display behaviors, and the lure display of co-occurring congener *L. cardium*, were captured. Despite having putative models in distinct phyla, both *L. fasciola* lure morphs have largely similar display behaviors that differ significantly from that of sympatric *L. cardium* individuals. Some minor differences in the behavior between the two *L. fasciola* morphs were observed, but we found no clear evidence for a behavioral component of the polymorphism given the criteria measured. Discovery of discrete within-brood inheritance of the lure polymorphism is the first such record for freshwater mussels and implies potential control by a single genetic locus. This result identifies Lampsilis fasciola as a promising study system to identify regulatory genes controlling mantle lure formation - a key adaptive trait of freshwater mussels.

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Perspectives on Conservation of Freshwater Mussels

Taxonomy and Systematics

Oral - 276

Anodontites trapesialis (UNIONIDA: MYCETOPODIDAE): A SINGLE WIDELY-DISTRIBUTED SPECIES OR A COMPLEX OF CRYPTIC SPECIES?

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Keywords: South America, freshwater mussels, conservation, distribution.

South America is home to two families of Unionida: Mycetopodidae and Hyriidae. The Mycetopodidae comprises 53 species, 32 of which are found in Brazil, though many require taxonomic revision. The most species-rich genus within Mycetopodidae is *Anodontites*, of which *Anodontites trapesialis* has been consistently recognized in all major taxonomic revisions. However, its broad geographic distribution has long raised questions about whether it represents a single species or a species complex. All specimens examined were initially identified as *Anodontites trapesialis* based on morphological and shell features. Samples were collected from various localities across four South American countries—Brazil, Paraguay, Argentina and Uruguay—covering most of its known distribution range. We used three molecular markers: COI, 16S and 28S. Sequence alignment was performed in MEGA, followed by a Maximum Likelihood (PhyML) and a Bayesian phylogenetic analysis (MrBayes). Additionally, an ASAP (Assemble Species by Automatic Partitioning) analysis was conducted to delineate potential species lineages within the dataset. We generated 131 new sequences, of which 98 of COI, 15 of 16S and 18 of 28S. ASAP analysis identified five major lineages within *A. trapesialis* (ASAP score = 2.0) for COI. This phylogenetic structure suggest a species complex under the name '*A. trapesialis*' where is grouped other similar, but distinct species. The most widespread lineage spans a broad geographic range, including Paraguay, Brazil (Northeast, Central-West, Southeast and South regions) and Uruguay. Notably, this widespread clade exhibited internal geographic structure, suggesting significant genetic differentiation among populations. The remaining lineages occupy more restricted areas: one in northern Brazil, another in northeastern Brazil, and two others in distinct regions of southern South America (Brazil, Argentina and Uruguay). Inside *A. trapesialis* complex, the widespread clade was more basal, the two northern lineages presented a sister-group relationship, as also the two southern lineages. The trees generated for 16S and 28S presented similar results. Taxonomic studies are currently being conducted to determine the identity of these lineages. Morphological identification of *Anodontites* species remains challenging due to their highly homogeneous shell and soft tissue characteristics, and the lack of distinctive shell features has historically hindered taxonomic studies of *Anodontites*. Genetic analysis thus serves as a crucial tool for uncovering hidden diversity within this genus. This is an ongoing study and results should be considered preliminary. More DNA sequences should be added, as also further analysis must be done. However, based in preliminary analysis, our data indicates a hidden diversity of Mycetopodidae in South America. This implies that ecological studies may be comparing different species and may be omitting the conservation of endemic and threatened species by considering them part of this species complex.

Funding Source: FAPERJ.

Perspectives on Conservation of Freshwater Mussels

Conservation

Oral - 314

LOCAL ADAPTATION AND FORECASTING RESPONSE IN THE ENDANGERED SCOTTISH FRESHWATER MUSSEL, *Margaritifera margaritifera*

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Keywords: conservation genomics, ecological modelling, freshwater mussel, Margaritifera.

Given the rapid pace of climate change, there is an urgent need to understand how endangered species will respond to changes in their environment. Species distribution modelling is a popular tool used to forecast a species range based on the relationship between surveyed occurrence data and explanatory (habitat) factors. However, it does not account for local adaptation and intraspecific response to change. Genomic offset offers an evolutionary dimension for forecasting species response to change and is defined as the mismatch between current adaptive composition and future optimal composition under a changed environment. The freshwater pearl mussel, *Margaritifera margaritifera*, has a widespread Holarctic distribution but many constituent populations are endangered or threatened, especially across its European range. Here, we compare predictions from an ensemble species distribution model of 462 presence points of *M. margaritifera* with genomic offset estimates derived from 417 putatively adaptive SNPs from 18 populations in Scotland to understand impacts from future climate change. First, Scottish populations have a particularly complex pattern of genomic population structure, partially explained by local climate. Both the species distribution model and genomic offset estimates forecast a loss of *M. margaritifera* from the eastern Scottish Highlands, with loss of suitable habitat and maladaptation of local populations. However, while the species distribution model indicates a future loss of suitable habitat on the Ardnamurchan Peninsula, these populations have a lower value of genomic offset suggesting these populations are more resilient to climate change through existing adaptation. As such, these findings indicate that although general trends are congruent among methods, there are fine scale differences that may go undetected without considering genomic composition. This study examines the use of both species distribution models and genomic offset and demonstrates the utility of an evolutionary perspective alongside species distribution models for forecasting species response to a changing climate.

Funding Source: No.

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Conservation

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BIODIVERSITY ASSESSMENT OF FRESHWATER MUSSELS IN COSTA RICA

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Keywords: Central America, Unionidae, Mycetopodidae, phylogenetics.

For over three decades, native freshwater mussels (Mycetopodidae & Unionidae) in Costa Rica have received minimal attention. Since Dwight W. Taylor compiled the country's first checklist of freshwater mollusc species in 1993—reporting only three native mussel species—most research efforts have focused on invasive species. In collaboration with four U.S. institutions (Shedd Aquarium, Field Museum, Smithsonian National Museum of Natural History, and Anacostia Watershed Society) and the University of Costa Rica, we conducted field surveys across freshwater basins in Costa Rica from December 2023 to 2025. Live mussels were collected, and preserved for anatomical study and DNA extraction. Sampling sites included rivers, wetlands, and lagoons across both Pacific and Caribbean drainages. We collected over 700 specimens and tentatively identified eight species using morphology and molecular characters. Three mitochondrial genes (COI, 16S, and ND1) were sequenced using Sanger and Nanopore sequencing methods. Phylogenetic analyses of concatenated gene sequences revealed eight distinct clades. Six were found in the Caribbean Basin, and four in the Pacific Basin, with *Anodontites tortilis* and the invasive *Sinanodonta pacifica* occurring in both basins. The results suggest that *Anodontites* and *Mycetopoda* species in Costa Rica are genetically and morphologically distinct from congeners in South America, potentially representing new species. Furthermore, phylogenetic differentiation was observed within *Anodontites trapesialis* between samples from Caribbean and Pacific basins. Within Unionidae, *Nephronaias tempisquensis* was confirmed as endemic to the Pacific drainages whereas the taxonomy of *Nephronaias* sp. in Caribbean drainages require further validation. Additionally, the presence of Arotonaias cyrenoides in Costa Rica was confirmed, likely distributed in the Río San Juan and adjacent Caribbean drainages. A comprehensive taxonomic evaluation is needed to estimate total species diversity in Costa Rica and describe potentially new species. As many populations are low in abundance, our findings underscore the urgent need for further taxonomic and conservation assessments focused on Costa Rica's native freshwater mussels.

Funding Source: This project was made possible thanks to the collaboration and support of Shedd Aquarium, the Field Museum, the Smithsonian National Museum of Natural History, the Anacostia Watershed Society, and the Walder Foundation through the Walder Grant.

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SHELL MORPHOMETRY OF *Castalia inflata* (D'ORBIGNY, 1935): IMPLICATIONS TO ECOLOGY AND SPECIES CONSERVATION

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Keywords: Bivalvia, Unionida, morphology, Pantanal.

Freshwater mussels are one of the groups with the highest documented extinction rates documented. The order Unionida, which has an obligatory parasitic life stage, is inherently more vulnerable to ecosystem changes. Morphological variation reveals species' adaptability and conservation needs. This study employs geometric morphometry to analyze sexual and geographic shell variations in *Castalia inflata*, a Unionida species widely distributed in the Pantanal, the world's largest humid continental biome. 112 specimens were collected from two localities in a floodplain in Pantanal located in central South America: Aricá-Açú Stream and Baúva Lake. Geometric morphometry analysis was performed using landmark-based methods, including General Procrustes Analysis (GPA) to extract morphometric data and assess correlations with individual sex and collection sites. Fourteen landmarks were digitized on the shell's internal surface using TpsDig software to obtain 2D coordinates. MorphoJ was then employed to conduct GPA, quantify shape and size variation, and analyze the relative displacement of configurations to assess differences between shapes. Finally, the GPA-aligned covariance matrix was used to perform a Procrustes ANOVA and Principal Component Analysis (PCA). While the variation in centroid size was minimal, Procrustes ANOVA revealed statistically significant shape differences. This significant morphological disparity validates subsequent analyses for identifying trends and distinguishing groups based on observed characteristics. Principal Component Analysis (PCA) of both valves yielded consistent results, with the first two axes collectively explaining 40% of the observed morphological variation. The analysis revealed significant differences between collection sites, while only a trend of sexual dimorphism was detected. PCA wireframe visualizations demonstrated distinct shape patterns: specimens from Aricá-Açú exhibited a more triangular morphology, characterized by dorsal displacement of landmarks 1 and 2 and lateral displacement of landmarks 4 and 6. In contrast, Baúva specimens showed ventral displacement of landmarks 1 and 2 with greater medial separation of landmarks 4 and 6, resulting in a more rounded shell contour. To further investigate sexual dimorphism, Canonical Variate Analysis (CVA) was performed, revealing more pronounced differences between sexes, particularly a more prominent anterior portion in female specimens compared to males. The distinct geographical settings expose each population to different environments: Aricá-Açú represents a calm stream, while Baúva constitutes a lacustrine habitat. The observed morphological differences between sites likely reflect these contrasting selective pressures. Additionally, the emerging pattern of sexual dimorphism may be linked with the reproductive strategies in this species. Conserving such diverse habitats remains essential for maintaining the species' genetic diversity and evolutionary potential.

Funding Source: FAPESP - Process number 2024/22065-1.

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Conservation

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DAMS AND DATA GAPS: ASSESSING SAMPLING BIAS IN FRESHWATER MUSSELS ACROSS THE AMAZON BASIN

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Keywords: Unionida, biomonitoring, hydroelectric plant, bivalve.

Several river basins in South America have been impacted by dam construction and expansion. These structures alter river ecosystems and affect sensitive organisms such as freshwater mussels. In the Amazon Basin, this scenario is exacerbated by data deficiency. We assess the sampling history of freshwater mussels across Amazonian ecoregions and its relationship with dam distribution, identifying knowledge gaps and priority areas for future research. To do so, we compiled data on the occurrence of freshwater mussels from the literature and online repositories, extracting the year and geographic coordinates of each record. We grouped species records and dam locations by ecoregion, and calculated the longest recording interval based on the first and last occurrence years. We then performed a correlation analysis between these intervals and the number of dams. Finally, we estimated priority areas by summing the normalized values of dam density and time since the last record. We found that the 1990s had nearly six times more records than the 1970s, with approximately one-third of all records occurring in the year 2000. This sampling concentration may be associated with the period of most intense dam construction in Brazil, suggesting that ecoregions under greater anthropogenic pressure are the most studied. Ecoregions in the northwest were less sampled, while the most recent records were concentrated in central and northeastern portions of the Amazon Basin. Only 22% of ecoregions had records from the past ten years, indicating large areas with decades-long gaps in biological monitoring. Recent records were positively correlated with ecoregions containing hydropower plants, suggesting a sampling bias linked to dam development. Five ecoregions showed high priority scores, indicating that major Amazonian rivers may harbor unassessed impacts from dam expansion. These findings suggest that anthropogenic pressure is associated with uneven sampling efforts — concentrated in already impacted regions, while others remain understudied or historically neglected. The data indicate that areas with a greater number of dams have more recent biological records, whereas others have not been updated for decades. This reveals a worrying pattern of reactive monitoring, which requires emergency strategies to fill gaps before new impacts are generated.

Funding Source: CNPq; INPP.

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Ecology

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SYNTHESIZING FUNCTIONAL TRAITS AND ENVIRONMENTAL DATA TO UNDERSTAND FRESHWATER MUSSEL DECLINES AND THEIR IMPLICATIONS FOR STREAM ECOSYSTEMS

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Keywords: Unionid, freshwater mussel, ecosystem function, life history theory, biogeochemistry.

The causes and consequences of declining freshwater mussel biodiversity and biomass (defaunation) depend on species response traits that regulate which species are vulnerable to particular stressors and effect traits which regulate the ecosystem-level consequences of declines. Areas with high levels of mussel species richness and endemism are especially vulnerable. We used a >30-year long-term monitoring dataset and a trait-based framework to identify defaunation in multi-species freshwater mussel aggregations. We used two complementary survey methods¬ across four rivers in southeastern Oklahoma, USA. First, we used semi-quantitative time searches to maximize spatial coverage and characterize species richness and relative abundance in three rivers. Then, we used quantitative surveys, where we excavated the sediment to a depth of 10-15 cm to quantify mussel density and to estimate mussel-driven ecosystem function in four rivers. In rivers where drought conditions were more severe during the study, mussel aggregations experienced changing assemblage structure and/or declines in density. Two out of three rivers that were semi-quantitatively surveyed showed changing assemblage composition, with declining relative abundances of drought-sensitive species, and increasing relative abundances of drought-tolerant species. Two out of four rivers that were quantitatively surveyed experienced declines in mussel density. Losses of mussel density were associated with biomass declines of 51–83%, and consequent losses of mussel-generated carbon and nutrient recycling and storage of 47–83%. Unexpectedly, declines did not differ among thermal tolerance guilds—both thermally sensitive and thermally tolerant species declined in defaunated streams. Rather, the taxa driving the declines in density and ecosystem function were equilibrium strategists adapted for stable hydrologic conditions (low fecundity, long lifespans, late age at maturity). We suggest that the ecophysiological traits that impact individual survival may be more important in governing drought-induced defaunation at shorter time scales, while life history traits that govern population recovery may be more important at longer time scales. Given the significant role that river ecosystems play in global biogeochemical processes, defaunation of mussel aggregations may have major consequences if continued unchecked.

Funding Source: National Science Foundation DEB and DBI.

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Ecology

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INFLUENCE OF ENVIRONMENTAL CONDITIONS ON THE BODY SIZE OF *Castalia inflata*

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Keywords: Unionida, Hyriidae, bivalve, wetland.

Individual size data are critical for conservation due to implications for recruitment, survival, and environmental responses. However, collecting such data is challenging, requiring extensive and long-term fieldwork. In countries like Brazil, with vast continental basins and limited research capacity, these challenges are amplified. Here, we investigated population size variation in *Castalia inflata* and assessed how environmental conditions influence body size across floodplain lakes in the Pantanal. *C. inflata* individuals were sampled from 10 lakes in Pantanal Mato Grosso between 2015 and 2017 in the central region of South America. The organisms were collected manually with hands and feet, with a two-hour sampling effort, and kept in containers with local water. The total length (Lt (mm)) was measured using a digital caliper before returning the individuals to the environment. Environmental variables, such as dissolved oxygen, percentage of organic matter, and sediment heterogeneity, were assessed in three subsamples from each pond. We calculated the most frequent Lt (mode) per pond and related it to environmental conditions using multiple linear regression. We found 1.249 individuals with Ltf between 6.8 mm and 33.66 mm. Individuals with higher Ltf values were found in lakes with higher dissolved oxygen and conductivity. This preference suggests that *C. inflata* individuals may have reduced growth rates in response to the most severe droughts in the region. Lakes that disconnect from the main river during drought contain more oxygen-consuming organic matter. It is likely that environmental stress not only impairs growth but also survival, as lakes with less oxygen have fewer individuals. This direct impact on individuals may have broader ecological consequences, affecting the ecological roles of *C. inflata*, such as decreasing its water filtration capacity. Smaller and fewer individuals filter less, thereby compromising the nutrient cycle and water quality. As lakes are increasingly less connected to the main river owing to climate change, these environments are becoming increasingly vulnerable. Our findings highlight the vulnerability of this species under scenarios of intensified drought. These responses indicate a direct impact of environmental stress on population dynamics, reinforcing the need to integrate morphometric and environmental data into conservation strategies for this species in the Pantanal environment.

Funding Source: CNPq; INAU.

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Conservation

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NEW RECORD OF *Bartlettia stefanensis* (MORICAND, 1858) IN THE PARAGUAY RIVER BASIN

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Keywords: freshwater mussels, conservation, Paraguay River Basin.

Mussels in freshwater ecosystems face a variety of anthropogenic pressures, resulting in global population decline. This study reports the occurrence of *Bartlettia stefanensis*, a crevice dweller mussel – formerly believed to be cementing - in the Paraguay River Basin (Brazil) with the discovery of an active population in the Cuiabazinho River (Rosário Oeste, Mato Grosso). A 300 meter stretch of the river was explored for three days in August 2024. Active search was conducted over a cumulative period of 4 person-hours by three researchers who used masks and snorkels and observed and searched the bottom sediment. Individuals were removed from the substrates using a pocketknife. Environmental variables such as depth, water velocity, and the length of the exposed posterior part outside the substrate and the total length and wet weight of each individual were recorded. At total, 12 individuals were found with a total length (mean + SD) of 48.94 (+ 5.99) mm and weight of 18.11 (+ 6.63). The mussels were at a depth of 448.5 (+ 43.30) mm, with approximately 65% of the shell out of the crevice (31.5 + 7.5 mm) and exposed to a water velocity of 0.075 (+ 0.03) m^3/s. The microhabitat was characterized by pH 7.53, dissolved oxygen 6.94 (mg/l^{-1}), conductivity 93 (uS/cm^{-1}) and temperature 24.72°C. The species was recorded in microhabitats consisting of large flat rock slabs transverse to the riverbed, with the presence of aquatic plants of the species *Tristicha trifari* (Podostemaceae) and finer sediments such as sand. All individuals were fixed with the anterior part immersed and embedded in the substrate, a highly fractured silty sandstone. We did not find large aggregations, and only two individuals were recorded in close proximity. This study represents the third record of *Bartlettia stefanensis* on Paraguay River Basin, and the second occurrence in Brazil. This discovery highlights the need to investigate the ecological requirements of *B. stefanensis*, such as its association with specific substrates and vulnerability to climate threats, including as intensified droughts.

Funding Source: CNPq (169359/2023-9); Sesc Pantanal – Parque Sesc Serra Azul.

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Conservation

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INVESTIGATING *Brycon hilarii* AS A MIGRATORY HOST FOR *Castalia inflata* IN THE UPPER PARAGUAY BASIN, BRAZIL

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Keywords: Unionida, Hyriidae, wetland.

Studies on fish hosts of freshwater mussels in South America are limited, despite their importance for conservation. The larval phase depends on host interaction for metamorphosis, making hosts essential for reproduction. Migratory species, like *Brycon hilarii*, play a key role by aiding dispersal. This study identifies *B. hilarii*, a migratory fish in the Upper Paraguay Basin (Brazil), as a potential host for *Castalia inflata*. Therefore, we conducted an artificial infestation experiment in the laboratory. Initially, we sampled five gravid *C. inflata* females and used their mature glochidia after release. We then added glochidia to thirteen individuals of *B. hilarii* individuals. The fish were kept individually in 10-liter aquaria, and the number of rejected glochidia and metamorphosed juveniles was quantified daily. The metamorphosis rate was calculated as the ratio between the juveniles formed and the total glochidia present in the aquariums and was normalized by the weight of the fish. Juveniles were recorded between the third and seventh days after exposure, with metamorphosis peaks on the fourth and fifth days. *Brycon hilarii* presented an average metamorphosis rate of 20.25% (± 4.04%) per gram of fish (mean ± standard deviation). Our results suggest that this migratory fish acts as a marginal host, although controlled experiments with South American mussels are lacking for a robust comparison. We can infer that this marginal use occurs for two main reasons: first, evolutionary equalization, since *C. inflata* does not occur in plateau rivers, which may have limited coevolution with *B. hilarii*; second, the time required for migration, which lasts days or weeks, is greater than the time required for metamorphosis, which may have led to the secondary use of this host over the course of evolution. However, other factors still need to be considered, such as the sediment characteristics and physical and chemical conditions of the water. These findings advance the understanding of Neotropical mussel ecology and highlight the importance of host–mussel interactions for effective conservation. Identifying natural hosts is key to ensuring reproductive success and guiding management, particularly in data-poor, human-impacted basins across South American ecoregions.

Funding Source: INPP; CNPq.

Perspectives on Conservation of Freshwater Mussels

Taxonomy and Systematics

Oral - 150

FRESHWATER MUSSELS (BIVALVIA: UNIONIDA) OF VIETNAM REVISITED

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Keywords: mussels, Bivalvia.

Vietnam has a high diversity of freshwater mussels in the Indo-Burma area. Fifty-nine freshwater mussel species of Unionoida have been reported from Vietnam. However, over the past seven years there has been a tremendous increase in integrative work on the phylogeny of the freshwater mussels of Asia. By carefully reviewing recent taxonomic analyses using modern phylogenetic analyses performed on the Unionida from across Asia has allowed us to update the taxonomic position of many genera that were of unknown affiliation and relationships. This review has permitted us to develop an updated the taxonomy of the Unionid fauna of Vietnam. This has resulted in the recognition of 5 new tribes, 6 new genera, 1 genus synonymized, 16 species transferred to different genera, 1 new species described, and another possible 3 new species discovered, but not yet described, and 4 species placed into synonymy. The result is a revised list of the Unionoidea of Vietnam recognizing 2 families, 4 subfamilies, 12 tribes, 29 genera, 57 species. Total freshwater mussel species recognized in Vietnam has decreased by two species but reflects a better understanding of the relationships of the Vietnamese fauna. These data are critical to the conservation of these species. The updated and revised list of unionid taxa from Vietnam now allows us to map the distribution of theses species and focus on research on the biology of these taxa and describe the new taxa. During the past seven years the IUCN Red List of Threatened Species has updated six assessments for Unionoidea from Vietnam. This resulted in two changes from Data Deficient to Least Concern. The taxonomic change of one species changed its conservation status from Not Examined to Endangered. Conservation status and basic biological information on these freshwater mussels is still under studied and information on host fish is lacking.

Funding Source: No.

SYMPOSIUM: YOUNG TAXONOMISTS

YOUNG TAXONOMISTS

Coordinators:

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The Young Taxonomists Symposium is a tradition at the Brazilian Malacology Meetings. The Brazilian Malacological Society recognizes that taxonomy is a scientific field that has faced significant discredit over the past decades, and the number of taxonomists among biologists, and consequently among malacologists, has been steadily decreasing. Therefore, this symposium aims to honor and highlight the taxonomic research carried out by young malacologists.

Young Taxonomists

Taxonomy and Systematics

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UNRAVELING THE SECRETS OF *Smaragdinella* MARINE SNAILS: THE ONLY ROCK-DWELLING GENUS OF CEPHALASPIDS

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Keywords: diversity, taxonomy, Mollusca, Indian Ocean, Pacific Ocean, haminoeid snail.

Smaragdinella is a genus in Haminoeidae and the only of the order Cephalaspidea inhabiting hard substrates. Restricted to the tropical Indo-West Pacific, it occurs in the upper tidal zone on rocky outcrops, Kiawe tree branches, and under pebbles. With three valid species and 16 nominal names, its taxonomy is problematic. This study investigates *Smaragdinella* diversity, species relationships, evolutionary origins, speciation patterns, and assesses whether diet drove habitat specialization. A total of 71 specimens were barcoded (COI gene), and a maximum likelihood phylogeny was inferred along with an ASAP species delimitation analysis to obtain a preliminary estimation of the number of candidate species. Two specimens per putative species were selected for whole genome sequencing, and phylogenetic hypotheses were reconstructed using maximum likelihood and Bayesian methods based on complete mitogenomes and ribosomal nuclear genes. Morphological characterization was conducted through anatomical dissections and scanning electron microscopy (SEM), focusing on key structures such as the jaws, radulae, gizzard plates, male reproductive system, and shell. Diet composition was analysed using SEM and metabarcoding of gut and faecal pellet contents. Maximum likelihood, Bayesian, and ASAP analyses based on complete mitogenomes, and nuclear ribosomal genes suggest the presence of approximately 11–14 species of *Smaragdinella* distributed from Easter Island to South Africa. Phylogenetic analyses identified two major clades, largely separated by geography: one comprising of Pacific and Red Sea species, and another consisting of Indian Ocean species. These geographic clades exhibit consistent anatomical differences, particularly in shell morphology, gizzard plates, radulae, jaw plates, and reproductive structures. Diet analyses showed a predominance of diatoms, rotifers, and small arthropods, with these components contributing equally to the snails' food intake. This challenges the long-held assumption that haminoid snails are strictly herbivorous, instead revealing a broader and more diverse feeding strategy. Mitogenome and nuclear ribosomal gene analyses, combined with ASAP species delimitation, revealed the presence of 11–14 candidate *Smaragdinella* species between Easter Island and South Africa—representing a six to sevenfold increase over the currently recognized taxonomic diversity in the genus. Metabarcoding and SEM analyses of gut content show these snails exhibit an omnivorous diet.

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Young Taxonomists

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THE MOLLUSCAN ODYSSEY: A NEW PANPULMONATA TREE OF LIFE ILLUMINATES GASTROPOD TERRESTRIALISATION

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Keywords: Heterobranchia, phylogenomics, ultra-conserved elements (UCEs), terrestrialisation.

Panpulmonata represents a highly diverse clade of gastropod molluscs, encompassing dozens of thousands of snail and slug species inhabiting marine, freshwater, and terrestrial environments. This group serves as an exceptional model for studying evolutionary habitat transitions. Despite their vast diversity— dominated by terrestrial stylommatophorans — several panpulmonate lineages remain underrepresented in phylogenomic studies, resulting in conflicting evolutionary hypotheses. We present a comprehensive phylogenetic analysis of Panpulmonata, incorporating a balanced taxon sampling across all ten recognised orders for the first time. Using high-throughput sequencing of ultra-conserved elements (UCEs), we assembled a genomic dataset of over 1,800 loci from up to 100 newly sequenced specimens. This robust phylogenetic framework enabled us to reconstruct habitat transitions across the evolutionary history of panpulmonates. Our results propose a novel Panpulmonata tree of life, revealing a new phylogenetic framework. We resolve long-standing debates by positioning Pyramidelloidea, an order of marine ectoparasitic snails, as the sister lineage to all remaining Pneumopulmonata, while identifying Acochlidimorpha as an earlier-diverging group. Additionally, we reveal a previously unrecognised sister relationship between Siphonariida limpets and the freshwater Hygrophila. Ancestral State Reconstruction indicates at least seven independent habitat transitions—three to freshwater and four to terrestrial environments. Unlike other major animal groups such as tetrapods, chelicerates, and hexapods, where terrestrialisation occurred only once, panpulmonates exhibit a uniquely dynamic evolutionary trajectory. Our findings further suggest that land colonisation was driven by taxa inhabiting transitional environments (e.g., intertidal zones, mangroves, estuaries) rather than from freshwater ancestors. We propose a revised evolutionary framework for Panpulmonata with direct implications for understanding terrestrialisation in gastropods. This study highlights the power of UCE-based phylogenies to resolve deep evolutionary divergences and provides a robust foundation for future comparative and evolutionary research within this ecologically hyper-diverse clade.

Funding Source: No.

Young Taxonomists

Taxonomy and Systematics

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CRYPTIC DIVERSITY AND PHYLOGENETIC RELATIONSHIPS WITHIN THE STREPTAXIDAE FROM BRAZIL (STYLOMMATOPHORA, EUPULMONATA)

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Keywords: species delimitation, molecular systematics, Neotropical land snails.

Streptaxidae Gray, 1860, which comprises carnivorous terrestrial gastropods that mainly prey on other gastropods, is one of the most species-rich among the 117 families of the order Stylommatophora. In Brazil, no genetic studies have been published on this group to date. Aiming to fill this gap, we conducted a genetic study in order to test the monophyly and phylogenetic relationships at species, genus and subfamily levels. The material used in this study was obtained from museum collections and recent field expeditions, with a total of 126 specimens. DNA extraction was performed using Qiagen commercial kits. DNA amplification comprised the genes COI, 16S rDNA, 28S rDNA and Actin. Sequence alignment was done using the MUSCLE algorithm in MEGA, and phylogenetic analyses were conducted with MrBayes 3.2.7 (Bayesian Inference) and PhyML 3.0 (Maximum Likelihood). Additionally, GenBank sequences of other Streptaxidae species were included. For potential species complexes, genetic 'p' distances were calculated in MEGA, and the ASAP software was used to objectively estimate the number of species within each complex. Based on the genetic data analysis, 184 sequences were generated (COI: 107; 16S: 31; 28S: 27; Actin: 19), resulting in the identification of 30 distinct species according to ASAP. The subfamily Streptaxinae, which includes South American Streptaxidae, was shown to be monophyletic. In contrast, *Streptartemon*, *Streptaxis* and *Rectartemon* were found to be polyphyletic. The creation of new genera may be necessary, although the lack of sequences of some type species still limits such taxonomic restructuring. Species complexes were also identified, with emphasis on *Streptartemon cookeanus* (Baker, 1914) and *Streptaxis contusus* (Férussac, 1819), which exhibit high internal genetic divergence. Additionally, the analysis revealed possible cases of synonymy, such as between *Streptaxis subregularis* Pfeiffer, 1846 and *Streptaxis cypsele* (Pfeiffer, 1849). The results indicate that the diversity of Streptaxidae in Brazil is underestimated, with cryptic species and unrecognized species complexes. The monophyly of the subfamily Streptaxinae reinforces its validity, while the polyphyly of some genera indicates the need for taxonomic revision.

Funding Source: Fundo Brasileiro para Biodiversidade (FUNBIO).

Young Taxonomists

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CHITONS FROM BRAZIL: SYSTEMATIC REVISION OF THE GENUS *Chaetopleura* (POLYPLACOPHORA, CHAETOPLEURIDAE)

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Keywords: integrative taxonomy, biodiversity.

Chaetopleura Shuttleworth, 1853, is characterized by prominent teeth on the insertion plates and tegumentum centrally sculptured by pustules arranged longitudinally. *Chaetopleura* worldwide distribution includes 31 species, six of which have been reported to Brazil. Its systematics require revision, the terminology is often ambiguous, and species diagnoses are brief. This study aims to review the systematics of *Chaetopleura* species found in Brazil, revisiting morphological traits and updating their geographical distribution. Literature data were critically reviewed, and specimens deposited in scientific collections (e.g. Museu de Zoologia da Universidade de São Paulo and coleção malacológica da Universidade Federal do Rio de Janeiro) were examined. Fresh specimens are also being collected along the coast of Rio de Janeiro State, with a total of 100 specimens (fresh and deposited) examined so far. Each specimen is analyzed using a stereomicroscope and compared to the type series and original descriptions of *Chaetopleura* species. A scanning electron microscope (SEM) is being utilized to examine detailed features of the valves, girdle, and radula. The geographical distribution of each species is being updated. Our preliminary results identified several morphological characteristics as particularly useful for distinguishing Brazilian species. Notably, the texture of the girdle can range from smooth to featuring spines, hair, or spicules. Additionally, the valve tegmentum may differ in size and the number of pustules present on the lateral areas. The arrangement and number of ribs in both the pleural and jugal regions of the valves are also important distinguishing features. These findings are consistent with the analysis conducted by Ferreira (1983), who emphasized the significance of the number and size of tegmental pustules as an important trait for species of *Chaetopleura* found in the eastern Pacific, but also highlights the intraspecific variation among individuals that may influence these characters. Although *Chaetopleura* is a diverse group of polyplacophorans, its systematics have been largely neglected and require significant revision. Our preliminary findings indicate that the diversity within this genus is likely underestimated. We hope that by the end of this study, we will contribute to enhancing the understanding of malacological diversity in Brazil.

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UNVEILING BIOMINERALIZATION PROCESSES AND GROWTH PATTERN IN *Corbula tryoni* SMITH, 1880 (BIVALVIA, CORBULIDAE)

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Keywords: *Corbula tryoni*, sclerochronology, growth pattern, daily growth lines, biomineralization, Raman spectroscopy.

The family Corbulidae, the most numerous within the order Myida, presents taxonomic challenges due to heterochrony and morphological variation. Their shells, composed of biomineralized layers and periostracum formed since gastrulation, develop growth lines and increments. These records allow the estimation of organism development time and are valuable for ecological and taxonomic studies. Sclerochronology techniques, commonly used in paleontological and population studies, were applied to 19 shells of *C. tryoni* from the benthic macroinvertebrate collection of the Federal University of São Carlos (Brazil), with average dimensions of 8.8 mm x 6.5 mm (length x height). The shells were embedded in epoxy resin, cut in half with a micro rotary tool, sanded, and stained with Mutvei solution. They were then photographed and the daily growth lines were counted. Additionally, micro-Raman Spectroscopy was used to identify mineralogical phases and organic compounds, and Scanning Electron Microscopy (SEM) was used to observe microstructural details. The investigation of *Corbula tryoni* shells revealed a growth pattern based on the formation of daily lines visible only in the mesoconch. The analysis of the daily growth lines indicates that shell growth can occur in three distinct phases after the deposition of the nepioconch; 1 Increase in thickness without growth in length; 2 Increase in length with little increase in thickness; 3 And a final marked increase in thickness in larger individuals. Structural analyses indicated that the deposition of organic material between calcium carbonate layers may be related to the development and age of the organisms. Smaller shells exhibit a single organic layer, while larger ones show two or more, suggesting progressive growth and structural organization over time. Our spectroscopic analysis demonstrated that *C. tryoni* is primarily composed of an aragonitic phase. Variations in the relative intensities of the peaks at low wavenumber range allowed us to estimate the chronology of shell biomineralization. Through SEM, it was observed that *C. tryoni* presents a crossed-lamellar microstructure both in the outer and inner layers, intercalated by one or more layers of conchiolin. Additionally, it was observed that right after the outermost conchiolin layer, a thin layer of prisms perpendicular to the conchiolin forms. Data analysis indicated that *C. tryoni* lives for about one year and a few months. Length and height are not good indicators of age, as calcium carbonate accretion occurs in phases that do not necessarily increase these dimensions. Thickness is more closely related to the number of daily lines, and analytical methods such as micro-Raman spectroscopy can confirm these observations.

Funding Source: No.

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RESOLVING TAXONOMIC COMPLEXITY IN THYASIRIDAE (BIVALVIA) THROUGH MORPHOMETRIC DATA

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Keywords: morphometry.

Thyasiridae is the second most frequent family in the deep-sea, commonly inhabiting reduced environments such as hydrothermal vents, cold seeps, and organic falls. Morphologically, these bivalves are known as having generally minute sizes and conchological similarity between species. They have undergone interesting adaptations related to their association with bacterial symbionts. These features drive morphological variation and contribute to taxonomic instability within the family. Three Thyasiridae genera were selected: *Thyasira* ('sensu strictu' and 'sensu lato'), *Parathyasira* and *Spinaxinus*. Approximately 10,000 valves were examined, including type and non-type specimens obtained from national and international museums such as: Museum of Comparative Zoology - Harvard University, Yale Peabody Museum, National Museum of Natural History of Smithsonian Institution, Bivalvia Collection of the Museum of Biological Diversity of the University of Campinas, National Museum and Malacological Collection of Federal University of Rio de Janeiro. Specimens were examined using stereomicroscopy and photographed with an attached camera, with some details analyzed by scanning electron microscopy (SEM). Geometric morphometrics using defined landmarks and morphometric data were processed via MorphoJ software. Morphometric analyses (PCA, CVA, Mahalanobis distance) revealed distinct groupings based on shell height and length, and consequently shell shape. These analyses separated the genera into two groups: (1) high and poligonal shells, including *Parathyasira* and *Thyasira* 'sensu stricto'; and (2) elongated shells, including *Spinaxinus* and *Thyasira* 'sensu lato'. Posterior curvature, determined by landmark displacements (ventral or dorsal), and the distances among them, further support the separation of the genera inside the groups. *Thyasira* was separated into two distinct morphological groups, reinforcing the hypothesis that this genus may encompass distinct subcategories. Taxonomic revisions were proposed for species such as *T. flexuosa*, *T. biplicata*, *T. gouldii*, *T. sarsi* and here, *T. trisinuata*, with expanded distributions to the Western Atlantic, and classified as representatives of *Thyasira* 'sensu stricto'. Conversely, species which differ from the type-species (*T. flexuosa*) are considered representatives of Thyasira 'sensu lato', suggesting *Thyasira* is an artificial grouping of sinuated shells. Key morphological differences between *Thyasira* 'sensu stricto' and *Thyasira* 'sensu lato' include: *Thyasira* s.s. shows three prominent points along the posterior margin, caused by the submarginal and posterior sulci; the anterior extreme is displaced dorsally, and the ventral extreme is located centrally, creating an angular, polygonal shell; Thyasira s.l. exhibits only two waves in the posterior margin; the anterior extreme is more ventrally displaced, and the ventral extreme is located more anteriorly, resulting in an oblique shell shape. Morphometric geometric analyses proved to be useful for distinguishing genera *Thyasiridae* species. This study reveals morphological differences within *Thyasira*, supporting its division into 'sensu stricto' and 'sensu lato', highlighting its artificial grouping as *Thyasira* and emphasizing the need for taxonomic revision.

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CONNECTIVITY, DISTRIBUTION, AND PHYLOGEOGRAPHY OF WEST ATLANTIC SPECIES OF CHITONS

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Keywords: Polyplacophora, biogeography, Brazilian fauna, Caribbean fauna.

Several species of western Atlantic chitons exhibit broad distributions, ranging from the Caribbean Sea to southern Brazil. However, numerous marine biogeographic barriers limit gene flow between these regions, and the expectation of connectivity becomes even more restrictive for coastal species with low mobility. This study aims to assess the genetic diversity of western Atlantic chitons as a case study to test role of biogeographic barriers in driving speciation. Specimens of four rocky intertidal species were obtained through field work and loans from scientific collections: *Ischnochiton striolatus* (Gray, 1828), *Ischnoplax pectinata* (Sowerby II, 1840), *Acanthochitona pygmaea* (Pilsbry, 1893), and *Calloplax janeirensis* (Gray, 1828). Species distribution was mapped combining specimen data and public databases such as GBIF. Genetic analyses used new sequences for the COI mitochondrial barcode region amplified from fresh and historical specimens. The resulting sequences were aligned and analysed using MEGA, and a haplotype network was constructed with the software POPArt. The four species exhibit similar distribution patterns, occurring in both the Caribbean Sea and along the coast of Brazil, with some differences in specific occurrence points for each species. Morphologically, each species remains consistent across its range. Genetic analyses, however, revealed significant differences, identifying two distinct and well-structured populations: one in southeastern and the other in northeastern Brazil. These results suggest that ocean currents and temperature gradients act as effective limits to dispersal, restricting gene flow between populations. Ongoing work to incorporate molecular data from Caribbean specimens into the analyses will test whether the biogeographic barriers between northeastern Brazil and the Caribbean Sea also restrict dispersal. This will also allow for a better understanding of the true diversity of chitons in the western Atlantic. These findings highlight the importance of marine biogeographic barriers in shaping genetic structure, even among morphologically uniform and widely distributed chiton species. The observed genetic divergence between northeastern and southeastern Brazilian populations supports the role of limited dispersal in promoting diversification. Expanding the analysis to include Caribbean specimens will be essential to clarify connectivity patterns and uncover the true evolutionary diversity of chitons in the western Atlantic.

Funding Source: SBMa, CAPES, FAPERJ, CNPq, Senckenberg Fellowship program, SOSA.

SYMPOSIUM: MULTIDISCIPLINARY APPROACHES TO MOLLUSCAN SYSTEMATICS AND TAXONOMY

MULTIDISCIPLINARY APPROACHES TO MOLLUSCAN SYSTEMATICS AND TAXONOMY

Coordinators:

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Several research approaches, such as anatomical, morphological, molecular aspects, among others, are important tools in elucidating the origin and vast diversity of the phylum Mollusca. Works that contribute to the areas of systematics and taxonomy of these organisms will be welcome in this symposium.

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EXIT THE CRYPTIC: INTEGRATING DNA AND 3D MODELS TO DISTINGUISH SPECIES IN THE *Unedogemmula unedo* COMPLEX (GASTROPODA, CONOIDEA)

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Keywords: 3D, morphometrics, species delimitation, taxonomic assignation, Gastropoda, *Unedogemmula unedo*.

DNA sequencing has revolutionized species delimitation in gastropods, revealing numerous cases of cryptic diversity. However, fewer than 5% of specimens are collected alive, and most type specimens are empty shells, limiting the scope of use of DNA for taxonomic and nomenclatural purposes. A robust morphological framework is therefore essential to include non-sequenced material into an integrative taxonomy approach. We investigated the *Unedogemmula unedo* complex (Kiener, 1839), for which previous molecular analyses delineated four MOTUs. Using a high-throughput phenotyping pipeline, we generated over fifty 3D models from both sequenced and non-sequenced specimens—including the syntype—from diverse Indo-Pacific localities. We developed a novel approach of 2D morphometrics based on 3D models that does not rely on strict structural homology. Instead, it models and compares individual shell growth trajectories, offering a more dynamic and developmentally informed way of quantifying morphological variation in gastropods. Our approach allows individuals to be rescaled to a standard size, improving comparability and reducing ontogenetic bias. Our analyses successfully distinguished the four MOTUs previously defined through molecular data, demonstrating that each corresponds to a distinct region in morphospace within the complex. We were also able to confidently assign the syntype, along with multiple non-sequenced museum specimens, to their most likely MOTUs—an essential step toward formal taxonomic revision. Beyond species-level differences, we detected significant geographical patterns in shell morphology, suggesting the influence of local environmental factors and raising new questions about the roles of phenotypic plasticity versus genetic differentiation. Our study shows that 3D models provide powerful, non-invasive tools for species delimitation and taxonomic clarification. Moreover, by incorporating growth dynamics, our method adds a developmental dimension often missing in traditional morphological studies. This study demonstrates the power of integrating DNA data with non-invasive, growth-based morphometrics for species delimitation in gastropods. Our pipeline enables the inclusion of historical and non-sequenced specimens—such as types—into a robust, developmentally informed taxonomic framework. This approach not only refines species boundaries but also helps disentangle environmental and genetic factors underlying morphological variation, opening new perspectives for taxonomy and evolutionary developmental biology in gastropods.

Funding Source: This project was founded by the Action Transversale du Muséum (ATM) for the year 2024 (grant DPT-UMR7205 904C5 ISYEB) and the Appel à Projets (AAP) Gratifications de Master du Muséum.

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TESTING THE HIDDEN DIVERSITY: DO MARINE GASTROPODS HAVE WIDE RANGES IN THE WEST ATLANTIC?

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Keywords: biogeography, DNA, species complex, taxonomy.

Most species of marine gastropods are solely known by their shells and some features of the internal morphology, which may result in taxonomic uncertainties when dealing with species complexes. This study comprises a genetic and morphological comparison of several marine gastropods that supposedly have wide ranges in the West Atlantic, testing whether species are truly distributed from northwestern to southwestern Atlantic, or whether there are hidden species with limited ranges. Samplings were conducted on several sites from USA and Brazil between 2013-2024. The investigated taxa are: *Alaba incerta* (d'Orbigny, 1841) [Litiopidae]; *Bittiolum varium* (Pfeiffer, 1840) and *Cerithium atratum* (Born, 1778) [Cerithiidae]; *Claremontiella nodulosa* (Adams, 1850) [Muricidae]; *Engina turbinella* (Kiener, 1836) [Pisaniidae]; *Eulithidium affine* (Adams, 1850) [Phasianellidae]; *Pilsbryspira albocincta* (Adams, 1845) [Pseudomelatomidae]; *Schwartziella catesbyana* (d'Orbigny, 1842) [Zebinidae]; and some species belonging to Triphoroidea and Pyramidellidae. The morphology was assessed by the study of the shell, operculum, jaw and radula, when present. The mitochondrial COI gene was sequenced for all species, complemented by the 16S gene in some cases. Phylogenetic trees (Maximum likelihood), genetic 'p' distances and the software ASAP were applied. Whereas some species indeed seem to maintain a gene flow along the tropical West Atlantic (*A. incerta*; *C. atratum*; *C. nodulosa*; *E. turbinella*; some triphorids), others are true species complexes (*B. varium*; *E. affine*; *P. albocincta*; *S. catesbyana*; several cerithiopsids and pyramidellids). In addition to the possible role of the Orinoco-Amazon freshwater discharge as a barrier for gene flow, some taxa also present clear allopatry within the Brazilian littoral, e.g. in the Cabo Frio upwelling system (Rio de Janeiro state). Albeit larval development is essential to explain these patterns, with species of low PLD (period of larval duration) having limited ranges, the feeding mode (generalists vs. specialists) seems also important. More samplings in the Caribbean are required in order to refine the ranges of species in the complexes, prioritizing the type localities. The present study also warns for the conservation of marine species, which is underestimated and sometimes with actual geographic ranges much narrower than previously considered.

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A NEW TAILED SPECIES OF *Falcidens* SALVINI-PLAWEN, 1968 (APLACOPHORA, CAUDOFOVEATA) FROM THE BRAZILIAN COAST

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Keywords: deep-sea, Chaetodermatidae, taxonomy, morphology.

Falcidens Salvini-Plawen, 1968 is one of the most speciose genus of Caudofoveata, currently bearing about 45 described species. This diversity is, however, still little explored for many places and among these is the Brazilian coast, that has some oil-rich areas from where many oceanographic campaigns have collected hundreds of samples of these molluscs. Here, we describe one more species of *Falcidens* from the northeastern and southeastern portions of this coast. The examined material was collected by four projects: in the southeastern by the Projects HABITATS (Campos Basin), AMBES (Espírito Santo Basin), and Santos (Santos Basin); and in the northeastern by the Project MARSEAL (Sergipe-Alagoas Basin). Also, additional lots were observed and came from the southeastern and southern coasts, now deposited at the collections of the Museum of Zoology of the University of São Paulo (MZSP) and the Brazilian National Museum (MNRJ). The general body morphology was observed and photographed under stereomicroscopes. The radula was isolated and its structure was recorded by the Scanning Electron Microscopy (SEM); by this and through birefringence microscopy details of the extracted sclerites were observed. The body of the new species reaches up to 7 mm in length. It is divided into weakly visible parts: an anterium, that has an “U” shaped oral disc; followed by a neck continuous to a trunk; and a posterior part, like a tail, formed by a shank and a knob. The sclerites are adpressed to the body and around the oral disc they are scale shaped. In general, the sclerites have a triangular shape, with a base bearing a shallow and almost indistinct notch and rounded ends, and a pointed blade ornamented with a central keel which widens towards the base, sometimes with a slightly abrupt tapering; they are more triangular in anterium, neck and shank, triangular elongated in the trunk, and needle shaped in knob. The radula has a pair of sickle-shaped teeth, connected each other by a symphysis, that is in turn connected to a cone-shaped central support. Around each tooth there is a lateral support, above them a central triangular plate. The species occurs in Brazilian coast, from Alagoas State (about 10°S) to Santa Catarina (about 27°S). A total of 38 lots with 48 specimens were analyzed, collected in a bathymetrical range of 114 to 1335 m depth. There are three other tailed species o *Falcidens* from the Brazilian coast that are clearly distinct from this new species: F. targatus and F. acutargatus, which have triangular shaped sclerites with a cris-crossed sculpture; and *F. australocaudatus*, that has lanceolate sclerites and a longer and well-marked tail. The recent explorations are continuously revealing thousands specimens of caudofoveates, currently known as totalizing ten 10 described species, five of them from the genus *Falcidens*. However, other areas, as in the northern part of the coast, are still unexplored and may hide an interesting biodiversity of these molluscs, with a consequent taxonomical, ecological and biogeographical importance for the study of these deep-sea animals.

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THE HYPERDIVERSE PROJECT - KEYS TO EVOLUTIONARY SUCCESS: UNTANGLING DRIVERS OF HYPERDIVERSIFICATION

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Keywords: Neogastropoda, systematics, evolution, toxins.

Explaining why some taxa are more diversified than their closest relatives remains one of the major challenges in evolutionary biology. To tackle this question, the HYPERDIVERSE project (2020-2026) focuses on a poorly known taxon of marine predators, the Neogastropoda. Their high species diversity (>15,000 species), unevenly distributed among lineages, and their specialized feeding habits make them a perfect model system to test hypotheses on the diversification of hyperdiverse taxa. The first objective of the project is to clarify the systematics of the neogastropods, both at the species and higher phylogenetic levels. The second objective is to explore the toxin diversity of the neogastropods, based on genomic and transcriptomic data, to eventually identify the molecular basis of their trophic specializations, which is regarded as the main driver of their diversification. The third objective is to combine the robust phylogenetic hypothesis and the estimations of toxin diversity in a comparative phylogenetic framework, to test if the diversification rates of specific clades within the Neogastropoda have been affected by the diversity of toxin families and specific gain/loss events. Using an integrative taxonomy approach, we discovered hundreds of new species, many of which have been (or are being) formally described. We then produced a genus-level phylogeny of neogastropods, including c.a. 750 terminal taxa, sequenced using an exon-capture strategy. Two genomes (*Monoplex corrugatus* and *Stramonita haemastoma*) have been published, and five others have been sequenced and are currently under analysis. Additionally, hundreds of transcriptomes, representing the family-level diversity of the neogastropods, have been sequenced and are currently being analysed, revealing hundreds of new putative toxins. We have entered the final phase of the project: its last year will be dedicated to inferring diversification rates and eventually correlating them with toxin diversity. The project marks a significant advancement in our understanding of the taxonomy, phylogeny and toxin diversity of the neogastropods. One major result is the detection of putative toxins in all the screened lineages, suggesting that all the neogastropods are venomous. However, much remains to be done, with potentially thousands of new species waiting to be described, and who-knows how many toxins to be discovered.

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THE FIRST STEPS OF HETEROBRANCHIA: REVEALING THE EVOLUTIONARY HISTORY OF THE 'LOWER HETEROBRANCHS'

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Keywords: phylogenomics, ultra-conserved elements, gastropod evolution, systematics.

Heterobranchia is one of the most diverse subclasses of gastropods. The 'lower heterobranchs' represent a grade of the earliest branches, with uncertain phylogenetic relationships. Here, we aim to shed light on known controversies, such as the position of Valvatoidea, and understand the emergence sequence of modern heterobranchs by analysing all the early lineages using innovative genomic tools. We employed the target enrichment of ultra-conserved elements (UCE) as a paradigmatic genomic technique in museomics. DNA was extracted from over 90 museum specimens covering all six recognised superfamilies of 'lower heterobranchs' plus Mesoneura and Euthyneura representatives, collected mostly in Japan and the Mediterranean. Library preparation, enrichment, and capture included the custom probe set of Moles & Giribet (2021). Sequence data were assembled, aligned, and filtered to generate a final 50% occupancy matrix of over 1,600 loci. To ensure the robustness of our phylogenetic reconstructions, we employed a combination of concatenated and coalescent-based approaches, including maximum likelihood (ML), Bayesian inference (BI), and multispecies coalescent/species tree (MSC) analyses. We provide a robust molecular framework that circumscribes the early evolutionary history of heterobranchs. The superfamilies "Omalogyroidea" (only including Ammonicera) + (Architectonicoidea + Mathildoidea) form the earliest divergent clade in Heterobranchia. Omalogyroidea was recovered as polyphyletic, with the smallest gastropod genus *Omalogyra* being a panpulmonate, as suggested by the sacoglossan-like radula and head characters. A second clade is composed of Valvatoidea + (Cimoidea + Orbitestelloidea) and positioned as the sister group to Mesoneura + Euthyneura. These novel findings augment and partially contradict previous taxonomic classifications based on morphology and limited molecular data, and are hinged on the inclusion of minute taxa, international community collaboration, and enhanced access to museum collections. This study shows that UCE-based molecular data can resolve disputed evolutionary relationships, even among the smallest marine taxa, and underscores the value of scientific collaboration. The so-called 'lower heterobranchs', once considered mostly prosobranchs, are now distributed across the heterobranch tree. Examples include pyramidellids and glacidorbids within Panpulmonata, acteonoids as sister to Ringipleura, and a grade of mostly shelled heterobranchs now placed in three major clades that are sister to Euthyneura.

Funding Source: No.

SYMPOSIUM: MOLLUSCS IN ONE PLANET: SPECIES DISTRIBUTIONS THROUGH SPACE AND TIME

MOLLUSCS IN ONE PLANET: SPECIES DISTRIBUTIONS THROUGH SPACE AND TIME

Coordinator:

STHEFANE D'ÁVILA – Museu de Malacologia Prof. Maury Pinto de Oliveira, Universidade Federal de Juiz de Fora – UFJF, Brazil

The scope of the symposium "Molluscs in One Planet: species distributions through space and time" includes all aspects of mollusc species distributions and methodological approaches such as (1) species distribution modeling, (2) ecological niche modeling, (3) updating geographic distributions of native and invasive species, (4) mapping species distributions for conservation assessments, (5) mollusc-borne diseases and geographic distribution of intermediate hosts, (6) projecting future distributions of mollusc species, (7) crop pests distribution and control, (8) spread and ecological impact of invasive species, (9) rare or endemic species and their conservation status, (10) biodiversity databases and malacological collections as sources of distributional data, (11) biotic and abiotic factors shaping species distributions, and (12) predicting the past distribution of species climatic niches, locations of past refugia, and migration pathways.

Molluscs in One Planet: Species Distributions through Space and Time

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REVISITING THE PHYLOGENY AND DIVERGENCE TIMES OF EASTERN PACIFIC *Argopecten* SPECIES

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Keywords: *Argopecten*, mitogenomics, bayesian phylogenetic inference.

The Eastern Pacific hosts two extant *Argopecten* species: *A. purpuratus* and *A. ventricosus*. Previous morphological analyses showed *A. purpuratus* more closely to Atlantic species (*A. gibbus*, *A. nucleus*), estimating their divergence around 7–6 Ma. However, molecular evidence suggests a different pattern, indicating a closer phylogenetic relationship between *A. purpuratus* and *A. ventricosus*. To assess this controversy, we reevaluated the phylogenetic relationships and divergence times of the Pacific and Atlantic *Argopecten* species, using a combination of updated fossil age ranges and protein-coding gene sequences from pectinid mitogenomes. We used 26 mitochondrial genomes from Pectininae, Palliolinae and Chlamydinae. Bayesian phylogenetic analysis was performed in BEAST2 using the Fossilized Birth-Death Process Model (FBD) under an uncorrelated log-normal relaxed clock. Maximum and minimum known stratigraphic ages were integrated into the molecular matrix as molecular clock prior calibrations. Fossil data were retrieved mainly from the Paleobiology database. The divergence event between *A. purpuratus* and *A. ventricosus* coincides with a 3°C cooling in the Caribbean Sea during late Oligocene (26.6 Ma). This cooling affected warm-water species and may have favored the proliferation of temperate to cold-water tolerant marine invertebrates. The MRCA of *A. purpuratus* was dated to 3.85 Ma. This divergence event coincided with the onset of a progressive global cooling during the Pliocene, contributing to the Plio-Pleistocene extinction of marine megafauna. This cooling may have favored the spread of cold-water adapted species into southern Chile. Our findings support the hypothesis that marine invertebrates in the Humboldt Current Ecosytem are ancient remnants of older tropical faunas and share a close relationship with the Tropical Eastern Pacific species associated to the Panama Province. The progressive decline in sea surface temperatures during the Plio-Pleistocene may have led to extant *A. purpuratus* tolerating cold waters. In addition, the climate variability related to the El Niño Southern Oscillation (ENSO) during the Pliocene and onwards likely contributed to promoting *A. purpuratus* adaptations to changing upwelling conditions in the Humboldt Current ecosystem.

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Molluscs in One Planet: Species Distributions through Space and Time

Conservation

Oral - 375

ECOLOGICAL NICHE AND ANATOMICAL CHARACTERIZATION OF *Drymaeus germaini* (ANCEY, 1892) (GASTROPODA, BULIMULIDAE)

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Keywords: Atlantic Forest, Cerrado, Amazon, Bulimulidae, conservation.

Drymaeus germaini Ancey, 1892 is a species originally ascribed to the genus *Bulimulus* Leach, 1814, based on a single dry shell, collected in Mato Grosso state, Brazil. The current knowledge on the distribution of *D. germaini* is based on few occurrence records taken from the original description and former literature. Occurrence records of *D. germaini* were obtained from the biodiversity databases Global Biodiversity Facilities GBIF and Sistema de Informação sobre a Biodiversidade Brasileira, besides published papers and records associated to specimens deposited in the malacological collection of the Museu de Malacologia Prof. Maury Pinto de Oliveira. To delineate the abiotic components of the model, we used 19 bioclimatic variables obtained from the WorldClim database at a spatial resolution of 30 arc seconds (~1 km^2). Multicollinearity among the variables was analyzed using the Variance Inflation Factor (VIF). Highly correlated variables were excluded from the previous step to construction of the niche modeling, resulting in seven bioclimatic variables for the analyses. In the present study, the bulimulid species *D. germaini* was revisited. We have redescribed this species based on the inner anatomy and shell sculpture, also providing the first comparative analysis with congeneric species. Using records from malacological collections, we have updated the geographic distribution of *D. germaini*, providing, for the first time, specific localities where this species occurs, which also allowed us to estimate its potential distribution. The ENM results revealed a narrow belt from Rio Grande do Norte to Rio Grande do Sul states including mid-to-high suitability areas in the Atlantic Forest. At Rio Grande do Norte, Paraíba, Alagoas, and Sergipe states these areas extended from the Atlantic Forest to the Caatinga. In the Rio Grande do Sul state, a continuous area of mid-to-high suitability included both the Atlantic Forest and the Pampas. The Atlantic Forest is considered as a biodiversity hotspot with high levels of endemism in both fauna and flora. It is also the most degraded biome in Brazil, enclosing most of threatened invertebrate species. Additional areas of mid suitability were found in Cerrado biome, in the Mid-East Goiás, Mid-East Minas Gerais, and North Maranhão state. Cerrado is the second most degraded biome in Brazil. The main threats to biodiversity conservation in these two biomes are the habitat fragmentation, fire, and habitat loss as consequence of urbanization pressure, large scale agriculture, and cattle raising. These facts highlight the need to monitor *D. germaini* and obtaining the information necessary to stablish its conservation status. Despites the scarcity of recent occurrence records for *D. germaini*, the fact that the records available correspond to unprotected areas (with the exception of the records from Ipaba, MG), and the fact that the ecologically suitable areas for *D. germaini* are located in regions disturbed by deforestation, fires, urbanization, habitat loss, mining, and flooding, this species should be classified as data deficient, according to the criteria of the IUCN.

Funding Source: No.

Molluscs in One Planet: Species Distributions through Space and Time

Evolution

Oral - 22

UNCOVERING THE DRIVERS AND PATTERNS OF FRESHWATER BIVALVE DIVERSIFICATION IN SOUTH AND SOUTHEAST ASIA

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Keywords: biogeography, phylogenetic, systematics, biodiversity hotspots, plate tectonics, ancient rivers.

The Oriental Region is one of the world hotspots of freshwater mussel diversity. Its water bodies host more than 200 species of the order Unionida, with an exceptional level of endemism. Here, we review research efforts on the freshwater bivalve fauna of the region and highlight key findings regarding the drivers and patterns of freshwater bivalve diversification in South and Southeast Asia. Our mussel research was based on shell and soft tissue samples collected from freshwater systems across the region since 2011, as well as on materials from museum collections and databases. For taxonomic revisions, we applied an integrative approach combining morphological investigation (comparative morphological analyses and geometric morphometry) with molecular techniques and biogeographic reconstructions using the COI, 16S rRNA, and 28S rRNA gene sequences. Biogeographic and macroevolutionary patterns were inferred from time-calibrated phylogenies based on fossil records and molecular evolution rates, along with ancestral area modeling and plate tectonic reconstructions. We used freshwater mussels (Unionidae) as a model to reconstruct spatial patterns of freshwater biogeographic divides throughout the Oriental freshwater biogeographic region. Based on the Unionidae phylogeny and endemism patterns, this area could be delineated to the Western Indochina, Sundaland, and Indian subregions. Our findings highlight that Southeast Asia's freshwater bivalve fauna primarily originated within three evolutionary hotspots (Western Indochina, Sundaland, and the East Asian subregion of the Palearctic) supplemented by ancient immigrants from the Indian Subcontinent. The subfamily Parreysiinae most likely originated in East Gondwana in the Jurassic and its representatives arrived to Asia on two Gondwanan fragments (Indian Plate and Burma Terrane). The Burma Terrane collided with mainland Asia in the Late Eocene, leading to the origin of the Mekong's Indochinellini radiation. The subfamily Gonideinae originated in Laurasia (Sunda Plate) and split to two large monophyletic radiations within the former paleo-Mekong catchment during the Late Eocene. This subfamily colonized the Burma Terrane after the collision of this tectonic block with the Sunda Plate. We found that the largest freshwater basins in tropical Asia represent more or less isolated evolutionary hotspots of the Unionidae with high levels of endemism. Mussel evolution within long-lived (ancient) river systems through the entire Cenozoic epoch has resulted in single-drainage and intra-drainage endemics. Our results indicate that the paleo-Mekong and paleo-Ayeyarwady rivers could have been initiated since the Late Cretaceous as did the paleo-Yangtze System. Additionally, the stream captures between freshwater basins facilitated the diversification of subregion endemics. The Southeast Asian freshwater mussel fauna originated primarily within three evolutionary hotspots (Western Indochina, Sundaland, and East Asian) supplemented by Late Miocene immigrants that colonized freshwater systems of Myanmar from the Indian Subcontinent. Our phylogenetic models support the assumption that a long-term freshwater basin history together with drainage re-arrangements and a plethora of relatively isolated tributaries are the main drivers of diversification processes in riverine unionoids.

Funding Source: This study was supported by the Ministry of Science and Higher Education of Russia (project No. FUUW-2025-0022).

Molluscs in One Planet: Species Distributions through Space and Time

Archaeomalacology

Oral - 40

PREHISTORIC SHELL MIDDEN SITES IN SOUTHWEST MINDORO, PHILIPPINES: AN ARCHAEOMALACOLOGY STUDY IN ISLAND SOUTHEAST ASIA

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Keywords: archaeomalacology, coastal archaeology, maritime environments, palaeoecology, prehistoric life ways.

From the Late Pleistocene to the early to mid-Holocene appears to have been a period of significant social change and technological innovation, as illustrated by the prehistoric shell middens as well as assemblages across the Philippine archipelago and Island Southeast Asia as far as Near Oceania. They presented a potential stepping stone to the main Philippine Archipelago based on the archaeological investigations and cultural assemblages unearthed in Mindoro cave sites. This research focused on shell middens at the Bubog rock shelter sites (Bubog 1 and Bubog 2) on the small island of Ilin just off the coast of Mindoro and shell assemblages at the Bilat Cave, located in the southwesternmost part of Mindoro Island, facing east of Ilin Island. All sites provided a three (3) shell column sampling of 1 × 0.50 m^2. Shells were sorted and identified at the species level, if possible. Abundance and diversity of shell species were analyzed quantitatively and were grouped according to their aquatic ecological background. The excavations in Bubog produced evidence of stratified sequences of human habitation at the two rock shelter sites in the form of dense shell middens that date to ca. 33,000 cal. BP onwards. They have 38 species and/or genera of gastropod and eight of bivalves recorded in Bubog 1 and 42 and 12 in Bubog 2, respectively (Pawlik et al., 2014 and 2025). While shell species adapted to rocky shore, estuarine, and mudflat conditions dominate the lower layers, coral reef species are more frequent in the layers above. They provide direct evidence on how variability in landscape formation, sea levels, and landmass during the terminal Pleistocene and early Holocene influenced the behavior of early human populations. Numerous species of molluscs were recorded, and provisional results indicate variations in the invertebrate faunas throughout the stratigraphic sequences, resulting from sea level rise and the establishment of coral reefs between Ilin and Mindoro at the end of the Pleistocene. Bilat Cave had several dated habitational layers from 7200 to 21800 cal. BP. All of them were dated from the shell assemblage. The mollusc assemblage is more diverse, with ten (10) families from the Class Bivalvia, with 40 genera, and 39 families with 141 genera representing gastropods. All of them live in marine and estuarine environments except for Thiaridae, whose habitat is freshwater environments. The midden sequence indicates exploitation strategies focused on the adjacent rocky shores and mid- and low-intertidal zones, with occasional forays to sandy beaches and mangrove areas. By integrating data from archaeological excavations where molluscan remains have been recovered, results contribute substantially to our understanding of the processes of human island adaptation, complement ongoing research into Island Southeast Asia's paleogeography, and enhance current knowledge of prehistoric subsistence strategies and socio-economic interaction across the region.

Funding Source: No.

Molluscs in One Planet: Species Distributions through Space and Time

Ecology

Oral - 147

BIODIVERSITY OF BENTHIC FAUNA ASSOCIATED WITH THE INVASIVE OYSTER *Saccostrea cucullata* (BORN, 1778) IN THE INTERTIDAL ZONE OF THREE BAYS IN RIO DE JANEIRO

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Keywords: biological invasion, habitat complexity, rocky intertidal, Guanabara Bay, Ilha Grande Bay, Sepetiba Bay.

Several Ostreidae species are considered "ecosystem engineers" due to their ability to generate biogenic habitats. Their three-dimensional structure provides protected interstitial spaces, foraging and breeding environments, and substrate for the settlement of sessile organisms (Aslam, 2020; Boudreaux et al., 2006). This study aims to describe the biogenic habitats created by the invasive oyster species *Saccostrea cucullata* and their associated fauna on rocky shores in three bays in Rio de Janeiro. Three rocky shores in each bay (Guanabara Bay - GB, Sepetiba Bay - SB, and Ilha Grande Bay - IGB) in the state of Rio de Janeiro were sampled in January and February 2024. Oyster layer scraping was performed on the rocky substrate in the mid-intertidal zone, within a delimited 400 cm^2 quadrat, with five replicates in each site. Specimens were sorted into broad taxonomic groups and are being identified to the lowest possible taxonomic level with the assistance of specialists. Organisms will be assigned to trophic groups based on available literature data. Multivariate and diversity analyses are being conducted using PRIMER version 6.1.13 & PERMANOVA+ Version 1.0.3 software. The composition of biogenic habitats varies between bays, with the invasive species *Saccostrea cucullata* predominating in GB and SB. In IGB, the native oyster *Crassostrea rhizophorae* Guilding, 1828 predominates. Of the three sites with the largest volume of sampled material (an indicator of substrate complexity), two are located in IGB and one in GB. Although they differ in composition, these sites have a common characteristic: the sampled substrate was a continuous rocky shore. Our results showed higher densities of associated fauna on rocky shores compared to boulders, likely due to their greater topographic complexity and therefore, more microhabitats. In line with studies on biogenic habitats provided by molluscs (Gestoso et al., 2013; Aslam et al., 2020; Cameron et al, 2024), we found 38,660 organisms distributed in 8 phyla, with Mollusca and Arthropoda being the most abundant. The two sites with the highest abundances of *S. cucullata* (BG) and the two with *C. rhizophorae* (IGB) showed high similarity in the cluster analysis, suggesting that the dominant species is not the determining factor for the associated faunal composition, but rather the total abundance of oysters. The abundance of associated organisms correlated positively with the volume of the samples ($r=0.82$; $p<0.05$), confirming the influence of habitat complexity. The bay also does not appear to be a determining factor for the associated faunal communities (PERMANOVA, $F=1.287$, $p=0.251$). However, the factor "site" showed a significant difference (PERMANOVA, $F=11.771$, $p=0.001$), suggesting that a local factor might exert the greatest influence on the composition of the communities. Habitat complexity appears to be a major influencing factor in the density of organisms supported by oyster beds, just as the site where the community is developing seems to affect the composition of the associated fauna. Thus, further study of the environmental factors that locally determine these habitats is necessary to better understand the dynamics between an ecosystem engineer, whether invasive or not, and the species with which it interacts.

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Molluscs in One Planet: Species Distributions through Space and Time

Conservation

Oral - 155

HISTORICAL AND CONTEMPORARY RECORD OF CONTINENTAL MOLLUSKS IN MEXICO CITY

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Keywords: Mexico City, urban malacofauna, new species, exotic species, freshwater mollusks, conservation, habitat degradation, invasive species.

Mexico City, one of the largest urban areas in America, surprisingly harbors a high diversity of continental mollusks, despite intense urbanization. Given the global vulnerability of these organisms and increasing habitat degradation, this study aimed to compile an updated inventory of continental mollusk species in the city, providing essential data to inform conservation and restoration efforts. Species records were compiled through field sampling at selected sites (e.g., UNAM Botanical Garden, Xochimilco canals, Magdalena River) and virtual consultation of zoological collections (CAS, ANSP, FLMNH, MCZ, USNM, etc.) and biodiversity databases (GBIF, Enciclovida). Museum specimens were reviewed, and specialized literature was consulted for exotic species. Field identification prioritized living organisms, with some shell-only occurrences interpreted cautiously to avoid misidentification. A total of 74 continental mollusk species were recorded, including 70 gastropods and 4 bivalves from 34 families. Twenty-eight gastropod species were exotic, mainly introduced via horticultural trade or aquarism. The first record of Menetus dilatatus in Mexico City was documented. Moreover, a possible new freshwater gastropod species was identified, requiring further taxonomic investigation. Two species, Anodonta impura and Valvata humeralis, appear to have been locally extirpated, likely due to environmental degradation and the introduction of invasive species. Additionally, specimens of Sphaerium sp. were recorded exclusively in the best-preserved areas of the Magdalena River, emphasizing the critical condition of native aquatic mollusk populations. These findings highlight the urgent need for biodiversity monitoring and ecological restoration strategies to safeguard molluscan diversity within the urban landscape. This work highlights the significant mollusk diversity surviving within an intensely urbanized environment. Continuous monitoring is vital to compare historical and contemporary records, informing conservation and restoration initiatives. Preventing further local extinctions demands effective ecological strategies. Inventories such as this provide indispensable baselines for modeling biodiversity responses to environmental pressures in urban contexts.

Funding Source: No.

Molluscs in One Planet: Species Distributions through Space and Time

Conservation

Oral - 156

FORGOTTEN MUSSELS BROUGHT TO LIGHT: AN EFFORT TO MAP THE MYCETOPODIDAE IN THE STATE OF SÃO PAULO, BRAZIL

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Keywords: Unionida, natural history collections, conservation, species distribution, Bivalvia.

Despite playing important roles in freshwater ecosystems, freshwater mussels are among the most endangered organisms worldwide, a trend observed across various regions of the globe. Drastic environmental changes driven by human activities, combined with the introduction of invasive species, as well as taxonomic challenges such as difficulty in species delimitation and lack of comprehensive distributional data, significantly hinder conservation efforts. We provide an updated checklist of the species of Mycetopodidae from the state of São Paulo, southeastern Brazil. Occurrence records for all species were reviewed based on collection specimens, online databases (e.g., GBIF, MusselProject), literature and citizen science (iNaturalist). Our primary data sources are the Malacological Collection of Ribeirão Preto (CMRP) and the Mollusca collection at the Museum of Zoology of the University of São Paulo (MZSP), which contain specimens collected in several hydrographic micro-basins across the state. Most of this material is unpublished and contains invaluable data on the occurrence of mycetopodids. This information was used to pinpoint the most species-rich areas and assess potential threats. Our work has so far resulted in 267 records across the state of São Paulo. The MZSP collection holds the largest number of records (106), followed by CMRP (64), GBIF (40), MusselProject (38) and iNaturalist (18). In São Paulo state, there are records of about 18 species of Mycetopodidae, although some identification needs further revisions. Among the 24 hydrographic micro-basins of the state, MZSP showed the broadest coverage, with records from 11 basins, and it is the only database with data from the Peixe micro-basin. Most records were found in micro-basins associated with the Tietê River. The micro-basins with the highest species richness were Pardo, Alto Tietê and Médio Tietê. Notably, there was very little overlap between species occurrences and established protected areas. Our preliminary results highlight the importance of collections like the MZSP and CMRP, which had numerous records that had never been published before. This is particularly true for smaller and provincial collections such as the CMRP, which has received little attention despite its rich material. As our study continues, we intend to use this data to discuss the conservation of these species by comparing records over time to detect potential changes in species richness and correlate these changes with environmental data to identify potential impacts. Considering that freshwater mussels are severely threatened worldwide, addressing the conservation of these species in Brazil should be a priority. Freshwater environments in São Paulo faced drastic anthropogenic changes, but little is known about the situation of its mussels. Our preliminary results show a rich fauna of mycetopodid mussels in the state that has gone unnoticed so far, serving as a basis for future studies on the subject.

Funding Source: No.

SYMPOSIUM: CITIZEN SCIENCE AND MOLLUSKS: BRIDGING COMMUNITIES AND RESEARCH / DIVERSITY, EQUITY AND INCLUSION IN MALACOLOGY

CITIZEN SCIENCE AND MOLLUSKS: BRIDGING COMMUNITIES AND RESEARCH / DIVERSITY, EQUITY, AND INCLUSION IN MALACOLOGY

Coordinators:

RUTHELA P. PAYAWAL – Polytechnic University of the Philippines, Philippines
RAFAEL MASSON ROSA – Universidade de São Paulo, Brazil

The session shall explore the growing field of citizen science, focusing on its contributions to mollusk research. From coastal surveys to biodiversity mapping, citizen scientists play a crucial role in collecting data on mollusk populations, helping researchers track changes in ecosystems, identify new species, and address conservation challenges. This discussion will highlight successful collaborations between professional scientists and the public, showcase cutting-edge projects, and offer practical strategies for engaging communities in mollusk research. In addition, the session will discuss the themes of gender inequality, racial diversity, and the inclusion of different social segments in malacology research. In the theme of gender inequality, data will be presented on the participation of women in leadership positions and in scientific production in this field and related areas. In the theme of ethnic-racial diversity, inequalities, respect for differences, and contributing to the elimination of discrimination and prejudice based on ethnicity or race will be discussed. Finally, in the theme of inclusion, we will present studies and reflections on quota laws and PWDs that also affect the malacology community. In this prestigious space within the Brazilian and international malacology community, the WCM cannot refrain from presenting the three current and relevant themes to its audience, and thus promote a conscious and objective reflection on the obstacles that a large part of its community, women, black people, and those with some kind of disability, face, seeking, and bringing to discuss strategies that help overcome these obstacles.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Education and Outreach

Oral - 113

BUILDING AWARENESS, OBSERVING THE OVERLOOKED: LESSONS FROM URBAN CITIZEN SCIENCE ON NONMARINE MOLLUSCS IN ITALY

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Keywords: citizen science, urban biodiversity, nonmarine molluscs, community engagement, iNaturalist, opportunistic data.

Land molluscs are essential to urban ecosystems but often overlooked in citizen science (CS) due to low public appeal and identification challenges. In 2021 we analysed iNaturalist data from Tuscany and found that in certain cases land molluscs could be detected through opportunistic CS contributions. This inspired CLIC! (Chiocciole e Lumache In Città i.e. “Snails and Slugs In Cities”), the first nationwide Italian CS project on urban nonmarine molluscs. CLIC! used an opportunistic CS model: supported by multimedia resources and identification tips but without formal training and protocols, volunteers uploaded observations to a dedicated iNaturalist project. In Siena, CLIC! overlapped spatially and temporally with Siena BiodiverCity (SBC), a broader local project on urban biodiversity, offering a unique opportunity to explore engagement and reporting patterns, particularly for low-charisma animals such as nonmarine molluscs. Awareness in Siena was promoted through school programs, biodiversity walks, public events, and an ongoing social media series ("malacological stickers") highlighting species traits in an engaging way. Already in early 2025, CLIC! has collected over 2000 observations representing 116 taxa of nonmarine molluscs in Italy, showing a well-known predominance of medium- to large-sized synanthropic species as well as common ones (e.g. *Cornu aspersum*, *Eobania vermiculata* and *Papillifera papillaris*). Despite its opportunistic nature, the project highlighted that volunteer-driven observations can yield ecologically valuable data, reveal overlooked distribution patterns (e.g. taxa most frequently encountered by generalist users are also the taxa that are usually not included in mainstream research datasets), and foster interest in traditionally neglected groups. Participants' willingness to join CLIC! and submit mollusc observations suggested relatively high motivation and curiosity. However, expert validation remains essential to ensure the reliability and scientific value of the data collected through citizen contributions. In SBC, expert-led initiatives significantly increased the diversity and quantity of mollusc records, showing statistically significant differences between BioBlitzes and unguided contributions. Nevertheless, spontaneous mollusc records outside expert-based events were also notable, suggesting underlying interest potentially amplified by CLIC! outreach activities. Although direct quantitative comparison is ongoing, our preliminary results indicate that fostering a culturally receptive context - through education and targeted engagement - can enhance participation and data collection efforts for low-charisma taxa. Public familiarity, built over time, appears to positively influence spontaneous CS contributions. CLIC! and SBC demonstrate that combining expert-led initiatives with spontaneous citizen-driven efforts can improve the monitoring of under-represented taxa. While guided events like BioBlitzes boost short-term participation and data quality (and quantity), outreach activities that build public awareness sustain engagement over time. Expert validation is crucial to maintain scientific robustness. Creating a receptive cultural context is equally important to increase the representation of low-charisma taxa in urban biodiversity research.

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Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Invasive Alien Species

Oral - 131

TRACKING ALIEN MOLLUSCS WITH CITIZEN SCIENCE: THE iNATURALIST EXPERIENCE

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Keywords: iNaturalist, citizen science, invasive species, biological invasions.

iNaturalist is a worldwide known citizen science platform focused on biodiversity data, with many useful applications in research, education, outreach and conservation. In recent years, molluscan research has increasingly incorporated data from iNaturalist, with a highlight to the opportunities it brings to the study of invasion biology. In this presentation, we share our experiences with iNaturalist and compare two projects focused on the exotic molluscs in Argentina and Brazil. For any geographic region, iNaturalist features an interactive present-taxa checklist based on internal and external data, which includes their establishment means. Following modern literature, we updated the mollusc species checklists of Argentina and Brazil, adding the "introduced" label to the relevant taxa. Then, we created two iNaturalist projects (up-to-date observation clusters derived from filter-based classification) set to compile existing records of exotic molluscs in each country. The resulting projects are self-updating and publicly visible, allowing users to keep track of all observations matching the selected criteria over time. We then compared the datasets produced by both projects to see how exotic molluscs are being observed in Argentina and Brazil. We found 7,385 observations of exotics molluscs in Brazil and 3,304 in Argentina. The proportion of exotics were similar in both countries, being 21.5% of all molluscan observations in Brazil and 19.1% in Argentina. The number of identified alien species in both countries was also similar (37 in Brazil and 33 in Argentina), but their composition and relative abundance were different, led by *Lissachatina fulica* and *Cornu aspersum*, respectively, as the most observed taxa. Remarkably, some records represent range expansions. Beyond the projects, we also found a few observations of unidentified molluscs that might represent newly introduced species. The number, frequency and geographic distribution of observations on iNaturalist are not a perfect reflection of these organisms' occurrence, as they are affected by several observer-related biases. Observations tend to be more frequent in more densely populated areas, taken at times when people are more active and focus mostly on conspicuous species. Exotic species are favored by those biases due to their synanthropic nature, which might influence their high rates of observations. We highlight the importance of expert identifiers, which are severely lacking for molluscs on iNaturalist. Identifying molluscs is not always trivial and some cases are limited by insufficient data. Inaccurate identifications by the algorithm and inexperienced users are also frequent. Ongoing efforts to review and identify observations are necessary to ensure more robust datasets. Lastly, we also discuss the potential of iNaturalist for science outreach and educational projects in the context of exotic molluscs. iNaturalist is an effective tool for monitoring exotic species, since its continuously updated database allows us to quickly assess their presence and distribution. Efforts to track the spread of established exotics and quickly detect new introductions are essential to inform management strategies. Beyond research, iNaturalist can be used to raise public awareness of these biological invasions and teach people how to distinguish exotic molluscs from their often endangered native counterparts.

Funding Source: No.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Conservation

Oral - 232

SOCIO-ECOLOGICAL ASSESSMENT OF THE MALACOFAUNA IN LAKE ECOSYSTEM: A CASE IN THE SEVEN LAKES OF SAN PABLO CITY, LAGUNA, PHILIPPINES

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Keywords: conservation, lakes, mollusks, socio-ecological systems, stakeholders.

Studying socio-ecological systems (SES) in lakes is essential for effective mollusk conservation management. This approach underscores the interaction between ecological factors and human activities, fostering a comprehensive understanding of the lake ecosystem. It addresses issues, such as pollution and habitat degradation, which directly impact mollusk populations. Furthermore, SES highlights the significance of local communities and their knowledge, making their participation in the planning and implementation of conservation strategies crucial for achieving successful outcomes. However, research on the socio-ecological system (SES), such as lakes for mollusk conservation and management in the Philippines, is currently limited. To address this gap, the study employed a variety of methodologies, including biophysical malacofauna surveys across seven lakes in San Pablo City, Laguna, and DNA barcoding to identify invasive species and its possible geographic origin. Additionally, human dimension data was collected through key informant interviews from government offices and organizations that have jurisdiction over the seven lakes, household surveys in communities surrounding the lakes, and focus group discussions with stakeholders. We comprehensively assessed several physicochemical water parameters, including water temperature, pH, conductivity, total dissolved solids (TDS), salinity, dissolved oxygen (DO), and water transparency. Gastropods and bivalves were collected from 158 sampling points randomly distributed across various lakes. Our three-year survey recorded 36,449 freshwater mollusks, representing 16 species (14 gastropods and 2 bivalves) from 11 families, with Stenothyra sp. being the most abundant. Moreover, we identified three introduced species: *Pomacea canaliculata*, *Sinotaia quadrata*, and *Sinanodonta woodiana*. Canonical correspondence analysis demonstrated that pH, electrical conductivity, TDS, and salinity were dominant factors influencing species distribution. The generalized linear mixed model revealed that salinity is the most significant predictor for species richness, while conductivity is for abundance. Analysis of the genetic characteristics of *P. canaliculata* through phylogenetic and haplotype network analyses revealed its possible undocumented multiple introductions beyond the original 1980s introduction in the seven lakes of San Pablo. Aquaculture, intentional release, pet trade, interconnected pathways, flooding, and other natural disasters might have facilitated the multiple introductions. The analysis of the knowledge, attitudes, and practices of the stakeholders on mollusks revealed a strong fundamental understanding of the ecological and economic roles of mollusks in the lakes. The stakeholders expressed strong support for mollusk conservation and sustainable utilization. This includes practices such as eating invasive species such as *P. canaliculata*, *S. woodiana*, and *S. quadrata*, and regular lake clean-up drives initiated by the local government units, Fisheries and Aquatic Resources Management Councils, and local communities, organizations, and cooperatives. The socio - ecological information gathered in this study underscores the rich malacofaunal diversity of Philippine maar lakes, providing essential information that empowers policymakers and agencies to implement effective, evidence - based mollusk conservation and sustainable management strategies in lake ecosystems.

Funding Source: Research fund from Department of Science and Technology Grants-in-Aid (DOST-GIA) Program with the National Research Council of the Philippines (NRCP) as Monitoring Agency. Vittorio Tonolli Fellowship Award of the International Society of Limnology (SIL). Early Career Research Grant Award of the Malacological Society of London (MSL).

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Other themes

Oral - 360

BIOPRINTING OF BONE MODELS USING CALCIUM CARBONATE FROM VALVES OF *Crassostrea gigas*: DEVELOPMENT OF BIOINK FOR THE STUDY OF DIAGNOSTIC METHODS

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Keywords: diagnostic methods, bioprinting, bioprospecting, marine molluscs, tissue enginering.

This study aims to develop a bone-mimetic bioink incorporating calcium carbonate derived from mollusc shells, a byproduct of malacoculture. Utilizing this sustainable biomaterial, the proposed bioink seeks to fabricate three-dimensional structures for modeling bone tissue. These constructs are intended to replicate key microenvironmental features, supporting future diagnostic applications. The calcium carbonate will be acquired from *Crassostrea gigas* shells, following a sanitizing, calcinating and milling process. Characterization of the particles will be done using Thermogravimetric Analysis, Granulometry and X-Ray Diffraction. The bioink will incorporate different concentrations of calcium carbonate, 5% alginate sodium, 20% Pluronic P-123 and 2% nanosilica into a hydrogel matrix, compared to conventional bioinks nowadays used. The following parameters will be evaluated: rheological properties (viscosity, shear rate), cell viability and biocompatibility (using the Live/Dead and MTT assays with fibroblasts 3T3), the topography aspects of the incorporation will be analyzed using Scanning Electron Microscopy. The developed material is expected to present rheological properties compatible with bioprinting, such as fluidity and viscosity suitable for the process, in addition to post-printing hardening capacity that mimics the characteristics of trabecular bone tissue. In addition, the material should be biocompatible, not presenting cytotoxicity, in order to enable its application as a basis for the development of new diagnostic strategies. After the evaluation of the bioink's performance, a putative product could contribute to advances in Tissue Engineering, maximizing accuracy among Diagnostic Methodologies and the discovery of a new destination for Malacoculture waste, contributing to the protection of the environmental and human health and becoming a new income source for coastal communities. The integration of calcium carbonate from *Crassostrea gigas* shells into bioink formulations seems to be a promissory option for bone bioprinting applications. This approach not only supports technological advances in diagnostics and regenerative medicine but also promotes sustainable practices by repurposing malacoculture waste. The proposed bioink could represent an innovative, eco-friendly alternative with socioeconomic and environmental benefits.

Funding Source: No.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Education and Outreach

Oral - 64

FANTASTIC MOLLUSKS AND WHERE THEY LIVE: A PLAYFUL ACTIVITY ABOUT MALACOFAUNA OF COASTAL ECOSYSTEMS

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Keywords: zoology teaching, marine mollusks, malacology, science popularization, environment.

Mollusca is the second most diverse phylum, but in the Elementary School the teaching of mollusks is precarious, making it difficult for students to approach Malacology. Despite beauty of shells, they are animals that cause strangeness and disgust. Didactic resources collaborate to bring the phylum closer to the public (Silva & Campos 2021). The project "Malacology at School" disseminates information about mollusks in formal and non-formal teaching environments (Santos). During the Environment Week 2024 (June 3 - 7), we present the exhibition " Sea Mollusks" in schools on the Costa Verde region, to publicize the mollusks present on rocky shores, beaches and mangroves. We developed and applied a game to correlate the animals to its habitat; We used posters, representing these environments and icons of the common mollusks in each environment. The purpose was to make students correlate the icons of mollusks to the places where they live, based on their previous knowledge. An exhibition of various shells, common in the region, acted as stimulator of the activity. Afterwards, there was a discussion about each animal and its adaptive characteristics. We visited two municipal schools: C.M. Hermínia de Oliveira Mattos (Conceição do Jacareí, Mangaratiba, RJ) and E.M. Brigadeiro Nóbrega (Vila do Abraão, Ilha Grande, Angra dos Reis, RJ) and the Science Club "Nas Ondas da Ciência" (Praia de Dois Rios, Ilha Grande, Angra dos Reis, RJ) totaling 960 students from the Costa Verde/RJ region. Children and teenagers were interested and curious about the shells of marine mollusks, which they were able to handle. With the game, they showed their personal knowledge about the malacofauna of the region. Students from Elementary School I and Early Childhood Education recognized most of the animals presented, while students from Elementary School II, in addition to identifying, were able to easily associate the mollusks with their respective habitats. As they are residents of coastal regions, accustomed to having the sea as their backyard, they are very familiar with the beach, the mangrove swamp and the rocky shores, and, therefore, have close contact with the animals on display. Some students reported that their parents are fishermen and that they are used to seeing and eating some of these mollusks. The application of the game was a success, with the enthusiastic participation of the students. Similar results were observed in similar activities carried out during the National Science and Technology Week 2023 (Ferreira et al. 2024), corroborating the importance and success of this type of activity. We emphasize the importance of using playful activities to bring the school commnunity closer to the natural environment that surrounds them, valuing their previous knowledge and disseminating knowledge about mollusks. Exhibitions are activities that arouse interest and curiosity in different age groups, breaking barriers, through scientific dissemination, between scientific knowledge and the previous knowledge of the school community, helping to popularize Malacology.

Funding Source: CETREINA/UERJ; Secretaria de Educação, Juventude e Inovação de Angra dos Reis; Prociência UERJ/PR2.

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Education and Outreach

Oral - 217

MALACOLOGY AND CONCHOLOGY FOR EVERYONE: AN OUTREACH STRATEGY FOR MEXICO

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Keywords: science communication, videos, interdisciplinary, workshops for children, infographics.

Regarding communication of science, dissemination and outreach has always been present in Mexico, but only in recent years have scientists been encouraged -even required- to share their results beyond academic circles. While newspapers, radio, and television have historically played important roles for disseminating knowledge outside the educational system, it is the rising trend of virtual social networks that has accelerated this trend. A public call was made on March 31st, 2025, during the joint meeting of the Western Society of Malacologists and the Malacological Society of Mexico that was held in Sonora, Mexico, to invite anyone interested in producing communication and outreach materials on malacology and conchology. This year-long effort involves virtual and in-person sessions focused on collaborative content creation to share on different social media networks. As a result, an interdisciplinary group of 29 members from eleven different Mexican institutions - including graphic designers, aquaculture engineers, illustrators, biologists, marine biologists, journalists, communicators, visual artists and students- was formed to develop a communication strategy. The organization was carried out through emails, as well as synchronous and asynchronous video meetings, to define the target audience, type of products, timeline, production, publication, and the implementation of workshops. In the first stage, content topics were chosen based on a review of existing infographics on mollusks in Spanish available online. Then three underrepresented topics were selected for development based on gaps in existing materials and participants' experience. The results describe the outcome of the first quarter and outlines the first year plan, which focuses on the creation of 1) infographics, 2) short videos, and 3) workshops, along with metrics related to social media networks. One of the main obstacles to the initiative has been meeting the needs of participants, so much of the follow-up has been done virtually and asynchronously. The workshops created have been standardized using the initiative of several institutions and outreach groups under the name "Repositorio Nacional de Ciencia Recreativa" (National Repository of Recreational Science), whose purpose is to ensure that all activities submitted to the repository can be replicated free of charge by anyone once they are published. The interdisciplinary nature of this effort has allowed the exchange of skills and knowledge between people of different ages, academic backgrounds, and professions, resulting in more enriching and diverse outreach products. Furthermore, it has provided a space for sharing different perspectives on malacology and how to share information, regardless of the diverse generational backgrounds between the participants.

Funding Source: No.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Education and Outreach

Oral - 346

ARE SHELL SHAPES A GOOD RESOURCE FOR INTERDISCIPLINARY TEACHING?

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Keywords: outreach, shell morphology, mathematics, interdisciplinary teaching.

Shell morphology has long been fundamental to biological systematics, from early taxonomic classifications to modern geometric morphometrics. Today, as interdisciplinary education becomes crucial for 21st-century science, we investigate whether shell shapes - both recent and fossilized - can serve as effective teaching tools. By integrating biology with mathematics (biomatics), this study explores their potential to enhance student engagement, species identification skills, and understanding of mathematical concepts through real-world applications. The study involved 20 undergraduate students in Mathematics and Physics. Fossil (*Wilkingia terminalis*, *Oriocrassatela piauiensis*, *Aviculopinna* sp.) and dead (*Diplodon aethiops*, *Castalia martensi*, *Monocondylaea corrientesensis*, *Anodontites trapezeus*, *Corbicula fluminea*, *Fossula fossiculifera*) specimens from the Parnaíba Basin and Ibicuí basin were used to demonstrate quadratic functions, parabola construction, linear geometry, and statistical analysis. Disjointed bivalves illustrated angular measurements and planar geometry. A pre-workshop assessment revealed participants' limited prior knowledge of shell shapes. The workshop included paleontological concepts, hands-on activities using GeoGebra software, drawings of shell shapes, and interdisciplinary applications, followed by a post-workshop evaluation to measure effectiveness and student perceptions. The morphological analysis of the shells used in the study revealed a diversity of geometric patterns with high pedagogical potential for interdisciplinary teaching, promoting the integration of biology, mathematics, and systematics. Disarticulated shells, such as those of *Castalia martensi* and *Corbicula fluminea*, enabled the exploration of plane geometry concepts, including angles, symmetry axes, and linear measurements, while elliptical and ovoid contours observed in Fossula fossiculifera allowed for discussions on proportionality and applications of the ellipse equation. Bilateral symmetry and intraspecific morphological variations supported the introduction of statistical analyses such as mean, standard deviation, and scatter plots, making these geometric patterns both visually accessible and mathematically quantifiable. Before the workshop, 90% of participants reported limited knowledge of shell shapes and species identification; post-intervention, 85% found the strategy effective in stimulating curiosity and critical thinking, and 63% rated the interdisciplinary approach highly (9 out of 10). Shell morphology effectively connected biological structures to mathematical and systematic principles, demonstrating the potential of paleontological resources in exact science education. Students reported increased engagement and autonomy in the learning process, indicating that such methods foster scientific literacy and help prepare future professionals for collaborative problem-solving, as emphasised in the literature on interdisciplinary pedagogy. Community participation, though limited to students, indicated a positive shift in perception toward shell shape-based learning. The study confirmed that shell shapes are a valuable interdisciplinary teaching resource, effectively bridging biology, mathematics, and correlated concepts. Objectives were achieved, with participants recognising the method's efficacy in enhancing scientific literacy. This approach supports the integration of palaeontology and malacology into exact science education, fostering a holistic and inquiry-based learning environment.

Funding Source: No.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Education and Outreach

Oral - 358

DIDACTIC SEQUENCE TO RECOGNIZE AND DIFFERENTIATE THE TERRESTRIAL SNAILS *Megalobulimus* spp AND *Lissachatina fulica*

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Keywords: teaching-learning, non-formal teaching, Science Club.

Megalobulimus spp. or aruá-do-mato, a native gastropod with endemic species of the Atlantic Forest, is threatened with extinction due to environmental degradation and by confusion with the invasive *Lissachatina fulica*. Due to the importance of preserving native species, it is essential to develop activities teaching how to recognize and differentiate these animals. We proposed a didactic sequence to classes in Elementary School 2, according to the moments proposed by Zabala. The didactic sequence was developed at the Science Club of Telêmaco Gonçalves Maia Municipal School (CTGM), in four meetings of 2 to 3 hours with the following moments: presentation of the theme, survey of previous knowledge, conversation circle with video presentation on a recent case of angiostrongylosis in Rio de Janeiro, practical activities of mollusk recognition (handling and drawing shells, observation of live animals), bibliographic search to deepen knowledge, production of didactic booklet, evaluation. For the practice, materials such as shells of both species, with varying colors and sizes, demonstration boxes with other genera of the Atlantic Forest such as Thaumastus and Orthalicus, as well as posters, were used. Thirteen students from CTGM participated in the activity. The previous survey showed that the students had never had contact with the shells, and that they believed that terrestrial gastropods were poisonous. During the conversation circles, the most debated topic was about the differences between the two gastropods and the impacts of the exotic. After the practical activity, the students were able to recognize the main differences between the shells of the native and exotic snails through contact and analysis of the structures, and subsequent illustration. Of these, four students recognized that the native snail is more bulging and has a rounded apex, in relation to the exotic, with a more elongated shell and pointed apex; two students clearly pointed out the highest number of whorls of the exotic; Three students, in addition to the shape of the shell, were able to identify the thickened opening edge of the native snail, absent in the African. At the end of the activity, the drawings were debated, and doubts were clarified. In the next moment, the students carried out a bibliographic search on the internet about the snails studied, noticing a greater availability of data on the African snail. In the end, the club members were divided into three groups to build an informative booklet, based on the observations and research carried out. The evaluation was carried out through a questionnaire in which all students answered more than half of the questions correctly. The proposed didactic sequence was able to motivate the students to learn, allowing them to quickly identify the shells of the native and exotic snails. The activity allowed the students to play a leading role in seeking knowledge and building pedagogical material. In addition, it allowed a real awareness of the subject, as several students began to recognize the presence of the exotic snails near the school and their homes.

Funding Source: CETREINA/UERJ scholarship to AEP.

Citizen Science and Mollusks: Bridging Communities and Research / Diversity, Equity, and Inclusion in Malacology

Other themes

Oral - 380

PARTICIPATION OF WOMEN LEADERSHIP POSITIONS IN MALACOLOGICAL SCIENTIFIC SOCIETIES

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Keywords: mollusks, equity, gender, scientific society.

Scientific societies (SS) bring together researchers, through the organization and support of events, awards, as well as financial support to members. Thus, SS are essential institutions for consolidating science fields (WITTER, 2007). However, despite its relevant role, until recently, SS have excluded women from their membership. This work aims to present the participation of women in malacological scientific societies settled in Brazil and in other countries (LEAL, 2023). The work is characterized as quantitative research and utilizes official documentation and information extracted from various sources to collect data on the occupation of different positions within malacological societies. The identification of malacological SS distributed worldwide was carried out through searches on official SS websites, websites of malacological groups, and freely accessible databases. Data on the SS members occupying leadership positions within these societies were organized and analyzed using Excel program. Based on a binary classification, each name identified was manually assigned as either man or woman. We found 1,203 names occupying different positions across the 36 surveyed malacological SS. Of these, 9 SS do not provide information on the occupants of their positions, 10 SS present complete data on positions (from their founding on to the present), and 17 only have data on the current mandate or a single period. In the most prestigious and leadership positions, we found 62 women among the 525 presidents (11.8%) and 16 women among the 53 vice-presidents (30.2%). In the second echelon, there were 46 women in 122 secretaries (37.7%) and 35 in 85 treasurers (41.2%). Looking in detail the societies, we found a different profile for the Brazilian society, where there were 14 women among 27 presidents (51.9%). The results show that women are a minority in the different positions within these scientific societies, and as the positions become more prestigious, the proportion of women decreases. We also observe a gradual increase in female participation in malacological SS over the decades, especially from the 70s onwards, although female representation remains lower than that of males. Nevertheless, this trend seems to be changing, with more women occupying leadership positions, such as presidencies. The present analysis reinforces the relevance of gender studies in science, as they allow us to identify and evaluate the persistence of hierarchical segregation in scientific environments and, thus, seek actions to reverse this general scenario in which women are still minority. For societies, such actions may include the elaboration of internal rules that guarantee equity in the occupation of positions, especially those command and prestige.

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SYMPOSIUM: MOLLUSCAN MACROECOLOGY AND BIOGEOGRAPHY

MOLLUSCAN MACROECOLOGY AND BIOGEOGRAPHY

Coordinator:

CARMEL MCDOUGALL – University of St Andrews

We will explore biogeographical patterns of mollusks across diverse habitats, addressing ecosystem roles to foster discussions on the implications of macroecological research in conservation strategies, climate change, and biodiversity management. This symposium will seek to illustrate both historical and contemporary perspectives.

Molluscan Macroecology and Biogeography

Invasive Alien Species

Oral - 212

SPECIES CONFIRMATION AND DISTRIBUTION OF NON-NATIVE MYSTERY SNAILS *Cipangopaludina japonica* AND *C. chinensis* WITHIN NORTH AMERICA

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Keywords: *Cipangopaludina japonica/chinensis*, invasion, North America, parasitism.

Japanese (*Cipangopaludina japonica*) and Chinese (*C. chinensis*) mystery snails were intentionally transported to North America in the early 1900s. They are now found throughout North America with *C. chinensis* being the most widely reported of the two species. The two appear morphologically identical. While genetic sequencing is a more reliable method of identification, it has yet to be widely used in the invasive range. Since 2021, mystery snails have been collected from 37 sites representing 14 US States and three Canadian and two Korean Provinces. Each snail was measured for length, dissected (and the number of brooded juveniles counted), and screened for parasites. DNA was extracted from foot tissue, the COI mitochondrial segment amplified, and then sequenced. Resulting sequences were compared to available sequences from genetic databases and a phylogenetic tree was created to confirm species and explore population structure. Differences in brood number between species and the impact of parasitism on brood number were explored using linear modeling. Of the 14 sampled US States, seven were confirmed *C. japonica* (VA, WV, MD, NC, PA, NY, and ME) and seven were *C. chinensis* (AL, NJ, MA, RI, CT, MN, and OH). All sampled Canadian (Ontario, Quebec, and Nova Scotia) and Korean sites (Gyeongsang and Incheon) were also *C. chinensis*. So far, *C. japonica* has been confirmed in a wider range than previously recorded (ME), and *C. chinensis* has been absent in some extensively sampled regions where they have been reported in the past (VA and MD). This suggests that misidentification has historically been a problem. Uncertainty in species identity and inaccurate reporting can confuse ecological and biological differences between the two species, as studies conducted on one species may have been of the other. Both species have a positive exponential relationship with shell length and brood size. Sampled *C. japonica* were larger in both mean and maximum length (49-82mm) in comparison to sampled *C. chinensis* (40-61mm) and had a higher abundance of brooding juveniles (median 42 vs 12, respectively). *Cipangopaludina japonica* were parasitized by up to 80% by the trematode Aspidogaster conchicola at two river sites in Virginia. Infected snails had a significantly lower number of brooding juveniles, suggesting an impact on fecundity due to infection. This project has provided clarity of the distribution of mystery snails in North America; sampling will continue through fall 2025. Going forward, individual shell mapping will be linked to genetic identification to address potential identifying characteristics for each species that could improve reporting without the need for genetics. Additional analyses of the population genetics will be used to explore patterns of historic spread and identify potential vectors.

Funding Source: Ann C. Powel memorial grant - George Mason University. American Museum of Natural History. American Malacological Society. Helminthological Society of Washington.

Molluscan Macroecology and Biogeography

Evolution

Oral - 3

BIOGEOGRAPHY OF INDIAN NON-MARINE MOLLUSCS

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Keywords: Into India, Gondwanan, Deccan volcanism, endemic radiation, conservation.

India's rich biodiversity is a result of its complex geological and climatic history, including plate tectonics and the Deccan volcanic events. In recent decades, numerous studies have investigated the influence of plate tectonics and climatic changes on the biogeographic patterns of dispersal and vicariance influencing the subcontinent's biota. However, research on invertebrates remains relatively limited. Invertebrates, with their distinct physiological tolerances, ecological behaviours, and dispersal mechanisms, provide unique insights into biogeographic histories compared to vertebrates. Our team has concentrated on understanding how the subcontinent's geological and climatic history has shaped the biogeography of various non-marine mollusc families. For the present study, the samples of *Filopaludina*, *Cipangopaludina* and *Angulyagra* (Viviparidae), *Indoplanorbis* (Bulinidae), *Brotia* and *Paracrostoma* (Pachychilidae), *Cremnoconchus* (Littorinidae), *Vitta* (Neritidae), *Paludomus* (Paludomidae), and *Cyclophorus* (Cyclophoridae) were collected across their entire distribution range in India. The genomic DNA was extracted using the modified CTAB method as per Chakraborty et al. (2020). Multiple mitochondrial (COI, 16S, 12S) and nuclear (18S, 28S and H3) markers were amplified. Thereafter, phylogenetic trees were constructed using Maximum Likelihood and Bayesian approaches for the concatenated dataset after cleaning the dataset. JModeltest was used to ascertain the appropriate substitution model. Molecular dating analysis was performed using appropriate fossils for each family listed above and biogeographic analysis was performed using the BioGeoBEARS package in R. For freshwater bivalves the data was procured from Bolotov et al. (2022). For the first time, we have compiled a biogeographic and timing of the evolution of Indian non-marine molluscs using molecular data. Four distinct biogeographic patterns were observed, which are listed below. a) Into India dispersal from Africa and SE Asia: Dispersal from Africa was seen in three genera, i.e *Pila*, *Indoplanorbis* and *Paludomus*. For *Pila*, dispersal from Africa occurred during the Eocene (50.3–36.1mya), and two back dispersal events from SE Asia to India during the Eocene Early Oligocene (42.6–27.0 mya and 42.4–25.2 mya). For Indoplanorbis the said dispersal took place during Oligocene (~35 mya)(5). *Paludomus* dispersed into India around 78 mya. Dispersal from SE Asia was seen in Viviparids, Brotia, *Paracrostoma*, and *Cyclophorus*. Two independent dispersal in Viviparids occurred during Eocene to Miocene (~50—25 mya) and Late Miocene (~7 mya). Similarly, *Brotia* showed two independent dispersal events into India, one during early Eocene and one during Oligocene while *Paracostoma* dispersed around 90 mya. Whereas *Cyclophorus* dispersed during the late Miocene period (between 6 and 10 mya) when the Indian monsoon started strengthening and seasonality set in. The into-India dispersal either from Africa or from Southeast Asia occurred after India docked to the Eurasian plate around 55 mya, when land bridges were formed on both the eastern and western sides. b) Out of India: Out of India to SE Asia was reported from Pila and Indoplanorbids. Members of these two genera, after it colonised India from Africa, dispersed out to SE Asia around 45.0–29.3 and 27.4–8.1 mya, respectively. Similarly, Viviparids also dispersed out of India to Africa after colonisation from SE Asia around 24–19 mya. c) Marine to freshwater: Marine to freshwater colonisation was observed in *Cremnoconchus*, which occurred during the 96 mya split between marine and freshwater, and around 56 mya, the North and Central Western Ghats. The Neritids, another group with marine relatives, distributed in the freshwater habitats in India, dispersed from a marine ancestor at around 50 mya. The colonisation of freshwater habitats might have occurred due to a gradual reduction in sea level during the early Eocene (Saha et al. 2022). d) Gondwanan origin: Among all non-marine molluscs, subfamily Parreysiinae from the Unionidae family likely originated in East Gondwana during the Jurassic period, and their representatives

arrived in Asia on two Gondwanan fragments viz., Indian Plate and Burma Terrane (Bolotov et al. 2022). Our research, combined with published information, indicates that non-marine molluscs of India exhibit four distinct biogeographic patterns: Into-India, Out-of-India, Marine-to-Freshwater, and Gondwanan. Similar to Indian tetrapods, most non-marine mollusc families originated outside India and colonised the region via terrestrial connections during periods of humid climate. Additionally, there have been two instances of marine-to-freshwater colonisation and one case of Gondwanan origin. India experienced significant geological upheavals, including volcanic activity and aridification, and these events likely had profound impacts on the region's flora and fauna, leading to a limited representation of Gondwanan elements compared to more recently colonised groups.

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Molluscan Macroecology and Biogeography

Ecology

Oral - 34

SMALL IN SIZE, BIG IN NUMBERS: CRYPTIC MOTILE MOLLUSKS IN AUTONOMOUS REEF MONITORING STRUCTURES OF SÃO PAULO COASTAL ISLANDS, BRAZIL

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Keywords: cryptic diversity, ARMS, marine ecology, benthic ecology.

Cryptic diversity in marine ecosystems remains understudied due to sampling challenges and lack of specialists. When it comes to small invertebrates; they are harder to collect and often present complex taxonomy. Autonomous Reef Monitoring Structures (ARMS) were conceived to enable researchers to study cryptic communities. This study aims to present a survey of cryptic mollusks collected from ARMS deployed in coastal islands of São Paulo, Brazil. ARMS were installed at four sites: two in the Alcatrazes archipelago, 34 km away from the mainland, and two in Cabras and Palmas isles, 6 km from the city of Ubatuba off the northern coast of São Paulo, in 2020. Approximately two years later, they were retrieved and processed. Fauna larger than 2 mm was retained using a mesh sieve by filtering seawater collected with the structures and preserved for subsequent identification. Only motile organisms were considered for this analysis, with richness and abundance compared across collected phyla. Among all taxa collected from the motile fraction of these ARMS, mollusks represented the second most abundant phylum, surpassed only by arthropods. Ubatuba stood out with 448 individuals (32%) out of 1,389 compared to 163 (33%) out of 493 from Alcatrazes. Gastropods were considerably more abundant than chitons and bivalves, representing over 80% of all motile mollusk fauna in both locations. In terms of richness, 13 taxa were recorded, of which nine were identified at the species level, and the other four were assigned to the genus due to taxonomic challenges. Five were common to both regions and each location had four exclusive organisms: *Bostrycapulus aculeatus* (Gmelin, 1791), *Lima caribaea* (A. d'Orbigny, 1853), *Leucozonia* sp. 1 (J. E. Gray, 1847) and *Vexillum* sp. (Röding, 1798) in Alcatrazes; and *Costoanachis sparsa* (Reeve, 1859), *Leucozonia ocellata* (Gmelin, 1791), *Calliostoma tupinamba* (Dornellas, 2012) and *Corambe* sp. (Bergh, 1869) in Ubatuba. Results indicate a proportional abundance of mollusks in both locations, but environmental variables and distance from the coast may play a significant role in shaping diversity. Differences in biomass were notable, with Ubatuba sites being significantly closer to the coast and subject to more significant continental discharges. Variations in richness also highlight the unique composition of each location despite their relative proximity. The ARMS facilitated the collection of organisms and showcased the significant role mollusks may play in rocky reefs' cryptic environment, given their high abundance. Standardized protocols are crucial for accessing and assessing neglected fauna, including many invertebrates. These methods also contribute to a more globalized and collaborative scientific process.

Funding Source: Coodenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

Molluscan Macroecology and Biogeography

Ecology

Oral - 48

HIDE AND SEEK: THE DIVERSITY OF CRYPTIC MOLLUSK COMMUNITIES ASSOCIATED WITH THE EPILITHIC ALGAL MATRIX (EAM) IN THE BRAZILIAN PROVINCE

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Keywords: cryptic diversity, turf algae, marine ecology, oceanic islands.

The epilithic algal matrix (EAM) is a complex assemblage of algae, detritus and microorganisms that dominates the benthic cover in tropical and subtropical reefs. Owing to the shelter and resources it provides, the EAM hosts a diverse cryptic fauna, including numerous mollusk species. Despite its widespread occurrence and ecological importance, both the EAM and its associated fauna have remained largely understudied, with limited knowledge of their taxonomic composition and ecology. This study aimed to survey the diversity of mollusks associated with the EAM across multiple locations within the Brazilian Province, encompassing a coastal subtropical reef (Arraial do Cabo, n = 30), a midshore tropical reef (Abrolhos, n = 20), and two tropical oceanic islands (Fernando de Noronha and Trindade Island, n = 10 each). At each site, mollusks were counted, and EAM characteristics were measured, including wet weight of algae and trapped sediment particles. Samples were collected from shallow reefs (3–10 m). To account for differences in sampling effort, data were standardized prior to analysis. A total of 921 individuals were recorded, representing 80 species: 65 gastropods, 12 bivalves, and 3 chitons. The most abundant families were Barleiidae (N = 384), Rissoidae (108), Caecidae (93), Cerithiidae (73) and Cystiscidae (50). Barleiidae dominated the communities at Abrolhos (~30%) and Fernando de Noronha (~76%), whereas at Arraial do Cabo, three families (Caecidae, Cerithiidae and Rissoidae) together accounted for ~60% of the total abundance. Trindade Island was the only site where a bivalve family (Mytilidae; Brachidontes sp.) was the main contributor (~30%). Although multiple species were recorded, only three accounted for approximately 50% of the total abundance, whereas over half of the remaining species were singletons or doubletons. The most abundant species was Barleeia creutzbergi (N = 377), which occurred at three of the four sites and dominated the communities of Fernando de Noronha (N = 359), contributing substantially to inter-site dissimilarity. Community composition differed significantly among sites, with Arraial do Cabo being the most distinct due to the high abundance of *Alvania auberiana*, *Bittiolum varium* and *Caecum brasilicum*. This site also exhibited the highest richness, averaging ~11 species per 100 cm² of EAM, followed by Abrolhos and Fernando de Noronha (~5 species), and Trindade Island (~2 species). At Arraial do Cabo, even with 30 samples, the rarefaction curve did not stabilize, underscoring the presence of many rare species. When analyzed at the phylum level, depth was the dominant driver, but species-level GLMs revealed a richer interplay, emphasizing the importance of taxonomic resolution. Our findings reveal that even within a few square centimeters of EAM lies a remarkably diverse mollusk community. Depth emerged as the dominant driver at the phylum level, but species-level models revealed additional influences of algae and particles. These results underscore the EAM's value as a reservoir of cryptic biodiversity and emphasize the importance of taxonomic resolution for understanding ecological patterns in reef ecosystems.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

Molluscan Macroecology and Biogeography

Ecology

Oral - 130

HOW FEEDING ECOLOGY AND PHYSIOLOGY CONTRIBUTE TO NICHE DIFFERENCES AMONG SYMPATRIC TROPICAL *Chiton*

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Keywords: Polyplacophora, stable isotopes, respirometry, thermal performance.

A longstanding goal in evolutionary ecology is understanding how species diversity is maintained, especially among closely related sympatric species. One approach to addressing this question is identifying how sympatric species partition available resources and occupy distinct ecological niches (i.e., roles in an ecosystem). Here, we investigated how niche differences in feeding ecology and physiology may help maintain species diversity among Central American *Chiton*. To learn how differences in diet may contribute to niche partitioning in *Chiton*, we quantified stable isotope ratios (of δ13C and δ15N) from chiton tissues and environmental epibenthic samples (i.e., potential food sources). Afterwards, we estimated and compared isotopic niche space among species. To see how physiological tolerances contribute to niche differences in *Chiton*, we estimated (1) aquatic metabolic rates as oxygen consumption in seawater at ambient temperatures (~23-29°C); and (2) aquatic thermal tolerances as the change in heart rate with increasing seawater temperature (25-41°C). We compared physiological responses of chitons across conditions via ANOVA followed by post-hoc Tukey tests. First, we found that three out of four sympatric species overlapped in isotopic niche space, suggesting that some, but not all, *Chiton* have similar dietary habits and occupy similar trophic positions (with results pointing towards a mainly herbivorous diet). However, it is important to consider that species might still partition their food sources based on spatial/seasonal availability or competitive impacts of other grazers. Second, we found that aquatic metabolic rates were associated with the vertical zonation of species, with high and mid-intertidal chitons tending to have lower aquatic respiration rates than low intertidal and subtidal chitons. This has been proposed as a compensatory mechanism to deal with the increased stresses of temperature variation, desiccation, and feeding opportunities in high and mid-intertidal microhabitats. Thus, lower aquatic oxygen consumption rates in high and mid-intertidal species may be indicative of an overall less active lifestyle. Third, we found that aquatic thermal tolerances were not significantly different among chiton species. Seawater temperatures are relatively stable and similar across the microhabitats these species inhabit, and considering they are rarely exposed to seawater temperatures exceeding 32°C, thermal tolerances above this threshold appear to reflect the general response of tropical chitons to thermal stress rather than adaptations to their distinct microhabitats. This study demonstrates how niche differences among ecologically similar, closely related species may help maintain species diversity. Further analyses of dietary habits and radular morphology are in progress to better ascertain how *Chiton* feeding ecologies are partitioned. Moreover, physiological experiments in air will allow for a better understanding of how metabolic rate and thermal tolerance contribute to niche partitioning among *Chiton*.

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Molluscan Macroecology and Biogeography

Ecology

Oral - 201

PREVIOUSLY UNDOCUMENTED TROPICAL OYSTER REEFS OF NORTHERN AUSTRALIA: STRUCTURE, FUNCTION, AND A NEWLY IDENTIFIED REEF-BUILDER

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Keywords: biodiversity, tropics, functional ecology.

Oyster reefs have collapsed around the globe due to overexploitation and other human activities. Surprisingly, we recently found seemingly healthy oyster reefs in tropical north-eastern Australia. Here we report the investigation of these reefs to provide baseline ecological data, determine which oyster species is (or are) responsible for their construction, and to explore whether the invertebrate communities they host are correlated with their physical attributes. Three intertidal oyster reefs in tropical Queensland were surveyed using aerial drone imagery and quadrat sampling to characterise reef structure and associated invertebrate communities. Reef area and percent cover were measured using ImageJ, and structural features such as reef height, reef shape, and substrate type were assessed. Oyster density was calculated, and oyster species were genetically identified using COI and 16S barcoding. Invertebrate communities were sampled from reef clumps, sieved into two size classes, identified to Class, and assigned to functional groups. Statistical analyses included NMDS and Bayesian hierarchical multivariate GLMs to explore invertebrate composition and associations with reef characteristics. Genetic analysis confirmed *Saccostrea* 'lineage B' as the dominant reef-building species across all reefs despite clear phenotypic plasticity between sites. This species has not previously been documented as 'reef-building'. Additional *Saccostrea* lineages and other reef-forming bivalves were also present at some reefs. Reef structures varied, ranging from dense continuous reefs on rocky substrate to larger, sparse patch reefs on shelly sediment, and mixed-type reefs with variable density and substrate. Invertebrate communities differed most strongly by location and substrate type, with larger invertebrates more commonly associated with lower intertidal zones and shelly sediments. Distinct community patterns were found between tidal zones at some sites, however location explained the greatest variation in invertebrate composition. Our results indicate that high oyster densities on rocky substrates may limit habitat complexity, reducing invertebrate abundance and size. Our study provides important insight into the ecology of tropical oyster reefs by investigating how reef characteristics influence invertebrate assemblages across multiple locations. We also find that *Saccostrea* 'lineage B' is likely to be a species of importance for future oyster reef research and restoration in the Indo-Pacific, and identify several important factors for consideration in intertidal oyster reef restorations in the tropics.

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Molluscan Macroecology and Biogeography

Anatomy and Physiology

Oral - 388

COMPARATIVE ACCLIMATION CAPACITY: LINKING THERMAL TOLERANCE WITH BIOGEOGRAPHY IN ANTARCTIC AND SUB-ANTARCTIC PERINWINKLES (*Laevilitorina* spp.)

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Keywords: ecophysiology, gastropods, climate change.

The Antarctic Circumpolar Current has acted as a barrier to species dispersal at southern higher latitudes since its formation ~34 Mya. However, keystone macroalgae like *Durvillaea antarctica* and *nonindigenous* species (e.g. mussels, decapods) have been known to cross this biogeographic barrier, likely aided by human activities and climate change. This challenges the notion of Antarctica ´s biological isolation and raises questions about invasion feasibility, consequences, and the role of global environmental change in facilitating such processes. This study aimed to evaluate the physiological constraints and potential to occupy and resist a warmer environment, as predicted by global climate change. We collected adult specimens of 3 periwinkle species: *Laevilitorina pepita*, a recently-described species with a restricted distribution in the Magellan Strait (sub-Antarctic region), *L. antarctica*, endemic to Antarctica, and *L. venusta*, broadly-distributed across Antarctica and sub-Antarctic islands. We performed long-term acclimation experiments using different temperatures: -1.5, 5, 11°C (*L. pepita*) and -1.5, 0, 2, 5,8, 11°C, (*L. venusta* and *L. antarctica*). Daily mortality was recorded over a period of 120 (*L. venusta*) and 60 (*L. pepita*) days. No statistically significant differences were found between treatments in *Laevilitorina pepita*. However, the overall trend suggests that survival at 11°C would be low for this species, in contrast to expectations based on its distribution. Interestingly, *L. pepita* is only found at this specific location and not at higher or lower latitudes (where temperatures are equal or higher). In the case of *L. venusta*, no statistically significant differences were found between treatments at -1.5, 0, 2, 5, and 8°C. However, significant differences were observed between the 11°C treatment and the other experimental temperatures, with a median survival of only 20 days. Results for *L. antarctica* are still pending as the study is ongoing. These findings suggest that, as expected based on their current distribution, *L. venusta* may exhibit abroader thermal tolerance compared to the endemic Antarctic species and the exclusively sub-Antarctic species. This could partially explain its wide distribution and higher thermal tolerance than the average summer temperature in Antarctica, where the specimens were collected. Both *L. venusta* and *L. pepita* are particularly sensitive to 11°C. However, the results for *L. pepita* raise questions about its ability to acclimate to temperatures slightly above the annual average (8°C) in the intertidal zone in the Strait of Magellan or to tolerate stressful events, such as heatwaves. Further analyses are needed to explore this matter. We found a high interspecific variability in thermal tolerance within this clade that does not necessarily reflect the thermal breadth across each species' geographic range, likely as a result of phylogenetic history. These results expand our knowledge about the physiological limits in high latitude mollusks, a field that has been relatively underexplored despite their ecological role and importance.

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SYMPOSIUM: INVASIVE GASTROPODS AS AGRICULTURAL PESTS / INVASIVE ALIEN SPECIES

INVASIVE GASTROPODS AS AGRICULTURAL PESTS / INVASIVE ALIEN SPECIES

Coordinator:

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Class Gastropoda, which includes snails and slugs, is a highly diverse group of animals that play important ecological roles, however many of these species are also considered significant agricultural pests. They cause substantial damage to crops in agriculture, horticulture, and forestry, often feeding on a variety of plants and compromising yield. Many gastropod species are classified as invasive, having been introduced to new regions through trade and commerce, where they disrupt local ecosystems and habitats. Recent efforts by malacologists have focused on identifying pest gastropod species, determining their distribution and abundance, and assessing the extent of the damage they inflict on crops. This research is critical for understanding the economic impact of these pests on agriculture. Future studies are expected to further evaluate the degree of crop damage caused by these mollusks, as well as their broader economic effects, helping to inform management strategies and mitigation measures to protect crops and prevent further spread of invasive species.

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Genetics / Genomics

Oral - 165

TRACKING THE ORIGINS AND SPREAD OF PEST SNAIL INVASIONS: AN AUSTRALIAN STUDY

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Keywords: *Cernuella virgata*, *Cochlicella barbara*, phylogeography, genetic diversity.

Invasive Mediterranean snails cause losses exceeding $100 million annually to the Australian grains industry through crop damage, grain contamination and management costs. *Cernuella virgata* and *Cochlicella barbara* have passively spread throughout agricultural regions of southern Australia, with limited information known of their genetic background and geographic invasion origins. Here, we aimed to investigate the genetic diversity, species composition, and global origins, of Mediterranean snails in Australia using a phylogenomic framework. *Cernuella virgata* and *C. barbara* populations were collected throughout their Australian, native Mediterranean/Western European and other invaded ranges (e.g. New Zealand) in locations where genetic data is presently lacking. DNA sequencing was undertaken at two mitochondrial loci (CO1, 16S), and a nuclear region consisting of three loci (5.8S-ITS2-28S) using Sanger and nanopore sequencing. As of April 2025, 38 *C. virgata* and 15 *C. barbara* Australian populations have been sequenced, with further sequencing to occur. Intraspecific phylogeographic relationships were established based on study generated and public database sequences, using Bayesian and Maximum likelihood analyses. Genetic data revealed new lineages and potential species origins or shared pathways for spread. For *C. virgata*, two genetically divergent Australian mtDNA lineages were observed (COI 10%). Each lineage revealed a widely distributed dominant haplotype from populations across southern Australia. Other haplotypes were locally distributed and displayed low divergence from the dominant haplotypes. From comparison with public database sequences, exact CO1 mtDNA matches for Australian haplotypes were found with individuals from Turkey and the United States, while low divergence was found with individuals from Balkan countries and Iran. For one lineage no closely related individuals from Mediterranean or Western European countries makes it difficult to determine putative origins. For *C. barbara*, haplotype diversity within Australia was high. A single dominant haplotype was observed to be widespread across southern Australia, while others revealed regional distributions. A population from Western Australia contained individuals with approximately 16% sequence divergence from individuals within the same population and from other Australian populations, suggesting the possibility of a cryptic species. Matching CO1 mtDNA sequences found among populations from both south-east Australia and South Africa suggest a likely introduction pathway. Further, low genetic diversity among some Australian/South African, French and Spanish individuals, indicates possible origins. Further work is required to determine putative origins of this species in Australia. Analysing genetic data from two Mediterranean snail species has given insight into possible introduction origins. While availability of source region data has limited our ability to determine origins of *C. virgata* and *C. barbara*, future work will target key locations. A better understanding of the genetic background of the pest snail complex in Australia will inform spread pathways and management of these species in Australian agriculture.

Funding Source: South Australian Grain Industry Trust (SAGIT).

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 38

EXAMINATION OF DISTRIBUTION OF TERRESTRIAL GASTROPODS IN THE DELTA REGION AND ITS IMPLICATIONS FOR FOOD SECURITY WITHIN EGYPT

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Keywords: distribution, terrestrial, gastropods, Egypt.

Egypt's fertile Delta, crucial for food security, is increasingly threatened by terrestrial gastropods. A comprehensive survey highlighted a widespread invasion of numerous species, driven by climate change and weak quarantine. This inventory documents gastropod diversity and the alarming expansion of invasive species in key crop fields, directly threatening agricultural productivity and food security. The study significantly advances understanding of this growing challenge to the region. The study's methodology involved systematic sampling during the active season for land snails and slugs, complemented by year-round field observations. These observations indicated the persistent presence of gastropods in Delta agricultural fields, even under harsh summer conditions. Live specimens were accurately collected from diverse sites and studied in detailed morphological examination and identification. Each species was illustrated and described, establishing a strong taxonomic basis. Precise geographical data was recorded, culminating in a comprehensive distribution report invasive gastropods across the Egyptian Delta Region. Additionally, the research aimed to correlate the presence and abundance of specific gastropod species with observed economic damage to various crops in the region. The detailed illustrations and descriptions of the collected snail and slug species, linked with the comprehensive distribution maps generated, provide a valuable resource for future research and identification efforts within Egypt. The study's findings obviously establish a clear and concerning link between the presence and proliferation of terrestrial gastropods, particularly the invasive species, and significant economic losses in crop production within the Delta region. The number of the terrestrial gastropod species had been collected: 10 land snail species, 5 land slugs, 4 land slug species still under study. The identified species were *Eobania vermiculata*, *Monacha obstructa*, *Cochlicella acuta*, *Theba pisana*, *Oxyloma elegans*, *Opeas pyrgula*, *Oxychilus* cf. *cellarius*, *Polygyra cereolus*, *Allopeas gracile* and *Zonitoides arboreus*, for the land slugs *Limacus flavus*, *Deroceras laeve*, *Ambigolimax valentianus*, *Laevicaulis alte* and *Laevicaulis stuhlmanni*. The land slugs that are under study are 2 species belonging to the Veronicellidae family and the second two species belong to the Parmacellidae family. The observed damage ranged from direct consumption of plant tissues, leading to reduced yields and compromised quality, to the fouling of produce, rendering it unmarketable. The widespread establishment of invasive species, often lacking natural predators and well-adapted to the local environmental conditions, exacerbates this problem. The influence of climatic shifts likely contributes to the establishment and spread of these non-native species by creating more favorable conditions or weakening the resilience of native ecosystems. Similarly, breaches in agricultural quarantine regulations have inadvertently facilitated the introduction and dispersal of these harmfulorganisms through the movement of agricultural products and materials. The persistent presence of these gastropods throughout the year, even during unfavorable climatic conditions, underscores their adaptability and the continuous threat they pose to agricultural productivity. The economic implications of these crop losses extend beyond individual farmers, potentially impacting national food supply chains and the overall economy of Egypt. Therefore, the findings of this study underscore the critical and urgent need for the development and implementation of targeted and effective management strategies aimed at minimizing the detrimental impact of terrestrial gastropods on agriculture in the Delta region. This comprehensive gastropod inventory in Egypt's Delta establishes a crucial baseline, revealing an escalating threat from invasive species to agricultural productivity and food security. Detailed distribution data and links to economic damage highlight the urgent need for collaborative management

strategies. Climate change and quarantine failures have fueled this invasion, demanding immediate, proactive intervention and further research into effective control measures to protect this vital agricultural region.

Funding Source: No.

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 176

ENHANCING BIOLOGICAL CONTROL OF INVASIVE CONICAL SNAILS IN AUSTRALIAN AGRICULTURE

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Keywords: parasitoid fly, biological control, *Sarcophaga villenueveanna*, revegetation.

The introduction of the parasitoid fly Sarcophaga villeneuveana is one component of an IPM strategy in Australia's battle against invasive conical snails. Originally sourced from France, this host-specific biocontrol agent was first released in South Australia 25 years ago to suppress *Cochlicella acuta* and *C. barbara*. The program has now expanded to new regions with an aim to protect grain crops and reduce economic losses through sustainable, targeted pest management. The impact of S. villeneuveana was assessed 20 years after release over two years across South Australia's Yorke Peninsula. Surveys were conducted at 19 sites, collecting >88,000 conical snails (*Cochlicella acuta* and *C. barbara*). Sampling involved four 25-meter transects with 2-meter-wide timed visual searches in exposed (elevated substrates) and cryptic (ground/plant refuges) habitats. Collected snails were dissected to identify fly larvae/pupae within shells and quantify parasitism rates. Recent biocontrol programs have focused on assessing fly nutrition uptake targets on survival and fecundity, the impact of revegetation on fly parasitism rates, and establishing the fly to new regions of South Australia and Western Australia. The effectiveness of S. villeneuveana as a biocontrol agent in South Australia varies considerably depending on habitat conditions and environmental factors. In areas with suitable habitat near flowering vegetation, parasitism levels can reach 30-50% on snails larger than 5mm. However, parasitism rates drop dramatically in areas lacking native vegetation, often falling below 3% even when conical snail populations are high. This observation highlights the critical importance of habitat diversity and flowering plant resources on fly distribution and effectiveness across agricultural landscapes. Adult parasitoid flies require carbohydrate and protein in the form of nectar and pollen for survival and reproduction. Nutritional studies found that total lifetime reproduction was greatest at a P:C ratio of 1:4. A recent study is investigating the impact of revegetation, with native spring- and summer-flowering plants, on the ability to boost S. villeneuveana parasitism rates and dispersal. The impact of revegetation will be measured by comparing parasitism rates and fly establishment between revegetated and non-revegetated control sites over multiple seasons. This project is the first large-scale, systematic effort to link native revegetation with enhanced biological control of conical snails, potentially providing a sustainable, habitat-based solution for South Australian grain growers. In addition, over the last four years, researchers at SARDI have mass-reared approximately 100,000 flies for release at new sites in South Australia and Western Australia to establish or boost local fly populations. The implementation of S. villeneuveana as a biocontrol agent for invasive conical snails represents an important component of a greater IPM strategy in Australia. From its initial introduction in the early 2000s to recent expansion into Western Australia, this parasitoid fly has shown promise as a sustainable tool for managing snail populations, particularly in areas with suitable floral resources. This study underscores the importance of habitat management for biocontrol success.

Funding Source: Grains Research and Development Corporation. South Australia Grain industry. Viterra Australia.

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 218

THE SECRET LIFE OF SNAILS: TRACKING MOVEMENT USING SMART SENSORS FOR PRECISION PEST MANAGEMENT

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Keywords: *Cernuella virgata*, *Theba pisana*, *Cochlicella acuta*, *Cochlicella barbara*.

Integrated management of Mediterranean snails is widely adopted by Australian grain farmers yet remains costly and only partly effective. Increased scale and mechanisation of Australian farms is driving the development of more effective tools for snail management that are increasingly automated and enable spatiotemporally targeted control. Here, we describe current trends in snail IPM in Australia, focusing on advances in remote camera-based monitoring, AI vision, and new mechanical controls. A network of autonomous sentinel camera stations was developed and deployed on Australian farms to track snail activity and environmental conditions in near real-time. Movement alerts were used to guide farmers on the optimal timing of molluscicide bait applications. A ground-based AI vision system was developed for spatial mapping of snail densities in crop fields to enable spatially targeted controls. A novel method is in development for mechanical destruction of snails in crop stubbles between cropping seasons. Sentinel snail camera stations reveal new insights into snail movement behavior. At the end of summer aestivation, snail movement was linked to levels of relative humidity, which can assist growers to better predict snail movement for optimal bait timing. AI-based vision shows promise for spatial mapping of snails which can facilitate spatially targeted and increasingly autonomous control in future. Mechanical destruction can potentially kill millions of snails per pass of a crop field. A range of other experimental research has provided insights into spatiotemporal distributions of snails in crop fields, feeding preferences, movement activity, biocontrol, behavioral responses to barriers, traps, and environmental conditions. The research support efforts to increase the snail IPM package available to farmers. Emerging technologies have potential to enable farmers to monitor and manage snails at larger agricultural scales. Fundamental knowledge of snail biology and ecology, and an integrated package of control methods, remain essential to effective snail management in Australian grain crops.

Funding Source: Grains Research and Development Corporation (code: UOA2205-005RTX).

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 185

HOST SELECTION BY A PARASITIC FISH IN INVADED COMMUNITIES: THE ROLE OF INVASIVE MUSSELS, COEVOLUTION, AND HOST QUALITY

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Keywords: fish.

Biological invasions reshape native host–parasite dynamics and test the flexibility of reproductive strategies. The European bitterling (*Rhodeus amarus*) depends on freshwater mussels to complete its life cycle. We examined whether this parasitic fish uses or avoids the invasive mussel *Sinanodonta woodiana*. We aimed to determine whether host selection is influenced by mussel quality, duration of coexistence, sympatry or consistent avoidance of unsuitable hosts across different populations. We used a two-pronged approach combining aquarium-based behavioural experiments and field surveys. In the laboratory, bitterling pairs from four populations differing in the duration of coexistence with *S. woodiana* were observed while choosing among mussels (*S. woodiana* or *Anodonta anatina*) from different sites. Reproductive behaviours of both male (spawning) and female (oviposition) were recorded. In the field, a total of 1076 mussels were collected across 12 sites and dissected to record bitterling embryos, mussel size, presence of glochidia, and macroparasites. Sites were categorised by the presence and invasion history of *S. woodiana*. Statistical models were used to identify factors influencing bitterling host use in both experimental and natural contexts. No *S. woodiana* individual was parasitised in the field (n = 152), and bitterling avoided spawning in this species during lab trials. Importantly, all fish populations showed strong avoidance of *S. woodiana* individuals from a population with the most recent (5 years) coexistence with bitterling. This consistent response suggests that mussels from invasion fronts are recognised as particularly unsuitable or risky hosts. In contrast, local sympatry and individual mussel quality did not influence bitterling response to *S. woodiana*. However, with native *A. anatina*, host selection was clearly driven by individual quality rather than population origin. In the field, bitterling parasitised all six native mussel species, with *Unio pictorum* and *U. tumidus* used most frequently. Mussel size and absence of glochidia increased the likelihood of parasitism, confirming a preference for large, unoccupied individuals. Although over half the mussels were infected with macroparasites, these had no detectable effect on bitterling prevalence or clutch size. This may reflect low sensitivity to parasite-induced damage or masking of negative effects. The results indicate that bitterling rely on generalised cues to avoid novel, poor-quality hosts while selecting native mussels based on reliable individual traits. These mechanisms operate similarly across populations and conditions, suggesting behavioural stability despite environmental change. Bitterling consistently avoided *S. woodiana*, particularly individuals from recently established populations, indicating recognition of low-quality hosts at invasion fronts. In contrast, native mussels were selected based on individual traits such as size and reproductive status. The absence of local adaptation or parasite-mediated effects suggests that bitterling relied on stable behavioural mechanisms rather than flexible responses to changing host communities.

Funding Source: This study was funded by the Polish National Science Grant 2021/41/B/NZ8/02567.

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 174

NICHE-BASED PROJECTIONS FOR ACHATININAE (GASTROPODA) IN EUROPE UNDER PRESENT AND FUTURE CLIMATE CONDITIONS

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Keywords: ecological niche modelling, species distribution, invasive species, MaxEnt.

The Achatininae subfamily (Mollusca: Gastropoda: Achatinidae) includes what are commonly known as "African giant snails". This group poses a threat to biodiversity, public health, and agriculture due to their invasive potential and their role as vectors of parasites and diseases. Although not yet naturalized in Europe, isolated introductions have been documented. It is essential to identify areas at higher risk of establishment to improve preventive management. To identify areas susceptible to invasion, the ecological niche of eight Achatininae taxa categorized as “priority” species due to their high invasive potential, was modeled. The potential distribution area was calculated using MaxEnt software, analyzing various climatic scenarios for current conditions and future climate change scenarios, as expected changes will affect environmental conditions and habitats in Europe. Distribution data were sourced from the GBIF platform, with filtering and validation of records. Environmental variables included the 19 bioclimatic variables widely used in biogeography and ecology studies, developed by the Euro-Mediterranean Center on Climate Change (CMCC). The results reveal notable variations in the potential habitat distribution among the different species, which reflect their specific ecological requirements. Overall, the results indicate a limited availability of suitable habitats for these species in Europe at present, with concentrations on the southern Mediterranean coasts, the Greek and Italian islands and the western Iberian Peninsula. However, under climate change scenarios, the availability of suitable habitats is expected to increase, particularly in the Mediterranean coastal areas of Italy, France and Spain and the Atlantic coast of the Iberian Peninsula, France and the British Isles. Species such as *Lissachatina fulica*, *Lissachatina inmaculata*, and *Cochlitoma varicosa* are expected to experience the most significant increases in their distribution range. These results suggest that these species could become more problematic in the future from both an ecological and management perspective. The increase in potential habitat availability due to climate change may exacerbate the threat posed by these snails, making early detection and proactive management even more critical. Although under current conditions there are not many susceptible areas for Achatininae colonisation, the study confirms that climate change conditions are likely to expand suitable sites for these invasive species in Europe, particularly along the coasts of the Mediterranean Sea and the southern Atlantic Ocean. Of the eight taxa analysed, *Lissachatina fulica*, *Lissachatina inmaculata* and *Cochlitoma varicosa* should be prioritised for future monitoring and management actions.

Funding Source: The study was conducted by the Spanish Malacological Society (SEM) for TRAGSATEC, commissioned by MITECO, and funded by the European Union – Next Generation EU funds.

Invasive Gastropods as Agricultural Pests / Invasive Alien Species

Invasive Alien Species

Oral - 70

A NEW LOOK AT THE SPREAD OF *Physella acuta* (DRAPARNAUD, 1805) (GASTROPODA: PHYSIDAE) IN BRAZIL: GEOGRAPHIC EXPANSION AND TEMPORAL TRENDS

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Keywords: invasive species, distribution, Quantum Gis, scientific collections, database.

Invasive species are one of the threats to the environment and native organisms, especially in freshwater ecosystems. The snail *Physella acuta* has a worldwide distribution, considered as exotic and invasive species in Brazil. Besides the great number of records, information about current distribution in Brazil remains unclear and outdated. We aimed to analyze *P. acuta* expansion in Brazil, using information provided by scientific collections, online platforms and bibliography. A database was built from the species records found by consulting data from scientific collection, open access platforms and published works using keywords. All records were filtered and validated according to some exclusion criteria. Those with incomplete information, without specific locality and duplicates were removed. Occurrences without coordinates, but with locality were georeferenced with the GEOLocate platform. Coordinates were converted to decimals, following the American Geocentric Reference System (SIRGAS-2000). Maps were built with Quantum Gis software (v. 3.16.3), using shapefile layers from the State Institute of Environmental (INEA/RJ) and Brazilian Institute of Geographic and Statistic (IBGE). A total of 654 records were compiled, of which 304 corresponding from scientific collections and 238 from literature (61 papers). After removing the duplicates (143 records) and imprecise locations (8 records), 212 records were georeferenced. The final dataset contained 483 unique records. These records were sourced from 40 journals, 15 collections, and 11 open access platforms. We reviewed 52 articles, five MSc dissertations, three PhD thesis, one specialization monograph, and one expanded abstract. Several surveys focused on parasitology, with 33 specifically addressing the topic. Among the 52 articles reviewed, only 14 contained images and 10 of them provided suitable figures. Most studies identified the species based on shell and only 47 used soft parts morphology as identification criteria, while only two cited diagnostic characters. The first *P. acuta* record in Brazil was in 1966, although scientific collections suggest an earlier invasion in the beginning of the 1960s. Over time, the number of records has increased, with many studies published in the last seven years. The species was recorded in 10 out of 12 Brazilian hydrographic regions, primarily in the southeast, where it was probably introduced before spreading to other regions. Records in Northern Brazil are scarce. The species was reported in 18 states, particularly in Rio de Janeiro and São Paulo, with 266 and 91 records, respectively. An absence of points is notable for the north region and Espírito Santo state. The lack of specific research and species monitoring is an impediment to an accurate determination of their distribution, track invasion risk areas, and potential parasite dissemination.

Funding Source: CNPq Universal 434964/2018-2 (S.B. Santos) CNPq Rede Mata Atlântica 441157/2023-B (H.G. Bergallo).

SYMPOSIUM: TERRESTRIAL GASTROPODS OF LATIN AMERICA

TERRESTRIAL GASTROPODS OF LATIN AMERICA

Coordinator:

RODRIGO BRINCALEPE SALVADOR – Finnish Museum of Natural History, University of Helsinki, Finland

The symposium 'Terrestrial gastropods of Latin America' will explore the latest research on land snails and slugs of Latin America, covering both native and exotic species. Topics will include advances in taxonomy, phylogenetics, biogeography, and natural history, offering fresh insights into terrestrial gastropods' diversity and evolutionary relationships in this biologically rich region.

Terrestrial Gastropods of Latin America

Anatomy and Physiology

Oral - 81

EARLY INSIGHTS ON THE COMPARATIVE ANATOMY OF TOMOGERIDAE (GASTROPODA, STYLOMMATOPHORA)

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Keywords: anatomy, systematics, terrestrial, Orthalicoidea, *Anostoma*.

Tomogeridae Jousseaume, 1877 is a family of terrestrial gastropods, including the up-mouth snails, endemic to Brazil, with 25 species distributed among five genera. Data about their anatomy is scarce, with little information available about *Anostoma* Fischer von Waldheim, 1807 and *Tomigerus* Spix, 1827 species. The goal of this study is to describe and compare the anatomy of the genera of Tomogeridae and analyze which anatomical characteristics are shared among them. Specimens of the type species of each genera of Tomogeridae, i.e. *Anostoma octodentatum* Fischer von Waldheim, 1807, *Biotocus cumingii* (L. Pfeiffer, 1849), *Clinispira insolita* Simone & Casati, 2013, *Hyperaulax ridleyi* (E. A. Smith, 1890), and *Tomigerus clausus* Spix, 1827 were obtained from Museu Nacional da Universidade Federal do Rio de Janeiro and Museu de Zoologia da Universidade de São Paulo, Brazil. Specimens were dissected under a stereo-microscope through standard techniques with specimens immersed in 70% ethanol. The pallial cavity, reproductive, digestive, and nervous systems were isolated and described. The pallial cavity of all species, except for *B. cumingii*, has numerous and highly conspicuous veins with a conspicuous collar vessel. The heart is slender with an additional thick vein, almost as large as the pulmonary vein, with a T shaped insertion right below the pericardium. Odontophore retractor muscles are subdivided into four uneven muscles, with the two most internal less than 1/5 as thick as the two most external. Salivary glands are small and simple, stomach and intestinal loop are very long. Anterior reproductive system is highly elongated, especially the penial complex and the bursa copulatrix duct. Albumen gland and hermaphroditic duct short and simple. Ovotestis with two to five lobes each formed by several ramifications leading to an arborescent shape. Nervous system symmetrical with very few nerves. Cerebral ganglia not fused, connected by a short connective. Posterior ganglia well separated, left parietal and visceral ganglia completely fused, except for *A. octadentatum*. Statocysts inserted postero-ventrally inside each pedal ganglion. Several distinctive characteristics among the soft parts were identified for Tomogeridae. Future steps in this study will include the analysis of microstructures of the hard parts, the inclusion of additional species, and the reconstruction of Tomogeridae phylogeny using both morphological and molecular characters. These efforts will facilitate a better understanding of the family's evolutionary history and morphology.

Funding Source: FAPERJ and CAPES.

Terrestrial Gastropods of Latin America

Conservation

Oral - 136

HOW THE SEARCH FOR A RARE SLUG LED TO NEW AND UNEXPECTED DATA

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Keywords: endangered species, pro-species program, malacofauna, native species, exotic species.

The Territorial Action Plan for the Conservation of Endangered Species of the Southern Plateau (PAT Planalto Sul, or PATPS) forms part of Brazil's National Strategy for the Conservation of Endangered Species (Pró-Espécies). The aim is to locate and preserve critically threatened species that are not supported by any official conservation policy, being one of the PATPS target species the slug *Phyllocaulis renschi* Thomé, 1965. The PATPS area encompasses 43 municipalities and approximately 32,000 km^2 of the Atlantic Forest Biome: from the northeast of the state of Rio Grande do Sul to the southeast of the state of Santa Catarina. A total of twenty survey expeditions were carried out between 2021 and 2024 in eight municipalities. The active search methodology was adopted for searching P. renschi. All molluscs collected were euthanised in accordance with the standard protocol for each group. Georeferencing was also conducted, and the specimens were registered in the malacological collection of the Museum of Natural Sciences of Rio Grande do Sul. Specialized taxonomic publications were used for specimen identification. Despite the substantial sampling effort, the target species could not be located. However, these expeditions provided the opportunity to collect a wide range of molluscs, including both Bivalvia and Gastropoda. Two bivalve species of different families were collected, one of which was non-native. A total of 43 species from 20 different families were identified within Gastropoda. Approximately half of the 43 species could be determined to species level so far, while the remainder has been identified to genus level. The study underscores the presence of a rare species, *Mirinaba fusoides* (Bequaert, 1948), and the first record of *Galba rupestris* (Paraense, 1982) in the state of Rio Grande do Sul. This species was previously documented solely from its type locality, which was geographically distant from the new locality, and it had not been observed for over three decades. Two terrestrial non-native species, *Deroceras laeve* (Müller, 1774) and *Meghimatium pictum* (Stoliczka, 1873), were identified in various sampled areas, constituting novel records of invasion. The families recorded in the PATPS area included Agriolimacidae (exotic), Bulimulidae, Charopidae, Chilinidae, Cyrenidae (exotic), Cystopeltidae, Euconulidae, Epiphragmophoridae, Helicinidae, Hyriidae, Lymnaeidae, Odontostomidae, Philomycidae (exotic), Planorbidae, Scolodontidae, Simpulopsidae, Streptaxidae, Strophocheilidae, Succineidae, Tateidae, Valloniidae, and Veronicellidae. The search for a threatened species has led to the investigation of malacofauna in areas not yet studied, the recording of non-native species in natural environments and the establishment of new records for the surveyed regions. All these data are important for the conservation of molluscs in the Atlantic Forest Biome.

Funding Source: Pro-Species Project.

Terrestrial Gastropods of Latin America

Conservation

Oral - 183

UPDATED DISTRIBUTION OF *Megalobulimus proclivis* (MARTENS, 1888), A THREATENED LAND SNAIL IN SOUTHERN BRAZIL ATLANTIC FOREST, AND IMPLICATIONS FOR ITS CONSERVATION

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Keywords: Gastropoda, area of occupancy, extent of occurrence, habitat preference, threats, Rio Grande do Sul.

Megalobulimus proclivis (Martens, 1888) is an endangered land gastropod. It was originally described from the Southern Brazil Atlantic Forest and, up to now, little is known about its natural history and geographic distribution. The aim of this study is to update the geographic distribution of *M. proclivis*, contributing to a more robust assessment of its threat status to support more effective conservation actions for the species. Geographic distribution data were obtained by examining the mollusks collection of the Museu de Ciências Naturais (MCN) of Rio Grande do Sul State (Brazil), databases (Gbif 2024, speciesLink 2024), citizen-science platform (iNaturalist 2024), bibliography, and field expeditions. The latter were conducted from 2006 to 2024 in the species' potential occurrence places and type localities, with a total of 500 field hours over 131 days by two collectors, during day and night. The geographical coordinates were recorded with a handheld GPS (datum WGS84) and a map was created using ArcGIS software. The GeoCAT tool was used to calculate the updated extent of occurrence and area of occupancy, according to IUCN. No new locality was obtained as a result of the MCN collection, bibliography and databases searches. Regarding the field expeditions, in only six of the 24 localities surveyed shells and/or specimens of *M. proclivis* were found. All six new records occurred in the municipalities of Maquiné or Itati, Rio Grande do Sul State. In relation to regions of the historical records, in the south of Brazil, no new specimen was obtained. These regions were drastically changed by the deforestation for agricultural production. In addition, the two specimens collected by Schade in Paraguay was probably confused with *Megalobulimus sanctaepauli* (Ihering & Pilsbry, 1900) which was recorded from Paraguay, Argentina and Brazil (Paraná) by Beltramino in 2013. *Megalobulimus proclivis* lives mainly on the slopes of the Atlantic Forest mountains at altitudes between ca. 100 and 300 meters. Even though it is occasionally found at 900 meters, this species probably does not establish populations in locations at this altitude. It was found exclusively in primary or old secondary-growth forests, mainly in Submontane Dense Ombrophylous Forest, and occasionally in Mixed Ombrophylous Forest. These gastropods require a stable microclimate and do not occur in anthropized areas like some other species of *Megalobulimus*. During daytime, the snails were observed burrowed in the ground, covered by leaf litter or using shelters under rocks or fallen trunks. The main threat is habitat loss, either by deforestation, agricultural expansion or the introduction of invasive exotic species such as wild boars (*Sus scrofa* Linnaeus, 1758). Considering all records from Rio Grande do Sul State, the estimated extent occurrence reduces from ca. 62,133 km^2 to ca. 2,355 km^2 and the area of occupation from 350 km^2 to 300 km^2, despite the six new records in this study. Furthermore, understanding the altitudinal range of occurrence of the species and its climatic optimum can help predict possible impacts of climate change on these gastropods.

Funding Source: Fundação Biodiversitas/CEPAN/CEPF, Fundação Zoobotânica do RS, SEMA-RS, and UFRGS/ Molluscs in One Planet: species distributions through space and time.

Terrestrial Gastropods of Latin America

Ecology

Oral - 253

THE LAND SNAILS IN AREAS OF ATLANTIC FOREST FRAGMENTS OF THE IFFAR CAMPUS SANTO AUGUSTO, RIO GRANDE DO SUL, BRAZIL

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Keywords: terrestrial gastropods, rainforest, edge effect, southern Brazil.

Due to the lack of studies presenting quantitative data of the natural land snail population in Brazil (SALVADOR, 2019), new efforts regarding the data collection of the Atlantic Forest seems necessary. The research's purpose was to identify and to distinguish the species that occur both in the edge and interior, in areas of Atlantic Forest fragments of the Instituto Federal Farroupilha (IFFar), campus Santo Augusto, Rio Grande do Sul. Land snails were collected from November 2024 to April 2025 in areas of Atlantic Forest fragments of the IFFar. Two samples were collected per month, totalling 12, in the interior and edge by using two methodologies: active search and samples of leaf litter. At the sample points, the temperature and relative humidity were recorded. The sampling effort corresponded to one collector an hour/day according to SANTOS & MONTEIRO (2001). For the leaf litter samples' collection, a square of 25cm x 25cm made of PVC pipe was used. The differences found between the samples collected in each point were analyzed using the Mann-Whitney test ($p < 0,05$). The total abundance resulted in 196 individuals, with a difference between the number of registered individuals in the interior (173) and in the edge (23), $p=0,0002$. The total richness amounted to 10 species, with 9 registered in the interior and 6 on the edge. *Deroceras laeve*, *Cyclodontina tudiculata*, *Radiodiscus* sp., *Habroconus semenlini* and *Bulimulus* sp. were found in both places. In all interior collections, 152 individuals of *D. laeve* were registered, meanwhile in the edge, there were 9 individuals. *Deroceras laeve* represented 81% of all collected individuals, it's an invasive species and a farm pest with a high fertility rate (FABERI et al, 2006). In the interior, 6 *C. tudiculata* were registered, while in the edge, there were 3. In the interior, 1 individual of *Radiosdiscus* sp., 1 *H. semenlini*, and 7 *Bulimulus* sp.; in the edge, 3 *Radiodiscus* sp., 2 *H. semenlini* and 1 *Bulimulus* sp. Exclusively in the interior 3 *Anthinus albolabiatus*, 1 *Megalobulimus* sp., 1 *Drymaeus interpunctus*, 1 *Bulimulus tenuissimus* were found. Only in the edge, 5 *Drepanostomella* sp. were registered. ESTEVES et al. (2025) account for a compositional change along the humidity's gradient, which suggests differences between the species according to the humidity, even in a fine scale. In this research, the humidity rate was higher in the interior (between 90% and 45%) than in the edge (78% to 45%) which could have influenced the amount of gastropods at the collection points. The edge effect amongst mollusks was reported by WIGHT et al (2017). A higher number of individuals and species were found in the interior of the Atlantic Forest's fragment than in its edge. The invasive species *D. laeve* was the most registered, probably due to the favorable humidity inside the forest fragment and presence of farming near it. According to the sample sufficiency curve, the richness has not yet stabilized, and, likely, new records will be added as new collections are made.

Funding Source: CNPq.

Terrestrial Gastropods of Latin America

Taxonomy and Systematics

Oral - 350

THE TRUE SLUGS (VERONICELLIDAE) OF ILHA GRANDE, ANGRA DOS REIS, RIO DE JANEIRO, RJ, BRAZIL: PRELIMINARY RESULTS

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Keywords: Mollusca, Gastropoda, slugs, zoology, taxonomy.

Veronicellidae is composed of terrestrial gastropods distributed in tropical and subtropical regions. They are identified by their long, bulging body, shell absence and anus located in a posterior position. This family is studied a little; then we are conducting a study on the diversity of these slugs in Ilha Grande, Angra dos Reis, RJ aiming to identify and to map island slugs, associating them with environmental characteristics and forest physiognomy. A search was carried out for specimens deposited in the Mollusk Collection of UERJ (Col.Mol.UERJ) which houses mollusks collected mainly in the Caxadaço, Parnaioca and Jararaca Trails and literature review. Collections are carried out using two methodologies: free collection, looking for individuals in rotten trunks, stones and litter and collection of 1m^2 of litter, stored in plastic bags and sorted in the laboratory; In addition, we carried out corrugated cardboard collection experiments. Environmental data are taken (temperature, humidity, litter depth, among others). Specimens are anesthetized and fixed for dissection. Samples from the foot are fixed in 96° alcohol and frozen for molecular biology. Among the samples of Col.Mol.UERJ, 19 belongs to the Veronicellidae. They were collected in Vila do Abraão, Vila Dois Rios and Parnaioca, Caxadaço and Pico do Papagaio Trails and were identified as *Potamojanuarius* sp, *Sarasinula* sp and *Sarasinula marginata* (Semper, 1885). Recent field collections resulted in five specimens, identified as belonging to the genus *Potamojanuarius*, mainly due to their reduced pedal gland and shape of the penial gland and penis; specific identification in process. The others are of the genus *Sarasinula*, as indicated by the pedal gland; however, they are very young, making it impossible to identify them in the species category, a problem that will be solved with the use of molecular data. The *Sarasinula* slugs were collected in anthropized environments while the Potamojanuarius slugs were collected in regenerating secondary forest environments. The corrugated cardboard methodology proved to be ineffective for slugs, but it is necessary to repeat the experiments for definitive conclusions; however, it proved to be efficient in collecting snails, attracting mainly Subulina and Happiella. The project's proposal is to collect throughout Ilha Grande territory, including the east and west modules of RAPELD Ilha Grande. The Veronicellidae on Ilha Grande are poorly documented, most of the records being occasional, from studies with other approaches. Considering the total area of Ilha Grande (193 km^2), a very small area were explored. It is necessary to expand collection efforts. Considering islands tend to have higher endemism rate, the present work, by associating morphology, molecular and environmental data, will contribute to the taxonomy, ecology and evolution of the group.

Funding Source: CNPq AP 441157/2023-8 PPBio-MA; PIBIC/CNPq scholarship to MPM).

SYMPOSIUM: EPIDEMIOLOGIC AND ECOLOGIC ASPECTS OF MALACOLOGY AND SNAIL CONTROL

EPIDEMIOLOGIC AND ECOLOGIC ASPECTS OF MALACOLOGY AND SNAIL CONTROL

Coordinator:

ELIANA NAKANO – Instituto Butantan, São Paulo, Brazil

In this symposium, the geospatial cartography of snails distribution, the predictive modeling, the species identification and control as well as the technologies and innovative approaches will be discussed.

Epidemiologic and Ecologic Aspects of Malacology and Snail Control

Ecology

Oral – 403

PERSPECTIVES ON SNAIL CONTROL IN SCHISTOSOMIASIS: CURRENT AND EMERGING APPROACHES

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Keywords: bioprospection, molluscicide, cercaricide, surveillance, eDNA.

The control of intermediate host snails with the use of chemical molluscicides has been recently reintroduced on the WHO Schistosomiasis Control Agenda after decades of chemotherapy prevalence. Our bioprospection studies started in the 1970's with the search for molluscicides, following the WHO guidelines. With the establishment of the entire life cycle of *Schistosoma mansoni* in the laboratory, the assays with parasites were included in the screening protocol to the assessment of activity against snails, *S. mansoni* adult and young worms, as well as cercariae larvae. So far, aiming to build a diverse library of scaffolds, we have isolated and identified 11 compounds from the screening of more than 60 different species of plants, seaweeds and poisonous animals with activity in at least one of the models. These compounds may be leads to develop both new drugs for chemotherapy and products to the environmental control of schistosomiasis. In another front, we are employing the eDNA technique as an alternative method to detect the presence of *S. mansoni* in environmental water samples, aiming to contribute to the surveillance of schistosomiasis with a more sensitive technique than the conventional snail-based surveys.

Funding Source: Fapesp, CNPq, Fundação Butantan.

Epidemiologic and Ecologic Aspects of Malacology and Snail Control

Ecology

Oral – 401

INTEGRATED RISK MAPPING AND SNAIL CONTROL TO SUPPORT SCHISTOSOMIASIS ELIMINATION IN BRAZIL: THE ADVANCE OF SCHISTOSOMIASIS SURVEILLANCE BASED ON A NEW CLASSIFICATION OF RISK AREAS USING LANDSCAPE PATTERNS

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Keywords: malacology, schistosomiasis, database, GIS.

Efforts to control schistosomiasis have evolved in response to changes in land use and urbanization, which have reshaped the geographic transmission landscape. Control strategies target both infected individuals and freshwater habitats where schistosomiasis vectors, specifically snails, release cercariae. Notably, shifts toward urban and peri-urban living, often accompanied by inadequate sanitation, have fragmented traditional transmission zones, leading to the emergence of geographically disconnected areas. To navigate the increasing complexity of schistosomiasis risk assessments, researchers have collaborated within the Belmont Forum-Fapesp framework to develop a novel model aimed at identifying geographic areas where the presence of snails and sanitation issues occur without human infection. This model employs an interdisciplinary approach incorporating malacology, environmental data, mathematical models, and machine learning techniques. Three distinct landscape categories were established based on their potential for schistosomiasis transmission: 1. Continuous Transmission Areas: Locations where transmission is ongoing and human infections are common. 2. Receptive Landscapes: Areas where conditions favor the initiation or reintroduction of transmission, albeit without observed human cases. 3. Resistant Landscapes: Environments that show a resistance to sustained transmission. In conclusion, this new model provides a robust framework for assessing schistosomiasis transmission risk in an evolving environmental landscape, focusing on the dynamics of snails and sanitation. By identifying areas at risk even in the absence of human infections, it paves the way for informed interventions and enhanced surveillance strategies.

Funding Source: FAPESP/BELMONT 19/23593-3.

Epidemiologic and Ecologic Aspects of Malacology and Snail Control

Ecology

Oral – 402

MALACOLOGICAL SURVEILLANCE IN BRAZIL: CHALLENGES AND PERSPECTIVES

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Keywords: neglected tropical diseases, malacology, *Schistosoma mansoni*, basic sanitation, epidemiological surveillance.

Brazil, with 8.5 million km², five regions, 27 Federal Units and 5,570 municipalities, has an estimated population of 213 million inhabitants and a universal health system. Schistosomiasis mansoni is endemic or focal in 19 states, mainly in seven states in the Northeast (Alagoas, Bahia, Maranhão, Paraíba, Pernambuco, Rio Grande do Norte and Sergipe) and two in the Southeast (Espírito Santo and Minas Gerais). The disease is related to poor environmental and sanitary conditions, common among vulnerable populations, and the country's geographic and socio-environmental diversity makes control complex. Transmission depends on snails of the genus *Biomphalaria*, which are intermediate hosts of *Schistosoma mansoni*, making malacological surveillance essential. The Schistosomiasis Control Program (PCE) guidelines, updated in 2024, reinforce integration with sanitation, diagnosis, treatment, and health education actions. However, challenges remain, such as lack of intersectoral coordination for environmental management, difficulty in maintaining trained teams for snail collection and identification, lack of technical and laboratory resources, and insufficient integration between Epidemiological Surveillance and Primary Health Care. Unplanned urban expansion without sanitation also increases the risks. To move forward, the Ministry of Health invests in technical training, data integration and health education, both in-person and online, in addition to partnerships with other sectors. Schistosomiasis has been included in the Healthy Brazil Program, expanding intersectoral actions focused on socio-environmental determinants. The Ministry of Health also conducts in-person training in endemic states on information systems, malacological surveillance and vector control, as well as online courses for health professionals, strengthening local and regional response capacity. These actions are fundamental to contain transmission, prevent the spread of the disease and protect new areas.

Funding Source: Ministry of Health of Brazil.

Epidemiologic and Ecologic Aspects of Malacology and Snail Control

Parasitology

Oral - 386

TOXICOLOGICAL EVALUATION OF *Rhinella diptycha* POISON ON *Biomphalaria glabrata* AND *Schistosoma mansoni* CERCARIAE

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Keywords: bioprospecting, natural products, toxins, drug discovery.

Schistosomiasis affects approximately 240 million people worldwide and relies on controlling intermediate hosts, such as Biomphalaria spp. in Brazil. The only WHO-approved molluscicide is costly and lacks selectivity. This study evaluated the molluscicidal and cercaricidal potential of crude poison from the amphibian *Rhinella diptycha* (Cope, 1862) on different stages of the parasite's life cycle, aiming to explore alternative control strategies with greater efficacy and lower environmental impact. Tests were conducted on *Biomphalaria glabrata* (Say, 1818) snails (adults and embryos) and *Schistosoma mansoni* (Sambon, 1907) cercariae. Adult snails were exposed to the poison (100 µg/mL) for 24 hours. Embryos at the blastulae, gastrulae, trochophore, and veliger stages were also exposed for 24 hours. *S. mansoni* cercariae were exposed for up to 2 hours at 100 µg/mL and 50 µg/mL concentrations. All tests included water and 1.5% dimethyl sulfoxide (DMSO) controls. The poison was obtained from the parotoid secretion of *R. diptycha*, dried, and later resuspended in DMSO (1.5%). Biological activity was assessed based on lethality and observable morphological and behavioral alterations. In adult snails exposed to 100 µg/mL, an 80% mortality rate was observed. For embryos, poison-induced mortality varied significantly by developmental stage: 100% in blastulae and gastrulae, 15.79% in trochophore, and 12.61% in veliger. Developmental delay was also observed in some surviving embryos, along with the presence of dead embryos retained within egg capsules, suggesting partial development followed by failed hatching and subsequent death. Regarding cercariae, the 100 µg/mL concentration caused 100% mortality within 60 minutes of exposure, while 50 µg/mL resulted in an average mortality of 93.3% after 2 hours of exposure. The data demonstrate that the poison acts swiftly and effectively on the parasite's cercariae and intermediate host. Overall, the crude poison of *R. diptycha* demonstrated high molluscicidal and cercaricidal potential, with effects on adult and early embryonic stages of *B. glabrata*, along with *S. mansoni* cercariae. These findings support further investigation of its bioactive compounds as potential alternatives to niclosamide.

Funding Source: No.

SYMPOSIUM: CEPHALOPOD BIOLOGY, ECOLOGY AND LIFE HISTORY / DIVERSITY AND EVOLUTION OF MOLLUSCA

CEPHALOPOD BIOLOGY, ECOLOGY AND LIFE HISTORY / DIVERSITY AND EVOLUTION OF MOLLUSCA

Coordinator:

TATIANA S. LEITE – Universidade Federal de Santa Catarina – Florianópolis, Brazil

The symposium will highlight recent advances in the study of cephalopods, and welcomes contributions from all fields of cephalopod research, aiming at promoting dialogue and facilitating future interdisciplinary collaborations. It will also provide a space to discuss the diversity and evolution of mollusks.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Ecology

Oral - 27

DIVERSITY AND DISTRIBUTION OF CEPHALOPODS IN BRAZIL: THE TAXONOMIC CATALOG OF THE BRAZILIAN FAUNA (TCBF)

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Keywords: Cephalopoda, taxonomy, species catalog, fauna survey.

After the expeditions of European naturalists, the first studies on the diversity of cephalopods in Brazil were carried out after the review by Pickford (1955). Between 1964 and 2021, seven octopus's species and one squid were described and two octopuses were redescribed. The first checklist of Cephalopoda was published in 1985, listing 35 species. Over the years, the number of species has been updated to a total of 86 species. As part of a broader effort to evaluate and organize data on diversity in Brazil, a comprehensive bibliographic search was conducted about the diversity and distribution of cephalopods in Brazil, and the information gathered was used to update the Taxonomic Catalog of the Brazilian Fauna (TCBF). The catalogue now provides detailed information on species occurrence, which we have categorized and analyzed in this study according to biogeographic areas and depth ranges. This comparison provided a clearer understanding of regional distribution patterns. Based on our evaluation, the known diversity of cephalopods in Brazil currently consists of 92 valid species distributed across 75 genera. Of these, 61 species are decapodiforms, represented by 24 families, while 31 species are octopodiforms distributed across 14 families. This diversity represents approximately 12% of the world's total cephalopod diversity. The most prominent biogeographic areas are Southeastern Brazil (55 species) and Rio Grande (29 sp) in the Warm Temperate Southwestern Atlantic, and in the Tropical Southwestern Atlantic, the Eastern Brazil (49 sp) and Northeastern Brazil (28 sp). Other regions of occurrence include Fernando de Noronha and Rocas Atoll (24 sp), São Pedro and São Paulo Islands (21 sp) and the Amazonian (5 sp). These occurrences reflect survey efforts in Southern Brazil in the 2000s and, more recently, in Northeastern Brazil and oceanic islands. Other regions of the Brazilian coast, particularly the Amazonian shelf, are likely to harbour significant unknown diversity. In terms of depth, cephalopods in Brazil occur from the surface and tide pools to depths of 2,136 meters. The majority of species studied and documented are from shallow waters and are of interest to fisheries. Given Brazil's vast coastline, its cephalopod diversity may be underestimated. Increased research on deep-sea fauna, along with greater financial support for diversity and taxonomic studies, and more sampling expeditions, may reveal a greater diversity of species. In addition, with advances in underwater research methods and the exploration of previously unexplored areas in Brazil, it is expected that undescribed species will be encountered and described by scientists.

Funding Source: No.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Conservation

Oral - 36

CEPHALOPOD CONSERVATION IN BRAZIL: THE FIRST NATIONAL LIST BASED ON IUCN CRITERIA

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Keywords: octopus, squid, red list.

The International Union for Conservation of Nature (IUCN) Red List of Threatened Species is a global checklist used to evaluate the conservation status of species and threats to biodiversity. In Brazil, the extinction risk assessment of cephalopods was formerly included with other mollusks in 2011, with only two species of octopus assessed. For the first time in 2022, the extinction risk of the Brazilian cephalopod was separately evaluated. The assessment follows the methodology proposed by the IUCN (2022). First, a list of cephalopod species based on the distribution and occurrence in Brazil was defined. Then, an extensive search was carried out in the literature on taxonomic classification, distribution, natural history, population, threats, exploitation, and conservation status. Information online was also obtained from citizens and researchers. The second phase was the evaluation by a group of cephalopod specialists, representatives of the fishing industry, and the Chico Mendes Institute for Biodiversity Conservation (ICMBio) team. The conservation status of each species was discussed, and an IUCN category was defined for the selected species. Forty-six species were assessed for their extinction risk. Most species were classified as Least Concerned (LC) basically because they are not targeted by specific fisheries or inhabit habitats with no present or potential impacts of human activities. A few demand more attention, some of them considered Data Deficient (DD), as the coastal loliginid *Lolliguncula brevis*, the pygmy octopus *Parocotpus cthulu*, which has only been found in association with marine debris in very shallow waters in densely populated regions, and the octopus Lepidoteuthis joaquini whose main habitat is the Great Amazon Reef System, an area that could be affected by oil exploration. On the other hand, a few species are targeted by small and large scales fisheries, including the squids *Doryteuthis pleii*, *Doryteuthis sanpaulenis* and *Illex argentinus*, and the octopuses *Octopus insularis* and *Octopus americanus*. These require (presently lacking) adequate landings reports, and further studies on ecology, population dynamics, spawning areas, genetic variability and behavior to define their status of conservation. The results were published in 2024 on the online platform SALVE (Biodiversity Extinction Risk Assessment System) as part of the Brazilian Red List of Aquatic Invertebrates (ICMBio 2024). This first list is an important step for conservation of cephalopods in Brazil. While the majority of the assessed species were classified as LC, the life cycle of most species remain poorly understood and further research are need, especially on recently described species. In addition, the lack of reliable landings data for octopus and squid makes it difficult to correctly assess the status of species targeted by Brazilian commercial fisheries.

Funding Source: Instituto Chico Mendes de Conservação da Biodiversidade.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Behaviour

Oral - 83

COMPARATIVE ANALYSIS OF BODY PATTERNS OF THE SQUID *Sepioteuthis* aff. *sepioidea* BLAINVILLE, 1823 BETWEEN THE CARIBBEAN AND BRAZIL

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Keywords: Cephalopoda, behaviour, taxonomy.

In cephalopods, body patterns are often related to species, specific behaviours and the environment. The analysis of these patterns can aid in species identification, as many exhibit unique characteristics. Our objetive is to analyse the patterns and their components exhibited by the population of the squid *Sepioteuthis* aff. *sepioidea* in Arraial do Cabo - Brazil, and compare them to those cataloged for the species in the Caribbean. The patterns were analyzed from in situ photographs and videos from the Cephalopoda Project archive. Fieldwork was conducted at the Marine Extractive Reserve of Arraial do Cabo (2023–2024) using snorkeling and scuba diving. The selected media were analyzed individually following Byrne et al., 2003; Mather et al., 2010 and Mather, 2016, to identify chromatic, textural, postural components, and overall body patterns. The videos allowed for observation of dynamic variations, so that the same individual may have been analyzed more than once, depending on the different expressions observed throughout the footage. The presence or absence of components was recorded, totaling 466 analyses of 357 individuals, based on 218 photographs and 44 videos. A total of 6 colors, 31 chromatic components, 1 textural component, 11 postural components and 12 body patterns were identified. The most frequent body pattern was the Basic Brown, already cataloged as a chronic pattern of the species in the Caribbean. Although most components and patterns had already been recorded for the Caribbean population (Moynihan & Rodaniche, 1982; Byrne et al., 2003; Mather et al., 2010; Mather, 2016), 4 chromatic components and 1 body pattern were observed for the first time in Brazil. This new pattern suggests a possible camouflage function in response to a local algae not found in the Caribbean. This observation supports the idea that habitat differences can directly influence the expression of body patterns, indicating adaptations to the Brazilian environment. The presence of a unique pattern also raises the possibility that the Brazilian population has its own repertoire, potentially even representing a distinct species. Genetic analyses are underway to evaluate this possibility. This is supported by significant physical and oceanographic barriers between the regions, which interfere with the dispersal of paralarvae through ocean currents. Furthermore, additional studies in different environmental and behavioral contexts are being conducted to explore possible variations in body patterns of this species in Brazil, ultimately leading to a comprehensive and detailed mapping of the body pattern repertoire of the Brazilian population.

Funding Source: No.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Ecology

Oral - 311

COUNTING STARS: ASSESSING THE *Octopus* IDENTIFICATION GUIDE'S EFFECTIVENESS BASED ON BODY PATTERNS TRAITS IN SITU

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Keywords: Cephalopoda, *Octopus*, identification guide, body patterns, citizen science, visual identification.

The "Shallow-Water *Octopus* Identification Guide of Brazil" was launched in June 2024 as an eBook, featuring eight species found in the country and body patterns´s components for non-invasive identification of animals capable of changing shape and colors. The tool aims to be accessible and connect with the non-scientific community. A method to assess its effectiveness was applied after lectures in which those components evaluated in the e-book were presented. To evaluate the effectiveness of the eBook, a questionnaire was conducted during four lectures, with 86 participants. In the original material, the components observed in octopus body patterns were rated using a star system (1-3), based on their frequency and exclusivity, which reflects their reliability in identifying species in the field. A selection of media (11 photos - 6 videos) featuring different species was presented for participants to identify. These media were categorized as easy, medium, or difficult depending on the presence and rating of the evaluated components. The Kruskal-Wallis test was applied to analyze differences in accuracy rates, and Spearman's test assessed the correlation between accuracy and difficulty levels. Among the 86 participants, 81.4% (n = 70) correctly identified more than 80% of the media, demonstrating a solid understanding of the material. A significant difference was found among difficulty levels (Kruskal-Wallis, $p = 0.043$), along with a moderate negative correlation between difficulty and accuracy rates (Spearman, $\rho = -0.61$; $p < 0.01$). Of the 17 images analyzed, four were classified as easy, five as medium, and two as difficult. The image with the highest error rate was number 6 (*Amphioctopus burryi*), with approximately 76% incorrect responses, most of which misidentified it as *Paroctopus cthulu* (chi-square, $p < 0.0001$). This pattern suggests an influence of visual context, as the presence of debris — a behavior observed in both species — is more strongly associated with *P. cthulu*, which is only recorded in littered environments. Among the videos, only one was classified as easy (100% accuracy). Video 1 (*Octopus insularis*) had the highest error rate (55%, n = 47), with frequent confusion with *A. burryi* (46%, n = 21) and *O. hummelincki* (40%, n = 18). The presence of traits such as the "eye bar" and prominent papillae may have contributed to the errors, as these features are shared by the misidentified species, respectively. The data indicate that identification accuracy improves when a greater number of exclusive morphological components are present. The analyses reinforce the usefulness of the identification guide and highlight the challenges posed by naturalistic observation, particularly in videos that capture the animals' dynamic body patterns. The results revealed that the eBook is effective in its purpose of identifying octopus species in situ in a non-invasive manner, contributing to the dissemination of knowledge about these mollusks and enhancing citizen science participation. The tool stands out by teaching how to recognize the animals based on their morphological characteristics and environmental observation. Moreover, it presents an unconventional methodology with potential for application to other taxa.

Funding Source: No.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Reproduction

Oral - 321

ULTRASTRUCTURAL INVESTIGATION OF TELLINOIDEAN SPERMATOZOA

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Keywords: SEM, TEM, sperm cells, phylogeny, Bivalvia.

Transmission and Scanning Electron Microscopies have contributed to the systematics of bivalves. In many cases, the results of these methodological tools have remarkably complemented molecular studies, comparative investigations of internal anatomy and conchological characters, expanding the understanding of the phylogenetic relationships among representatives of the Bivalvia class. Tellinoidea has hundreds of living species. Although the ecological importance of this superfamily is unquestionable, the literature repeatedly mentions the scarcity of knowledge about the ultrastructure of gametes produced by species of the Tellinidae, Psammobiidae and Semelidae families. This work studies the ultrastructure of spermatozoa from the bivalve species *Strigilla pisiformis*, *S. carnaria*, *Austromacoma constricta*, *Austromacoma biota*, *Psammotreta brevifrons*, *Eurytellina lineata*, *Eurytellina punicea*, *Eurytellina angulosa*, *Ameritella versicolor*, *Ameritella janeiroensis* (Tellinidae), *Sanguinolaria sanguinolenta*, *Nuttalia japonica* (Psammobiidae), *Semele proficua* and *Ervilia nitens* (Semelidae) with the aim of collecting sperm morphology data for species or genera never studied before, in an attempt to obtain characters for phylogenetic studies. Comparative analysis of the morphology of spermatozoa from the three families showed conspicuous differences including morphological traits of the nucleus, acrosome and mitochondrial elements. The spermatozoa produced by Macominae and Semelidae are of the ect-aquasperm type, while the morphology of male gamete cells of Tellininae, Strigillinae and Psammobiidae is considered modified, with a short, conical acrosome, a long, helical nucleus, generally elongated mitochondria that overlap the periphery of the nuclear base and a simple flagellum. In the literature on Bivalvia, the slim head is considered more efficient in penetrating eggs that have a large gelatinous layer. In conclusion, the helical nucleus could be a characteristic shared (synapomorphy) by all species studied here belonging to Tellininae and Strigillinae, but interestingly, it also occurs in at least two species of Psammobiidae. This similarity may correspond to a phylogenetic proximity between Psammobiidae and Tellininae+Strigillinae or represent an adaptive convergence. Hence, our work highlights the need to reassess the taxonomy of Psammobiidae. Finally, it seems reasonable to believe that the paraspermatozoa found in *Ameritella versicolor*, *Ameritella janeiroensis* and *Eurytellina angulosa* play an anti-dispersive role, which contributes to minimizing the dissipation of gametes by turbulent waters, thus triggering an increase in reproductive efficiency, as it would increase the probability of fertilization in an external environment.

Funding Source: Funding Number: 2009/07679-3 FAPESP.

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Reproduction

Oral - 163

Milax gagates, THE BIOLOGY AND ECOLOGY OF AN AUSTRALIAN ALIEN SPECIES

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Keywords: *Milax gagates*, reproduction, mortality, fecundity.

Milax gagates is a significant pest that has been introduced in many regions globally and damages important economic crops. Globally, canola is an important but susceptible crop to damage from *M. gagates*. Despite its economic importance, little is known about its biology and ecology, which is crucial to develop effective management strategies in Australian crops. This study aims address the role of temperature in egg and slug development. Adult *M. gagates*, collected from a population at the Waite institute, Adelaide, South Australia, were allowed to mate and breed over a period of three weeks in an incubator at 15°C. Clutches of eggs were extracted, washed and sealed into 55mm Petri dishes with parafilm. Petri dishes with eggs were randomly assigned to six temperatures (5, 10, 15, 20, 22.5 and 25°C) and checked weekly for neonates. Upon emergence, neonates were weighed and 100 individuals placed into individual Petri dishes, to monitor weight and development through their neonate and juvenile stages. Egg-laying by 30 of these slugs is currently being measured but will not be reported here. Emergence of individuals was generally low, with 14.6% of all egg clutches having zero emergence. Temperature influenced emergence, with failure of emergence in 25°C, very low emergence in 5 and 22.5°C (3 and 5% respectfully), while the highest emergence was observed in 10°C (41.6%), followed by 15°C (31.6%) and 20°C (21.2%). The earliest emergence was observed in the warmer temperatures, with eggs at 20 and 22.5°C emerging in 43 days, while eggs at 10 and 15°C emerged around 46-47 days on average. Emergence at 5°C took approximate 207 days. As the experiment is still ongoing and slugs in different temperatures are at different life stages, not all data are available at the time of writing. Total fecundity, time to reproduction, longevity and next generation emergence rates will be presented when data are available. Optimum temperatures for the development and survival of *M. gagates* eggs were between 10 and 15°C, consistent with other temperate slug species such as Deroceras reticulatum (Shirley et al., 2020). This biological and ecological data are part of a larger project and is being used to create a population model to determine risk factors for farmers in the Australian broadacre industry.

Funding Source: Grains Research and Development Corportation (GRDC) UOA2308-004RTX.

Cephalopod Biology, Ecology and Life History / Diversity and Evolution of Mollusca

Invasive Alien Species

Oral - 115

XenoDOMuS PROJECT: TROPICAL GREENHOUSES AS HOTSPOTS OF ALIEN MOLLUSC DIVERSITY IN ITALIAN BOTANICAL GARDENS

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Keywords: geographical distribution, non-indigenous molluscs, taxonomy, translocated species, tropical greenhouses.

The horticultural trade is a major pathway for alien species worldwide. In this context, the XenoDOMuS project was launched as a collaboration between the Museum of Natural History Accademia dei Fisiocritici, the Molluscan Biodiversity Research Group of the University of Siena, and the National Biodiversity Future Centre (NBFC). The project investigates the diversity of alien nonmarine molluscs accidentally introduced into Italian botanical gardens and science centers with tropical greenhouses. Since its inception, XenoDOMuS has conducted targeted sampling campaigns in nine botanical gardens and two science centers across Italy. The sampling focused on soil, litter, plant debris, pools and structural elements in tropical greenhouses, areas where exotic molluscs can find suitable microhabitats. Specimens were analysed by morphological and molecular approaches to obtain sound species identification and to detect any new records or undescribed taxa. The project emphasized the synergy between scientific institutions, museums and research networks, demonstrating the importance of strategic cooperation in biodiversity-monitoring efforts. More than 3000 specimens of nonmarine molluscs have been collected, representing over 50 species. Among them, a remarkable discovery was a tiny slug belonging to the Rathouisiidae family, a little-known group occurring from East Asia to Australia, found in the tropical greenhouse of the MUSE Science Museum in Trento. Morphological and genetic analysis confirmed it to be a new species and a new genus, subsequently described as *Barkeriella museensis*. In addition to this discovery, seven alien species, hitherto unrecorded in Italy, were identified, including a species never previously reported in Europe (*Geostilbia aperta*). These findings confirm the role of tropical greenhouses as hotspots of introduction of alien species and highlight the potential of systematic monitoring programs for revealing hidden biodiversity. Access to specimens through targeted sampling also provides valuable opportunities for taxonomic research, contributing to the description of new taxa and the updating of regional faunal lists. XenoDOMuS continues to expand its activities across Italy, fostering integrated research on biological invasions. The XenoDOMuS project demonstrates that collaborative efforts between museums, research institutions and biodiversity networks can achieve significant results based on solid scientific evidence. By strategically monitoring overlooked environments like tropical greenhouses, it is possible to detect alien species early, support taxonomic research, and better understand the dynamics of biological invasions in Italy.

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SYMPOSIUM: DIVERSITY AND EVOLUTION OF MARINE HETEROBRANCHIA

DIVERSITY AND EVOLUTION OF MARINE HETEROBRANCHIA

Coordinators:

VINÍCIUS PADULA – National Museum, Federal University of Rio de Janeiro, Brazil
KARA LAYTON – University of Toronto, Canada
JUAN MOLES – University of Barcelona, Spain
JESSICA GOODHEART – American Museum of Natural History, USA

Heterobranchia includes nudibranchs, sea hares, and other slugs and snail groups. They are known for their varied morphologies, vibrant colors, and complex behaviors, exhibiting a wide range of feeding strategies and ecological roles, including interstitial groups. While some are herbivorous, others prey on sponges, cnidarians, or even other molluscs. This symposium brings together studies on the systematics, taxonomy, ecology, and evolution of marine heterobranch representatives.

Diversity and Evolution of Marine Heterobranchia

Ecology

Oral - 206

ECOLOGICAL INSIGHTS FROM HETEROBRANCH SEA SLUGS IN MEXICAN CORAL COMMUNITIES FROM THE TROPICAL EASTERN PACIFIC

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Keywords: biodiversity, coral reefs, Heterobranchia, community ecology, Huatulco, Oaxaca.

Heterobranch sea slugs are among the most popular coral reef creatures in the world. They exhibit a wide variety of colors and shapes that make them interesting for divers, but also have relevant ecological roles as intermediaries in the communities they inhabit. The goal of this study was to analyze the sea slug community structure in four coral communities in the Tropical Pacific of Mexico during two seasons. Sampling was made during dry and rainy seasons using specialized direct and indirect methods for sea slug collection at four localities in Huatulco, Oaxaca, Mexico: Conejos, San Agustín, Entrega and Arrocito. In San Agustin, however, data were collected exclusively through observations, as it is a Natural Protected Area. Sea slugs were recorded based on observation time (number of individuals h-1 observer-1) and were identified either in situ or in the field laboratory with specialized literature of the region. Specimens were collected when necessary, anesthetized using magnesium chloride and preserved in ethanol 70%. A total of 457 organisms belonging to five orders, 20 families and 44 species were recorded. This represents 11% of the total sea slug species previously known for the Eastern Pacific, from Alaska to Peru. In addition, we report two distribution extensions, two new records for the Mexican Pacific coast and six species previously recorded in other localities of the region, but undescribed. The ecological attributes for each locality were analyzed using data obtained exclusively from direct sampling methods. The species accumulation curve was asymptotic, and it was far from reaching the maximum expected. Sea slug communities at Arrocito exhibited higher values of species richness (20), followed by Entrega and San Agustín (14), and Conejos (13). *Aplysia hooveri* showed high relative abundance (53.5%; 66.7%) and density (15 ind./h; 22 ind./h) in San Agustín and Entrega. At the same time, most of the species were observed on substrates associated with their feeding habits. However, this distribution was not exclusive, as individuals were also found on more than two types of substrates, including unusual ones. Furthermore, sea slug communities differed significantly between seasons (PERMANOVA, Pseudo-$F(1)=2.829$, $p<0.05$), and between localities (PERMANOVA, Pseudo-$F(3)=3.369$, $p<0.05$), except between Entrega and San Agustín, which showed similar communities according to the pair-wise test. The interaction between season and locality was not significantly different (PERMANOVA, Pseudo-$F(3)=0.937$, $p>0.05$). Huatulco Bays harbor a high diversity of sea slugs compared to other localities in the region. This study contributes to our understanding of sea slugs' temporal and spatial ecology in coral communities of the Tropical Eastern Pacific and provides valuable information on the marine invertebrates within a Natural Protected Area.

Funding Source: No.

Diversity and Evolution of Marine Heterobranchia

Ecology

Oral - 273

DIVERSITY AND PHENOLOGICAL PATTERNS OF MARINE HETEROBRANCH GASTROPODS ACROSS MULTIPLE YEARS ALONG THE CATALAN COAST, MEDITERRANEAN SEA

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Keywords: marine heterobranch gastropods, community science, transects, phenology, diversity.

Marine heterobranchs are exceptionally diverse and charismatic, yet their phenology and community structures remain underexplored. By integrating observations from community science efforts and expert-driven data in the Mediterranean Sea, we aim to clarify spatiotemporal patterns in heterobranch assemblages. Here, we also leverage robust databases able to serve as a foundation for future ecological studies on these captivating organisms. We profited from the two community science platforms GROC1 and MINKA2, containing data from 2009 to the present, along roughly 700 km of coastline in northeastern Spain (Catalonia) in the western Mediterranean. GROC also integrates expert-led transect surveys conducted between 2013 and 2018. We used these data primarily to investigate the phenology and diversity of heterobranch communities and whether there is a south-to-north gradient increase in species richness. The expert transect data enabled us to define marine heterobranch assemblages at four sites within this region, considering habitat heterogeneity (number of microhabitats per transect). All analyses were performed in R Studio, using the vegan and zoo packages. 1https://opistobranquis.org/es/home 2 http://www.minka-sdg.org/. A total of 263 heterobranch species were found across both databases. Transects took place in four diving sites, while the community science observations took place in up to 2000 diving sites from 2012 to 2024. Analyses using community science data confirmed a south-to-north gradient, largely driven by latitude-related differences in habitat heterogeneity. Specifically, the city of Blanes marks a turning point, with a wider continental shelf with sandy substrates and low rock coverage dominating south to this point, while rockier seafloors—featuring caves, vertical walls, and other microhabitats—prevail in the northern region, promoting higher species richness and abundance. Within the dataset, the orders Nudibranchia and Sacoglossa, demonstrated the highest richness (96 and 15 species, respectively) and abundance (10,041 and 4,892 records, respectively) out of all orders recorded. Moreover, the transect data revealed a consistent pattern of nudibranch dominance in both richness and abundance relative to cephalaspideans and sacoglossans, mirroring the broader trends observed in the community science analyses. Concerning phenological patterns, we used the expert transect data to calibrate the community science data to describe the annual variation in abundance for the species with the highest abundance in the dataset. After obtaining the phenological patterns for these more common species, we compared those with the seasonality of their food availability with their reproductive season. We were able to define some marine heterobranch communities along the Catalan coast across space and time, confirming that there is an increase in richness and abundance of species from the south to the north coast, highlighting the importance of management and conservation in specific areas. In the future, it is essential to better define transects along the Catalan Coast, paying special attention to the region southward of Blanes.

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Diversity and Evolution of Marine Heterobranchia

Evolution

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PHYLOGENOMICS OF ELLOBIOID GASTROPODS AND THEIR MULTIPLE INVASIONS OF THE LAND

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Keywords: Ellobioidea, Ellobiidae, *Pythia*, phylogeny, early development, terrestrialization.

Animal terrestrialization is one of the most significant events in the Earth's history of life, contributing to shaping the current biodiversity on land. Gastropods have been exceptionally successful in this habitat shift with at least ten colonization events. Of these, two independent invasions have been suggested for the eupulmonate family Ellobiidae; all species of its subfamily Carychiinae and a few in the genus *Pythia* (Pythiinae) exclusively occur in terrestrial habitats. Here, we show new molecular phylogenetic trees for the superfamily Ellobioidea, including the families Ellobiidae, Otinidae, Smeagolidae and Trimusculidae, based on (1) genome skim data for their basal relationships and (2) traditional nuclear rDNA and mitochondrial markers for more recent divergences. Special emphasis was placed on the genus *Pythia* by incorporating as many coastal to inland-forest species as possible. Moreover, the mode of early development was inferred from the observation of eggs, hatched larvae and protoconchs as well as population genetic analyses and was mapped on the reconstructed phylogeny to explore its significance in the evolutionary process leading to full terrestrialization. Our phylogenomic trees recognized two major clades in Ellobioidea, one of which included the nominal families Otinidae, Smeagolidae and Trimusculidae as well as some genera from the ellobiid subfamilies Melampodinae and Pedipedinae. The other clade comprised the remaining Ellobiidae including Carychiinae and Pythiinae with terrestrial species, thereby necessitating familial and subfamilial reclassification. Terrestrial species of *Pythia* were found polyphyletic; four independent invasions of the land were suggested within the genus in the tropical and subtropical West Pacific. The common ancestor of the Ellobioidea was inferred to live in the intertidal zone and develop as planktotrophic swimming larvae, whereas direct development has evolved multiple times and independently paved the way for the land invasion, sometimes with lecithotrophy as a transitional condition. The acquisition of the direct development and subsequent land invasion in the *P. nana* species complex in Okinawa seem to have occurred in the late Miocene and Pleistocene, respectively, representing one of the most recent terrestrialization events documented to date for the entire Animalia. This study is the first to infer multiple land invasions within an animal genus based on molecular phylogenetic reconstruction. Independent acquisitions of direct development might have triggered these habitat shifts in the Cenozoic, including one in the late Miocene. The genus *Pythia* has a great potential to serve as a model system for studying animal terrestrialization from ecological, morphological, physiological and genetic points of view.

Funding Source: No.

Diversity and Evolution of Marine Heterobranchia

Taxonomy and Systematics

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THE SYSTEMATICS OF THE GENUS *Aplysia* IN THE EASTERN PACIFIC: RESOLVING LONG-STANDING TAXONOMIC AMBIGUITIES

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Keywords: systematics, Heterobranchia, morphology.

Although the genus *Aplysia* has been the focus of numerous taxonomic and physiological studies, its worldwide systematics remains poorly understood due to both ontogenetic variability and high levels of phenotypic diversity. One region that is in critical need of taxonomic revision is the Eastern Pacific, where more than ten species have been described, but some are only known by its original description and others were introduced without proper comparative analyses. Also, some widely distributed species, such as *A. dactylomela* and *A. juliana* have been reported from this region, but their presence is uncertain due to persistent taxonomic confusion. In this study, we performed a phylogenetic analysis based on a concatenated dataset of COI, 16S rRNA, and H3 gene fragments, as well as whole mitochondrial genomes to enhance phylogenetic resolution, using specimens collected from California to Peru. Examinations of external morphology, digestive system, and reproductive structures were conducted to identify diagnostic traits for species. Additionally, scanning electron microscopy was used to examine radulae, jaws, and penises, and type material for most species was examined. The results support the presence of six distinct species in the Eastern Pacific and provide data to help clarify the identity and synonymy of several nominal taxa. Some names previously thought to represent valid species are proposed to be junior synonyms, while others—historically misidentified or known only from their original descriptions—are re-evaluated. Additionally, no molecular or morphological evidence was found to support the occurrence of *A. dactylomela* or *A. juliana* in the region, despite previous records. Species ranges suggest latitudinal expansion during El Niño events, and morphological characters—particularly of the reproductive system—proved useful for distinguishing taxa. These findings not only resolve long-standing taxonomic ambiguities in the Eastern Pacific but also provide a critical regional framework for broader systematic studies of *Aplysia* worldwide, contributing to the understanding of the global phylogeny and evolutionary history of the genus.

Funding Source: No.

Diversity and Evolution of Marine Heterobranchia

Taxonomy and Systematics

Oral - 337

A WORLDWIDE MARINE TRAVELER: TAXONOMY AND POPULATION GENETICS OF *Polycera hedgpethi* (GASTROPODA: NUDIBRANCHIA)

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Keywords: Heterobranchia, exotic species, sea slugs, rafting, *Bugula*.

The nudibranch *Polycera hedgpethi* Er. Marcus, 1964 was originally described from the coast of California, USA, and has since been reported from several regions worldwide. It has been hypothesized that *P. hedgpethi* disperses via ship hulls, associated with bryozoans. However, records have been primarily relied in external morphology. In this study, we reevaluate the taxonomy and natural history of *P. hedgpethi* using integrated morphological, molecular phylogenetic, and population genetic approaches. Over 70 specimens from California, northern Peru, Brazil, Spain, France, Italy, and Australia were collected and sequenced. Molecular analyses were based on the COI and 16S genes. Phylogenetic reconstruction was carried out using Bayesian inference (MrBayes) and maximum likelihood methods (IQ-TREE) including additional species of Polycera and Polycerinae obtained from GenBank. Population studies included haplotype networks (POPART), assessments of haplotype and nucleotide diversity, segregation sites (AMOVA), and FST values (conducted with DNASP and Arlequin). Morphological analyses involved external and internal features, including micrographs of the radula and jaws, as well as schematic illustrations of the reproductive system. Polycera is polyphyletic, with species grouped into seven distinct clades. The *P. hedgpethi* clade is distant from the other species in the genus, except for *Polycera tricolor*. There is no subdivision into clades that would suggest that *P. hedgpethi* represents more than one species. For the COI gene, 27 haplotypes were identified among 40 individuals, and for the 16S gene, 13 haplotypes were found among 62 individuals. There is no population structure in both genes, with haplotypes from different regions recovered across the network. California (USA) and New South Wales (Australia) show the highest number of individuals and haplotypes for the COI gene. Venice (Italy) has the highest number of samples for the 16S gene (33), but only four distinct haplotypes, followed by California (USA) with 16 samples but eight distinct haplotypes. In external morphology, the mantle varies from white or translucent white densely covered with small irregular spots to an almost completely black mantle. Extrabranchial processes are white at the base, sometimes with small black spots. In internal morphology, the jaws are strong, wing-shaped; the ligament region between the two parts is robust, V-shaped. The radula is mostly dark brown in color; rachidian teeth are absent. The lateral teeth are bicuspid, with triangular cusps. The marginal teeth smaller and plate-shaped. In the reproductive morphology, the seminal receptacle is elongated, ranging from narrow to broad, connected to the bursa copulatrix by a thin uterine duct. Morphological and molecular data confirm that *P. hedgpethi* represents a single species with a wide distribution across multiple ocean basins. Variation is observed in body size, mantle pigmentation, and the size and shape of the seminal receptacle. Population genetic analyses suggest California as the most likely origin and dispersal center for the species, although further sampling is needed to more rigorously test this hypothesis.

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REVISITING PHYLOGENETIC UNCERTAINTY IN DORID NUDIBRANCHS WITH GENOME-WIDE DATA

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Keywords: phylogenomics, exon capture, speciation, Doridoidei.

A scarcity of genomic resources in many diverse marine invertebrate groups limits our ability to establish robust phylogenetic frameworks that are fundamental to our understanding of evolution. Here, we use a sequence capture dataset targeting hundreds of phylogenetically informative genes to address this deficit in the hyperdiverse dorid nudibranchs. Dorids exhibit incredible phenotypic and ecological diversity, but the lack of a well-resolved phylogeny hinders deeper understanding of their biology and ecology. We generate data from 300 genes in 18 families and 48 genera of dorid nudibranch to resolve phylogeny using both maximum-likelihood and multi-species coalescent methods. Then, we use a hypothesis-testing framework through gene genealogy interrogation to resolve recalcitrant nodes, and we use a newly discovered geminate pair to establish the first time-calibrated phylogeny for this group. Next, we employ a phylogenetic network approach to investigate the prevalence of introgression across the dorid tree. Lastly, we revise the multiple non-monophyletic genera recovered here. This study is the first to use genome-wide data to establish a resolved phylogeny for dorid nudibranchs, a critical framework that will support future work, and it improves our understanding of the evolutionary processes generating diversity in this group.

Funding Source: No.

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Taxonomy and Systematics

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INTEGRATIVE SYSTEMATICS OF *Nanuca* (GASTROPODA: NUDIBRANCHIA: MYRRHINIDAE) REVEAL FIVE NEW SPECIES AND PROVIDE INSIGHTS INTO WESTERN ATLANTIC BIOGEOGRAPHY

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Keywords: Cladobranchia, *Dondice*, Gastropoda, new species, phylogeny, pseudocryptic species, speciation, species delimitation.

The genus *Nanuca* comprises a single species, *N. sebastiani*, which is distributed widely along the tropical Western Atlantic. The taxonomy of *Nanuca* has not been comprehensively examined and its relationship with the genus *Dondice* is a topic of discussion (Furfaro & Mariottini, 2021; García Méndez et al. 2022). In this study, both molecular and morphological datasets were extended to include multiple *N. sebastiani* specimens for the first time. The type material of *N. sebastiani* was rediscovered in the historical slides collection of Ernst and Eveline Marcus. 40 new specimens were collected from various locations spanning the south of Florida, USA, to the Cabo Frio region, southeastern Brazil. Using newly generated sequences, the most comprehensive dataset to date for studying Myrrhinidae evolution (with 68.9% of global species diversity) was created. An integrative framework was adopted, combining phylogenetic analyses (Maximum likelihood and Bayesian inference), species delimitation methods (ABGD, ASAP, GMYC and PTP) with mitochondrial (COI and 16S) and nuclear (28S LSU D1-D2) genes, genetic distances, haplotype network for COI, molecular diagnostic characters, morpho-anatomical and biogeographical evidence. Phylogenetic reconstruction recovered the six genera of Myrrhinidae as monophyletic, reinforcing Dondice and Nanuca as distinct taxa. The diversity in Nanuca is much higher than that currently recognized. All molecular phylogenetics, species delimitation, genetic distances, haplotype network, and morphological data support that the widespread nominal species *N. sebastiani* represent six distinct lineages with a restricted geographical distribution. All delimited species were pseudocryptic and supported by external or internal morpho-anatomical characters, or by a combination of these. Based on this, polymorphic *N. sebastiani* was redescribed, and five new species were formally described. Geographic separation in the *N. sebastiani* complex corresponds to the major biogeographic barriers proposed for marine reef fish in the Caribbean and Brazil, such as the Amazon River, which acts as a barrier in the Western Atlantic (Floeter et al. 2008; Luiz et al. 2012). Environmental similarities between the Caribbean and Rocas Atoll, the warmer waters in northeastern Brazil, and upwelling region in southeastern Brazil, play an important role in species diversification (Rocha et al. 2005; Cord et al. 2022). The hypothesis of dispersal by sweep events and subsequent isolation across the Amazon River barrier was proposed to explain the origin of the Brazilian and Rocas Atoll lineages. Additionally, larval development may influence the dispersal capacity of Nanuca species, thereby affecting genetic connectivity between populations. This study provides an integrative framework rejecting the hypothesis of synonymy between Nanuca and Dondice, the recovery of several Nanuca lineages, their delineation as distinct species, and highlight another case of colour polymorphism in nudibranchs. The results shed light on biogeographic features' role in nudibranch speciation in the Western Atlantic and highlight the importance of considering nudibranch diversity in an evolutionary context.

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EXPLORING GEOGRAPHIC VARIATION IN MIMIC-MODEL RESEMBLANCE IN NUDIBRANCHS THROUGH CITIZEN SCIENCE

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Keywords: Nudibranchia, aposematism, mimicry.

Nudibranchs in the family Chromodorididae serve as excellent models of aposematism, as they display diverse conspicuous colors while also being unpalatable. Aposematism is particularly intriguing in the genus *Felimida* since this is one of only two chromodorid genera with which mimicry has recently been uncovered. In this system, trans-Atlantic *F. binza* displays drastically different morphotypes on either side of its range, appearing to mimic other congeners. More recently, dozens of images of Felimida have become available on citizen science repositories and have demonstrated more extensive color pattern variation than originally reported. As such, we collected, edited, and standardized research grade images of Felimida from iNaturalist for color pattern analyses, spanning the full distribution of this genus. We used the recolorize package in R to standardize and segment images to create zone maps that were then used for pattern complexity and adjacency analysis. We used principal component analysis (PCA) to explore geographic variation in color pattern complexity and found that *F. binza* in the eastern Atlantic typically display a striped morphology, similar to *F. krohni*, while *F. binza* in the western Atlantic typically display circular spots, similar to *F. clenchi*. However, several individuals from locations in Portugal and Bermuda appeared to have intermediate phenotypes and may indicate introgression among species. Additionally, we quantitatively compared color transitions and color diversity to demonstrate how well models and mimics resemble each other. These findings have provided insight into the regional drivers of spatio-chromatic variation in this mimetic complex. Next, we plan to incorporate an exon capture dataset to explore relationships among Felimida species and provide a molecular framework for understanding this phenotypic variation.

Funding Source: No.

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NEW CONTRIBUTIONS TO THE EUTHYNEURA BIODIVERSITY OF COLOMBIA'S PACIFIC AND CARIBBEAN COASTS

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Keywords: rocky reef, coral reef, Heterobranchia, nudibranchs, shallow subtidal, intertidal.

Euthyneuran heterobranchs, including sea slugs and sea hares, are a morphologically and ecologically diverse group widely used in evolutionary, ecological, and chemical studies. Despite Colombia's extensive Pacific and Caribbean coasts—home to key ecosystems such as coral reefs and rocky shores—the biodiversity of these mollusks remains understudied. This research contributes new data to the Colombian inventory from two contrasting regions: the Seaflower Biosphere Reserve and Uramba Bahía Málaga National Park. To expand the inventory of Euthyneura in Colombia, rapid biodiversity assessments and artificial hard substrates (AHS) were employed in two contrasting ecosystems: coral reefs in Courtown Cay (Seaflower Biosphere Reserve, Caribbean) and rocky reefs in Los Negros and Los Negritos (Uramba Bahía Málaga National Natural Park, Pacific). Fieldwork was conducted between July and December 2022 using SCUBA diving and snorkeling at depths of 1–40 m. AHS units, filled with coral rubble and shell fragments, were deployed in the Pacific intertidal and subtidal zones and retrieved after four months to assess sea slug colonization. All specimens were photographed, taxonomically identified, and preserved for databasing. A total of 31 Euthyneuran species in 16 families were recorded: 14 from the Caribbean and 17 from the Pacific. Of these, 11 are new records for Colombia (3 from Courtown Cay and 8 from Los Negros and Los Negritos). Nudibranchs represented 58% of the species; Aplysiidae was the most diverse family (5 spp.), followed by Facelinidae (4 spp.), and Aeolidiidae, Discodorididae, Chromodorididae, and Plakobranchidae (3 spp. each). Species richness was higher in the Pacific, particularly at Los Negritos, and new records were over twice as frequent there compared to the Caribbean. This aligns with the historical under-sampling of the Colombian Pacific, despite its potential, and contrasts with the better-documented Caribbean, where most new records filled known distribution gaps. Sampling effort influenced outcomes: 40 h in the Caribbean yielded only 4.5% of the expected fauna, while 20 h in the Pacific yielded 7.1%. Pacific habitats allowed more effective intertidal searches due to wider tidal ranges and more accessible microhabitats. In contrast, Caribbean coral reefs limited substrate inspection. This study increases the known heterobranch fauna to 131 species in the Caribbean and 111 in the Pacific. However, many species were represented by single individuals, underscoring the need for expanded sampling and molecular confirmation. Future research should adopt region-specific strategies and target underexplored habitats—particularly in the northern Colombian Pacific, where rocky reefs remain poorly studied. Combining increased sampling effort with integrative approaches, including detailed morphological, ecological, and molecular analyses, will be essential to uncover hidden diversity, clarify species identities, and better understand the biogeography and ecological roles of Euthyneura in Colombian marine ecosystems.

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CHALLENGING THE CURRENT TAXONOMY OF *Haminoea*: INTEGRATING MOLECULAR PHYLOGENETICS AND MORPHOLOGICAL TRAITS TO REDEFINE SPECIES BOUNDARIES

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Keywords: Heterobranchia, mollusc, diversity, taxonomy.

Haminoea is a genus of cephalaspidean gastropods characterized by having a globose, thin, semi-translucent shell. The number of valid species is unsettled, varying between 14–20. Species are distributed across the Atlantic and eastern Pacific Oceans, with one lineage along the temperate coastline of South Africa in the Indian Ocean. This study aims to determine the number of valid species within the genus and to clarify their phylogenetic relationships. A total of 263 specimens were sequenced for the cytochrome c oxidase I gene (COI). Maximum likelihood (ML) and Bayesian inference (BI) phylogenetic analyses, along with the Assemble Species by Automatic Partitioning (ASAP) species delimitation method, were employed to infer the number of candidate species. Two individuals per putative species were shotgun sequenced to infer phylogenetic hypotheses under ML and BI analyses based on complete mitochondrial genomes and nuclear ribosomal gene cluster (18S, ITS1, 5.8S, ITS2, 28S). ASAP analyses were conducted with mitochondrial and nuclear ribosomal datasets. Morphological traits were examined through dissections and scanning electron microscopy (SEM), focusing on jaws, radulae, gizzard plates, male reproductive tracts, and shells. Phylogenetic inference and ASAP analyses, based on both mitogenomes and the nuclear genes, identified between 9 and 22 candidate species. The nuclear ribosomal genes appeared to be conserved, offering lower resolution for species delimitation and clustering lineages which, according to other genetic data and morpho-anatomical traits, were recognized as distinct species. In contrast, the rapidly evolving nuclear ITS genes provided good resolution for species discrimination, supporting a hypothesis of 12 lineages largely consistent with mitochondrial and morphological data. Analyses of mitochondrial genome data alone was, in a few cases, affected by high mutation rates in some specimens, leading to issues such as long-branch attraction and the artificial splitting of otherwise well-supported species into multiple lineages. The best-resolved phylogenetic tree, with maximum support at all nodes, was obtained by combining mitochondrial genome sequences with the two ITS genes. Resolving the *H. alfredensis*–*H. antillarum*1–*H. antillarum*2–*H. orbignyana* species complex remained challenging. All species delimitation scenarios suggested a single lineage, and uncorrected COI genetic distances were low, ranging from 2–5% between species in the complex, compared to 8–13% among other sister lineages. Nevertheless, these four lineages consistently formed clades with maximum support in our phylogenies, were geographically allopatric, and exhibited distinct reproductive systems. Species delimitation in *Haminoea* based solely on genetic data is challenging due to different molecular evolutionary rates among candidate species, long-branch attraction issues in mitochondrial genes, and low resolution in nuclear ribosomal genes. The combined analysis of nuclear ITS genes and complete mitochondrial genomes produced the best-supported phylogenetic hypothesis. Additionally, morpho-anatomical data proved crucial for understanding the diversity in the genus, which likely comprises 15 valid species.

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Taxonomy and Systematics

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COMMUNITY SCIENCE AND NUDIBRANCHS: A NATURAL PARTNERSHIP?

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Keywords: community science, nudibranch, cryptic species, range extension, ocean warming.

Community science has strong potential for studying biodiversity. Nudibranchs, being highly charismatic and potential bioindicators of ocean warming, are ideal for testing its applicability. Tracking them using community science may reveal new insights into climate change impacts on sea slugs. Here, we tested the accuracy of community science species-level nudibranch identifications to evaluate the reliability of such data. We used the community science platform iNaturalist, downloading all "Research Grade" observations for three pairs of northeastern Pacific cryptic nudibranch species: *Hermissenda crassicornis* and *H. opalescens*, *Triopha modesta* and *T. catalinae*, and *Diaulula odonghuei* and *D. sandiegensis*. These species have subtle but diagnostic morphological characters which are documented in the scientific literature. We identified 250 iNaturalist observations per species (1500 observations total) using the morphological descriptions documented in the literature. Each observation was identified by two researchers. We compared the species identifications between the two researchers and the researcher identification to the community identification on iNaturalist to quantify disagreement between community and traditional science. We found relatively high agreement between researchers (81-96%). The *Diaulula* genus had the highest agreement (93-96%), *Hermissenda* species had slightly lower (90-91%), and *Triopha* had the lowest agreement (81-88%). When comparing identification mismatches between researchers and community scientists, a similar pattern was found. *Diaulula* nudibranchs had the highest agreement (93-94%), *Hermissenda* was a bit lower (85-86%), and *Triopha* had the lowest (66% and 87%). This matches with our predictions based on the ease of identification of the morphologies noted in the literature. *Diaulula* and *Hermissenda* species. are relatively easy to tell apart, using the dorsal spots or ceratal stripes. *Triopha* species are harder to distinguish, as the shape of the dorsal tubercles must be seen clearly in the given photograph. Community science data has been shown to have high species identification accuracy in some taxa, but the exception is often cryptic species. In the case of cryptic nudibranchs, community scientists seem to be fairly accurate in their species identifications. We found high accuracy in community science species-level identifications of cryptic nudibranchs. However, accuracy is dependent on species, with some being easier to identify than other. This indicates that this data can be used to make meaningful observations surrounding nudibranchs, including using the data to track range shifts associated with climate change. Next, we will use iNaturalist to track species range changes given the high accuracy of community science data.

Funding Source: Natural Sciences and Engineering Research Council of Canada. Simon Fraser University.

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Anatomy and Physiology

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LOOK A HETEROBRANCH IN THE MOUTH: STUDIES OF THE BUCCAL ARMATURE FORMATION IN EUTHYNEURA

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Keywords: radula, jaws, ultrastructure, odontoblasts, gnathoblasts.

The gastropod buccal armature (radula and jaws) is a taxonomically significant structure notable for its ability of continuous renewal. The buccal armature in Heterobranchia, a highly diverse gastropod clade, exhibits remarkable morphological diversity, reflecting adaptive feeding strategies and suggesting varied renewal mechanisms. However, the existing diversity of these processes remains understudied. To address this gap, we conducted a comprehensive study of buccal armature formation across different heterobranch taxa. We have studied the general morphology and ultrastructure of the radula and jaws in different heterobranch species, all belonging to Euthyneura, including various species of Nudibranchia, Pteropoda, Sacoglossa, and Acochlidimorpha. In our work, we utilized a combination of classic and modern morphological methods, including light and confocal laser scanning microscopy, transmission and scanning electron microscopy, micro-computed tomography, and computer-based 3D-reconstruction. Our findings demonstrate a consistent pattern of radula formation across all studied species: each tooth is synthesized by a small group of specialized odontoblasts via microvillar activity. Notably, odontoblasts in these species are significantly larger than those in non-Euthyneuran gastropods. Given the correlation between cell size and ploidy, we propose that Euthyneuran odontoblasts are polyploid, representing another case of somatic polyploidy — a common phenomenon in this clade. Additionally, we identified morphological variation in the radula formation zone, reflecting adaptations to radula width and size of radular teeth. For instance, species with broad radulae possess a connective-tissue collostyle, which likely prevents the deformation of the formation zone during radular movements. Concerning the synthesis of jaws and jaw-like structures (e.g., labial cuticle, buccal hooks), our results reveal two distinct synthesis mechanisms in Euthyneura. In the first type, observed in aliform jaw plate, specialized cells called gnathoblasts synthesize its fibrous middle layer that becomes covered by the cuticle of buccal epithelium. The second mechanism occurs in jaw-like structures (e.g., labial cuticle) consisting of solitary elements (rodlets) embedded in a common matrix. In that case, each rodlet is secreted by a single gnathoblast. Furthermore, we identified morphological features of gnathoblasts suggesting their periodic replacement throughout the mollusc's lifespan. Our findings provide new insights into the cellular mechanisms of buccal armature synthesis in Euthyneura. These results enable us to elucidate the structural adaptations underlying the diversity of buccal armature in Euthyneurans and to identify the main patterns of the buccal armature synthesis.

Funding Source: The study was conducted under the state assignment of Lomonosov Moscow State University.

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Taxonomy and Systematics

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FROM CLADES TO FORM: REDEFINING *Felimare* THROUGH MOLECULAR PHYLOGENETICS AND MORPHOLOGICAL ANALYSES

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Keywords: Heterobranchia, Nudipleura, phylogeny, *Hypselodoris*, *Mexichromis*.

Chromodorididae stands out as one of the most remarkable nudibranch families due to the high diversity of body color patterns. The genus *Felimare* was resurrected to include some species previously classified under *Hypselodoris* and *Mexichromis*. However, *Felimare* remains controversial, as it currently includes species with different external features, radular and jaw morphologies, and distinct reproductive traits. This study integrates molecular and morphological analyses to improve the understanding of *Felimare* systematics. Phylogenetic analyses were based on COI and 16S genes. Fourteen *Felimare* species and eight from other *Chromodorididae* genera (*Chromodoris*, *Mexichromis*, *Ceratosoma*, *Miamira*), including their type species, were analyzed, using *Cadlinella ornatissima* to root the trees. Most sequences were retrieved from GenBank, along with new sequences of *F. kempfi* and *F. juliae*. Sequences were edited in Geneious and screened for contamination using BLAST-n. Alignments were performed in MEGA 11 (MUSCLE), with 16S masked using GBlocks. Phylogenetic analyses were conducted using Bayesian inference (MrBayes) and Maximum Likelihood (RAxML). Morphological analysis included external and internal characters, such as SEM micrographs of the radula and jaws, and reproductive anatomy. The tree topology indicates that *Felimare* is divided into two well-supported clades. The first comprises *Felimare bayeri*, the type species of the genus, along with other large-bodied species (up to 130 mm), predominantly distributed in the tropical Western Atlantic. The second clade includes smaller species (up to 30 mm), such as *F. porterae* (Eastern Pacific), and the Atlantic species *F. kempfi*, *F. francoisae*, and *F. sisalensis*. This group shares internal morphological traits distinct from *Felimare*, including jaw elements with 3–5 cusps resembling a mole's paw and a reduced radula with teeth bearing cusps of similar size. These differ markedly from typical *Felimare*, which exhibit unicuspid jaw elements and numerous, strongly bicuspid radular teeth. Additionally, the reproductive system in this group is characterized by a short, undifferentiated prostate and a seminal receptacle connected near the base of the bursa copulatrix and curved toward the gonopore. In contrast, *Felimare* presents a long, coiled prostate and a seminal receptacle inserted in the middle of the vagina, curving toward the bursa copulatrix. These findings support the separation of these clades and the proposal of a new genus, composed of small chromodorids distributed in the Eastern Pacific and Atlantic Ocean. This study provides robust molecular and morphological evidence supporting the recognition of a new genus in Chromodorididae, distinct from *Felimare*. The discovery represents a step forward in expanding our knowledge of the family. Comprehensive morphological descriptions and revisions remain crucial for the study of chromodoridids, enabling a thorough evaluation of diagnostic traits and the effective integration of morphological data with molecular information.

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FROM DISCOVERY TO RECLASSIFICATION: A NEW GENUS AND TAXONOMIC REVISION OF *Felimida grahami* (THOMPSON, 1980) (NUDIBRANCHIA, CHROMODORIDIDAE)

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Keywords: Gastropoda, Heterobranchia, integrative systematics, color variation, sea slugs.

Nudibranch genus *Felimida* has been recovered as polyphyletic. One of the clades includes the Eastern Atlantic and Mediterranean *Felimida purpurea* and similar species. Color patterns in *Felimida* can mislead taxonomists due to the presence of species with similar coloration. We integrate molecular phylogenetics and morphology to investigate the systematics of the *F. purpurea* clade and to evaluate the range of color in *F. paulomarcioi* and its relationship to *F. grahami*. Specimens of *Felimida purpurea*, *F. grahami* and *F. paulomarcioi* were collected and photographed alive; General morphology was based on the photos of living specimens, and preserved specimens under a stereomicroscope Nikon SMZ 1500. The phylogenetic analysis was based on the COI and 16S genes, including other Felimida species as also *Chromolaichma*, and *Chromodoris*. The phylogenetic trees were rooted using *Tyrinna evelinae* (Er. Marcus, 1958). Bayesian runs consisted of 10 million generations for two independent runs in MrBayes and maximum likelihood analysis of concatenated–gene dataset was executed in RAxML. In addition to the molecular phylogeny, species diversity in *Felimida purpurea* clade was estimated through different species delimitation analyses. Bayesian and ML trees show the same overall topology. The clade including *F. purpurea*, *F. atlantica*, *F. fentoni*, *F. grahami* and *F. krohni* comb. nov. is highly supported and separated to the remaining *Felimida*, *Chromolaichma* and *Chromodoris* species. All species delimitation analyses recovered *F. grahami* and *F. paulomarcioi* as a single species. Species of the *F. purpurea* clade share characteristics in external and internal morphology, including purple and white rhinophores and gill, presence of a yellow band on the dorsal mantle edge, absence of rachidian teeth, first lateral teeth with a main central cusp and large inner and outer cusps, and a very long, thin, and coiled vagina. *Felimida grahami* presents a wide variation in the body color, the dorsal mantle ranges from white with orange or light red dots or lines to a light orange, salmon, or almost red mantle. Darker former is most commonly observed in larger specimens. Based on molecular and morphological evidence the *Felimida purpurea* clade represents a new genus, and *Felimida paulomarcioi* is a junior synonym of *Felimida grahami*. We observed wide variation in color patterns among some species, a phenomenon previously documented in certain Atlantic Chromodorididae. We demonstrate that analyzing larger number of individuals and evaluating color variation alongside other morphological and molecular evidence provides a deeper understanding of the diversity within the family.

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SHEDDING LIGHT ON THE ORIGINS OF BIOLUMINESCENCE IN DORID NUDIBRANCHS

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Keywords: bioluminescence, dorid nudibranchs.

Gastropods are the only major animal lineage in which bioluminescence evolved in freshwater, marine, and terrestrial systems, but the number of independent origins for this trait remains uncertain. Nudibranch gastropods have diverse ways to produce light, even within smaller clades like the family Polyceridae. The objective of our study is to assess how many times bioluminescence evolved in Polyceridae and investigate how bioluminescence may have evolved in this group. We collected exon-capture sequence data using an existing Doridina bait set from 44 dorids (31 Polyceridae including *Kaloplocamus*, *Plocamopherus*, and *Kalinga* specimens, and 13 outgroup taxa). We used the Qiagen Bood and Soil DNeasy kit for DNA sequencing and sent gDNA to Arbor Biosciences for exon capture library preparation and Illumina sequencing. We trimmed reads with Trimmomatic and used HybPiper to assemble target regions from read data and build data matrices, and we reconstructed phylogenies using maximum likelihood analyses implemented in IQ - TREE. We conducted species delimitation analysis to assess species numbers and investigated morphology for species descriptions and to look for potential bioluminescence tissues. Within Polyceridae, currently accepted classifications suggest at least two origins of bioluminescence; once in the subfamily Triophinae (if *Plocamopherus* and *Kaloplocamus* are sister taxa), and once in *Kalinga*, the only genus in the subfamily Kalinginae. Moreover, a recent study on *Plocamopherus* and *Kaloplocamus* highlighted that the limited information available on light production in these two genera is insufficient for determining whether bioluminescence is produced via the same mechanism. Even less information is available for Kalinga. Our preliminary analyses support the monophyly of the subfamily Triophinae in Polyceridae, including at least *Triopha*, *Kaloplocamus*, and *Plocamopherus*, which is consistent with some previous phylogenies. *Kaloplocamus* and *Plocamopherus* are also sister clades in this analysis, suggesting that these represent one origin of bioluminescence and contradicts more recent phylogenies resolving other groups in Triophinae as more closely related to Kaloplocamus. The implication of these results is a single origin of bioluminescence in Triophinae followed by diversification of the bioluminescence mechanism (intracellular vs. extracellular). Further analysis is ongoing with regard to the potential additional origin in the genus Kalinga. Investigations into the evolution of bioluminescence rely on well-supported phylogenies to determine bioluminescent origins. Our study in one nudibranch family (Polyceridae) suggests a single origin of bioluminescence in this group (for *Plocamopherus* and *Kaloplocamus*), and that the diverse bioluminescence mechanism in these two lineages is due to diversification rather than evolutionary independence. These results provide context for further investigations into how diverse modes of bioluminescence may originate and diversify.

Funding Source: No.

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A NOVEL STING: CHARACTERIZATION OF VENOM-STEALING TISSUES IN THE NUDIBRANCH *Berghia stephanieae*

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Keywords: Gastropoda, Heterobranchia, novelty, defense, immune evolution.

The emergence of novel phenotypes is an important driver of molluscan diversification, yet we do not fully understand how new traits arise. As shell-less gastropods, nudibranchs use novel defenses to protect themselves. For example, some nudibranchs steal stinging organelles (nematocysts) from their cnidarian prey, and store these nematocysts in a unique organ called the cnidosac. Despite its biological importance, the genetic and evolutionary underpinnings of this stolen defense remain unclear. To address this gap in knowledge, we established the first-ever nudibranch spatial-transcriptomic dataset in the model nudibranch *Berghia stephanieae*. We used 10x Genomics Visium Spatial Gene Expression to combine gene expression data with corresponding histological images, identifying which genes are expressed in the cnidosac. First, we cryosectioned adult *B. stephanieae* samples and placed sections on barcoded 10x Visium gene expression slides. These sections were stained with hematoxylin and eosin for morphological analysis. Next, we conducted library preparation and sequenced the Visium gene expression slides. We used 10x Genomics Cell Ranger to map reads to the *B. stephanieae* genome, and then analyzed tissue clusters using the Seurat package in R. We resolved the transcriptional identity of diverse tissues in the nudibranch *B. stephanieae*. From our data, we compared gene expression across phagocytic tissues, including the digestive gland and cnidosac. We confirmed cnidosac expression of a previously identified gene, C-type lectin macrophage mannose receptor 1. C-type lectins are a highly conserved gene family of pattern recognition receptors, typically used in innate immunity. Interestingly, we found multiple C-type lectins and other immune-related genes expressed in the cnidosac. We also found numerous C-type lectins expressed outside of the cnidosac, suggesting that only some genes in this conserved gene family are involved in nematocyst theft. Our results suggest that conserved phagocytic genetic mechanisms (e.g. those involved in innate immunity and digestion) have been co-opted for nematocyst theft in some nudibranchs, like *B. stephanieae*. These phagocytic alterations mirror those found in molluscan symbioses, where conserved pattern recognition receptors evolved new roles for identifying symbionts instead of pathogens. Through studying the genetic underpinnings of nematocyst theft, we can broaden our understanding of how gene evolution (e.g. expansion and co-option of pattern recognition receptors) leads to molluscan novelties and diversification. Here we reveal tissue-level gene expression patterns in the cnidosacs of *B. stephanieae*. Future work should combine our spatial gene expression data with single-cell RNA-sequencing to understand how phagocytic cells within the cnidosac identify nematocysts. Together,our results provide a new layer of morphological and transcriptomic information that not only furthers our knowledge of nematocyst sequestration in nudibranchs, but also enhances our broader understanding of molluscan novelty and evolution.

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BAGONG BAKAWAN SA BAKAWAN: A NEW SPECIES OF MANGROVE BUBBLE SNAIL FROM ORIENTAL MINDORO, PHILIPPINES

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Keywords: bubble snail, mangrove-associate, new species, Oriental Mindoro.

Being situated at the center of global marine biodiversity, it is no surprise that one stumbles upon an undescribed species, both in the terresetrial and marine environments. Only two species of mangrove-associated bubble snails (Heterobranchia: Haminoeidae) have so far been documented in the Philippines. Here, we report the first observation of the haminoeid *Bakawan* in Oriental Mindoro, and the description of a new species. Specimens were collected from abandoned fishponds that were recolonized by mangroves in the municipalities of Bongabong and Mansalay, Oriental Mindoro. Comparative analyses included examination and measurement of shells and buccal apparatuses (i.e. radula and gizzard plates), and DNA barcoding using cytochrome c oxidase 1 (COI) gene. All available COI sequences of Haminoeidae species from GenBank were included in the molecular analyses. Examination of the genital anatomy is still ongoing. Morphologically, *Bakawan* n.sp. is most similar to *Bakawan fusca* in that the ridges and pattern of the gizzard plates are diagonal and tapering. Though similar in shape and overlapping in size ranges, the shells of *Bakawan* n.sp. are citrine whereas fusca´s are rufous in color. Most notable is the COI sequence divergence between the two, which was 11% for uncorrected distance and 17-19% for K2P distance. We are currently examining the genital anatomy of our samples for further comparison. Neighbor-joining (NJ) and maximum likelihood (ML) gene trees of our COI sequences together with other Haminoeidae sequences rendered *Bakawan* n.sp. as a group separate from other described species of *Bakawan*. The discovery of this species in an abandoned fishpond recolonized by mangroves underscores the diversity that such environments can harbor. The spotty occurrence data on *Bakawan* in the Philippines necessitates more expeditions in mangrove ecosystems across the country.

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MACROEVOLUTIONARY PATTERNS OF FEEDING HABITS IN NUDIBRANCHIA

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Keywords: sea slugs, trophic specialization, trait evolution, diversification.

The diversification of Nudibranchia is commonly associated with their feeding preferences. Shifts in prey selection and the exploitation of new resources, including nematocyst sequestration and symbiotic relationships, seem pivotal in their evolutionary radiation. However, limited number of phylogenies integrated to ecological data constrains our better understanding of nudibranch diversification. This study aims to explore patterns of feeding habits in nudibranch evolution. Nudibranchia nucleotide sequences of mitochondrial COI and 16S genes were retrieved from public databases and refined using Perl scripts. Dietary information was compiled from literature sources and organized by species level feeding preference. Phylogenetic analyses included sequence alignment, model selection and maximum likelihood (ML) tree estimation. Divergence times were estimated based on indirect fossil calibrations from shelled heterobranchs. Ancestral feeding preferences were reconstructed, and diversification rates were estimated using a Bayesian algorithm. Diversification rates were analyzed according to food preference. A total of 1,142 species were included in the analyses. The ML tree recovered both Cladobranchia and Doridina monophyletic as well as most families and genera. Initial radiation of Nudibranchia is estimated for the Triassic period, approximately 204 Mya, and the reconstruction of the ancestral state indicates Nudibranchia last common ancestor feeding on sponges. In the Early Cretaceous, the common ancestor of Cladobranchia shift to a diet based on hydrozoans. Later, the preference for Anthozoa arose three times during the evolution of Cladobranchia. An independent transition to feeding on bryozoans has been identified in Cladobranchia about 88 mya. For Doridina, the common ancestor maintained a diet based on Porifera. Transitions in feeding habits of Doridina occurred over the time, with a shift to bryozoans in the Early Cretaceous, followed by two reversals to feeding on sponges, approximately 128 and 119 Mya. Other feeding habits, such as the consumption of ascidians, appear to have arisen twice independently in Doridina, possibly as a result of a transition from a generalist habit. Our results support previous hypothesis in indicating that the last common ancestor of Cladobranchia fed on hydrozoans, while the last common ancestor of Doridina fed on sponges. Using a comprehensive phylogeny, we were able to thoroughly map transitions between different feeding habits, including reversals to the ancestral trophic state, as observed in Doridina. Diversification analyses reveal that hydrozoan-feeding species exhibit higher diversification rates than other Nudibranchia lineages. In this study, we provide the first estimates of diversification rates in Nudibranchia. Our preliminary findings support diet as a key driver of nudibranch diversification. Multiple independent transitions in feeding habits were observed. Cladobranchia's feeding-associated traits, including nematocyst sequestration and zooxanthellae symbiosis, may underlie their elevated diversification rates. Our results underscore the importance of integrating ecological and phylogenetic data to better understand the processes shaping marine biodiversity.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES, Brazil. Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro, FAPERJ, Brazil.

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Ecology

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PICKY EATERS? SHEDDING LIGHT ON TROPHIC SPECIFICITY ACROSS NUDIBRANCHIA

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Keywords: Nudibranchia.

Diet is considered a crucial driver of diversification across the Tree of Life including nudibranch gastropods. A broadly hypothesized high trophic specificity in most species underpins many ecological and evolutionary studies. Consistent and comparable evidence of dietary specificity is, however, lacking for most lineages. We aim to shed further light on the trophic specificity of nudibranchs using DNA metabarcoding in comparison to traditional methods for the inference of prey preference. We are establishing a protocol that will (1) allow the identification of prey organisms present in nudibranch gastropod fecal pellets and to (2) test for the taxonomic diversity, or lack thereof, in nudibranch diets through DNA metabarcoding. To do so, we collected fecal samples from a diverse array of nudibranch sea slugs from New York City and Florida in 2024 and 2025. DNA was extracted from fecal samples using low-molecular weight eDNA protocols. DNA barcodes for metabarcoding were amplified using primers targeting the universally used mitochondrial CO1 and 16S regions. After amplicon sequencing, taxonomic assignments of prey taxa and diversity estimates were analyzed using tools like BOLDigger and TaxonTableTools. Despite tremendous efforts based on field observations and visual and biochemical analyses of gut contents, the sheer number of nudibranch taxa renders obtaining and comparing detailed information on the dietary ecology of nudibranch gastropods challenging. Results obtained through this pipeline will allow us to obtain high amounts of information on the trophic ecology of nudibranch gastropods alongside field observations in an integrative approach. Novel information on the taxonomic composition of prey taxa, as well as information of relative proportions of prey taxa and diversity estimates through DNA metabarcoding from fecal samples will allow the detailed comparison of the dietary diversity vs. specificity across nudibranch taxa allowing for a more comprehensive understanding of their trophic ecology. DNA metabarcoding of nudibranch gastropod gut contents will allow the scalable and comparable inference of the dietary ecology of nudibranch gastropods in concert with traditionally applied methods for the inference of their dietary preferences. The detailed information obtained through this pipeline will allow for implementation in integrative taxonomy as well as the testing of long-standing hypotheses on evolutionary scenarios and the ecological drivers of speciation in nudibranch gastropods. Understanding an organism's diet is crucial for understanding its general biology and its role in complex and changing ecosystems. Molecular dietary diversity assessments hold the potential to help us answer a plethora of evolutionary and ecological questions including the role of nudibranch gastropods in trophic networks, their abilities to adapt to changing landscapes, putative drivers of speciation, their population-scale ecology as well as their chemical and visual ecology and evolution.

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ASSESSING THE LIMITS OF EXON CAPTURE EFFICIENCY FOR PHYLOGENOMICS, USING NUDIBRANCH GASTROPODS AS A CASE STUDY

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Keywords: Nudibranchia, Doridina, Cladobranchia, exon capture.

Target capture is a powerful and cost-effective tool for phylogenomics that allows the use of older or poorly preserved specimens. A key criterion for its success is the bait-to-target DNA distance, related to the divergence rate of the group under study. In Nudibranchia, an exon capture baitset was designed for Doridina, but its broader utility remains unexplored. This study evaluates its efficacy for phylogenetic reconstruction across other nudibranch clades. Seventy-six species of nudibranchs were newly sequenced with short-read sequencing using an exon capture bait set designed for Doridina, covering both suborders and 12 of the 13 superfamilies into which Nudibranchia is currently divided. After trimming, clean reads were analyzed using the software HybPiper, which maps the reads against the baitset, assembles and retrieves the genes. Maximum Likelihood analyses were performed using IQtree. Capture efficiency was measured as sensitivity (percentage of exons covered) and specificity (the percentage of mapped reads that map to target regions), in relation with bait-to-target DNA distance. Our analyses showed a negative correlation of sensitivity and specificity with respect to the distance of the target DNA and the original bait set, varying between taxa. Doridina species extracted most of the genes from the bait set, but there was a decrease in the percentage of sequenced genes in Cladobranchia taxa, showing that the capture efficiency decreases after a threshold bait-to-target distance of approximately 30%. Previous studies have reported this distance ranging from 10% to 30%. Furthermore, the percentage of mapped reads that map to target regions also decays with distance. Although overall efficiency was lower in Cladobranchia taxa, the number of genes recovered was sufficient for phylogenetic inference. The phylogenetic relationships recovered are consistent with those previously obtained through transcriptome analyses for cladobranchs. Results of phylogenetic analyses shed light on questions that have remained controversial due to the lack of support in previous analyses, such as the position of the genus *Doridoxa* within Doridina, supporting Phyllidioidea as a monophyletic group, or the paraphyletic nature of Chromodoridoidea. Although target capture efficiency depends on the distance between bait and target genes, our analyses suggest that the threshold at which exon capture efficiency declines is around 30%. However, despite lower gene recovery in Cladobranchia compared to Doridina, we obtained well-supported phylogenetic relationships from suborder to genus level. Our findings can guide future bait set design for mollusks and allow researchers to better assess cross-lineage use of existing bait sets.

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FROM LOST TO FOUND: REDISCOVERY OF TYPE MATERIAL OF SACOGLOSSA SPECIES DESCRIBED BY ERNST AND EVELINE MARCUS

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Keywords: Heterobranchia, *Elysia*, sea slugs, collection, taxonomy.

Sacoglossan gastropods, known for their ability to retain functional chloroplasts from algal food sources, comprise 371 described species, 33 of which are found along the Brazilian coast. Of these, nine were described by Ernst and Eveline Marcus from specimens collected along the coast of São Paulo in southeastern Brazil. For decades, the type material for these species was considered lost or untraceable. Since 2022, a collection of microscope slides prepared by Ernst and Eveline Marcus and housed in the Mollusca collection at the Museu de Zoologia da Universidade de São Paulo (MZUSP) has been rediscovered and is currently under review. The material includes histological sections, radulae, cerata, and whole specimens. Reproductive and radular slides were re-examined in comparison with the original species descriptions, incorporating anatomical features, collection locality, slide labels, and handwriting by the authors. Well-stained sections were photographed using a digital camera attached to a light microscope to highlight diagnostic structures. The identified material is now catalogued in the MZUSP Malacological Collection. A total of 63 slides of Brazilian sacoglossan species described by Marcus were examined. These include: *Elysia chitwa* Er. Marcus, 1955; *Elysia evelinae* Er. Marcus, 1957; *Elysia serca* Er. Marcus, 1955; *Elysia canguzua* Er. Marcus, 1955; *Elysia cauze* Er. Marcus, 1957 – a junior synonym of *Elysia subornata* A. *E. Verrill*, 1901); and *Stiliger vanellus* Er. Marcus, 1970 – a junior synonym of *Ercolania fuscata* (Gould, 1870). Of these, 58 slides were confirmed as syntypes through comparisons with originals descriptions. With the exception of *Elysia* cauze, whose a type specimen is preserved in ethanol at the Museum of Comparative Zoology, Harvard, all other species now have their type material recovered, catalogued and accessible for further studies. The rediscovery and reidentification of these historical slides represent a valuable contribution to the taxonomy of Western Atlantic sacoglossans. By recovering original type material thought to be lost, this work restores essential taxonomic references, clarifies species identities, and highlights the enduring scientific value of museum collections and archival materials in modern biodiversity research.

Funding Source: Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro, FAPERJ, Brazil. Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPQ, Brazil. Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES, Brazil.

Diversity and Evolution of Marine Heterobranchia

Taxonomy and Systematics

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CONTRIBUTIONS TO NUDIBRANCH DIVERSITY IN SOUTH AMERICA AND THE ATLANTIC ISLANDS

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Keywords: biodiversity, Nudibranchia, sea slugs, Nudipleura, conservation.

Nudibranchs are among the most colorful and charismatic creatures in the oceans. They are shell-less marine gastropods that live on the substrate, mainly on reefs and rocky shores. They feed on other invertebrates, such as cnidarians, bryozoans, and sponges, and are sensitive to environmental changes that affect the availability of their prey. Most of the knowledge about nudibranchs in the tropical Western Atlantic and nearby regions originates from the work of Ernst Marcus and Eveline Marcus, conducted between the 1950s and 1980s. In this synthesis, we present studies on the diversity of nudibranchs along the coasts of Brazil and Argentina, as well as from certain Atlantic islands and Eastern Pacific regions. These studies were selected based on research conducted over the past 20 years. In particular, we highlight the work carried out as part of Projeto Nudibranchia over the last seven years, following the fire at the Museu Nacional in Rio de Janeiro, which completely destroyed our laboratory infrastructure. We compile results from faunal surveys conducted across various regions, studies of species complexes using an integrative approach, and discussions on the geographic distribution patterns of nudibranch species. These patterns include endemic species, species occurring both in the Caribbean and southeastern/southern Brazil - highlighting the role of the Amazon River mouth as a biogeographic barrier - and species with wide distributions across the Atlantic Ocean and other ocean basins, including exotic species. Recent research has helped clarify species complexes, uncover hidden diversity, and expand knowledge of under-sampled regions such as the northeastern Brazilian coast and South Atlantic islands. Despite the 2018 fire at our museum and the loss of our laboratory, research activities have continued through collaborative efforts, including student training. These initiatives have contributed to a deeper understanding of biogeographic patterns, larval dispersal potential, and the influence of habitat specificity on nudibranch distribution. Continued integrative taxonomic studies, the training of new specialists, and genuine collaborations, especially involving researchers from the Global South, are essential for advancing our understanding of nudibranchs and supporting the conservation of their habitats. Anthropogenic impacts on coastal ecosystems, along with climate change, pose significant threats to many species, including those that are rare or yet to be described by science.

Funding Source: Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro, FAPERJ, Brazil. Conselho Nacional de Desenvolvimento Científico e Tecnológico, CNPQ, Brazil. Coordenação de Aperfeiçoamento de Pessoal de Nível Superior, CAPES, Brazil. DAAD, German Academic Exchange Service.

Diversity and Evolution of Marine Heterobranchia

Taxonomy and Systematics

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TOWARDS A CONSENSUS NOMENCLATURE OF HETEROBRANCH GASTROPODS: THE SEARCH FOR STABILITY

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Keywords: Heterobranchs, phylogenetics, classification, nomenclature.

With the advent of modern phylogenetic systematics, principles were outlined that would hopefully produce a stable nomenclature for recognized monophyletic lineages. However, within the Heterobranchia there has been a clear lack of consensus and great nomenclatural instability, based on differing approaches to naming clades, rather than differences in phylogenetic understanding or tree topology. A series of guiding principles are recommended to help remedy this pervasive nomenclatural issue. A review of recent systematic literature of heterobranch molluscs was undertaken to determine where competing classification systems exist. After identifying where different interpretations of essentially the same phylogeny occur, careful analysis of the underlying taxonomic principles that formed the basis for these incongruities were made. Examination of philosophical differences that resulted in differing classifications were then conducted to determine commonality of issues that require greater consensus to produce more stable classifications. It is clear that this instability of classifications is problematic and that ongoing instability undermines the utility of taxonomy and taxonomists to end users of classification systems. Review of cases of recent conflicting classifications reveals several core issues that permeate taxonomic literature. In some cases, new classifications are proposed that are in conflict with fundamental principles of contemporary phylogenetic systematics. Monophyly is the core principle that it often not adhered to and new taxa are created that render existing taxa paraphyletic or polyphyletic. In other cases, new taxa are erected instances where the phylogeny is not fully resolved and polytomies are present in the consensus phylogenetic trees. In other cases, new higher taxa are described in groups where large numbers of new taxa are known to exist but remain undescribed and have not been included in phylogenies. In these cases, interim solutions should be proposed, but creation of new higher taxa should be avoided. In many cases, new phylogenetic trees generate new understanding of relationships that require significant adjustments to our phylogenies and the resulting classification is absolutely required. In other cases, phylogenies further illuminate the diversity of lineages within known taxa, but major taxonomic changes in higher taxonomy are proposed simply because there is greater species richness and morphological diversity recognized. These types of changes cause unnecessary disruption of taxonomy and should be avoided. There is also a propensity for taxonomic inflation of names and ranks that is not reflective of new understanding of relationships, just more taxa included within those lineages. Resisting the temptation to create taxonomic inflation is paramount to achieving greater stability in our classifications. The issue of creating stable nomenclature has plagued taxonomy since its beginning. Modern phylogenetic systematics has created new opportunities for generating greater stability, but this goal has fallen short of its potential promise. New understandings of diversity must be reflective of changing views of relationships, but creation of new higher taxa must be tempered with serving end users of our classification systems if taxonomists want to remain relevant and valued.

Funding Source: This work was supported by the California Academy of Sciences Hope for Reefs Initiative and funding from the National Science Foundation DEB 1856407.

AMS PRESIDENT'S SYMPOSIUM – TEACHING AN OLD MOLLUSK NEW TRICKS: INNOVATIVE RESEARCH USING MUSEUM COLLECTIONS

AMS PRESIDENT'S SYMPOSIUM – TEACHING AN OLD MOLLUSK NEW TRICKS: INNOVATIVE RESEARCH USING MUSEUM COLLECTIONS

Coordinator:

JINGCHUN LI – CU Natural History Museum, Dept. of Ecology & Evolutionary Biology, University of Colorado, USA

Combined Symposium Day on Innovation and Care of Mollusk Museum Collections

This year, the American Malacological Society and the Society for the Preservation of Natural History Collections (SPNHC) are excited to collaborate on a special symposium centered around Innovation and Care of Mollusk Museum Collections. The event highlights the crucial role of museum collections in advancing research and conservation efforts within malacology, while also focusing on innovative methods for maintaining and utilizing these invaluable resources.

Morning Session: AMS President's Symposium – Teaching an Old Mollusk New Tricks: Innovative Research Using Museum Collections. The morning symposium will feature invited speakers who are pioneering research projects utilizing mollusk museum collections in novel and groundbreaking ways. These presentations will demonstrate how historical collections can drive modern scientific discoveries, from evolutionary studies to ecological restoration and beyond.

Afternoon Session: Participant Symposium

In the afternoon, the symposium will feature presentations from meeting participants, showcasing diverse perspectives and new research centered on the care, digitization, and application of mollusk collections. This session will offer an opportunity for attendees to engage directly with the wider community, fostering collaboration and the exchange of ideas.

Join us for a day of cutting-edge research and thoughtful discussion on the future of mollusk museum collections.

AMS President's Symposium – Teaching an Old Mollusk New Tricks: Innovative Research Using Museum Collections

Collections

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UNLOCKING THE UNLIMITED: REALIZING THE POTENCIAL OF MUSEUM COLLECTIONS IN A MODERN WORLD

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Keywords: natural history, wet and dry collections, Indian Ocean, innovation, applications, molluscs.

Research utilizing museum collections of molluscs informs about new species, local extinctions, range shifts, key innovations, family trees, ocean acidification, marine reservoir effects not to mention the intersection between art and science and social history. Innovative methods to elicit new information from legacy specimens coupled with the increased challenge of obtaining new material, makes existing collections precious and valuable. The WA Museum based in Perth, Australia is one of the most isolated institutions in the world and is the hub for arguably the most exciting biodiversity frontier, the Indian Ocean. However, from a collection's perspective, it is also located in one of the most highly regulated countries in the world. Featured projects are shared that highlight how our team supports innovative research despite massive challenges to ensure 'no mollusc gets left behind'.

Funding Source: No.

AMS President's Symposium – Teaching an Old Mollusk New Tricks: Innovative Research Using Museum Collections

Collections

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THE MOLLUSC COLLECTION OF OSWALDO CRUZ INSTITUTE – FIOCRUZ: FROM PROMINENT DISCOVERIES FOR PUBLIC HEALTH IN BRAZIL TO INNOVATIVELY PROMOTING MOLLUSCS IN A PLAYFUL WAY

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Keywords: non-marine molluscs, integrative studies, public health, agricultural pests, biodiversity repository.

The Mollusc Collection of the Oswaldo Cruz Institute (CMIOC), initiated in 1948, was founded on the pioneering taxonomic work of Dr. Lobato Paraense on *Biomphalaria*—vectors of schistosomiasis, a major public health concern in Brazil. Since then, CMIOC has evolved into a multidisciplinary resource, supporting studies in taxonomy, ecology, and conservation of non-marine molluscs, highlighting its growing relevance to science and society. Examples of some of those studies will be presented. CMIOC's holdings were initially built through extensive fieldwork by Dr. Paraense and later expanded by the Laboratory of Malacology team, with collections from type localities across Brazil, South America, and the Caribbean. Continuous contributions from specialists through specimen donations and collaborative studies have enriched the collection. This study analyzes the trajectory of scientific output based on CMIOC specimens—ranging from classical taxonomy to phylogeography and ecology—over the last 77 years. It also documents public engagement strategies, including participation in science fairs and institutional education projects, aimed at promoting awareness of scientific collections among students and the broader community. The CMIOC currently houses 15,773 lots comprising approximately 200,000 specimens from 61 countries, predominantly freshwater and terrestrial gastropods. These include species relevant to public health (e.g., vectors of schistosomiasis, fascioliasis, angiostrongyliasis), agriculture (notably exotic pest species), and native fauna from all Brazilian biomes. The freshwater gastropods represent 24 families, while terrestrial gastropods span 42 families and bivalves 6 families. Planorbidae is the most represented family (7,853 lots), followed by Ampullariidae (1,968 lots). From foundational conchological and morphological studies by Paraense to recent research on evolutionary relationships, species invasions, and ecological interactions, CMIOC has supported a diverse scientific agenda. The collection's legacy also extends to public health services and education. Its outreach includes interactive displays at national science events such as "Fiocruz Pra Você" and the "Semana Nacional de Ciência e Tecnologia", fostering public interest in medical and applied malacology. Moreover, institutional programs bring scientific collections into public school classrooms, emphasizing the role of molluscs and collections in science and conservation. These initiatives have increased the collection's visibility and engagement with a broader audience. Initially developed for public health research, CMIOC has become a multifaceted center for science, education, and outreach. In the face of accelerating biodiversity loss, CMIOC stands as a critical repository of molluscan diversity from Brazil and beyond. Its integrated approach not only supports research but also fosters societal appreciation for biodiversity and the vital role scientific collections play in conservation and knowledge preservation.

Funding Source: FIOCRUZ, FAPERJ, CAPES, CNPQ, NIH.

AMS President's Symposium – Teaching an Old Mollusk New Tricks: Innovative Research Using Museum Collections

Taxonomy and Systematics

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TAXON-OMICS AND MUSEOMICS PERSPECTIVES ON HETEROBRANCHIA – A CASE STUDY OF ACTEONIMORPHA AND RINGIPLEURA

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Keywords: phylogenomics, target enrichment, systematics, Nudibranchia, sea slugs.

The phylogeny of Heterobranchia—a clade of ~44,000 gastropod species—remains incompletely resolved. Here, we clarify Acteonimorpha as sister to Ringipleura and resolve family- and genus-level relationships in Pleurobranchida and Nudibranchia (Cladobranchia, Doridina). By integrating UCE phylogenomics with Sanger-sequenced markers and dense taxon sampling, we fill major backbone gaps. Future phases will assess COI mini-barcoding via portable nanopore sequencing of museum specimens to extend this framework to underrepresented taxa. We applied a custom UCE target-enrichment probe set (2,259 loci) to genomic DNA extracted from both fresh and century-old museum specimens, with libraries sequenced on Illumina platforms to establish a robust phylogenomic backbone of Heterobranchia. To resolve shallow divergences, we generated multilocus Sanger sequences (COI, 16S, 28S, H3) from the same specimens and incorporated publicly available datasets. Raw reads underwent quality trimming, assembly, and alignment via established bioinformatic pipelines; UCE loci and Sanger markers were concatenated for joint analyses. Phylogenetic inference employed maximum-likelihood (IQ-TREE) and coalescent (ASTRAL) methods. Future phases will assess MinION nanopore workflows using 313 bp COI mini-barcodes. Our combined UCE and Sanger-sequenced matrices deliver a robust, multilocus phylogeny that resolves key relationships within Heterobranchia. Acteonimorpha is unambiguously recovered as sister to Ringipleura, settling a century-old debate. In Pleurobranchida, analyses of 94 taxa—including type species of all genera—reveal a novel superfamily Tomthompsonioidea as the earliest-diverging lineage, characterised by a helicoid shell and absent acidic oral gland, while *Euselenops* nests within Pleurobranchaeidae and *Berthella* is split into four clades, including the new *Tomoberthella*. Regarding Nudibranchia with up to 200 species, Doridina is monophyletic and includes Bathyodoridoidea as the sister group to all other dorids; *Vayssierea* and *Gymnodoris* affiliate with Polyceridae; and Onchidoridoidea is paraphyletic, indicating the need for revision. Cladobranchia encompass the superfamilies Aeolidoidea, Fionoidea, Dendronotoidea, Arminoidea, Proctonotoidea, Doridoxoidea and Tritonioidea. Elusive genera such as *Curnon*, *Pseudotritonia*, *Heterodoris* and *Doridoxa* find their places for the first time, filling long-standing gaps. While our Sanger markers strengthen resolution of recent divergences and validate species boundaries where UCE data remain sparse, the promising future application of COI mini-barcodes via portable nanopore sequencing will further extend this framework to underrepresented and degraded museum specimens. By integrating UCE phylogenomics with Sanger-sequenced markers and dense taxon sampling—core lines of research at The Slug Lab—we have resolved key Heterobranchia relationships: confirming Acteonimorpha as sister to Ringipleura, clarifying Pleurobranchida and Nudibranchia lineages, and placing elusive genera within a unified phylogeny. This multilocus framework fills major backbone gaps and sets the stage for future portable nanopore COI mini-barcoding of museum specimens, advancing biodiversity discovery, taxonomy, and conservation.

Funding Source: Spanish Ministry of Science, HETGEN1000 project (PID2021-127037NA-I00/MCIN/AEI/10.13039/501100011033/ and by FEDER una manera de hacer Europa).

SYMPOSIUM: MOLLUSCAN MICROBIOME / EMERGING IMAGING TECHNOLOGIES IN MALACOLOGICAL STUDIES

MOLLUSCAN MICROBIOME / EMERGING IMAGING TECHNOLOGIES IN MALACOLOGICAL STUDIES

Coordinators:

PRISCILA M. SALLOUM – University of Otago, New Zealand
DANIEL CARACANHAS CAVALLARI – USP, São Paulo, Brazil

Microbes are everywhere, including within animals. Molluscs are incredibly diverse and understanding how their associated microbes interact with them will help shed light not only on the specifics of molluscan microbiomes, but also on the overall evolution of the most diverse dynamics between hosts and their microbial symbionts. Microbiomes have the superpower to modulate their hosts characteristics and how their hosts interact with their surroundings. The number of microbiome studies in molluscan research has been growing pointedly in recent years – highlighting the interest of the malacological community in this new field of study, as well as its potential for innovation. This symposium will aim at covering all microbiome research involving molluscs as hosts of a microbial community, comprising aquaculture, response to anthropogenic and environmental stress, ecological and evolutionary perspectives on molluscs-microbes associations, and descriptions and isolations of microbes from molluscs. In addition, the symposium will bring together researchers and experts to explore how innovative imaging techniques are advancing our understanding of mollusks. We intend to focus on a range of imaging methods, including Micro-Computed Tomography (Micro-CT), Magnetic Resonance Imaging (MRI), fluorescence imaging, Optical Coherence Tomography (OCT), Synchrotron Radiation Microcomputer Tomography (SRμCT), and other cutting-edge technologies. Participants will examine how these techniques are integrated into malacological studies and how they enhance our ability to visualise and analyse mollusk anatomy, physiology, development, diversity, and evolution. In addition to presentations, the symposium will create a dynamic environment for researchers to exchange experiences, encouraging discussions on methodologies, findings, and best practices.

Molluscan Microbiome / Emerging Imaging Technologies in Malacological Studies

Other themes

Oral - 50

TRENDS, GAPS, AND FUTURE PERSPECTIVES IN MOLLUSCAN MICROBIOME RESEARCH

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Keywords: Mollusca, microbiome, systematic review, anthropogenic stress, host–microbe interactions.

Our understanding of host-microbiome interactions is limited. Research on animal microbiomes has mostly been done in a select group of organisms, failing to represent the large diversity of these interactions. To understand the impact of host-microbiome associations in the overall evolution of life, microbiome research needs to diversify. Groups such as molluscs, with large diversity and widespread distribution, hold huge potential to elucidate the ecological and evolutionary impacts of microbiomes. In April 2024, we undertook a systematic review of the literature on molluscan microbiomes. Our aim was to describe the current focus of microbiome research in malacology, identify strengths, point out knowledge gaps, and propose future directions. We searched the Web of Science for the keywords Mollusc* AND Microbiome*, which resulted in 921 articles. This raw dataset was then filtered to 276 articles, all of which matched a set of rules that ensured our final dataset was suitable to answer our questions. Of the studies in our dataset, 64% were on bivalves, while Polyplacophora, Scaphopoda, Monoplacophora and Aplacophora were not represented. The habitat of 70% of the molluscs assessed in these studies was marine, but more research is needed on terrestrial molluscs, those in mangroves, and in the deep sea. Most studies assessed the microbiome in the molluscan gut, in line with the overall microbiome literature, but there are studies of molluscan microbiomes focusing on a diverse range of tissues (e.g., haemolymph, gills). The microbiome can be tissue-specific, and assessing it in different tissues can reveal its impact on host traits that are not necessarily influenced by the microbial community in the gut. We identified that many studies in our dataset aimed to describe the role of the microbiome in molluscan stress responses to various factors, mostly related to anthropogenic pressure. However, the methodological approaches used mostly enable characterisation of the taxonomic composition of bacterial communities, possibly due to challenges involved in functional microbiome analyses and in assessing other components of the complex microbial community (e.g., fungi and viruses). Despite this, although still slow, there has been an increase in studies targeting functional microbiome characterisation, as well as a more holistic approach towards assessing microbiomes beyond bacterial communities. Commercial species in aquaculture facilities are likely the most accessible models for more complex microbiome studies, and partnerships with the aquaculture sector are one of the strengths in malacology. Our literature review highlighted that research in malacology has contributed to the overall knowledge of microbiome interactions with animal hosts, particularly in the context of anthropogenic pressure. However, our review also reiterates that there are biases in terms of molluscan species and habitats studied. The huge molluscan diversity remains largely untapped and has unparalleled potential to advance our understanding of the eco-evolutionary impacts of microbiome-host interactions.

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Molluscan Microbiome / Emerging Imaging Technologies in Malacological Studies

Evolution

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DRIVERS OF MICROBIAL DIVERSITY IN VENOMOUS MARINE SNAILS

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Keywords: Conidae, microbiome, geography, Pacific Islands, symbiosis.

Conus sponsalis, a species of marine venomous snails, occurs widely across the Indo-West Pacific and represents an excellent system for determining how microbial communities associated with marine organisms vary across geographic scales and what factors drive this variation. This research sheds light on ecological and evolutionary associations over different scales, elucidating biogeographical relationships between cone snails and microbes. We collected *Conus sponsalis* samples from populations in Hawaii, Guam, American Samoa, and multiple islands in French Polynesia (Huahine, Rangiroa, Rurutu, and Makemo). We characterized the venom duct microbiome using the V4 region of the 16S rRNA. To identify the microbiome structure, we used alpha (Shannon, Simpson) and beta diversity metrics (Bray-Curtis dissimilarity). We determined if there are correlations between microbial composition and geographic distances over small and large geographic scales (>400-10,000 km) using Mantel tests to identify whether closer locations have more similar microbiomes than distant ones. Finally, we used machine learning modeling (Random Forest) to predict associations between microbiome composition and geographic locations. We found more than 2,900 amplicon sequence variants (ASVs) of both Bacteria and Archaea. We identified Proteobacteria, Bacteroidota, and Campilobacterota as the most abundant bacterial phyla. We also identified bacteria previously described in cone snails and other venomous marine and terrestrial taxa (Stenotrophomonas, Nocardiopsis, Actinomycete). Dissimilarity in microbial communities was observed across islands with a significant difference and structure of the cone snails' microbiome that is associated with geography (Bray-Curtis, $p < 0.01$; Mantel test, $p < 0.004$). Moreover, our predictive machine-learning model showed good performance and a high (0.7) classification accuracy when using our microbial communities to predict the location of collected samples with a low false positive rate at various threshold settings. The results suggest that geography plays a significant role in the structure of *C. sponsalis* population microbiomes, and particularly, our predictive modeling also supports geographic location as being important in microbial community structuring. Finally, the presence of bacteria in multiple venomous taxa might suggest that these microbes could be adapted to this microenvironment, but also that they can be participating in the venom production, acting as potential symbionts in venomous mollusks and other animals. Geography plays a significant role in the structure of Conus microbiomes across West Indo-Pacific, but the factors driving differences tend to be host-dependent. Venom could be a relevant factor driving microbiome diversity in venomous snails that should be contemplated in future research. It is important to perform multifactor approaches (testing both host-related and environmental factors) to better identify how mollusk microbiomes assemble and persist through time (holobiont approach).

Funding Source: EEB Department and Rackham Graduate School (University of Michigan), Award from Belmont Forum and NSF (Award no. 2022885).

Molluscan Microbiome / Emerging Imaging Technologies in Malacological Studies

Anatomy and Physiology

Oral - 65

FREEZING TOLERANCE IN MOLLUSC, WHAT WE KNOW ABOUT MICROBIOM IN SNAILS?

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Keywords: microbial inoculation, microbiota, *Helix pomatia*, supercooling point, cold stress.

Molluscs characterize a large amount of water content, therefore, they are good models for the investigation of general aspects of freezing tolerance including processes of adaptation e.g. microbiota having ice-nucleating activity and storing cryoprotectants. The aim of study was to check 1) if microbial communities help snails of temperate zone survive freezing during winter and 2) how they lower the supercooling piont of hosts body fluids. Experiments were performed on *Helix pomatia* L. snails gathered from their natural habitat in the vicinity of Toruń (central Poland, 53°02'N, 18°35'E) during the year. The middle part of the intestine was chosen for identification of the snails' gut microbiota. The piece of the gut was homogenized in saline solution (0.85% NaCl). Microorganisms isolated from snails intestine were identified on the basis of the 16S rDNA gene sequence. The strains were applied to the different groups of snails in the form of the microbial preparation. The next experiments relaying on measurement of the supercooling point of snails body fluids (SCP) were performed. The microbiological preparation contained the following strains: *Microbacterium algeriense*, *Buttiauxella agrestis*, *Luteimonas* sp. and *Chryseobacterium balustinum*. The microbial preparation, used as a diet supplement, isolated from overwintering snails, had an impact on the lowering of the supercooling point of the *H. pomatia* snails. It is possible that supplemented bacterial strains work as ice nucleating agents, but they could also overproduce cryoprotective substances. Moreover, it is also possible that their metabolites enter the reaction cascades or cycles, leading to a decrease in the supercooling point temperature. This allows us to plan further projects aimed at understanding the mechanisms responsible for partial freezing tolerance of *H. pomatia* snails on many different levels of unit organization. The overwintering of *Helix pomatia* snails can be analyzed on many levels, starting from microbial composition and low molecular mass cryoprotectants accumulation and ending with the elevation of production of HSPs and CSPs (Idczak-Figiel et al., 2023 unpublished), making an intricate mechanism that allows them to survive temperatures below the freezing point of their body fluids.

Funding Source: This work was partially supported by Grants4NCUStudents grant "SUPPLEMENTS FOR SNAILS: WHAT, WHEN AND WHY" under the "Excellence Initiative - Research University" program at Nicolaus Copernicus University in Toruń.

Molluscan Microbiome / Emerging Imaging Technologies in Malacological Studies

Ecology

Oral - 160

NOT JUST FILTER FEEDERS: INVESTIGATING BIVALVES AS BIOLOGICAL BARRIERS TO PARASITE TRANSMISSION

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Keywords: freshwater mussels, filtration, bivalves, ecosystem functions.

Freshwater bivalves are key ecosystem engineers, influencing aquatic communities through habitat modification and filtration. They may also modulate parasite populations with aquatic life stages. We investigated their role in the dynamics of *Angiostrongylus cantonensis*, a parasitic nematode occurring in water in two life stages and potentially using bivalves as paratenic hosts. Ecological interactions between freshwater bivalves and nematode *Angiostrongylus cantonensis* were investigated through a series of controlled microcosm experiments. We assessed the ability of selected bivalves found in central European waters (*Anodonta anatina*, *Sinanodonta woodiana*, *Dreissena polymorpha* and *Corbicula fluminea*) to reduce parasite density in the water column, their potential to support development of first-stage larvae into the infectious third stage, and their suitability as paratenic hosts for third-stage larvae. Additionally, we included freshwater gastropods (*Biomphalaria glabrata*) in selected trials with *C. fluminea* to evaluate whether bivalves can limit parasite transmission to intermediate hosts under varying turbulence regimes. Our study demonstrated a stage-specific interaction between freshwater bivalves and *A. cantonensis* larvae. First-stage larvae were significantly reduced by bivalves, with no evidence of successful development to the infectious third stage within bivalve tissues. In contrast, free-living third-stage larvae were not removed from the water column and were able to infect certain bivalve species, reaching densities of up to 2.48 larvae per gram in *S. woodiana*. The observed reduction in first-stage larvae appears to result from both filtration and increased environmental complexity via shell production; however, only filtration significantly impacted parasite transmission to sympatric intermediate hosts. Notably, these effects were absent under stagnant water conditions, highlighting the influence of hydrodynamic regimes on bivalve-mediated parasite control. Freshwater bivalves show potential significantly reduce spread of aquatic stages of parasitic organisms, as demonstrated on the model system including selected freshwater bivalves and parasitic nematode. However, the complexity of parasite life cycle has to be considered, as the bivalves can serve as a potential paratenic hosts for more developed life stages.

Funding Source: The study was supported by the Czech Science Foundation [22-26136S]. Animal handling and experimental procedures were conducted in full compliance with ethical standards and under the authorization of the Ministry of Education, Youth and Sports (No. MSMT-23125/2022-4).

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Parasitology

Oral - 148

PARASITES CAN MODIFY THERMAL PREFERENCES OF FRESHWATER SNAIL HOSTS - IS THE HOST IN THE WIZARD'S HANDS?

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Keywords: parasites.

An exciting group of parasites connected with freshwater (mainly) molluscs are trematodes. Most species use freshwater snails as first intermediate hosts of Digenea - trematodes with a complex life cycle. Digenetic larvae can alter host populations' parameters, because infected hosts can differ from non-infected ones in behaviour and/or susceptibility to environmental conditions. In the face of global changes, we ask about parasites' s influence on host' s thermal preferences. We studied the seasonality of natural infection of Digenea in *Lymnaea stagnalis* and *Planorbarius corneus*, collecting snails in lakes of normal conditions for temperate climate and thermally polluted ones. Thermal preferences of snails were investigated experimentally using an oblong thermal gradient. The factors influencing thermal behaviour were parasites and, additionally, pathogen pyrogens. We observed host survival, fecundity, and parasite larval productivity by keeping snails in a constant thermal condition (according to the results of the previous experiment) and using natural photoperiod in a laboratory. In both experimental studies, we used naturally infected snails and parasite-free individuals. We examined nearly 12.000 individuals. The changes in parasite prevalence in snail populations depended on the season. The seasonal algorithm of some parasite species differed in snail populations from lakes with a natural thermal regime compared to those from thermally polluted lakes. Studies on the thermal behaviour of snails establish that both parasite species and parasite stage affect the thermal preferences of hosts. Snails under the influence of bacterial or fungal pyrogens can generate behavioural fever, and individuals infected with fluke larvae generate the opposite reaction, called behavioural anapyrexia. Some species disrupt this defence reaction, contributing to increased mortality of hosts. Increased temperature of laboratory culture also affected the shortening of snail life, especially in the group of infected individuals. Increased mortality of hosts could result from an increased rate of release of parasitic larvae, causing damage to the snails' bodies. Depending on how parasites are transmitted, such increased mortality of hosts could be essential to maintaining the parasite in the environment. Temperature is an essential factor in seasonal changes in parasite prevalence in populations of the studied snail species. The decrease in several infected snails in the shore zone of lakes has resulted from increased snail mortality and/or a change in the hosts' thermal preferences. Differences in the parasitic invasion in snails from thermally polluted lakes compared to those from lakes with a natural regime result from adaptations in snail-fluke system.

Funding Source: No.

Molluscan Microbiome / Emerging Imaging Technologies in Malacological Studies

Evolution

Oral - 397

SPATIO-TEMPORAL CHARACTERIZATION OF LIGHT ORGAN GENES AND PROTEINS DURING EMBRYOGENESIS: HOW THE SYMBIOTIC ORGAN SHAPES ITS INTERNAL ENVIRONMENT FOR SYMBIONT INTEGRATION

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Keywords: *Euprymna scolopes*, *Vibrio fischeri*, host-microbe symbiosis, embryonic development, antimicrobials.

The Hawaiian bobtail squid *Euprymna scolopes*, from hatching through the entire lifespan, maintains a symbiotic association with the bioluminescent bacterium *Vibrio fischeri*. Decades of research have elucidated postembryonic development and maturation of the light organ (LO). However, in this association and other horizontally transmitted symbioses, little is known about how the host embryo prepares the nascent tissues for initial symbiont colonization. In this study, we characterized genomic features and biogeographic expression of specific genes and their associated proteins during and following embryogenesis. We used Hi-C (high-throughput chromosome conformation capture-based technologies), chromatin accessibility mapping, and transcriptomic profiling to investigate the regulatory landscape of LO-associated genes. We visualized the transcripts by in situ hybridization chain reaction (HCR) and the corresponding proteins were detected via confocal immunocytochemistry (ICC). Finally, to gain spatially resolved molecular insights, we applied a combination of immunocytochemistry and NanoSIMS (nanoscale secondary ion mass spectrometry) to analyze isotopic labeling patterns and subcellular localization of biomolecules. Our study revealed that several LO genes show precipitous increases in expression during late embryogenesis. Members of two families of 'antimicrobials', galaxin (EsGal1E) and a halide peroxidase (HPO), were among these upregulated genes. During embryogenesis, the initiation of EsGal1 and HPO production occurs as the first pair of crypts begins to form, indicating co-evolution between the proteins and the host's development of biogeographic conditions that will facilitate the reception, selection, and eventual accommodation of these bacterial partners. We also characterized the patterns of these genes and proteins following embryogenesis. As previous studies had shown that symbiont light production is critical for persistent colonization, we used mutants in *V. fischeri* light production (Dlux) to explore whether normal biogeographic patterns of the antimicrobials occur in colonization with dark mutants. NanoSIMS analysis revealed that dark mutants fail to develop the normal patterns in hatchling animals. These findings highlight the crucial role of light production in antimicrobial protein expression and the host's embryonic preparation for symbiosis. The patterns of embryonic preparation for symbiosis described in this study are likely conserved across other bacterial-epithelial associations in the animal kingdom.

Funding Source: No.

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Anatomy and Physiology

Oral - 229

SNAILS FROM THE INSIDE OUT: EXPLORING THE SOFT ANATOMY OF GASTROPODS THROUGH CT

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Keywords: computed tomography, specimen digitization, three-dimensional anatomical atlas, anatomical imaging.

Computed tomography (CT) has become an increasingly important tool in molluscan research over the past decades. Although it has been most extensively applied to shells, CT has also been shown to be a powerful tool in examining and describing the complex soft anatomy of molluscs. In this presentation, we discuss the potential of this technology for anatomical research on gastropods, based on recent and ongoing studies by our research group. In a recent example, we used CT to describe the anatomy of the magician tree snail *Drymaeus magus* (Stylommatophora: Bulimulidae). We employed a tailored contrast-enhancing protocol based on PTA to highlight the soft tissues of the studied specimens, which were subsequently scanned in a high-resolution CT scanner at Centro para Documentação da Biodiversidade (FFCLRP-USP), Ribeirão Preto, Brazil. The resulting images were used to reconstruct 3D models of the internal organs of *D. magus* and serve as the basis for the entire description of its soft anatomy. Similar methodologies, including other contrasting solutions and protocols, are being developed and refined in ongoing studies by our research group. The high-definition CT images obtained were used to produce a comprehensive description of *D. magus*, reaching a level of complexity similar to traditional anatomical studies. In addition to their high resolution, CT images also provided a more integrated view of the snail body plan by showing the topology of organs inside an intact organism. The resulting 3D anatomical atlas of *D. magus*, now available on the MorphoMuseuM platform, is the most complete reconstruction of a land snail to date, providing valuable and easily accessible data on its anatomy for future studies. Remarkably, the images were obtained in a relatively short processing period and with minimal damage to the specimens. Taking from our experience with *D. magus*, we now seek to expand our usage of CT to larger-scale studies and different gastropod taxa, building a database of 3D anatomical atlases of gastropods. Among our next steps, we are conducting a taxonomic review of the limpet genus *Lottia* (Patellogastropoda: Lottiidae) in Brazil, employing CT to perform a highly detailed comparative anatomical study of the four closely related species that occur in the country. We also intend to continue testing and optimising contrast-enhancing protocols and image acquisition techniques to push the boundaries of CT in molluscan research. Our results highlight the potential of CT for research on gastropod anatomy and taxonomy. Its main advantages over traditional techniques are its non-invasive nature, relatively faster processing time, and greater accuracy in representing volumetric proportions and organ topology. We expect that CT will be increasingly incorporated into future studies on molluscs, representing a new frontier in molluscan anatomical research.

Funding Source: MSc fellowship by FAPESP (process 2024/18231-3) to RMR.

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Taxonomy and Systematics

Oral - 252

THE TOMOGRAPHY BY SYNCHROTRON LIGHT AS A NEW TOOL FOR MORPHOLOGICAL STUDIES OF MOLLUSCA: OBSERVATIONS OF A SPECIES OF CAUDOFOVEATA

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Keywords: MOGNO, Brazil, Caudofoveata, morphology.

The morphological features of molluscs are studied by different techniques of microscopy. Those of Caudofoveata, however, are often observed by only light and scanning electron microscopes, and for this, knowledge about their tissues is still very restricted, especially for small species. This work seeks to show some results obtained by tomography using synchrotron light. Specimens of *Scutopus variabilis* Passos, Corrêa & Miranda, 2021 were collected in the Brazilian southeastern coast, then fixed in 4% formaldehyde and maintained in 70% ethanol. After passing in a contrast solution of 0,3% of phosphotungstic acid (PTA) with 3% of dimethylsulfoxide (DMSO), they were observed in two ways – in liquid (100% alcohol) and solid (embedded in historesin) conditions – in the MOGNO beamline of the Brazilian Center for Research in Energies and Materials (CNPEM), where high-resolution images of these samples are obtained by absorption tomography. In both conditions, 3D images show important features used in the taxonomy of caudofoveates, such as details off the oral disc, the ornamentation and the spatial arrangement of the spicules on the animal's body, and the structure of the radula. Also, details of the pallial cavity were clearly distinguished, as the bipectinate gills, as well as internal characters, such the structure of nervous system (including the pairs of ganglia and the nerve cords), and the organs of the digestive system. Interestingly, these observations could be compared and complemented by conventional histology made by microtomization of the same samples. The results confirm the applicability of PTA + DMSO, as all specimens exhibited tissues with good contrast; 12 hours of staining in this solution were enough. Each sample was tomographed in about ten minutes. The small size of aplacophorans - which in general reach a few millimeters - imposes difficulties in dissections but is not an impediment for tomography using synchrotron light. However, admittedly, this is not an easily accessible technique, as beamlines are linked to particle accelerators. Anyway, the success of this modern methodology is evident, allowing important characters to be greatly improved.

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SYMPOSIUM: PALAEONTOLOGY OF MARINE CENOZOIC MOLLUSCS

PALAEONTOLOGY OF MARINE CENOZOIC MOLLUSCS

Coordinator:

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Molluscs appear in the fossil record in the Cambrian Period, have had a rich evolutionary history and represent today the largest group of animals – in terms of species diversity – in marine environments. During the Cenozoic, molluscs have witnessed major climatic changes, undergone periods of rapid diversification or extinctions, and now face various risks due to human activities and rapid climate change. Their ecological adaptations, good preservation potential in the fossil record and ability to record environmental conditions in their shells make them a key material for understanding a wide array of research questions. The Symposium welcomes presentations on all aspects of the study of fossil and sub-fossil molluscs of the Cenozoic (incl. Holocene), such as: (1) Taxonomy and Systematics of molluscs; (2) Molluscs through rapid environmental changes and crises; (3) Evolution of molluscs; (4) Paleoecology of molluscs and (5) Molluscs in conservation paleobiology.

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Palaeontology

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INTEGRATING GASTROPOD AND MICROFOSSIL DIVERSITY TO UNRAVEL PALEOENVIRONMENTAL TRENDS OF THE MIOCENE SUCCESSION OF THE DWARKA BASIN, WESTERN INDIA

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Keywords: gastropods, microfossils, Miocene, diversity, paleoenvironment.

The Neogene marine succession of the Dwarka Basin, western India, is rich in diverse molluscs but lacks detailed diversity studies. In the Miocene succession of this basin, the Gaj Formation (Aquitanian - Langian) has seven members, many with molluscan fossil-bearing beds (Jain, 2014; Bose et al., 2023). This study examines the temporal variation in gastropod and microfossil diversity and paleo-community structure to reconstruct the depositional history of Gaj Formation. Sample-size of 11495 gastropod specimens was analysed for the diversity study, collected from eight distinct units of the Gaj Formation - namely, Nma, Nmb, Kur, Ran, Asm, Chk, Low, and DM. To visualize the temporal variation in taxonomic diversity, diversity metrics like species richness, dominance, etc, were employed. Ecological diversity was assessed through construction of 3-D ecological morphospace defined by three axes representing key gastropod life habits: Tiering, Motility, and Diet. Temporal abundance data were further analysed using cluster analysis and ordinated with multivariate techniques such as Correspondence Analysis and nMDS to evaluate the structure of gastropod paleo-communities. Additionally, thin sections were studied to document the associated foraminiferal diversity. The overall gastropod diversity from the Gaj Formation comprises 95 species belonging to 70 genera. Cluster and multivariate analyses reveal four distinct gastropod paleo-communities (PCs) corresponding to specific stratigraphic units. PC1, represented by the Nmb UNit, is a turritelline-dominated assemblage (TDA) with turritelline gastropods - semi-infaunal suspension feeders - accounting for 96% of the assemblage. The presence of associated microfossil assemblage of Rotallida group, Ammonia, and other benthic foraminifers indicates a warm, tropical, nutrient-rich, subtidal-intertidal setting. PC2, represented by the Asm Unit, hosts a Vicarya-rich assemblage, with Vicarya - an epifaunal herbivore-grazer known to inhabit mud flats and mangrove swamps - being the dominant taxon in association with strombid, naticid, and conid gastropods. The unit lacks microfossils, likely due to their poor preservation potential in mangroves. These features support an intertidal-mudflat/mangrove environment. PC3, from the DM unit, exhibits a strombid-dominated assemblage, with strombid gastropods constituting 53% of the assemblage, along with ampullinids, naticids, cypraeids, nassarids, and conids. The associated microfossil assemblage is abundant in Archaias, indicative of a shallow, warm, low-energy, back-reef setting. PC4 includes the remaining units (Nma, Kur, Ran, Chk, Low) and shows a mixed assemblage of abundant strombids, naticids, cypraeids, conids, ampullinids, and volutids. The associated microfossils - Rotillida, Ammonia, Archaias, and Miliolida - suggest a deposition in a low-energy, open marine environment within a middle to inner ramp setting. The results highlight the dynamic nature of marine depositional environments and their close relationship with marine ecosystems. The study successfully demonstrates the temporal variation in Miocene gastropod community structures and associated foraminifera assemblages in the Dwarka Basin of western India, in conjunction with shifting paleoenvironment settings.

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Palaeontology of Marine Cenozoic Molluscs

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TEMPORAL CHANGES IN THE PALEO-COMMUNITY STRUCTURE OF GASTROPODS: A CASE STUDY FROM THE EOCENE STRATA OF THE JAISALMER BASIN, WESTERN INDIA

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Keywords: Eocene, gastropod, diversity, paleo-community, depositional environment.

During the Eocene Epoch, successive transient hyperthermal events and the northward drift of the Indian subcontinent significantly impacted marine ecosystems (Speijer et al. 2012; Self-Trail et al. 2017). The Eocene marine deposits of the Jaisalmer Basin, western India, preserve a diverse but understudied molluscan assemblage. This study aims to evaluate temporal changes in the gastropod paleo-communities, focusing on variations in both taxonomic and ecological diversity. Gastropod specimens (N = 1047) were collected from five fossiliferous litho-units (SB1–SB5) of the Khuiala (early Eocene) and Bandah (middle Eocene) formations in the Jaisalmer Basin. Shareholder Quorum Subsampling (SQS) standardized species counts across samples. Taxonomic diversity was quantified using diversity measures such as species richness, dominance, Simpson Index, etc. An ecological database documenting three life habits of gastropods– tiering, motility, and diet– was compiled from the Paleobiology Database (PBDB:2025). The abundance data were subjected to multivariate analyses, including Cluster Analysis (based on Bray-Curtis Similarity Index) and Detrended Correspondence Analysis (DCA), to assess the faunal similarities among units and delineate gastropod paleo-communities in relation to varying environmental settings. The study documents a rich gastropod diversity of 62 species, 47 genera, and 22 families from the Eocene successions of the Jaisalmer Basin. Multivariate analyses reveal that SB2 and SB3 cluster together due to their considerable taxonomic similarities, while SB1, SB4, and SB5 plot separately, delineating four distinct gastropod paleo-communities. SB1 is dominated by Rimella sp., an epifaunal omnivore-grazer constituting 89.6% of the assemblage alongside a few ampullinids, conids, and naticid gastropods. The bio-micritic limestone lithology and faunal assemblage suggests a warm, tropical, low-energy, restricted marginal marine environment. SB2 and SB3 are abundant in ampullinids such as *Globularia* sp. and *Ampullospira* sp., associated with conids, volutids, naticids, and rostellarid gastropods. These units, characterized by bio-sparitic limestone with abundant terrigenous quartz grains and larger benthic foraminifera (Assilina, Nummulites), indicate a warm, high energy, shoal, or intertidal depositional settings. SB4 is dominated by potamidid gastropods, *Potamides* sp., an epifaunal herbivore-grazer (98.6% of the assemblage), along with *Tympanotonos*. Hosted in shale, this assemblage suggests a mangrove/mud flat depositional environment. Finally, SB5 is characterized by abundant seraphsid gastropod, *Terebellum* sp., an epifaunal omnivore-grazer, with associated cassids, rostellariids, naticids, and conids, occurring alongside solitary and compound corals. The biosparitic to biomicritic limestone lithology alongside the assemblage indicate deposition in a reef to back-reef environmental setting. The gastropod assemblages from different litho-units studied, indicate deposition in an overall warm, tropical, shallow marine environment, mostly within inner shelf settings. However, variations in lithology and gastropod paleo-community structure suggest a highly heterogeneous depositional environment across the basin during the Eocene. This heterogeneity was likely influenced by climatic changes driven by successive hyperthermal events and fluctuations in sea-level.

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Evolution

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PLEUROTOMARIID GASTROPODS FROM THE JURASSIC TO RECENT: A RELATIONSHIP BETWEEN BODY SIZE AND LATITUDINAL DISTRIBUTION

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Keywords: Pleurotomariidae, body size, latitudinal zones.

The family Pleurotomariidae appears continuously in the fossil record since the Middle Triassic. They shifted from shallow to deep waters during the end Cretaceous. In the recent times, they inhabit depths of 100–1000 meters (Harasewych, 2002). This study investigates the relationship between the latitudinal distribution and body size of Pleurotomariidae over time, from the Jurassic to the present, offering insights into their long-term ecological and evolutionary patterns. Extensive global bibliographic data and our own collection data from the Indian subcontinent were compiled for this study. Although Pleurotomariidae originated in the Middle Triassic, this research focuses on the Jurassic to Recent. It includes 15 Mesozoic and 5 Cenozoic pleurotomariid genera, with only two Mesozoic genera surviving past the K-Pg boundary. Specimens were classified into seven shell size classes (S1 to L4; ranging from 0–200 mm shell diameter). The analysis covers three latitudinal zones—Polar, Temperate, and Tropical—spaced 30° apart in both hemispheres. The global body size distribution pattern of pleurotomariid gastropods is notably marked by the complete disappearance of small-sized forms (S1 and S2) during the end-Cretaceous. These smaller taxa vanished in a sequential latitudinal pattern: first from the Polar region in the Early Jurassic, then from the Tropical region in the Late Jurassic, and finally from the Temperate region in the Late Cretaceous. Medium-sized forms (M1 and M2) emerged during the Early Jurassic, initially in the Temperate region, where they persist through to the Recent. Their subsequent appearances occurred in the Tropical region during the Middle Jurassic and finally in the Polar region by the Late Cretaceous. Large-sized pleurotomariids (L1, L2, L3, L4) showed a parallel pattern of expansion. They first appeared in the Early Jurassic Temperate region alongside the medium-sized forms, followed by their appearance in the Tropical region during the Late Jurassic, and eventually reaching the Polar region in the Late Cretaceous. The Temperate region exhibits a continuous record of pleurotomariid gastropods across all size classes throughout the studied interval. The Polar region has yielded relatively sparse fossil evidence mainly occurring in the Early Jurassic, end Cretaceous (Maastrichtian) and Paleocene. The Tropical region, despite a richer record overall, shows two notable gaps in pleurotomariid presence—during the Paleocene–Eocene and the Pliocene–Pleistocene intervals—indicating potential environmental or preservational biases. The finding highlights the complex interplay between body size evolution and latitudinal distribution over time within this ancient gastropod family. Also, shifting to the deep marine environment in the Cenozoic offered a favourable condition for the medium to large sized forms of the family.

Funding Source: This work was supported by the Indian Statistical Institute [5480I for the Year 2024–2025].

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Palaeontology

Oral - 392

ADVANCING CONSERVATION PALEOBIOLOGY IN SOUTH AMERICA: THE MOLLUSKS' POTENTIAL BY INTEGRATING PALEONTOLOGICAL AND ZOOLOGICAL INFORMATION

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Keywords: climate changes, taphonomy, Mollusca.

Since Charles Darwin's first observations, the southern South American coast has been recognized as a natural laboratory for addressing major scientific questions. Since the 1990s, taphonomy research has been conducted, including pioneering time-averaging estimates and establishing marine baselines for Conservation Paleobiology (CP). However, significant challenges have been continuous throughout this journey into the unknown. The Patos Lagoon (Brazil) and Río de La Plata (Uruguay and Argentina) are among the world's largest lagoons and estuaries. Southern Brazil, Uruguay, and Northeastern Argentina are rich in river basins containing Quaternary fossils that provide crucial baseline data. South America, with its rich, although vulnerable, biodiversity, unique geology, and rich fossil diversity, is a natural laboratory for understanding ecosystems over time. However, it is concerning that South America is still underrepresented in CP, contributing only 5% of total publications worldwide, with 67% of these coming from Brazil (Assumpção & Ritter, 2025). Most South American authors are from geosciences areas (especially Paleontology) who primarily publish on mollusks, representing roughly 67% of the zoological groups studied (Assumpção & Ritter, 2025). Mollusks have a relatively excellent fossil record, and most paleontological and zoological studies are based on empty shells, the "empty shells" syndrome (Kowalewski et al., 2023). These empty shells accumulating on the modern seafloor can be hundreds to thousands of years old (Ritter et al., 2023). Still, there is an urgent need for integration with zoological research to incorporate accurate data on living biodiversity that will be helpful to CP. Given the current scenario of anthropogenic global change, environmental changes may be assessed by analysing modern ecosystems through paleoenvironmental information derived from geological, paleontological, and modern records in these marine, coastal, and continental aquatic environments, integrating with current data. The application of this integrated data to better understand environmental change over timescales longer than a few decades should be expanded in South America.

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Palaeontology of Marine Cenozoic Molluscs

Palaeontology

Oral - 119

BIVALVE ASSEMBLAGES INDICATE DEPTH OF DEPOSITION DURING THE EARLY–MIDDLE PLEISTOCENE TRANSITION IN THE EASTERN MEDITERRANEAN

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Keywords: bivalves, scaphopods, Quaternary, climate, Greece.

Bivalve molluscs have specific depth ranges in which they thrive and are able to record their environmental conditions, including climate. They can be used in the fossil record for investigations that focus on reconstructing depositional depth environments and climatic events. Here, we focus on the Eastern Mediterranean, specifically the island of Rhodes (southeastern Aegean Sea, Greece), which exhibits onshore bathyal deposits of the Early Middle Pleistocene Transition (EMPT). The aim of this work is to investigate deep-sea bivalve community changes during this important time for Earth climate evolution. Fifteen bulk sediment samples were taken from two sections; they were sieved using a 250 µm mesh in order to retrieve all bivalves, including minute forms. The samples cover Marine Isotopic Stages (MIS) 32 to 18. A non-metric Multidimensional Scaling (NMDS) analysis was performed on presence-absence data to examine changes in community composition between samples. Depth preferences of each recovered species are based on available information from both modern representatives and fossil occurrences. The preliminary results show changes in community composition during the EMPT, and new assemblages emerge in MIS 19 and 18. The two studied successions are showing gradual changes in the assemblage taxonomic composition during the EMPT. The species of bivalves and scaphopods found here are living in bathyal depths. Different assemblages emerge during glacial and interglacial intervals (MIS), which can contain bathyal species with cold-water affinities. Most of the bivalves are nuculoids, which are common elements of bathyal environments mainly because they are infaunal and feed on detritus. The bivalve *Bathspinula excisa* and the scaphopod *Cadulus ovulum* are documented for the first time in Eastern Mediterranean; in the two sections studied in the present analysis, they are only found in cooler intervals (MIS). Two successions covering the EPMT are studied, displaying differences in community composition during this peculiar time of the Quaternary. Four of the recovered species are now extinct; these were living in cold-water conditions and their disappearance suggests a warming of the water body at depths of 300 to 500 m after the EMPT.

Funding Source: No.

SYMPOSIUM: GENETICS AND GENOMICS IN MALACOLOGY

GENETICS AND GENOMICS IN MALACOLOGY

Coordinator:

ROBERTO EUGENIO VOGLER – Universidad Nacional de Misiones / CONICET, Argentina
ARIEL ANÍBAL BELTRAMINO – Universidad Nacional de Misiones / CONICET, Argentina

This symposium explores how genomic and genetic approaches are advancing the study of mollusks, from shell formation, regeneration, and gene expression to phylogeny, population structure, and adaptation. Emphasis is placed on linking molecular mechanisms with ecological and evolutionary processes across diverse molluscan groups.

Genetics and Genomics in Malacology

Genetics / Genomics

Oral - 12

HOW DO MOLLUSCS BUILD THEIR SHELLS? DECIPHERING CALCIUM TRANSPORT MECHANISMS IN SHELLFISH BIOMINERALIZATION USING GENE EDITING

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Keywords: CRISPR, *Crepidula fornicata*, bulk RNA sequencing, HCR, gene editing, development, biomineralization.

Calcium carbonate is the primary component of biomineralized shells. There are two hypothesised routes of calcium transport for biomineralization: paracellular (between cells) and transcellular (through cells). Prior research indicates that molluscs likely use a combination of both paracellular and transcellular pathways to transport calcium for shell deposition. To date, the genetic control of calcium transport for biomineralization remains uncharacterised. Using the slipper limpet, *Crepidula fornicata*, as a model, we gathered bulk RNA-sequencing from a range of developmental stages to identify candidate genes for calcium transport through a differential expression and weighted gene co-expression network analysis. Hybridization chain reaction (HCR) confirmed the precise cellular location of candidate gene expression, and candidates expressed in the shell gland and developing mantle edge were selected as primary targets. CRISPR-cas9 was used to create F0 gene knock-out limpets for three genes and the resulting phenotypes were studied in relation to calcium transport. Nineteen putative candidate calcium transport genes were identified using a differential expression analysis and a weighted gene co-expression network analysis (WGCNA). Six were differentially expressed between early- and late-mineralization larval stages. Eleven were significantly correlated to the adult mantle tissue and expression of two shell gland specific shell matrix proteins. Ten candidates were screened using HCR and two had expression in the shell gland and developing mantle. These two shell gland specific candidates, along with a positive control for method development, were used to generate CRISPR-cas9 F0 knockouts. Crispant embryos were collected for genotyping and potential phenotypes were observed using a combination of HCR to examine the level of mRNA expression and microscopy for morphological analysis. Two genes were identified as putative candidates for calcium transport in molluscan larval biomineralization using the model organism, *Crepidula fornicata*. The spatial localisation of expression in the shell gland and developing mantle edge led us to a novel hypothesis for calcium transport in molluscs. F0 knock-outs were generated and studied, proving that CRISPR/Cas9 can be used to study loss-of-function mutations in gastropods at an F0 generation.

Funding Source: This work is funded by the East of Scotland Bioscience Doctoral Training Partnership (EASTBIO DTP) and the Biotechnology and Biological Sciences Research Council (BBSRC). This work has been supported by the School of Biological Sciences at the University of Aberdeen PGR and PGT scholarships (Sutherland, Clyne, and Stephen Funds).

Genetics and Genomics in Malacology

Genetics / Genomics

Oral - 125

A GENOME-BASED PHYLOGENY FOR MOLLUSCA IS CONCORDANT WITH FOSSILS AND MORPHOLOGY

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Keywords: BUSCO genes, evolutionary relationships, monoplachophoran genome, Panmollusca.

Extreme morphological disparity within Mollusca has long confounded efforts to reconstruct a stable backbone phylogeny for the phylum. Familiar molluscan groups-gastropods, bivalves, and cephalopods-each represent a diverse radiation with myriad morphological, ecological, and behavioral adaptations. The phylum further encompasses many more unfamiliar experiments in animal body-plan evolution. Whole-genome sequencing enables a deeper understanding of evolutionary relationships and the mechanisms underlying morphological diversity in Mollusca at the molecular level. In this work, we reconstructed the phylogeny for living Mollusca on the basis of metazoan BUSCO (Benchmarking Universal Single-Copy Orthologs) genes extracted from 77 (13 new) genomes, including multiple members of all eight classes with two high-quality genome assemblies for monoplacophorans. Using both concatenated and coalescent methods, we inferred the molluscan phylogeny and evaluated support for previously contested hypotheses based on our genomic data. Our phylogenetic analysis confirms the origin of the phylum in the Cambrian and a rapid split into the major clades Aculifera and Conchifera. Congruent with the extensive fossil record of Mollusca and phylogenetic hypotheses proposed from morphology, we found that Monoplacophora is sister to the remaining Conchifera, and Cephalopoda is sister to the clade Gastropoda + Diasoma (Scaphopoda + Bivalvia), and this latter clade (Gastropoda+ Scaphopoda + Bivalvia) has been named Megalopodifera. Based on this new phylogeny, we infer that the molluscan ancestor had a solid dorsal shell, a foot, multiple dorsal-ventral and oblique foot-retractor muscles, a radula, and no eyes. Broad taxon sampling reveals that many molluscan genomes have extremely high heterozygosity and a high proportion of repetitive sequences. Large-scale genomic analyses of representative species from all eight molluscan classes confirm their phylogenetic relationships, consistent with morphological and fossil evidence, and show widespread genomic variation. Throughout the long evolutionary history of Mollusca and continuing today, aspects of a flexible genome led to a flexible phenome: The endless forms of molluscs showcase the power of animal evolution.

Funding Source: This work is funded by the Leibniz Association project PHENOME (P123/2021).

Genetics and Genomics in Malacology

Genetics / Genomics

Oral - 140

POPULATION GENOMICS REVEALS FINE SCALE GENETIC STRUCTURE OF A SUB-ANTARCTIC FALSE LIMPET (*Siphonaria fuegiensis*) AND LOCAL ADAPTATION PATTERNS

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Keywords: SNPs, rafting, environmental asociation analyses.

In the Southern Ocean (SO), various benthic invertebrates have a broad distribution across sub-Antarctic islands. For species without pelagic larvae, long-distance dispersal (LDD) via rafting has been recognized as key, but are these events enough to maintain gene flow? Population genomic studies may reveal fine-scale patterns and determine environmental features playing a role in shaping the genetic structure of populations and their local adaptation, improving our understanding of the region. Therefore, we studied the pulmonated limpet *Siphonaria fuegiensis*, found in the rocky intertidal of southern South America and sub-Antarctic islands. We sequenced >50 individuals from Atlantic and Pacific coasts, Kerguelen and Crozet islands, obtaining a neutral dataset of ~4000 SNPs. We performed genetic diversity analyses, assessed population structure (FST, PCA, STRUCTURE) and environmental influence (RDA) of 35 oceanographic variables, and evaluated patterns of contemporary gene flow with BA3. To study local adaptation, we used an environmental-association approach to detect SNPs with high correlation to SST and salinity with Bayenv2 and used an RDA to determine the adaptive structure and which oceanographic variables explained most of the adaptive differentiation. Genetic diversity was highest in the Atlantic, and lowest in sub-Antarctic islands. Neutral genetic structure analyses consistently recovered 3 genetic groups: 1) the Atlantic, 2) the Pacific and sub-Antarctic islands, and 3) the Strait of Magellan (in the Pacific). These patterns evidence low differentiation between distant populations (southern South America vs sub-Antarctic islands), and high differentiation between geographically close populations (the Strait vs the rest of the Pacific populations), where the RDA indicated that average salinity and minimum current velocities are relevant variables in explaining the genetic variation. Gene flow results indicated low and asymmetrical migration between populations, mainly sustained by self-recruitment. Considering these results, we've found a significant degree of differentiation at fine scale (Strait of Magellan) that has not been previously reported through the analysis of COI and nuclear sequences from *Siphonaria fuegiensis*, nor other sub-Antarctic species. On the other hand, the environmental-association approach detected 716 putatively adaptive SNPs associated to maximum, average and minimum SST and salinity. Adaptive structure was similar to the neutral structure yet recovered a 4th genetic group; Diego Ramirez Island (within the Pacific). Within the RDA model, oceanographic variables had small yet significant weight in the genetic differentiation, where the SSTmax and maximum salinity explained most of the genetic variation (~12% and ~5% respectively). These results indicate that there are significant patterns of local adaptation. Therefore, using population genomic tools, our results offer low evidence for continuous gene flow via LDD-events across the Southern Ocean, highlighting the need to reevaluate contemporary connectivity patterns. Additionally, genomic analyses revealed that oceanographic variables (SST and salinity) are playing a significant role in the divergence and adaptation of local populations, allowing us to understand with finer detail the evolutionary and ecological processes shaping the Southern Ocean benthic fauna.

Funding Source: Proyecto MILENIO BASE ICN_2021-002, ANID 21230929 scholarship.

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Genetics / Genomics

Oral - 207

ELUCIDATING PRINCIPLES OF REGENERATION IN MOLLUSKS

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Keywords: regeneration, *Berghia stephanieae*, scRNA-seq, position information.

Regeneration involves fundamental yet poorly understood processes, such as the source of new proliferative cells and the maintenance and reestablishment of positional information following injury. Mollusks are interesting for studying regeneration, given their poorly understood regenerative capacity and their close evolutionary relationship to other phyla holding regenerative species. We are developing the mollusk *Berghia stephanieae* as a novel regeneration model to elucidate the fundamental mechanisms underlying regeneration. By generating a single-cell RNA sequencing (scRNA-seq) atlas followed by expression validation using hybridization chain reaction fluorescence in situ hybridization (HCR-FISH) we are currently exploring: i) the identity and molecular signature of proliferative cell populations during tissue maintenance and regeneration; ii) candidate positional information genes; and iii) the transcriptomes for all major cell types comprising an adult mollusk. We generated uniform manifold approximation and projection (UMAP) plots of scRNA-seq data for approximately 130,000 cells from *B. stephanieae* body regions and regenerative and non-regenerative wound sites at 0 hours, 3 days, and 8 days post-injury. *B. stephanieae* has the ability to regenerate its posterior body parts and various appendages, such as oral tentacles, rhinophores, foot tentacles, and cerata. During regeneration, wounds heal within a few hours, and the blastema is formed within ~3 days. Next, structures start to grow and differentiate, completing regeneration within 10 to 80 days, depending on how much tissue was lost. However, these animals are unable to regenerate heads. This makes it possible to address the underlying basis for different regenerative capacities in the same animal. Within the single-cell data, we were able to determine the identity of different clusters (e.g. neuronal, muscle, germline), including rare cells types found in the animal such as in the rhinophores and cerata, and we confirmed the expression of genes for these cell types using HCR-FISH. We also identified different clusters of dividing cell populations by utilizing proliferative and cell cycle gene expression markers. The findings indicate the presence of distinct populations of proliferative cells, which may contribute to the formation of diverse tissues, implying a heterogeneity in the adult pluripotent stem cell compartment. Moving forward, we hope to thoroughly characterize all mollusk cell populations and to compare homologous cell types across other animal species. Additionally, we aim to investigate the positional information and progenitor cell populations present in the dataset. Studying regenerative mechanisms in mollusks will provide valuable insights into the fundamental principles of regenerative biology and enable comparative analyses of the evolutionary origins of regenerative capacities.

Funding Source: The Pew Latin American Fellows Program; Howard Hughes Medical Institute; WIPDA Educational Award Committee.

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Genetics / Genomics

Oral - 309

ESTABLISHING GENOMIC RESOURCES FOR *Nacella*: A COMPARATIVE FRAMEWORK FOR PATELLOGASTROPODS OF THE SOUTHERN OCEAN

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Keywords: genomics, Patellogastropoda, Southern Ocean, hybrid genome assembly.

The genus *Nacella* (Patellogastropoda) includes nearshore intertidal limpets with Antarctic and sub-Antarctic distributions. Accordingly, this genus represents an excellent model for studying genomic adaptation in the Southern Ocean. Nevertheless, so far genomic information in members of the genus remains limited. This study aims to generate and assemble high-quality reference genomes for multiple *Nacella* species, providing a framework for comparative genomic analyses and evolutionary inference. High-molecular-weight DNA was extracted from foot tissue of *Nacella clypeater* using Monarch HMW DNA extraction kit (BioLabs). Sequencing libraries were generated with 200 ng of input DNA and processed using Oxford Nanopore (long-reads) and MGI DNBSEQ (short-reads) technologies. Genome assembly libraries for *Scurria scurra* were retrieved from GenBank and used as reference for assembly. Hybrid genome assemblies were performed combining long-read contigs with short-read polishing. Genome completeness was evaluated using BUSCO with Metazoa database. Short-read data from additional *Nacella* species were aligned to the assembled genomes using Bowtie2, generating mapping files for downstream comparative analyses like variant calling and interspecific alignment-based metrics. Among the three assembly strategies tested for *Nacella clypeater*, the hybrid approach combining Oxford Nanopore long reads with short-read polishing using MGI data yielded the most complete and contiguous genome. This strategy resulted in an assembled genome size of approximately 758 Mb, with 83.3% completeness based on BUSCO scores against the Mollusca database. The assemblies generated from other strategies—long-read only and hybrid without polishing—produced lower completeness and more fragmented assemblies, underscoring the value of short-read polishing in molluscan genome recovery. Using this reference genome, short-read data from four additional *Nacella* species were aligned using Bowtie2. Mapping rates exceeded 60% for all species, with *N. flammea* showing the highest alignment (81.07%). These results suggest a relatively conserved genomic architecture among Nacella species, reinforcing the utility of *N. clypeater* as a reference for cross-species genomic comparisons. The incorporation of *Scurria scurra* genome data from Giles et al. (2025) provided an external reference framework to guide assembly and facilitate gene structure validation. This intergeneric reference usage supports synteny-informed assembly optimization for non-model molluscs. These preliminary results are the platform for future comparative analyses among Nacella species, including exploration of structural variants, gene content variation, and signals of local adaptation. Furthermore, by establishing a high-quality draft genome and standardized mapping pipeline, this study contributes valuable genomic resources for Patellogastropoda in the southern hemisphere, and particularly in the Southern Ocean, a region historically underrepresented in molluscan genomics. This study successfully assembled a high-quality draft genome for *Nacella clypeater* using a hybrid sequencing strategy and a patellogasteropod reference genome. The assembled genome served as a robust reference for cross-species alignment, confirming its utility in comparative genomic analyses. These results meet the initial objective of establishing foundational genomic resources for *Nacella*, enabling future studies on evolutionary processes and genetic divergence in Southern Ocean limpets.

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Oral - 390

SALIVARY GLANDS GENE EXPRESSION UNDERLIES TROPHIC ASSOCIATION IN A CORALLIVOROUS MARINE SNAIL

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Keywords: trophic ecology, adaptation, symbiosis, transcriptomics, proteomics.

Several gastropod groups have evolved the ability to feed on Cnidaria, despite their toxicity, but the molecular basis of this adaptation have been neglected. Among them, Coralliophilinae (Neogastropoda, Muricidae) include species with different degrees of specialization. *Coralliophila meyendorffii*, common in the Mediterranean Sea, can feed on multiple hosts ranging from sea anemones to scleractinians and zoantharians, offering the possibility to explore the link between gene expression and trophic association. We used a proteotranscriptomic approach to characterize gene expression in salivary glands and gland of Leiblein from two different ecotypes of *C. meyendorffi*, associated respectively with *Parazoanthus axinellae* and Astroides calycularis, two distantly related Anthozoa species with a different toxicity profile. Samples were pooled in three replicates from which total RNA was extracted and used to build libraries that were sequenced on an Illumina HiSeq 2500. A de novo assembly was built with Trinity and annotated with Trinotate. Tissue specific differential expression analyses were carried out with DESeq2. In parallel, total proteins were extracted from tissue-specific samples digested with trypsin, shotgun sequenced by LC-MS/MS, and de novo analyzed with PEAKS. We were able to characterize tissue-specific gene expression for the two ecotypes of *C. meyendorffi*, highlighting clear differences in salivary glands gene expression between snails feeding, respectively, on the zoantharian *P. axinellae* and the scleractinian A. calycularis. In particular, the latter ecotype showed a higher level of overexpression of protease inhibitors genes, that might be related to the need to neutralize proteases in the nematocyst venom. On the other hand, the salivary transcriptome of the snails feeding on *P. axinellae* showed overexpression of genes encoding proteins involved in digestion and cell maintenance. In contrast to what was observed for the salivary glands, gene expression in the gland of Leiblein did not display a high level of diversification between the two ecotypes. Proteomic data are in agreement with transcriptomics. These findings support the hypothesis that salivary glands, discharging their products directly on the host, are responsible of mediating the trophic specialization, through a fine-tuned regulation of gene expression. On the other hand, the gland of Leiblein seems to be involved into host-independent digestion processes. This is the first study addressing the biochemical basis of trophic association in a corallivorous marine snail. Our results indicate that *C. meyendorffi* is able to regulate tissue-specific gene expression according to their host, making this species an interesting model to investigate the interplay between phenotypic plasticity and genetic adaptations in shaping trophic specialization. Our findings help to clarify the mechanisms underlying trophic interaction in marine communities.

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Oral - 262

IMPACT ASSESSMENT OF SOIL POLLUTION ON THE MICROBIOTA OF THE TERRESTRIAL SLUG *Ambigolimax valentianus* (A. FÉRUSSAC, 1821)

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Keywords: microbial composition, bioindicators, terrestrial gastropods, alpha diversity, heavy metals.

Understanding how environmental pollution affects terrestrial organisms is crucial for assessing ecosystem health. The balance of microbial populations within the host's gut reflects an evolutionary adaptation that enables gastropods to exploit environmental resources effectively. The present study aims to assess the impact of soil pollution on the microbiome of *Ambigolimax valentianus* by analyzing microbial community composition and diversity under different pollution scenarios. Specimens of *A. valentianus* and soil samples were collected from three sites: Atlangatepec, Atilhuetzia, and we reared in lab a control population. Heavy metal concentrations (Ni, Mn, Pb, Hg, Cd, As) were measured in soils and slug tissues using standardized analytical techniques. Gut compartments (buccal mass, stomach, intestine) were dissected, and bacterial DNA was extracted. Libraries of the V3 region 16S rRNA gene were sequenced using the MiniSeq platform (300 cycles, 2 × 150 bp paired-end), following the manufacturer's protocol, and sequenced at the CIAD in Mazatlán, Sinaloa, Mexico. Principal coordinates analysis (PCoA) based on Hellinger distances was used to evaluate microbial community structure according to site and gut region. Heavy metal concentrations varied by site, with Atlangatepec showing elevated levels of Cd, Pb, and Hg in slug tissues. Mn levels were high across all locations. PCoA revealed distinct clustering of bacterial communities by site, with Atlangatepec samples displaying low variability and strong dominance of Enterobacteriaceae and Moraxellaceae. Atilhuetzia showed greater microbial diversity and dispersion, suggesting environmental heterogeneity. Control samples exhibited the most balanced bacterial profiles, with higher richness and taxa such as Burkholderiaceae and Micrococcaceae. Each gut region contributed to taxonomic variation, but site differences were more influential. These findings indicate environmental conditions significantly shape gut microbiota and metal accumulation in *A. valentianus*, highlighting its utility as a bioindicator. The study shows that heavy metal accumulation and gut microbiota composition in *A. valentianus* vary with site conditions (environmental pollution), samples from Atilhuetzia displayed greater dispersion, indicative of higher variability in bacterial composition, possibly driven by more heterogeneous or disturbed habitat conditions. These slugs effectively reflect environmental contamination levels, supporting their role as possible sentinel organisms in terrestrial ecosystems.

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Genetics and Genomics in Malacology

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Oral - 293

EVIDENCE OF TRANS-APF LONG-DISTANCE DISPERSAL IN A NEARSHORE MARINE INVERTEBRATE IN THE SOUTHERN OCEAN

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Keywords: long-distance dispersal, *Laevilitorina venusta*, Antarctic Polar Front, Southern Ocean.

Long-distance dispersal (LDD) represents a main biogeographic mechanism in the Southern Ocean but most of the examples have been recorded around the Antarctic continent and among sub-Antarctic provinces. Although occasional LDD occurred over long (evolutionary) timescales there is little evidence of ongoing gene flow across the Antarctic Polar Front (APF). A recent study in the littorinid *L. venusta* showed a broad distribution in Antarctic and sub-Antarctic provinces across the APF. Species of *Laevilitorina* are very abundant in shallow rocky bottom ecosystems and exhibit benthic protected development without free-living larval stages. Here, we performed population-based molecular analyses including more than 586 individuals from 17 localities across the species' distribution using tradition mtDNA (COI) and SNPs. For this, we included in the analyses populations from maritime Antarctica (11) and from geographically distant sub-Antarctic Islands of the Southern Ocean such as South Georgia, Marion, Crozet, Kerguelen and Macquarie. In general, *L. venusta* showed low to medium levels of genetic diversity and exhibits a short genealogy with the presence of several dominant haplotypes. Sub-Antarctic populations of *L. venusta*, particularly Macquarie Island, exhibited higher levels of genetic diversity than maritime Antarctica ones. General patterns of population structure showed six clearly differentiated genetic genetic groups: 1) maritime Antarctic + Signy Island; 2) South Georgia; 3) Marion; 4) Crozet; 5) Kerguelen and 6) Macquarie Island. Interestingly, each of the sub-Antarctic islands here analyzed represents a different genetic group. Moreover, mtDNA analyses detected evidence of bi-directional and asymmetrical gene flow in *L. venusta* between Antarctic and sub-Antarctic provinces. Population structure analyses using SNPs corroborate the mtDNA pattern with a marked distinction between Antarctic and sub-Antarctic populations. At the same time population-based analyses based on SNPs failed to identify evidence of contemporary connectivity between geographically distant Antarctic and sub-Antarctic populations. *Laevilitorina venusta* represents one of the nearshore marine benthic invertebrate with the broadest distribution in the Southern Ocean with populations in Antarctic and sub-Antarctic provinces, across one of the most powerful oceanographic boundaries of the planet, the APF. Considering the reproductive mode in *Laevilitorina* recent LDD mediated by rafting at the scale of thousands of year seems to best explanation for the expanded distribution of *L. venusta*.

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TOXIN PRODUCTION AND DIVERSITY IN PREDATORY GASTROPODS: THE EXAMPLES OF *Monoplex corrugatus* (CYMATIIDAE) AND *Stramonita haemastoma* (MURICIDAE)

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Keywords: Caenogastropods, toxin, genomics, transcriptomics, evolution.

The exploration of toxins diversity is crucial for understanding evolutionary adaptation of venomous taxa. Despite being active venomous predators, neogastropods are largely understudied beyond Conidae. This study targets two predatory gastropods, *Monoplex corrugatus* and *Stramonita haemastoma*, aiming to characterize their toxin-producing tissues, evaluate the diversity and function of toxins, and compare expression profiles across tissues. Specimens of both species were dissected to isolate multiple samples of both secretory glands and other tissues. Transcriptomic data were generated and complemented by shotgun proteomics for *S. haemastoma*. Transcriptomes were used to identify putative toxin genes using the DeTox pipeline, followed by filtering by expression levels and sequence features. Differential expression was assessed via STAR and featureCount, followed by SARTools for statistical analysis. Differentially expressed toxins were further manually annotated using functional databases and structural prediction tools. Orthologous toxins were identified using OrthoFinder, and proteomic data for *S. haemastoma* were analyzed using PEAKS. The study identified 2,565 and 1,777 putative toxins in *S. haemastoma* and *M. corrugatus*, respectively. Salivary glands were confirmed as the major toxin-producing organ in both species, with additional toxin expression in mid-oesophageal and accessory salivary glands. Manual annotation confidently identified 115 and 143 venom proteins in *S. haemastoma* and *M. corrugatus*, highlighting significant interspecies and intertissue differences. Functional categorization revealed enzymatic and peptide toxins, as well as venom-processing proteins, with *M. corrugatus* showing expression in non-secretory tissues. Despite their phylogenetic distance, shared orthologs were identified between the two species, namely for venom-processing proteins like calglandulin and disulfide isomerases, suggesting a conserved functions. Species-specific toxins, including echotoxins and plancitoxins in *M. corrugatus*, indicate lineage-specific venom adaptations. Proteomic validation supported transcriptomic predictions in *S. haemastoma*. This underscores the value of multi-omics approaches for toxin discovery and for investigating the complexity of gastropod venom evolution. The study successfully achieved its objectives, characterizing toxin-producing tissues and characterizing toxin repertoires in both species. Results reveal the presence of both conserved and lineage-specific venom traits, highlighting the key role of salivary glands in toxin production and demonstrating the evolutionary and functional diversity of gastropod venoms.

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SYMPOSIUM: BRIDGING TRADITION AND TECHNOLOGY: ADVANCING MOLLUSK COLLECTION STEWARDSHIP AND RESEARCH SOCIETY FOR THE PRESERVATION OF NATURAL HISTORY COLLECTIONS (SPNHC)

BRIDGING TRADITION AND TECHNOLOGY: ADVANCING MOLLUSK COLLECTION STEWARDSHIP AND RESEARCH SOCIETY FOR THE PRESERVATION OF NATURAL HISTORY COLLECTIONS (SPNHC) SYMPOSIUM

Coordinator:

JINGCHUN LI – CU Natural History Museum, Dept. of Ecology & Evolutionary Biology, University of Colorado, USA

This year, the American Malacological Society and the Society for the Preservation of Natural History Collections (SPNHC) are excited to collaborate on a special symposium centered around Innovation and Care of Mollusk Museum Collections. The event highlights the crucial role of museum collections in advancing research and conservation efforts within malacology, while also focusing on innovative methods for maintaining and utilizing these invaluable resources.

Afternoon Session: Participant Symposium In the afternoon, the symposium will feature presentations from meeting participants, showcasing diverse perspectives and new research centered on the care, digitization, and application of mollusk collections. This session will offer an opportunity for attendees to engage directly with the wider community, fostering collaboration and the exchange of ideas. Join us for a day of cutting-edge research and thoughtful discussion on the future of mollusk museum collections.

Bridging Tradition and Technology: Advancing Mollusk Collection Stewardship and Research Society for the Preservation of Natural History Collections (SPNHC)

Collections

Oral - 385

MULTI-INSTITUTIONAL DIGITIZATION OF MOLLUSKS FROM THE EASTERN SEABOARD OF THE UNITED STATES

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Keywords: digitization, georeferencing, vitality, extended specimen, natural history collection.

The ongoing digitization of natural history collections in the USA has made museum specimens widely available to researchers, educators, students, and the general public. Eastern Seaboard (ESB) and DigIn are two coordinated, multi-institutional Thematic Collections Networks (TCNs) funded by the National Science Foundation that are currently digitizing records of marine species. In addition to traditional digitization activities such as georeferencing and photographing, mollusk digitization now includes recording whether specimens were collected alive or dead (vitality), a trait that can refine species distributions by restricting them to live-only records. One of the most innovative facets of the project is the use of Collaborative Georeferencing, a procedure through which collections form groups for mutually reviewing and editing, to combine and share georeferencing data. The collaborating institutions contain > 85% of all the known records of marine mollusks from the Eastern Seaboard of the USA. Working together, we have mobilized over 4 million mollusk specimens into online data portals and made them freely available to users. As part of this effort, ESB and DigIn members worked with the International Working Group on Taxonomic Databases (TDWG) to integrate the new term “vitality” into the Darwin Core lexicon to track live-collected and dead-collected specimens. Future activities may include scoring other ecologically and evolutionarily important features such as evidence of predation and the presence of shell-associated fauna (e.g., barnacles) as well as linking to external datasets with biographical information on collectors. Together, these new traits create extended specimen records and provide new opportunities for ecological research and informal STEAM education. Working collaboratively across institutions has expedited the delivery of high-quality data to online portals and allowed for innovative solutions to common problems. This growing, free, primary resource is available for research, education and outreach activities, and highlights the value of natural history collections.

Funding Source: National Science Foundation, USA.

Bridging Tradition and Technology: Advancing Mollusk Collection Stewardship and Research Society for the Preservation of Natural History Collections (SPNHC)

Other themes

Oral - 382

MARINE GEOREFERENCING

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Keywords: databases, collections, coordinates.

Mollusk collections have been georeferencing since the 1970s. The standards, however, have evolved and continue to be refined. At first some fields that are now considered standard were not included: datum, error radius, source of coordinates, method of georeferencing, who did the georeferencing, and when it was done. We propose that the context of georeferencing also be recorded. If the goal is only to put points on a coarse-scale map, that might be done with bulk processing. If the goal is to take the habitat or biology of the taxon into account, considerably more nuance might be achieved. For example, some taxa are known to be primarily intertidal whereas others are subtidal. The date collected can be taken into account, since some coastal areas change relatively rapidly. The technology for determining depth also changes and boundaries and landmarks can change, so contemporary maps should be used. The structure of the database might also be changed, allowing one-to-many relationships in the tables associated with georeferencing, so that, rather than lose the history of georeferencing, it can be preserved and refined as needed. It should be possible to georeference a sample more than once. The context of georeferencing should be documented and iterated georeferencing should be possible. Rather than overwriting the coordinates associated with an object in a collection, they would be refined, and both versions would be part of the record's history.

Funding Source: U. S. National Science Foundation.

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Collections

Oral - 237

NHM UNLOCKED: UNLOCKING THE TALES OF THE COLLECTION AND REUNITING THE "MOLLUSCOIDEA"

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Keywords: molluscoidea, collections.

The Natural History Museum in London is undergoing some big changes. We are currently in the midst of an exciting project, NHM Unlocked, the culmination of which will be the opening of our new facility at the Thames Valley Science Park (TVSP) in Reading, Berkshire. 38 million specimens will be moving, across the recent and palaeontological collections, encompassing mammals and non-insect invertebrates. This move will improve the collections storage and facilities and provide space for the collections to grow. Significant preparation work is underway, with a plethora of work streams underway to get the collection ready to move. This has included assessing the conservation requirements of the collections moving. The entire palaeontological collection has been assessed, and the interventions have begun. It is not just the physical collections we are assessing; this project is giving us a great opportunity to get a handle on our documentation and paperwork. In preparing the collections to move we are uncovering all manner of stories and exciting information, all whilst improving the collections storage and ensuring the collections are stable to move. I will be sharing tales of individual specimens, collections, excavations and expeditions, the details of which have just come to light. We are also keen to illustrate some of the innovative projects which are being completed to protect our collections and prepare them to move. Additionally we have an appeal, if you have datasets containing NHM specimens, especially images or transcribed specimen metadata, this could help us prepare the collections. Please get that information to us. If you have overdue loans of NHM material, please contact up to arrange sending them back. If anything we are doing to prepare to move can help you, please get in touch. We want to reduce the impact on our collections users as much as possible, if you may require the NHM collections in the period up until 2030, please reach out and discuss your collections access needs with the relevant curatorial teams as soon as possible.

Funding Source: No.

Bridging Tradition and Technology: Advancing Mollusk Collection Stewardship and Research Society for the Preservation of Natural History Collections (SPNHC)

Collections

Oral - 43

EDUCATIONAL APPLICATIONS OF MALACOLOGICAL MUSEUM COLLECTIONS FOR UNDERREPRESENTED STUDENTS IN COLORADO

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Keywords: malacological museum specimens, outreach, education.

Girls at the Museum Exploring Science (GAMES) is a program created by and implemented at the Museum of Natural History, University of Colorado Boulder. In its 22nd year, this program exists to introduce museum research and collections to elementary and middle school girls from rural and underrepresented districts in Colorado. This program delivers science to students who need it most, demonstrating significant success through the use of malacological museum specimens. The Museum hosts two cohorts each school year for an 8-week duration. The goal of 2025 Spring semester is to expose students to malacological museum specimens and to connect these tangible specimens with concepts of animal behavior, evolution, and diversification. Additionally, we hope to inspire students to pursue the sciences. Post-pandemic, this program has adopted virtual sessions in addition to in-person sessions. In person, students visited the Invertebrate Zoology (IZ) collection, listened to a presentation from the Li Lab about mollusc defense and morphology, and then did a DNA extraction activity. Virtually, classes were sent shells from our educational collection to correlate with a virtual presentation from the Li Lab. We obtained data on how many individual students handled shells and how many classes handled shells; we also collected data on responses regarding whether it mattered that the shells were from a museum, how the shells changed students' perception of museums, scientists, and the ocean, and what the students would like to see next. At the end of the in-person session, there were statistically significant changes in the way students saw science and scientists, and students from both cohorts reported wanting to pursue marine biology as a career path. For the virtual experience, there were more students that handled malacological specimens than expected; the shells that were shipped from the Museum to one class were then passed along to additional classes and kept for longer durations than expected due to teacher and student enthusiasm about what they were seeing. Students used mollusc shells to understand animal behavior, evolution, and diversification. Given the unexpected increase in use of shells during the virtual sessions, it is evident that malacological museum collections are powerful tools of exposure for rural and underrepresented students. These specimens afford them the opportunity to encounter invertebrate diversity. The uniqueness of GAMES improves attitudes towards science and helps students realize their own potential in the sciences.

Funding Source: GAMES has received funding from the Public & Community Engaged Scholarship (PACES) and from NSF federal grants as support for execution of the work, and personnel salary support through the University of Colorado Museum of Natural History. The Li Lab's participation in GAMES is funded by NSF DBI 2001640.

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Collections

Oral - 362

THE CONTRIBUTION OF JOHN ANTHONY ALLEN TO THE STUDY OF THYASIRIDAE (BIVALVIA): A HISTORICAL OVERVIEW

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Keywords: taxonomy.

The eminent malacologist John Anthony Allen, born in 1956, made a significant contribution to the study of the Thyasiridae (Bivalvia), in collaboration with Cathy Payne, when they studied twenty-eight species of this family from the deep Atlantic. This work was fundamental to understanding their taxonomical and anatomical features and laid the foundation for future studies. Here, these species are reviewed, incorporating recent advances undergone in their taxonomy. Twelve eight species reviewed and redescribed by Payne & Allen (1991) were taxonomically verified using the World Register of Marine Species (WoRMS) and MolluscaBase databases. The nomenclatural status and current classification of each species were confirmed with the most recent updates. Additionally, based on sample lists provided by them and donated to the Museum of Comparative Zoology (MCZ), specimens were re-examined and compared with type-materials from the National Museum of Natural History (USNM), Museum of Comparative Zoology (MCZ), and Yale Peabody Museum - Invertebrate Zoology (YPM). John Anthony Allen, in collaboration with Cathy Payne, made na influential contribution to the scientific understanding of Thyasiridae. They reviewed twenty-eight species: one assigned to *Axinus* and twenty-seven to *Thyasira*, which they divided into five subgenera: *Thyasira* 'sensu stricto' (2 species), *Thyasira* 'sensu lato' (3 species), *Parathyasira* (8 species), *Leptaxinus* (1 species), *Axinulus* (4 species), and *Mendicula* (9 species). Twelve of those species were new to science and originally placed in the genus *Thyasira*. Historically, *Thyasira* has multiple subcategories placed on it which contribute to taxonomic instability of the genus. Over time, these subgenera were elevated to full genus status and are now valid and the new species have since been reclassified. Two species were transferred to other genera: *T.* (*M.*) *transversa* to *Adontorhina transversa* and *T.* (*P.*) *subequatoria* to *A. subequatorius* according to WorMs. Also three subspecies were reclassified: *T.* (*T.*) *succisa atlantica* as *T. succisa*, *T.* (*P.*) *atlantica* as *T.* (*P.*) *tortuosa*, and *T.* (*P.*) *subovata minuta* as *L. minutus*. Through re-examination of the specimens, it was possible to link the samples and the "List of Specimens Examined" and identify some inconsistencies in the redescriptions of some species. One example of this is *T.* (*T.*) *trisinuata*: the samples in their examined material are of two other species, not *T. trisinuata*. In the sample used to illustrate its external view (MCZ 355957), the individuals found are of *T. biplicata*; and in the sample USNM 45715, the specimen used to illustrate the hinge is of *T. flexuosa*. The work of John Anthony Allen, in collaboration with Cathy Payne, was pioneering and highly relevant for Thyasiridae, but recent taxonomic updates reveal that many of their proposed classifications have been revised or modified. The current analysis, based on updated databases and reexamination of type specimens, corrects previous identifications and highlights inconsistencies in some of the original descriptions, reinforcing the importance of continuous revision in taxonomy.

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Other themes

Oral - 79

A NON-BINARY TAKE ON THE BINARY: A SUGGESTION ON HOW TO NAME SPECIES HONORING NON-BINARY PEOPLE WITHOUT BREAKING TRADITION

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Keywords: nomenclature, taxonomy, non-binary, suffixes, inclusion.

Article 31.1.2 of the International Code of Zoological Nomenclature regulates species-group names formed from personal names, citing rules for adding genitive suffixes for names of men and women. As it stands, this does not include non-binary people. In this sense, a solution to this underrepresentation is proposed using the same rules as utilized by Article 31.1.2 of the Code, aiming not to affect its stability. The rules of Article 31.1.2 consist in the addition of suffixes coming from the endings of the declensions of the Latin genitive case to the personal name used. The endings -ae and -arum, used, respectively, for species names formed from the personal name of a woman and women, come from the first declension of the Latin genitive, while the endings -i and -orum, used, respectively, for names of species formed from the personal name of a man, men, or a man/men and a woman/women together, come from the second declension of the Latin genitive. We suggest the use of the third declension of the Latin genitive to name species honoring non-binary people. This would not imply a drastic change to Article 31.1.2 or the Code more broadly, but simply an addition to the suffixes used, including -is for names formed from the name of any person (including non-binary ones) and -ium for names formed from the name of any group of people (including those that include non-binary people). One could argue that the current edition of the Code allows the proposal of names in any spelling as long as there are two or more letters, so the endings discussed here could already be used. One could also argue that Article 31.1.2 does not restrict the uses of genitive endings, which means it is possible to use the first declension for names of men, the second declension for names of women, other declensions, such as those of the forth and fifth cases, or even no genitive endings at all. However, the main objective of this proposition is not merely procedural, but to highlight how non-binary people are not included in our traditional naming practices, as seen by the wording of Article 31.1.2 using only the words “man” and “woman”, which does not include non-binary people. The main objective of this proposition is to give all people equal representation and treatment by the Code, regardless of gender, and include non-binary people in the wording of the Code. Adding more explicit rules to Article 31.1.2 is not only a matter of providing the possibility for non-binary people to be honored in species names in an inclusive manner, but also of ensuring that non-binary people are treated equally to men and women by the words and regulations of the Code, making the Code more inclusive to all people without jeopardizing its stability.

Funding Source: No.

SYMPOSIUM: MOLLUSCS AS BIOINDICATORS

MOLLUSCS AS BIOINDICATORS

Coordinator:

LENITA DE FREITAS TALLARICO – Instituto Butantan (IB), Brazil
ELISABETE TEIXEIRA TSUKADA SOARES – UNICAMP, São Paulo, Brazil

Molluscs, especially bivalves, have long been studied as bio-indicators of pollution. Bivalves' sessile nature combined with filter-feeding behaviour has made them a useful tool to understand pollution profiles in marine and freshwater environments. However, examples, such as the induction of imposex in gastropod molluscs worldwide also demonstrate that molluscs can have unique and unexpected susceptibility to certain types of chemical pollution. Pollution is known to be a major risk to molluscan populations. Molluscs living in various aquatic and terrestrial habitats are exposed to a myriad of contaminants from metals, biocides and industrial chemicals to pharmaceutical and personal care products. Despite this, molluscs are often under-represented in chemical risk assessments and a better understanding of the impacts of pollution on molluscs is needed to help protect vulnerable groups. In this symposium, studies (laboratory and field) addressing the impacts of pollution at different biological scales, from molecular, cellular, individual and population are welcome.

Molluscs as Bioindicators

Conservation

Oral - 268

MICROPLASTICS IN FRESHWATER MOLLUSCS: EVIDENCE FROM *Pomacea figulina* (SPIX IN WAGNER, 1827) IN A BRAZILIAN NEOTROPICAL RIVER

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Keywords: bioindicator, *Pomacea figulina*, Gastropoda, microplastic, freshwater, Neotropical, ecology, Mollusca.

Microplastic pollution poses a significant environmental threat. The gastropod *Pomacea figulina* (Spix in Wagner, 1827) is an omnivorous species that thrives in sediment and aquatic plant environments and is abundant in water reservoirs in Sorocaba, Brazil. Given its biological and ecological attributes, the species has been considered to be a bioindicator. This study investigates its potential as a sentinel organism for monitoring microplastic pollution. In September 2024, 13 specimens of *Pomacea figulina* (Spix in Wagner, 1827) were collected from the Pirajibu-Mirim River (23o 29'23.62"S 47o), which feeds into a water reservoir in Sorocaba, Brazil, in September 2024. The organisms were transported alive to the UFSCar laboratory, where they were measured and weighed. Their soft tissues were extracted from the shells and individually digested using H_2O_2(35%). Each digested sample was subsequently filtered in a plastic clean room and deposited onto a membrane. These membranes were then examined under a stereomicroscope at magnifications of up to 80x. The microplastics found were classified based on morphotype and color. Thirteen specimens of *Pomacea figulina* collected during winter months were analyzed. Consistent with their life cycle stage, these individuals exhibited smaller morphometrics (average weight: ~0.9 g; shell width: ~15 mm) compared to typical adults of the species (50–60 mm), suggesting a juvenile status. Of the 13 plastic particles identified, fibers predominated, alongside near-rectangular fragments and rubber particles, with sizes ranging from 0.04 to 1 mm. They were of different colors, black, various shades of blue, purple and white. This evidence indicates that they are of different origins. As *P. figulina* is a fully aquatic species—obtaining oxygen, foraging, and ingesting water directly from its environment—it likely serves as a bioindicator for microplastic contamination. The presence of microplastics in these specimens implies uptake and retention through environmental exposure. While comparative data are lacking due to the absence of prior studies, we posit that larger individuals may accumulate higher microplastic loads. Ongoing complementary analyses of summer-collected specimens (which exhibit significantly larger body sizes) aim to test this hypothesis and evaluate potential seasonal or size-dependent accumulation patterns. size, supporting its potential utility as a bioindicator species for microplastic contamination. Furthermore, the detection of these anthropogenic particles implies possible pollution of aquatic systems in the Sorocaba region. While these findings are promising, additional investigations are necessary to evaluate *P. figulina*'s effectiveness. Current research efforts are addressing this knowledge gap through expanded sampling and analysis.

Funding Source: This project had a scientific initiation (undergraduate) grant sponsored by CNPQ (National Council for Scientific and Technological Development - Ministry of Science, Technology and Innovation - Brazil).

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Conservation

Oral - 264

USE OF *Pomacea figulina* FOR THE IDENTIFICATION OF MICROPLASTICS IN THE PIRAJIBU-MIRIM RIVER

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Keywords: microplastics, gastropods, urban pollution, freshwater biomonitoring, *Pomacea figulina*, Pirajibu-Mirim River.

Microplastic pollution poses risks to aquatic biota and human health. Benthic organisms like gastropods are effective bioindicators due to their ability to accumulate and excrete contaminants. This study evaluated the potential of *Pomacea figulina* as a biomonitor by analyzing the presence and morphology of plastic particles excreted by individuals collected from the Pirajibu-Mirim River. Twenty-four *Pomacea figulina* individuals were collected from the Pirajibu-Mirim River in Sorocaba. They were kept in glass aquariums at 24°C with continuous aeration and fed daily with a clean, protein-rich diet. Feces were collected every four days and stored in glass containers. Samples underwent chemical digestion with 35% hydrogen peroxide for 72 hours, followed by vacuum filtration using 5 µm nylon membranes. Residues on the membranes were analyzed under a stereomicroscope for visual identification and morphological classification of particles by shape, color, and size. Monitoring continued until microplastics were no longer detected in the feces. Feces were monitored for 40 days, after which microplastics became rarely detected. A total of 468 microplastic particles were found, 64% of which were fibers. The predominance of fibers in *Pomacea figulina* feces suggests this is a major pollutant category in the Pirajibu-Mirim River, often linked to synthetic fiber release from laundry, pointing to domestic effluents and the textile sector as key contamination sources. Other particle types included irregular fragments, spheres, and foam-like particles, indicating diverse origins such as industrial products and degraded urban waste. Most particles were blue (37.72%), black (16.38%), or transparent (10.78%), reflecting pollution sources like textiles and plastic packaging. Contaminant entry into the river is likely tied to improper waste disposal, as the Pirajibu-Mirim flows through several urban neighborhoods, facilitating pollutant accumulation. The wide range of particle types underscores the complexity of microplastic entry routes in freshwater ecosystems and the need for ongoing monitoring in human-impacted areas. The ability of *P. figulina* to excrete synthetic particles after a depuration period confirms its ingestion of environmental microplastics and supports its potential as a freshwater biomonitor. Its ease of handling and sensitivity to contamination make it a promising sentinel organism for ecotoxicological studies. These results align with literature promoting aquatic gastropods as indicators of microplastic pollution and contribute to advancing monitoring and pollution control strategies. The results confirm microplastic presence in the Pirajibu-Mirim River, mainly fibers, along with fragments, spheres, and foams, indicating diverse pollution sources. *Pomacea figulina* proved to be a promising biomonitor due to its ability to ingest and excrete microplastics. The detection of particles in feces after depuration highlights the species' sensitivity to microplastic pollution and its potential relevance in ecotoxicological monitoring studies.

Funding Source: National Council for Scientific and Technological Development (CNPQ).

Molluscs as Bioindicators

Behaviour

Oral - 381

ARDUINO-BASED VALVOMETRY APPLIED TO ECOTOXICOLOGY. A NEW INSIGHT INTO NEOTROPICAL FRESHWATER BIVALVES' BEHAVIOR UNDER STRESS

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Keywords: ecotoxicology.

Bivalves are widely used in aquatic biomonitoring due to their sensitivity to environmental changes, sedentary lifestyle, and aptitude to accumulate contaminants. Monitoring their valve movements provides real-time insight into behavioral responses to water quality fluctuations. This approach offers a non-invasive and continuous method to assess valuable etological biomarkers. This study aimed to prototype, assemble and program a valvometry device, validating its sensor readings to monitor bivalve behavior in ecotoxicological assays. The design followed a modular approach, with an Arduino microcontroller serving as the main processing unit. Six analog Hall effect sensors were connected to a custom single-layer PCB to detect changes in the magnetic field caused by shell movements attached to a magnet. Firmware was programmed to manage continuous data acquisition and real-time visualization through a graphical interface. A 2×2 factorial design was used to assess the effects of nutritional condition (fed/unfed) and chemical exposure to a glyphosate based herbicide (GBH, exposed/non-exposed) on six individuals of *Corbicula largillierti* and *Anodontites trapesialis*. Sensor data was standardized to perform a Principal Component Analysis (PCA) and a mixed generalized linear model (MGLM). The 2D PCA model accounted for 64.1% of the total variance in *C. largillierti* and 72% in *A. trapesialis*, effectively reducing data dimensionality and revealing clustering patterns in behavioral responses based on valve opening activity. Scatter plots indicated partial separation between treatments, with distinct groupings of individuals under different experimental conditions, suggesting treatment-specific behavioral modulation. Multivariate generalized linear model (MGLM) results revealed a significant interaction between GBH exposure and nutritional condition ($p < 0.05$). Exposure to GBH induced behavioral shifts in both species, characterized by reduced overall valve opening duration and intermittent episodes of elevated gaping frequency. Furthermore, the presence of food modulated gaping behavior in both species, indicating a switch in frequency patterns in response to nutritional availability ($p < 0.05$). The Arduino-Based valvometer proved effective in capturing behavioral patterns under controlled experimental conditions, validating the accuracy and consistency of sensor readings. This approach offers a non-invasive, continuous method for obtaining valuable ecotoxicological information, supporting its potential application in laboratory assays and future biomonitoring programs.

Funding Source: Mohamed bin Zayed Species Conservation Fund (MBZ Project 242534346).

Molluscs as Bioindicators

Conservation

Oral - 245

INTERTIDAL GASTROPODS AS BIOMONITORS: *Littoraria flava* (KING, 1832) AS A MODEL AND SENTINEL SPECIES FOR MICROPLASTIC POLLUTION STUDIES

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Keywords: species selection criteria, captivity tolerance, environmental indicators.

Coastal environments are increasingly affected by microplastic pollution, which can impact marine biodiversity at various trophic levels. Selecting appropriate bioindicator species is essential for monitoring and assessing contamination. This study aimed to evaluate four intertidal gastropod species to identify the most suitable for microplastic biomonitoring, considering both environmental relevance and laboratory viability, and to test the species' tolerance to captivity for potential use in experimental studies. The research was conducted in two phases. In the first phase, four gastropod species were collected in Baraqueçaba Beach, São Sebastião, São Paulo, Brazil: *Stramonita brasiliensis* (Claremont & D.Reid, 2011), *Littoraria flava* (King, 1832), *Echinolittorina lineolata* (A. d'Orbigny, 1841), and *Hastula cinerea* (Born, 1778). Each species was evaluated based on its abundance, ease of collection and handling, and feasibility of microplastic analysis. Based on these criteria, *L. flava* was selected for a second sampling phase in Indaiá Beach, Bertioga, São Paulo, Brazil, where individuals were collected and maintained in laboratory conditions to assess their survival, adaptability, reproduction, and potential use in controlled microplastic exposure experiments. Microplastic contamination was detected in 94% of the 50 individuals analyzed in the first phase, totaling 126 particles in the four species. The most frequent type was fiber (85%), followed by fragments (6,3%) and films (8,7%). These findings confirm that intertidal gastropods are widely exposed to microplastics exposed to microplastics at both collection points. Although all species were contaminated, *L. flava* was notably the most suitable for biomonitoring purposes due to its high field availability, ease of handling, and efficient laboratory processing. Specifically for *L. flava*, the fiber size was not homogeneously distributed; the transparent fibers were significantly larger than the others. After the second collection made in Bertioga, the individuals of *L. flava* have been successfully maintained in laboratory conditions, exhibiting good survival, stable behavior, and feeding activity. These observations suggest that it combines ecological relevance with practical advantages for use in experimental protocols, reinforcing its potential as a sentinel species and also for laboratory bioassays to monitor and better understand the effects of microplastic pollution. The study achieved its objectives by identifying *L. flava* as a promising biomonitor species for microplastic pollution, and possibly for other pollutants. The species demonstrated consistent contamination, practical advantages for field and laboratory work, and adaptability to captive conditions. These findings support its use in future monitoring programs and controlled exposure experiments in coastal environmental assessments.

Funding Source: This research was funded by CAPES (Coordination for the Improvement of Higher Education Personnel - Brazil).

Molluscs as Bioindicators

Ecology

Oral - 260

ASSESSING MICROPLASTIC RETENTION AND BIOACCUMULATION IN *Anodontites trapesialis*: A FRESHWATER BIOINDICATOR STUDY

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Keywords: freshwater bivalves, microplastic pollution, depuration of microplastics, environmental monitoring.

Microplastics (MPs) are contaminants that can bioaccumulate, interact with pollutants, and release additives, intensifying their environmental impacts. *Anodontites trapesialis*, a freshwater bivalve widely distributed in Brazil, is an effective bioindicator due to its high filtration capacity and its importance in water quality and nutrient cycling. This study evaluates the potential for bioaccumulation of MP, the sizes ingested, fragmentation, and the residence time of these contaminants. Twenty-eight individuals were collected in the Pirajibu-Mirim River (SP, Brazil) and acclimated in 3 L aerated aquaria. Temperature and ammonia concentration were monitored daily; organisms were fed 1 mL/day of *Nannochloropsis* sp. Egestions were collected every two days, for 15 days, digested with H_2O_2 (50 °C, 48 h), filtered (5 µm), and analyzed via stereomicroscopy. Individuals were exposed for 48 h to 0.0375 g/L of polyester fibers (0.7 mm – 4 mm); controls included aquaria with and without mussels. Post-exposure depuration was analyzed using the same procedure as during acclimation. Afterwards, individuals were dissected, their viscera were digested, and analyzed. The collected individuals were depurated for 15 days until no more microplastics and sediments were in the egesta. A total of 7 spheres, 59 fibers, 1 pellet, 37 fragments, and 3 fiber clusters were identified. This same period was sufficient to stabilize ammonia levels in the water. After exposition, during the depuration, we noticed that the average size of the fibers did not change significantly over time. The number of fibers egested on day 1 was not counted due to the excessive number of fibers overlapping each other. From the third day of egestion, it was counted 370 fibers, which decreased continuously until there were 7 fibers on day 22. Filter membranes revealed twisted, agglomerated, and possibly fragmented fibers with morphology and size distinct from the material originally supplied. The size difference and the morphology of the extremities, analyzed throughout scanning electron microscopy (SEM), showed possible evidence of the fragmentation action by the digestive system. During dissection, an agglomerate of fibers was found firmly adhered in the crystalline style of one individual, a structure possibly involved in material alteration. Regarding the number of modified fibers, we found 5 agglomerates and 20 twisted structures in the whole experiment, temporally distributed along the experiment. After these days, no other evidence of fiber bioaccumulation was observed in the viscera. Analysis of the depuration of 0.7 mm fibers is ongoing. Based on the obtained data, *Anodontites trapesialis* demonstrates potential as a microplastic contamination monitor, depurating a plethora of microplastics of several shapes and colors in about 15 days. For the 4.00 mm fibers, there was no evidence of bioaccumulation in viscera after 22 days, although the digestive system modified the microplastics morphology.

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Molluscs as Bioindicators

Conservation

Oral - 263

DEVELOPMENT OF A PROTOCOL FOR LABORATORY REARING OF *Pomacea figulina* (SPIX IN WAGNER, 1827)

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Keywords: *Pomacea figulina*, growth performance, laboratory rearing, feeding protocol.

The use of gastropods in ecotoxicology is growing due to their sensitivity to pollutants and easy handling. *Pomacea figulina* emerges as a promising native biomonitor among Neotropical mollusks, yet lacks standardized rearing protocols. This study aimed to establish a cultivation protocol for *P. figulina* under laboratory conditions, focusing on growth and survival, to support its application in future ecotoxicological bioassays. Egg masses of *Pomacea figulina* were collected in Sorocaba (SP) and incubated under controlled conditions for 20 days. After hatching, 120 individuals were randomly assigned to 40 aquaria (3 per tank; 10 replicates/treatment) and maintained for 8 weeks with constant temperature and aeration. Four diets were tested: (1) commercial fish feed, (2) fresh kale, (3) feed + kale, and (4) a lab-made feed (fish feed, eggshell, agar, water). Each individual received 0.3 g of food every 3 days. Weekly, shell length, weight, and mortality were recorded. Data were analyzed using the Kruskal-Wallis test and Dunn's post hoc test ($p < 0.05$). This analysis showed that individuals in Treatment 4 achieved the best biological performance, with the lowest mortality rate (6.7%) and the highest mean gains in mass (0.2554 g) and shell length (9.615 mm), with significant growth observed from the second week. Treatments 2 and 3 showed intermediate and similar development patterns, with gradual growth and stable survival rates, averaging Treatment 2 (0.0936 g / 6.9375 mm) and Treatment 3 (0.1975 g / 9.430 mm). Although similar overall, Treatment 2 differed significantly from Treatment 4 in shell length, with lower performance. Treatment 1 showed modest and continuous growth (0.1986 g / 8.335 mm) and a mortality rate of 43.3%, which was lower than the 70% observed in Treatment 2 (21 individuals), the highest among all groups. This may be attributed to external factors such as fluctuations in water quality, food quality, or the broodstock's condition. Statistical analysis using the non-parametric Kruskal-Wallis test revealed significant differences between treatments for both variables (mass and length), and a positive correlation between them. Treatment 4 stood out significantly, being the only one with superior performance in both parameters. Treatment 1 differed significantly from Treatment 4 in length, though its mass gain was comparable to Treatment 3. Treatment 2 performed the worst overall, recording the lowest averages for both variables. These findings establish Treatment 4 as the most effective feeding strategy for cultivating *Pomacea figulina*, providing a foundation for developing laboratory rearing protocols and supporting its application as a model organism in ecotoxicological studies. Treatment 4 proved most effective for *Pomacea figulina*, showing superior growth and lower mortality. Treatments 2 and 3 had intermediate outcomes, while Treatment 1 showed poor performance. Diet was a key factor in development, though water quality and brood traits may also influence results. These findings support the species' suitability for ecotoxicological research and environmental biomonitoring.

Funding Source: National Council for Scientific and Technological Development (CNPq). Foundation for the Coordination of Improvement of Higher Education Personnel (CAPES).

Molluscs as Bioindicators

Evolution

Oral - 285

EDIBLE INVADERS: USING INVASIVE ALIEN FRESHWATER MOLLUSKS TO MONITOR MICROPLASTIC CONTAMINATION IN TROPICAL MAAR LAKES OF THE PHILIPPINES

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Keywords: invasive alien species, mollusks, maar lakes, microplastics.

The Philippines is one of the leading countries in microplastic (MP) pollution. Most MPs diverted to marine ecosystems originate from rivers and lakes. However, MP research in lakes is still limited in the country. This is complicated by the presence of invasive alien mollusks (IAM). Interestingly, most Filipinos consume these species. Thus, this study examined MP contamination in IAM, *Pomacea canaliculata*, *Sinotaia quadrata*, and *Sinanodonta woodiana*, in selected maar lakes. Mollusks collected from various locations within the maar lakes (Sampaloc, Yambo, Palakpakin, and Mohicap) were covered with aluminum foil prior to storage in the laboratory. Water parameters (pH, temperature, turbidity, and depth) were measured while anthropogenic activities were also noted. Around 20-30 adult *P. canaliculata*, *S. quadrata*, and *S. woodiana* were utilized per lake followed by tissue digestion using 10% potassium hydroxide for ≥ 72 hrs. The digested tissue mixtures were filtered through 1.2 µm GC/F Whatman glass filter to trap the MPs. Isolated MPs were identified under a stereomicroscope and confirmed using a hot needle test. The MPs were classified based on form, size, and color. The abundance of MPs in *P. canaliculata* and *S. quadrata* ranged from 0.53 - 1.37 MP/g and from 0.88 - 2.28 MP/individual. Samples from Lake Palakpakin have the highest MP contamination followed by those from Lakes Sampaloc, Mohicap and Yambo. Microplastic sizes varied across the lakes, with 57% above 1 mm. The detected MPs were dominantly fibers (90%) with black color (50%) suggesting the most likely origin of these particles are the dark-colored fish nets scattered within the lakes. Principal component analysis showed distinct variation in MP distribution between Lakes Sampaloc, Palakpakin, and Mohicap with heavy anthropogenic encroachment and aquaculture activities, compared to Lake Yambo which is relatively pristine and mainly utilized for ecotourism. Results of this study suggest widespread MP contamination in edible invasive mollusks that might post health risk upon human consumption. This also provided evidence on the potential of IAM as bioindicators for MP monitoring in different freshwater habitats in the country. Moreover, the data can be used by local government units and other stakeholders for science-based policy and management of plastic wastes.

Funding Source: Research fund from Department of Science and Technology Grants-in-Aid (DOST-GIA) Program with the National Research Council of the Philippines (NRCP) as Monitoring Agency for Project 1. Surveillance of Invasive Alien Species in Tropical Maars: Biology and Ecology of Invasive Mollusks and Fish in the San Pablo Lakes (under the 7 LAMPS Program Phase 2).

Molluscs as Bioindicators

Ecology

Oral - 240

ACUTE ECOTOXICITY EVALUATION OF *Biomphalaria glabrata* AND *Lymnaea stagnalis* (MOLLUSCA: GASTROPODA) EXPOSED TO THE ANIONIC SURFACTANTS LINEAR ALKYLBENZENE SULFONATE (LAS) AND SODIUM DODECYL SULFATE (SDS)

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Keywords: ecotoxicological assay, native snail, pond snail, freshwater.

Linear alkylbenzene sulfonate (LAS) and sodium dodecyl sulfate (SDS) are anionic surfactants widely used in several products, such as pharmaceutical and industrial.They are frequently released into aquatic environments through effluents,and there is a lack of knowledge about the effects,especially in mollusks.In this work,the aim was to evaluate the acute toxicity effects of the LAS and SDS on the freshwater gastropods *Lymnaea stagnalis* (Linnaeus, 1758) and *Biomphalaria glabrata* (Say, 1818). Adult snails of the species *L. stagnalis* and *B. glabrata* were exposed in a semi-static system for 24 hours, analyzed during five days, and the assays were repeated three times. The mollusks were evaluated through exposure to five concentrations of both surfactants. A negative control group was maintained under the same experimental conditions. The endpoint for acute toxicity assays were physiological changes and mortality, the median lethal concentration (LC_{50}) was established. The LAS-LC_{50} observed was 17.25 mg L^{-1} to *L. stagnalis* and 19.17 mg L^{-1} to *B. glabrata*. The SDS-LC_{50} observed was 33.2 mg L^{-1} to *L. stagnalis*, and this result was compared with previous data with *B. glabrata* of 36.9 mg L^{-1}. Observed effects during exposure included hemolymph release, mucus secretion, and body protrusion from the shell. The sensitivity of the species *L. stagnalis* compared with the endemic snail *B. glabrata* demonstrated similar results for both surfactants. An advantage of using *B. glabrata* in ecotoxicological tests in countries with a tropical climate is that the amount of test solution used and consequently the waste disposal is smaller, also reducing the economic investment in the test. For standardization procedures in countries that require the regulation of new tests, the comparison between organisms already validated worldwide, as *L. stagnalis*, and endemic species helps in the development of guidelines in countries that require new testing regulations. treatment for this group of contaminants to minimize the environmental impacts of this pollutant. The use of a species representative of ecosystems in tropical regions, such as *B. glabrata*, is a relevant and recommended tool for the monitoring and evaluation of chemical substances and products, effluents and continental waters of greater environmental significance for Brazil and Latin America.

Funding Source: Supported by: Scholarship - Secretaria de Estado da Saúde de São Paulo.

SYMPOSIUM: INVASIVE ALIEN SPECIES IN MALACOLOGY

SYMPOSIUM INVASIVE ALIEN SPECIES IN MALACOLOGY

Coordinator:

MARTIN HAASE – University of Greifswald, Germany

JANINE OLIVEIRA ARRUDA – Secretaria Estadual do Meio Ambiente do Rio Grande do Sul, Brazil

This symposium explores the spread and impact of invasive molluscs, addressing detection challenges, ecological consequences, and management strategies across different regions.

Invasive Alien Species in Malacology

Invasive Alien Species

Oral - 109

OUT OF NEW ZEALAND: THE GLOBAL SPREAD OF *Potamopyrgus antipodarum*

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Keywords: Caenogastropoda, freshwater, invasive species, parthenogenesis, Tateidae.

Potamopyrgus antipodarum is among the globally most successful invasive freshwater gastropods. It has reached Australia and Europe already in the 19th, North America and Japan in the late 20th, and Chile in the 21st century. Parthenogenesis, ovoviviparity, and broad ecological tolerances are perfect preconditions for colonizing new habitats and generating extremely dense populations. We analysed the spread in order to understand its dynamics as prerequisite for developing effective management strategies. Published records in literature and data bases until including 2023 were collated to map the spread of *P. antipodarum* and compare continental-wide patterns. Based on SNPs typed in 1617 specimens, 1) the genetic differentiation of samples from New Zealand, Europe and North America was analysed using clustering methods and discriminant analysis of principal components, and 2) the colonization of Europe and North America was inferred in an approximate Bayesian computation framework. Evidence for genetic adaptation of the clonal lineages since colonization is provided from common garden experiments conducted in different contexts. 148803 records from 43 countries on five continents were compiled. While in Australia, North America and Japan, *P. antipodarum* spread initially fast to slow down already after 10-20 years, the expansion in Europe started slowly and only after several decades picked up speed in several waves to reach the Middle East and lately also Northern Africa. The arrival in Chile roughly ten years ago is too recent for meaningful comparisons. Of course, the picture mainly reflects the documentation of the range changes and records certainly lag behind the actual dispersal events to varying degrees. Directions and distances suggest different dispersal mechanisms, hence, different measures to face the invasion. The introduction of *P. antipodarum* to Europe and North America happened in ballast water of ships. Europe received two lineages from the North and South Islands of New Zealand, respectively. The invasion of North America was more complex. One of the European lineages probably gave rise to the cluster dominating the East of the US. The other cluster mainly occurring in the Western US had affinities to the other European lineage as well as to two clusters from New Zealand. Our analyses suggest that only very few clonal genotypes were responsible for invading entire continents raising the question if only a few lineages are really capable of becoming invasive. Evidence from common garden experiments suggests that the invasive lineages also accumulate beneficial mutations, i.e. evolve, despite the lack of recombination. Our analyses stress the importance of continuous monitoring of freshwater sites to mitigate the ecological impact and further spread of *P. antipodarum*. Our results have certainly relevance for our understanding of the establishment and evolution of clonal lineages and may also support modelling the potential future spread.

Funding Source: German Science Foundation (DFG): RTG 2010 RESPONSE.

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Invasive Alien Species

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TOLERANCE OF *Limnoperna fortunei* (DUNKER, 1857) (BIVALVIA: MYTILIDAE) JUVENILES TO AIR EXPOSURE

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Keywords: air exposure, invasive species, bioassays, dispersal control.

Limnoperna fortunei (Dunker, 1857) is an invasive bivalve introduced to Brazil in the 1990s, causing environmental and economic problems in aquatic ecosystems and hydroelectric plants. To mitigate these impacts, tolerance studies, including air exposure experiments, have been conducted, especially with juveniles, which are hard to detect and have high dispersal potential. Understanding tolerance and mortality in these conditions aids in adopting more effective control and management strategies. Tests were conducted to analyze the tolerance of *Limnoperna fortunei* juveniles (3–5 mm and 10–15 mm) to air exposure at 20°C and 25°C, under 50% and 70% relative humidity, with a 12h:12h light:dark photoperiod. The experimental group was exposed to air, while the control group was maintained in dechlorinated water under the same environmental conditions. Mussels were placed in six-well plates and stored in BOD (Biological Oxygen Demand) incubators for five days without feeding. Daily, one plate from each group was observed, and mortality was recorded. The endpoints considered were lack of response to physical stimulation, shell closure, and absence of heartbeat or gill movement. The collected data showed that both temperature and relative humidity influenced the mortality curve of *Limnoperna fortunei* juveniles within the selected size ranges, although these factors did not have a strong impact on the time required for total mortality. In the group of 3–5 mm juveniles, high mortality was observed after just one day of air exposure, reaching 100% mortality within two days, regardless of the condition tested. Among juveniles measuring 10–15 mm, only those kept at 25°C and 70% humidity exhibited mortality on the first day. In the other experimental conditions, mortality began on the second day, reaching 50% after three days and 100% after four days, except for individuals maintained at 20°C and 70% humidity, in which 6% of the mussels survived until the fifth day. Analyzing these data provides a better understanding of the factors affecting the mortality of *L. fortunei* juveniles under air exposure. Recognizing how relative humidity and temperature influence the mortality curve enables the development of more efficient techniques for sterilizing fouled surfaces and controlling the spread of the golden mussel, helping to mitigate its impacts on Brazilian river basins and industries.

Funding Source: No.

Invasive Alien Species in Malacology

Invasive Alien Species

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WHO IS TO BLAME? FIRST RECORDS OF THE NON-NATIVE PREDATORY SNAIL *Tomostele musaecola* IN MEXICO AND IMPLICATIONS FOR ITS POTENTIAL SPREAD IN CANCÚN

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Keywords: Streptaxidae, protected natural area, malacophagous, tourism, urban developments.

Tomostele musaecola is a predatory gastropod whose spread into new habitats has raised concerns about its potential impact on native land snails. In island ecosystems, it has been linked to local declines of native mollusks, although its behavior in mainland settings remains poorly understood. Cancún is characterized by rapid urban expansion and the proliferation of large-scale tourist developments, factors that can inadvertently facilitate the introduction of non-native species. This study investigated the presence and density of *T. musaecola* in Parque Ecológico Kabah, an urban protected area in Cancún, Quintana Roo, México. Sampling took place in June 2022 at five distinct sites. Each site featured a 50 m transect laid perpendicular to the trail road, with 10 randomly chosen points for collecting soil and leaf litter samples, which were subsequently sieved to recover adult snails with complete shells. Within the park, soil is routinely imported and redistributed to tourist resorts through government assistance, creating pathways for the accidental introduction and dispersal of non-native fauna. This is the first record of *Tomostele musaecola* in Mexico. The results indicated that *T. musaecola* occurs in only two sites, areas with heavy foot traffic and active soil transport. Statistical analysis showed that this species acts as an indicator in one of those sites, where its presence is characteristic and mainly localized, and the overall gastropod density there was significantly lower than in the best-preserved zone. The presence of juveniles points to an established population, and its association with disturbed environments underscores its potential possible negative effects on native malacofauna. Authorities in Quintana Roo have been alerted to the discovery of *T. musaecola*, but no preventive actions have been currently implemented. No further studies are being conducted on *T. musaecola* at the site, highlighting the urgent need for additional research. Investigations in other tourist complexes and developments that have imported soil from the park could help determine whether *T. musaecola* has successfully colonized additional sites around the city.

Funding Source: No.

Invasive Alien Species in Malacology

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CHALLENGES IN ZEBRA MUSSEL DETECTION USING ENVIRONMENTAL DNA IN THE IBERIAN PENINSULA

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Keywords: *Dreissena polymorpha*, eDNA, monitoring, freshwater.

The zebra mussel *Dreissena polymorpha* is considered one of the most invasive species in the world and causes significant economic damages. Early detection is crucial to prevent rapid expansion. The use of environmental DNA (eDNA) is increasingly being used to this aim but is often pointed as producing unreliable results. The objective of this study was to test eDNA methods for early detection of zebra mussel in the Iberian Peninsula. Adult zebra mussel samples were collected, along with other sympatric bivalve species in the Iberian Peninsula. Water samples were collected and filtered from a wide range of locations, with and without zebra mussels and other bivalves. eDNA was extracted and quantitative PCR was used to detect *Dreissena polymorpha*, using published primers and our own design. New primers were designed using published COI genes from Genebank. Conditions for qPCR were adjusted to optimize results. Our results show that published primers lack specificity, as they amplify DNA from other sympatric bivalves as well. Using adult specimens' samples, it was relatively easy to identify *Dreissena polymorpha* in the qPCR, as it needs less cycles to amplify and shows a different melt peak temperature around 86°C. However, Unio tumidiformis showed a similar, melt peak temperature. Furthermore, due to the reduced and variable amount of DNA present in water samples, the number of PCR cycles showed to produce unreliable results. Consequently, in the studied systems there was the possibility of false positive results. Additionally, some water samples from locations where the species is present did not produce positive eDNA results, showing the importance of considering field replication and the need to revise factors such as volume filtered, temperature patterns, etc. Testing of these factors, laboratory procedures and new primers are ongoing. Our results show the importance of considering local conditions, including the presence of sympatric species, in developing and interpreting results from eDNA analysis for detection of the zebra mussel. This knowledge allows to optimize field and laboratory procedures to increase reliability of the results and therefore have a cost-effective tool to manage this species invasion.

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NON-NATIVE MOLLUSC SPECIES IN BRAZIL

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Keywords: exotic species, biological invasions, terrestrial molluscs, marine molluscs, limnic molluscs, scientific cooperation.

Alien species are among the main causes of biodiversity loss on the planet, altering the native biota, causing economic damage, and posing human health risks. In this study we compare results of the three initiatives from Brazilian specialists in order to produce the country's first list of non-native molluscs (NNM) based on analysis of geographical reports and current taxonomic knowledge of these species. The initiative was prompted by letter 021/2003 from the General Fauna Coordination of the Brazilian Institute for the Environment and Renewable Natural Resources. Three working groups were set up, bringing together specialists at the Brazilian Malacology Meetings (EBRAM) in 2011, 2021, and 2023. The lists generated were organized according to the categories: 1) naturalized species, established in the wild in Brazil; 2) species kept only in captivity ; 3) potential invasive species not yet observed in Brazil. In 2021, a fourth category was added, 4) cryptogenic species. For data search, only scientific articles were considered when drawing up the list. In 2011, category 1 included 22 species (three marine, seven limnic, and 12 terrestrial), category 2 had four species (one marine and three terrestrial), and category 3 included one marine species. In 2021, 16 species were added to category 1 (two limnic, seven marine, and seven terrestrial), six to category 3 (three limnic and three marine), and two terrestrial species to category 4. In 2023, another 16 species were added to category 1 (three marine and 13 terrestrial) and six to category 4 (all terrestrial). One terrestrial species initially allocated to category 1 in 2011 was subsequently relocated to category 4. Since 2023, the list of alien species has been updated according to the new articles published. In 2024, three species (one limnic and two marine), and in 2025, one terrestrial species were added to category 1. A total of 21 species were listed for category 1 in 2011; 17 species in 2021, 16 species in 2023; three species in 2024, and a single species so far in 2025. It is noteworthy that in the interval between only 2021 and 2023, 16 species were added to category 1 while between 2011 and 2021 the rate was of just 1.7 species/year. In total, 79 non-native mollusc species are known from Brazil, 57

species are established (56% terrestrial, 26% marine, and 18% limnic) (Category 1), four are kept only in captivity (Category 2), and nine in categories 3 and 4. This project represents a comprehensive survey of exotic mollusks within Brazilian territory until present. Evaluating the diversity and distribution of these species is an essential step toward determining necessary management or containment strategies, contributing to conservation planning and biosecurity efforts.

Funding Source: No.

Invasive Alien Species in Malacology

Invasive Alien Species

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MODELLING ENVIRONMENTAL SUITABILITY FOR THE SOUTHERN LINEAGE OF THE INVASIVE BIVALVE *Mytilopsis leucophaeata*

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Keywords: false mussel, invasive species, MaxEnt.

Environmental suitability models help predict the geographic distribution of species in both native and invaded regions. *Mytilopsis leucophaeata* is native from Gulf of Mexico, and has two invasive lineages: the "northern" (northeastern U.S.A. and Eurasia) and the "southern" (South America). This study aims to develop environmental suitability models for the southern lineage of *M. leucophaeata* in native and non-native areas. We compiled a global database of occurrence records for the southern lineage of *M. leucophaeata* (native and non-native) up to 2024. Six environmental variables that may influence the distribution of *Mytilopsis* spp. were retrieved from Bio-ORACLE using R (i.e., salinity, mean sea surface temperature, mean bathymetry, mean chlorophyll-a, dissolved oxygen, and mean bottom light). Environmental suitability models were generated in MaxEnt, and model performance was assessed via the AUC (Area Under the Curve) metric. The models achieved high accuracy (AUC > 0.9), indicating broader environmental suitability than the species' current range in both native and non-native areas. High suitability regions include tropical and subtropical coasts of South America, the Caribbean, western Africa, southeast Asia, and parts of the Pacific. Among the environmental variables, light at the bottom was the most influential factor, followed by mean sea surface temperature and mean chlorophyll-a. The southern lineage of *M. leucophaeata* has been expanding its distribution in recent years, especially in Brazil, where it forms dense clusters of individuals. These findings may indicate that the environmental conditions in tropical countries favor the establishment and spread of this species. Its broad physiological tolerance and high filtration rates enhance water clarity and facilite colonization. Another invasive *Mytilopsis* species - *Mytilopsis* sallei - native to the Caribbean, has been introduced in several regions around the world, particularly in southeast Asia. According to the generated models, there is an overlap in native occurrence areas between the two species, as previously reported in the literature, and a potential overlap in non-native areas, mainly in China, where *M. sallei* has already been recorded. These results suggest that the southern lineage of *M. leucophaeata* may further expand its distribution if introduction vectors, such as ballast water discharge, are not properly managed and monitored. The study successfully identified global regions environmentally suitable for the southern lineage of *M. leucophaeata*. Therefore, management measures should be developed to prevent the spread of this species to new environments, considering the potential ecological impacts following its introduction, such as competition with native species and disruptions to ecosystem functioning.

Funding Source: CAPES; FAPERJ; UNIRIO.

Invasive Alien Species in Malacology

Invasive Alien Species

Oral - 315

COMPARATIVE ANALYSIS OF THE SEX RATIO OF *Limnoperna fortunei* (DUNKER, 1857) IN A HYDROPOWER RESERVOIR IN THE LOWER IGUAÇU RIVER - BRAZIL

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Keywords: invasive bivalves, limnic molluscs, sex determination, reproductive allocation, population dynamics, mollusk reproduction.

Limnoperna fortunei (Golden Mussel) is a freshwater bivalve dioecious, with occasional reports of hermaphroditism. It reaches sexual maturity at approximately 1 year and 5–6mm in length. The sex ratio is reported as 1:1, with regional variations. Studies on the sexual ratio and maturity are essential for assessing fertility and population balance, particularly in organisms that have undergone chromosomal manipulation. Individuals were collected from distinct beds in the Baixo Iguaçu Hydroelectric Power Plant (HPP) reservoir and transported to the laboratory at the State University of Ponta Grossa. Shell length (L) was measured using a digital caliper with a precision of 0.01 mm. After mechanical opening, sex (male, female, or undetermined) was identified based on gonadal coloration and gamete morphology under an optical microscope. A systematic review was conducted for this species to identify patterns in its sex ratio. The sex ratio was evaluated using the chi-square test (X^2), considering the 1:1 ratio hypothesis. All analyzed specimens exhibited gonadal tissue, corroborating the maturation size (< 5 mm) described in the literature (Darrigran et al., 1999; Boltovskoy et al., 2015). Although studies suggest a balanced sex ratio (1:1) in *L. fortunei* (Ut et al., 2013; Nakano et al., 2017), variations were observed among the sampled banks in the studied reservoir. The present sample was compared with 11 previous studies (Mansur et al., 2012). The overall mean indicated 52.45% females, 39.38% males, 7.77% undetermined individuals, and 0.400% hermaphrodites (the latter recorded only in two studies at low frequency). In 9 out of 12 studies, including the present one, a predominance of females was observed. The chi-square test (X^2) revealed significant differences ($\alpha = 0.05$) in only four studies, three showing a female-biased ratio and one a male-biased ratio. The lowest p-value ($p = 0.013$) was reported by Marcelo & Callil (2006) with a proportion of 1.22:1 (F:M), while the highest p-value ($p=0.148$) occurred in Pestana et al. (2008), with a proportion of 0.48:1 (F:M) and a variation of 0.135. No clear geographic pattern was detected for these differences, which may be attributed to local phenotypic factors. The presence of undetermined individuals may be explained by gonadal immaturity, parasitic castration, and/or reproductive resting periods. The majority (66.66%) of the studies did not show a significant difference in the proportion between males and females. The low frequency of hermaphrodites reinforces that *L. fortunei* exhibits predominantly dioecious behavior, while the presence of undetermined individuals suggests methodological limitations or potential sexual plasticity. Future studies should investigate environmental and genetic factors underlying these patterns, with applications for population control strategies and ecological monitoring of the species.

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Invasive Alien Species in Malacology

Invasive Alien Species

Oral - 345

GOLDEN MUSSELS IN THE AMAZONIAN AQUATIC ECOSYSTEM: AN ALERT FOR LOCAL DIVERSITY AND ECONOMY

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Keywords: Amazonian Basin, *Limnoperna fortunei*, exotic species, ballast water, biofouling, integrative taxonomy, impacts.

Establishment of *Limnoperna fortunei* (Dunker, 1857) populations in the Tocantins-Araguaia River basin, a recent invasion in Amazon. Golden mussels were firstly notified in South America in the early 1990s (Darrigran; Pastorino, 1995) quickly spreading by biofouling and ballast water, due to its high larval dispersion. Acting as an ecosystem engineer, it alters nutrient cycles, increases water transparency, and modifies habitats, impacting native species and affecting local economy. Samples were collected on November and December 2024, in the upper portion of the Araguaia-Tocantins rivers from Amazonian aquatic ecosystem (2°4'48.52" S,49°25'18.04" W; 1°45'31.63" S,49°1'46.14" W; 4°59'37.38" S, 49°20'21.15" W and nearby locations). Bivalves were sorted and initially identified based on morphological characteristics. Taxonomic confirmation was performed using DNA barcoding of the mitochondrial cox1 and 16S markers. Phylogenetic reconstruction was conducted using the maximum likelihood method in the IQ-TREE software version 2, and mean uncorrected P-distances, both within and between Limnoperna species, were estimated using MEGA version 11.0. Specimens were then photographed using an Ivesta 3 stereomicroscope (Leica) and deposited in the mollusc collection of the "Museu Paraense Emílio Goeldi (MPEG)". Individual golden mussels were mostly between 15.01-20 mm and 20.01-25 mm in length, with total lengths ranging from 2.2 to 28.0 mm. 96.7% of the individuals were larger than 5 mm (adults). Analysed organisms were deposited at the Museu Paraense Emílio Goeldi (voucher numbers MPEG 004375, 004397–004401, 004417). Species identification was confirmed by morphology (Pereira et al., 2012) and DNA barcoding (this study), forming a monophyletic clade with intra-specific cox1 genetic divergence below 2% and 16S rRNA congruent topologies. In addition to its known distribution in the Paraná River, São Francisco River, and Pantanal wetlands (Chagas et al., 2025), new dense aggregations have recently been recorded in the Araguaia-Tocantins River basin. This evidences the species' continued expansion into the Amazon, progressing faster than previously predicted. Although ecological models had estimated its arrival in northern Brazil around the 2030s (Barbosa et al., 2018), field observations—supported by fishermen reports—now confirm its presence, revealing its ability to adhere to various substrates, tolerate environmental variation (including estuarine dynamics), and cause macrofouling. Molecular analyses support this invasion scenario. Haplotype network analysis of the cox1 gene revealed shared haplotypes between South American and East Asian populations (China, Japan, and Taiwan), indicating recent introductions likely mediated by maritime transport, e.g., ballast water (Zhang et al., 2022). Phylogenetic analyses of cox1 and 16S rRNA genes showed congruent topologies, with South American samples clustering within Asian clades. These results support the hypothesis of multiple introductions, rapid expansion, and a potential genetic bottleneck in the invaded region. The rapid invasion of the Amazonian aquatic ecosystem by golden mussels is a warning sign that stakeholders and decision-makers need to be aware of. Integrative taxonomy is essential for accurate identification and monitoring species, including invasive ones. Native bivalve species from Amazon basin,

other organisms, particularly fish, which are exploited resources, and economically significant human activities are all being impacted by this spread.

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SYMPOSIUM: ARCHITAENIOGLOSSA TO NEOGASTROPODA – SYSTEMATICS AND EVOLUTION OF CAENOGASTROPODS

ARCHITAENIOGLOSSA TO NEOGASTROPODA – SYSTEMATICS AND EVOLUTION OF CAENOGASTROPODS

Coordinators:

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The symposium 'From Architaenioglossa to Neogastropoda – systematics and evolution of caenogastropods' will focus on the taxonomy and phylogenetic relationships among caenogastropods, in particular based on genomics approaches, and on the use of systematic hypotheses to tackle evolutionary questions about their diversification.

Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Taxonomy and Systematics

Oral - 63

UPDATED PHYLOGENY OF THE NEOGASTROPODA: RESOLVED ROOT, NOVEL DEEP LINEAGES, AND OUTLINES OF THE UPCOMING CLASSIFICATION

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Keywords: Neogastropoda, phylogenetics, systematics, new taxa.

With over 15,000 living species, Neogastropoda is the largest order of marine gastropods. Its members are ubiquitous in marine realm and play an important role in benthic communities and economics of coastal countries. Fossil record suggests that the major lineages of Neogastropoda originated as a result of explosive radiation, making their relationships difficult to disentangle and their evolutionary history poorly understood. We applied an exon-capture methodology to reconstruct the relationships of Neogastropoda, based on 575 ingroup taxa, thus increasing taxonomic coverage by almost 6-fold compared to previous studies. Additionally, our dataset included a broad range of higher Caenogastropoda lineages, allowing to clarify relationships at the root of the Neogastropoda radiation. Furthermore, the inclusion of type genera for 94 neogastropod family-level taxa provided, for the first time, a solid basis for a systematic revision of the entire order. We recover strong support for the monophyly of the Neogastropoda, while a close relationship with the superfamilies Tonnoidea and Ficoidea, proposed by previous studies, is not supported by our results. The extensive taxonomic sampling employed in this work allowed us to define, for the first time, the placement of some enigmatic taxa, and to clarify the affinities of lineages previously unresolved. Based on the reconstructed phylogeny we propose notable changes in the family-level systematics of the Neogastropoda: six new families are proposed or raised from subfamily rank, to include deep lineages possessing unique morphology, and one family is reduced to subfamily. Three new superfamilies are proposed to accommodate the phylogenetic diversity of the order emerging from this study. While our results solve most long-standing questions in Neogastropoda systematics, the affinities of Strepsiduridae and Ptychatractidae remain unassessed, and the paraphyletic Borsoniidae could not be tackled at present due to insufficient taxon sampling. The presented results significantly advance our understanding of the Neogastropoda phylogenetic relationships and evolutionary history, concluding a long journey initiated more than a decade ago. The reconstructed phylogeny will provide a robust and comprehensive framework to test major macroevolutionary hypotheses, whereas forthcoming classification of the order will be essential for efficient taxonomic treatment of the huge number of Neogastropoda species that are still awaiting their description.

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Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Evolution

Oral - 77

WINNERS AND LOSERS IN A HYPERDIVERSE CLADE: THE MACROEVOLUTION OF NEOGASTROPODA

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Keywords: diversification, speciation, extinction, macro-evolution, Neogastropda, evolution.

Neogastropods are a hyperdiverse clade of marine predators (>15,000 species), but diversity is unevenly distributed across lineages, with some species-rich lineages but also lineages with a poor extant species richness. Until now, a lack of robust phylogenetic frameworks has limited the potential to test macroevolutionary hypotheses on diversification, extinction, and ecological radiation in this emblematic group. In the context of the HYPERDIVERSE project (2020-2026), an exon-capture based backbone tree on nearly 600 ingroup taxa was reconstructed and dated. In addition, ~15,000 barcode (cox-1) sequences were produced, bringing the total number of available barcode sequences to nearly 50,000. Using a combination of automated species-delimitation and grafting procedures, we combined the exon-capture backbone tree with barcode data to increase taxon sampling and thus maximizing statistical power. Additionally, depth and geographical ranges were inferred for each molecularly delimited species (MOTU). Our integrative approach yielded the largest dated phylogeny of mollusks to date, including nearly 6,000 MOTUs. By comparing several state-of-the-art diversification rate inference methods, we revealed complex dynamics of lineage accumulation in Neogastropoda. Some clades show clear signals of increasing speciation rates, while others exhibit more stable or even declining rates. Methodological discrepancies, especially concerning rate shifts and extinction estimates, are discussed. Ecological hypotheses, such as the latitudinal diversity gradient and the bathyal diversity gradient, were tested using bathymetric and geographical data in association with diversification rates. Some lineages appear to have repeatedly colonized and radiated in deep-sea environments, while others are restricted to shallow tropical waters. These results emphasize the importance of ecological transitions and historical contingencies in driving the rise and fall of neogastropod lineages. They also highlight the power of combining phylogenomic backbones with large-scale DNA barcode data for macroevolutionary analyses. Our study establishes a new phylogenetic and macroevolutionary framework for Neogastropoda, revealing dynamic diversification patterns shaped by ecological and historical factors. By integrating genomic and barcode data, we robustly test large-scale evolutionary hypotheses. This approach uncovers the evolutionary trajectories of major clades and highlights how ecological shifts—particularly in depth and latitude—drive both the rise and decline of neogastropod biodiversity.

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Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Ecology

Oral - 91

WHAT IS THE POPULATION STRUCTURE OF POECILOGONIC SPECIES? EVIDENCE FROM LARGE SCALE GENOTYPING IN A NEOGASTROPOD LINEAGE (CONOIDEA: RAPHITOMA)

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Keywords: population genetics, larval ecology, poecilogony, *Raphitoma*, species delimitation.

'Poecilogony' is a peculiar condition in which different larval developmental modes are present in the same species or population (Giard, 1905). In non-sacoglossan gastropods, almost all claims of poecilogony have been confidently dismissed (Bouchet, 1989). However, some taxa in the neogastropod genus *Raphitoma* Bellardi, 1847 may represent rare exceptions (Russini et al., 2020). But what is the effect of poecilogony on the population genetics of a species? A dataset of 80 individuals of three Mediterranean species of *Raphitoma* was assembled and larval development was inferred from protoconch morphology: multispiral and cancellate for planktotrophic development and paucispiral for non-planktotrophic development (Jablonski & Lutz, 1983; Shuto, 1974). Through a Specific Locus Amplified Fragment (SLAF) sequencing protocol (Sun et al., 2013), a large number of loci was obtained. The resulting dataset was analysed to perform species delimitation analyses with the intent to confirm or disprove poecilogony. Furthermore, the population structure of one poecilogonic species was assessed to verify the co-presence of low- and high-dispersal features. The high-throughput sequencing produced ~10k SNPs. The number of retrieved lineages corresponded with three taxa as previously delimited using mitochondrial and nuclear markers, namely *R. philberti* (Michaud, 1829), *R.* sp. C, and *R. laviae* (R. A. Philippi, 1844), with possibly an additional cryptic species split from the latter. Specimens with contrasting larval development were present in both R. philberti and *R. laviae* s.s. The alternative hypothesis with planktotrophic and non-planktotrophic developers reciprocally segregated was not supported and therefore rejected. In *R. laviae* s.s., the population from Corsica lacked a geographic structure, whereas the one from Croatia showed a remarkable geographic structure, with a clear Isolation by Distance pattern. Congruently, all specimens from Corsica were planktotrophic developers, and all samples from Croatia were lecithotrophic developers. Conversely, in *R. laviae* s.l. specimens of differing larval development are found sympatrically in Croatia, but with remarkable genetic distance between the two and no evidence of interbreeding. Two scenarios are drawn on the emergence of poecilogony depending on the possibility that *R. laviae* comprises two species: (i) triggered by an unknown past event (e.g., the prolonged isolation of Croatia from the rest of the Mediterranean), loss of planktotrophic occurred in the Croatian population. Even if planktotrophic specimens from other regions occasionally reach Croatia coasts, they retain a reproductive barrier with the lecithotrophic population; (ii) the environmental conditions in Croatia promote a developmental strategy with lower dispersal capacity. Planktotrophic larvae that arrive in Croatia 'switch' as adults to a different reproductive strategy, generating lecithotrophic offspring. This is the first study addressing the population genetic of poecilogonic species using high-throughput sequencing. Results support the poecilogonic status of two species in the genus *Raphitoma*, allowing the evaluation of both the features of long-distance dispersal and high local recruitment in one of them. The multi loci approach was not conclusive concerning the taxonomy of *R. laviae*, which should be subject to further revision from an integrative viewpoint.

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Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Palaeontology

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AT THE DAWN OF HIGHER CAENOGASTROPODS-POSSIBLE ANCESTORS OF NEOGASTROPODA, TONNOIDEA AND CYPRAEIDAE

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Keywords: Gastropoda, Neogastropoda, Maturifusidae, Pseudotritoniidae, Purpurinidae, Colombellinidae.

In spite of many years of investigations the origin of higher caenogastropods (i.e. Neogastropoda, Tonnoidea and Cypraeidae remained poorly understood. We traced possible ancestors of these groups in the Triassic, Jurassic and Cretaceous fossil record and argue on possible links with higher caenogastropods. We traced all published accounts on four families of gastropods (i.e. Maturifusidae, Pseudotritoniidae, Purpurinidae, and Colombellinidae) that were considered in the past as possible ancestors of neogastropods (and/or other higher caenogastropods). We also examined several historical collections (Kolkata, Lyon, Munich, Ostrava, Palermo, Sofia) and investigated newly collected specimens from the Dolomites in Italy, Žemaitija in Lithuania, Tennessee and Mississippi in the USA, Dorset, Kent, and Yorkshire in the United Kingdom as well as several localities in Poland. The investigated families differ in taxonomic richness, stratigraphic distribution, and morphology—especially the protoconch, which is crucial for identifying high level taxa. We conclude, that all four families should be kept as separate clades. The monogeneric Maturifusidae ranges from Early to Late Jurassic and is monogeneric. The family Pseudotritoniidae is also monogeneric and ranges from Early to Late Triassic. The family Purpurinidae ranges Middle Triassic to Early Cretaceous and includes genera: *Angularia*, *Cretadmete*, *Fossacerithium*, *Khetella*, *Pseudoscalites*, and *Purpurina*. *Angularia* consists of nine Middle to Late Triassic species. The genus *Cretadmete* is represented by three Late Jurassic to Early Cretaceous species. Two species are attributed to the genus *Fossacerithium*, which ranges from Middle to Late Jurassic. *Khetella* ranges Middle Jurassic to Early Cretaceous and consists of five species. *Pseudoscalites* is represented by three Middle to Late Triassic species. The genus *Purpurina* is species rich and its composition requires separate detailed study. The morphological similarity between Jurassic purpurinids and recent tonnoids is suggestive of an evolutionary connection from the oldest species of Khetella and Cretadmete to the recent tonnoids, with the intermediate genus of *Paladmete* from the Late Cretaceous on the one hand and a number of tonnoid species from the Late Cretaceous and Eocene on the other hand. Colombellinidae ranges from Middle Jurassic to early Late Cretaceous and comprises two genera: *Colombellina* and *Zittelia*. We conclude that purpurinids were already divided into two groups in the Jurassic. One of them, represented by *Khetella*, lead to Tonnoidea and Cypraeidae (through Colombellinidae), while the other branch represented by *Fossacerithium*, could lead to Neogastropoda—a hypothesis, to be tested by future studies. The colombellid genus *Zittelia* is most likely and ancestral taxon for Cypraeidae with the earliest cypraeid *Coffeacypraea* known from the latest Jurassic (Tithonian).

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Palaeontology

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CRETACEOUS RADIATION OF NEOGASTROPODA

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Keywords: Gastropoda, Cretaceous, fossil record, diversification.

Neogastropods are highly diverse group of predominantly marine benthic organisms that currently comprise about a quarter of all living gastropod species. Despite their modern evolutionary success, the origin and early diversification of the group remain poorly understood. We compiled all known records of Cretaceous Neogastropoda, with a particular focus on the Early Cretaceous, to identify potential centres of diversification. Our research is based on compilation of the published taxonomic data with stratigraphic ranges gathered from the original descriptions as well as revisions and the examination of gastropod collections from various institutions, including the Institute of Paleobiology PAS (Warsaw, Poland), the State Museum of Natural History NASU (Lviv, Ukraine), National Museum of Natural History BAS (Sofia, Bulgaria), and the Geological Survey of India (Kolkata, India). We found out that 10 neogastropod families and at least 21 genera have been documented from the Early Cretaceous. The earliest record consists of a juvenile shell assigned to the Buccinoidea from the Valanginian of Poland and Switzerland. These are followed by a turbinellid shell from the Barremian of Bulgaria. A remarkable increase in diversity is observed in the Albian, with the first appearance of 19 genera. Among these, 15 neogastropod species have been recorded from Madagascar, representing the most diverse Early Cretaceous assemblage. Additional records from the Albian of Mexico, England, and Austria further support this trend of increasing diversity. In the Late Cretaceous, neogastropods became more widespread, with 21 families and 159 genera documented worldwide. While the majority of Cretaceous genera went extinct at the Cretaceous-Paleogene (K/Pg) boundary, 26 genera representing 12 families survived. The research reveals a significant radiation of neogastropods in the late Early Cretaceous, with the Albian as a key period in the evolutionary history of the group. The increasing taxonomic richness towards the Late Cretaceous, followed by partial survival across the K/Pg boundary, suggests that the group had already achieved broad ecological and evolutionary success by the end of the Mesozoic.

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Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Evolution

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LIMPET STORIES THROUGH SHELLS AND ANATOMY

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Keywords: limpetisation, microCT, comparative anatomy, body constraints.

Limpet-shaped body plans have evolved multiple times in Mollusca, typically associated with substrate adhesion, protection, and mechanical stability. However, it remains unclear whether convergence extends beyond external shell shape. This study investigates whether flattened morphologies impose anatomical constraints that drive internal reorganization. By comparing gastropods, parasitic limpets, and other molluscan groups, we explore how functional demands reshape internal body plans across unrelated lineages sharing the limpet form. We examined five focal species—*Tectura virginea*, *Ancylus fluviatilis*, *Thyca crystallina*, *Pedicularia elegantissima*, and *Neopilina galathea*—and additional taxa including Caecum and Enigmonia. Specimens were analysed through micro-CT scanning, histology, and 3D reconstruction to compare shell structure, musculature, and major organ systems. We measured and quantified anatomical volumes and generated mathematical models of organ space occupation to assess structural constraints imposed by dorsoventral compression. Comparisons were made between free-living, parasitic, and sessile limpets to identify general and lineage-specific anatomical innovations associated with limpetisation, and to infer how these patterns reflect functional, rather than purely morphological, convergence across Mollusca. Limpet-like molluscs exhibit consistent internal reorganization to meet the demands of dorsoventral compression, adhesion, and environmental interaction. Free-living limpets such as *Tectura*, *Ancylus*, and *Neopilina* show muscular reinforcement and dorsoventral flattening, while sessile limpets like *Enigmonia* rely on shell cementation. Parasitic limpets (*Thyca*, *Pedicularia*) evolve highly compacted and reoriented body plans centered around host adhesion, with modifications to visceral and sensory systems. In contrast, *Caecum*—a derived, scaphopod-like gastropod—represents a rare case of “reverse” limpetisation: it elongates its shell for a burrowing lifestyle but retains key flattened-body anatomical elements. Despite varying life histories, these taxa converge on structural solutions such as reorganized muscle arrangements and minimized body height. Our comparative approach demonstrates that external limpet shape often masks diverse internal strategies for coping with similar physical constraints. These anatomical shifts provide a mechanistic explanation for the success of limpet forms across disparate molluscan groups—and perhaps also for their absence in others. Rather than a fixed outcome, the limpet form emerges as an adaptable, functionally driven architecture. This framework highlights the utility of limpetisation as a model for exploring morphological constraint, evolutionary flexibility, and functional convergence across Mollusca. The limpet form represents a flexible anatomical template repeatedly modified to meet ecological demands. Internally, this convergence involves muscular reinforcement, body compression, and organ repositioning. Our findings reveal that limpetisation is more than superficial resemblance—it reflects adaptive anatomical innovation. These reconfigurations help explain both the repeated emergence and evolutionary limits of the limpet form, offering insights into morphological constraint and the functional evolution of molluscan body plans.

Funding Source: This work is funded by the Leibniz Association project PHENOME (P123/2021).

Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Taxonomy and Systematics

Oral - 259

DIVERSITY OF COLUMBELLIDAE (NEOGASTROPODA): MOLECULAR INSIGHTS INTO THE TAXONOMY OF WESTERN ATLANTIC SPECIES

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Keywords: DNA barcoding, Caenogastropoda, dove snails, systematics, Buccinoidea.

Columbellidae comprises almost 1,000 valid extant species of marine snails classified in about 80 genera. Despite this remarkable diversity, integrative taxonomy has recently revealed cryptic species within this family in the Mediterranean area. However, molecular approaches in the alpha-taxonomy of columbellids are still scarce, especially in the western Atlantic. In the present study, we conducted a species delimitation approach based on a single-locus DNA barcode. Specimens used in this study were collected mainly by the authors in Florida, USA, and along the Brazilian coast. We compiled a dataset of 248 COI sequences (136 new and 112 from the GenBank database) of columbellids from the western Atlantic. Available individuals range from Massachusetts, USA (North limit) to Santa Catarina, Brazil (South limit). Species delimitation using ASAP (substitution model: p-distance) and phylogenetic analyses (Maximum likelihood and Bayesian Inference) were performed. The dataset contains preliminary identification of 18 nominal species, besides other sequences determined up to genus or family level, considering our determinations and those existing in the GenBank. The partition with the lowest score (6.00) in ASAP resulted in 41 subsets. The results suggest that the number of species of Columbellidae in the western Atlantic is underestimated, with potential species complexes related mainly to the taxa *Astyris lunata* (five subsets), *Columbella mercatoria* (two subsets), *Falsuzafrona idalina* (two subsets), *Mitrella ocellata* (two subsets) and *Parvanachis obesa* (three subsets). Current knowledge suggests that these species have a wide geographic range in the western Atlantic, but our results suggest that specimens morphologically assigned to these nominal species hide cryptic speciation. In general, populations from the northern and southern hemispheres differ genetically, but A. lunata has a complex scenario of lineages even in Florida. On the other hand, we confirm some species with a wide distributional range, with no clear distinction between the Caribbean and the Brazilian coast (e.g., Costoanachis sertulariarum and Mitrella dichroa). The complex diversity of Columbellidae needs a taxonomic reassessment based on an integrative approach. Our results suggest the presence of at least five species complexes. It is necessary to advance in the morphological study of these taxa to aid future taxonomic decisions. Also, the effort of DNA barcode in western Atlantic columbellids is still necessary, toward a more robust inventory in this region.

Funding Source: Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

Architaenioglossa to Neogastropoda – Systematics and Evolution of Caenogastropods

Taxonomy and Systematics

Oral - 290

BIOGEOGRAPHICAL PATTERNS IN HIGHER LATITUDE LITTORINIDS (*Laevilitorina*, *Laevilacunaria* AND *Pellilitorina*)

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Keywords: biogeography, Southern Ocean, littorinids, *Laevilitorina*, *Laevilacunaria*, *Pellilitorina*.

Southern Ocean littorinids includes three genera of small nearshore benthic marine snails: *Laevilitorina*, *Laevilacunaria* and *Pellilitorina*. *Laevilitorina* comprises at least 25 nominal species distributed in southern South America, the Antarctic Peninsula, Australia, New Zealand and sub-Antarctic islands of the Southern Ocean (i.e. South Georgia, Marion, Crozet, Kerguelen, Heard, Macquarie). Higher latitude littorinids are gonochoric, exhibit low dispersal potential with benthic protected development and most of them are narrow endemics. We performed an integrative biogeographic study in higher latitude littorinids using multi-locus phylogenetic reconstructions (maximum parsimony, maximum likelihood and bayesian analyses) based on mtDNA (COI, 12S rRNA, 16S rRNA) and nucDNA (28S rRNA and 18S rRNA) sequences, species delimitation analyses (ABGD, mPTP and GMYC) divergence time estimations, radular configuration analyses and geometric morphometric analyses in higher latitude littorinids across their distributions. For this, all the nominal species of *Laevilacunaria* and *Pellilitorina* as well as species of *Laevilitorina* from southern South America, the Antarctic Peninsula, New Zealand, Australia and sub-Antarctic Islands of the Southern Ocean. The systematic of the analyzed groups is much more complex than previously thought and require major revisions. Both, *Laevilitorina* and *Laevilacunaria* are paraphyletic and separated into five major lineages. Species delimitation analyses discriminated most of the nominal species here analyzed. However, within *L. caliginosa* we detected hidden diversity including at least nine different species-level clades. Contrarily, Antarctic species *L. antarctica*, *L. claviformis* and *L. umbilicata* are conspecifics. Divergence time estimations in Laevilitorininae suggest that the origin of the subfamily occurred around 90 million years ago (Ma) associated to the separation of Gondwanan continental landmasses. Most of *Laevilitorina* species are restricted to particular areas of the southern hemisphere. However, one species (*Laevilitorina venusta*), shows a broad distribution in Antarctic Peninsula and sub-Antarctic Islands (South Georgia, Marion, Crozet, Kerguelen and Macquarie). In southern South America we recognized eight different species of *Laevilitorina*. Three of them (*L. magellanica*, *L. pepita*, *L. fueguina*) are found in the Strait of Magellan, two in Cape Horn (*L. caliginosa* and *L. hicana*) and three species (*L. latior* and two new species) in the Falkland/Malvinas Islands. Three different species were recorded in New Zealand sub-Antarctic Islands (*L. delli*, *L. bifasciata*, *L. aucklandica*) while a fourth new species was found in New Zealand South Island. The New Zealand species *L. delli* and *L. bifasciata* are closely associated to South American species of the genus. Finally, Tasmanian species (*L. mariae* and *L. bruniensis*) are more closely associated to New Zealand species. Biogeographical patterns in Laevilitorininae reflect the relevance of plate tectonic vicariance together as well as evidence of recent long-distance dispersal events. Here, we demonstrate how the separation of lineages in different areas of the southern hemisphere are associated to the separation of continental landmasses. This study is most detailed integrative study of littorinids worldwide and reveals an unforeseen diversity across the Southern Ocean.

Funding Source: Fondecyt Regular Project 1210787, Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos Mi-BASE (ICN2021_002), Centro Fondap IDEAL (15150003).

SYMPOSIUM: MOLLUSCAN BEHAVIOUR IN AN EVOLUTIONARY ECOLOGY CONTEXT

MOLLUSCAN BEHAVIOUR IN AN EVOLUTIONARY ECOLOGY CONTEXT

Coordinator:

BARBARA M. TOMOTANI – The Arctic University of Norway, Tromsø, Norway

The symposium 'Molluscan behaviour in an evolutionary ecology context' will highlight recent advances in the study of molluscan behaviour, with a focus on evolutionary ecology. Contributions are welcomed from all classes of molluscs across various environments — marine, freshwater, and terrestrial — offering a broad perspective on how behavioural traits have evolved and adapted in diverse ecological settings.

Molluscan Behaviour in an Evolutionary Ecology Context

Behaviour

Oral - 16

WHY AND HOW TO STUDY LAND SNAIL BEHAVIOUR - EXPERIENCES FROM RESEARCH IN THE ARCTIC

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Keywords: activity patterns, circadian rhythms, evolutionary ecology, hibernation, seasonality.

Our lab studies how organisms adapt to environmental changes, particularly how they deal with novel and extreme environmental challenges. These challenges are particularly prevalent due to global impacts such as urbanization and/or climate change, where human activities rapidly modify natural areas. Our focus is on behavioural and circadian traits (e.g., activity patterns), as well as seasonality (e.g., traits involved in hibernation), which would allow animals to cope with extreme conditions and successfully colonize novel environments. In this talk, we will tell you about our recently started research program with the copse snail, *Arianta arbustorum* (Helicidae), a widespread European species that naturally occurs above the Arctic Circle in Fennoscandia. Our research questions include if and how a nocturnal animal maintains rhythmicity during the "Midnight Sun" period, when there is continuous daylight for 24 hours, and how activity patterns of arctic population compare to those of southern ("standard") populations. Our project did not have a smooth start, and we will share our methodological constraints and how we have been troubleshooting them. Our challenges include determining appropriate darkness treatment parameters and recording the behaviour of slow-moving, cold-blooded animals using video and/or motion sensors. A crucial part of the work is defining the best setup, involving cages, lighting, cameras and sensors, followed by usage of motion-tracking software and the subsequent data processing. We hope that our experiences can help and encourage future studies in snail behaviour and evolution, so we can better understand whether and how snails adapt to environmental challenges. Our lab is set on establishing land snails as good models for evolutionary ecology studies, including areas stretching from chronobiology to neurobiology.

Funding Source: Velux Stiftung (Proj. 1974).

Molluscan Behaviour in an Evolutionary Ecology Context

Evolution

Oral - 5

HOW MUTUALISTIC SYMBIOSIS SHAPES MACROEVOLUTION: INSIGHTS FROM PHYLOGENOMIC RECONSTRUCTION OF THE SUBFAMILY FRAGINAE (FAMILY: CARDIIDAE)

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Keywords: symbiosis, macroevolution, phylogenomic, Cardiidae, Fraginae.

Mutualistic symbiosis is a widespread biotic interaction in marine ecosystems, and it reshapes organismal physiology, ecology, and evolution, often driving novel traits and niche expansion. However, the macroevolutionary impact of mutualistic symbiosis remains debated: does it lead to evolutionary dead ends or drive rapid diversification into new niches? In this study, we investigate this question using the bivalve subfamily Fraginae (Family: Cardiidae), one of only two obligate photosymbiotic bivalve lineages. Fraginae contains more than fifty species found in the tropical waters worldwide. Photosymbiosis is restricted to one clade within Fraginae. We reconstructed the most comprehensive Fraginae phylogeny to date with exon sequencing data of 272 specimens from 45 species from natural history museums worldwide, and calibrated it with fossil records. Additionally, we used microCT scans of 142 shells from 22 species to examine the morphological adaptations associated with photosymbiosis. The phylogeny reveals paraphyly in the genera *Fragum*, *Corculum*, *Americardia*, and *Ctenocardia*. We found greater intraspecific morphological disparity within the symbiotic lineage, posing significant challenges for traditional morphology-based taxonomy. Symbiotic species experience restricted distributions due to their reliance on shallow waters, limiting their dispersal across wide deep-water barriers, or even at local scales. Conversely, non-symbiotic species were able to cross these barriers, which likely resulted in allopatric speciation. Moreover, photosymbiosis significantly influences shell morphology, but these morphological adaptations follow diverse trajectories, reflecting different ecological strategies for adapting to photosymbiosis in Fraginae. Our results indicate that symbiotic and non-symbiotic lineages share similar diversification rates, suggesting that symbiosis does not necessarily lead to adaptive radiation but instead imposes trade-offs between ecological specialization and evolutionary potential. Overall, our findings demonstrate that photosymbiosis can profoundly influence animal macroevolution trajectories, but not necessarily drive rapid adaptive radiations. While symbiotic species display increased morphological disparity, their reliance on shallow waters restricts their geographic range, limiting opportunities for speciation. Mutualistic interactions can promote functional innovation while constraining diversification.

Funding Source: CU Boulder Museum Student Research Award (RL). CU Boulder EBIO Student Research Grant (RL). Packard Fellowship for Science and Enginerring 2019-69653 (JL).

Molluscan Behaviour in an Evolutionary Ecology Context

Evolution

Oral - 10

PATTERNS OF VARIATION OF PREY UTILIZATION OF A PREDATORY CONE SNAIL

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Keywords: Conoidea, feeding ecology, population genetics.

Conus miliaris is a broadly distributed predatory gastropod species that exhibits tremendous differences in feeding ecology among different regions of the Indo-West Pacific, including a wide dietary breadth at Rapa Nui that may have arisen through competitive release. Here we evaluated patterns of variation in diets of populations of *C. miliaris* from four sites in French Polynesia to determine if and how diets differ within smaller geographic regions. We determined the identity of prey items of populations at these sites through sequencing of a region of the mitochondrial 16S gene from fecal samples obtained from specimens. We then compared diets of these populations to those of populations at Guam, American Samoa, and Rapa Nui that were characterized previously. To evaluate population genetic patterns, we obtained sequences of regions of a mitochondrial (i.e., cytochrome oxidase subunit I (COI)) and two nuclear (i.e., conotoxin) loci and compared these to sequences from Guam, American Samoa, and Rapa Nui that were also characterized previously. Populations at four sites in French Polynesia (Rangiroa and Makemo in the Tuamotu Archipelago, Huahine in the Society Islands, and Rurutu in the Austral Islands) show overlapping diets; their diets are generally distinct from those of populations at Guam and American Samoa but share some prey items in common with and in some cases show similar dietary breadths as the population at Rapa Nui. While examination of COI sequences shows little to no differentiation among populations from Guam, American Samoa, and French Polynesia and strong divergence of these populations from the population at Rapa Nui, analyses of the conotoxin loci reveal some admixture between French Polynesia and Rapa Nui populations. These results suggest that the broad dietary breadth and similarity in diets of populations of *C. miliaris* from French Polynesia and Rapa Nui reflect the origin of this ecological phenotype in Rapa Nui and the subsequent migration of it into French Polynesia.

Funding Source: The study was supported by an award from the Belmont Forum and the National Science Foundation of the United States of America.

Molluscan Behaviour in an Evolutionary Ecology Context

Reproduction

Oral - 219

INDUCED TRANSFORMATION OF *Crepipatella peruviana* TO AN ADELPHOPHAGOUS STRATEGY: EFFECTS OF EXTRAEMBRYONIC FOOD ON EMBRYONIC, LARVAL DEVELOPMENT

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Keywords: adelphophagous strategy, development, embryonic, larvae.

The mode of development in some gastropod species depends on the availability of intracapsular food (Collin & Moran, 2018). This study evaluates the ability of *Crepipatella peruviana*, a species with mixed-planktotrophic development, to adopt an induced adelphophagic condition through the provision of extraembryonic food during the encapsulated phase. It also investigates the impact of this extra food on biochemical and physiological characteristics during the pelagic larval phase. Capsules incubated by *C. peruviana* females containing larvae at the intermediate veliger stage were collected. Sibling capsules were divided into control and experimental groups. In the treatments, half of the encapsulated embryos were sacrificed to generate extraembryonic food for the survivors. The encapsulated embryos were cultured until larval hatching. The larvae were maintained until 12 days post-hatching, just before settlement. During larval development, physiological changes were assessed through measurements of oxygen consumption rates (OCR) and clearance rates (CR) (days 0, 7, and 12 post-hatching), as well as biochemical composition (total proteins, lipids, and carbohydrates) (days 0 and 7 post-hatching). Experimental ('cannibal') larvae exhibited higher clearance rates (CR) throughout the pelagic phase, with significant differences between cannibals and controls on days 7 and 12 ($p < 0.001$). OCR increased progressively in cannibal larvae (0.015 on day 0; 0.0697 on day 7; 0.0844 on day 12), with significant differences compared to control larvae (Dunn's test, $p < 0.05$). From a biochemical perspective, newly hatched cannibal larvae (day 0) showed a higher protein content (3.76 $\mu g \cdot ind^{-1}$), with significant differences compared to day 7 cannibal larvae (2.425 $\mu g \cdot ind^{-1}$) and the control group on the same day (2.187 $\mu g \cdot ind^{-1}$) ($p = 0.003$). Regarding lipid content, newly hatched cannibal larvae also significantly surpassed day 7 controls ($p < 0.05$). As for carbohydrates, day 7 post-hatching cannibal larvae exhibited significantly higher values (0.262 $\mu g \cdot ind^{-1}$) compared to the day 0 treated group (0.0655 $\mu g \cdot ind^{-1}$) ($p = 0.03$). These results demonstrate a better physiological and nutritional condition in cannibal larvae, attributable to the exogenous feeding received during the encapsulated period. The provision of extraembryonic food to encapsulated *C. peruviana* larvae significantly enhances energy performance and physiological functioning during the pelagic larval phase, revealing positive carry-over effects. This extra food "transformed" the encapsulated development of *C. peruviana* from a mixed-planktotrophic strategy to an induced adelphophagic condition during the encapsulated stage. This research strengthens our understanding of larval developmental plasticity.

Funding Source: This work was funded by the ANID-CHILE FONDECYT Regular project 1230222.

SYMPOSIUM: ECOLOGY AND CONSERVATION OF MOLLUSCA

ECOLOGY AND CONSERVATION OF MOLLUSCA

Coordinator:

HAROLD BASOC LIPAE – University of The Philippines Manila, Philippines

This symposium explores the ecology, distribution, and functional traits of mollusks across terrestrial and aquatic habitats. Presentations focus on species interactions, reproductive and feeding patterns, and environmental responses, highlighting their role in ecosystem function and informing conservation strategies.

Ecology and Conservation of Mollusca

Ecology

Oral - 236

TRAIT DISPERSION OF MACRO LAND SNAILS IN SELECTED KARST AND NON-KARST FORESTS OF THE PHILIPPINES

HAROLD BASOC LIPAE[1], RAFAEL RYNO G. SANCHEZ[2], KINSLEY MEG GUIA PEREZ[2], JULIUS A. PARCON[2], FRETZELJANE O. POGADO[3], IAN KENDRICH C. FONTANILLA[4], ANNA PAULINE O. DE GUIA[2], EMMANUEL RYAN CELZO DE CHAVEZ[2]

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Keywords: competition, functional traits, forest over limestone, environmental filtering, trait-based ecology.

Ecological studies on land snails have gradually increased over the years in the Philippines. However, trait-based ecological research, including investigations into how species are assembled in communities, remains largely unexplored. In this study, we aimed to determine how macro land snail communities are shaped in karst and non-karst forests in the Philippines using functional traits. A total of eight sites (four karst and four non-karst) and 80 macro land snail species were included in this study. Six traits under the categories of life history, morphology, and habitat were analyzed. Standard effect size (SES) was calculated using a null model approach, and a one-sided permutation test was performed. Positive and negative SES p-values indicate trait overdispersion and underdispersion, respectively. Analyses revealed the presence of both trait dispersion processes in karst and non-karst forests. All karst sites exhibited SES values above zero, indicating that these sites harbor competition-driven land snail communities (trait overdispersion), resulting in high variation in functional traits. This finding also supports the commonly observed pattern of high competition in snail communities within calcium-rich areas. In contrast, only two non-karst sites, Baybay and Mt. Makiling ($p > 0.05$), exhibited trait underdispersion, suggesting that environmental filtering plays a greater role in community assembly at these sites, leading to greater ecological similarity in traits. Overall, trait overdispersion appears to be relatively more prevalent than underdispersion, occurring in six of the studied sites. Further analyses will help elucidate the underlying mechansims explaining these results. This study is the first attempt to examine the trait ecology of land snails in the Philippines. It contributes to a better understanding of the processes shaping land snail communities in both limestone (karst) and non-karst forest ecosystems, as well as the broader ecological factors influencing biodiversity patterns across different forest types in the country.

Funding Source: No.

Ecology and Conservation of Mollusca

Ecology

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LATITUDINAL DISTRIBUTION OF MOLLUSKS ASSOCIATED WITH MACROALGAE ALONG THE BRAZILIAN COAST, OCEANIC ISLANDS, AND THE CARIBBEAN

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Keywords: mollusks, macroalgae, association, faunistic survey, latitudinal distribution.

Macroalgae provide shelter, food, and protection for a variety of associated species of animals, among which the malacofauna is particularly prominent, being abundant and ecologically important, influencing marine trophic dynamics. However, standardized studies on these organisms and their associations along a latitudinal gradient in the Atlantic South American coast are still lacking, and this represents a critical gap that hinders taxonomic advancement, also hampering investigations on biogeography. Sampling encompassed 31 sites along the Caribbean and the Brazilian coast, including both coastal and oceanic islands. Algal fronds were collected at depths of 1–5 m, using a 0.2 mm mesh to retain juveniles. The associated fauna was fixed in absolute ethanol, and the molluscan specimens were sorted under a stereomicroscope, quantified, and identified to the highest possible taxonomic resolution. Non-metric multidimensional scaling (nMDS) analyses were performed using Bray-Curtis dissimilarity (abundance) and Simpson dissimilarity (incidence) to investigate latitudinal patterns. Well preserved specimens of each species were photographed, and the material has been deposited in the collection of the Museum of Biological Diversity of the University of Campinas (MDBio-UNICAMP). A total of 3,495 individuals have been recorded to date. Of these, 3,000 have been identified to at least the family level and, when possible, to genus and species; 37 species were recognized. The classes Polyplacophora, Bivalvia, and Gastropoda were present, the latter being the most diverse and abundant, represented by 16 families. Among the identified species, *Eulithidium affine* stood out as the most abundant and widely distributed, contributing to the dominance of the family Phasianellidae. *Cylindrobulla beauii*, although restricted to the Saint Peter and Saint Paul Archipelago and associated with *Caulerpa* sp., accounted for the highest number of individuals collected at that location. The family Columbellidae exhibited the highest species richness, with eight identified and three additional unidentified species. Non-metric multidimensional scaling (nMDS) analyses based on both mollusk abundance and incidence data revealed four main groupings: Caribbean, Brazilian oceanic islands, and the coastal regions of the North–Northeast and Southeast–South of Brazil. When considering only species turnover based on incidence data, the separation was even more pronounced between the Caribbean, the oceanic islands, and the Brazilian Southeast–South coast. The observed patterns partially reflect not only previously described biogeographic ecoregions, but also highlight a strong insularity effect, which appears to outweigh the influence of latitudinal variation. These preliminary trends require validation with complete datasets, more robust statistical analyses, and incorporation of other dimensions of diversity—such as functional diversity—as well as the inclusion of local environmental variables and macroalgal bed characteristics in predictive models. This study emphasizes the malacofauna as important in algae-invertebrates associations, with gastropods being the most abundant and diverse. The distribution of assemblages partially reflects the biogeographic ecoregions, but the degree of insularity appears to be more influential than latitude. Considering the ecological role of mollusks associated with algal beds, understanding their distribution patterns is essential to elucidate environmental dynamics and to make future predictions, subsidizing future conservation efforts.

Funding Source: Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP) (Processo 2023/16683-1).

Ecology and Conservation of Mollusca

Conservation

Oral - 342

FIRST RESULTS OF FIELD MONITORING OF OVIPOSITION PATTERNS IN THE IGUAZÚ SNAIL (*Pomacea americanista*) AT THE IGUAZÚ NATIONAL PARK (ARGENTINA)

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Keywords: Iguazú snail, *Pomacea*, egg masses, development.

Pomacea americanista is a freshwater snail, belonging to the Ampullariidae family, endemic to the Iguazú and Upper Paraná rivers. It has been categorized as Endangered at the regional level due to the reduction in its area of occupancy, extent of occurrence and habitat suitability. The objective of this work was to carry out field monitoring and analysis of the egg masses of this vulnerable species. To this end, egg masses laid on visible emergent substrates along the upper and lower trails of Iguazú Falls at Iguazú National Park, Argentina, were monitored. For 15 consecutive days, data were recorded on date, time, weather, developmental stage of the egg masses (fresh, advanced, very advanced, hatched, fully hatched) and substrate type. Egg masses were photographed daily, and some were collected to estimate the average egg size. Clutch size and distance from the waterline were measured using scaled photographs. Additionally, substrate coverage and egg mass counts by substrate type (woody, herbaceous, artificial and basalt rock) were recorded to assess oviposition preferences. A total of 75 egg masses were initially recorded, 58.9% of which were at an advanced developmental stage. By the end of the study, 101 egg masses had been documented, due to the addition of new clutches at the selected sites, where in total 51.5% were in the hatched stages. Eighteen egg masses were already hatched at the beginning of monitoring, 26 never hatched, 28 hatched during the first week, 23 during the second week, and 11 completed development (from fresh to hatched) in 11.55 days on average. The average egg size was 3.18 mm (± 0.09 mm). Among fresh egg masses, 30.3% (33) were located less than 10 cm from the water, considering the lowest egg. The average egg mass length was 4.76 cm (± 1.95 cm). No significant correlation was found between clutch size and its distance from the waterline. Substrate preference data suggests a positive tendency towards woody substrates, with no apparent preference among the remaining types. The Iguazú snail showed a clear oviposition preference for woody substrates, a novel finding for the species. Hatching success was relatively high, with many clutches completing development within two weeks, in line with lab data. The total number of egg masses observed was notably higher than in previous years, suggesting favorable reproductive conditions. A second sampling will complement the preliminary substrate use patterns observed in this first stage.

Funding Source: To the National Scientific and Technical Research Council (CONICET) for the scholarship granted for the development of my doctoral thesis, within which this work is framed. To the Conchological Society of Great Britain and Ireland and the Rufford Foundation for the grants awarded to support this study. To Iguazú National Park and its staff for their support during fieldwork and their willingness to assist at all times.

Ecology and Conservation of Mollusca

Ecology

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"MOLLUSCS ARE NOT FRIENDS, THEY ARE FOOD" - DIET OF *Astropecten brasiliensis* MÜLLER & TROSCHEL, 1842, *Astropecten cingulatus* SLADEN, 1889 AND *Luidia senegalensis* (LAMARCK, 1816) (ECHINODERMATA: ASTEROIDEA) ON THE COAST OF ILHÉUS (BAHIA)

ERMINDA DA CONCEIÇÃO GUERREIRO COUTO[1], GABRIELA SILVA PEREGO[1]

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Keywords: prey selection, Gastropoda, Bivalvia, trophic ecology.

Asteroids of the order Paxillosida are efficient predators, consuming mainly mollusks and crustaceans. They are characterized by intra-oral feeding, since they are not able to evert their stomachs. The genera *Astropecten* and *Luidia* demonstrate great variation in feeding habits, with some considered specialists and others generalists. Studies have been conducted to determine how sympatric species use common resources through mechanisms of prey selection, by species and size, to attenuate competition. Individuals were collected monthly (April 2003 to November 2004), using door trawls with a mesh size of 20 mm in the pan and 16 mm in the bag, off the coast of Ilhéus, at a depth of 16 m. Incisions were made in the aboral region of 347 specimens (82 of *A. brasiliensis*, 209 of *A. cingulatus* and 56 of *L. senegalensis*). The prey were separated into the following groups: Gastropoda, Bivalvia, Scaphopoda, Crustacea and Miscellanea. The variation in diet composition was statistically analyzed using the X^2 test and a cluster analysis verified the similarity between size classes using the Bray-Curtis index. The diet differed significantly (X^2 (8) = 597.83; $p<0.01$). *Astropecten brasiliensis* and *A. cingulatus* fed mainly on gastropods, while *Luidia senegalensis* fed on bivalves. *Astropecten brasiliensis* consumed gastropods mainly (88%). The species *Natica* sp represented approximately 80% of the mollusks consumed and 60% of all food items. *Astropecten cingulatus* also consumed mainly gastropods (53%). *Natica* sp was the most consumed species, representing 30% of mollusks and 15% of all food items. Bivalves accounted for 14% of the diet, while scaphopods accounted for 9%. Mollusks were also the main group consumed by *Luidia senegalensis*; however, for this species, bivalves were dominant (77%), while gastropods accounted for 12%. When considering size, the diet also differed significantly within and between species (X^2 (45) = 785.77; $p<0.01$). In *A. brasiliensis*, the proportion of gastropods, already high, increases as individuals grow. Bivalves were the most consumed item in all classes of *Luidia senegalensis*, decreasing in larger individuals. Cluster analysis allowed us to verify the similarity of the diets of the different size classes of the three species. Trophically, *A. brasiliensis* would be essentially a tertiary consumer, since it feeds primarily on endofauna predators, such as Natica sp.; *A. cingulatus* would be both a secondary consumer, since it consumes bivalves, and a tertiary consumer, since it also feeds on *Natica* sp.; and *L. senegalensis* would be a secondary consumer, since it feeds on bivalves. A comparison between the diets of asteroids of different length classes suggests a distinct division in the exploitation of food resources. Based on the differences indicated, it is likely that the species respond to the pressure exerted by the habitat, having specialized in consuming prey in different proportions. This differential feeding must be a strategy to avoid competition between these species.

Funding Source: CNPq (AFAPESCA Project), FAPESB and UESC.

Ecology and Conservation of Mollusca

Ecology

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RADULAR TOOTH COMPOSITION IN GASTROPODS UNDER DISTINCT PH CONDITIONS

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Keywords: mechanical properties, elements, chitin, wear.

Mollusks are profoundly impacted by water acidification. Caused by increased CO_2 absorption by seawater, lowers pH levels and reduced availability of carbonate ions, acidification weakens their calcium carbonate shells, impairs physiological functions, and adversely affects survival and reproductive success. The susceptibility of mollusks to these changes can disrupt ecosystems, making it crucial to understand and mitigate the effects of acidification to preserve mollusk biodiversity and maintain healthy environments. This study investigates the impact of acidification on the composition of radular teeth used to scrape algae from surfaces. Two gastropod model species, the marine *Littorina littorea* and the freshwater *Planorbella duryi*, were exposed to pH levels of 7.5 and 8.1 for six weeks, and their radulae were compared with those of a control group (pH of 8.1). We documented the tooth morphology and wear by scanning electron microscopy (SEM), tested the elemental composition of teeth by energy-dispersive X-ray spectroscopy (EDX), documented material heterogeneity by confocal laser scanning microscopy (CLSM), and the mechanical properties by nanoindentation. SEM revealed increased wear on the radular teeth of individuals from both pH-groups compared to the controls (pH of 8.1). Further analysis of the elemental composition of the teeth showed that the outer surfaces of the control group's teeth contained high proportions of silicon and calcium in both species. In contrast, teeth from the 7.5 pH group exhibited significantly reduced silicon levels, while those from the 8.1 pH group showed lower calcium levels. These differences were corroborated using CLSM, which highlighted material differences. Mechanical properties of the teeth, including effective Young's modulus and hardness, were assessed. Teeth from the 7.5 and 8.1 pH groups were significantly softer and more flexible compared to those of the control group. These findings strongly suggest that water acidification affects the feeding apparatus of gastropods, potentially compromising their survival and reproductive success under adverse environmental conditions. The results also hint at possible phenotypic plasticity changes in radula composition induced by food, warranting further investigation.

Funding Source: Deutsche Forschungsgemeinschaft.

SYMPOSIUM: EVOLUTION OF MOLLUSCAN WEIRDNESS II / DIVERSITY AND EVOLUTION OF MOLLUSCA

EVOLUTION OF MOLLUSCAN WEIRDNESS II / DIVERSITY AND EVOLUTION OF MOLLUSCA

Coordinator:

JULIA SIGWART – Senckenberg Research Institute and Museum, Germany
FABRIZIO M. MACHADO – Universidade Estadual de Campinas, Brazil

Molluscs are capable of evolving rapid and dramatic changes to the body plan. The goal of this symposium is to showcase the incredible disparity of mollusc species and to discuss the challenges of interpreting convergence and rapid adaptations in understanding animal evolution. Presentations on molluscan body plan evolution, phylogeny, rapid phenotypic changes, adaptations, and natural history are all absolutely welcomed. In this symposium we want to consider the capacity of the molluscan body plan, genome, and diversity, and celebrate the weirdest molluscs.

Evolution of Molluscan Weirdness II / Diversity and Evolution of Mollusca

Evolution

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MOLECULAR PHYLOGENY OF FILE CLAMS (LIMIDAE) AND THEIR EVOLUTION OF VISION-GUIDED DEFENSES

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Keywords: file clam, phylogenetics, evolution of vision, life history, defense.

Predator-prey interactions promote dramatic innovations, such as eyes, through coevolutionary arms races. However, studies of such interactions often focus on the eyesight of predators, overshadowing prey vision as an important contributor to prey-predator dynamics. To date, there is no systematic investigation on the evolutionary connections between defense and vision in bivalves. We propose File Clams (Limidae) as a novel marine molluscan system to assess trait covariation between defense and vision. We established a Limidae molecular phylogeny using three genes. Consisting of 46 Limidae species covering eight out of the 10 extant genera (2-fold in generic representation from the last Limidae tree), we examine the relationships within the family and subfamilies, as well as between the known genera. Ancestral state reconstructions and trait correlation tests were conducted between assigned defense profile and bathymetry of the limid species included based on literature search. Combining their diverse yet unconventional defense strategies with a truly cosmopolitan distribution across all depths (from shallow reefs to deep sea >4000 m), Limidae is uniquely suitable for examining multi-trait covariations in relation to predator/prey-induced natural selection. Although defense strategies may confer survival advantages, their deployment may impose energetic and somatic costs. While all Limidae are known to possess noxious chemicals in their tissues, making them unpalatable to predators, chemical defense and tentacle autotomy require somatic sacrifices, making these behaviors costly and may at times prove lethal to the deployer themselves. Our phylogenetic reconstructions show that Limidae is monophyletic. Support for most major genera are strong. However, the subfamily Limatulinae, which traditionally includes *Limaria*, *Limatula*, and *Limea*, is paraphyletic. *Divarilima* and *Limea* are nested within *Lima* and *Limatula* respectively, making both latter genera non-monophyletic. Proactive defense appears to be ancestral for Limidae and appears to be strongly maintained. Most transitions in defense profile occur while limids are in the neritic zone. Observation of such correlations concurs with our hypothesis that visual detection by predators could be a strong selection pressure in the shallows, where light is ample. There are higher rates transitioning toward shallow and proactive states. No transition in defense profile happens when the taxa are in the bathyal zone. Interestingly, transitioning into the depth while having a reactive defense profile appears to be an evolutionary dead-end without any exit transitions. Visual detection of predators can play a pivotal role in curtailing the need for costly defensive mechanisms by enabling preemptive behaviors. Our work suggests that visual detection may enable a shift from reactive to proactive, minimizing reliance on high-cost strategies. Future work would include histological identification of eye complexity in Limidae to directly characterize their visual abilities to further our investigation into multi-trait evolution in response to predation pressures.

Funding Source: No.

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Taxonomy and Systematics

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IDENTIFYING MOLLUSK SPECIES IN THE FRESHWATER BODIES OF NEW MEXICO

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Keywords: phenotypic plasticity, freshwater, taxonomy, environmental variation, shell morphology.

Due to its proximity to the Chihuahuan Desert, New Mexico has an arid environment with sparse water bodies that are remote and undocumented but can also be biodiverse oases. As a result, little research has been done on its native freshwater organisms, leading to the inquiry of what mollusk species reside there. To answer this question, I collected organisms from an ephemeral spring called Ojo del Abo on the southeastern edge of the Manzano Mountains and a pond that was cut off from the Rio Grande River. Preliminary observation of the collected organisms revealed that the vast majority were sinistral snails, a rare trait that allowed for me to recognize them to be a part of the Physidae family. Physidae freshwater snails are known for their unique ability of phenotypic plasticity, which enables them to change their shell morphology in response to biotic and abiotic factors in their immediate environment. This enhances their ability to adapt and causes generations and even individuals to look different from each other. As a result, shell morphology alone could not be used to identify the species, and penial morphology and behavior were used as complementary. Identified species from Ojo del Abo included the freshwater snail species of *Lymnaea cockerelli*, *Lymnaea cubensis/viator*, and *Physa gyrina* as well as the freshwater clam species of *Sphaerium striatinum*. The Rio Grande pond was less diverse and less abundant, with only the species of *Lymnaea cubensis/viator* and *Physa gyrina* being collected. Phenotypic plasticity was most evident in the *Physa gyrina*, whose varying shell colors and aperture sizes allowed for inferences about the environmental conditions faced by these organisms. These results led to the implication that because climate change and global warming will have significant impacts on the environments of these organisms, it will also impact their morphologies. The objective of identifying the underexplored organisms was achieved through this experiment. The species are now documented at both sites, with notable abundance and variation. These results will provide a foundation for future research on mollusks and hopefully influence future studies on their ability to adapt to arid environments. All collected specimens were donated to the collection at the University of New Mexico's Museum of Southwestern Biology.

Funding Source: NSF REU at the University of New Mexico and the Sevilleta National Wildlife Refuge.

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Taxonomy and Systematics

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PHYLOGENETIC INSIGHTS INTO THE FAMILY ACANTHOCHITONIDAE (MOLLUSCA: POLYPLACOPHORA) USING A TARGET ENRICHMENT APPROACH

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Keywords: Acanthochitonidae, Cryptoplacoidea, phylogenomics, Polyplacophora, ultraconserved elements.

Chitons are a morphologically conservative yet taxonomically challenging group of molluscs, with many families in need of systematic revision. The family Acanthochitonidae is known for its taxonomic complexity and limited molecular data. Genomic tools have been underutilized in chiton systematics, partly due to the scarcity of fresh material for rare or undersampled taxa. Here, we implement target enrichment of ultraconserved elements to understand relationships within Acanthochitonidae and its relatives. We designed a mixed probe set combining 9,177 genomic probes targeting 3,271 UCE loci and 9,903 exon probes targeting 2,459 conserved exon loci, covering 5,730 loci in total. In silico testing recovered an average of 3,148 and 1,152 loci from 18 chiton genomes and 28 transcriptomes, respectively. These baits were then employed to target and enrich UCE and exon loci from over 80 chiton samples, including recent (stored in 96% ethanol) and degraded (low-grade ethanol and dry specimens stored at room temperature). Taxon sampling focused on the family Acanthochitonidae from the superfamily Cryptoplacoidea, and its sister clade Mopalioidea. In vitro, our probe set successfully captured up to 3,328 UCEs, with an average of 1,701 loci per sample. Despite variable preservation, degraded specimens yielded between 2 and 2,229 loci, with an average of 998 and a median of 359 loci. Both concatenated maximum likelihood and coalescent-based analyses produced well-supported trees that confirmed the monophyly of Cryptoplacoidea and Mopalioidea. Notably, Nuttallochiton and Plaxiphora were placed outside Mopalioidea, consistent with prior studies. This dataset represents the most extensive taxon sampling for Acanthochitonina and Cryptoplacoidea to date. The resulting phylogeny clarifies the positions of several long-debated taxa. While morphological convergence and parallel evolution obscure true relationships, geographic affinity appears to play a stronger role in shaping evolutionary lineages. We formally reinstate the genus *Meturoplax* Pilsbry, 1894, supported by both morphological and molecular evidence. Not all genera were recovered as monophyletic, highlighting the need for systematic revisions. Our findings suggest chitons are less morphologically conserved than previously assumed – morphologically similar taxa were recovered polyphyletic, likely reflecting convergence in similar habitats. This apparent morphological plasticity may relate to their high rates of chromosomal rearrangement, even at the genus level. Finally, we successfully enriched and sequenced DNA from specimens stored dry at room temperature for up to 140 years, demonstrating the potential of target enrichment for integrating historical material into modern phylogenomic frameworks. Our study brings long-needed clarification of the evolutionary relationships within Acanthochitonina, offering a robust foundation for revising outdated taxonomies. The recovery of non-monophyletic genera highlights the limits of morphology-based classification. By reinstating genera such as *Meturoplax* we lay the groundwork for a more natural classification. Moreover, our study demonstrates the effectiveness of target enrichment in resolving phylogenetic relationships in chitons, even from highly degraded historical specimens.

Funding Source: This study was supported by Senckenberg Ocean Species Alliance (SOSA).

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Taxonomy and Systematics

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THE SENCKENBERG OCEAN SPECIES ALLIANCE AS A NOVEL APPROACH TO ACCELERATING MARINE INVERTEBRATE SPECIES DESCRIPTIONS

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Keywords: new species, alpha taxonomy, taxonomy service, marine invertebrates, Mollusca, biodiversity discovery.

Human impacts increasingly threaten the survival of marine molluscs, yet many species have remained undiscovered, undescribed, and consequently unprotected. The Senckenberg Ocean Species Alliance initiative was founded to develop innovative and transferrable approaches to accelerate and streamline high-quality species description and publication for marine invertebrates in times of anthropogenically-driven biodiversity loss. In the current research landscape that offers limited incentives to describe new species, the Ocean Species Alliance provides two complementary support lines to taxonomists: First, technical help through its taxonomic service unit. The new taxonomy lab in Senckenberg, Germany, is being developed as a service provider, offering on demand technical support for the laborious aspects of morphological species descriptions. Second, in another, complementary project, the open-access, peer-reviewed 'Ocean Species Discoveries' article series combines concise descriptions of multiple species from different animal phyla into modular 'mega publications'. This new format increases the visibility and impact of each single contributor by reaching a wider audience. Within one year of operation, the Ocean Species Alliance has facilitated (re-)descriptions of 76 marine invertebrate species new to science through its scientific network, lab and publication services, including 29 molluscs from five classes: Polyplacophora (5 spp.), Monoplacophora (2 spp.), Gastropoda (17 spp.), Bivalvia (4 spp.) and Scaphopoda (1 sp.). These description projects encompassed diverse laboratory methods, including macrophotography, optical, confocal and scanning electron microscopy (SEM), barcoding, dissection, scientific drawing, and micro computed tomography (µCT). We have tracked the needs of collaborating international scientists and skilled amateurs, which have included access to special infrastructure (e.g., SEM and µCT), specimen processing, access to taxonomic expertise and advice, and facilitating publication of species descriptions. In every interaction with clients (interested taxonomists) and their study material, invaluable knowledge transfer takes place, novel technical challenges are met, and feedback is received, translating into increasingly efficient description workflows. Our ongoing work is clarifying the major bottlenecks to describing species, and providing and developing solutions through taxonomic services. The Ocean Species Alliance has become a dynamic, inclusive and growing network aiming at accelerating alpha taxonomy in times of anthropogenically-driven biodiversity loss. We are looking forward to sharing our progress to date, and invite you to discuss potential future collaborations.

Funding Source: The Senckenberg Ocean Species Alliance project was funded by a generous philanthropic donation.

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Taxonomy and Systematics

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SHELL GAMES: MULTI-LOCUS PHYLOGENY OF PHILIPPINE CYCLOPHORIDAE (GASTROPODA: CAENOGASTROPODA) UNCOVERS SPECIES FOR TAXONOMIC RE-EVALUATION

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Keywords: integrative taxonomy, land snail, molecular systematics, polyphyly, species complex.

The family Cyclophoridae is a terrestrial family of gastropods distributed across Africa, Asia, Australia, and various Pacific Islands. Globally, the family contains approximately 34 extant genera with around 810 species, with the Philippines having around 8 genera and 190 species. While extensive studies on species under this family have been conducted by neighboring countries in Southeast Asia and East Asia, similar studies remain limited in the Philippines. Our study aimed to reconstruct the phylogeny of Philippine cyclophorids using multiple loci.Loaned museum specimens and fieldwork collections at various sites in Luzon Island were used.DNA was extracted following the CTAB method of extraction following amplification of three loci namely cytochrome oxidase I (COI),16S rRNA and 28S rRNA gene fragments.75 COI sequences (573 bp),42 16S rRNA sequences (311 bp),and 35 28S rRNA sequences (349bp)representing 25 species belonging to six genera of Philippine cyclophorids.Maximum likelihood (ML) and Neighbor-joining (NJ) trees were constructed using iq-tree, and PAUP respectively,using the appropriate models for the individual loci and concatenated datasets. ABGD and ASAP methods of molecular species delimitation analysis were also done. Our results show that most Philippine Cyclophoridae were found to nest in their respective genera. Philippine *Leptopoma* is paraphyletic with two *Cyclophorus* species and one *Lagochielus* species nested within. Philippine *Cyclophorus* is also paraphyletic—*Cyclophorus quadrasi* of Palawan is sister to all other species from the Philippines and mainland Asia. Philippine and Bornean *Opisthoporus* as well as Philippine *Cyclotus* and Vietnam *Cyclotus* were found to be polyphyletic. A Shimodaira-Hasegawa test of monophyly was conducted to determine the monophyly of *Opisthoporus*, to which the generated optimal tree was found to be significantly different ($p<0.05$) from the tree where *Opisthoporus* from Borneo and the Philippines are constrained to be monophyletic suggesting that Philippine and Bornean *Opisthoporus* are not sisters.We also flag several species for taxonomic re-evaluation due to their phylogenetic placements—*C. woodianus* and *C. appendiculatus* might be synonymous with *C. woodianus* forming a possible species complex, *L. vitreum* of the Philippines might be a distinct species from the Thailand population, and *L. perlucidum* of the Philippines might be a species complex. Our study provides the initial phylogenetic framework of Philippine Cyclophoridae which shows that there is much to be explored about the evolution of the Cyclophoridae. We hope to then further query different populations for the said Philippine species flagged for taxonomic re-evaluation.

Funding Source: Natural Sciences Research Institute (NSRI) of the University of the Philippines (UP) Diliman (Grant numbers: BIO-21-1-01). Department of Science and Technology Accelerated Science and Technology Human Resource Development Program (DOST-ASTHRDP) Outright Thesis Grant Malacological Society of Australasia Grant.

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Taxonomy and Systematics

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TOO FAR FROM RELATIVES? IMPACT OF THE GENETIC DISTANCE ON THE SUCCESS OF EXON CAPTURE IN PHYLOGENOMICS

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Keywords: Neogastropoda, exon capture, phylogenomic.

The exon capture approach allows for sequencing a large number of loci to reconstruct phylogenetic relationships at varying taxonomic levels. In order to efficiently recover the targeted loci, the probes designed to capture the exons need to be genetically sufficiently similar to bind to the DNA, with a proposed limit of 10% of divergence. However, this threshold has never been tested with a specific protocol. We have designed a set of probes to capture 1,125 exons in the Neogastropoda (Mollusca, Gastropoda), processed with the same protocol from the field to the DNA sequencing to control for potential bias in DNA quantity and quality. We sequenced 30 different species, including 14 species of Neogastropoda and 16 species of Caenogastropoda non-Neogastropoda. Each species includes 5 specimens, for a total of 150 specimens, and for four specimens among the 150, DNA extracts were aliquoted in four samples, sequenced separately, to estimate the intraspecific and intra-specimen variability in capture success. Our results confirm the impact of genetic distance on the success of exon capture with a negative linear correlation between the genetic distance and the number of exons captured for each sample. Consequently, designing new capture probes would allow for capturing exons in genetically more distant groups without the need to redesign a new set of exons. The difference between ingroups and outgroups is also illustrated by the significant correlation between the number of reconstructed exons and the average p-distance between the reconstructed exons and the corresponding baits for each species: the higher the genetic distance, the lower the number of reconstructed exons. It does not seem possible to identify a clear threshold of genetic distances above which the exon capture efficiency significantly decreases, and thus to readily identify which lineages would necessitate the design of new baits. On the contrary, the decrease in capture efficiency is quite gradual. Designing probes using more transcriptomic and/or genomic data from a more representative set of taxa will help to maintain a high level of capture success. Thus, ideally, when designing a probe set for exon capture, each new lineage, significantly diverging from the previously sampled ones, would benefit from adding new probes based on a transcriptome from this lineage.

Funding Source: This project was founded by the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement no. 865101).

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Conservation

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BETA DIVERSITY PATTERNS OF THE GENUS *Hungerfordia* (CAENOGASTROPODA:DIPLOMMATINIDAE) IN PALAU (MICRONESIA)

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Keywords: land snail, beta diversity, Micronesia, Palau, Pacific, SLOSS, conservation.

Palau, in the western tropical Pacific, has more than 600 islands, most smaller than one square kilometer. Nearly all these islands were joined together during various glacial intervals of the Pleistocene. The land snail genus *Hungerfordia* includes 41 species endemic to this archipelago, which presents an interesting opportunity to study diversity patterns on what is essentially a 12,000 year lowland tropical rainforest fragmentation experiment. In this study we summarize locality data for the genus *Hungerfordia* from a series of monographs by Yamazaki, Yamazaki, & Ueshima, collections by Yoshio Kondo at the Bishop Museum (Hawaii, USA), and our own fieldwork in Palau. Using various beta diversity metrics, we show that there are distinct regions of Palau with representative *Hungerfordia* taxa, despite the lack of obvious environmental gradients within the study region. We explore the consequences of this high level of turnover for the SLOSS (Single Large or Several Small) problem. *Hungerfordia* are entirely confined to the limestone habitats of Palau, in the southern half of the Palau archipelago. Within this region, relatively few species are widespread, and most only occur in a cluster of islands. Four main regions are defined by relatively similar species membership within them and relatively high species turnover among them. Sixteen species have been recorded from the largest limestone outcrop, the island of Ngeruktabel, which is about 18 square kilometers. However, the relatively high species turnover across the archipelago results in support for “Several Small” islands frequently having more species than the “Single Large” island if three or four regions are represented. We still don't understand what drives the high species turnover among the island groups of Palau. However, this underscores the importances of continuing exploration and fieldwork for land snails throughout the world, which might not have species ranges that are straight-forward to predict from climate or other environmental data. The SLOSS results support the value of conserving habitats, even small ones.

Funding Source: Indicate here the funding sources/projects, if any.

SYMPOSIUM: DEEP-SEA MOLLUSCS: A SYNTHESIS

DEEP-SEA MOLLUSCS: A SYNTHESIS

Coordinator:

FLÁVIO DIAS PASSOS – Universidade Estadual de Campinas, Brazil

The symposium “Deep-sea molluscs: a synthesis” will address contributions on taxonomy, biogeography, ecology, genomics and other topics related to molluscs from the deep sea.

Deep-sea Molluscs: a Synthesis

Deep-sea

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COMPOSITION, DISTRIBUTION AND ECOLOGICAL CHARACTERISTICS OF THE HADAL FAUNA: INFERENCE FROM THE MOLLUSCAN ASSEMBLAGE OF JAPAN AND KURIL-KAMCHATKA TRENCHES

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Keywords: abyssal, deep sea, diversity, ecology, rarity, trawling, trench.

Difficulty of access in combination with low population density have hampered detailed understanding of the diversity, distributions and speciation of animals in ocean trenches. Wire length and strength as well as ship time for lowering and retrieving a trawl or a sledge are among the primary reasons for the previous lack of dense sampling at depths below 6 km. We have developed a new method for effective deep-sea sampling by video recording and analysing the attitude of trawls underwater. Standard textbook procedures may require a 15 km wire and 12 hours for a trawl cast to 10 km deep, which are reduced to 10.1–10.5 km and 8 hours with our method. This enabled us to conduct the densest ever sampling of the trench fauna during two recent cruises (KH-22-8 and KH-23-5). The sampling encompassed 32 stations below 5 km deep in the Kuril–Kamchatka and Japan Trench area of the Northwest Pacific, where high surface productivity supports among the highest population densities of abyssal and hadal communities. Combined morphological and genetic analyses recognized 156 species among ca. 18,000 molluscan specimens from the 32 stations. Species composition analysis showed a clear faunal difference between shallower (5,013–6,562 m) and deeper (6,646–8,014 m) stations, thereby identifying the border of the abyssal and hadal zones for the first time with quantitative data at around 6,600 m. The community structure within each zone was also correlated with depth but not with other factors including geographic and topographic settings. Gastropods vastly outnumbered other classes in the species count (91) and consisted of numerous rare species that were singletons (36) or with specimens found only at a single station (34). In contrast, bivalves represented 94% of the molluscan specimens collected, with many (30 out of 41) species occurring at more than one station. The common and ubiquitous Bivalvia seemed best suited for exploring animal distribution and speciation in trenches (see our poster paper by Asada et al. for results and discussion). The observed trends of species richness and diversity in Gastropoda and Bivalvia can be explained by their contrasting ecological characteristics. The patchy distributions of the gastropod species might be attributable to specialized food items or different (including direct) modes of early development. Their low population densities are maintained with copulation and/or hermaphroditism that would increase the chances of gametes meeting and fertilizing. Most of the bivalve species are, on the contrary, general deposit feeders with separate sexes; fertilization is external and eggs develop into lecithotrophic swimming larvae. We hypothesize that the depth itself (i.e. hydrostatic pressure) serves as a primary controlling factor in species' distributions in ocean trenches, where temperature, salinity, and dissolved oxygen and nutrient concentrations are known to be homogeneous across the entire depth range. This hypothesis will be tested with denser sampling and environmental characterization at 6–10 km deep during our forthcoming cruise to Japan and Izu–Ogasawara Trenches.

Funding Source: Financial support was provided by the Japan Society for the Promotion of Science (KAKENHI grants nos 19H00999, 19KK0385 and 22H02681).

Deep-sea Molluscs: a Synthesis

Deep-sea

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ENDEMICITY ANALYSIS SHOWS AREAS AND DIFFERENT PATTERNS OF DISTRIBUTION AMONG CAUDOFOVEATE (APLACOPHORA) FAMILIES

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Keywords: deep-sea, Chaetodermatidae, taxonomy, morphology.

The deep-sea is among the least studied areas of the world oceans, from where many groups are characteristic, like the caudofoveate aplacophorans. As such, little is known about the biogeography of these molluscs. Here an endemicity analysis was done for the caudofoveates, aiming to understand their distribution patterns and to find possible areas of endemism. A dataset of all species described for the Atlantic Ocean, Caribbean Sea, Gulf of Mexico, Mediterranean Sea and North Sea was compiled, based on literature and materials observed by the author in collections of museums from Brazil and the United States of America; a total of 2935 records was gathered, belonging to 76 species, 61 being formally described and other 16 being unknown to science yet. For endemicity analysis, data was analyzed with the full dataset and also separated into three bathymetric zones: 0-200, 200-1000, and 1000-4000 meters depths. For grid size, three sizes were used: 1° x 1°, 2° x 2° e 3° x 3°. Endemism areas were found in all bathymetrical zones and grid sizes, except in the 0-200 m zone with 1° x 1° grid. In the remaining analysis, two endemism areas were consistently found: one in the Gulf of Mexico and another on the Brazilian coast. In the zone 200-1000 m and global data with 1° x 1° grid, the Brazilian Northeast also appears as an endemism area inside the Brazilian coast. In Brazil, the species that contributed more to the scores of endemism areas were *Falcidens australocaudatus*, two undescribed, endemic species of *Falcidens*, and one unknown of *Chaetoderma*. In the Brazilian Northeast area, one species of *Prochaetoderma*, an endemic Psilodens and a third undescribed species of *Falcidens* contributed for the appearance of the area. The main contributing species for the Gulf of Mexico were *Chaetoderma felderi*, *Chevroderma cuspidatum*, an endemic Psilodens, and two other undescribed endemic species of *Falcidens*. In total, 14 species contribute for the endemism areas, nine of Chaetodermatidae, three of Limifossoridae, and two of Prochaetodermatidae. This pattern suggests that most species of Chaetodermatidae tend to be more endemic than the other two families. On the other hand, this reinforces that the Prochaetodermatidae species tends to be widely distributed, as already known in the literature. The Limifossoridae comprise a few described species; it is still hard to delimit a pattern for this family. Endemicity analysis showed the existence of two endemism areas in the Atlantic, one in the Gulf of Mexico and other in Brazilian coast. Moreover, caudofoveate families differ in their distribution patterns. The small number of species described contributing to endemism areas suggests that our knowledge of the biogeography of this group is still restricted. Future taxonomical studies and collections from unexplored areas may reveal important information to understand their distributions.

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Deep-sea Molluscs: a Synthesis

Deep-sea

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DEEP IN THE DARK: EYE LOSS, REGRESSION AND VISUAL ADAPTATIONS IN SCALLOPS AND RELATIVES (PECTINOIDEA) FROM DIFFERENT OCEAN DEPTHS

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Keywords: Propeamussiidae, phylogenomics, visual systems, comparative biology.

Eyes frequently regress in anatomical complexity or are lost in environments with reduced or no light. However, macroevolutionary patterns of eye regression are still poorly understood for many taxonomic groups in the deep sea. The pectinoidean bivalves, with multiple eyes, different life habits, and diverse bathymetric distribution, are a suitable group for examining eye regression in environments where light trade-offs are extreme. We used the Pectinoidea as a model group of invertebrates to understand eye evolution in association with functional and ecological changes that may drive eye regression and loss in the deep sea. We compared morphological predictors, such as eye presence, size, number, and pupil diameter, for more than 250 samples, including 50 species from the families Cyclochlamydidae, Entoliidae, Pectinidae, Propeamussiidae, and Spondylidae. In addition, we utilized an anchored hybrid enrichment (AHE) approach to capture orthologous loci from across the genome of 67 individuals. The anchored phylogenomics based on 1527 loci was used to provide a robust phylogenetic framework to assess the evolution of eye investment and morphology in Pectinoidea. We sequenced a range between 384-1487 loci per sample, with an average of 1247 loci. One individual was dropped due to low coverage. Using a 70% data matrix, we produced a robust phylogeny containing 66 individuals that span across five families: Limidae (1), Spondylidae (3), Entoliidae (1), Propeamussidae (23), and Pectinidae (38). We found strong support for Pectinidae and Propeamussidea as monophyletic sister clades. Our results reveal that eyes are restricted to pectinoideans in the photic (0–200 m) and disphotic (200–1,000 m) zones, while those in aphotic depths are eyeless. Interestingly, larger eyes and pupils are found in animals living in the disphotic zone, a dim-light environment where adaptations are expected for increased sensibility. Most of these morphological deviations are concentrated in propeamussiids. Eye and pupil size are allometrically related to body size and correlated to ocean depth, as small eyes with narrow pupils belong to shallow-water dwellers. Interestingly, relative eye size (corrected for body size) and relative pupil size (corrected for eye size) do not vary with ocean domains. Furthermore, eye abundance drastically reduces with ocean depth, as illustrated by propeamussiids with only four eyes in contrast to shallow-dwelling scallops with more than 60. In general, the results suggest eye regression in deep-dwelling species, with reduced investment in the visual system and adaptive changes in eye morphology. Our findings suggest an evolutionary trajectory for pectinoideans whose eyes maximize light capture (photosensitivity) at the expense of image clarity (spatial resolution) in dim-light environments, while they are entirely lost in aphotic habitats. Consequently, we provide a robust model to investigate evolutionary changes in visual systems in response to transitions to different ocean photic environments.

Funding Source: NSF DEB 1754331. FAPESP 2019/18834-1, 2022/14347-1.

Deep-sea Molluscs: a Synthesis

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TALES OF LIGHT AND DARKNESS: ASSESSING COMPARATIVE EYE ANATOMY IN DEEP SEA PROPEAMUSSIIDAE (BIVALVIA, PECTINOIDEA)

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Keywords: mollusks, bivalves, eyes, Propeamussiidae.

Photoreceptor systems in bivalves exhibit wide morphofunctional diversity, making them excellent models for evolution and adaptation. However, studies addressing the visual system of Propeamussiidae are scarce, as these animals are fragile and rarely collected with soft parts. Considering that propeamussiids occur in aphotic and disphotic zones of the deep sea, they are relevant for investigating morphofunctional variations in the visual system in response to different photic environments. We investigated the histology of eyes from six species of Propeamussiidae and four species of Pectinidae, from the Muséum National d'Histoire Naturelle (MNHN, Paris), and three additional species from the Museu de Diversidade Biológica (ZUEC-BIV - UNICAMP). Additionally, the sampling covered a wide taxonomic (14 species) and geographic diversity, including the Atlantic, Pacific, and Indian Oceans, as well as the Mediterranean Sea, from 0 m to 682 m. Sections of 3 µm were stained with toluidine blue and fuchsin for analysis. External eye morphology was also investigated, contributing to data for comparative anatomy. The data obtained were analyzed for interspecific variation and compared with other families, i.e., Pectinidae and Spondylidae. Comparative histology revealed some recurring variation in the ocular structure of propeamussiids compared to the eye pattern found in Pectinidae (the best-studied and most taxonomically diverse family) including: loss of the reflective layer (mirror); narrow retina contained within the diameter of the ocular opening (pupil); reduction of the inner and outer pigment layers; expansion of the ciliary portion of the distal retina; reduction of the rhabdomeric portion of the proximal retina; lens regression. These changes align with the theoretical framework discussed in the literature regarding modifications in visual systems resulting from the invasion of disphotic environments. The observed changes in ocular structure suggest a hypothesis of visual trade-off due to the absence of selective pressure for visual acuity (resolution) in the deep sea, coupled with a selective pressure for greater optical sensitivity, as seen in deep-sea fishes and crustaceans. In addition, it is possible to speculate that the high energetic cost of maintaining visual systems may favor a scenario of reduced ocular investment, considering a well-discussed framework of structural reduction due to energy savings in dark environments. The absence of selective pressures for maintaining specific ocular components may be involved in the morphofunctional changes observed in the visual system of deep-sea propeamussiids. Further phylogenetic studies are required to test whether they were subjected to similar selective pressures with greater ocean depth, resulting in parallel evolution. Overall, we hypothesize that a trade-off that favors sensitivity over visual acuity, along with energetic savings, has impacted the propeamussiid visual system.

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MICROSATELLITE-BASED PATERNITY ANALYSIS OF PAIR FORMING OCEANIC SQUID, *Thysanoteuthis major*

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Keywords: pairing, microsatellite marker, sperm, diamond squid, reproductive behaviour.

The social organization of oceanic diamond squid, *Thysanoteuthis major* is unique among squids. They are often observed in pairs of one male and one female. Their pairing begins at immature stage and continues into adulthood, indicating behavioral monogamy. However, there is no evidence supporting genetic monogamy, which led us to investigate the molecular basis of these relationships. Therefore, a study was conducted to investigate whether these squids are truly monogamous. The research was carried out by genotyping the stored sperm in the female's multiple seminal receptacles (SRs) which are ventrally located on the female's buccal membrane. Polymorphic microsatellite markers were developed through PCR-PAGE-Fragment length analysis workflow for genotyping the stored sperm. The peak area and peak height of the electropherograms obtained from fragment length analysis during genotyping process were quantified to analyze the proportion of sperm contributed by the mated males. Four highly polymorphic microsatellite markers were newly developed for genotyping the sperm. The microsatellite-based fragment length analysis (FLA) showed that one female mated with at least 2 to 5 males, indicating that they are not monogamous. Even each SR within the females also exhibited multiple paternity. Interestingly, the FLA electropherograms showed multi-allelic peaks with significant similarity in peak patterns among SRs within female. Despite mixed paternity being evident, we found that paternity share in all the SRs within a female was biased to presumably a single male. This contrasts with the case of the oceanic Japanese common squid, Todarodes pacificus, where each SR exhibits different pattern of paternity composition and wider distribution of paternity share. However, dominancy of a single male in paternity sharing in diamond squid supports their pairing behavior and is somewhat related to extra pair copulations. The findings from the study show the first genetic evidence of mating behaviour of oceanic diamond squids. These infer that regardless of pairing, the female diamond squids practice extra pair copulations outside the pair-bonded partner to have genetically diversified offspring.

Funding Source: No.

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OCULAR AND EXTRAOCULAR TISSUES REVEAL COMPLEX OPSIN DIVERSITY ACROSS PTERIOMORPHIAN BIVALVES

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Keywords: eyes, vision, photoreception, phylogeny, diversity.

Animals use diverse anatomical structures to detect light, but most rely on highly conserved opsin-based photopigments. As eyes have evolved tens of times in metazoans, visual systems likely co-opted opsins from light-sensing, but otherwise nonvisual contexts. How opsins are recruited to new functions, like vision, remains largely unknown. Understanding this process is therefore critical to linking the evolution of photoreceptor organs to their molecular repertoires and functional roles. We investigated how opsin repertoire varies among ocular and extraocular tissues of pteriomorphians, a diverse group of bivalves with multiple photoreceptor systems. We generated transcriptomes for 12 species, including eyed and eyeless bivalves, and analyzed published transcriptomes from six additional species across all orders and eye types. We retrieved opsin candidates among the expressed transcripts and performed phylogenetically informed annotations to classify them. To investigate whether opsin repertoire matches functional complexity in eye and mantle tissues, we tested whether eye presence, photoreception type, and mobility are evolutionarily associated with the number of expressed opsins and which are widely used. In total, we identified and classified 103 opsins expressed in the mantle and eyes of 17 species using phylogenetically informed annotation. We identified visual and nonvisual opsins used in eyes and dermal photoreception. While the pearl oyster species express only three opsins, ark clams and scallops exhibit up to 13 opsins. Our results demonstrate that retinochrome is the only opsin type expressed in the eyes and mantle of all species. Similarly, rhabdomeric opsin types, including canonical r-opsin, primarily associated with invertebrate vision, have a taxonomically diverse expression pattern, regardless of tissue type. When comparing relative opsin expression between eye and mantle samples, r-opsins are remarkably more abundant in the eyes. Consequently, our findings support that the rhodopsin-retinochrome system is pervasive across bivalves. Our results suggest that eye opsins are likely derived from the repertoire used by the ancestral mantle with five main types: retinochrome, canonical r-opsin, noncanonical r-opsin, Go-opsin, and xenopsin. In addition, the photoreception system, encompassing non-directional, directional, and low-resolution vision, correlates with differences in the total number of expressed opsins, with a significant distinction between non-directional (extraocular mantle margin) and low-resolution vision (eyes). More specifically, the number of expressed opsins suggests an evolutionary increase in repertoire complexity in eyes. However, no association was found between mobility and opsin repertoire, indicating that both mobile and sessile species exhibit similar opsin expression variations. In conclusion, opsins are likely derived from the repertoire used by the ancestral mantle, and bivalve eyes generally express more opsins than extraocular tissues. Our findings reveal a complex molecular diversity associated with expression patterns and functional implications. Overall, we provide a foundation for comparative investigations into photoreception in invertebrates and demonstrate the potential of bivalve photosensitive tissues to explore the evolution and mechanisms of light detection.

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GETTING A WIGGLE ON: SPIRALS AND DERAILMENTS FROM SPIRALS IN CONCHIFERAN MOLLUSCS

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Keywords: morphometrics, ontogeny, Conchifera, shell morphospaces.

Perhaps one of the most striking characteristics of Mollusca as a phylum is the disparity of the taxa included. Despite their long fossil record, worldwide distribution, and functionally-informative shell, the conchiferan molluscs are underused as a model organism for studying tempo and mode in morphological evolution because it has proven almost impossible to design a measurement scheme that can usefully compare taxa at any level higher than the family. There is an element of arc or spiral growth to mollusc shells. Using CT scanning, we extract the curved path that describes the growth trajectory of a shell, and record changes in pitch and yaw of the aperture through ontogeny, producing an empirically-derived moving-reference-frame shell model, and morphospace, which can accommodate and compare both regular and irregularly coiled shapes across classes. We present a pilot study using taxa which either naturally or through damage exhibit changes in their coiling pattern through ontogeny, to demonstrate the utility of the method for analysing shape change both within an individual's lifespan and between taxa. Using rates of change in aperture pitch and yaw as analogous to the Raupian parameters of T and W respectively, as well as aperture shape change (Raup's S), we are able to demonstrate several things: first, that an empirically-derived morphospace that accommodates both regular and irregularly coiled shells, of multiple classes, is possible. Second, that there are commonalities in post-damage shell growth in gastropods (one subset of our data) which suggest that the T component is more labile than W or S. And third, that this lability of T is also apparent in that, in rare specimens of *Helix* and *Cornu* which exhibit deviation from the normal growth pattern, only scalariform individuals have been seen, and the degree of scalariformity is highly variable. No instances of more planispiral or trochiform *Helix* or *Cornu* (which would indicate lability of the W parameter) are known to the authors. We are now at the cusp of having an empirically-derived morphospace of the conchiferan mollusca as a feasible tool for the study of their form. Measuring spirals rather than discrete landmarks gives us a holistic view of shell form that captures ontogenetic change and allows us to observe patterns that otherwise would be missed due to methodological issues such as landmark mismatch.

Funding Source: No.

Deep-sea Molluscs: a Synthesis

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LIMITATIONS IN BIVALVE RECOGNITION: HISTOLOGICAL AND TRANSCRIPTOMIC PERSPECTIVES OF FUSION AND REJECTION IN XENOGRAFTS

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Keywords: allorecognition, xenograft, immunity.

Distinguishing self from non-self is crucial for immune systems in multicellular organisms. However, evidence from cultured pearl industry practices and transmissible cancers in bivalves indicates that they may have a limited capacity to detect and reject cells from other individuals, whether from the same or closely related species. This has not currently been systematically explored. My project aims to understand the extent to which fusion occurs in bivalves. Small mantle tissue pieces from *Magallana gigas* were placed next to those from *Mytilus edulis* (another bivalve), and *Patella vulgata*, (a gastropod), under tissue culture conditions. Cultures were histologically examined after two weeks to determine any physical reactions to foreign tissue, and differentially expressed genes are currently being explored to determine pathways related to recognition strategies. DiI, a lipophilic tracer, has been used to visualise the movement of cells between these grafts. The two tissue samples could not be clearly distinguished by histology, from the same, closely related and distantly related species, indicating fusion. Differentially expressed genes are currently being analysed through transcriptomics to assess responses between the different species, assisting in determining which pathways are involved in the tissue response. Fusion between the bivalve and gastropod samples indicates a significant limitation to recognition. Changes in differentially expressed genes between closely and distantly related species may provide some indication of underlying processes that provide no physical reaction. These results confirm limited recognition ability even from more distantly related species and suggest that the spread of transmissible cancers between species could be due to a lack of recognition ability against foreign cells in general. These findings will unveil the processes and limitations of recognition in bivalves, facilitating future research from an evolutionary perspective to thoroughly comprehend the origins of xenorecognition in multicellular organisms. Additionally, it contributes valuable insight into an under-explored area of bivalve immunity. It provides a fundamental understanding when considering the infection methods of transmissible cancer, which significantly affects bivalves worldwide.

Funding Source: The American Malacological Society funded this work through the Melbourne R. Carriker student research award.

SYMPOSIUM: MOLLUSCS IN CAVE ENVIRONMENTS / DIVERSITY AND EVOLUTION OF MOLLUSCA

MOLLUSCS IN CAVE ENVIRONMENTS / DIVERSITY AND EVOLUTION OF MOLLUSCA

Coordinator:

SÉRGIO MENDONÇA DE ALMEIDA – Universidade Católica de Pernambuco, Brazil

The symposium 'Molluscs in cave environments' will bring together researchers interested in the molluscan fauna of subterranean habitats worldwide. These environments serve as natural laboratories of biodiversity and can often act as refuges or speciation engines. Both bivalves and gastropods, whether terrestrial or aquatic, are included, and any topics related to them — from taxonomy to ecology to conservation — are welcome.

Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Taxonomy and Systematics

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DUNGEONS DEEP AND CAVERNS OLD: ARE SUBTERRANEAN ENVIRONMENTS REFUGIA OR SPECIATION LABS FOR BRAZILIAN SNAILS?

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Keywords: freshwater snails, Gastropoda, land snails, Truncatelloidea, Urocoptoidea.

Brazil is home to over 20,000 caves, more than half of which are found in limestone rock formations. Among the country's approximately 900 species of land and freshwater gastropods, fewer than twenty are troglobitic. However, this number is likely an underestimate, as Brazil's terrestrial and freshwater malacofauna remains incompletely documented, and its subterranean environments are even less studied. Recent collection efforts and taxonomic studies, supported by molecular phylogenetics whenever possible, are beginning to reveal intriguing aspects of Brazil's cave malacofauna. Such collections have taken place across the country, particularly in Pará, Rio Grande do Norte, Bahia, Minas Gerais, Mato Grosso do Sul and São Paulo states. New records and new species have been revealed by such efforts, with broader implications for the history and evolution of the involved groups in Brazil and South America. In some cases, subterranean environments function as natural laboratories of speciation, where multiple endemic cave species evolve in isolation. This phenomenon has been observed, for instance, in the freshwater truncatelloidean genus *Potamolithus* (Tateidae) in southeastern Brazil. However, the extent of such radiation remains unclear and requires further phylogenetic and phylogeographic studies. Conversely, caves can also serve as refugia for lineages that are rare or even absent from surface environments. A striking example is the discovery of members of the superfamily Urocoptoidea in southeastern Brazil — a group of land snails predominantly distributed in the Caribbean and otherwise absent from present-day Brazil, though a few fossils have been found from the Paleogene of Rio de Janeiro. Finally, in some cases, caves can simultaneously act as both speciation laboratories and refugia, as seen in the freshwater genus *Idiopyrgus*. This group of truncatelloidean snails was recently identified as a lineage of the relict family Tomichiidae, which has only a few representatives across Gondwanan regions, including Australia, South Africa, and Brazil. Despite being a relict genus, *Idiopyrgus* appears to have undergone some radiation in subterranean environments, with cave-endemic species being recently described. We hope that future collections and studies will continue to unveil the diversity and evolutionary history of cave snails in Brazil. However, it is important to recognize that many caves across the country are threatened by human activities, particularly mining. As in other tropical regions, we fear that cave snail biodiversity is being lost to these threats before species are even discovered and formally described.

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Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Other themes

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TROGLODYTE FAUNA OR CAVE TRAMPS OF FAUNA: QUINTANA ROO (MEXICO)

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Keywords: stygobiont, sink holes, Gastropoda, Yucatan Peninsula, Playa del Carmen, Caribbean.

Caves in the Yucatan Peninsula are a product of the dissolution of a carbonate matrix. In the caves of Quintana Roo a new species of *Miradiscops* was located. Our objective was to collect some new specimens of it, in turn we found some other cave species. Its number increases the knowledge of the molluscan fauna from the Yucatan Peninsula, and a listing of species is provided. Four caves near Playa del Carmen, Quintana Roo, Mexico, were searched for land molluscs (outside and inside the Trono Cave System, and three other caves were searched inside). Molluscs were taken directly by hand from the floor, and from crevices on the cave; at the inside of these sites, only shells were collected. The specimens were placed in plastic jars and labelled with relevant data. Live specimens were relaxed with water and minutiae of tobbaco. When no movement was noticed, they were changed to a 70% alcohol solution. At the laboratory, shells were cleaned, rinsed and brushed under clear water, and then separated and identified with specialized literature. A total of 382 specimens were found in four caves of Quintana Roo, divided in 35 species and subspecies from 17 families of land (29), marine (5) and freshwater (1) molluscs, with the literature review this sums 67 species and subspecies in 28 families of freshwater (5), land (54) and marine (8) molluscs recorded for the entire Peninsula. Twenty nine taxa were not previously recorded in the literature. Of the freshwater families, the most diverse was Planorbidae with four species, from terrestrial molluscs the most diverse families were Spiraxidae with 10 species and Achatinidae with eight. Of the marine molluscs, the family Potamididae had two recorded species. Of the four caves (Calavera, La Milla, Papalote and Systema Trono), Papalote and Trono were the most diverse with 17 species, Calavera has 16; Trono was the closest to the sea, so it has marine influence showing 5 marine molluscs; La Milla had 7 species and this one is inside the city, so it is unlikely it will trap more molluscs. Fourteen species had not been previously recorded in the caves of the Yucatan Peninsula, including the introduced *Melanoides tuberculata* (Müller, 1774), which was present as a juvenile at Papalote cave. *Allopeas gracile* (Hutton, 1934) occurred at both Papalote and Calavera, this introduced species was already recorded in other studies. Live specimens inside the caves were not recorded, that agrees with Bequaert and Clench (1938) that concluded that molluscs are not true cave-dwelling species; rather, they are trapped as soon as they come into the cave, in contrast to *Teinostoma brakovitsi*, *Mexicenotica xochii* and *Pyrgophorus thompsoni* that dwell at Yucatan State caves; the last two are associated with *Pisidium* sp.

Funding Source: Annual stipend from the University to Edna Naranjo.

Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Taxonomy and Systematics

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PEEK-A-BOO: CRYPTIC DIVERSITY IN CARRIER SNAILS REVEAL PHYLOGEOGRAPHIC BOUNDARIES

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Keywords: *Xenophora*, cryptic species, biogeography.

Cryptic speciation, hybridization, and the evolution of complex traits such as behaviour embattle the classification of biodiversity. Although cryptic speciation – the formation of species with minor morphological differences – is a widely documented phenomenon, the scarcity of genetic samples from deep-sea molluscs complicates unbiased assessment of diversity. The carrier snails (family Xenophoridae) are mesophotic and coastal offshore marine gastropods, long celebrated by naturalists for their unique behaviour of collecting and affixing foreign objects, such as rocks, shells, and corals, to their shells for camouflage or physical defense. With a rich alpha-taxonomic history, species limits and classification are largely stable with 28 species across six genera currently recognized. We present the first diversity assessment of xenophorids based on molecular species delimitation. Our integrative species delimitation approach, incorporating morphological, ecological, and cytochrome oxidase I (cox-1) barcode sequences from nearly 600 specimens, supports a 49-species scenario – a near two-fold increase in species richness. Single-locus species delimitation further supports the validity of several sister species pairs diagnosed with inconspicuous features. By analyzing the pattern of divergence across all cryptic species complexes, we found that the separation of Pacific and Indian Ocean basins is a significant phylogeographic boundary, across which multiple morphospecies form two genetically differentiated but morphologically cryptic clades. Within the *Xenophora regularis* complex, a species group that primarily cements rocks to their highly rugose shells, we recovered six distinct mitochondrial lineages, three of which we describe as new species. Species within each cryptic complex do not cluster into a single clade, suggesting that xenophorids may have undergone repeated evolution of a highly rugose shell that may be associated with rock-collecting behaviour. We plan to use a target-capture approach to infer a robust phylogeny that better reflects species and generic relationships and to further investigate correlations between the evolution of specific shell morphology and collecting behaviour. This study affirms the potential of mass barcoding to discover cryptic species, to reveal biogeographic patterns and evolutionary trends in complex behaviours.

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Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Taxonomy and Systematics

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GASTROPOD BIODIVERSITY IN PARQUE NACIONAL DA TIJUCA, RIO DE JANEIRO: A COMPREHENSIVE CHECKLIST AND COMPARATIVE INSIGHTS WITH ADJACENT PROTECTED AREAS

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Keywords: conservation, distribution, Atlantic Rainforest, systematics.

Tijuca National Park (PNT) is recognized as one of the largest Brazilian urban forests and plays a vital role in influencing the climate and air quality of Rio de Janeiro. The park is divided into four sectors, with Sector A being the largest. Despite its importance, the terrestrial malacofauna remains largely unexamined. This study aims to conduct a comprehensive inventory of the terrestrial gastropods found within Tijuca Forest Sector A. Field expeditions in PNT were conducted on random dates between 2019 and 2025 along several trails accessible to tourists in Sector A. Active search methods were employed at different times throughout the day to sample species without regard to their preferred periods of activity. All specimens obtained during these expeditions were deposited in the Malacological Collection of the Biological Institute at the Universidade Federal do Rio de Janeiro. Preliminary results indicate the presence of 22 species across 11 families in the studied area. The Bulimulidae family is the most prevalent, with five species, followed by Veronicellidae, which has four species. Additionally, there are four families represented by two species each: Helicinidae, Scolodontidae, Simpulopsidae, and Solaropsidae. Five other families have one species each: Achatinidae, Helicarionidae, Megaspiridae, Odontostomidae, and Streptaxidae. The high number of native species (21 species) suggests a strong level of conservation, indicating that Tijuca Forest remains a hotspot for malacofauna in Rio de Janeiro. A study by Fernandes et al. (2025) analyzed the Municipal Natural Park of the City (PNMC), a fragment of the Atlantic Forest located near the PNT. The most diverse family in the PNMC was Achatinidae, with five species, while Bulimulidae was represented by only one species. Notably, despite being two important adjacent areas, only four species are common to both PNT and PNMC. In part, this discrepancy in species diversity may be explained by the distinction between sampling methods in both studies: in PNMC sampling methods concentrated much of its effort on the microgastropods from leaf litter. Nevertheless, the discrepancy between arboreal or shrub-dwelling species in both PNT and PNMC are still speculative and under debate. In Rio de Janeiro, the Tijuca Forest serves as a crucial refuge for the diversity of terrestrial gastropods. It offers significant opportunities for ongoing research and documentation of biodiversity across various areas of the biological sciences. Further studies are necessary to evaluate the species richness of gastropods in different sections of the forest and less-explored habitats.

Funding Source: This work was supported by the Fundação Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) - Brasil [Finance Code 001].

Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Anatomy and Physiology

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THE IDENTITY OF *Vaginulus taunaisii* FÉRUSSAC, 1821 (GASTROPODA, VERONICELLIDAE): MORPHOANATOMICAL REDESCRIPTION OF A SLUG ENDEMIC TO PARQUE NACIONAL DA TIJUCA (PNT), RIO DE JANEIRO

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Keywords: biodiversity, Mollusca, slug, terrestrial, taxonomy, phylogeny.

Vaginulus taunaisii Férussac, 1821 is a terrestrial slug that can grow up to 20 cm in length. It has a brown-olive body, dark brown cephalic tentacles, a broad perinotum, and a tapered pedal sole. Originally described from Parque Nacional da Tijuca (PNT) in Rio de Janeiro, it is commonly found, especially during the rainy season. However, despite its presence in a heavily visited area, it remains poorly known. Fresh specimens were periodically collected in PNT between December 2023 and March 2025, with further sampling planned through December 2025. Field activities occurred during different seasons, aiming to sample at the same locations whenever possible. In the field, data such as substrate type, activity time, and diet were recorded. In the laboratory, specimens were anesthetized and preserved in 90% alcohol. A total of 30 individuals were examined for external morphological analysis, and 21 of these were dissected to study their nervous, digestive, and reproductive systems. The dissection followed standard protocols for Veronicellidae and utilized a stereomicroscope, along with appropriate tools, including ophthalmic scissors, precision forceps, and entomological pins. The results provided important insights into the external morphology and internal anatomy of the analyzed systems. The nervous system is highly branched and complex, originating from a circumesophageal ring, with long pedal nerves extending throughout the body in a comb-like arrangement. The digestive system includes elongated yellowish salivary glands connected to the radular bulb, a short and thin esophagus, a long crop, a muscular U-shaped stomach, and a thin, extensive intestine that penetrates the tegument and opens at the anus. The visceral system is covered by the hepatopancreas. Notably, the reproductive system features a highly distinctive penis that is prominent and bears two lateral ridges. The penis gland tubules are long and folded at the tip, a common trait within the Veronicellidae family. The next steps involve describing and comparing the ecological data of the species with that of other veronicelids, as well as DNA sequencing for future phylogenetic analyses. The anatomical and morphological data presented here enhance our understanding of *Vaginulus taunaisii*, a species that has received little attention despite its abundance in Tijuca National Park. The distinct features observed, particularly in the nervous and reproductive systems, contribute to a better understanding of Veronicellidae diversity and support future taxonomic studies. This underscores the importance of continued sampling and anatomical investigation of native terrestrial mollusks in Brazil.

Funding Source: No.

Molluscs in Cave Environments / Diversity and Evolution of Mollusca

Evolution

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STREAMS OF SPECIATION: HIGH DIVERSIFICATION IN TWO FRESHWATER MOLLUSC GENERA OF THE WESTERN GHATS, INDIA

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Keywords: Western Ghats, biogeographic gaps, endemic freshwater molluscs, diversification.

The Western Ghats, a biodiversity hotspot, is interrupted by three major gaps or valleys that have played a crucial role in shaping species distributions. The region's freshwater habitats harbour endemic and unique genera and species. Several freshwater molluscan genera, restricted to perennial lotic systems, are endemic to this region. This study investigates diversification patterns in the Western Ghats' freshwater molluscs, using two endemic genera, *Paludomus* and *Cremnoconchus*, as model organisms. The freshwater mollusc samples belonging to *Paludomus* and *Cremnoconchus* were collected across their distribution range and preserved in absolute ethanol. Genomic DNA was extracted using a modified CTAB method and amplified for one mitochondrial gene (COI) and one nuclear gene (28S). The concatenated dataset (COI and 28S) was used for Maximum Likelihood analysis in IQTree. Species delimitation analysis was performed using ASAP and PTP. Molecular divergence dating analysis was conducted with the concatenated dataset in BEAST to obtain time-calibrated phylogenetic trees and estimate divergence times. A Lineage Through Time (ltt) plot was created to assess the diversification rates of *Paludomus* and *Cremnoconchus* in the Western Ghats. The maximum likelihood tree shows that *Paludomus* from the Northern Western Ghats (NWG) (16˚-21˚N) forms a sister clade to the Central Western Ghats (CWG) samples (12˚–16˚N). They, in turn, form a sister clade to the Southern Western Ghats (SWG) (8˚–12˚N) samples. Similarly, *Cremnoconchus*, which is distributed on the western slopes of the waterfalls in northern and central Western Ghats, formed two clades- NWG and CWG. Preliminary analysis has shown that the biogeographic gaps play a role in species segregation. The species delimitation analysis suggests that *Paludomus* comprises 31 putative species, of which 10 have been described, and *Cremnoconchus* has 38 putative species, of which nine have been described. The divergence dating analysis suggests that *Paludomus* reached the Western Ghats around 87 mya (million years ago), and subsequently started diversifying in the region around 56 mya. The SWG *Paludomus* predates the NWG and CWG ones, and back dispersal to SWG occurred around 37 mya. The age of diversification of *Cremnoconchus* suggests an ancient split that occurred around 90 mya from its marine counterparts. A major split within the genus *Cremnoconchus* took place around 56 mya, which separated the NWG species from the ones from CWG. The lotic system of the Western Ghats harbours a species-rich community, many of which are novel to science. This high diversity faces an imminent threat from rapid urbanisation and other land use changes, such as dam construction. Documenting these ancient lineages is vital as it will enhance the conservation value of not only the study organisms but the freshwater systems of the Western Ghats.

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POSTERS

ANATOMY AND PHYSIOLOGY

Anatomy and Physiology

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BIOCHEMICAL COMPOSITION OF SNAIL MUCIN OF GIANT AFRICAN LAND SNAILS (*Archachatina marginata* AND *Achatina achatina*) AND THEIR CARDIOTONIC POTENTIAL

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Keywords: mucin, metabolite, minerals, *Achachatina marginata*, *Achatina achatina*, cardiac function.

The African giant snail, a nocturnal mollusk, has long been valued in traditional medicine. Its mucin, a high-molecular-weight glycoprotein secreted in large quantities, has been studied for its biochemical properties. While the haemolymph of different snail species has been analyzed, little is known about the biochemical composition of mucins. One hundred snails (mean weight: 150.64±2.35g) were obtained from the Department of Forestry and Wildlife Management, Federal University of Agriculture, Abeokuta, and their mucin was processed into powder. Biochemical (protein, albumin, globulin, cholesterol, and triglycerides) and mineral (Mg^{2+}, Fe^{2+}, Na^{+}, K^{+}, P, and Ca^{2+}) analyses were conducted using standard methods, and a t-test determined statistical significance. The mucin extract of *A. marginata* was light brown and more viscous, whereas *A. achatina* mucin was dark brown and less viscous. No significant differences ($p<0.05$) were found in their biochemical compositions. However, protein levels were higher in *A. achatina* (5.05±1.34) than in *A. marginata* (3.69±1.06), while triglycerides were higher in *A. marginata* (22.55±1.84) than in *A. achatina* (19.56±1.46). Magnesium (Mg^{2+}) and calcium (Ca^{2+}) concentrations were significantly higher ($p<0.05$) in *A. achatina* (4.58±1.46 and 17.17±3.69, respectively) compared to *A. marginata* (1.91±0.80 and 9.50±3.55, respectively). No significant differences ($p<0.05$) were observed in Fe^{2+}, Na^{+}, K^{+}, and phosphorus levels between species. Mucin from both species reduced heart contractility and heart rate in toads, though no significant differences were observed between them. The most pronounced reductions occurred in toads treated with mucin from *A. marginata* and *A. achatina* compared to conventional drugs. These findings suggest that mucin from *A. marginata* and *A. achatina* may influence cardiac function by reducing heart rate and contractility, highlighting its potential for future therapeutic applications. Mucin possess wonderful therapeutic biochemical activities as regards wound healing and some other ailment. the mucin extracted from it during processing can offers another useful product for medical application

Funding Source: No.

Anatomy and Physiology

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ANATOMIC DESCRIPTION OF *Graptacme obtura* (SCAPHOPODA: DENTALIIDAE) FROM TRINDADE ISLAND, BRAZIL

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Keywords: Dentaliida, anatomy, taxonomy, Southern Atlantic, oceanic island, archipelago.

As research and sampling of the Trindade and Martin Vaz oceanic archipelago are increasing in recent years, one of these sampling efforts awarded a new, and so far endemic, species of scaphopod mollusks. Said species is *Graptacme obtura* Fogarolli & Simone, 2024, which was described through conchological aspects. The aim of this work is to add upon the characterization of the species with a full anatomic description. Dissections were made by standard techniques, with the specimens under a stereomicroscope, immersed in fixative (ethanol 70%). Photos of all dissection steps were taken. All drawings were made through a camera lucida. The presented measurements were obtained from selected specimens, normally dissected; these specimens are labeled at the collection. Types: Holotype MZSP 166760, spm. Paratypes: MZSP 121837, 6 spm from type locality. Material examined: BRAZIL. Espírito Santo: Ilha da Trindade (J.B. Mendonça col.), Ponta da Calheta, 20°30'18.72"S, 29°18'31.6"W, 1 spm, MZSP 162494 (16.XI.2017), 20°30'18.72"S, 29°18'31.67"W, 5 spm, MZSP 162593 (04.XII.2017), 1 spm, MZSP 154841 (10.VIII.2018). The detailed anatomical study revealed that *Graptacme obtura* has the same general conformities of Scaphopoda from the Dentaliidae family. Although some structures have distinct differences that are significant for differentiation of species, some of them have been previously considered in the literature but in few works, while others mentioned here can be considered as new suggestions to the anatomy study of this group. Such structures that deserve more attention, in general, are: the oral tube and its internal chambers and folds; the size and proportion of the muscles and cartilages which compose the odontophore; radula teeth and its structures; intestine loops; shape and size of posterior mantle border; the general shape of the foot and its epipodial lobes. Unfortunately there are no anatomies of the genus *Graptacme* present in the literature. This study, thus, is the first anatomical description of the genus. A future study of the congeneric species is possible and welcome to have a better basis for the comparative studies of this group of Scaphopoda. In conclusion with the results, *G. obtura* sheds light on good anatomical features to take note when studying Scaphopoda. Which opens more opportunities to keep exploring and sampling the waters around Trindade and Martin Vaz, along with other less explored places in Brazil. And it further proves the necessity for the better development of anatomic studies with Scaphopoda, as well as other less known mollusk clades.

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RELATIONSHIP BETWEEN FOOT SIZE AND SHELL DIMENSIONS OF INTERTIDAL GASTROPODS

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Keywords: morfometry, intertidal gastropods, shell, foot.

Foot size combined with shell shape are determining factors for the survival of intertidal gastropods and are directly connected with their ecological niche. Intertidal fauna is among the most threatened by climate change, making it essential to study and understand these species to conservate them. This study aims to check if there is a correlation between shell and foot measurements among individuals of the same species and between species. The species *Agathistoma viridulum*, *Vitta meleagris* and *Stramonita brasiliensis* were collected two times at Pacheco beach and one at Dois Coqueiros beach, both in the municipality of Caucaia, between November 2024 and January 2025. 50 individuals of each species were analysed in the field. Shell Height (AC) and length (CC) of the shell, opening height (AA) and length (CA) and foot height (AP) and length (CP) were measured, photographs of the fully expanded foot were taken and submitted to ImageJ software to obtain foot area (ÁP). For the statistical analysis of the data, the Shapiro-Wilk normality test was performed, we used Pearson and Spearman correlation analysis performed in RStudio software. Our data indicated a moderate to strong positive correlation between AC (R = 0.67) and AA (R=0.55) measurements with ÁP in *S. brasiliensis*. This species has predatory habits, but it's preyed upon by the gastropod *Aurantilaria aurantiaca*. The positive relationship between the size of the opening and the size of the foot could be a reflection of the movement for hunting and escaping, in addition to greater speed in the expansion and contraction of the foot. *A. viridulum* showed a moderate positive correlation between AC (R=0.53) and LC (R=0.43) measurements with ÁP. This species is herbivorous, found mainly under rocks, with little tolerance to unconsolidated substrate. The limited niche could justify a reasonably sized foot in relation to the shell, keeping the animal always attached to the rock even with the tide's influence. The relationship between shell and foot measurements in *V. meleagris* was weak or nonexistent, suggesting that shell, aperture and foot size are shaped by other factors. This species is a grazer on sandy bottoms, in other parts of the world they are known for living and reproducing in estuaries, however the studied population is well established and reproducing at Pacheco and Dois Coqueiros beaches, which are near of Ceará river estuary, but not a part of it. Among the studied species *V. meleagris* had the most globosus shell with practically no spire and no columella, a unique structure that could explain the absence of correlation between shell and foot size. The present study demonstrated that the relationship between shell and foot measurements is strongly correlated in *S. brasiliensis*, moderate in *A. viridulum*, and practically nonexistent in *V. meleagris*, demonstrating that the degree of correlation varies between species. Since the present study compared species with different feeding habits and predator/prey relationships, further research could compare species with similar ecological habits to verify whether the observed relationships are maintained.

Funding Source: No.

Anatomy and Physiology

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COMPARATIVE EXTERNAL MORPHOLOGY OF THREE POPULATIONS OF *Chaetopleura angulata* (POLYPLACOPHORA, CHAETOPLEURIDAE)

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Keywords: Polyplacophora, comparative morphology.

Chaetopleura angulata (Spengler, 1797) is a relatively large species of chiton, reaching a length of 50mm. The most evident features are beaked valves, apparently leathery girdle and central area of valves sculptured with longitudinal beaded lirae. It lives at depths of 0-50m in a disjunct distribution in the South America east coast and Iberian Peninsula, with a remarkable geographic gap between the populations. The study compares samples from these areas. This work focused on bibliographic research and a first anatomical analysis of the external characteristics of the species. A map of distribution was created using data from the material deposited in the Malacological Collection of the Museu de Zoologia da Universidade de São Paulo (MZUSP), preserved in 70% ethanol. For the images, material from three locations where *Chaetopleura angulata* is present was used: Southern Brazil, Portugal and Argentina. The entire animal was observed and photographed dorsally and ventrally under a stereo-microscope and then the valves were gently removed to observe their visible characteristics and also those covered by the mantle and girdle. The documented distribution of *C. angulata* shows an unusual pattern for chitons, considering these animals have a relatively restricted distribution, and can suggest that the specimen was shipped to the coast of Portugal by traders, since that animal was already found climbing anchor chains. The shell morphology and external features looks, in fact, similar in the specimens of the three locations analyzed, the greatest similarities were found, mainly, between the specimens from Brazil and Portugal, however, Argentina specimens look smaller than the Brazil and Portugal ones, and the beaded lines are more diffuse and the insertion plates appear wider compared to the size of the valve, having a more opaque color. As expected, all three populations do not have any aberrant differences. However, some aspects of distribution, species history and valve characteristics may be taken into account in a more in-depth study, and because of a lack of anatomical studies of the genera there are few taxonomic relevant characteristics of the internal anatomy, which show the importance of continuing this study for a proper review of the species.

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SLEEPING LIKE AN OCTOPUS: A COMPARATIVE STUDY OF MOLLUSKS SLEEP

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Keywords: mollusks, sleep, cephalopods, octopus.

Sleep in mollusks remains understudied, however emerging research reveals evolutionary gradients. Cephalopods display complex sleep architecture, including REM-like phases. Gastropods exhibit behavioral quiescence, neural correlates still unconfirmed. While bivalves show only primitive inactivity patterns. The convergence of sophisticated sleep states in intelligent cephalopods and vertebrates suggests sleep is linked with cognitive evolution. These findings evidence the need for comparative studies across molluscan taxa to elucidate sleep's evolutionary origins. This study used a comparative approach to analyze sleep-like states across mollusk classes (cephalopods, gastropods, bivalves) from a review of published papers through Google Scholar using mainly the terms: Mollusks, Sleep, Rest, Activity, Rhythm, Circadian. Behavioral and physiological data were evaluated based on sleep criteria: (1) behavioral quiescence, (2) reduced responsiveness, (3) rapid reversibility, (4) homeostasis, (5) physiological changes and (6) cyclic phases. For cephalopods, we looked in the literature for evidence of these criteria, including cyclic quiescence states combined with electrophysiological data. For bivalve and gastropod, we focused on studies showing behavioral quiescence, changes in responsiveness thresholds, cyclic resting/active states and rebound after deprivation of inactivity patterns. Among cephalopods, octopus and cuttlefish exhibited sleep-related features including behavioral quiescence, reduced responsiveness, homeostatic rebound (octopus), and cyclic REM-like phases. Octopus and cuttlefish species (*Octopus vulgaris*, *Octopus insularis*, *Octopus laqueus*, *Sepia officinalis*) showed cyclical alternation between active sleep (characterized by rapid skin patterning changes) and quiet sleep periods. No published studies on squids were found. Gastropods (*Lymnaea stagnalis*, *Aplysia californica*, *Stylommatophora*) met criteria for behavioral quiescence and showed increased responsiveness thresholds during resting, but lacked clear cyclicity while bivalves (*Crassostrea gigas*, genus *Mytilus*) displayed only inactivity patterns with circadian and circatidal rhythms. No published studies were found for other molluscan classes. This comparative analysis reveals a complexity gradient in molluscan sleep that parallels neurological sophistication. Cephalopods' vertebrate-like sleep patterns, including their REM-like states, correlate with their centralized nervous systems and complex cognition. The independent evolution of sophisticated sleep states in cephalopods and vertebrates suggests functional convergence, supporting the hypothesis that sleep complexity evolves with neural organization. These findings highlight cephalopods as exceptional models for studying sleep evolution, particularly regarding the emergence of complex sleep states. However, the lack of data for most molluscan classes underscores the need for broader comparative studies to understand sleep evolution, its functions, and its relationship with cognition within this phylum. Cephalopods, mainly coleoids, connect invertebrate and vertebrate sleep studies, exhibiting complex sleep patterns through unique neural mechanisms absent in simpler mollusks. Their sleep correlates with the ability to adapt to the environment, highlighting its evolutionary role in cognition. Future investigations are necessary to elucidate sleep diversity in mollusks, enabling deeper understanding of its neural mechanisms, adaptive significance, and evolutionary origins of sleep in these taxa.

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COMPARATIVE ANALYSIS OF THE PROBOSCIS STRUCTURE OF *Admete viridula* (GASTROPODA: NEOGASTROPODA) WITH AN ASSUMPTION ABOUT THE TYPE OF NUTRITION

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Keywords: Neogastropoda, Cancellariidae, proboscis, jaw.

Neogastropoda is a large and widespread order of gastropod mollusks. The main distinguishing feature of its representatives is the proboscis, which contains the anterior part of the digestive system. Highly modified proboscis was observed among the sister group to Neogastropoda – family Cancellariidae, whose representatives often do not have a radula, the type of nutrition for most is unknown, therefore, the study of their feeding apparatus and behaviour seems relevant. The aim of this work was a comparative anatomical analysis of the proboscis and anterior digestive system of cancellariid mollusks with the assumption of type of nutrition. For the study *Admete viridula*, widespread mollusks in the Arctic seas, were chosen. The material was collected in the Kandalaksha Bay of the White Sea, mainly with Sigsby trawl. For two weeks, in a cold room at a water temperature of 2°C, living adult mollusks were observed. Three-dimensional reconstruction methods and confocal laser scanning microscopy were used to investigate general morphology of proboscis and to describe a whole muscular system. Scanning and transmission electron microscopy were used to study the fine morphology. Observations have shown that mollusks were burrowing into the ground. They may find their prey both above and below ground. The very long thin proboscis has multidirectional muscle fibers. There is a main ventrolateral retractor, which plays an important role in contraction. The salivary glands, esophagus and buccal mass have their own muscles, performing form-building and supporting functions. Diagonal muscles were found, and a mechanism of jaw moving in the buccal complex during feeding was suggested, similar to rolling up the sleeves of a shirt: when the diagonal fibers contract, they expand the lumen of the oral tube and the buccal complex moves forward. However, several types of common neogastropod muscles were not found, thus, it is impossible to describe whole-proboscis locomotion. Accessory salivary glands are possibly not associated with digestion, because their ducts open near the mouth. The buccal mass consists of vacuolated cells with myofilaments that indicates their contractility. In our analysis, we called this tissue 'supporting', since it is possible that its contractility changes the width of the lumen of the buccal cavity. The jaw is a layer of chitin lining the buccal cavity. Microvilli of the buccal epithelium are embedded in this layer, which indicates an active process of its thickening. The basal part of the jaw consists of amorphous chitin. The polymerized distal part is needed for direct interaction with prey and can pierce soft tissues. In the studied specimens, valve of Leiblein is much simpler in structure than in other neogastropods (Conoidea, Muricoidea). For the first time, a detailed morphology of the cancellariid proboscis using many methods has been described, many unique features have been revealed: a thin jaw structure, 'supporting' tissue, a variety of muscles. Analysis of morphological features of the proboscis and behaviour made it possible to suggest a sucking type of nutrition, in which a thin long proboscis reaches inaccessible places, for example, polychaetes in tubes.

Funding Source: No

Anatomy and Physiology

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REVIEW OF THE IDENTIFICATION OF SPECIMENS OF THE GENUS *Biomphalaria* (SAY, 1818) FROM THE MALACOLOGICAL COLLECTION OF THE TAXONOMIC COLLECTIONS CENTER OF THE FEDERAL UNIVERSITY OF MINAS GERAIS (BRAZIL) THROUGH ANATOMICAL STUDIES

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Keywords: Planorbidae, taxonomy, anatomy, sistematics, dissection.

The Malacological Collection of the Taxonomic Collections Center of UFMG (CCT–UFMG) includes 5,677 specimens. 1,123 of them belong to the genus *Biomphalaria* from various regions of Brazil. Of these, 48% remain unidentified at the species level. Considering the genus's medical relevance, the need for accurate identification and the training of new systematists, this study aims to perform morphological identification of *Biomphalaria* specimens, increasing the scientific value of the collection. Initially, training and studies on fixation, dissection, and the analysis of anatomical structures relevant to the taxonomy of the genus were conducted. A review of the collection's specimens was carried out to identify those containing soft tissue and those with only shells. A visual inspection of the material was then performed to select specimens suitable for dissection. Dissections were conducted using a stereomicroscope and forceps to expose structures following classical planorbid systematics literature. After identification at the species level, the data were updated in the collection's database. Out of a total of 539 available exemplars in the collection, 30 specimens previously identified at the genus level (*Biomphalaria*) were dissected. The mantle was removed to observe the renal tube located on the roof of the pallial cavity, and the reproductive system was exposed to examine proportions and diagnostic characters relevant to taxonomy of the genus. Based on these observations and the literature, the species *B. straminea*, *B. glabrata*, and *B. tenagophila* were identified and the data were changed in database. There is a lot of work to be done and there are still many specimens to be observed. Over 500 'exemplars' will be dissected to be identified at species level. Classical morphological identification of planorbids requires dedication and significant time for the training of a systematist. This training is crucial for developing skilled professionals who can later conduct molecular studies supported by validated morphological analyses. Accurate identification of the collection not only demands time and study but also contributes to advancing the planorbid distribution map of the country and provides valuable information for the scientific knowledge of the collection.

Funding Source: No

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DEFENSE IN SEA SLUGS: MORPHOLOGY AND GENE EXPRESSION ALONG THE CERATAL AUTOTOMY PLANE OF THE NUDIBRANCH *Berghia stephanieae*

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Keywords: Gastropoda, Heterobranchia, candidate genes, immune system, muscle response.

Autotomy is a defense strategy that involves the self-detachment of body structures at predetermined breakage points. This defense has more than one evolutionary origin, and is widely among marine invertebrates. In the gastropod group Nudibranchia, some species can autotomize appendages, while others lack this ability. The aim of this work was to use the laboratory model *Berghia stephanieae* to investigate the morphological and molecular features of autotomizing tissues in nudibranchs. We first investigated the general anatomy of autotomy plane in *B. stephanieae* using microcomputed tomography (microCT). We further observed the cerata and autotomy plane in detail using histological sections embedded in both paraffin (cuts of 7µm) and Technovit 7100 resin (2.5µm). We collected short read transcriptomes from different body regions, including (i) two autotomy response areas and (ii) three additional non-autotomizing. We then performed differential gene expression analysis to study the candidate genes that may be involved in autotomy process. Histological sections revealed that the autotomy plane in *Berghia stephanieae* is formed by longitudinal and transverse muscle fibers that surround and constrict the plane, including the portion of the digestive system entering the cerata. Axons innervating this musculature, along with a layer of connective tissue containing dense granules, were also observed. The anatomy of this plane differs from that described in *Melibe leonina*, the only ceratal autotomy system previously studied in detail. Following autotomy, the mantle epidermis disintegrates, and putative hemocytes (cells involved in the immune response) appear after mantle rupture. Differential gene expression analysis identified 1,304 genes upregulated in autotomy response areas compared to non-autotomizing areas. These genes were linked to 24 functional terms across the three main gene ontology (GO) categories. A large number were involved in biological processes, particularly transmembrane transport and proteolysis, as well as the molecular function of metalloendopeptidase activity. The predominance of these biological processes likely relates to wound healing, nutrient transport, and tissue breakdown in the affected area. Among the upregulated genes, those related to muscle response, injury repair, and regeneration were particularly prominent. These findings are consistent with histological observations, highlighting the role of muscle constriction at the autotomy plane and the rapid appearance of hemocytes. The autotomy mechanism is often associated with structures that serve other defensive roles, such as nematocyst sequestration in aeolid and dendronotid cerata. Comparative studies of autotomy across different lineages may shed light on the evolution of defense strategies in nudibranchs. Numerous cladobranch and few dorids species use autotomy as a defense. We studied it in *Berghia stephanieae* and found that the autotomy plane has an anatomical structure predisposed to rupture, controlled by transverse and longitudinal muscles that constrict the area, facilitating tissue rupture, wound closure, and immune response. This suggests the acquisition of the trait at a specific evolutionary stage, but further comparative studies in Nudibranchia and Metazoa are needed.

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MORPHOGENESIS AND CHEMICAL COMPOSITION OF SUBEPIDERMAL SPICULES IN HETEROBRANCH MOLLUSCS

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Keywords: spicule complex, sclerocytes, biomineralization, calcification, micro-CT, Raman spectroscopy.

Calcareous skeletal structures are widespread among molluscs, typically being external and synthesized extracellularly (e.g., shells, sclerites). However, some heterobranch gastropods possess subepidermal spicules that are synthesized and retained intracellularly — a rare trait in molluscs and Metazoa. Current knowledge of their morphology, structure, and formation remains insufficient to clarify their origin and homology across Heterobranchia. To address this, we conducted a comprehensive study of subepidermal spicules in two heterobranch groups. Using morphological methods and experimental techniques, we investigated the morphology, structure, and formation of subepidermal spicules in five nudibranch species: *Onchidoris muricata*, *Adalaria proxima*, and *Acanthodoris pilosa* (all Onchidoriddidae); *Cadlina laevis* (Cadlinidae); *Palio dubia* (Polyceridae); and one acochlidimorph species, *Asperspina murmanica*. The spicule tract configuration was revealed by micro-computed tomography. Light microscopy, scanning, and transmission electron microscopy were used to investigate the general morphology and ultrastructure of spicules and adjacent tissues. Immunocytochemical analysis and incubation with calcein were utilized to reveal chemical composition, and Raman spectroscopy was used to determine mineral composition. This integrative methodology provides a comprehensive analysis of spicule characteristics across studied taxa. Body wall morphology is generally conserved across studied species, comprising a glandular epithelium and a collagen matrix containing embedded sclerocytes (each with a spicule) beneath the epithelium. We revealed minor variations in the cellular composition of the epidermis, musculature organization, and spicule arrangement, which likely reflect functional differences in the spicule complex among Heterobranchia. In body regions lacking well-developed spicule tracts, the collagen matrix becomes thinner. This suggests that the composition and degree of development of the collagen matrix correlates with the degree of spicule tracts development. Sclerocyte ultrastructure is consistent across studied species: a nucleus lies peripherally, a perinuclear region contains organelles, and a vacuole occupies most of a cell volume. The internal structure of spicules in all studied nudibranch species changes during ontogenesis, transitioning from organic (containing collagen) and spongy in juveniles to mineralized and monolithic in adults through intermediate stages (exhibiting mixed structures with concentric layers and radial striation). Spicule growth patterns differ across the taxa: calcite spicules of Onchidoriddidae actively grow in juveniles, with calcium accumulation near the tips and along a periphery, while Cadlinidae spicules exhibit distinct growth and mineralization patterns. We propose asynchronous spicule formation in Cadlinidae, likely related to their extended metamorphosis from a veliger-like larva to an adult-resembling juvenile. Raman spectroscopy data confirm that the spicules of Onchidoriddidae are calcium carbonate, while in other Doridina there is variability in the mineral composition of the spicules from amorphous calcium carbonate to calcite. Our findings demonstrated conserved morphology of spicules and sclerocytes in distant groups of Heterobranchia (Nudibranchia and Acochlidimorpha), potentially indicating homoplasy. However, to prove this suggestion, we need further investigations of other heterobranch species with subepidermal spicules. Moreover, spicule mineral composition and mineralization patterns vary even among dorid nudibranchs. Therefore, we still cannot make definitive conclusions about the origin of subepidermal spicules and their homology within Heterobranchia.

Funding Source: This study was supported by the Russian Science Foundation, Grant Number 24-24-00028.

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REDUCTION AND AESTHETE PATTERNS IN CRYPTOPLACOIDEA (POLYPLACOPHORA: CHITONIDA)

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Keywords: aesthetes, Cryptoplacoidea, Mopalioidea, sensory systems, Polyplacophora.

Chitons possess an extensive sensory system embedded in their shells, called aesthetes. The superfamily Cryptoplacoidea is characterised by varying degrees of tegmentum reduction – the upper layer of the chiton valve – raising questions about its effects on sensory ability. Additionally, we investigated several species with reduced valves from the sister clade, Mopalioidea, to determine potential constraints on modification of the aesthete network. We used synchrotron-based µCT scanning to obtain high-resolution images that reveal the internal structures within chiton valves from 13 species across Cryptoplacoidea and Mopalioidea. Intermediate valves were selected for consistency. The aesthete channels were segmented as digital volumes using the software Dragonfly, and these models were compared across species. These were used to identify a matrix of characters representing the patterns in each region of the valve (lateral, pleural and jugum). In Cryptoplacoidea, we observed a stepwise reduction in the complexity and density of the aesthete network with increasing reduction of the dorsal tegmentum. Some taxa retain scattered lateral aesthetes, greatly reduced in density, suggesting partial functional retention. In *Cryptoconchus*, this architectural shift reaches an extreme, with an apparent loss of lateral channel networks altogether. Members of Mopalioidea with reduced tegmentum show a different modification in the aesthete network, maintaining a radial pattern. This system illustrates several responses to valve reduction: (1) near-complete loss of the aesthete system; (2) reduction or simplification of pleurolateral aesthete channels; (3) reorientation of the jugal aesthete network; and (4) novel additional sensory structures, as observed in *Cryptoplax*. Expanded girdles and adjacent epidermal sensory cells in some species may compensate for reduced valve-based sensing. These findings refine our understanding of how molluscan clades adapt to ecological pressures while navigating material and functional constraints. Chiton shell architecture serves dual role in protection and perception, and aesthete network reorganisation is a consistent outcome of shell simplification. Despite morphological loss, sensory connectivity may persist in alternate tissues or microstructures. These findings expand our view of molluscan sensory evolution, showing how changes in protective anatomy reshape not just external form, but internal systems of perception and information processing.

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A STUDY OF PHENOTYPIC VARIATION IN *Phyllaplysia taylori* AND TRENDS IN SEAGRASS HABITAT ALONG THE NORTH AMERICAN WEST COAST

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Keywords: marine gastropod, phenotype, seagrass habitat, ecology.

Phyllaplysia taylori, commonly known as Taylor's sea hare, is a marine gastropod in the family Aplysiidae (Dall, 1900). This species inhabits subtidal eelgrass *Zostera marina* beds and remains on the plant during all stages of its life. Previous research has indicated drastic morphological and physiological variations in individuals. Variation in pigmentation as well as habitat stability were studied. Images of *P. taylori* posted on iNaturalist.org were identified for the host type and morphological phenotypes of the specimen, noting the color morph and dorsal stripe patterns. Seagrass survey data from SeagrassNet.org sites located within *P. taylori* species range were studied to estimate *Z. marina* abundance. The pooled data were then used to determine the relationships between latitude, host, Euclidean distance, and time to color morph and dorsal pattern, as well as trends in *Z. marina* abundance in *P. taylori*'s species range over time. This thesis found a potential subpopulation of *P. taylori* with unique translucent pigmentation distinct from the common green morph in color and lack of dark dorsal stripes. They are found within a relatively short latitudinal distance and may indicate that they are an isolated population. A weak relationship between latitude and certain phenotypic similarity was found. Additionally, Euclidean distance to phenotypic sameness was not statistically significant; however, it displayed a weak positive relationship. The distribution of dorsal stripe pattern and host type is likely dependent on each other, whereas the distribution of color morph and host type is not. Changes in the probability of phenotypes suggest seasonally dependent phenotypic patterns. A weak link between color morph and stripe pattern was found. Analyzing seagrass survey data indicated that as *Z. marina* abundance increases, the probability of *P. taylori* presence also increases. Overall, *Z. marina* abundance in *P. taylori*'s species range showed negative trends across time. The observed discontinuity of populations and *Z. marina* patches, infrequency of *P. taylori* observed on abiotic surfaces, and phenotype distribution reinforce the argument for high genetic connectivity between populations via rafting. It is conceivable that with climate change and declining abundance of *Z. marina*, *P. taylori* population structure and abundance may be altered in the future.

Funding Source: Reed College – Initiative Grants in Undergraduate Research.

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THE ANATOMY OF THE EYES IN THE OPTIC SIPHONAL TENTACLES OF THE ANTARCTIC BIVALVE *Laternula elliptica* (P. P. KING, 1832) (LATERNULIDAE)

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Keywords: *Laternula elliptica*, eyes, siphons, retinal cells, bivalves.

Bivalves of the family Laternulidae are known as having eyes on the tip of tentacles surrounding the distal ends of both siphons. They live deeply burrowed in the substratum, with the optical tentacles oriented towards the water column. In the single laternulid from Antarctica, *Laternula elliptica* (P. P. King, 1832), these eyes remain poorly studied; this research aims to describe them, in comparison with those from other bivalve families. Specimens of *L. elliptica* were collected in Admiralty Bay, King George Island (South Shetland Archipelago), in the austral summers of 1996/97 and 1997/98. Fragments of the siphonal endings or isolated optic tentacles were fixed in two solutions: Bouin's, and Karnovsky modified for marine organisms. For histological sections, they were embedded in glycol methacrylate resin; sections of 5 µm thickness were then stained with toluidine blue and basic fuchsin, or Gomori's trichrome and glacial acetic acid. Samples fixed in Bouin's solution were tomographed in the MOGNO beamline of the Brazilian Center for Research in Energy and Materials (CNPEM). The histological sections revealed noticeable similarities and differences between the eyes of *L. elliptica* and those of other bivalves. Like species of Pectinidae, Spondylidae, and *L. truncata* (Lamarck, 1818) [now accepted as *Exolaternula spengleri* (Gmelin, 1791)], its eyes have a complex mirror structure, being "camera-type eyes", composed by a cornea, lens, tapetum, and retina. There is, however, one main difference: while *L. elliptica* exhibits a single layer of retinal cells, the other bivalve species are recorded as possessing a double retina, i.e. they have two layers of retinal cells. As the families Pectinidae and Spondylidae belong to the Infraclass Pteriomorphia, they are not directly related to the Laternulidae, which in turn is classified in a distinct bivalve branch: the Supeorder Anomalodesmata of the Infraclass Heteroconchia. This would imply that the eyes in these bivalve groups have different evolutionary origins, and so distinct structure too (with the corresponding distinct placement, since in laternulids the eyes occur in the siphons, not in the mantle margins). Interestingly, differences in the number of retinal layers were also found between *L. elliptica* and *E. spengleri*, showing that variations may occur in the family level. The analysis of the 3D tomographical images are in progress and through them the occurrence of a single layer of retinal cells in *L. elliptica* will surely be confirmed. Examination of other species of Laternulidae are also necessary.

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ARMED OR ALARMED? A LIMPET SECRETIONS UNDER THE MICROSCOPE

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Keywords: Patellogastropoda, repugnatorial glands, ultrastructure.

Molluscan secretory glands perform diverse functions such as adhesion, maintenance, and defence. The limpet *Tectura virginea* has conspicuous mantle-margin glands, previously hypothesized as repugnatorial, though never experimentally tested. This is unusual within Patellogastropoda, a group not known for chemical defences. We investigated these glands' morphology, behaviour, and chemistry to assess their function and explore whether they reflect a broader evolutionary pattern within this otherwise conservative lineage. Live *T. virginea* specimens were collected intertidally in Strangford Lough, Northern Ireland. Mechanical stimulation triggered filament secretion from marginal glands. These were collected and fixed in methanol for chemical analysis. Animals were fixed in paraformaldehyde, decalcified, and sectioned for light and electron microscopy. Semi-thin Richardson-stained sections were used for 3D reconstruction (Dragonfly), while ultrathin sections were stained and imaged on a ZEISS EM 10CR TEM. Extracts were analysed via HPLC and LC-MS to identify compounds. Anatomical features such as gland structure, vesicle maturation, and innervation were examined to determine gland function and neural control mechanisms. The mantle-margin glands in *T. virginea* are numerous (~640 per individual), and each secretion event is localized to the area directly stimulated. The glands are large (~78 µm), unicellular, and filled with vesicles that transition from dense granules to clear vacuoles, discharged by a whole-cell mechanism under neural control. Adjacent nerve fibres and surrounding muscle suggest regulated release. Chemical analysis identified glucuronic acid as the primary compound. Although this molecule is commonly associated with detoxification, here it likely functions as a repellent, supporting the historical interpretation of these structures as repugnatorial glands. The secretion forms white filaments that dissolve slowly in seawater, potentially providing a sensory or physical deterrent. While marginal glands exist in other molluscs, this is rare in Patellogastropoda, where defensive glands are largely undocumented. Given that *T. virginea* is sister to Lottioidea, the presence of chemically active glands raises evolutionary questions: is this a retained ancestral feature, or a unique adaptation in this lineage? The findings challenge the perception of limpets as behaviourally passive and anatomically simple, revealing hidden complexity in a morphologically conserved clade. This discovery contributes to a broader understanding of molluscan chemical ecology and highlights the need for further investigations into overlooked defensive traits in other limpet species. *Tectura virginea* possesses mantle-margin glands that release glucuronic acid upon stimulation, functioning through a whole-cell discharge mechanism. This supports their proposed role as repugnatorial glands, providing a chemical deterrent against predators. The species' phylogenetic position suggests that such secretory strategies might be more widespread than previously assumed within Patellogastropoda. This finding prompts a reevaluation of defensive adaptations in limpets and highlights unexplored physiological diversity in conservative molluscan lineages.

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BEHAVIOUR

Behaviour

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CIRCADIAN RHYTHMS AND LOCOMOTION OF THE *Limnoperna fortunei* (DUNKER, 1857) (BIVALVIA: MYTILIDAE): IMPLICATIONS FOR CONTROL AND MANAGEMENT

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Keywords: circadian behavior, invasive, locomotion.

Limnoperna fortunei (golden mussel) is an invasive bivalve that causes obstructions and corrosion in water systems. In Brazil, it is present in the South, Southeast, Midwest, and Northeast regions, and recently in the North, where it threatens aquatic ecosystems and the hydroelectric sector. This study aims to analyze circadian behavior, comparing the responses of juveniles and adults. These data can assist in more effective control and management of the species. The specimens collected from the Furnas Reservoir, São José da Barra/MG, were divided into two groups: juveniles (≤ 5 mm) and adults (21-27 mm), with 6 individuals per group. The bivalves were acclimated to a 12h light/12h dark photoperiod in dechlorinated water at 20 °C and pH 7.6, without feeding for 48 hours. During the experiment, the animals were individually placed in Petri dishes under identical conditions to acclimation. A camera in the BOD (Biochemical Oxygen Demand) incubator recorded the behavior for 24 hours. The light and dark behavior records were analyzed using Tracker software. After 24 hours, all mussels, both adults and juveniles, were found attached to the Petri dishes which they were subjected to during the scotophase and photophase. A repeated measures ANOVA was used to evaluate differences in rotation between the life stages of the golden mussel during the photophase and scotophase. A significant difference ($P = 0.027094$, $P < 0.05$) was observed in the photophase between juveniles and adults: juveniles exhibited greater rotation compared to adults. However, adult rotations were similar between the light and dark periods. The speed analysis did not indicate significant differences between juveniles and adults, which showed similar speeds during the scotophase and photophase. Although adults exhibited a tendency towards slightly lower speeds than juveniles, this difference did not reach statistical significance. The displacement analysis also did not indicate significant differences between juveniles and adults, which showed similar displacements during the scotophase and photophase. Although golden mussels exhibited a tendency towards greater displacement in the photophase than in the scotophase, this difference also did not reach significance. This study revealed that juvenile golden mussels exhibit greater rotation in the presence of light, while adults maintain constant rotation patterns. Speed and distance traveled did not show significant differences between light and dark phases, suggesting that locomotor activity is more related to substrate searching than to illumination. The fixation observed highlights the species adaptability, reinforcing the need for management strategies that consider the circadian behavior of the golden mussel.

Funding Source: Fundação de Amparo à Pesquisa do Estado de Minas Gerais – Fapemig.

COLLECTIONS

Collections

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CEPHALOPOD COLLECTION OF THE "MUSEU DE ZOOLOGIA DA UNIVERSIDADE DE SÃO PAULO" (MZUSP)

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Keywords: cephalopod diversity, faunal inventory, safeguarding, museums collections, Cephalopoda.

The malacological collection at the Museu de Zoologia da Universidade de São Paulo (MZUSP) began in 1880s with around 2,000 specimens, including six cephalopods, primarily cuttlefish fragmatocones, brought from Europe by Ihering. Since then, the collection has been curated by six prominent malacologists. Over the years, the collection has grown significantly, eventually becoming the largest malacological collection in Latin America in terms both, specimen numbers and lots. In recent years the collection has been fully computerized and is accessible via a platform called Specify. The cephalopod data from the collection was entered into Specify and subsequently transferred to an Excel spreadsheet for analysis. The number of lots in the cephalopod collection has been compared across orders, families, and the countries, regions, and states within Brazil Where the specimens were collected. The MZUSP cephalopod collection is the largest collection of its kind in Brazil, containing 1,015 lots, which include specimens, shells, suckers, beaks, and eggs. The collection also houses seven lots of type material, which include three paratypes from the squid *Doryteuthis sanpaulensis*, two paratypes and the holotype of the octopus *Eledone massyae*, and one paratype of *E. gaucha*. The collection represents three subclasses: Coleoidea, Ammonoidea, and Nautiloidea, with 973, 27, and 15 lots, respectively. Among the orders in Coleoidea, those most associated with coastal waters—such as the squids of Myopsida and benthic octopods (Octopoda)—are most prominent, with 332 and 302 lots, respectively. These are followed by Oegopsida (117 lots), Spirulida (96 lots, shells), Sepiolida (95 lots), Sepiida (28 lots, shells), and the extinct Belemnitida (3 lots). The Oegopsida and Octopoda orders exhibit the greatest diversity in terms of families represented. Oegopsida includes 12 families, with the most abundant being Ommastrephidae (46 lots), Pholidoteuthidae (17 lots), and Enoploteuthidae (17 lots). The octopods are represented by seven families, with the most numerous being Octopodidae (157 lots), Argonautidae (76 lots), and Eledonidae (53 lots). Although Brazil is the primary country of origin for the specimens (737 lots), the MZUSP cephalopod collection also contains specimens from 30 other countries. Within Brazil, the Southeastern (332 lots) and Northeastern (160 lots) regions are most represented, particularly from the states of São Paulo (220 lots) and Bahia (93 lots). The cephalopod collection at MZUSP is a valuable resource, offering a diverse representation of cephalopods from around the world, with a particular emphasis on Brazil. It remains an important repository in South America and continues to be a relevant collection for taxonomic and distributional studies.

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GASTROPOD TYPE SPECIMENS IN THE UNIVERSITY OF MICHIGAN MUSEUM OF ZOOLOGY (UMMZ)

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Keywords: UMMZ, type, Gastropoda.

The UMMZ Mollusk Collection has long ranked among the most important freshwater and land snail collections in North America, noted especially for its excellent taxonomic and geographic coverage, relative age, and type collection. To make the collection more accessible to the broader scientific community, we have reviewed and compiled a list of our gastropod type holdings. A comprehensive, though by no means exhaustive, list of annotated type specimens was entered into the UMMZ Specify database. Where possible, the type status of each specimen was verified using the original publication, and its systematic arrangement and current valid combinations were updated to conform with MolluscaBase. In addition, the following metadata have been linked to voucher specimens: scanned copies of original descriptions (where available), photographs of the specimens and their labels, their acquisition records, and their sampling localities taken from the labels and/or the original descriptions (georeferenced where possible). This work-in-progress currently enumerates 2,806 type lots, including 449 holotypes (including 102 subspecies and 13 questionable lots), 6 lectotypes, 1,010 syntypes, and 1,108 paratypes. A total of 5,089 image files (photographs and scans) have been directly attached to the specimen records. The freshwater family Planorbidae is the most represented, with 178 lots, followed by another freshwater family, Pleuroceridae (144 lots), and then the land snail families Polygyridae (103 lots) and Helicidae (102 lots). UMMZ holdings contain a significant number of holotype lots of taxa described by F. C. Baker, H. B. Baker, L. Hubricht, A. Solem, F. G. Thompson, D. W. Taylor, and B. Walker. Nearly 1,000 lots are from the United States (915 lots), followed by Australia (188 lots), Guatemala (158 lots), Mexico (138 lots), and South Africa (111 lots). The type status of numerous lots still requires close examination by specialists – e.g., more than 300 lots of small land snails (many belonging to the families Charopidae, Diplommatinidae, Microcystidae, Punctidae and Urocyclidae) collected from Norfolk and Lord Howe Islands by H. B. Preston. All type material belonging to the class Gastropoda in the UMMZ Mollusk Division has been reviewed and digitized into the Specify database. These data and images will soon be available through Symbiota web portals (InvertEbase.org and PILSBRy.org), national resources (GBIF.org, iDigBio.org) and the University of Michigan Digital Library (lib.umich.edu/collections/digital-collections).

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INCREASING ROCKY MOUNTAIN AND GREAT PLAINS REGION INVERTEBRATE REPRESENTATION IN DIGITAL NATURAL HISTORY COLLECTION DATABASES

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Keywords: Natural History Collections, invertebrates, digitization, Western United States, Rockies and Great Plains.

Partnering with the InvertEBase TCN, the University of Colorado Museum of Natural History (UCM) augmented existing taxonomic and geographic digital representations of Western North American invertebrates from the Rocky Mountain and the Great Plains regions of Colorado through a 4-year-long digitization effort. Focusing on four key phyla – Mollusca, Arthropoda, Porifera, and Annelida – images of type specimens, mounted historical slides and exemplar specimens of regionally significant taxa were prioritized. In this project, we accessioned, cataloged, georeferenced, and mobilized the focal specimen lot records onto our Specify 6.8 database. Images of specimens were taken via focus stacking using Helicon Focus. Mounted microscope slide specimens were scanned using a whole slide imaging scanner. Upon completion of the grant work, UCM invertebrate zoology data will be published to the InvertEBase, iDigBio, and Symbiota Collections of Arthropods (SCAN) portals. UCM digitized and mobilized 64,526 specimen lot records, georeferenced 9,531 lots and digitally imaged 287 type lots, > 1,000 exemplar specimens of significant taxa and approximately 200 historical microscopic slides, exceeding 100% of our total digitization and georeferencing goals. The UCM invertebrate zoology recently acquired additional collections of regional freshwater and terrestrial (including pitfall trapped) non-insect taxa and expanded our Colorado freshwater sponge and leech collections to be the largest in the Great Plains region. The project has increased the digital coverage of four important invertebrate phyla in the Western United States by 7852%. This newly added geographical focus is important because the burgeoning human populations in the Western US is drastically altering associated natural environments, calling for urgent and better assessments of ecosystem change through time. Historical museum collections are ideal for reconstructions of community distribution patterns over time to quantify anthropogenic impacts on biodiversity. The UCM collections date back to the early 1900s and researchers, often frequenting similar localities, have been continually collecting specimens throughout this century of human population growth. Digitizing these invertebrate phyla will reveal information about invertebrate community shifts, population dynamics, and isolated or rare taxa from the Rocky Mountains and Great Plains, which may subsequently inform biodiversity monitoring and management policies. A digitized and mobilized collection will promote progress in diverse and important research areas that are impacted by anthropogenic environmental disturbances, including invertebrate-mediated parasite transmission, and invertebrate microbial symbiont communities. The NSF PEN Digitization grant allowed dark data from the UCM Invertebrate Zoology collection to be mobilized and made available to researchers, land managers, and the general public. Hopefully, the distribution of this data will greatly improve our understanding of these significant and sensitive invertebrate groups in Colorado.

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REDISCOVERING HISTORICAL TYPE AND FIGURED FOSSIL SPECIMENS IN GREEK COLLECTIONS THROUGH THE DISSCO INFRASTRUCTURE

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Keywords: molluscs, type specimen, museum collection, Neogene.

The digitisation of historical fossil collections is critical for advancing taxonomic and biodiversity research. Within the "SUB4 Digitisation of Greek Natural History Collections" project, included in the European DiSSCo initiative, we examined the paleontological collections of the Museum of Geology and Paleontology of the National and Kapodistrian University of Athens. Our aim was to recover and digitize type and figured specimens while implementing international FAIR principles (Findable, Accessible, Interoperable, Reusable). Our work focused on fossil collections of Adolf Papp (1953), Sarantis N. Charalambakis (1948), and Panagiotis S. Psarianos (1940), covering both marine and lacustrine deposits. Specimens were reviewed, photographed, and catalogued using a collection management system based on Darwin Core standards. Digital imaging was conducted according to SUB4 protocols, including high-resolution photography. All digital files were marked with persistent identifiers and QR codes, ensuring metadata traceability and alignment with FAIR principles. This allowed for seamless integration into DiSSCo's infrastructure and enhanced discoverability across digital platforms. We identified several significant Type and Figured specimens across the under-digitized fossil collections of Athens, Greece. Some key species include *Ostrea iphigeniae* Charalambakis, 1948 and *Lithophaga mitzopoulosi* (Charalambakis, 1948) from Pliocene marine deposits in Attica; *Melanopsis costatiformis* A. Papp, 1953 and *Melanopsis scalaritesta* A. Papp, 1953 from the Plio-Pleistocene lacustrine deposits of Western Peloponnese; and *Viviparus mitzopoulosi* Psarianos, 1953 from the Plio-Pleistocene deposits of Patras in Peloponnese. These specimens had not previously been digitally catalogued or made accessible for research. Their digitisation now allows for improved taxonomic resolution, supports reproducible research, and enhances data interoperability across institutions. The use of standardized formats, controlled vocabularies, and persistent identifiers ensures long-term usability and integration into global databases. The rediscovery process also highlighted the value of legacy collections and their potential to contribute to contemporary scientific inquiries, such as paleoenvironments, species distribution shifts, and evolutionary dynamics. This work illustrates the necessity of systematic digitisation efforts, particularly in regions with rich but previously inaccessible paleontological resources. By applying DiSSCo and SUB4 protocols, we successfully digitised and integrated historically significant type specimens from Greek fossil collections. These efforts not only preserve scientific heritage but also empower collaborative research through FAIR data practices. The project demonstrates how local paleontological collections, when made accessible through digital infrastructures, can contribute meaningfully to understanding past biodiversity, evolutionary processes, and long-term ecological change.

Funding Source: This work was supported by the SUB4 Digitisation of Greek Natural History Collections project and the DiSSCo Research Infrastructure.

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THE MALACOLOGICAL COLLECTION OF THE CENTER FOR TAXONOMIC COLLECTIONS AT THE FEDERAL UNIVERSITY OF MINAS GERAIS: A REVIEW

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Keywords: conservation, systematics, biodiversity.

The Malacological Collection of the Center for Taxonomic Collections at UFMG (CCT-UFMG) houses a wide variety of mollusks of medical and environmental importance, representing Brazil's malacofaunal diversity. Its holdings support scientific research and studies in systematics, molecular phylogeny, and genetics. Given the need for constant maintenance, this study aimed to improve material conservation through formal cataloging and data organization into spreadsheets. The animals were sorted and stored, with the shells preserved in dry storage and the soft parts preserved in wet storage. For dry preservation, the material was placed in acrylic containers lined with layers of cotton or stored in zip-lock bags to prevent deterioration. For wet preservation, tissues were fixed in 70% alcohol and kept in amber glass bottles. Each specimen was assigned a catalog number, and its data were recorded on labels placed inside each container and later entered into a spreadsheet corresponding to the collection's database. Lots were stored in separate cabinets (dry and wet), and are periodically inspected for fixative replacement. A total of 5,677 lots of mollusks were properly preserved, stored, and had their information entered into the database. The collection includes specimens from the classes Gastropoda (4,369), Bivalvia (872), Polyplacophora (22), and Scaphopoda (2). Gastropoda stands out, particularly due to the large representation of the genus *Omalonyx*, comprising approximately 1,307 lots. Other representative genera include *Biomphalaria* (1,123), *Physa* (502), *Onchidella* (436), *Melanoides* (136), and *Lymnaea* (91), as well as specimens from other genera such as *Chilina*, *Succinea*, *Pomacea*, *Drymaeus*, *Thaumastus*, and *Achatina*. The collection also receives materials donated by collaborators from other countries; thus, the holdings include specimens from Argentina (179), the Caribbean (74), French Guiana (57), Venezuela (57), Japan (31), Paraguay (26), United States (16), China (15), France (15), and Cuba (4). Nevertheless, approximately 4,804 samples are native to Brazil, highlighting the collection's relevance to the conservation of local biodiversity. Through the activities carried out in this study, it was possible to ensure that the collection is in suitable condition to fulfill its potential for research, teaching, and outreach activities. It is therefore concluded that the Malacological Collection of CCT-UFMG is a rich repository of information on malacofauna, playing a crucial role in the study of natural history, biodiversity conservation, and medical-sanitary and environmental research.

Funding Source: PRPQ. PROEX. MEC (PET).

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CATALOGUE OF TERRESTRIAL GASTROPODS (MOLLUSCA: GASTROPODA) FROM THE MUSEU DE HISTÓRIA NATURAL DO CEARÁ PROF. DIAS DA ROCHA (MHNCE-UECE)

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Keywords: terrestrial gastropods, biological collection, Brazilian northeast, Ceará.

Malacological collections are essential tools for understanding biodiversity, as they allow for the preservation and access to specimens, providing information about the natural history of these animals. Gastropoda is the most diverse molluscan class and includes 748 species in Brazil, being the only one to colonize terrestrial environments. This study aims to catalog the gastropod species deposited in the MHNCE malacological collection. To achieve this, data from each specimen recorded in the inventory spreadsheet of the Malacological Collection at the Museu de História Natural do Ceará Prof. Dias da Rocha were selected and organized to build a database containing taxonomic information of the deposited terrestrial gastropods. Based on this data, the richness and abundance of the species were calculated, as well as the locations and collection periods of the specimens. The results revealed 88 lots of terrestrial gastropods, totaling 277 specimens belonging to 3 orders, 17 families, 30 genera, and 41 species. The collection includes specimens from 12 municipalities of Ceará, with 5 from the Maciço de Baturité, a mountainous region where the museum is located. In the order Cycloneritida, usually marine, there is one terrestrial arboreal species, *Helicina schereri* (n=4), from the family Helicinidae. In Systellommatophora, native slugs with no shell and cutaneous respiration, there is one specimen of the genus *Sarasinula*, family Veronicellidae. The order Stylommatophora, which includes most land snails and slugs, is represented by 15 families. Among these, Achatinidae had the highest number of specimens (n=120), including six species, two of which are non-native: *Lissachatina fulica* (n=17) and *Subulina octona* (n=46). Tomogeridae, widely distributed in Northeast Brazil, had the highest richness (n=6), with abundant genera like *Tomigerus* (n=39) and rarer ones like *Biotocus* (n=2). The collection also includes endemic species from Ceará such as *Streptartemon cf. quixadaensis* (n=4, Streptaxidae), *Solaropsis cearana* (n=3, Solaropsidae) and *Bahiensis ciaranus* (n=1, Cyclodontinidae). This study made it possible to quantify the diversity of terrestrial gastropods deposited in the Malacological Collection of the Museu de História Natural do Ceará Prof. Dias da Rocha, highlighting its importance for understanding the molluscs diversity of the state of Ceará and the conservation of these species.

Funding Source: We would like to thank the Museu de História Natural do Ceará Prof. Dias da Rocha (MHNCE) at the Universidade Estadual do Ceará (UECE) for providing structural support for this work. I am also grateful to the Programa de Pós-Graduação em Sistemática, Uso e Conservação da Biodiversidade (PPGSIS) at the Universidade Federal do Ceará (UFC), Fundação Cearense de Apoio ao Desenvolvimento Científico e Tecnológico (FUNCAP), and to the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), under the Ministério da Educação (MEC) of the Governo Federal do Brasil, for their financial support.

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UNCOVERING HIDDEN GEMS: REORGANIZING THE BAHIA NATURAL HISTORY MUSEUM'S DRY MOLLUSK COLLECTION

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Keywords: mollusk biodiversity, taxonomic validation, natural history collections.

The lack of resources and the decline in taxonomists severely impact global biodiversity research and conservation efforts. This study focuses on revitalizing the Mollusk Collection at the Bahia Natural History Museum by reorganizing the physical collection, digitizing it, and conducting taxonomic validation of the specimens collected since 1962. The collection data were retrieved from the accession register of the Gastropoda and Bivalvia collections. A thorough verification was conducted, comparing the collection specimens with the register entries, checking the labels for each lot, and confirming the number of specimens per record. The data were then standardized and tabulated. Taxonomic validation was performed based on current specialized literature and online databases. Upon completion of this stage, the data were analyzed to identify the most representative families, collection periods, and locations for each accessioned item. The records reveal the existence of 935 lots of the Class Gastropoda and 578 lots of the Class Bivalvia. The gastropod collection encompasses 79 families. Among these, the families Muricidae (62 lots), Olividae (50), Naticidae (48), Turbinidae (47), Cypraeidae (43), Fissurellidae (43), and Bullidae (40) stand out. These specimens were collected between 1962 and 2000, along the Brazilian coast, particularly in Bahia, as well as in states from the Northeast, Southeast, and South regions, and also from the United States. Regarding the bivalve collection, it includes 31 families. The most numerous are Veneridae (139 lots), Arcidae (79), Lucinidae (50), Cardiidae (41), Tellinidae (35), and Mytilidae (34). The bivalve collection comprises specimens collected between 1965 and 2005, mostly from the Brazilian coast, particularly Bahia, but also includes lots from different regions of Northeast, Southeast, and South Brazil. The collection also contains specimens from Argentina, Chile, Uruguay, Spain, Italy, Greece, and New Zealand. The set of information from this collection documents the richness of mollusk biodiversity along the Brazilian coast, particularly in the state of Bahia. The reorganization of the collection has improved its management and conservation, sparking interest in its expansion. Preliminary data support the role of collections in understanding biodiversity, fostering scientific and technological advancements. It also contributes to the training of new taxonomists, encouraging undergraduate and graduate students to pursue careers in Malacology in the state of Bahia.

Funding Source: No.

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ANALYZING PREDATION PATTERNS ON DREDGED ARCIDAE BIVALVE SHELLS IN NORTHEASTERN BRAZIL BY CARNIVOROUS GASTROPODS

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Keywords: Naticidae, Muricidae, dredgins, marine ecology, radula.

This study examines shell predation by malacophagous gastropods, primarily from the Naticidae and Muricidae families, key players in marine ecosystems. These predators bore holes into shells using radula and accessory boring organ (ABO) to consume the inner organisms. The selection of boring sites varies; some gastropods show no preference, while others choose sites likely based on how the prey is held. Boring over the gonadal region may maximize energy gain. The mollusk collection at the Universidade Federal Rural do Semi-Árido in Brazil began in the 1970s, featuring a diverse assortment of native and exotic species. This collection includes specimens dredged during expeditions, notably by the vessels Akaroa, Canopus, and NOc Almirante Saldanha in the 1960s off Sergipe's coast. These specimens are preserved in UFERSA's Malacological Collection. Specifically, lots containing Arcidae family individuals were studied, with predated samples separated and quantified. The perforations, typically made by muricid and naticid gastropods, feature smooth walls, decreasing diameter with depth, and usually circular or elliptical shapes. Predation was evaluated based on drilling site location: dorsal-anterior, dorsal-posterior, ventral-anterior and ventral-posterior quadrants following. Ninety-two marine bivalve lots from the Arcidae family, collected by the Akaroa, were analyzed, totaling 277 specimens, with 13% showing boring marks. Species with predation marks included *Anadara chemnitzi*, *Anadara notabilis*, *Anadara secernenda*, *Barbatia domingensis*, *Fugleria tenera*, *Lunarca ovalis*, *Lamarcka ventricosa*, *Lamarcka imbricata*, and *Paranadara taludae*. These specimens had shells only, lacking soft parts. This family typically inhabits intertidal zones and can be found in various substrates, making them vulnerable to gastropod predation. Only three species showed no predation signs: *A. secernenda*, *F. tenera*, and *L. imbricata*. Predation marks appeared in two types: circular holes with uncut margins and elliptical or semi-elliptical with sharply cut margins. Analysis showed that 70% of holes were on the dorsal side, with only 26% on the ventral area. Authors suggest this might be due to predators being conditioned to drill these areas for higher energy yields from the digestive gland. There were no significant differences between anterior and posterior sites. Holes in the umbonal region of valves were frequent, occurring in about 40% of cases, though the ventral region is thinner. In all bivalve shells, the dorsal margin was most frequently perforated, aligning with the visceral mass's location for possibly greater nutritional gain. It is clear that multiple taxonomic groups contributed to Arcidae predation, with perforations often by Naticidae and Muricidae family members, depending on whether the prey was sediment-buried or epifaunal.

Funding Source: No.

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CURATORSHIP AND TAXONOMIC REVISION OF FOSSIL MOLLUSKS OF THE MALACOLOGICAL COLLECTION MAURY PINTO DE OLIVEIRA, BRAZIL

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Keywords: taxonomic review, collection, fossil mollusks.

Established in 1967, the Prof. Maury Pinto de Oliveira Malacology Museum - MMPMPO - houses one of Brazil's most important malacological collections, comprising over 15,000 lots and over 1 million specimens, including both recent and fossil species worldwide. We aimed to review the taxonomic identification and taxonomic status of fossil representatives and to make available species distributional data, contributing to a broader understanding of the biodiversity represented in this collection. All lots of fossil mollusks in the CMMPO were examined, and the information associated with the specimens were compiled. Taxonomic identification was carried out through morphological comparisons based on diagnostic criteria described in specialized taxonomic literature, prioritizing original species descriptions and systematic revisions. Nomenclatural updates adhered to the rules set forth by the International Code of Zoological Nomenclature (ICZN) and were supported by online databases such as the World Register of Marine Species (WoRMS, 2025) for validation of names and synonymies. This study is part of sustained efforts to update the taxonomic classification of the specimens present in the MMPMPO collection, initiated in 2014, when a decade-long period without formal curatorship came to an end. We reviewed the taxonomic identification of 28 species, including 17 gastropods and one bivalve, distributed among the following taxa: *Streptaxis intermedius* (Eupulmonata, Streptaxidae) (7 specimens); *Rhinus heterotrichus* (Eupulmonata, Simpulopsidae) (3); *Thaumastus magnificus othoni* † (Eupulmonata, Megaspiridae) (2); *Cyclodontina coelhoi* (Eupulmonata, Cyclodontinidae) (1); *Bulimulus trindadeae* † (Eupulmonata, Bulimulidae) (1); *Brasilennea minor* † (1), *Brasilennea arethusae* † (Eupulmonata, Cerionidae) (4); *Eoborus sanctijosephi* † (4), *Eoborus cf. sanctijosephi* † (1), *Eoborus rotundus* † (5), *Eoborus fusiformis* † (Eupulmonata, Strophocheilidae) (2); 5 fragments of *Polygyratia polygyrata* (Eupulmonata, Scolodontidae); *Planorbella duryi* (Higrophyla, Planorbidae) (2); *Tylostoma crandalli* † (Caenogastropoda incerta sedis, Tylostomatidae †) (1); *Crommium acutum* † (Caenogastropoda incerta sedis, Ampullinidae) (4); *Tritia clathrata* † (Neogastropoda, Nassariidae) (3); *Clavilithes* cf. *noae* † (3), *Clavilithes* sp. (Neogastropoda incerta sedis Clavilithidae †) (3); *Pinzonella illusa* † (Megalodontidae †) (9). Two gastropods, three bivalves, and five ammonites remained unidentified, with two ammonites determined only to the family level (Ataxioceratidae † and Vascoceratidae †). Among the recorded species, 17 belong to extinct lineages known exclusively from fossil records. The geographic origin of the fossils includes Brazil, the United States, France, and Italy, with specimens derived from key sedimentary basins such as São José de Itaboraí (Paleocene), Paraná (Corumbataí Formation, Late Permian–Early Triassic), Potiguar (Upper Cretaceous), Sergipe (Cotinguiba Formation, Cenomanian–Turonian), and Paris (Paris Formation, Lutetian). Three specimens still lack identification, two are currently classified only to family level, and eight are pending further review. Studies of this nature are crucial for museological curatorship, providing foundation for future paleontological research, besides studies in taxonomy, ecology, and conservation. Our results emphasize the significance of small collections, which despite being located outside major research centers, can substantially contribute to taxonomic advancement and to a deeper understanding of biodiversity.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

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SMALL BIOLOGICAL COLLECTIONS AND BIODIVERSITY: LYMNAEIDAE IN THE MAURY PINTO DE OLIVEIRA MALACOLOGICAL COLLECTION, BRAZIL

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Keywords: malacological collections, lymnaeids, CMMPO.

The Maury Pinto de Oliveira Malacological Collection is one of the most expressive in Brazil, both taxonomically and geographically, housing over 1 million specimens of mollusks from various groups, including the family Lymnaeidae Rafinesque, 1815. Lymnaeids hold significant economic, medical, and veterinary importance, as they act as intermediate hosts of *Fasciola hepatica* Linnaeus, 1758, agent of fasciolosis. This study aims to review the Lymnaeidae species present in the CMMPO. All lots of Lymnaeidae in the CMMPO were examined, and the information associated with the specimens were compiled. The taxonomic identification and status of all the species were checked. The information assembled included accession number, species attribution on the original record, updated taxonomic classification including species, genus and family, collection date, collection locality, collector, links to MolluscaBase and the species original description paper, number of specimens, and preservation method. Species representativeness in collections worldwide was assessed through searches in the Global Biodiversity Heritage Library, using species names and the filters. We recorded 31 lots representing 12 different species, including *Ampullaceana balthica* Linnaeus, 1758 (3 specimens), *Bulastra lessoni* Deshayes, 1831 (1), *Galba truncatula* O. F. Müller, 1774 (2), *Ladislavella catascopium* Say, 1817 (1), *Ladislavella emarginata* Say, 1821 (1), *Lymnaea stagnalis* Linnaeus, 1758 (4), *Omphiscola glabra* O. F. Müller, 1774 (1), *Peregriana peregra* O. F. Müller, 1774 (4), *Pseudosuccinea columella* Say, 1817 (5), *Radix auricularia* Linnaeus, 1758 (3), *Stagnicola corvus* Gmelin, 1791 (1) and *Stagnicola palustris* O. F. Müller, 1774 (5). From the 171 specimens examined, most were represented by dry-preserved shells. Only one specimen presented both the shell and body preserved in ethanol. The Lymnaeidae collection is geographically diverse, with specimens from Europe, North America, and Oceania. The lots originate from Romania (7), Belgium (4), Germany (2), USA (3), Austria (1), Spain (1), Italy (1), Netherlands (1), Canada (1), and Australia (1). Those lots were donated by researchers from all over the world, with significant contributions from prominent figures such as the Romanian Alexandru Grossu, the Belgian Richard Van Belle and the American Willian Old Jr., reflecting the scientific exchange promoted by Prof. Maury Pinto de Oliveira. Only four lots were collected in Brazil, three in Juiz de Fora, MG (where the museum is based) and one in Piúma, ES. All representing *Pseudosuccinea columella*, the most common and widespread lymnaeid species in the South and Southeast regions of the country. Additionally, five lots lacked collector information and came from Belgium (2), Canada (1), and Brazil (2). This study reviewed the Lymnaeidae species in the CMMPO, highlighting the importance of small biological collections and their potential contribution to biodiversity knowledge. The exchange conducted by Prof. Maury Pinto de Oliveira with malacologists from around the world has significantly enriched the collection, enhancing its role in biodiversity research and underscoring the importance of international collaboration.

Funding Source: No.

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MALACOLOGICAL COLLECTION - STATE UNIVERSITY OF PONTA GROSSA, PR, BRAZIL

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Keywords: collection, mollusk, Campos Gerais of Paraná.

The malacological collection housed at the Zoology Laboratory of the State University of Ponta Grossa (UEPG), Paraná, comprises specimens preserved by both dry and wet methods. This collection is associated with the Research Line in Ecology and Biology of Mollusks at the institution above. In 2016, the collection received material from a private donation, bringing the total to approximately 9,000 specimens, representing all classes of the phylum Mollusca. The collection is organized into two components: a didactic collection and a scientific collection. Currently, it comprises around 12,000 specimens. The mollusk collection includes an archive of 304 bibliographic records, including books, manuals, and manuscripts covering taxonomy, ecology, phylogeny, and paleontology. This library features descriptions and citations from leading malacologists in Brazil and other parts of the world. The collection aims to contribute to human development through research projects, including undergraduate scientific initiation, final course projects, master's, and doctoral studies. Another important aspect is the use of this collection to foster the exchange of material and knowledge among researchers from various national and international institutions. This interaction is currently being conducted through lectures, workshops, and extension courses that utilize the deposited material, addressing topics such as the diagnostic characteristics of bivalves and gastropods, distribution, conservation, taxonomy, and ecology. Plans include exchanging specimens with other institutions and collaborating with leading malacologists to develop advanced courses in the Campos Gerais region and to establish a mollusk research center in southern Brazil. In terms of outreach, the collection also contributes to the dissemination of information, particularly to elementary and high school students and the broader community. This knowledge is shared through lectures and exhibitions held in schools in Ponta Grossa, Curitiba, and other regions of Paraná, where students have the opportunity to learn about shell diversity from around the world, the significance of the phylum Mollusca, the morphological characteristics and distinctions of these organisms, and their economic importance. This collection represents a significant asset for the Campos Gerais region of Paraná, as it contributes to the training of students. The shells can be utilized in scientific research and extension programs across various fields, including biology, History, Geography, Ecology, and Mathematics. As such, the collection and the professionals associated with it form a new hub of invertebrate specialists with an integrated approach to research, teaching, and education.

Funding Source: No.

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THE MALACOLOGICAL COLLECTION OF UERJ (COL. MOL. UERJ): A RICH AND THEMATIC ARCHIVE

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Keywords: curatorship, scientific collection, malacology.

Zoological Collections are important repositories and testimonies for the understanding of biodiversity. The UERJ Mollusk Collection (Col. Mol. UERJ) began to be formed in 1989. Today, it has 12,674 listed lots (marine, terrestrial and freshwater). The collection has been used to subsidize lines of research in Systematics and Taxonomy, favoring the preparation of undergraduate and specialization monographs, dissertations, theses and article publications. After receiving the lots accompanied by an identification form, the curatorship is carried out through sorting, cleaning, prior identification and taxonomic organization. Shells are preserved dry; soft tissues in 70% alcohol or Railliet-Henry, for dissection; more recently, in 96% alcohol due to the adoption of Molecular Biology techniques. In parallel, a bank of tissues is being organized, fixed in 96% alcohol and frozen. Curatorship involves the routine replacement of fasteners, the making of labels and bureaucratic procedures for sending and receiving loans and/or donations for research, analysis or identification purposes. Constantly, new samples are registered in the Catalogue Book, whose digitization is still in progress. The Malacological Collection of the State University of Rio de Janeiro (Col.Mol.UERJ) currently comprises 12,674 registered samples, totaling more than 100,000 specimens, including shells, soft tissues and tissues for molecular analysis. Gastropoda has the highest representativeness, with 10,762 lots, of which 6,295 (57.3%) come from Ilha Grande, Angra dos Reis, RJ, reinforcing its thematic character. The collection focuses on material from the Atlantic Forest Biome, with more than 10,000 lots from the State of Rio de Janeiro, about 70% of which are from Ilha Grande, where the Center for Environmental Studies and Sustainable Development (CEADS) is located, a fundamental infrastructure for the development of research in systematics, phylogeny and biogeography. To maintain this collection, in a time frame of one year, the replacement of fasteners of 3,531 lots and inclusion of 308 cataloged lots was carried out, as well as digitization of 586 lots. The collection provided the preparation of about 20 monographs, 10 dissertations, seven theses; now, four graduate studies at UERJ and other institutions are in progress. Considering the growing threats to the Atlantic Forest, such as deforestation, urban expansion and fires, added to the impacts of climate change, the collection assumes a strategic role. It is a repository of historical and contemporary data, which subsidizes not only taxonomic studies, but also investigations on changes in the composition of malacological communities in the face of ongoing environmental transformations. Despite the importance of COl.Mol.UERJ, advances in the discussions on the institutionalization of UERJ's Scientific Collections, concrete efforts are still needed for its recognition as institutional heritage, as recommended by PPBio. This is essential to ensure continuity, adequate infrastructure, specialized staff, and resource allocation. The maintenance of the collection is an act of respect for the data obtained, and a fundamental action to subsidize future projects.

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CURATORSHIP AND TAXONOMIC REVISION OF STROPHOCHEILIDAE FROM THE MALACOLOGICAL COLLECTION MAURY PINTO DE OLIVEIRA, BRAZIL

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Keywords: scientific initiation, backlog, biological collections, land snails.

The Malacological Museum Prof. Maury Pinto de Oliveira houses one of the most expressive collections of molluscs in Brazil. However, for many groups, there are lots that have not been reviewed in decades. The present work involved the curatorship, taxonomic revision and inclusion of new lots from the backlog, contributing to the expansion of the number of specimens of Strophocheillidae, as well as the taxonomic and geographic representativeness of this family, in the collection. Herein, we present the main impacts of the development of a scientific initiation project aimed at the curatorship and taxonomic revision of the specimens of Strophocheilidae deposited in the MMPMO collection, as well as the backlog material. The methodology performed by an undergraduate student, included the review of the taxonomic attributions of the specimens, the taxonomic attribution of unidentified specimens, reconditioning of the specimens in containers and casings suitable for their conservation, inclusion of records written in India ink in addition to the original files (often damaged) and image acquisition of all specimens. The development of this scientific initiation project allowed the compilation of unprecedented data on the occurrence of the analyzed species, which will allow the updating of the geographic distribution, directing efforts to the collection of species that have not been revisited since their description, as well as the accomplishment of ecological modeling studies. By carrying out these processes, the undergraduate student acquired knowledge about the curatorial processes in a biological collection and practical skills related to the work routine of a taxonomist. At the same time, the curatorial and taxonomic review work carried out by the student contributed to the safeguarding of the collection, its expansion, and ensured the reliability of the data associated with the specimens. The acquisition of images contributes to the digitization of the collection, an indispensable action for the integration of the collection into the digital age of biological collections. Thus, students who carry out scientific initiation projects around the collection constitute an invaluable workforce for the MMPMPO. The analysis of backlog material allowed the identification of ontogeny series of gastropod shells of the genus *Megalobulimus*, reared in the laboratory in past decades. The information associated with these specimens can be useful in studies on the development and life history of these species. The curatorial work, review of the taxonomic identifications, and taxonomic attribution of unidentified specimens has contributed to the expansion of the MMPMPO collection. In this process, we have discovered true gems such as this semi-fossil specimen of a species of the genus Megalobulimus. The training of young taxonomists and curators is essential in a scenario of biodiversity crisis. In addition, it is interesting that these young people are working on biological collections, since these may house species unknown to science, in addition to a large set of unpublished temporal and geographic data on the distribution of species, creating opportunities for scientific research.

Funding Source: No.

CONSERVATION

Conservation

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REVIEW ABOUT THE BIODIVERSITY OF PILL CLAMS (BIVALVIA, SPHAERIIDAE) IN THE CONFINES OF THE WORLD, THE ARGENTINEAN PATAGONIA

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Keywords: Bivalvia, freshwater, conservation, Patagonia, Sphaeriidae.

Sphaeriidae, also known as "pills," "peas," or "fingernail clams," are the smallest freshwater bivalves, with shells rarely exceeding 25 mm. Despite their small size, they are crucial in freshwater ecosystems, often being dominant in benthic communities and playing a key role in nutrient and energy cycling. This study aims to update the knowledge on Sphaeriidae diversity and distribution in Argentine Patagonia, particularly in Santa Cruz Province. Between 2015 and 2023, specimens were collected from various aquatic habitats, including rivers, lakes, lagoons, and wetlands, using both manual techniques and sieve-based methods. This fieldwork was complemented by a comprehensive literature review and an analysis of major malacological collections in Argentina. Geographic and taxonomic data were processed to create distribution maps using QGIS. Localities without geographic coordinates were georeferenced following established protocols. Species identification and classification were conducted based on the works of Ituarte and collaborators, utilizing updated dichotomous keys and a standardized taxonomic framework. A total of 121 records of the family Sphaeriidae were examined, comprising 74 records from malacological collections, 30 from bibliographic sources, and 17 from new field surveys. Of these records, 101 were identified to belong to the species level, 14 to the genus level, and six to the family level. We identified four species within the genus *Pisidium* and two species for the genus *Musculium*. *Pisidium magellanicum* and *Pisidium patagonicum* were the most frequently recorded, with 26 and 14 records, respectively. *Musculium patagonicum* had the broadest distribution range in Argentine Patagonia, extending from northern Neuquén Province to southern Tierra del Fuego Province. The Santa Cruz Province had the highest number of records (57), followed by Chubut with 24 records. The provinces with the fewest records were Río Negro (four) and Tierra del Fuego (11). The results of this study provide a comprehensive synthesis of the diversity and distribution patterns of Sphaeriidae species in the Argentine Patagonia (from 37° S to 56° S). The data collected through sampling address information gaps in the relatively underexplored region of southern Patagonia and update the known distribution ranges of the identified species. This study synthesizes Sphaeriidae diversity and distribution in Argentine Patagonia, identifying six species. *Pisidium magellanicum* and *Musculium patagonicum* have the widest distributions, with Santa Cruz Province showing the most records. The discovery of *Pisidium chilense* in Neuquén highlights the need for ongoing surveys. Updated identification keys have improved taxonomic accuracy. Species face conservation threats from habitat degradation, invasive species, and climate change, posing risks to regional ecosystems.

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BIOGEOGRAPHIC REGIONS OF ARGENTINA BASED ON THE PRESENCE OF FRESHWATER BIVALVES

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Keywords: biogeography, conservation, Unionida, Sphaeriida, Venerida.

Freshwater bivalves are vital components of biodiversity in continental aquatic ecosystems, playing essential roles in water filtration, sediment stabilization, and nutrient cycling. Despite being one of the most threatened animal groups, their distribution patterns in South America are still poorly understood. Argentina supports over 60 recorded freshwater bivalve species across various aquatic environments. This study presents preliminary results aimed at establishing a biogeographic framework for freshwater bivalves in Argentina. We compiled 3789 georeferenced records from malacological collections, scientific literature, and recent field surveys. A 20 km buffer was applied around each presence point to estimate species' areas of occupancy. Using this data, we generated a presence/absence matrix for each hydrographic basin and performed multivariate analyses with the Kulczinski similarity index and Hierarchical Agglomerative Clustering. Cluster significance was assessed using ANOSIM, and species contributions to group similarity were analyzed through SIMPER. This study identified five major biogeographic groups of freshwater bivalves corresponding to Argentina's main drainage systems: (1) the Plata Basins, (2) the Patagonian Basins, (3) the Northwestern Region, (4) the Cuyo Region along with the Colorado and Negro Basins, and (5) the Central and Southern areas of Buenos Aires Province. ANOSIM results revealed statistically significant differences among these groups, indicating well-structured faunal assemblages. SIMPER analysis determined the species contributing most to the similarities within each biogeographic group. Group (1) was mainly represented by *Anodontites trapesialis*, *A. patagonicus*, *Castalia inflata*, and *Rhipidodonta charruana*. Group (2) included *Musculium patagonicum*, *Pisidium magellanicum*, and *P. patagonicum*. In group (3), the most representative species were *P. chicha*, *P. ocloya*, and *P. omaguaca*, while group (4) featured *P. chiquitanum* and *A. patagonicus*. Group (5) was characterized by *Musculium argentinum*, *A. trapesialis*, and *Diplodon delodontus*. These findings emphasize the role of drainage basins as biogeographic barriers and reflect distinct patterns of species composition among regions. When compared to biogeographic models proposed for Argentine freshwater gastropods—which recognize eight malacological provinces—our results suggest that freshwater bivalves exhibit broader and more cohesive distribution patterns. This contrast highlights the importance of using taxon-specific approaches in biogeographic studies and suggests that bivalves may respond differently to historical and ecological drivers shaping regional biodiversity. Overall, our study provides new insights into the biogeography of South American freshwater bivalves and offers a baseline for future research and conservation efforts focused on this understudied group. These findings provide an initial framework for understanding the spatial distribution of freshwater bivalves in Argentina, offering a basis for future biodiversity surveys, conservation prioritization, and evidence-based policy development. Ongoing efforts focus on identifying undetermined specimens to refine and enhance the resolution of these biogeographic patterns.

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DISTRIBUTION AND CONSERVATION OF THE GENUS *Mycetopoda* (BIVALVIA: MYCETOPODIDAE): ENVIRONMENTAL PREFERENCES AND PROTECTED AREA EFFECTIVENESS FOR SPECIES CONSERVANCY IN SOUTH AMERICA

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Keywords: *M. legumen*, *M. siliquosa*, *M. soleniformis*.

Freshwater bivalves are one of the biggest anthropic victims, however the absence of species basic information delays extinction risk estimations. *Mycetopoda* is the type genus of Mycetopodidae (Unionida) and is composed by tree species: *M. legumen*, *M. siliquosa* and *M. soleniformis*, to this day respectively classified as Endangered, Least Concern and Data Deficient. Therefore, this work examines its distribution pattern and conservation for the *Mycetopoda* genus, associated with environmental variables. Occurrence data were collected from online repositories, scientific collections, and literature, using only georeferenced records. Environmental variables, "The Freshwater Ecoregions of the World" and "The Terrestrial Ecoregions of the World", were used for distribution analysis. The collection year was used to evaluate species conservation and research evolution throughout the decades. For "World Protected Areas", only observations inside or within one kilometer were counted. *Mycetopoda siliquosa* represented more than a half of the observations, and showed a wide distribution with higher density in Argentina and Uruguay, with low preferences regarding environmental variables. *Mycetopoda legumen* exhibited tendencies for low altitudes, precipitation, and temperatures, restricted to the La Plata and Lagoa dos Patos basins. *Mycetopoda soleniformis* preferred higher altitudes and precipitation, associated with floodplains, and was separated into two main groups, one near the Peruvian and Bolivian Andes and the other following the Paraguay River. Concerning the Freshwater Ecoregions, the three species only coexisted in three regions: Paraguay, Lower Paraná, and Lower Uruguay. All species exhibited significant aggregation behavior and preference for low-slope terrain. Most dated occurrences were around the 1980s, probably due to the flourish of Malacology in Brazil, Argentina and Uruguay; as also previously to the impact of invasive species. Only 22% of the observations were associated with a protected area. Half of *M. soleniformis* occurrences were close or inside protected areas, although with lower records, mapping gaps are possible. *Mycetopoda legumen* were mostly found outside protection, as its presence in places most used as fluvial pathways and harbours; *M. siliquosa* also had low protection percentage, with some records near the Amazonian forest within partial protection. In conclusion, *Mycetopoda* species showed unique environmental preferences, even though *M. siliquosa* showed higher adaptability. The genus showed a low protection rate for two species and, possibly incorrectly, a higher rate for *M. soleniformis*. These data represent a first effort to understand the distribution of *Mycetopoda* species in South America and are essential for future conservation and management actions.

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DIVERSITY AND DISTRIBUTION OF MYCETOPODIDAE (BIVALVIA: UNIONIDA) IN RÍO NEGRO BASIN (BRAZIL - URUGUAY)

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Keywords: freshwater mussels, conservation, *Anodontites*.

The freshwater bivalve family Mycetopodidae, endemic to the Neotropical region, comprises 53 species in 11 genera and is critically endangered. Given the number of records, existing knowledge, and the biogeographic significance of the Rio Negro Basin (RNB), this study analyzes the distribution of the family in the area. The results offer valuable information to support conservation and management efforts for these threatened freshwater mussels. The RNB is shared by Uruguay and Brazil, with a length of 750 km and a basin area of more than 73,000 km^2, is part of the Uruguay River Basin. For this study, collections from the FZB (Brazil), MACN and MLP (both in Argentina), and MNHN (Uruguay) were revised. Records obtained from recent surveys conducted between 2015 and 2024 were also included. Records from collections were considered as old data and from the recent surveys as new data. A data matrix was created that included lot number, specimen identification, location with geographic coordinates, Strahler Order of the river, collection date, and collectors. The data was analyzed using QGIS. A total of 494 records were obtained from 126 localities, of which 413 correspond to old data (1901 to 2014) and 81 to new data records (2015 to 2024). The localities were not evenly distributed, concentrated in the lower part of the RNB and at sub-basin of Yí River. A total of 12 species were recorded for RNB: *Anodontites ferrarisii*, *A. lucida*, *A. patagonica*, *A. trapesialis*, *A. trapezea*, *A. tenebricosa*, *Leila blainvilliana*, *Mycetopoda legumen*, *M. siliquosa*, *Monocondylaea corrientesensis*, *M. minuana* and *M. paraguayana*. The most distributed species were *A. trapesialis* and *A. patagonica*, with 129 and 91 records, respectively. In contrast, *L. blainvilliana* and *M. paraguayana* had the most restricted distributions, with 3 and 13 records, respectively. A comparison of new and old data highlights the absence of *M. paraguayana* in recent collections at RNB, and of *A. tenebricosa* upstream of the Rio Negro reservoirs. For the first time, the habitat preferences of Mycetopodidae were described using numerical data (Strahler's orders). The results of this work describe the distribution of a rich fauna of Mycetopodidae in the Río Negro Basin, identify information gaps, and point to potential threats and important conservation sites. Further analysis will detail the distribution of these species in sub-basins, as also some environmental factors that influence their distribution.

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GEOGRAPHIC DISTRIBUTION OF *Megalobulimus valenciennesii* (PFEIFFER, 1842), A BRAZILIAN GIANT SNAIL ENDEMIC TO SOUTHERN BAHIA

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Keywords: Atlantic Forest, endemism, land snails, Southern Bahia State.

The land snail genus *Megalobulimus* (Miller, 1878) includes about 80 species, of which approximately 60 occur in Brazil, including *M. valenciennesii*, endemic to the Atlantic Forest at Southern Bahia. Distributional data in the literature for most of the species of *Megalobulimus* is scarce and refers mostly to Brazilian states with few available records of specific occurrence localities. In the present study, we have updated the geographic distribution of *M. valenciennesii*. Specimens of *M. valenciennesii* were recently collected in different municipalities in Southern Bahia. Living specimens were photographed in nature to visualize the coloration of the soft tissues. The shells were measured with a digital caliper. A distribution map was constructed with QGIS 3.22.10, based on our original occurrence records, literature data and records available at the online biodiversity database, namely GBIF, SiBBr and iNaturalist. Taxonomic attribution in iNaturalist was verified by checking the correspondence of the shell traits of the specimens in the images with species diagnosis. Herein, all the analyzed specimens present shell characteristics that are typical of *M. valenciennesii*, such as the presence of uncolored areas in zigzag and an evident callus at the superior part of the parietal wall of the peristome. Besides, one live specimen was photographed in nature, allowing the visualization of the orangish pigmentation of its soft parts. *Megalobulimus valenciennesii* is rarely mentioned in malacological survey studies and appears to be the only species of the genus present in the Cabruca, a traditional agroforest system in Southern Bahia. According to current data in the literature, the distribution of *M. valenciennesii* is restricted to the municipalities of Una, Itapebi and Ilhéus, Bahia. Herein, we expand the knowledge about the geographic distribution of the species, including records for the municipalities of Barro Preto, Gandu, Igrapiúna, Itabuna, Itacaré, Ituberá, Maraú and Valença, all located in Southern Bahia. The conservation status of this species is still unknown. Brazil is considered one of the most megadiverse countries on the planet and our knowledge on land snails' diversity and distribution do not reflect the multiplicity of biomes and ecoregions found in Brazil. The high level of extinction already documented for this group justifies the need of monitoring and updating species distribution to provide useful information to access their conservation status. This is especially important for those species occurring in the Atlantic Forest, a biodiversity hotspot with high levels of endemicity and degradation. After a comprehensive analysis of occurrence records, excluding those deemed doubtful, misidentified, or with shell images insufficient for reliable species identification, we confirmed that *Megalobulimus valenciennesii* is indeed endemic to the Atlantic Forest of southern Bahia, underscoring the need to assess the conservation status of this species.

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ARTIFICIAL HYDROLOGICAL PATTERNS AND THEIR IMPACT ON EGG MASSES OF THE IGUAZÚ SNAIL (*Pomacea americanista*) IN IGUAZÚ NATIONAL PARK (ARGENTINA)

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Keywords: Iguazú snail, *Pomacea*, hydrological patterns, dams.

Pomacea americanista is an endangered freshwater gastropod endemic to the Iguazú and Alto Paraná rivers. Among the potential threats to its survival are hydrological alterations caused by upstream hydroelectric dams during working days, which may compromise the viability of aerial egg masses through submersion. This study aimed to identify patterns of hydrological change and evaluate their potential impact on egg viability and recruitment success in this vulnerable species. At Iguazú National Park (INP), egg masses and water levels were monitored daily at four sites over 15 days. Scaled photographs documented water level changes and submersion of egg masses. Daily water-level data from the Iguazú River, spanning eighteen months, were obtained from the Argentine Naval Prefecture (ANP) and analyzed using seasonal and trend decomposition with Loess (STL). Submersion risk was assessed for egg masses laid on different days of the week, and the frequency of various submersion durations was estimated. Additionally, *P. americanista* development data under fluctuating laboratory temperatures were analyzed to calculate threshold temperature and degree-days for hatching, using four different estimation methods. A total of 101 egg masses were recorded, 11 of which completed development (mean duration: 11.55 days). Eight masses were partially or fully submerged (height above water: 10.73 ±4.22 cm; length: 3.29 ±1.26 cm); four hatched in 13 days after submersion on days 9–10 of development, and one in 8 days after being submerged on days 4–6. During the monitoring period water levels varied by 14.53 cm, peaking on Thursday and dropping by Monday. These values strongly correlate with daily water levels from the ANP (r = 0.856). STL revealed a weekly flood cycle, with peaks on Thursdays to Fridays and lows on Mondays (amplitude: 1.42 ±0.21 m). Considering the distribution of distances to water level of egg masses from 7.3 to 51.5 cm (mean: 22.94 ±12 cm), of the egg masses laid in one week, 30.95% would remain unsubmerged, 26.19% would be submerged for 2 days, 26.19% for 4 days, 3.57% for 5 days, and 13.1% for 6 days. The two methods with lower deviation estimated threshold temperatures for development of 12.3 and 12.4 days, and the corresponding accumulated degree-days were 225.15 (± 75.05) and 239.005 (±34.19) days. These models predict that the development time during summer will be 17.05 to 18.13 days, suggesting that total submersion times would be 2.6 times higher. Hydrological fluctuations driven by upstream dams pose a significant risk to *Pomacea americanista* egg viability by increasing submersion frequency. This study highlights the sensitivity of development timing to water-level dynamics and provides key temperature thresholds for hatching. Identifying critical exposure periods and submersion risks supports future conservation efforts aimed at mitigating recruitment failure in this endangered species through improved management of water flow and habitat protection strategies.

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DEEP-SEA

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BATHYMETRIC ZONATION AND SPECIATION IN OCEAN TRENCHES: THE CASE OF NORTHWESTERN PACIFIC BIVALVES

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Keywords: hadal zone, species composition, sister species, larval dispersal, ecological speciation, Japan Trench, Kuril-Kamchatka Trench.

Trench is an oceanic topography encompassing the deepest point on Earth. Past trench explorations revealed highly endemic species assemblages and led researchers to distinguish the trench fauna from the shallower abyssal fauna and to name its distribution range as the hadal zone. However, difficulty of sampling and low population density have hampered detailed understanding of their diversity, distributions and speciation. In this study, Bivalvia, an exceptionally abundant taxon in the hadal zone, was studied to overcome these fundamental obstacles. Specimens were collected with beam trawls and an epibenthic sledge during two cruises on the R/V Hakuho-maru (KH-22-8 and KH-23-5) in the Kuril–Kamchatka and Japan Trenches of the Northwest Pacific. Collected bivalves were identified at the species level based on both shell morphology and DNA sequences. Two pairs of closely-related abyssal and hadal species were further subjected to population genetic and morphometric analyses. A total of 41 species were identified among 16,975 individuals from 32 stations below 5,000 m deep. Species composition analysis showed a clear faunal difference between 16 shallower (5,013–6,562 m) and 13 deeper (6,646–8,014 m) stations, identifying the border of the abyssal and hadal zones for the first time with quantitative data at around 6,600 m. The community structure within each zone was also correlated with depth but not with other factors including latitude and topographic setting. Each of the abyssal–hadal sisters, with 1.3–2.5% divergence in mitochondrial COI sequences, exhibited reproductive isolation and slight bathymetric overlap in the lowermost abyssal zone (6,523–6,562 m in *Bathyspinula* spp. and 6,523–6,539 m in *Neilonella* spp.). Most interestingly, the hadal ones of the species pairs did not show population genetic structuring despite their apparently discontinuous distributions as benthic adults with a shallow (6,280 m) gap between the Japan and Kuril–Kamchatka Trenches. Depth-driven ecological speciation in the face of gene flow seems to be prevalent among bivalves in trenches with ontogenetic vertical migration and dispersal as lecithotrophic swimming larvae. Abyssal plains often exceed 6,000 m in depth but seldom reach 6,500 m worldwide. The adults of abyssal species may have adapted to hydrostatic pressure in this depth range, perhaps accounting for their absence below ca. 6,600 m, where hadal endemics occur. Recent divergence between abyssal–hadal sisters might suggest that depth-driven ecological speciation has repeatedly occurred potentially due to instability of trench habitats on an evolutionary timescale.

Funding Source: No.

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THERE IS AN ABUNDANT SPECIES OF BATHYMODIOLINAE (BIVALVIA: MYTILIDAE) LIVING ON ORGANIC FALLS IN THE SOUTHEASTERN BRAZILIAN COAST – WHO IS IT?

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Keywords: Bathymodiolinae, organical falls, deep-sea fauna, Brazil, taxonomy, morphology.

Mussels of the subfamily Bathymodiolinae are interesting habitants of the deep-sea, being frequently recorded associated with reducing environments. In the southwestern Atlantic Ocean, only one species of these bivalves is known, *Adipicola leticiae* Signorelli & Crespo, 2017, described as living on whale bones in the Argentinean coast. In the southeastern Brazil, one small species was abundantly collected and its shell and soft parts are here characterized. The specimens were obtained by the research vessel "Alucia", which recovered pieces of wood and whale bones that were sunk in 2017 and stayed ten months on the seabed. It was a part of an experiment on the fauna associated to organic falls (the BioSuOr Project), performed at a depth of 550 meters, in a point of the coast of São Paulo (26°36'S, 46°09'W). The animals were fixed in ethanol 70% and through dissections were examined under a stereomicroscope; one individual had its soft parts extracted from the shell and prepared for conventional histological techniques. The scanning electron microscopy (SEM) was employed for the observation of shell characters. Over 500 specimens with soft parts were collected, including juvenile animals that represent a complete growth series. The shell is elliptical in outline, small (up to 1.7 cm in length), equivalve; inequilateral, with prosogyrate, subterminal umbones positioned anteriorly at about 1/5 of the shell length; outer surface smooth, with indehiscent, thin, translucent, yellowish periostracum. Prodissoconch evident, reddish brown; limits between PI and PII well visible by the SEM; PI D-shaped, ~100 µm (n=4), PII equilateral, rounded, ~400 µm. Juveniles similar in outline to the adults. Inner margins smooth. Inner surface nacreous, smooth. Conspicuous muscle scars, heteromyarian. Hinge line straight, toothless; smaller individuals bear a posterior crenulation which appears to be covered by the opisthodetic ligament in posterior stages of development. The foot is well developed with an evident byssal groove. The gills are composed by only the inner demibranchs, which have filaments with elongated abfrontal surfaces suggesting the presence of chemoautotrophic bacterial symbionts. This species is distinct from *A. leticiae*, that was described as having an antero-posterior elongated, sub-rectangular outline and with more anteriorly displaced umbones. Comparisons with other described species of Bathymodiolinae are in need, as some of them are known as widely distributed. Also, the generic placement of this Brazilian remains uncertain, pending on a detailed study of the taxonomic puzzle that occurs in this bivalve group. Some species of Bathymodiolinae are known as large animals, living in hydrothermal vents, and this is the part of the diversity of this subfamily which is better investigated, while a larger amount, composed by small sized species, remains almost unrecognized. Bearing an extensive coast, the Brazilian littoral is probably rich in small bathymodiolines, the present study representing just the beginning of the discovery of this malacofauna.

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ECOLOGY

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UNVEILING THE ECOSYSTEM SERVICES OF FRESHWATER MOLLUSKS: A CRITICAL REVIEW OF KNOWLEDGE GAPS AND CONSERVATION IMPLICATIONS

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Keywords: freshwater mollusks, ecosystem services, unionid mussels, gastropods, water quality, bioindicators, conservation planning, aquatic biodiversity, nutrient cycling, invasive species impacts

Freshwater mollusks' essential roles in aquatic ecosystems were recognized for their contributions to water purification, nutrient cycling, and food web stability. Unionid mussels and gastropods, including species such as *Biomphalaria*, *Pomacea*, and *Radix*, were highlighted for their ecological importance. Despite these contributions, many of these species remained among the most threatened aquatic organisms. This review was conducted to examine the ecosystem services provided by freshwater mollusks. A narrative literature review drew from peer-reviewed articles published over the past decade. Studies were selected based on their focus on freshwater mussels and gastropods, covering ecological, functional, and toxicological dimensions. Thematic analysis was applied to categorize information under provisioning, regulating, supporting, and cultural services. Emphasis was placed on the roles of specific species, spatial patterns, and their documented contributions across rivers, reservoirs, and wetland habitats. Ecosystem functions were supported by species such as *Unio pictorum*, *Anodonta anatina*, and *Sinanodonta woodiana*, which were shown to enhance water filtration, sediment bioturbation, and nutrient retention. Habitat complexity and macroinvertebrate diversity were facilitated by their presence. Gastropods like *Biomphalaria glabrata*, *Pomacea canaliculata*, and *Physella acuta* were identified as key parasite transmission regulators and effective bioindicators of environmental pollution. The production of bioactive compounds by *Pomacea* species also suggested potential biomedical applications. These mollusks were found to be negatively affected by pollution, habitat alteration, invasive competitors such as *Dreissena polymorpha*, and hydrological shifts linked to climate change. Research was determined to be limited in geographic scope, particularly across tropical and subtropical regions, and few long-term ecological datasets or service valuation frameworks were reported. The review's objectives were achieved by consolidating evidence that unionid mussels and pulmonate gastropods are crucial providers of ecosystem services. However, their conservation was constrained by knowledge gaps, weak policy integration, and limited ecological monitoring. Future efforts were recommended to incorporate multidisciplinary research and adaptive conservation planning to ensure the long-term viability of these mollusk-driven services.

Funding Source: No.

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REVIEW AND COMPARISON OF IN SITU OCTOPUS ABUNDANCE ASSESSMENT METHODOLOGIES

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Keywords: Cephalopoda, subaquatic methodologies, roving diver, transects, visual census.

The assessment of octopus abundance in natural environments is essential for understanding their ecology and for developing management and conservation strategies. Visual census techniques during diving have been applied in these studies and can serve as an alternative to CPUE calculated from fishing. The aim of this review was to compare the different abundance assessment techniques used for in situ studies of octopuses and to discuss their applications. A bibliographic review was carried out using the platforms Google Scholar, Web of Science and Scopus in order to identify relevant studies related to octopus abundance estimative. Searches were performed by combining the terms "roving diver", "quadrats", "transect", "CPUE" and "abundance" with the term "octopus", ensuring that the results specifically targeted studies focused on abundance evaluation techniques. To maintain the quality and reliability of the information gathered, the document type filter was selected "article," thus including exclusively peer-reviewed research publications. This approach aimed to compile a solid scientific foundation for the analysis of methodologies employed in octopus abundance studies across different environments. A total of 29 articles were found, with 10 estimating octopus abundance using transects, 5 using quadrats, 1 using the Roving Diver Technique (RDT), and the remaining using CPUE calculated from fishing. Two publications used more than one method. The RDT method involves an active search based on time rather than area and is effective for quickly estimating abundance over large areas at low cost, enabling regular monitoring. Leite et al. (2009) was the only study to adapt the RDT for octopus research and has been cited 60 times according to Web of Science. This study is also notable among those using quadrats, where a fixed area is searched and organisms documented. The three most impactful studies (Leite et al., 2009; Bouth et al., 2011; Batista and Leite, 2016) used 50x50m quadrats, which allow for standardized, repeatable sampling useful for monitoring over time. Among transect-based studies, the size and layout varied considerably. Transects involve moving along a defined line to record nearby organisms, making them suitable for studies along environmental gradients. However, both quadrats and transects face limitations when applied to highly mobile species, potentially affecting abundance estimates. Therefore, methods should be adapted to the species' ecology. For instance, 50x50m quadrats were effective for species like *Octopus insularis* and *O. vulgaris*, which inhabit large dens in reef areas. In contrast, species like *Callistoctopus furvus* and *O. briareus*, or burrow-building species like *Macrotritopus* cf. *defilippi*, require alternative approaches such as the Roving Diver Technique. Challenges in adapting scientific diving methods reveal the need for more publications that systematize techniques suited to diverse ecological and behavioral contexts. Such studies are key to improving reproducibility and adjusting methods to specific environments and species. In octopus research, underwater methodologies have proven efficient, offering a non-invasive alternative for in situ studies without the need for capture.

Funding Source: No.

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SURVIVAL IN THE SEMI-ARID: RESISTANT FUNCTIONAL TRAITS ENABLE THE PERSISTENCE OF LIMNIC MALACOFAUNA IN TROPICAL ECOSYSTEMS

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Keywords: functional composition, functional homogenization, limnic malacofauna, northeast, semiarid reservoirs.

Functional traits are biological characteristics that help us understand how communities respond to environmental variations and disturbances. Moreover, these indicators reveal the ecological performance of species within ecosystem functioning. This information is especially relevant in semiarid reservoirs, which, despite their importance in providing ecosystem services, are susceptible to environmental degradation. We aimed to identify the functional traits that enable the survival of freshwater mollusk fauna in semiarid ecosystems. The study was conducted in seven reservoirs of the Paraíba River basin and one reservoir in the Mamanguape River basin (Brazilian semiarid). The malacofauna and environmental variables were sampled at 15 littoral sites of the reservoirs during the dry and rainy periods, from 2021 to 2024. The group was characterized by 12 attributes and 34 functional categories related to its colonization and persistence capacity. Differences in environmental parameters and malacofauna were analyzed using PERMANOVA. The community weighted mean (CWM) was calculated for each functional attribute. PERMANOVA was applied to the CWM values, and Spearman's correlations were performed to evaluate the relationship between CWM values and explanatory variables. A total of 43,799 mollusks were collected, belonging to seven taxa: Cochliopidae, Planorbidae, *Pomacea*, *Stenophysa*, *Melanoides tuberculata* (Gastropoda), *Eupera*, and *Corbicula largillierti* (Bivalvia). The invasive mollusk *M. tuberculata* was the most abundant taxon (90.31%) and dominated across all reservoirs, particularly in Argemiro de Figueiredo, which had the highest number of individuals (29.99%), with *M. tuberculata* representing 99.79% of the local fauna. Both the composition of the mollusk fauna and the environmental structure varied significantly among reservoirs (Pseudo-$F_{7,553}$ = 18.87; p = 0.001; R^2 = 0.19) and (Pseudo-$F_{7,451}$ = 4.21; p = 0.001; R^2 = 0.61), respectively. The CWM analysis revealed dominance of generalist species (100%) from lentic habitats (100%), of medium size (93.09%), with spiral-shaped (93.91%) and thin shells (99.52%). Predominant respiratory mode was gill-based (94.48%), and locomotion occurred mainly through crawling (93.91%) and burrowing (91.68%). There was also a predominance of parthenogenesis (86.16%), internal fertilization (93.91%), multivoltinism (93.91%), estivation (89.01%), and scraping (88.87%) and detritivorous feeding (93.91%). PERMANOVA on the community-weighted means of functional traits indicated significant functional variation among reservoirs (Pseudo-$F_{7,553}$ = 14.683; p = 0.001; R^2 = 0.16). Spearman's correlation analysis identified five relevant predictors for the functional structure: four abiotic variables (coarse sand, ORP, NO2, and SRP) and one biotic variable (*M. tuberculata*). Our results show the dominance of functional traits associated with persistence and rapid colonization, typical of unstable environments. These traits reflect adaptations to environmental stresses, such as poor water quality and biological invasion, indicating resistance but with low functional diversity. We conclude that degraded environments, combined with the presence of invasive species, reduce functional structure by favoring organisms with resistant traits, such as *M. tuberculata*. This simplification can lead to the formation of functionally homogeneous communities, compromising essential ecological functions and reducing ecosystem resilience to disturbances and changes.

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UNDER THE DOMINANCE OF AN INVADER: THE PORTRAIT OF THE LIMNIC MALACOFAUNA IN SEMIARID ECOSYSTEMS

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Keywords: taxonomic structure, biotic homogenization, freshwater mollusks, northeast, semiarid reservoirs.

Taxonomic diversity studies are essential for understanding ecological patterns and environmental impacts, especially in vulnerable regions such as the Brazilian semi-arid. Water scarcity and climatic and anthropogenic pressures directly affect the environmental conditions of semi-arid reservoirs, making it crucial to understand how these changes influence the diversity of mollusks. We aimed to identify the main ecological factors (biotic and abiotic) influencing the taxonomic diversity of freshwater mollusks in semiarid ecosystems. The study was conducted in eight reservoirs (Brazilian semi-arid region). Malacofauna and environmental variables were sampled at 15 sites during the dry and wet periods between 2021 and 2024. Differences in environmental parameters and malacofauna were analyzed using PERMANOVA, and the SIMPER analysis identified the contributions of species. Taxonomic diversity was assessed using Hill indices (q0, q1, q2), and their relationships with environmental variables were investigated using Spearman correlation. A total of 43,799 mollusks were recorded, belonging to seven taxa: Cochliopidae, Planorbidae, *Pomacea*, *Stenophysa*, *Melanoides tuberculata* (Gastropoda), *Eupera*, and *Corbicula largillierti* (Bivalvia). The invasive species *M. tuberculata* was the most abundant, accounting for 90.31% of the total. It dominated all reservoirs, particularly in the Argemiro de Figueiredo Reservoir, which exhibited the highest number of individuals (29.99%), with *M. tuberculata* comprising 99.79% of the local fauna. The composition of the malacofauna and environmental structure varied significantly among reservoirs (Pseudo-F7,553 = 18.87; p = 0.001; R^2 = 0.19) and (Pseudo-F7,451 = 4.21; p = 0.001; R^2 = 0.61), respectively. An average dissimilarity of 68.82% among taxa across reservoirs was observed, with *M. tuberculata* contributing 56.3%, while other species contributed less than 4%. Mollusk diversity was low, with seven taxa (q0) and reduced effective diversity (q1 = 1.61; q2 = 5.48). Spearman correlation identified eight relevant predictor variables for taxonomic diversity: seven abiotic (CSand, Chl-a, Air°C, Sal, NO2, SRP, and DIN) and one biotic (*M. tuberculata*). Environments with a higher proportion of coarse sand favored species richness (q0). In contrast, eutrophic conditions and high temperatures reduced diversity (q0 and q1), favoring tolerant species such as *M. tuberculata*. The dominance of this species resulted in low evenness and greater variation in diversity indices, indicating an uneven community structure and potential ecological instability. The q2 index was influenced by higher salinity and phosphorus, reflecting a community dominated by a single species. Our results indicate that local impact conditions favor resistant taxa, evidencing a process of biotic homogenization. The dominance of the invasive mollusk *M. tuberculata* contributed to a reduction in diversity, leading to more uniform communities in terms of composition and increased susceptibility to change, particularly in degraded semiarid reservoirs.

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GEOCHEMISTRY METHODS IN THE SHELL STUDY OF CALCIPHILE LAND SNAIL *Caucasotachea vindobonensis*

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Keywords: *Caucasotachea vindobonensis*, shell, crossed-lamellar structure, chemical composition, phase identification, environmental factors, calcium substrate.

The geographic distribution of *Caucasotachea vindobonensis* spans south-eastern Europe. In Poland, at the northern edge of its distribution, the species' continuous range includes the belt of calcium-rich uplands. In contrast, the insular range includes the river valleys where the substrate is poor in calcium. The occurrence of *C. vindobonensis* in such extreme environmental conditions has served as the basis for studies exploring the relationship between substrate chemistry and shell characteristics. Calcium content in the habitats of both the continuous and insular ranges of *C. vindobonensis* was determined using inductively coupled plasma optical emission spectrometry (ICP-OES). Shell structure was examined using a scanning electron microscope (SEM) and a KEYENCE VHX-5000 digital microscope. The chemical composition of the shells was analysed with energy-dispersive X-ray spectroscopy (EDS), while crystal phase identification was conducted using X-ray diffraction (XRD). Shell microhardness was measured using the Vickers method. Relationships between substrate calcium content and shell features of *C. vindobonensis* were investigated through statistical analysis. Substrate analysis confirmed that habitats within the continuous and insular ranges of *C. vindobonensis* differ significantly in calcium availability. The species' occurence in calcium-poor environment result from passive dispersal along watercourses. In Poland, this process moves from the south and southeast toward the north and northwest. Shells collected from both types of habitats are characterized by a typical crossed-lamellar structure. The average shell wall thickness is 215.8 µm. A positive correlation was found between calcium content in the substrate and shell wall thickness. Chemical and crystal phase analyses of the shells revealed that approximately 97% of their weight comprises the major elements making up calcium carbonate in its aragonite phase. In addition to the major elements, trace elements such as magnesium, iron, and manganese are also present, accounting for around 3% by weight. Similar results were obtained in studies of the structure and physicochemical properties of the shells of *Cepaea nemoralis*. Positive correlations were found between calcium levels in the substrate and the total content of major elements in the shells, while negative correlations were observed between this factor and the total content of impurity-forming elements. The average shell microhardness was 337 HV under a load of F=0.025 HV. A negative correlation was noted between calcium concentration in the substrate and shell microhardness. Furthermore, the chemical composition of the shell was shown to be a significant factor influencing microhardness. Negative correlations were observed between the major-element content and shell microhardness, whereas positive correlations emerged with elements occurring as impurities. Calcium availability in the substrate is an important factor influencing the properties of *C. vindobonensis* shells. These findings are part of a broader project investigating how environmental factors associated with the substrate affect population density, distribution, and shell growth in *C. vindobonensis*. This research aims to improve our understanding of this species, which is threatened with extinction in Europe, and to contribute to the development of effective conservation strategies.

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ECOLOGICAL VARIATION IN *Octopus insularis*: DIET AND HABITAT USE IN OCEANIC ISLANDS OF BRAZIL AND THE LUCAYAN ARCHIPELAGO

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Keywords: Cephalopoda, ecology, octopus, diet, habitat use, niche.

Octopus insularis is a tropical octopus species with populations in oceanic islands in Brazil, where it dominates shallow warm waters, and in the Lucayan Archipelago, western North Atlantic Ocean, where it coexists with other octopus species. No study has directly compared the ecological strategies of these two populations separated by oceanic gyres. Data collected from Fernando de Noronha Archipelago, Brazil (2003–2005) consisting of 473 prey items obtained from 117 different dens was compared to data from the Turks and Caicos Islands (2020–2024), consisting of 512 prey items from 55 dens. Diet was assessed by categorizing prey remains by taxonomic group (crustaceans, bivalves, gastropods) while habitat use was assessed through den type and substrate composition. 254 dens were characterized in Brazil, and 115 in Turks and Caicos. Standardized field methods were applied in both regions to ensure comparability. Data are presented as relative frequencies to highlight regional contrasts. Diet composition differed markedly between regions. In Fernando de Noronha, small crustaceans dominated (69.98% of prey items), primarily *Pitho sp*. (26.85%) and *Mithrax forceps* (23.89%), while bivalves accounted for only 17.55% of the diet. In contrast, Turks and Caicos populations favored bivalves (50.20% of prey items), with a single species (*Johnsonella fausta*) representing 33.79% of the diet, while crustaceans represented 24.61%. Turks and Caicos also showed chitons as part of the diet (0.2%), which has not been observed in Brazil. Only three prey species overlapped in the two locations: *Calappa gallus*, *Chorinus heros* and *Codakia orbicularis*. Despite marked dietary differences, both populations shared similar habitat preferences. Horizontal crevices were frequently used in both regions (Brazil: 46.85%; Turks and Caicos: 35.66%), though Turks and Caicos showed higher use of caves (46.96% vs. 12.20% in Brazil), possibly due to local reef complexity. Substrates were predominantly bedrock or flat reefs (Brazil: 70.87%; Turks and Caicos: 93.91%), though dead coral (0.97%) occurred exclusively in Turks and Caicos. The dietary divergence with crustacean-dominated in Brazil versus bivalve-focused in Turks and Caicos, likely reflects adaptation to differences in prey availability, such as abundant bivalve beds associated with algal banks in the Turks and Caicos, leading to prey specialization. These findings demonstrate that *O. insularis* maintains consistent habitat requirements while having great flexibility in adjusting its diet to local resource conditions as a time-minimizer hunter (Leite et al, 2009). This study reveals striking regional differences in *O. insularis* diet, from prey specialization (crustaceans vs. bivalves), likely driven by prey availability. These findings establish a critical baseline for future experimental studies on niche plasticity in shallow water octopuses, particularly those inhabiting oceanic islands. Such comparisons are vital for understanding cephalopod adaptability in changing oceans.

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FOREST STRUCTURE AND WATER QUALITY FACILITATE THE ESTABLISHMENT OF THE INVASIVE SLUG *Meghimatium pictum* (STOLICZKA, 1873) (STYLOMMATOPHORA: PHILOMYCIDAE) IN SUBTROPICAL TREE-HOLE MICROCOSMS

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Keywords: detritivore, exotic plantations, phytotelmata, invasion ecology.

Forest conversion and plantation management can alter canopy structure and water chemistry, favoring invasive detritivores like *Meghimatium pictum*, mainly in tree-hole habitats. Despite its rapid spread across South America, the environmental filters influencing its abundance remain unclear. Given the threat biological invasions pose to subtropical forests, this study aimed to identify environmental thresholds associated with *M. pictum* abundance in managed forest landscapes. We deployed 144 rain-filled microcosms containing four litter species along three transects spanning native forest fragments, abandoned pine stands, and active eucalyptus plantations. Each 800-mL microcosm was suspended at 1.5 m height and equipped with hourly temperature logging. We measured turbidity, dissolved oxygen, conductivity, nitrate, ammonia, pH, redox potential, and pigment concentrations (chlorophyll and pheophytinin) the water, alongside canopy openness assessed via fisheye lens photography. After 120 days, *M. pictum* individuals were enumerated. *M. pictum* abundance was modeled using one-way generalized linear mixed-effects model with plot identity as a random factor, and multivariate regression trees (MRT) were used to identify the strongest environmental predictors of slug abundance. The PCA clearly separated plantation from native forest sites along a dissolved oxygen–turbidity versus ion-rich gradient, capturing 41% of the total environmental variance, indicating that forest type significantly influences the physicochemical properties of tree-hole habitats. *M. pictum* abundance varied significantly across forest types (χ^2 = 8.27, p = 0.015), with the highest mean abundances recorded in active eucalyptus plantations (17.9 ± 4.8 individuals' microcosm), followed by abandoned pine stands (8.8 ± 3.2), and the lowest in native fragments (1.6 ± 0.7), suggesting that habitat fragmentation promotes invasion processes by facilitating resource access and environmental suitability. The regression tree analysis identified canopy openness as the primary environmental filter, confirming that forest type transitions toward more anthropized landscapes accelerate invasion success. Microcosms located under canopy gaps ≥17% supported over tenfold higher slug abundances than shaded cavities. Within shaded sites (<17% openness), turbidity ≥206 NTU further tripled *M. pictum* abundance, indicating a compensatory pathway through suspended particulate resources. These results suggest that thinning, understory removal, and soil disturbance in plantation stands create light-rich, particulate-laden microhabitats that serve as invasion hubs, whereas intact native forest fragments with closed canopies and clear water resist slug establishment. Importantly, these simple thresholds (17% canopy openness and 206 NTU turbidity) provide actionable targets for invasion mitigation. By quantifying canopy and water-quality thresholds, our study demonstrates that light penetration and suspended solids jointly promote *Meghimatium pictum* outbreaks in subtropical forest mosaics. Maintaining canopy closure and minimizing sediment inputs emerge as effective, evidence-based strategies to curb the spread of this invasive detritivore and preserve ecosystem functioning in managed forest landscapes.

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TERRESTRIAL GASTROPODS IN SOUTH AMERICAN MOUNTAINS: A REVIEW OF CURRENT KNOWLEDGE AND GAPS

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Keywords: highland, altitudinal gradient, distribution, biogeography.

Mountains have unique environmental conditions, which offer a complexity of microhabitats, due to the marked variations in terrain, rainfall, temperature, atmospheric pressure and wind associated with the altitudinal gradient. These features may limit dispersion and favours micro endemism patterns in taxa with a low dispersal capacity, such as terrestrial gastropods. South America is home to 440 mountain ranges, most of which are still unexplored in search of terrestrial gastropods. We investigated the status of studies on terrestrial gastropods in mountains of South America. We conducted bibliographic survey in online databases, combining keywords related to the animals (e.g. terrestrial gastropod; land snail; land slugs), localities (e.g. South America; and its countries) and topography (e.g. hills, massifs, mountains), in English, Spanish and Portuguese. We disconsidered works of marine, freshwater, fossil or exotic gastropods; papers without concrete data on geographical distribution or without direct mention of mountains/altitudinal relief; and urban/high anthropogenic influenced areas. We georeferenced all valid coordinates, and restrained to mountains (sensu Snethlage et al. 2022). Data was analyzed in R (packages terra, raster, st and sp). We identified 148 published papers on terrestrial gastropods in South American mountains, of which only 66 had georeferenced records. Of the 433 coordinates extracted, only 259 (59.8%) were located in areas classified as mountainous. The countries with the highest number of records were Peru (63 records), Chile (54), Brazil (52) and Argentina (34). Only 54 (12.2%) of the 440 mountains in South America had records of terrestrial gastropods. The mountains with most records were the Cordillera Occidental (Ecuador), Serra Geral (Brazil) and the Cordillera Urubamba (Peru). The majority of records have been located in mountains near the coast, while extensive regions, such as the Amazon biome, remain barely explored. Among the taxa recorded, species from the Bulimulidae family were frequent, reflecting a possible taxonomic bias due to the concentration of specialists in the group. Our results highlight the large gap in knowledge about the diversity of terrestrial gastropods in South American mountain environments. We believe that the difficulty of accessing these areas may contribute to this lack of data, reinforcing the need for new sampling and study efforts, given the potential of these environments to harbor a high diversity of terrestrial molluscs.

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SEA SLUGS ASSOCIATED WITH MACROALGAE IN THE ROCKY INTERTIDAL OF PUNTA AMAPALA, EL SALVADOR, AND A NEW SPECIES RECORD

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Keywords: Heterobranchia, Chlorophyta, ecology, rocky intertidal, Eastern Tropical Pacific.

Some orders of marine heterobranchs, known as sea slugs, have a close association with macroalgae, which serve as their main food source (Mikhlina et al, 2024). Many species are characterized by cryptic coloration derived from the pigments of the algae they consume, allowing them to blend into their surroundings. A particularly remarkable feature in certain species is their ability to retain functional chloroplasts from macroalgaes in their diet (Martín-Hervas, 2020). This study was conducted on the eastern beaches of El Salvador, Central America, located at the eastern tropical Pacific. Those beaches areas feature rocky intertidal zones with communities of marine macroalgae and have been relatively understudied in relation to heterobranchs. Ten species of macroalgae were collected over a 15-hour effort during low tide in the dry season of December 2021. The algae were placed separately in trays, and observations were made to determine whether heterobranchs were present on the water surface seeking oxygen. In addition, a thorough search was carried out among the algae to collect any specimens that might still be present within them. A total of 10 species of marine macroalgae were collected and carefully analyzed in separate trays at the field laboratory. The collected macroalgae species, classified into three major divisions, were: red algae: *Ceramium* sp., *Galaxaura* sp., and *Gelidium* sp.; brown algae: *Dictyota* sp. and *Padina* sp.; and green algae: *Acetabularia* sp., *Bryopsis* sp., *Caulerpa* sp., *Chaetomorpha* sp., and *Halimeda* sp. Among these macroalgae, sea slugs were found on four species, with most records associated with green algae. The total number of marine heterobranch individuals was six, belonging to three species: *Aplysia hooveri*, associated with the macroalgae *Dictyota* sp. and *Ceramium* sp.; *Elysia pusilla*, found on *Halimeda* sp.; and *Phyllaplysia padinae*, found on *Padina* sp. Notably, *Phyllaplysia padinae* represents a new record for El Salvador. The presence of *A. hooveri* on multiple macroalgae aligns with various studies indicating that most sea slugs can feed on a wide variety of macroalgal species. There are also documented cases of a single sea slug species using two or more algal genera as food sources (Hernández-Álmaraz et al., 2018). *P. padinae* was recorded exclusively on *Padina* sp., consistent with previous records from the Pacific coast of Costa Rica (García & Camacho-García, 2015). However, Clark (2008) notes that *P. padinae* shows preferences for both brown and green algae, particularly favoring the seagrass Zostera marina. This species was not collected from the El Salvador reef during this study, suggesting the potential for such an association, although it has not yet been documented in the country. The presence of marine heterobranchs was limited to four out of ten species of macroalgae collected, with a majority of individuals found on *Halimeda* sp., suggesting a possible habitat preference or selectivity by these sea slugs. The new record of the slug *Phyllaplysia padinae* for El Salvador expands the current knowledge of the country's heterobranch biodiversity and highlights the need for continued systematic studies in underexplored regions.

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DOES THE BATHYMETRIC ZONE OCCUPIED BY BRAZILIAN INSULAR GASTROPOD SPECIES INFLUENCE THEIR GEOGRAPHIC DISTRIBUTIONS?

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Keywords: marine, prosobranchs, Southwestern Atlantic.

The geographic distribution of marine gastropods is predicted primarily by the type of larval development, followed by depth range and use of multiple habitats. However, a study with Azorean marine gastropods showed that bathymetric zonation was also an influencing factor, with intertidal species being more prone to rafting. Thus, our objective was to analyze whether this influence of the bathymetric zonation is observed in other insular gastropod assemblages. To build the database, we used published data of shallow prosobranch gastropods (up to 50 m depth) from four Brazilian oceanic islands. To analyze the effects on the geographic distribution, we used a linear mixed model (LMM), treating geographical distribution (range in degrees of latitude) as response variable and type of larval development (planktotrophic, lecithotrophic, and intracapsular metamorphosis), bathymetric zonation (intertidal or no intertidal) and habitat diversity (number of used habitats), as fixed variables. We also conducted a partitioning of variance analysis to determine the relative importance of each fixed variable in the model. Records of endemic insular species and empty shells were not considered. We analyzed 62 marine gastropod species (43 intertidal and 19 non-intertidal). Among intertidal and non-intertidal species, we observed respectively 23 and 11 species with planktotrophic larvae, 17 and six with lecithotrophic larvae, three and two with intracapsular metamorphosis, 31 and 13 occupying one habitat, 12 and six using multiple habitats, four and one with geographic distribution less than 30 degrees latitude, and 39 and 18 with geographic distribution greater than 30 degrees latitude. The results of the LMM and partitioning of variance analysis showed that the bathymetric distribution (whether the species is intertidal or not), by itself, is not a good predictor of their geographic distribution, with the type of larval development being the main predictor of this distribution. The chosen model showed the joint influence of the type of larval development, habitat, and bathymetric zonation on the distribution. Furthermore, it also showed that the interaction between the type of larval development and bathymetric distribution can influence the geographic distribution of insular species (the interaction between lecithotrophic and intertidal was significant in the model). Rafting, therefore, may be an explanatory factor for the broad geographic distributions found in species with lecithotrophic larval development, together with other factors discussed in previous studies, such as passive transport, dispersion by steppingstones, dispersion by other animals, changes in ocean currents, ecological requirements, and use of different types of habitats. Thus, our results partially corroborate what was observed for the marine gastropod assemblage of the Azores Archipelago, since the intertidal condition is important when also considering the type of larval development in predicting the geographic distribution of marine insular gastropods.

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BETWEEN ROOTS AND MICROORGANISMS: *Littoraria angulifera* AS A BIOINDICATOR OF ANTHROPOGENIC CONTAMINATION IN A SEMI-ARID MANGROVE IN NORTHEAST BRAZIL

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Keywords: environmental monitoring, public health, One Health.

Mangroves are vital tropical coastal ecosystems, hosting rich biodiversity and providing key ecosystem services. Among resident species, *Littoraria angulifera* stands out as an ideal model for biomonitoring due to its abundance, easy identification, and adaptation to the intertidal zone. This study investigated the presence of pathogenic microorganisms associated with *L. angulifera* in a Brazilian semi-arid mangrove to evaluate its potential as an environmental quality and public health indicator. Thirty adult *L. angulifera* were manually collected with sterile gloves from mangrove roots and trunks in the Pacoti River estuary (Eusébio, Ceará, Brazil). Individuals were placed in sterile tubes with BHI broth and transported to the laboratory. After maceration, samples were inoculated on Blood Agar and MacConkey Agar and incubated at 37 °C for 48 hours. Colonies were identified using the VITEK® 2 Compact system (BioMérieux), enabling the detection of clinically and environmentally relevant bacteria. The presence of these microorganisms was analyzed to assess environmental contamination and potential risks, contributing to the understanding of microbial dynamics in anthropogenically influenced mangrove ecosystems. Microbiological analysis of *L. angulifera* revealed several bacterial species, including *Vibrio fluvialis*, *Enterobacter cloacae*, *Pantoea spp.*, *Klebsiella oxytoca*, *Streptococcus iniae*, *Streptococcus thoraltensis*, *Staphylococcus xylosus*, and *Corynebacterium spp.* Many of these organisms are of clinical relevance and have pathogenic potential, indicating environmental degradation. *Vibrio fluvialis*, typically found in estuarine waters, is linked to gastroenteritis outbreaks via raw seafood consumption. *Enterobacter cloacae* and *Klebsiella oxytoca*, associated with human opportunistic infections, pose health risks to populations relying on mangrove resources. *Streptococcus thoraltensis* has been reported in animal infections, while *Streptococcus iniae* is a zoonotic pathogen affecting fish. The detection of *Pantoea spp.*, often linked to plants and water, may suggest influence from agricultural or urban runoff. Although *Staphylococcus xylosus* is commonly used in food fermentation, it can act as an opportunistic pathogen. *Corynebacterium spp.* includes species from human microbiota that may cause infection in immunocompromised individuals. These findings emphasize the utility of *L. angulifera* as a bioindicator of environmental quality and highlight the threat posed by climate change, which may favor the persistence and proliferation of such microbes. Conservation and environmental surveillance, informed by the One Health framework, are essential for mitigating risks emerging from the intersection of environmental, human, and animal health in tropical coastal ecosystems under increasing anthropogenic pressure. *L. angulifera* proved effective as a bioindicator of anthropogenic contamination in mangroves, harboring bacteria of medical and zoonotic concern. These findings signal environmental degradation and potential public health risks, especially in the context of climate change. The study reinforces the urgency of integrated public policies under the One Health perspective, aiming to conserve coastal ecosystems and mitigate emerging risks driven by intensified human activities.

Funding Source: No.

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ECOPHYSIOLOGICAL RESPONSES OF *Littoraria angulifera* TO SPATIO-TEMPORAL GRADIENTS IN A SEMI-ARID ESTUARY IN NORTHEAST BRAZIL

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Keywords: Littorinidae, ecophysiology, mangrove ecology.

Mangrove ecosystems are vulnerable to climate change, especially in semi-arid regions, where rainfall variability and high evaporation affect salinity and oxygen availability. *Littoraria angulifera*, a common mangrove gastropod, is a sensitive bioindicator of environmental stress. This study investigated its ecophysiological responses to seasonal and vertical tidal gradients in the Pacoti River estuary, evaluating temperature, salinity, oxygen, and organismal distribution. Monthly sampling was conducted from September 2020 to September 2021 in the Pacoti River estuary (Ceará, Brazil), using three perpendicular transects with three 100 m² plots each. Ten adults *Littoraria angulifera* were collected per plot (five above and five below breast height). Internal temperature, oxygen saturation, and pallial cavity salinity were measured. Shell height and wet biomass were recorded. Environmental data (rainfall, air/water temperature, oxygen, salinity) and mangrove structure (height, diameter, basal area) were obtained. The analyses compared physiological and biometric parameters of individuals with spatial and seasonal variations in the estuary. A total of 1080 specimens were analyzed. Physiological parameters varied with seasonality and tree position. Individuals near the river had larger shells, higher biomass, and greater internal salinity and oxygen, indicating favorable conditions. In contrast, those in higher, inland plots showed elevated internal temperatures during the dry season and lower oxygen, indicating stress. Internal salinity strongly correlated with water salinity, while oxygen was lower in dry months and farther from the river. Mangrove structure positively influenced individual size and biomass. Larger individuals occurred above breast height in drier plots, suggesting thermoregulatory behavior. Greater similarity was found among plots near the river, with salinity best explaining distribution patterns. These findings highlight *L. angulifera*'s ecological plasticity and its vulnerability to prolonged drought and increased salinity, which may lead to habitat contraction. The data suggest that reduced rainfall in future climate scenarios could restrict the species to more humid mangrove zones. This study reinforces the value of *L. angulifera* as a bioindicator in long-term climate monitoring programs. Ecophysiological parameters and the spatial distribution of *L. angulifera* varied significantly in response to environmental gradients. The species demonstrated resilience under moderate conditions but showed signs of stress during extreme drought and salinity. These results confirm its sensitivity to climate change and its importance as an ecological indicator. Continuous estuarine monitoring is essential given projected future climate scenarios.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

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DIVERSITY AND SEASONAL VARIATION OF BENTHIC MICROMOLLUSKS IN CORAL-ALGAL SEDIMENTS FROM THE NORTHERN COAST OF BAHIA, BRAZIL

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Keywords: diversity micromollusks, seasonal variation, coral-algal sediments.

Mollusks are ecologically important benthic invertebrates due to their diversity and dominance across trophic levels. Reef sediment micro-habitats increase local biodiversity and warrant further study. This research investigates the composition, structure, and seasonal variation of mollusk assemblages in coral sediments along Bahia's north coast, aiming to generate ecological data that enhances understanding of these communities and supports long-term environmental monitoring efforts. Seasonal collections were conducted on Bahia's north coast in 2023 and 2024. In 2023, collections occurred during the rainy season, while in 2024, both dry and rainy seasons were sampled. Material was collected using 8 deployments of a Holme grab (0.08 m^2) at 20-25m depths. Samples were sieved through screens (5 mm, 2 mm, 1 mm) and transported for lab, where specimens were identified to the lowest possible taxonomic level. The total number of individuals was recorded, and relative abundance was calculated. Preliminary statistical analysis included univariate indices: (i) Shannon diversity (H') and (ii) Pielou's evenness (J), using RStudio software (version 2024.12.1). A total of 962 benthic micromollusks were collected, distributed among 67 species and 41 families. The families Corbulidae (7 spp), Nassariidae (4 spp), Semelidae (4 spp), Architectonicidae (3 spp), Cardiidae (3 spp), and Naticidae (3 spp) stood out for their higher species richness. The highest abundance was recorded during the rainy season of 2024 (506 individuals). In the dry season of 2024, 393 individuals were recorded, and in the rainy season of 2023, only 62 individuals were recorded. The species *Semele proficua*, *Crassinella lunulata*, and *Caryocorbula ira* presented the highest relative abundances. Some species were recorded in only one period: (i) dry/2024 = 27 species; (ii) rainy/2023 = 18 species; (iii) rainy/2024 = 18 species. The average diversity was H'=1.93. The highest value was recorded in the dry season/2024 (H'=2.19) and the lowest in the rainy season/2023 (H'=1.64). The average evenness index was J=0.63. The highest value was recorded in the rainy season/2023 (J=0.79) and the lowest in the rainy season/2024 (J=0.54). Considering that the sampled sediments come from an oligotrophic oceanic region, the univariate index values are within the expected range, indicating moderate diversity and relatively heterogeneous distribution of organisms. However, diversity was influenced by the dominance of some species. This heterogeneous dominance, particularly in the rainy season, appears to be associated with temperature variations, El Niño events, and storms that occurred before the collection periods. Considering that it is an oligotrophic oceanic environment, this study revealed a significant diversity of micromollusks, with 67 species of gastropods and bivalves, associated with sediment variation (muddy, sandy, and mixed). *Semele proficua* and *Crassinella lunulata* were the most abundant species. Diversity was higher during the dry period. New collections are planned to further understand the dynamics of micromollusks in the study area.

Funding Source: No.

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FIRST CONTRIBUTION TO THE KNOWLEDGE OF TERRESTRIAL GASTROPODS (HETEROBRANCHIA) IN TLAXCALA, MEXICO WITHIN THREE LOCATIONS WITH DIFFERENT DEGREES OF DISTURBANCE

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Keywords: terrestrial mollusks, heavy metals, anthropogenic, richness, diversity.

Ecosystems near urban areas or used for agriculture are constantly exposed to chemical pollutants. Anthropogenic activity and other local factors, can alter the composition and distribution of gastropods. Due to the importance of understanding the response of terrestrial gastropods to environmental changes, and the limited information for Tlaxcala, a comparative study was conducted on the terrestrial gastropod community in three localities of the state with different levels of disturbance. The collections of organisms was carried out in the localities Atlihuetzia, Atlangatepec y Parque Natural El Rey, this involved direct searching for macromollusks and a transect method for micromollusks. In addition, soil samples were collected for heavy metal analysis using atomic absorption spectrometry. Subsequently, the specimens were processed for identification with the help of specialized literature. Species richness and abundance were quantified for each locality to calculate the Shannon-Wiener diversity index (H') and Pielou's evenness index (J') using the PAST software. A total of 504 individuals were obtained, including 261 organisms larger than 10 mm and 243 organisms smaller than 10 mm, belonging to 17 families, 18 genera, and 23 species. The locality with the highest richness and diversity was El Parque Natural El Rey, where more micromollusks were recorded, with *Paralaoma servilis* and *Radiodiscus millecostatus* being the most abundant species. This result is attributed to the lower level of pollution in El Parque, unlike the other localities (Atlihuetzia and Atlangatepec), which are located near urban areas, offer recreational activities, and receive wastewater discharges in their water bodies, resulting in high concentrations of heavy metals such as Ni, Mn, Cd, Pb, Hg, and As. The greater richness and diversity may also be influenced by other local factors such as humidity and vegetation cover (Rosin et al., 2017). In this regard, abundant trees, logs, vegetation, and rocks were observed in both El Rey and Atlihuetzia, which support a greater establishment and expansion of terrestrial gastropods. The high richness and diversity of terrestrial gastropods recorded in El Parque Natural El Rey is attributed to lower anthropogenic disturbance, but also to factors such as humidity, vegetation cover, and availability of refuges. In contrast, the lower richness recorded in Atlihuetzia and Atlangatepec suggests that human activities, such as urban expansion and wastewater discharge, may be affecting the diversity and abundance of these species.

Funding Source: No.

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FIRST RECORD OF *Lissachatina fulica* (BOWDICH, 1822) (GASTROPODA: ACHATINIDAE) IN A BRAZILIAN MANGROVE

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Keywords: bioinvasion, Brazil, estuary, invasive alien species, urban mangrove.

Mangroves are coastal ecosystems of high ecological and socioeconomic importance, but are increasingly threatened by urbanization. *Lissachatina fulica*, the giant African snail, is an invasive species widely reported in urban and agricultural environments in Brazil, yet there were no consolidated records of its presence in mangrove ecosystems. This study aimed to document the occurrence of *Lissachatina fulica* in an urban mangrove in the municipality of Acaraú, northeastern Brazil. The investigation was carried out through active search in a mangrove area of the Acaraú River estuary (2°52'49 " S; 40°07'18 " W) in April 2025. Three researchers walked 250 meters during 30 minutes in the early morning at spring low tide, manually inspecting mangrove vegetation substrates composed of Rhizophora mangle, Avicennia sp., and Laguncularia racemosa. Individuals were collected using gloves, stored in labeled containers, and taken to the laboratory for morphometric analysis using a digital caliper. Water salinity was measured with a portable refractometer. A total of 24 *Lissachatina fulica* specimens were collected—two individuals were observed on pneumatophores, while the remaining ones were found among Avicennia sp. propagules. The mean shell height and width were 70.73 ± 13.34 mm and 39.21 ± 5.66 mm, respectively. The water salinity at the collection site measured 10 ppt, and the temperature was recorded at 29°C. This unprecedented observation indicates a possible expansion of the species' ecological range, showing its tolerance to environments with moderate salinity and capacity to use mangrove structures as both shelter and substrate. The site also presented signs of environmental degradation, which may have reduced ecological resistance and thus facilitated this invasive species' establishment. This study presents the first documented occurrence of *L. fulica* in a Brazilian mangrove, contributing new information for invasive species monitoring and emphasizing the urgent need for effective conservation strategies focused on protecting increasingly degraded and vulnerable urban mangrove ecosystems.

Funding Source: No.

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SPATIAL DISTRIBUTION AND SHELL SIZE VARIATION OF *Melampus coffea* (LINNAEUS, 1758) AND *M. monile* (BRUGUIÈRE, 1789) IN A MANGROVE FOREST IN NORTHEASTERN BRAZIL

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Keywords: estuarine gastropods, mangrove forest, niche partitioning, shell morphology.

The genus *Melampus* (Ellobiidae) is part of a group of pulmonate gastropods adapted to amphibious life in tropical and subtropical estuarine environments. In Brazil, *M. coffea* is frequently recorded in mangroves, while *M. monile* has a more elusive occurrence. This study evaluates variation in shell density and size in relation to mangrove forest structure and investigates spatial zonation patterns associated with distance from the main river channel. The study was conducted in the Guriú River estuary (02°53'42 " S, 40°26'57 " W), located between the municipalities of Jijoca de Jericoacoara and Camocim, Ceará, in northeastern Brazil. The area is characterized by quartz sand sediments and silt–clay substrates in flooded zones, which enable mangrove development. Three transects were established, each containing three 100 m² plots where vegetation was surveyed and mollusks were sampled within five 1 m² subplots per plot. Specimens were measured in the laboratory and a variance analysis was applied to verify the relationship between shell size and density across plots, as well as a correlation test between species and environmental factors. No significant differences in shell size were found among plots for either species. However, *M. coffea* showed higher densities in plots closer to the river, suggesting a zonation pattern ($F_{2.6} = 11.44$, $p = 0.008$). In contrast *M. monile* was evenly distributed. A negative correlation was observed between *M. coffea* density and *M. monile* shell size ($r = -0.85$), and between *M. coffea* shell size and *M. monile* density ($r = -0.98$). Additionally, *M. monile* shell size was negatively related to tree height ($r = -0.84$) and basal area ($r = -0.81$), suggesting a preference for less shaded, open-canopy areas. These findings suggest potential niche partitioning between the two sympatric species. The inverse relationships indicate that in areas where *M. coffea* is more abundant, *M. monile* individuals tend to be smaller. Such patterns imply that both species may be reducing overlap through spatial segregation or differential use of microhabitats and resources. This ecological adjustment likely minimizes direct competition, promoting coexistence in habitats where both species are present. Moreover, vegetation structure and interspecific interactions influence their spatial distribution, reinforcing the importance of preserving habitat heterogeneity and forest structure to support mangrove biodiversity conservation.

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UNDERSTANDING PREDATION IN *Octopus insularis*: A STUDY OF SHELL OPENING TECHNIQUE ON CLAMS

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Keywords: ecology, pulling, drilling.

Octopus insularis, a dominant cephalopod species within the shallow water marine ecosystems along the Brazilian coastline, demonstrates proficient predatory behaviors that enhance foraging efficiency. Leveraging principles of the Optimal Foraging Theory (OFT), these octopuses exhibit selective predation on bivalves, notably the clam *Chione cancellata*, utilizing advanced sensory and cognitive mechanisms during foraging. This study focuses on evaluating the size-selective predation strategies employed by *O. insularis* during different shell-opening technique. The research was conducted on a sandstone reef at Ponta do Mel beach in Northeastern Brazil. Shells were extracted from octopus burrows for analysis. Measurements included the mantle length of the octopuses, shell dimensions, and identification of drilling sites using a tape measure and digital caliper. Statistical analyses employed included t-tests for comparing shell sizes, chi-square tests to assess drilling site frequencies, Pearson correlation to evaluate size relationships, and ANOVA to analyze differences in prey sizes across octopus size categories. A total of 135 *C. cancellata* shells were collected from 35 *O. insularis* dens. The analysis revealed that drilled shells had a significantly smaller mean size (16.31 mm) compared to non-drilled shells (16.87 mm; p=0.015), consistent with the Optimal Foraging Theory's indication that the selection of smaller shells maximizes energy returns. No significant correlation was found between octopus mantle length and shell size (r=0.09, p=0.18), underscoring that predation choices are guided more by strategic considerations than predator size. ANOVA highlighted significant prey size differences between octopuses in the EP and P categories (F=3.85, p=0.025). However, no statistically significant relationship was discovered between octopus size categories and drilling site choice (p=0.11), suggesting that site selection is independent of octopus size. This supports an efficient generalist predation strategy, aligning with observations in various cephalopod species. Despite there being no statistical size category difference between octopuses using pulling versus drilling, 66% of the non-drilled shells were found in small octopus dens. This study reaffirms that *O. insularis* optimizes its foraging strategy by selecting smaller shells for drilling, maximizing energy efficiency. This behavior underscores strategic predation that is less about the predator's size and more about effective energy acquisition, consistent with the OFT. The tendency for smaller octopuses to predominantly choose non-drilled shells further illustrates a nuanced approach to prey handling, reflective of individual behavioral tactics.

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DETERMINANTS OF BETA-DIVERSITY IN MOLLUSC ASSEMBLAGES ACROSS INTERMITTENT RIVERS AND EPHEMERAL STREAMS

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Keywords: beta-diversity, environmental filters, geographical distances, small rivers.

Freshwater molluscs are among the most diverse and abundant taxa in intermittent rivers and ephemeral streams. However, we know little about the factors influencing their presence and abundance in these environments. To fill this knowledge gap, we investigated variation in mollusc assemblages along rivers in the Parnaíba Basin, northeastern Brazil, to understand the influence of spatial structuring and environmental filtering on their diversity and distribution. We collected molluscs associated with macrophytes and sediments near the confluence with the Parnaíba River, the intermediate stretch, and the headwaters of each of the eight main rivers in the basin. Collections occurred during the dry seasons of 2022 and 2023. We calculated and partitioned beta-diversity among sites. We used Principal Component Analysis to reduce the dimensionality of environmental data (physicochemical data - measured during sampling, and in geospatial data - extracted from GeoFRESH platform). Variation in species composition among sites in response to environmental filtering (environmental data) and spatial structuring (geographic distance) was assessed using a Generalised Dissimilarity Modelling approach. We also calculated and partitioned beta-diversity among sites. A total of 5,938 molluscs were collected, comprising 19 species of Gastropoda and Bivalvia. Beta-diversity among sampled sites was high (βtotal = 0.86) with a major contribution from species turnover (βturnover = 0.76; βnestedness = 0.11), indicating that mollusc species composition in the Parnaíba River Basin varies greatly. Model results indicate that response variables explained more than 50% of the differences in species composition among sites, with environmental filtering (57.5%) more important than geographic distance (2.7%) in explaining mollusc beta-diversity. Specific environmental conditions generated by heterogeneous hydrology and geomorphology, such as river intermittency, allow the occurrence of particular mollusc species (habitat specialists) and lead to greater dissimilarity among sites. The partitioning of environmental variables allowed us to identify that soil and topography were the environmental gradients with the greatest influence on the beta-diversity of limnic molluscs. These gradients are strongly linked to important environmental filters for limnic molluscs, such as pH, water temperature, and intermittency level, confirming the influence of the terrestrial environment on aquatic molluscs. Although our results explain a great part of the dissimilarity between mollusc assemblages, this still leaves a large amount of unexplained variation, indicating that other factors not considered in our study may also influence the occurrence of mollusc species. Future research should prioritise a more integrative approach to fill this gap, incorporating other factors, such as ecological interactions between species at multiple spatial scales, to better understand mollusc diversity patterns.

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UPWELLING CONDITIONS IMPACT THE RESPIRATORY PHYSIOLOGY OF ENCAPSULATED *Acanthina monodon* EMBRYOS, BUT DO NOT PRODUCE LATENT EFFECTS IN JUVENILES

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Keywords: upwelling, oxygen consumption, encapsule embryos.

Coastal upwelling zones are characterised by the upwelling of subsurface waters with low temperature, low oxygen and low pH compared to surface waters. These parameters can affect the performance of marine invertebrates inhabiting these zones, and this effect is likely to be greater in the early stages of their development. In this study, capsules of the gastropod *Acanthina monodon* containing embryos at different developmental stages (early, intermediate and advanced stages) were exposed to upwelling conditions (T° = 9°C; O2= 3mg/L; pH = 7.6) for 7 days. The immediate respiratory response and the subsequent latent effects on larval respiration, feeding and mortality during the first 30 days after hatching were assessed. Upwelling conditions had a negative effect on oxygen consumption rate in all stages of encapsulated *A. monodon* embryos. However, the advanced encapsulated stages (veliger larvae) were most affected, with an almost immediate reduction in oxygen consumption rate and a possible oxygen debt at the end of the exposure period. On the other hand, no latent effects were observed in the responses of the oxygen consumption rate, the feeding rate and the mortality rate of the juveniles at 30 days after hatching. The juvenile responses in this study are associated with a short exposure period. However, in the natural environment upwelling conditions are more frequent and prolonged, and climate change is expected to increase upwelling periods. Exposure to upwelling conditions for 7 days caused a decrease in oxygen consumption rates in encapsulated stages of the gastropod *A. monodon*. However, there were no latent effects on mortality and respiratory and feeding physiology of the juveniles after capsular hatching.

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THE GENERATION OF NON-CONSUMPTIVE EFFECTS IN A PREY SPECIES DEPENDS ON THE EXUDATE OF THE PREDATOR SPECIES

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Keywords: non-consumptive effects, prey, predator exudate.

Non-consumptive effects (NCEs) are all those indirect effects of the predator on the prey. These stressors may affect the behavior, morphology, physiology or life history traits of prey. Prey may detect signs of predator exudates in the vicinity, of attacked conspecifics, or even predator feces with signs of consumed conspecifics. In this research, ENC were determined in *Crepipatella peruviana* (protandric hermaphrodite gastropod with mixed embryonic development) on their physiological rates of oxygen consumption (OCR) and clearance rate (CR) at three life cycle stages (encapsulated veliger larvae, males and females), when exposed to exudate from the predators *Meyenaster gelatinosus* (top predator in coastal environments with high wave exposure) and *Argobuccinum pustulosum* (sympatric species with *C. peruviana* prey), and to the exudate of injured conspecifics of *C. peruviana*. Finally, the actual feeding capacity and attack rate of *M. gelatinosus* and *A. pustulosum* on specimens of the prey *C. peruviana* were evaluated. *M. gelatinosus* exudate did not induce ENC in any of the life stages of *C. peruviana*. In contrast, all life stages responded to the risk of predation by *A. pustulosum*. In the latter case, an increase in OCR was observed in larvae and females, and an increase in CR in males. A decrease in CR was also observed in females. On the other hand, the presence of exudate from injured conspecifics caused a decrease in CR in females and males of *C. peruviana*, but no changes in OCR were recorded. *M. gelatinosus* did not attack and consume prey when attached to the substrate, but did so when detached (0.5 indiv. day-1 seastar-1). However, *A. pustulosum* was able to effectively attack prey attached to the substrate (0.34 indiv. day-1 snail^{-1}, shell perforation with ABO as the attack mechanism). The lack of ENC in *C. peruviana* against the exudate of *M. gelatinosus* seems to be a response to the fact that the two species do not share the same habitat, so that prey are not able to detect a potential predation risk. It is possible that the attack mechanism of *M. gelatinosus* does not pose a risk to prey due to its shell shape and adhesive capacity. The increase in OCR or CR in males of *C. peruviana* exposed to the exudate of the predatory snail may be related to possible escape responses, and the decrease in CR in injured conspecifics may be considered as an anti-predatory response. Individuals of *C. peruviana*, at all stages of their life cycle, are able to recognise the danger signal of a sympatric predator such as *A. pustulosum*, as well as the signal of injured conspecifics, and respond with changes in some physiological rates. However, they do not recognise the danger signal of the top predator *M. gelatinosus*, a non-sympatric species with *C. peruviana*.

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DIVERSITY OF TERRESTRIAL MOLLUSCS IN FOREST AREAS OF THE FIOCRUZ MATA ATLÂNTICA BIOLOGICAL STATION, RIO DE JANEIRO, BRAZIL

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Keywords: environmental variables, seasonality, native species, forest, terrestrial gastropods.

Terrestrial gastropods are diverse and considered excellent models for ecological studies, being good bioindicators of environmental quality. In this study, we evaluated the diversity of this group, in two forest areas at the Fiocruz Atlantic Forest Biological Station (EFMA), Rio de Janeiro, RJ. Our objective was to investigate possible differences in the malacofauna composition of the two areas, and possible effects of the environmental factors and seasonality. The two selected areas were: Transition area (close to main EFMA trail), and recovered and preserved Forest area (far from the main trail). Three plots were selected (10 m x 20 m) in each area, with collections carried out by active search in 2020 and 2021. In each plot a portion of soil (200 g) was collected. The collected specimens were deposited in the Mollusk Collection of the Oswaldo Cruz Institute (CMIOC). Data on temperature (°C), relative humidity (%) and precipitation (mm) were obtained from the website of the National Institute of Meteorology - INMET. The information was organized in an electronic spreadsheet, and data treatment in RStudio version 4.2.2. In total, 122 individuals were found (64 live and 58 shells), and 15 native species were identified. The diversity analyses showed no significant differences between the species communities of the areas studied. The highest abundance of live individuals was recorded in the autumn, (n=19), where the humidity recorded was higher (80.6%). For the analysis of the percentage of contribution of each species per plot and per seasonal season, the SIMPER analysis showed that *Neocyclotus prominulus* was the species that contributed the most to the community in the areas, representing 44.8% of the total species found. The species *Habroconus semenlini*, *Anthinus multicolor*, *Simpulopsis tryoni*, *Cochlorina aurisleporis*, *Gonyostomus goniostomus* and *Rectartemom costulosus* were considered specialists, due to their low abundance, found only in the recovered forest area. None of the environmental factors evaluated (moisture, temperature, precipitation, seasonality) and soil physicochemical parameter (calcium) significantly affected the pattern of organization of the species in the studied areas. Despite this, it was possible to verify the correlation of the abundance of the species *Leiostracus perlucidus* with precipitation, an arboreal species common in areas of the Atlantic Forest of southeastern Brazil. These results demonstrate the importance of continuous efforts to identify terrestrial and native malacofauna in the EFMA area and in nearby areas, such as the Pedra Branca State Park, which possibly includes a diverse fauna with species not yet identified in these places. We also suggest conducting studies focused on the ecology of the species, aiming to establish preservation strategies for the group.

Funding Source: CAPES - Fundação Coordenação de Aperfeiçoamento de Pessoal de Nível Superior.

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CHANGES IN OXYGEN CONSUMPTION AS A NON-CONSUMPTIVE EFFECT IN ENCAPSULATED VELIGER LARVAE EXPOSED TO TOP PREDATOR EXUDATE

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Keywords: non-consumptive effects, prey, predator exudate, encapsulated larvae.

The presence of chemical signals from predators can induce the generation of non-consumptive effects (NCEs) in prey, modifying aspects such as their behavior and physiology. There is considerable information on NCEs in adult prey, but little information in early developmental stages of marine invertebrates. The respiratory physiological response of 4 species of gastropods in their veliger larval stages, 2 species with direct encapsulated development (*Acanthina monodon* and *Crepipatella dilatata*) and 2 species with mixed encapsulated development (*Concholepas concholepas* and *Crepipatella peruviana*), was evaluated in the presence of a chemical signal (exudate) from the top predator *Meyenaster gelatinosus*. During the experiments, the oxygen consumption rates of the encapsulated larvae were quantified without and with the risk signal (exudate) of seastar predation. Not all veliger stages have the same respiratory response (OCR) to predator exudate and this response appears to be species specific. The results seem to indicate that the response is conditioned by the mode of embryonic development; veliger larvae of species with direct encapsulated development tend to decrease their oxygen consumption in the face of predator exudate, whereas veliger larvae of species with mixed encapsulated development tend to increase their oxygen consumption. As indicated in previous studies, the reduction in OCR is often associated with an antipredator response and this is often related to the intensity of stress. In terms of the life cycle of the species, it is interesting to note that gastropod larvae already have predator detection mechanisms, but this is an understudied subject. The larval stages of the species studied are able to detect the presence of a top predator, as evidenced by changes in their oxygen consumption rates. The direction of the response seems to be related to the developmental mode of the species studied.

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INTERTIDAL ENCAPSULATED EMBRYOS EXPOSED TO ENVIRONMENTAL STRESSORS ASSOCIATED WITH THE TIDAL CYCLE: A STUDY BASED ON OXIDATIVE STRESS AND ANTIOXIDANT RESPONSE IN EARLY STAGES OF THE MURICID SNAIL *Acanthina monodon*

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Keywords: oxidative stress, intertidal encapsuled, tidal cycle.

Encapsulated embryos of intertidal species are exposed to extreme environmental fluctuations that threaten their viability. This study investigates the antioxidant mechanisms in encapsulated *Acanthina monodon* embryos exposed to emersion conditions during the tidal cycle, with the aim of identifying the role of antioxidant capacity at different developmental stages in mitigating oxidative cellular damage. During the summer season, *A. monodon* egg capsules were collected from the rocky intertidal zone in Calfuco (Southern Chile). Embryos were categorized into early, intermediate, and late developmental stages. A simulated tidal cycle (immersion, 3-hour emersion, and re-immersion) was conducted under controlled environmental conditions. Temperature, relative humidity, photosynthetically active radiation (PAR), and UV-B radiation were recorded. Oxidative damage (lipid peroxidation and protein carbonylation) and total antioxidant capacity were assessed in encapsulated embryos. During emersion, the ambient temperature increased from 18.8 °C to 32 °C, while the relative humidity decreased to 35%. Emersion caused a significant increase in oxidative damage at all developmental stages, as evidenced by increrased lipid peroxidation and protein carbonyl levels. However, early-stage embryos exhibited higher antioxidant capacity, likely due to maternally derived compounds such as carotenoids and glutathione, suggesting an adaptive strategy to environmental stress. Upon re-immersion, embryos activated antioxidant repair mechanisms, reducing accumulated damage and highlighting their physiological resilience to the dynamic conditions of the intertidal zone. No mortality was recorded 24 hours after exposure, indicating a high tolerance to short-term emersion events. These findings contribute to the understanding of how physical intertidal conditions influence early ontogenetic processes and may affect subsequent juvenile performance. This study demonstrates that *A. monodon* embryos exhibit stage-specific antioxidant responses that effectively mitigate oxidative damage induced by tidal emersion-re-inmersion cycles. The enhanced antioxidant capacity observed in early-stage embryos, likely due to maternal provisioning, highlights a crucial adaptive mechanism that ensures embryo viability under extreme and fluctuating intertidal conditions.

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SEASONAL RESPONSES OF AN AMPULLARIIDAE SPECIES TO ENVIRONMENTAL VARIATION IN BRAZILIAN SEMIARID RESERVOIRS

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Keywords: freshwater molluscs, population dynamics, environmental drivers.

Pomacea is the most diverse and widely distributed genus of apple snails within Ampullariidae. Although recognised for its economic and ecological–sanitary importance, the population dynamics of its natural species remain poorly explored. To address this gap, we investigated the seasonal variation in shell size and abundance of Pomacea sp. in artificial reservoirs in the Brazilian semiarid, a region marked by a hydrology strongly influenced by dry and rainy periods. Molluscs and environmental variables (water depth and temperature) were sampled monthly (June 2017–May 2019) in three reservoirs in São Julião, Piauí: DMZVA and Emparedade (rural zone) and São Julião (urban zone). Morphometric traits (shell length, width and height) were measured and analysed using Redundancy Analysis (RDA) to assess temporal (dry vs. rainy season) and spatial (reservoir) variation. Seasonal abundance patterns were assessed using circular models. The influence of environmental variables and seasonality on the abundance of *Pomacea* sp. was modelled using Generalised Linear Models (GLMs) with negative binomial distribution. We collected 509 individuals of *Pomacea* sp. across the three reservoirs, with higher abundance in São Julião (n=241) and Emparedade (n=238), and lower in DMZVA (n=30). Morphometric analyses indicated that 26.5% of shell size variation was explained by spatio-temporal factors, with reservoirs accounting for 63% of this variation (p=0.001). Shell size patterns mirrored those of abundance, with larger individuals found in São Julião and Emparedade. Abundance differed significantly between reservoirs (p=0.0001) and between seasons (p=0.0001), peaking in the dry season. GLM models explained 14% (Pseudo-R^2=0.14) of the variation in species abundance. The dry season, combined with higher temperatures, had a positive influence ($p<0.002$; $z=2.8$), while greater depths and the rainy season had a negative effect on abundance ($p<0.0002$; $z= -2.46$; $p<0.03$; $z=-1.54$). This negative effect may reflect changes in water column dynamics, such as thermal stratification in deeper waters, which limits benthic resources and oxygen, and leads to sulphide accumulation in anoxic sediment layers. This condition is toxic to most invertebrates, including molluscs. Circular analyses confirmed seasonal aggregation (rho=0.62; p=0.001), with a peak oriented towards the dry season (≈169°), reinforcing the role of seasonality in population dynamics. By investigating seasonal variation in shell size and abundance of *Pomacea* sp. in reservoirs of the Brazilian semiarid, we confirmed the species responds strongly to seasonal shifts, with higher abundance and larger individuals during the dry season. The significant influence of temperature and depth highlights the species' sensitivity to hydrological variation, providing valuable insights for management in ecosystems subject to climatic extremes.

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BEYOND THE SHELL: A GLOBAL SYNTHESIS OF GENETIC AND TAXONOMIC DIVERSITY IN AMPULLARIIDAE

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Keywords: apple snail, barcoding, completeness, taxonomic representativeness.

Ampullariids are freshwater molluscs of ecological and economic importance, yet their global distribution, genetic data and conservation status remain poorly documented, hindering the understanding of patterns of their biological diversity. To overcome these barriers, integrating data from different sources is necessary. This study investigates global distribution patterns, visibility, and genetic coverage in Ampullariidae species, emphasising the identification of geographic and taxonomic biases that limit biodiversity knowledge. We compiled georeferenced records from GBIF, SpeciesLink and BOLD genetic sequences for all valid family Ampullariidae species listed in MolluscaBase. A total of 10,340 occurrences (dated between 1853 and 2024) and 2,072 sequences were validated for spatial, taxonomic and biogeographic accuracy. Occurrences were differentiated by: i) origin – native or invasive; and ii) type – citizen science or biological collections. Sampling completeness was estimated using grids from 10 to 220 km², restricted to aquatic habitats (GLWD3). Taxonomic visibility was defined by presence in GBIF and/or BOLD platforms. Genetic data were analysed in terms of BINs, marker types and representativeness. Although covering 61% of described species, globally validated data on ampullariids reveal strong spatial and taxonomic biases. Most occurrences are derived from citizen science (63.1%), emphasising invasive species, mainly from the genus *Pomacea*. Countries with high native diversity, such as Brazil (>30 spp.), remain under-represented. Only 17.7% of species are simultaneously represented in occurrence and genetic databases, while 37.5% are “invisible”, with no public data. Sampling completeness remains critically low across all regions and spatial scales, with means below 2% at 60 km² resolution in North America, Sub-Saharan Africa, Central Asia and the Near East. Even at a 220 km² scale, over 90% of the expected diversity remains undocumented. Regarding genetic data, 36 Linnaean species were identified from 70 BINs, predominantly *Pomacea canaliculata* (74.3%), while native genera such as *Forbesopomus* and *Afropomus* lack any sequencing. Sixteen species were assigned to more than one BIN, notably *Pila pesmei* (n=8), *Lanistes ovum* and *Pomacea maculata* (n=6 each). Most genetic sequences originate from Asia, especially China (n=1,150), Taiwan (n=267) and Hong Kong (n=162). The Americas contributed 153 sequences, mainly from the USA (n=53), Brazil (n=35), and Argentina (n=35). Other countries contributed fewer than 30 sequences. This disproportion in occurrence records limits evolutionary and biogeographic inferences. Ampullariids remain under-represented, with efforts prioritising invasive taxa. These gaps hinder the monitoring of declines in native species and the understanding of the group’s evolutionary processes. Overcoming this bias requires taxonomic revisions, field expeditions, and integrative, targeted genetic efforts, which are essential to achieving the goals of the One Health approach, which ensures the conservation of continental aquatic ecosystems and the diversity of molluscs.

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COLONIAL SHADOWS IN MODERN TAXONOMY: A CASE STUDY ON TERRESTRIAL MOLLUSCS

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Keywords: biodiversity, knowledge gap, neocolonial practices, parachute discovery.

Although over 2.3 million species have been described, a substantial portion of biodiversity remains unknown, particularly in the Global South. This knowledge gap reflects historical inequalities and asymmetrical scientific practices. By analysing terrestrial mollusc descriptions over the past two decades, we examine how geopolitical and economic factors contribute to the exclusion and marginalisation of Global South researchers, as well as their limited access to analytical tools in mollusc species discovery. We analysed original descriptions of 2,414 terrestrial mollusc species published between 2002 and 2022 to extract data on resident researcher involvement, first-author nationality, and indicators of comprehensiveness, including the number of type specimens, publication length, and lines of evidence covered in each species description. We classified descriptions as domestic, collaborative, or parachute research using type-localities and authors' affiliations. We used Kruskal-Wallis and chi-square tests to verify whether descriptions from the Global North and South differed in terms of local researcher exclusion, marginalisation, and taxonomic comprehensiveness. All analyses were conducted in R (version 4.3.3). Despite harbouring most of the world's biodiversity, countries in the Global South remain underrepresented in scientific production. Our results show that 76% of species described between 2002 and 2022 originated in the Global South, yet only 27.1% were led by local researchers. Most foreign-led discoveries (78.2%) lacked resident participation, characterising parachute science. A positive correlation emerged between per capita GDP and the number of foreign discoveries ($R = 0.489$; $p = 0.001$), with the USA, Hungary, and the Netherlands accounting for 58% of such cases. Biodiverse hotspots like Southeast Asia and the Pacific Islands hosted 55% of these discoveries. Descriptions in the Global South used fewer anatomical and molecular analyses and had type series 1.6 times smaller, reflecting disparities in access to tools and infrastructure. Lack of reciprocity was also evident: 93% of Global South collaborations involved authors from the North, whereas only 7% of Northern-led works included authors from the South. These patterns reflect a persistent academic hierarchy in which the South acts primarily as a data provider, with limited intellectual leadership in biodiversity science. Our findings expose a systemic imbalance: the Global South hosts biodiversity, while the Global North retains leadership, technology, and academic rewards. Closing the taxonomic gap requires sustained investment in infrastructure, training, and funding within the South and equitable partnerships that share data, authorship, and tools. Extractive practices will continue undermining local capacity and global biodiversity knowledge without these changes.

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LAST GLACIAL MAXIMUM TO PRESENT: MODELING *Agathistoma* SPECIES' RESPONSES TO GLACIAL-INTERGLACIAL TRANSITIONS IN THE WESTERN ATLANTIC

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Keywords: paleoclimatic variable, marine biogeography, SDM.

The Pleistocene glacial cycles, particularly during the Last Glacial Maximum (LGM), profoundly influenced marine species distributions. The marine gastropod genus *Agathistoma* represents a compelling biogeography study system due to its restricted ranges yet poorly understood historical distributional responses to climatic fluctuations. This study applied Species Distribution Models (SDMs) to six Western Atlantic *Agathistoma* species to predict their distribution and changes in environmental suitability since the LGM. We compiled contemporary occurrence records for six *Agathistoma* species and paired these with high-resolution paleoclimatic data layers representing current conditions, the Mid-Holocene (MH), and the LGM. These environmental datasets were spatially calibrated using vector boundaries of Atlantic marine biogeographic realms. Using an ensemble modeling approach, we developed Species Distribution Models (SDMs) evaluated through rigorous validation protocols (AUC and TSS metrics), which we then projected across all three temporal scenarios. From these model outputs, we generated composite species richness maps, enabling quantitative analysis of spatiotemporal distributional changes in Agathistoma assemblages throughout the late Quaternary. The richness maps revealed lower species diversity during the LGM with progressive recovery through MH to present maxima. The distance to shore and sea surface temperature as primary drivers, except for *A. viridulum* and *A. nordestinum*. Projections revealed severe contraction during the LGM, especially for *A. hotessierianum*, *A. fasciatum*, and *A. lividomaculatum*. *Agathistoma patagonicum* exhibited a pronounced latitudinal range shift from the LGM to present, with temperature variation emerging as the primary driver of this distributional change. In contrast, *A. viridulum* maintained a widespread distribution throughout all three climatic periods, a pattern consistent with its weaker temperature dependence in SDMs and indicative of broader thermal tolerance compared to congeners. *A. nordestinum* exhibited a constrained distribution, possibly explained by its sensitivity to salinity fluctuations, with the mean annual sea surface salinity emerging as the second-most influential variable in our models. This restricted distribution suggests lower tolerance to salinity variations, where riverine discharge zones appear to function as effective biogeographic barriers. Our results demonstrate that Pleistocene glacial cycles significantly impacted on Agathistoma distribution patterns accross the Western Atlantic, particularly during the LGM. We successfully reconstructed temporal shifts in both environmental suitability and biogeographic ranges, while simultaneously validating SDM approaches as powerful tools for elucidating historical biogeographic processes and marine species' responses to Quaternary climate oscillations.

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POPULATION DYNAMICS OF FRESHWATER GASTROPODS IN BRAZILIAN SEMIARID RESERVOIRS

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Keywords: invasive species, dry-forest reservoirs, Gastropoda, seasonality.

The Caatinga biome, characterised by high temperatures and irregular rainfall, relies on reservoirs for water management. However, such structures can foster invasive gastropods that disrupt native populations and increase disease-transmission risks. This study assessed how climatic seasonality shapes populations of the medically necessary native *Biomphalaria straminea* and the exotic *Melanoides tuberculata* in three artificial reservoirs of the semiarid region. Monthly surveys (Jun 2017 – Mar 2020) were conducted at three reservoirs (Emparedade, DMZVA and São Julião) in São Julião, Piauí. Age structure was determined from counts of juveniles and adults based on linear shell measurements. Shell measurements were subjected to principal-components analysis, with PC-1 used as a proxy for body size. Inter-reservoir differences in size were tested with Tukey's. Seasonal concentration of abundance was evaluated with circular statistics (Rayleigh test, mean vector length ρ). Finally, negative-binomial generalised linear models assessed the effects of season (dry vs wet) and water temperature on species abundance. We collected 72.677 gastropods: 5.555 *B. straminea* and 67.122 *M. tuberculata*. Abundance was highest in Emparedade (57 %), followed by DMZVA (24 %) and São Julião (19 %). More individuals occurred in the dry season (49.597) than in the rainy season (23.080). Abundances of both species varied significantly by reservoir and season. During the dry season, 3.896 juvenile and 989 adult *B. straminea*, and 3.917 juveniles plus 5.771 adults *M. tuberculata* were recorded; rainy season counts fell to 512 juveniles and 158 adults (*B. straminea*) and 1,934 juveniles plus 3,225 adults (*M. tuberculata*). Circular analysis showed a seasonal distribution for *B. straminea* (ρ = 0.58) but not for *M. tuberculata* (ρ < 0.5). GLMs indicated significant effects of season and temperature on *B. straminea* (pseudo-R^2 = 0.36): negative for the wet season (β = -1.63; p = 0.007) and water temperature (β = -0.64; p = 0.037), positive for the dry season (β = 5.30; p = 0.007). Environmental variables were not significant for *M. tuberculata* (pseudo-R^2 = 0.12). Mean shell length was 5.11 ± 1.16 mm for *B. straminea* and 3.80 ± 1.22 mm for *M. tuberculata*; size varied significantly among reservoirs for both species, more strongly for *B. straminea* (η^2 = 0.10; p < 0.001, largest at São Julião) than for *M. tuberculata* (η^2 = 0.06; p < 0.001, Emparedade and São Julião larger than DMZVA). Although both species coexist, *M. tuberculata* dominates the three reservoirs, demonstrating high adaptability and resilience and likely impacts on native fauna. Contrasts in size and distribution, particularly for *B. straminea*, suggest local environmental influences. These findings enhance understanding of gastropod dynamics in semi-arid systems and inform the management of invasive species and medically relevant vectors.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

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LETHAL AND SUBLETHAL RESPONSES OF THE INVASIVE BIVALVE *Mytilopsis leucophaeata* TO BIS(2-ETHYLHEXYL) PHTHALATE (DEHP)

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Keywords: ecotoxicology, false mussel, plasticizers, Rodrigo de Freitas Lagoon.

DEHP (bis(2-ethylhexyl) phthalate) is a plasticizer used to increase the flexibility and durability of plastic materials, and can contaminate aquatic environments such as Rodrigo de Freitas Lagoon (Rio de Janeiro, Brazil). In this lagoon, the invasive bivalve *Mytilopsis leucophaeata* is present and can act as a bioindicator of DEHP toxicity. The present study aims to evaluate the lethal and sublethal responses of *M. leucophaeata* to different concentrations of DEHP. In the experimental assays, five individuals of *M. leucophaeata* were used by replicate to evaluate the lethal and sublethal responses during the exposure times of 24, 48, 72 and 96 hours, at eight different concentrations of DEHP (0.045, 0.094, 0.187, 0.375, 0.750, 1.50, 3.00 and 6.00 mg L–1), in triplicates, with constant salinity (12.6) and temperature (25 ± 1° C). The negative control consisted of the same number of individuals and conditions, but without DEHP. Lethality was observed when the individuals were completely open or floating, while the sublethal responses were analyzed from three aspects: 1) response to stimulus, 2) byssus production, and 3) cluster formation. The survival of *M. leucophaeata* individuals was observed across all eight DEHP concentrations tested during the first 48 hours. After 72 hours, mortality occurred, reaching a cumulative mortality rate of 20% at the concentration of 1.50 mg L^{-1} after 96 hours. No significant differences were observed among concentrations (PERMANOVA, $p = 0.15$) and exposure time (PERMANOVA, $p = 0.84$) on the lethality of *M. leucophaeata*. Regarding the sublethal responses, concentrations showed significant effects on the response to stimulus (PERMANOVA, $p = 0.0001$), while for the production of byssus and cluster formation, significant differences were observed between the concentrations (PERMANOVA, $p = 0.0001$ for both) and exposure time (PERMANOVA, $p = 0.0105$ and $p = 0.04$, respectively). The interaction between concentration and time was significant only for byssus production (PERMANOVA, $p = 0.0023$). For the first time, this study presents the effects of DEHP exposure on a *Mytilopsis* species. Similar patterns were observed in previous studies for other bivalves, especially Mytilus species, with no mortality at different DEHP concentrations for M. coruscus, *M. galloprovincialis* and M. edulis. The response to stimulus seems to be a good indicator for ecotoxicological assays, although significant results were detected at concentrations above environmentally relevant levels (≤ 0.168 mg L^{-1}). Byssus production and cluster formation were reduced even in the negative control after 72 hours, indicating that these sublethal responses may not be suitable for assessing such effects. The invasive bivalve *M. leucophaeata* showed broad tolerance to different concentrations of DEHP, although sublethal responses did not provide clear evidence of negative effects on the species. However, increased DEHP contamination in aquatic ecosystems can affect a wide range of organisms, potentially including humans. Therefore, preventive measures must be taken to reduce DEHP contamination and mitigate the impacts on biota.

Funding Source: CAPES; CNPq; FAPERJ; INOVA UNIRIO.

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MORPHOGEOMETRIC PATTERNS OF *Anomalocardia flexuosa* (LINNAEUS, 1767) (BIVALVIA: VENERIDAE) ALONG THE BRAZILIAN COAST

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Keywords: molluscs, morphology, ecology, geometrics morphometrics.

Anomalocardia flexuosa is a shallow-burrowing bivalve mollusk that can be found in various habitats along the Brazilian coast, playing a significant socioeconomic role for many human communities. Mollusk shells reflect the diversity of life modes they exhibit, and several environmental factors can influence their shape. Quantitative approaches to biological forms, such as geometric morphometrics, introduce the mathematical and statistical rigor necessary for the accurate description and comparison of these forms. A total of 1,872 adult *Anomalocardia flexuosa* specimens (≥13.80 mm shell length) were collected along the Brazilian coast, with soft tissues removed and shells photographed under standardized conditions. Fourteen homologous landmarks, representing key shell structures such as the hinge, adductor muscles, escutcheon, and lunule, were digitized. Generalized Procrustes Analysis (GPA) was applied to isolate shape variation by removing effects of position, scale, and orientation. The aligned coordinates were projected into Euclidean space to generate a variance-covariance matrix, which served as the basis for subsequent analyses: shell shape was assessed in relation to size, population-level variation via Principal Component Analysis (PCA), and group differentiation through Canonical Variate Analysis (CVA). The study analyzed 1,872 individuals of *A. flexuosa* collected from 12 Brazilian states, with shell lengths ranging from 13.81 to 36.29 mm. Specimens from Bragança (Pará) were identified as the largest, while those from Icapuí (Ceará), Rio Tinto (Paraíba), and Camocim (Ceará) were among the smallest. ANOVA results indicated that shell shape varied significantly with both individual size and among sampling locations. The first three PCA axes accounted for 60.78% of the total shape variation, with prominent changes observed in the posterior extremity and shell margins. CVA yielded two principal axes, revealing some overlap among samples but also differences that contributed to distinguishing between groups. The most notable differences were detected in the shell margin region and in the orientation of the posterior adductor muscle and dentition, as well as in landmarks associated with the pallial sinus and dentition. Habitat and climate differences appear to result in larger shells at the extremes of the species' distribution. Resource availability may directly influence adult body size. Body size is shaped by ecological and evolutionary trade-offs involving growth, resource availability, reproduction, predation, longevity, and other factors, including historical events. The results demonstrated significant shape variation in shells of *A. flexuosa* across its distribution along the Brazilian coast. GPA and PCA provided detailed insights into shell shape variation. The morphogeometric methods employed in this study proved to be an effective, precise, and low-cost approach for investigating shell shape variation in *A. flexuosa*, and are applicable to other marine invertebrate populations, particularly bivalves.

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MALACOFAUNA FROM THE GEOMAR II AND III OCEANOGRAPHIC EXPEDITIONS: AN ASSOCIATION WITH THE MESOPHOTIC REEFS OF NORTHERNMOST BRAZIL

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Keywords: GEOMAR, mesophotic reefs, continental shelf.

The Amazon shelf is environmentally and economically important, yet its benthic fauna remains poorly understood. The GEOMAR expeditions in the 1970s revealed new mollusk species. More recently, the discovery of the Amazon Reef System (GARS) has renewed scientific interest. This study analyzes mollusks collected during those expeditions, contributing to the knowledge of biodiversity and species distribution in the northern region of Brazil. Samples were collected by dredging conducted by the Oceanographic Vessel Almirante Saldanha between 1969 and 1971. Part of the material was initially stored at the Marine Sciences Laboratory of UFC, now held at the Zoobenthos Laboratory. Malacological specimens are cataloged in the Professor Henry Ramos Matthews Malacological Collection (CMPHRM), series "A," though most remain unexamined. A total of 56 sampling stations were investigated, covering sandy, muddy, transitional, and shelf sediments, reflecting the region's environmental heterogeneity. Malacofauna distribution was analyzed based on substrate texture, using data from the GEOMAR II and III expeditions, provided by the Hydrography and Navigation Directorate (DHT) of the Brazilian Navy. A total of 311 mollusk taxa were identified, distributed among the classes Gastropoda, Bivalvia, and Scaphopoda, with a predominance of bivalves, especially in sandy-biodetritic facies associated with consolidated substrates. The highest diversity was observed in areas under the influence of the Great Amazon Reef System (GARS), suggesting a positive relationship between biogenic reefs and malacological richness, with notable species such as *Acar domingensis*, *Arca zebra*, and *Nuculana acuta*. Despite the high species richness found, the analyses indicated that the molluscan richness in the region is underestimated, highlighting the need for complementary studies to achieve a more comprehensive assessment. The analyzed material was incorporated into the Professor Henry Ramos Matthews Malacological Collection (CMPHRM), contributing to the preservation and expansion of knowledge about the marine biodiversity of the Amazon shelf. This study reinforces the importance of environmental monitoring initiatives, especially in light of the growing economic activities in the region, such as oil exploration, which may threaten the integrity of these unique reef ecosystems. The malacofauna of the Amapá shelf is quite rich, indicating potential for new species. The diversity of mollusks is still underestimated in the region. Areas near the Great Amazon Reef System show that greater reef complexity is linked to higher diversity. The materials from the GEOMAR II and III expeditions, stored at CMPHRM, are essential for expanding knowledge about the biodiversity of northern Brazil.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior – Capes.

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NEW RECORDS OF SEA SLUGS (GASTROPODA: HETEROBRANCHIA) FROM CLARION ISLAND, REVILLAGIGEDO ISLANDS, MÉXICO

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Keywords: gastropods, Eastern Tropical Pacific, intertidal zone, oceanic island, marine biodiversity.

The Revillagigedo Archipelago is located on the East Tropical Pacific; its consists of four volcanic islands. Clarion Island is the most Western and remote island of this Marine National Park. The region is influenced by the cold currents from California and the warm waters of the North Equatorial current, creating a convergence zone, with high marine biodiversity. The objective of this contribution is to provide a species list. The study was performed from January to March of 2023, and February to March 2024, through a continual survey of the beaches, intertidal pools and shallow reef areas in the south side of the island. The shallow intertidal sampling sites were selected for their accessibility during low tide, as these are the times when active searches for specimens can be conducted in the area. For the same reason, searches in the deep intertidal zone were conducted during high tide. In total, 143 specimens of gastropod mollusks of the Heterobranchia subclass belonging to 14 species were recorded at the 5 intertidal sites of Clarión Island. 13 were new records for this island and 5 new records for the Revillagigedo Archipelago. With the new records presented in this study, the number of sea slugs increases from 42 to 47 species in the Archipelago National Park, and from 5 to 18 species in Clarión Island.This richness of sea slug species in the archipelago is comparable to the richness recorded in other islands and archipelagos of the PET, such as Clipperton Island, France (Kaiser, 2007), Cocos Island, Costa Rica (García-Méndez and Camacho-García, 2015), Malpelo Island, Colombia (Kaiser and Bryce, 2001) and the Galapagos Islands, Ecuador (Kaiser, 1997). This study significantly contributes to the knowledge of the biodiversity of island heterobranch sea slugs of the Tropical Pacific. It is important to complement this contribution with molecular studies to confirm some of the current taxonomic uncertainties and to conduct phylogeographic and connectivity studies in the Eastern Tropical Pacific.

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HOLE IN THE SHELL: PREY SELECTIVITY BY PREDATORY GASTROPODS OF THE FAMILIES MURICIDAE AND NATICIDAE

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Keywords: Mollusca, predatory drilling, Holocene, thanatocenoses, ecological interactions.

The study of modern shell beds allows for a better understanding of ecological and evolutionary interactions, such as predation by Naticidae and Muricidae gastropods, which drill into bivalve shells, leaving a predatory borehole. This study analyzed predatory drill holes and diversity in bivalve mollusk thanatocoenoses from a beach (Matinhos City) on the Paraná (Brazil), aiming to investigate predation patterns, gastropod feeding preferences, and the ecological relationship between predator and prey. Four replicas of a shell bed were collected with a corer sampler, sieved, and divided into ≥2 mm and <2 mm fractions. Samples from the first fraction were analyzed under a stereo microscope to identify predatory drill holes. The position of each hole on the valves (dorsal, central, ventral, indeterminate) was determined, and the internal and external diameters (mm) were measured using ImageJ. The Predatory Drill Hole Difference (PDHD) index was applied to infer the predator (Naticidae or Muricidae). Predated bivalves were identified (family, genus, species). Samples from the second fraction were analyzed for the presence/absence of drill holes. Data were analyzed using frequency, ANOVA, and Tukey's test in STATISTICA. Screening resulted in 1,298 bivalve shells ≥2 mm, of which 6.3% (82) exhibited predatory drill holes. Holes were concentrated in the dorsal region of the valves (60.76%), followed by the central (22.26%), ventral (9.16%), and indeterminate (7.82%) regions. Among the predated bivalves, the most representative families were Tellinidae (32), Ostreidae (10), Lucinidae (9), and Mactridae (9), along with Arcidae, Cardiidae, Corbulidae, Myidae, Mytilidae, Plicatulidae, and Veneridae. The identified prey included *Lunarca ovalis* (Bruguière, 1789), *Cucullaearca candida* (Helbling, 1779), *Corbula* sp. (Bruguière, 1797), *Codakia* sp. (Scopoli, 1777), *Divalinga quadrisulcata* (A. d'Orbigny, 1846), *Mulinia cleryana* (A. d'Orbigny, 1846), *Sphenia fragilis* (H. Adams & A. Adams, 1854), *Perna* sp. (Philipsson, 1788), *Perna perna* (Linnaeus, 1758), *Modiolus* sp. (Lamarck, 1799), *Plicatula gibbosa* (Lamarck, 1801), *Tivela* sp. (Link, 1807), and *Strigilla* sp. (W. Turton, 1822). Prey-predator relationship indicated that Naticidae were the main predators of Tellinidae in the dorsal region, especially in *Strigilla* sp., as well as of Corbulidae, Mactridae, and Lucinidae. This suggests dietary preference and a predatory pattern towards areas of higher visceral mass of the bivalves. Muricidae primarily preyed on Mytilidae and Ostreidae, with no specific drill hole position pattern. Bivalves <2 mm, 37 specimens exhibited drill holes (4.81%), and 717 were not (95.19%). However, only intact valves (<2 mm) were considered in this analysis, due to the fragmentation of many specimens, which hindered the identification of drill holes and limited inferences regarding size and age selectivity in the prey-predator relationship due to information loss. The diversity analysis revealed the bivalve families most affected by predation from Naticidae and Muricidae. These results, combined with the higher occurrence of dorsal drill holes in Tellinidae, indicate selective behavior by predators, enhancing the understanding of trophic interactions and predatory patterns in the shell record. Expanded sampling, including analysis of drill size and valve biometrics, may further clarify prey preferences, age ranges involved, and the cost-benefit relationships underlying predation.

Funding Source: No.

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MALACOFAUNA ASSOCIATED WITH TRAWLING FISHERY BYCATCH OF *Xiphopenaeus* spp (HELLER, 1862), THE SEVEN-BEARD SHRIMP FROM OFF THE COAST OF BAHIA, NORTHEASTERN BRAZIL

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Keywords: mollusks, Brazilian coast.

Mollusks contribute significantly to the biomass recorded in trawling worldwide. In Brazil, this type of activity has been taking place since 1960, and is of great economic importance, despite its impacts on several marine habitats, threatening coastal environments. Our objective was to describe the spatial and temporal distribution of mollusk assemblages captured as bycatch during the seven-beard shrimp fishery off the coast of Ilhéus, southern Bahia. Between March 2003 and February 2005, monthly door trawls were carried out in three locations (Olivença, Aeroporto and São Domingos), at approximately 16 m water depth, off the coast of Ilhéus-BA, Brazil. The nets were 20 mm between knots when panned and 16 mm mesh when bagged. The captured specimens were preserved in alcohol 70%, identified using specialized bibliography and validated by an expert in the area. The total abundance and frequency of occurrence of each species were calculated, in addition to the nonparametric Kruskal-Wallis and Mann-Whitney tests to verify the variation of richness among stations; and among the averages of the capture sites, respectively. We collected a total of 1,158 individuals. Considering the sum of the three stations, among the individuals alive at the time of collection (with the soft part present), 51 bivalves (5%), 278 gastropods (26%) and 729 cephalopods (69%) were identified; while among the dead individuals, but with intact shells, one bivalve and 81 gastropods were recorded. As for the distribution, Olivença rendered the lowest abundance, followed by São Domingos, while Aeroporto had the highest. No significant difference was observed between the specific richness of the capture stations (p-value = 0.0916). Regarding the differences in the composition of the malacofauna accompanying the trawling of the seven-barba shrimp, the Mann-Whitney test revealed that Station 1 presented significant differences, (p-level = 0.01933) considering the abundances of collected mollusks, alive and dead, with alive ones being more frequent. Stations 2 (p-level = 0.2132) and 3 (p-level = 0.2525) did not show significant differences. Studies identifying species of shrimp caught in shrimp fishing are rare off the Brazilian coast. The coast of Sergipe showed greater richness (54 species), but sampling, was carried out up to 30 m. On the coast of Santa Catarina, 22 species were identified, with greater richness of gastropods. This study presents new information on the malacofauna captured along the coast of Bahia, including new records for state, in addition to providing data on abundance and temporal distribution. We are proposing to implement public policies aimed at studying and managing fishing resources, mainly the fauna accompanying mollusk species, as well as increasing partnerships between researchers.

Funding Source: CNPq “Projeto AFAPESCA”, CAPES e UESC.

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TEMPORAL DISTRIBUTION OF THE SQUID *Loliguncula brevis* (BLAINVILLE, 1823) PRESENT IN THE BYCATCH OF THE TRAWL FISHERY FOR THE SEVEN-BEARDED SHRIMP *Xiphopenaeus* spp (HELLER, 1862) ON COAST OF BAHIA, NORTHEASTERN BRAZIL

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Keywords: mollusks, ecology, Brazilian coast.

Trawling activities are intense along the Brazilian coast. Mollusks make up most of species richness and abundance caught accidentally in the shrimp fisheries, with Cephalopods being the best represented. *Loliguncula brevis* is the most abundant species, with no information available for the coast of Bahia. Our objective was to evaluate the temporal distribution of *Loliguncula brevis* caught in the shrimp trawl fishery in Ilhéus, Bahia. Between March 2003 and February 2005, monthly door trawls were carried out in three locations (Olivença, Aeroporto and São Domingos), at water depth of approximately 16 m, off the coast of Ilhéus-BA, Brazil. The nets mesh size was 20 mm between knots when panning and 16 mm when bagging. After sampling, the specimens were preserved in 70% alcohol and identified using a stereoscopic microscope, using specialized bibliography and validation by an expert in the area. The total abundance and frequency of occurrence of the species were calculated. In the first year (March/2003 to February/2004), the best results were those of August, totaling 193 animals. On the second year (March/2004 to February/2005), in May station three (81 inds) was more numerous, and January/2005 only one individual was recorded in station 1. Regarding the sampling points, Station 2 (Airport) rendered the best results, recording 365 squid; followed by Station 3 (São Domingos) with 305. Station 1 (Olivença) resulted in only 59 individuals. Several species of mollusks are recorded as bycatch from trawl fisheries, such as squid of genus Doryteuthis, the coastal squid *L. brevis* and octopuses of the genus *Octopus*. The large representation of the Loliginidae family observed in this study reflects the findings of previous studies, which also collected large quantities of squid and *Octopus*. As to the relative frequency (%) of the species and their classification, *L. brevis* was the most frequent (90.5%). *L. brevis* was the only cephalopod present at high occurrence, having been recorded in all seasons. The species is economically important, but is not commercialized in the region and is discarded in most fisheries, although some fishermen sell it as bait for other types of fishing. This study provides the first record of the occurrence and monthly distribution of *Loliguncula brevis* off the coast of Ilhéus, Bahia, northeastern Brazil. Despite the high number of individuals captured in fishing, this species has no economic importance in the region, and is discarded during sorting. The impacts of this activity on the local population are still unknown.

Funding Source: CAPES “Projeto AFAPESCA” e UESC.

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LONG TERM CHANGES ON ABUNDANCE AND POPULATION STRUCTURE OF THE DYE PURPLE SNAIL ON THE COAST OF JALISCO, MEXICO; IMPLICATION FOR THE SPECIES CONSERVATION.

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Keywords: Gastropods, Dye purple snail, abundance, conservation.

The dye purple snail is a marine mollusk that is characterized for its production of a natural purple dye. It inhabits the rocky intertidal zone from Pacific Panamic Province. It´s main characteristic against all other mollusk, is that it's not necessary to sacrifice the animal to obtain the dye. It is considered an important economic and cultural resource since the pre-Columbian era, the snail has been used to dye ceremonial dresses. To assess long-term changes in the abundance and population structure of the snail, surveys were conducted in 1991, 2006, and 2023, covering a period of 3 decades. Line transects were carried out in the intertidal area of nine rocky shores along the Jalisco coast. Sampling was carried out using transects, running parallel to the coast on a 50-m-long, 2-m-wide rope line, covering a total of 100 m^2. To estimate relative abundance, the transects were placed in the snail's distribution zones, which are the middle and upper mesolitoral zones. Each snail collected was measured with a digital vernier caliper and the sex of each specimen was determined (Michel-Mofin, et al, 2000). Although the snail has been a specially protected species under Mexican environmental laws since 1994, and is considered a cultural resource, reserving it use and use for indigenous group on the Pacific coast of Mexico. Despite this, the results obtained indicate a decrease in the abundance of the snail over time and a significant decrease in the average size and number of large snails due to two main hazards. First, a growing fishery for all types of invertebrates found in the rocky intertidal zone, capturing species such as snails, oysters, limpets, and chitons, which are then marketed regionally. And secondly, habitat loss due to the construction of tourist developments. The analysis of the available information indicates the main threat for the survival of the snail, is the growing fisheries over this species and its preys on several states of the pacific coast that could affect its populations in the short term. A new conservation status could be required.

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DRAWING LINES FROM SEA TO SEA: MAPPING GLOBAL BIOGEOGRAPHIC REGIONS OF NUDIBRANCH SPECIES

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Keywords: bioregionalization, Cladobranchia, Doridina, infomap bioregions, marine biogeography, Nudibranchia.

The definition of biogeographical regions, or 'bioregions', has been essential in historical biogeography. Studies have focused on terrestrial animals and plants, while marine invertebrate groups have received less attention. Nudibranchs are a diverse marine gastropod group with unique life strategies and varied dispersal capacities, although their biogeography remains understudied. This study identifies global-scale bioregions for nudibranchs across different taxonomic levels, filling a major gap in our understanding of their distribution. We based our bioregionalization on point occurrences of globally distributed nudibranchs compiled from the GBIF and OBIS repositories. We applied automated cleaning using 'CoordinateCleaner' package in R. Species names were cross-validated with the WoRMS. To define bioregions, we worked at the species and suborder levels using grid cells as geographic units, applying the Infomap Bioregions 2 network method with 20 trials. The bipartite network had 2,793 nodes, comprising 1,733 species connected to 1,060 grid cells with 46145 links weighted by range size. We set adaptive resolution of grid cells from 1° to 4° with a cell capacity of 10 to 100, balancing sampling bias and regional representation. Species occurrences are unevenly distributed, with higher concentrations in the Indo-Pacific, Eastern Pacific, North Atlantic, and Mediterranean Sea. In contrast, the Caribbean Sea and West Atlantic are the most underrepresented regions. The Infomap Bioregions 2 identified a hierarchy of biogeographical regions with up to three nested levels. The bioregions identified for Cladobranchia and Doridina subsets were generally similar, with some minor differences. For this study, we investigated the first two levels, termed as regions and subregions. At the first level, we found four regions: (1) Indo-Pacific, (2) Eastern Pacific and Tropical West Atlantic, (3) North Atlantic and Mediterranean Sea, and (4) Southern Ocean and South Atlantic region. At the second level, we identified 52 clusters nested within these regions. We highlight the most extensive and coherent subregions, named following Spalding et al. (2007), Costello et al. (2017), and Victorero et al. (2023): (1.1) Central Indo-Pacific, (1.2) Western Indo-Pacific, (1.3) South Australia, (1.4) New Zealand, (1.5) Subtropical Japan, (2.1) Temperate Northern Pacific, (2.2) Tropical Eastern Pacific, (2.3) Tropical Western Atlantic, (3.1) Temperate Northern Atlantic, (3.2) Mediterranean Sea and (3.3) Red Sea. Large areas in coastal South America and Western Africa resulted in the absence of distributional data, likely due to insufficient sampling. In general, some bioregions matched previous global marine frameworks, while others emerged uniquely from our analysis. This study reinforces the need for increased marine biodiversity data collection in undersampled regions. Our analysis identified four major regions and multiple subregions globally, influenced in part by uneven data availability. This highlights the urgent need for improved biodiversity sampling and provides a foundation for marine conservation planning in key hotspot areas. Future phases will explore the influence of environmental and geological drivers, assess endemism, turnover, and connectivity among bioregions, and expand this biogeographic framework to other taxonomic levels, including superfamilies, families, and genera.

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ECOSYSTEM ENGINEERS: MEGA-FILTERING BIVALVES CREATE BIOGEOCHEMICAL HOTSPOTS ON THE BOTTOM OF A CHILEAN LAKE

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Keywords: ecosystem engineers.

Freshwater mussels such as *Diplodon chilensis* (Hyriidae) are the largest, most biomass-dominant and long-lived invertebrates in Chilean freshwater ecosystems, considered megafilter feeders compared to smaller filtering invertebrates. This study aimed to evaluate the role of *D. chilensis* as an ecosystem engineer, experimentally analyzing its capacity to generate biogeochemical hotspots and modify the structure of benthic communities in the sediments of a eutrophic lake in southern Chile. The study was conducted in Laguna Chica de San Pedro (36°50'40"S;73°04'59"W),a meso-eutrophic lake in south-central Chile,where dense but declining populations of *Diplodon chilensis* (up to ~400 ind./m^2) persist.A randomized complete block design was implemented using in situ experimental mesocosms submerged for 8 weeks at 6–7 m depth.The experiment was repeated every three months between October 2023 and October 2024.Four plastic racks (50 × 50 cm), each with nine aluminum trays filled with pre-washed fine sand,were assigned to three treatments:(1)sand only (Control 1);(2)sand plus four sealed shells of dead *D. chilensis* (Control 2);and (3)sand plus five live adults(Treatment).Sediments were analyzed for TOM, Total-N, Total-P, meiofauna, macrofauna, and shell-associated chlorophyll-a and fauna. The presence of live *Diplodon chilensis* significantly increased biogeochemical and biological variables in the sediment. Compared to both controls, the treatment showed maximum increases of 30.5% in total organic matter (TOM) and 28.3% in total nitrogen (Total-N) during summer (January 2024), coinciding with higher temperatures and increased chlorophyll in the water column. In winter (July 2024), increases were lower (12.6% in TOM and 10.2% in Total-N), while spring and autumn showed intermediate values. This suggests that the functional activity of bivalves intensifies under warm and productive conditions. Total phosphorus (Total-P) showed high variability across treatments and seasons, with no statistically significant differences attributable to bivalves. Regarding benthic fauna, higher infauna abundances (Nematoda, Hydracarina, Oligochaeta, Chironomidae) were observed in the *D. chilensis* treatment, with a general trend of increasing abundance toward summer. This indicates a positive response of benthic communities to bivalve-induced enrichment, especially during warmer periods. In contrast, Control 2 showed higher epifaunal densities (notably Harpacticoida), likely related to the stability of dead shells. Control 1 consistently showed low infaunal and epifaunal abundances across all seasons. Finally, Control 2 shells exhibited more chlorophyll-a and attached fauna than those in the Treatment, suggesting that live bivalve movement and sand abrasion limit the development of biofilms and epibionts. Bivalve *Diplodon chilensis* acts as an ecosystem engineer in temperate lakes of southern Chile, increasing organic matter, nitrogen, and benthic diversity in lake sediments. Its effects are seasonally variable, being more intense in spring and summer. These results highlight its functional role in nutrient recycling and habitat structuring.

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MOLLUSCAN HORIZONS: A JOURNAL FOR ADVANCING MALACOLOGICAL RESEARCH IN THE GLOBAL SOUTH

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Keywords: malacology, open-acess research, scientific publication.

Malacological research in the Global South often faces significant challenges, including limited access to funding and publishing opportunities. In an initiative led by the Sociedade Brasileira de Malacologia (SBMa, Brazilian Society of Malacology) and supported by other Latin American malacological societies, we proudly announce a new journal dedicated to studying our favourite phylum. Molluscan Horizons is an open-access journal dedicated to advancing malacological research in the Global South by offering a more accessible platform for high-quality studies across all aspects of malacology. Our scope includes, but is not limited to, taxonomy, systematics, ecology, evolution, palaeontology, biogeography, medical malacology, fisheries, heliciculture, archaeomalacology, and education and outreach. The journal operates exclusively in an electronic format, with articles published continuously throughout the year. It is free of charge for researchers from the Global South. We invite researchers worldwide to submit original scientific articles and contribute to the advancement of malacology in the Global South and beyond. Additionally, we are seeking dedicated experts to join our editorial team and help shape the future of Molluscan Horizons. By promoting inclusivity and supporting researchers from underrepresented regions, we aim to strengthen collaborations and ensure a more equitable dissemination of malacological knowledge. Join us in building a journal that amplifies voices from the Global South. We have chosen the theme 'Advances in the Knowledge of Molluscs from the Global South' for our first special volume. We encourage submissions within this broad theme, aiming to engage a diverse array of colleagues in contributing to the growth and establishment of Molluscan Horizons as a prominent reference in malacology. Within the scope of studies focused on Global South malacofauna, we emphasize that submissions for this first volume must be led by researchers based in that region (manuscripts focusing on other topics can also be submitted for further volumes). Although the challenge of establishing a journal is significant, while we may go faster alone, together — and molluscs are a large group — we can go much further.

Funding Source: Sociedade Brasileira de Malacologia (SBMa).

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CRITICAL AWARENESS IN BIODIVERSITY: A PEDAGOGICAL PRACTICE INVESTIGATING THE IMPACTS OF INVASIVE SPECIES

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Keywords: exotic species, biological invasions, pedagogical tools.

Short courses for professional development are excellent pedagogical tools for introducing students to specific topics, such as invasive alien species. The activity aimed to discuss the impacts of these species on biodiversity, management challenges, and the importance of public policies for conservation. The experience sought to raise academic awareness and encourage strategies for mitigating environmental damage. The short course focused on exotic species in Brazil, particularly mollusks, highlighting their ecological consequences. The study was conducted in four stages: theoretical introduction, practical activities, group discussions, and fieldwork. Basic concepts of native, exotic, and invasive species were presented. In the practical session, students categorized native and exotic specimens. The theoretical closing involved discussions on the impacts caused by these species and strategies for control and conservation. Fieldwork took place at a tourist site within the Campos Gerais National Park Conservation Unit, where students learned to use equipment for collecting aquatic invertebrates. The sharing of knowledge on exotic, invasive, and native species revealed significant ecological and socio-environmental implications for the public and course participants. Results from classroom and field activities show that environments heavily modified by human activities, such as urban and agricultural areas, are more susceptible to the introduction and spread of invasive species. Inefficient public policies and a lack of environmental awareness exacerbate the issue. Discussions, like those held in the short course Exotic and Invasive Animals: Impacts on Biodiversity during the XXXVI Academic Week of Biology (SAEB/UEPG) & VII Symposium of the Evolutionary Biology Graduate Program (PPG BIOEVOL/UEPG), highlight the importance of environmental monitoring, education, and strict control of new species introductions. The clarity of the difference between native and invasive exotic species is crucial and plays a fundamental role in maintaining ecological balance. It promotes complex, coevolutionary interactions linked to human activities within ecosystems where new species are introduced. These factors contribute to negative impacts, including competition with native species, disruption of ecological dynamics, habitat degradation, and biodiversity loss.

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ORGANISMO: FEELING LIFE WITH YOUR HANDS

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Keywords: biodiversity, sensorial education, science popularization.

The Organismo project is an initiative of permanent development promoted by the Prof. Maury Pinto de Oliveira Malacology Museum – MMPMPO. Organismo integrates science, art, and education, awakening interest in biodiversity through the sensory and plastic experience provided by the interaction with papier maché sculptures of different organisms of the Brazilian fauna, flora, and microbiota, also establishing a connection between the museum's research on biodiversity and science popularization actions. The project integrates teaching, outreach, and science communication, and is conducted within the museum's facilities. The proposal combines sensory, playful, and virtual experiences and is structured in three main stages: (1) the conceptualization of the exhibition design, including narrative development, selection of specimens, identification of the target audience, and spatial planning; (2) the organization of workshops for the production of papier-mâché sculptures using recycled paper and other environmentally sustainable materials, alongside the creation of audiovisual content for dissemination via the project's Instagram profile; and (3) the installation of the exhibition at the museum's facilities, followed by training sessions for mediators who will support visitor engagement throughout the exhibition period. Museums and biological collections play a critical role in scientific research, education, and biodiversity conservation, with their relevance increasingly amplified by science communication initiatives. MMPMPO stands out due to its longstanding engagement in educational activities and university-integrated outreach projects, including original approaches that bridge biodiversity research with science popularization efforts. This year, the main action promoted by the Organismo project is an exhibition on Brazilian coral reefs, emphasizing the significance of marine ecosystem preservation and the impacts of global climate change on biodiversity loss. About sixty sculptures of corals, anemones, hydras, sponges, turtles, fishes, cephalopods, gastropods, crustaceans, planarians, sea urchins, star fishes, algae, ciliate protists, among other organisms, were made from recycled material, using papier maché and cold ceramic techniques and exhibited at the MMPMPO hall. The real-sized sculptures were integrated into a showcase structure, recreating a coral reef. Microscopic metazoans and ciliate protists were represented in large-sized sculptures exhibited in separated showcases. Fossil cephalopod species were also integrated in a separate scenario representing past marine biodiversity. Notable outcomes include the enhanced academic training of about forty undergraduate students in Biological Sciences who, through participation in the project activities, had the opportunity to acquire competencies typically underrepresented in standard curricula, such as pedagogical mediation and the development of educational materials. On a broader societal scale, the initiative contributes to science dissemination and aligns with both national and international biodiversity conservation agendas. Through exhibitions and interactive activities, the project promotes public engagement with biodiversity conservation and strengthens environmental education and awareness. The development of the coral reef exhibition, carried out as part of the project Organismo: Feeling Life with Your Hands, constitutes an interdisciplinary initiative that innovatively integrates teaching, research, and outreach. It aims to influence public perception of global biodiversity complexity and the need for biodiversity conservation, while also reinforcing the intrinsic importance of biological collections whose central mission is the safeguarding of biodiversity.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

Education and Outreach

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DISSEMINATING FRESHWATER MUSSELS: SCIENTIFIC COMMUNICATION STRATEGIES OF THE BIVAAS PROJECT

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Keywords: social networks, communication strategies, accessible science.

Knowledge about South American freshwater mussels remains limited due to barriers to accessibility and their scarce presence in mainstream media. In this context, social media has emerged as a valuable tool for broadening public engagement in science. This study aimed to analyze the communication strategies used by the Freshwater Bivalves of South America (BIVAAS) on digital platforms and evaluate their impact on public understanding and appreciation of freshwater mussels. BIVAAS developed science communication strategies in 2017. Initially, profiles were created on Facebook, Instagram, and YouTube to share live broadcasts, short interviews, and scientific articles, both classical and contemporary. During the COVID-19 pandemic, the strategy shifted toward online thematic conferences, focusing on topics such as the importance of biological collections and contributions of key researchers. In recent years, this approach has evolved into an in-person outreach. Activities included visits to educational institutions at various levels and participation in science fairs. These efforts featured interactive tools, such as educational games and curated teaching collections, aimed at young audiences to facilitate learning and engagement with scientific content. Over nearly a decade, more than five countries have collaborated to promote and communicate knowledge of freshwater mussels. At least ten universities have taken part in this initiative, and the content has reached over 110,000 people. A notable example is an event held in Brazil's central plateau, where 50,000 people engaged with the diversity of freshwater shell shapes and observed glochidia. In Uruguay, more than 1,000 children and adolescents participated in activities that explored the diversity of native and exotic species, fostering the knowledge and appreciation of local natural heritage. In general, when researchers use playful approaches and carry out activities in non-scientific settings, they succeed in sparking greater public interest. Moreover, initiating dialogue through curiosity-driven questions before introducing bivalves has proved to be a particularly effective and promising strategy. BIVAAS communication strategies have proven to be effective in enhancing public understanding and appreciation of freshwater mussels. By adapting to both virtual and in-person formats and prioritizing community engagement, the initiative has significantly contributed to increasing the visibility of these organisms. The results underscore the importance of inclusive science communication in addressing knowledge gaps related to biodiversity, especially for less charismatic species.

Funding Source: No.

EVOLUTION

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ONTOLOGY OF SHELL MATRIX PROTEINS (SMPS) ACROSS MOLLUSCS

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Keywords: mollusca, evolution, shell matrix proteins.

Molluscan shells are highly diverse. The mechanisms controlling shell formation are not fully understood and the evolutionary drivers of morphological shell diversity also remain elusive. Shell matrix proteins (SMPs) are diverse and often lineage restricted, suggesting they may control variation in shell phenotypes. To date, most SMP research has been conducted in bivalves, limiting our ability to make inferences across molluscs. Using OrthoFinder, we compared the proteome homology of over 100 species of Metazoa, including 68 species of Molluscs (21 bivalves, 34 gastropods, 5 cephalopods, 1 monoplacophoran, 3 polyplacophorans, 1 scaphopod, 3 aplacophorans). Using a published molluscan SMP database, we examined putative SMP homology across shelled molluscs and compared intra-class and intra-genus SMP homology in both gastropods and bivalves. Intra-genus SMP homology focussed on comparing *Crepidula*, a gastropod genus, and *Mytilus*, a bivalve genus, to further investigate and compare the levels of conserved SMPs. We also identified SMP-related protein domains conserved across all shelled molluscs. We found a high degree of SMP conservation, with nine SMP orthogroups shared across all shelled Molluscs. These conserved domains included those that have been hypothesised to form a molluscan 'biomineralization toolkit'; tyrosinase, carbonic anhydrase, chitin-binding and von Willebrand Factor A. We also found three SMP orthogroups shared across all metazoan species included (fibronectin, chitin binding and von Willebrand factors). This is a much greater level of SMP conservation than has been previously reported. Gastropods had a greater level of SMP conservation within class than bivalves, sharing a total of 18 SMPs across all species included, while bivalves shared 13 SMPs. Gastropods also had a higher average number of shared SMPs between species, indicating that bivalves have a higher degree of SMP lineage restriction than gastropods. Similarly, *Crepidula* shared a high number of SMPs within genus than *Mytilus* (three times less than *Crepidula*). The proteomes sourced for this analysis included different sampling (whole animal, tissue specific, pooled developmental etc.) and sequencing methods (genome, transcriptome or true proteome), meaning that some of the differences seen between species may be a result of technical inconsistency. In our approach and interpretation, we assume that more extensively studied, economically important biomineralisation "model" species in the bivalve class are likely to have more complete proteomes than the less studied gastropod class. Overall, we can be reasonably confident in our findings that SMP lineage restriction is greater in bivalves than gastropods. Our results suggest that SMPs are more conserved across shelled molluscs than previously thought, supporting and expanding the hypothesised 'biomineralization toolkit'. Contrasting class and genus-level degrees of SMP lineage specificity seen between bivalves and gastropods could imply the previously identified high degree of SMP lineage restriction is a bivalve specific phenomenon. Further research including more molluscan classes is required to understand the phylum level species specificity and evolution of SMPs.

Funding Source: No.

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DETOX: A PIPELINE FOR THE DETECTION OF TOXINS IN VENOMOUS ORGANISMS

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Keywords: toxin detection, pipeline, bioinformatics.

Venoms have independently evolved over 100 times, giving rise to more than 200,000 venomous species and a vast diversity of toxin molecules. These toxins offer unique opportunities for drug development and studying genetic innovation. However, challenges remain in accurately identifying toxins from RNA sequencing data. This study presents DeTox, a pipeline that integrates sequence and structural analyses to address these limitations and improve toxin discovery in diverse taxa. We developed DeTox, a customizable and parallelizable pipeline designed for efficient analysis of venom transcriptomes. The toolkit processes raw transcriptomic data, applying filters based on sequence similarity, structural features (e.g., cysteine patterns and disulfide bridges), and expression levels to predict putative toxins. It supports modular workflows, batch processing, and accessible usage for researchers without programming expertise. DeTox was tested across datasets from multiple venomous lineages—including gastropods, cnidarians, and snakes—validating known toxins and identifying novel candidates. A recent update improved the reporting of performance metrics. DeTox consistently recovered the majority of known toxins in tested datasets, confirming its reliability on all the different venomous lineages considered. Moreover, it detected numerous novel toxin candidates previously overlooked by sequence-based approaches alone. By combining structural and homology-based evidence, DeTox offers a more comprehensive analysis of venom repertoires. Moreover, by associating each putative toxin to tags, it provides an estimation of the reliability of the annotation, which helps the user in choosing the most significant putative toxins. Its ease of use makes it accessible to a wide research community, fostering discovery in poorly characterized species. Application across diverse taxa demonstrated its versatility and highlighted its role in standardizing toxin annotation. The objectives were fully achieved thanks to the DeTox pipeline, integrating toxin discovery from transcriptomic data, recovering known toxins efficiently, and identifying novel toxin candidates. It serves as a powerful tool to accelerate venom research, especially in non-model and understudied organisms.

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EVOLUTIONARY CHANGE OF THE MITOGENOME IN CEPHALOPODS

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Keywords: mitogenome, evolution, cephalopods.

The size and organisation of mitochondrial genomes in metazoans demonstrate diverse patterns among taxa in terms of size and composition, independent of their complexity. This variation may be attributable to metabolic rate, distribution, or life history traits. The objective of this study is to evaluate the evolution of the cephalopod mitogenome concerning distribution (latitude, depth, and distribution area), and body size. A database was constructed with 81 cephalopod species, including body size, metabolism, latitude, depth, distribution area, and mitogenome. The complete mitogenome of all species was downloaded from GenBank, separated into 13 coding mitochondrial genes, and aligned. These genes were concatenated to carry out the Bayesian phylogenetic analysis. Phylogenetic regression was employed to analyse the correlations between the size and composition of the mitochondrial genome and body size and distribution. The ancestral reconstruction of cephalopods with the size and composition of the mitogenome was performed. The mitochondrial phylogeny obtained showed high support values, thus confirming the monophyly of the primary clades Octopodiformes and Decapodiformes. A wide variation in the size and composition of the mitogenome was observed among the groups, Spirulida, Bathyteuthida and Oegopsida, have incoporated new elements in their mitogenome increasing in turn the size of the mitogenome (~20 kb), while other groups that have no additional elements their size is smaller (~14 kb). A significant association was found between the size of the mitogenome, body size, depth, and distribution area. However, mitogenome composition was only related to body size and depth. Ancestral reconstruction revealed that the evolution of the mitogenome in terms of size (kb) and composition (number of genes) has occurred independently in different lineages. This could reflect adaptations to different habitats, as well as positive selection of metabolic genes. The present study demonstrates that the size and composition of the mitogenome in cephalopods are significantly related to body size, depth, and area of distribution. Mitogenomic evolution is indicative of adaptive processes associated with the diversity and ecological success of this group, thereby providing novel perspectives for comparative genomic investigations. The next stage will be to expand the database with the mitogenomes of other species and other life history traits.

Funding Source: PH-scholarship: Andres Bello University.

FISHERIES, AQUACULTURE AND CULTURE

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INFESTATION OF FARMED AND WILD MOLLUSCS BY SHELL-BORING POLYDORID SPECIES (ANNELIDA, SPIONIDAE) ALONG THE COAST OF NORTHERN JAPAN

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Keywords: molluscan aquaculture pest, shell-boring worms, alien species, habitat preference.

Polydorid species (Annelida, Spionidae) bore into the shells of molluscs, causing negative impacts to their hosts. Their infestations have become a serious concern, as the global trade of commercially important molluscs facilitates the unintentional spread of the polydorid species. To better understand the infestation patterns of polydorid species among different host species and environmental conditions, a comprehensive survey was conducted along the coasts of northern Japan. From 2020 to 2023, molluscs were collected from farmed areas (5–20 m depth), sown areas (40–50 m depth), and wild intertidal zones, including oysters (*Crassostrea gigas*), scallops (*Patinopecten yessoensis*), and gastropods (*Neptunea arthritica*, *Ocinebrellus inornatus*, *Omphalius rusticus*). Polydorid worms were extracted from the shells, counted, and identified to the species level through morphological examination and molecular analysis of 18S rRNA and COI sequences. Five polydorid species—*Polydora brevipalpa*, *P. websteri*, *P. onagawaensis*, *P. cornuta*, and *Dipolydora bidentata*—were identified, with the first three species causing heavy mollusc infestation. Variations in infestation levels and species composition among different regions were suggested to be associated with host molluscs species and habitat condition, including water depth, sediment type, and farming methods. Sown scallops from Abashiri Bay (40–50 m depth) were heavily infested by *P. brevipalpa*, with up to 205 individuals per host. Wild oysters from Obuchinuma and Gamo Lagoon (muddy intertidal zones) were infested by *P. websteri*, with up to 234 individuals per host. The species favored the shallow and muddy environment, as it used mud as a material to form mud blisters on the inner shell surface. In Lake Notoro (sandy intertidal zone), *P. onagawaensis* largely infested wild oysters, scallops, and gastropods, as well as suspended cultured oysters in Akkeshi Bay (5–20 m depth), with up to 217 individuals per host. This species was recorded for the second time in Hokkaido and exhibited the widest distribution, with a broad host range. Its extensive distribution and habitat adaptability indicated a high potential for establishment in both aquaculture and natural environments. These findings highlight that the habitat preferences are key factors in the successful colonization of the polydorid species among diverse environments. Insights into invasion potential are essential for predicting the establishment of polydorid species in new regions and for developing effective management strategies for sustainable molluscan aquaculture and coastal ecosystems.

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OCCURRENCE OF TRACE AND RARE EARTH ELEMENTS IN FARMED SNAILS DURING 2022 AND 2024 IN NORTHWESTERN ITALY

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Keywords: heliciculture, snail, bioindicator, metal, REE.

Terrestrial snails are used as bioindicators for monitoring metal contamination in soil ecosystems due to their accumulation capacities [Gomot De Vaufleury and Pihan, 2000]. They play an important role in transferring pollutants directly to the food chain. We investigated the occurrence of 40 trace elements and rare earth elements (REEs) among populations of *Cornu aspersum* and *Helix pomatia* in Northwestern Italy, a well-known snail species used for human consumption. Twenty-five pooled samples of H. pomatia (n= 19) and *C. aspersum* (n= 6) were collected from 10 different local farms during 2022 and 2024. Each sample consisted of 6-15 individuals. A homogenised extract from each sample (0.5 g) was subjected to mineralisation with HNO_3 and H_2O_2. The quantification of trace metals and lanthanides was performed by means of inductively coupled plasma mass spectrometry (ICP-MS 7800, Agilent). The limit of quantification (LOQ) for trace metals was 0.010 mg kg^{-1} and for REEs was 0.001 mg kg^{-1}. The most prevalent metals detected were aluminium (range: 118-665 mg kg^{-1}) and barium (range: 101-204 mg kg^{-1}). Four (16%) of the samples revealed cadmium concentrations above 1 mg kg^{-1}, the maximum permissible level for edible molluscs in the EU [EC, 2006]. The average ∑REE was 0.29 mg kg^{-1} and REEs occurrence was comparable among all samples, thus confirming lanthanides usefulness in geological tracing. Moreover, the REE profile, after chondrite normalisation, overlays with others from Northern Italian biota [Squadrone et al., 2019], suggesting their potential for determining the geographical origin of snails. Indeed, these results indicate that REE values differed for area of origin and seasons, thus revealing the area where the snails came from and the microparticle composition in the heliciculture soils. Few samples showed relevant values of several elements, including aluminium, cadmium, arsenic, vanadium, chromium and some REEs. Specifically, one sample, consisting of dead *H. pomatia* snails which were harvested in Romania and transported to Italy for farming purposes, revealed high concentration levels of many metals especially aluminium, barium, cadmium and iron. These snails were potentially harvested from contaminated areas. Additional samples of living snails from the same batch showed the presence of aluminium and barium at levels that were of concern. These results need to be interpreted with caution, given the absence of established toxicity limits for terrestrial snails. Nonetheless, the high concentrations measured in this sample might have negatively affected the health status of individuals, potentially contributing to their mortality. To our knowledge this is the first study in Northwestern Italy that explores the use of farmed terrestrial snails as environmental bioindicators. Our results highlight that both wild and farmed snails could accumulate significant concentrations of trace elements. Further research on metal concentration levels on terrestrial molluscs is needed in order to define toxicity limits for snails and establish acceptable limits of metals in snails consumed as food. This research was supported by the Italian Ministry of Health (project ID: IZS PLV 06/23 RC).

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EVALUATION OF ANTIFOULING COATING ON NET CAGES FOR FISH FARMING

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Keywords: *Limnoperna fortunei*, antifouling, net cages, invasive species.

The biofouling caused by the golden mussel (*Limnoperna fortunei*) compromises net cage farming structures, increasing costs and sanitary risks in aquaculture. As an environmentally safe alternative to conventional biocides, this study evaluated the use of hybrid silicone and epoxy resin as an antifouling coating to reduce mollusk adhesion. In November 2020, 18 net panels (30×30 cm, ¾" mesh) made from three materials (stainless steel with and without coating and coated galvanized wire) were installed at three fish farming sites (P1, P2, and P3) in the Chavantes Reservoir (SP/PR), and removed in May 2021. Monthly (except March), limnological parameters were recorded with a multiparameter probe. Additionally, 1,000 L of water were collected for analysis of *L. fortunei* planktonic larval density, filtered using a 40 µm mesh net. Fouling was quantified on 225 cm^2 of panels by counting juveniles and adults and analyzing adhered plantigrade larvae (≤ 250 µm) microscopically. Data were analyzed using two-way ANOVA and Tukey's test ($p < 0.05$). Limnological parameters remained within tolerable ranges for mussel development, with mean values of 25.85 °C, pH 6.53, and dissolved oxygen at 5.49 mg/L. The density of planktonic larvae in the water column confirmed reproductive activity during summer, peaking at 6,850 larvae/m^3 in January. By April, values dropped to 184 larvae/m^3, indicating the onset of the reproductive resting period. The highest density of adhered plantigrade larvae was observed in February, while juvenile and adult densities peaked in April. The overall decrease in fouling density observed in May across all substrates may be linked to predation combined with lack of new larval recruitment. The stainless steel with resin showed the highest densities of both plantigrade larvae and juveniles/adults. Uncoated stainless steel had intermediate adhesion levels, while the lowest values were recorded for the coated galvanized wire. Statistical analysis showed significant differences across both time and materials. For larvae, significant differences were found among all three materials, with the best antifouling performance seen in the coated wire, followed by uncoated stainless steel and coated stainless steel. For juveniles and adults, the highest density occurred on the coated stainless steel panels (16,245 ind./m^2), followed by uncoated stainless steel (5,408 ind./m^2) and coated wire (4,326 ind./m^2). The difference between coated stainless steel and coated wire was statistically significant ($p = 0.0041$). The hybrid silicone-epoxy resin coating did not demonstrate antifouling potential when applied to stainless steel net panels. The resin actually increased adhesion compared to the uncoated net, the standard market material. Antifouling potential was only observed on galvanized wire panels, particularly during the initial mollusk settlement phase. Further studies are being conducted with support from FAPESP (Grant No. 2023/08026-0) to confirm these preliminary results.

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A DECADE OF CHANGE IN *Octopus insularis* FISHERIES: EXPANSION WITHOUT FISHERIES MANAGEMENT

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Keywords: fisheries expansion, sustainability challenges, fishing practices.

Artisanal octopus fishing represents about 10% of global cephalopod landings and has grown in recent decades due to high prices, market demand, and depletion of other species. This growth stems from increased fishing effort, emphasizing its economic significance and sustainability challenges. This study aims to describe the main changes in the fishing of *Octopus insularis* ten years after the adoption of pots in Rio do Fogo, RN. The municipality of Rio do Fogo, in Rio Grande do Norte, is the main producer of octopus through artisanal fishing in Brazil. Between 2011 and 2013, fishers participated in a participatory research project testing pot longlines, which the community recognized as viable. At that time, 45 fishers were individually interviewed to characterize the activity. Ten years later, we returned to the municipality and interviewed 35 fishers using the snowball sampling method to understand the current context of *Octopus insularis* fishing. The collected data was categorized and analyzed exploratorily to identify the main changes over this period. Fishing was previously carried out by approximately 210 fishers using 70 vessels (mostly 4.5 m long), employing longlines with plastic and cement pots. Each vessel operated with about 220 pots, deployed in traditionally productive areas and located with the help of GPS. However, there was no guarantee that the pots would remain on substrates preferred by octopuses, and the catch was made directly from the vessel, without the need for diving. The activity took place in gravel and reef areas, lasting an average of 8 hours, with catches of up to 30 kg per vessel. Currently, around 330 fishers operate 116 vessels (mostly 6 m long). With larger vessels, they can carry more pots and operate with greater autonomy. The use of longlines was abandoned; cement pots are now placed directly on the seabed and marked with GPS, and catches are made by diving with a compressor and a gaff (bicheiro). This shift is associated with the greater durability and lower cost of cement pots, as well as concerns over the theft of longlines. Today, each fisher maintains, on average, 4,200 pots distributed in the sea. Deploying individual pots allows for substrate assessment during diving, increasing the likelihood of octopus occupancy compared to longlines. Fishing now lasts an average of 12 hours, with catches reaching up to 100 kg per vessel on productive days, in deeper areas of gravel, reef, risca, and parecer. Artisanal fishing has expanded, with more vessels operating in deeper waters and using unlimited pots, tripling *Octopus insularis* catches. However, in the past decade, no progress has been made in species management, lacking a minimum catch size, specific studies, or regulation of the new practice. The absence of monitoring and management threatens the development and sustainability of the activity.

Funding Source: No.

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HARVESTING SHELLFISH: TECHNIQUES AND PRACTICES ON NORTHEAST BRAZIL

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Keywords: fisheries, socieconomic impact, *Anomalocardia flexuosa*, mollusk collection.

Artisanal invertebrate fishing plays a crucial socioeconomic role in Latin American countries, providing both a source of subsistence and employment. Despite its significance, the details of these activities remain relatively understudied. In Brazil, countless families rely on collecting or harvesting coastal resources, particularly mollusks, across the extensive Brazilian coastline. This study aimed to describe the primary capture techniques utilized in shellfish gathering along the Costa Branca coast, located in northeastern Brazil, and to identify the predominantly captured species. Research was conducted in the Apodi/Mossoró estuary—linking the municipalities of Grossos and Areia Branca—and the Piranhas/Açu estuary in Porto de Mangue. Data was collected using visual observations, monitoring records, and interviews with shellfish collectors. In the Apodi/Mossoró estuary, the primary species targeted was *Anomalocardia flexuosa*, predominantly harvested through a manual technique known locally as “catação do búzio” (clams fishing), with women constituting 93% of the workforce. Fishermen also employ various tools such as buckets, monoblocs, pickers, shovels, and the "jereré" net to aid in collection. Similarly, in the Piranhas/Açu region, *Anomalocardia flexuosa* accounted for 67% of the catch; other species such as *Mytella guyanensis* and *Crassostrea rhizophorae* were noted as well. Here too, manual collection was prevalent, sometimes supplemented with the same tools used in Apodi/Mossoró. Technique choice often depends on personal preference, although it was observed that older collectors favor manual gathering. When present, men frequently utilize tools such as shovels or pickers to excavate shellfish for enhanced productivity. The manual collection technique for *A. flexuosa* involves searching by hand during low tide when the substrate is most exposed. A bucket filled with water may be used to rinse the sediment, improving visibility of the specimens. Pickers and shovels facilitate removing individuals from the substrate, while monoblocs assist in washing and sorting the material. The research indicates that manual collection is the dominant method for shellfish harvesting in the Costa Branca region, a practice known for its selectivity. However, alternative methods are emerging, with unknown impacts on the substrate, the biology of exploited species, and overall ecosystem health. Continuous and frequent monitoring and documentation of these practices are necessary, alongside research that evaluates both the efficiency and ecological consequences of these harvesting techniques.

Funding Source: No.

GENETICS / GENOMICS

Genetics / Genomics

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EXPLORING THE MOLLUSCAN MICROBIOME: DIVERSITY, FUNCTION, AND ECOLOGICAL IMPLICATIONS

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Keywords: molluscan microbiome, host–microbe interactions, environmental stress, functional diversity, conservation biology, aquaculture, One Health, Proteobacteria, vertical transmission, mollusk-associated bacteria.

Molluscs are diverse invertebrates occupying marine, freshwater, and terrestrial habitats. They host complex microbiomes that influence digestion, immunity, and environmental adaptation. These microbial communities are shaped by host species, tissue type, and environmental stress. Despite recent advances, the full ecological and applied significance of molluscan microbiomes remains underexplored. This review investigates microbial diversity, function, and relevance to ecosystem health, conservation, and aquaculture. A structured literature review was conducted using PubMed, Scopus, and Web of Science. Studies were selected based on relevance to molluscan microbiome composition, host specificity, functional roles, environmental stress responses, and applied significance. A thematic synthesis approach was applied to categorize findings into taxonomic profiles, host–microbe interactions, and ecological functions. Data were further stratified by habitat, tissue type, host developmental stage, and experimental design. Functional annotations were interpreted from metagenomic and metatranscriptomic studies, including predictive tools such as PICRUSt. Attention was given to evidence of vertical transmission, functional redundancy, and microbial resilience across environmental conditions. Molluscan microbiomes were dominated by Proteobacteria, Bacteroidetes, Firmicutes, and Tenericutes. Oreohelix strigosa harbored over 7,000 OTUs, far exceeding *Radix auricularia* (1,196) and *Lissachatina fulica* (228). Vertical transmission was supported by OTU overlap across developmental stages. In Mytilus edulis, exposure to 34 °C increased bacterial load by 132-fold and reduced microbial diversity. Hatchery-reared *Biomphalaria straminea* lost over 60% of wild-associated ASVs within 50 days, illustrating environmental influence. Tissue-specific microbiota were evident in gills, gut, and haemolymph, with core taxa varying across species. Functional roles included digestion, vitamin biosynthesis, nitrogen cycling, and pathogen defense. Genera such as Mycoplasma and Cloacibacterium exhibited stable associations, reflecting adaptation. Functional redundancy and resilience were noted under stress. While community participation was absent, the review underscored the microbiome's potential in aquaculture, conservation, and health monitoring. Microbial shifts corresponded to pollution, climate change, and habitat disturbance, positioning mollusks as effective bioindicators under One Health frameworks. The review confirmed that molluscan microbiomes are vital to host function, environmental adaptation, and ecological monitoring. Core microbiota demonstrated host specificity, tissue differentiation, and vertical transmission. These microbial communities hold promise as tools for aquaculture optimization, pathogen surveillance, and biodiversity conservation. A multidisciplinary approach is recommended to address knowledge gaps and unlock their full potential across ecosystems and applied contexts.

Funding Source: No.

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WHY SO DIVERSE? INCLUDING MITROIDEA IN THE NEOGASTROPOD GENOME EVOLUTION INVESTIGATION

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Keywords: genomics, transciptomics, *Mitra mitra*, Neogastropoda, evolution, venom.

The order Neogastropoda represents one of the most diversified taxon of marine invertebrates. The mechanisms behind their wondrous radiation have inspired many evolutionary theories, which can now be tested from a genomic perspective. Regrettably, most genome-scale research is restricted to the superfamily Conoidea, and more neogastropod superfamilies need to be included to expand the scope to all neogastropods. Five specimens of *Mitra mitra* Linnaeus, 1758 were collected in Koumac (New Caledonia), and four were dissected to extract the foot, mid-oesophageal gland, and salivary glands. The tissue transcriptomes and the genome of a whole specimen were sequenced and a chromosome level assembly was produced. Repeated elements were masked and annotated from the assembled genome, and genes were automatically mapped and annotated using the transcriptomic data and a custom peptide database. A differential expression analysis was carried out between the three tissues dissected. The annotated genome was analysed with a focus on two important evolutionary drivers in Neogastropoda: gene duplication and venom production. The assembly length for the genome of *Mitra mitra* had a size of 2.17Gb, with 42% GC content, 93% completeness BUSCO score (17% duplicated), and a N50 value of 56Mb. Repeated elements accounted for 54.40% of the assembly. The full pipeline for automatic genome mapping was organized as a nextflow workflow to make this analysis fully accessible and repeatable. Preliminary analyses identified 45,514 genes in *Mitra mitra*, including genes coding for secreted substances common in gastropod venoms (peptidases, lectins, etc.), although the signature toxins of conoideans ("conotoxins") appear absent. The genome annotation statistics of *Mitra mitra* are coherent with other neogastropods. They are also in line with the hypothesis of a whole gene duplication event prior to the radiation of conoideans, and probably Neogastropoda (Farhat et al., 2023). Functional annotation of genes, in particular those related to toxin secretion, and the differential expression analyses are still undergoing, and they will reveal if the components produced by mitrids are substantially different from those in other known neogastropod venoms. The first genome in the superfamily Mitroidea was produced and investigated, expanding the taxonomic coverage on gastropod available genomic data. Preliminary results showed evidence of whole genome duplication, as well as the possible presence of toxic components in the secretome. These outcomes support the hypothesis that some of the adaptations that promoted the radiation of Conoidea may be shared by all neogastropods.

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ISLAND-DRIVEN LINEAGE DIVERSIFICATION: INSIGHTS FROM INTERTIDAL SNAIL SPECIES AROUND JAPAN

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Keywords: island biogeography, genetic structure, ddRAD-seq, endemism.

Islands generally play a pivotal role in fostering endemic lineages within terrestrial system. In particular, oceanic islands are often referred to as "natural laboratories of evolution" due to their significant role in genetic diversification with endemicity. However, in highly connected marine environments, how islands shape genetic endemism remains poorly understood. Here, our present study aims to understand the relationship between island systems and genetic divergence in marine species. We focused on *Monodonta perplexa*, an intertidal snail species widely distributed across the Japanese and Ryukyu archipelagos. These regions comprise a complex array of islands, including oceanic islands such as the Izu and Ogasawara Islands, making them ideal for exploring island-driven diversification. Previous molecular study using partial mtDNA sequences has suggested the presence of island-endemic genetic lineages in *M. perplexa* (Yamazaki et al., 2017). To further assess the existence of endemic lineages, we expanded the mtDNA dataset and, in addition, performed population genetic analyses using genome-wide SNPs obtained from double-digest restriction-site associated DNA sequencing (ddRAD-seq). Our molecular analyses—based on both mtDNA and genome-wide SNPs datasets— revealed that *M. perplexa* harbors multiple island-endemic lineages. However, the two markers showed some phylogenetic incongruence. Mitochondrial data identified an endemic lineage in the Izu Islands (Miyakejima Island, Mikurajima Island, and Hachijojima Island), coexisting with the mainland lineage in both Miyakejima Island and Hachijojima Island. In contrast, the genome-wide SNPs data indicated that populations on the Izu Islands south of Kozushima Island represent an endemic lineage. Additionally, unique lineages were also detected in the Ryukyu Archipelago and the Ogasawara Islands. Cluster analysis revealed the presence of island populations with mixed genetic components in the Ryukyu Archipelago. The complex genetic structure observed in the Ryukyu Islands is thought to have been shaped by a geological history of intermittent connections and isolations among populations. Our study demonstrated that *M. perplexa* exhibits a high degree of genetic divergence and endemism within complex island systems of Japan. Oceanic islands, such as the Izu Islands, can promote and persist the genetic endemism of marine species, despite their contact with the mainland lineage. Hence, our findings suggest that island structures play a more significant evolutionary role in shaping marine biodiversity than previously recognized.

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THE GENOME OF A MINUTE FRESHWATER SNAIL FROM NEW CALEDONIA

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Keywords: PacBio sequencing, New Caledonia, Tateidae.

New Caledonia is known as a hotspot for flora and fauna with many endemic species due to its unique geology and geological history. Ultramafic rocks, containing at least 90% mafic minerals, cover one-third of the island's surface, posing a physiological challenge for organisms. We sequenced and annotated the genome of the minute (1.2 mm), recently described gastropod *Viriiella touaouroua* inhabiting springs and streams on ultramafic bedrock. Specimens were collected in 2016 from ultramafic terrains in the Southeast of New Caledonia and fixed in 96% ethanol. Two Pacific Biosciences (PacBio) ultra-low input libraries were prepared according to the PacBio ultra-low input protocol. Input DNA for each library was 10 ng. Genome assembly was performed using Hifiasm. In order to reduce the degree of haplotypic contigs in the final assembly, Redundans was used. Identification and masking of Repetitive Regions was conducted with EarlGrey and structural annotation of the genome assembly was performed with BRAKER2, using protein predictions from other Gastropoda. The assemblies were tested for quality with BUSCO. Preliminary results indicate that the genome of the tateid *V. touaouroua* has a total length of 726.76 Mb (N = 7,573 total contigs), with the longest contig calculated at 2.3Mb. In comparison, this genome is almost 200 Mb longer than the ones of its closest available relatives *Potamopyrgus estuarinus*, *P. kaitunuparaoa* and *P. antipodarum*, while the max contig length is almost double in size. As far as the annotation is concerned, BRAKER was able to predict 44,672 protein-coding genes, which results in 88.9% complete BUSCOs and 4.6% fragmentation when compared with metazoa_odb10. When compared with the *Potamopyrgus* spp. quality results were similar, but there were almost 10,000 more genes predicted in *V. touaouroua*. The observed differences can partly be explained by the still preliminary nature of our results, but also by the lack of annotated genomes of evolutionarily less distant species. In addition, BRAKER tends to overestimate the gene number in larger genomes. Even though further analysis is expected to improve the provided results, the BUSCO scores indicate that our assemblies are already quite complete. The annotated genome will support phylogenomic studies analysing the biogeographic history of New Caledonia, and it will be used to shed light on the adaptations required to survive ultramafic conditions.

Funding Source: No.

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CAPTURING REEF GASTROPOD DIVERSITY ALONG THE CENTRE OF THE CORAL TRIANGLE USING ARMS AND THE NOVEL GASTRO16 METABARCODING MARKER

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Keywords: environmental DNA, metabarcoding, Gastropoda, biodiversity, Philippines, Indonesia.

Gastropods are key trophic and structural components in reef ecosystems and have evolved to become some of the planet's most diverse organisms. Their hyper-diversity is attributed to the specialisation of cryptic (i.e., concealed within microhabitats) and the often-overlooked meio- and microbenthic taxa, failing to sample which largely leads to underestimation of biodiversity. This challenge can be addressed by complementing traditional surveys with DNA metabarcoding approaches. Using Autonomous Reef Monitoring Structures (ARMS), we evaluated gastropod diversity at five sites across the Philippines and five in the Spermonde Archipelago, Indonesia. A total of 31 ARMS units were retrieved in 2018 and 2022 after 12–16 months of continuous underwater deployment on forereefs at ~10 m depths. Gastropods and other motile fauna >2 mm, encrusting sessile organisms, and sediment were collected from each unit. Community and environmental DNA were extracted from homogenised ARMS plate scrapings and sediment (500- and 125-µm fractions). High-throughput sequencing was performed on PCR-amplified Gastro16, a novel 16S-based metabarcoding marker (89–100 bp) developed for gastropods. Sequence data were processed using the MJOLNIR metabarcoding pipeline. Taxonomic annotation was successfully conducted using a custom reference sequence library comprising 7,335 sequences representing 306 gastropod families, along with 596 additional families from other molluscan classes and 12 other animal phyla. Across all ARMS units, we identified 49,516 metazoan MOTUs, of which 742 (1.5%) are gastropods, representing 16% of the total sequencing reads. We report the occurrence of 111 gastropod families across five subclasses detected using Gastro16 (versus 56 families with COI metabarcoding) in both regions and present their relative abundances at each site. Comparisons with motile recruit voucher specimens collected from the ARMS underscore the significance of integrating DNA metabarcoding with traditional surveys for a more comprehensive assessment of reef biodiversity. Gastro16 is shown to be effective in detecting gastropod diversity in both sediment and bulk samples. Its short length could also prove useful for metabarcoding typically degraded DNA from ancient environmental samples, which can be further tested. In this presentation, we introduce Gastro16 – a novel gastropod-specialised metabarcoding marker and its de novo constructed reference sequence database which will be made live post-publication. Our metabarcoding results demonstrate its effectiveness in detecting gastropod taxa in environmental samples even from high-diversity regions like the Coral Triangle. We underline its potential and value for monitoring biodiversity as well as understanding ecological processes past and present.

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INSIGHTS INTO SHELL FORMATION AND PIGMENTATION FROM TRANSCRIPTOMIC DATA OF *Humboldtiana* sp. nov. IN SIERRA GORDA, MÉXICO

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Keywords: transcriptomics, terrestrial mollusks, genes, Mexican biodiversity, signaling pathway.

The Sierra Gorda (SG) of México is part of the distribution range of snails from the genus *Humboldtiana* including *Humboldtiana* sp. nov. (description in progress). Recent studies demonstrate that there is a possible polymorphism in shell coloration. For this reason, the purpose is to identify the genes potentially involved in the pigmentation and formation of the shells of *H.* sp. nov. of the SG, using a transcriptomic approach. Adult specimens of *Humboldtiana* sp. nov. were collected in the SG, a portion of the muscular foot from four specimens were sent to mRNA extraction, cDNA library construction and sequencing on the Illumina Novaseq 6000 platform. The quality control of the raw reads was carried out by trimming the adapter sequences, low-quality sequences (phred > 28), duplicates, and poly X seq. From the high quality reads an assembly de novo was obtained. Finally, to identify those genes involved in the shell formation and pigmentation, the ORFs of transcripts were obtained and used for the functional annotation in the Kyoto Encyclopedia of Genes and Genomes (KEGG) using the GhostKOALA tool. The transcriptome assembly showed 136,310 genes, 209,504 transcripts, N50 of 922, and a total of 34,286 proteins. These results were compared with those reported to the species *Cepaea nemoralis* which was taken as a reference, for which 147,397 genes, 147,397 transcripts, N50 of 968 and 38,675 proteins were obtained. A total of 432 metabolic pathways were identified for *Humboldtiana* sp. nov. and 431 from *C. nemoralis*, with a higher percentage of those related to the processing of genetic information highlighting the calcium, melanogenesis and Notch signaling pathways for both of theme, approximately 11 previously reported genes related to shell formation and pigmentation were annotated, including HES, HEY, MAML, CALM, ErbB4, ErbB1, MITF, TYR, DCT, TYRP1 and DCT. The preliminary results obtained in this work show similarity with those obtained previously for the genes involved in pigmentation and formation of the shell of mollusks, despite being a group with many representatives, the processes of formation and pigmentation of the shell are still not fully known or clear, so it is necessary to continue researching and deepening the subject.

Funding Source: No.

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GENETIC INSIGHTS INTO TERRESTRIAL NATIVE LAND SLUGS OF THE GENUS *Phyllocaulis* (GASTROPODA: VERONICELLIDAE) IN SOUTHERN SOUTH AMERICA

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Keywords: Argentina, haplotypes, mitochondrial DNA, native species.

Phyllocaulis is a genus of terrestrial slugs and the southernmost representative of the family Veronicellidae in the Neotropics. It is endemic to Brazil, Uruguay, Paraguay, Argentina, and Chile. The genus comprises six species, three of which occur in Argentina: *P. soleiformis*, *P. tuberculosus*, and *P. variegatus*. The study aimed to initiate the exploration of intra- and interspecific genetic variability among these slugs in Argentina using a mitochondrial marker. Molecular analyses were conducted by sequencing a partial region of the mitochondrial cytochrome c oxidase subunit I (COI) gene from specimens deposited in the malacological collection of the Instituto de Biología Subtropical (CONICET – Universidad Nacional de Misiones). The examined material included 63 specimens collected from 21 localities in Misiones Province, as well as from additional sites in the Argentine provinces of Córdoba (3), Entre Ríos (2), Buenos Aires (1), and Santa Fe (1). Based on both newly generated sequences and additional data retrieved from GenBank, we assessed genetic variability, estimated genetic distances, evaluated phylogenetic relationships, and constructed haplotype networks. Comparison of the 63 sequences obtained in this study with those available in GenBank enabled the molecular identification of the three *Phyllocaulis* species occurring in Argentina: *P. variegatus* (41 sequences), *P. soleiformis* (21), and *P. tuberculosus* (1). Phylogenetic analyses revealed that all Argentine sequences clustered with their conspecifics from Brazil, forming well-supported monophyletic groups. High haplotype and nucleotide diversity was detected for *P. variegatus* and *P. soleiformis* in Argentina, with nine and eight distinct haplotypes identified, respectively. For *P. tuberculosus*, the presence of only one individual limited our ability to assess genetic diversity. In terms of geographic distribution, all three species were recorded in different areas of Misiones Province, whereas *P. soleiformis* was the only species found in the other represented provinces. Notably, none of the haplotypes identified in Argentina matched those available in GenBank for Brazilian specimens, indicating the presence of previously unreported mitochondrial haplotypes for all three species. Finally, the combined analysis of Argentine and Brazilian sequences revealed interspecific divergences ranging from 10.54% to 16.42% for the COI marker. This study provided new molecular data and valuable insights into a poorly studied genus of native terrestrial slugs, based on material from Argentina. These results establish a baseline for future research on genetic variability and evolutionary relationships within this group.

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THE *Acrorbis* (GASTROPODA: PLANORBIDAE) PUZZLE: A NEW PIECE IN THE PHYLOGEOGRAPHIC AND EVOLUTIONARY HISTORY OF ENDEMIC FRESHWATER SNAILS FROM THE UPPER PARANÁ ATLANTIC FOREST

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Keywords: Argentina, genetic lineages, mitochondrial DNA, new records, waterfall environments.

Freshwater snails of the genus *Acrorbis* are endemic to waterfalls and rapids of the Upper Paraná Atlantic Forest, a biodiversity hotspot. Although historically considered monotypic, previous studies have revealed significant genetic structuring with differentiated lineages among Argentine populations. This study expands the phylogeographic framework of Acrorbis by incorporating recently collected individuals from the northwestern region of Misiones Province, Argentina, and assesses their evolutionary affinities using mitochondrial DNA markers. Specimens were manually collected from two waterfall environments in northwestern Misiones, Argentina. Individuals were relaxed using menthol, preserved in 96% ethanol, and deposited in the malacological collection of the Instituto de Biología Subtropical (CONICET – Universidad Nacional de Misiones). Genomic DNA was extracted with a commercial kit. Partial sequences of the mitochondrial markers cytochrome c oxidase subunit I (COI) and 16S-rRNA were amplified and sequenced. Twenty new sequences were added to an existing dataset of 118 individuals from 20 localities to assess genetic variability, estimate genetic distances, perform species delimitation analyses and explore phylogenetic relationships. The analysis of individuals from northern Misiones revealed a previously genetically undocumented clade, referred to here as "*neglectus*". Phylogenetic reconstructions and species delimitation analyses consistently recovered neglectus as a monophyletic lineage, clearly separated from the previously defined "*petricola*," "*submersus*," and "*venustus*" clades. Four new COI and four new 16S-rRNA haplotypes were identified within the neglectus clade, with no shared haplotypes between the two sites, resulting in a total of five concatenated haplotypes. Mean genetic distances between neglectus and other clades ranged from 8.30% to 8.98% for COI and 8.20% to 9.44% for 16S-rRNA. Complementary morphological studies are still needed to accurately assess their taxonomic status and determine whether they possess distinguishing morphological traits or represent a cryptic lineage. The identification of the *neglectus* clade provides new insights into the diversification of *Acrorbis*, particularly regarding geographically isolated populations within the Upper Paraná Atlantic Forest. The findings underscore the importance of continued exploration of waterfalls microhabitats, as they are likely to harbor further undiscovered diversity within this endemic group. This study successfully expands the genetic landscape of *Acrorbis* by incorporating new populations from northern Misiones, bringing the total number of known populations in the Upper Paraná Atlantic Forest of Argentina to 22 localities. The identification of a new differentiated lineage underscores the genetic complexity and diversity of *Acrorbis*, adding new pieces to the puzzle of its intricate evolutionary history as a unique endemic genus.

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QUESTIONING GENERIC BOUNDARIES: WHAT MITOCHONDRIAL DNA TELLS US ABOUT *Anisancylus obliquus* (PLANORBIDAE: ANCYLINAE) IN ARGENTINA

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Keywords: endemic gastropods, freshwater limpets, mitochondrial DNA, evolutionary affinities.

The subfamily Ancylinae (Gastropoda: Planorbidae) comprises small freshwater gastropods with limpet-like shells. *Anisancylus obliquus* is one of seven species in the group inhabiting Argentina, and it also occurs in southern Brazil, Chile, Peru, and Uruguay. Understanding its evolutionary relationships is essential for clarifying the biogeographic history of the group. This study investigates the phylogenetic position of *A. obliquus* based on specimens from central Argentina using mitochondrial DNA. Partial sequences (655 bp) of the mitochondrial cytochrome c oxidase subunit I (COI) gene were analyzed from four *Anisancylus obliquus* individuals collected in Córdoba Province, Argentina, from three populations inhabiting the Ctalamochita (Tercero) and Los Molinos rivers. Species identification was confirmed through shell morphology and muscle scar patterns. Phylogenetic relationships were inferred using Maximum Likelihood (ML) and Bayesian Inference (BI). Genetic distances were estimated using the number of differences (p). To explore species boundaries, four algorithms were applied to the COI dataset: Automatic Barcode Gap Discovery (ABGD), Assemble Species by Automatic Partitioning (ASAP), and the Poisson Tree Processes models (mPTP and bPTP). Phylogenetic reconstructions based on the mitochondrial COI marker yielded consistent results across methods. *Anisancylus obliquus* from Córdoba, Argentina, clustered within a highly supported clade that also included two *Uncancylus* species: *U. concentricus* and *U. bonaerensis*, with *U. paulistanus* forming a sister group to this clade, also with strong support values. These findings suggest close evolutionary relationships among these taxa, potentially indicating taxonomic inconsistencies within current generic boundaries. The genetic distances between *A. obliquus* from Córdoba and *U. concentricus* from Uruguay ranged from 1.40% to 1.41%, while comparisons with *U. bonaerensis* from Buenos Aires Province, Argentina, showed divergences of 1.37% to 2.47%. In contrast, divergence between *A. obliquus* and *U. paulistanus* from Brazil ranged from 5.30% to 5.75%, supporting a more distant relationship. Furthermore, although the four species delimitation methods identified different numbers of species within the dataset, all consistently grouped *A. obliquus*, *U. concentricus*, and *U. bonaerensis* as a single taxonomic unit, while recognizing U. paulistanus as a distinct species. These results challenge the current generic distinction between *Uncancylus* and *Anisancylus*, as well as the species-level separation among *A. obliquus*, *U. concentricus*, and *U. bonaerensis*. The phylogenetic reconstructions conducted here represent the first assessment of the evolutionary affinities of *Anisancylus obliquus* in Argentina within a phylogenetic framework that includes other Neotropical species. Our findings suggest that the generic distinction between *Anisancylus* and *Uncancylus* may be artificial, highlighting the need for more comprehensive morphological and molecular analyses. Incorporating material from the type locality of *A. obliquus* in Chile will be crucial to clarify its phylogenetic placement.

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INVASIVE ALIEN SPECIES

Invasive Alien Species

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NEW OCCURRENCE OF *Electroma vexillum* (REEVE, 1857) (BIVALVIA, PTERIOIDEA, VULSELLIDAE) ON THE BRAZILIAN COAST

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Keywords: taxonomy, alien species, marine protected areas, morphology.

Biological invasions pose significant threats to biodiversity and economies, as highly reproductive and dispersive species often alter ecosystems. The number of alien species has increased in Brazil. *Electroma vexillum* (Reeve, 1857) is originally native to the Red Sea and the Indian Ocean, and has since spread to other regions of the world. Here, we record and describe this species from Brazil, where it appears to have been recently introduced. Specimens were collected in the Cumuruxatiba Marine Reserve, located on the northeastern coast of Brazil (Bahia), in March 2023, and preserved in 96% ethanol. The animals were dissected, measured, and their shell characteristics were observed and photographed, with particular emphasis on outline, sculpture, coloration, and hinge structure. Additionally, the type series of E. electra Simone, Gomes & Molozzi, 2024—previously recorded along the northeastern and southeastern coasts of Brazil—was examined for comparison with the *E. vexillum* specimens under investigation. The Cumuruxatiba specimens exhibit small, fragile, and translucent shells (up to 7.4 mm in length and 7.1 mm in height), inequilateral and inequivalve, with a pterioid shape. The valves are decorated with zigzag patterns, brown markings, and equidistant commarginal riblets. The prodissoconch is indistinct, and the umbones are slightly inflated and pointed, located in the anterior third of the straight, edentulous hinge line. The ligament is small and opisthodetic. The pallial line and adductor muscle scars are not visible. These specimens are very similar to those described as *E. vexillum* from the Mediterranean and Caribbean Seas and also closely resemble *E. electra* from Brazil. However, E. electra can be distinguished by its smaller size, more oblique shell outline, more inflated and less pointed umbones, and a less straight dorsal margin. The specimens collected were putatively identified as *E. vexillum*, representing a new record of an alien species in Brazil. Moreover, the great abundance of this collection (> 500 specimens) suggests that this species might be well stablished and can be a threat, specially for native Pteriidae(e.g, *Pinctada imbricata* Röding, 1798). The fact that it was collected within marine protected areas highlights its threat potential to sensitive ecosystems.

Funding Source: Brazilian Malacological Society.

Invasive Alien Species

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ECOLOGICAL FITTING AND HOST EXPLOITATION BY THE INVASIVE MUSSEL *Sinanodonta woodiana* ALONG A SYMPATRY GRADIENT

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Keywords: host–parasite interactions, freshwater mussels, glochidia load, host infestation, sympatry gradient, biological invasion.

Invasive freshwater mussels can disrupt native host–parasite systems via novel infection strategies and immune interference. The Chinese pond mussel *Sinanodonta woodiana* has spread across Europe, exploiting a broad range of hosts. However, the extent to which it displaces native mussels through host competition remains unclear. We investigated natural infestation patterns of *S. woodiana* and native unionids along a sympatry gradient to evaluate differences in host use and infestation intensity. We surveyed six freshwater sites in Poland that differed in invasion history of *S. woodiana*, covering both lentic and lotic environments. A total of 601 fish representing eight species were collected using electrofishing and dissected for parasitological examination. Glochidia were identified morphologically, and their prevalence, intensity, and attachment sites (gills, fins, skin) were recorded. Statistical models were used to compare infection patterns across host species, sites, and mussel taxa. We evaluated potential spatial partitioning and interactions between native and invasive mussels by analyzing co-infections. Host body mass and habitat type were tested as covariates affecting parasite load, and differences in site-specific infestation were analyzed along the sympatry gradient. Glochidia of *S. woodiana* were found on all fish species, with higher prevalence and intensity in lentic habitats. Infection rates varied significantly among hosts, with *Carassius gibelio*, *Rhodeus amarus*, and *Pseudorasbora parva* showing highest parasite loads. *Glochidia* were commonly found on both fins and gills, suggesting flexible attachment strategies. In contrast, native mussel (mainly *Unio pictorum*) infested fewer hosts, with gill-specific attachment and lower prevalence. Although the potential for immune-mediated interference existed, and some fish hosted multiple mussel species, statistical analysis showed no direct exclusion of native glochidia by *S. woodiana*. Fish body size positively correlated with *glochidia* abundance, and fin infestation was more common in heavily parasitized individuals, especially in *C. gibelio* and *R. amarus*. These results suggest that *S. woodiana* benefits from ecological fitting to East Asian-origin fish and may outcompete native mussels by saturating shared hosts. Higher infestation levels in lakes likely reflect habitat-specific differences in transmission dynamics rather than solely longer invasion histories. The broad host range and flexible attachment strategy of *S. woodiana* highlight its invasive potential. While our study found no direct evidence for immune interference with native mussels, such indirect effects remain a plausible concern in invaded communities. *S. woodiana* demonstrates broader host use and higher glochidia loads than native mussels, particularly in lentic habitats. While no direct displacement of native larvae was observed, immune interactions or preferential host saturation may impede native reproduction. The species' generalist strategy likely contributes to its invasive success. Conservation of native unionids requires site-specific management and further investigation of host compatibility, reproductive timing, and immune-mediated effects of biological invasions.

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Invasive Alien Species

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BIOLOGICAL PERFORMANCE ASSESSMENT OF PLANTIGRADE LARVAE AND JUVENILES OF *Limnoperna fortunei* (BIVALVIA: MYTILIDAE) UNDER THE EFFECT OF DIFFERENT ANTIFOULING COATINGS

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Keywords: golden mussel, impacts, net cage fish farming, antifouling coatings.

The introduction of the golden mussel (*Limnoperna fortunei*) in Brazil has generated environmental and economic impacts, affecting net cage fish farming in reservoirs, making it urgent to seek methods for its control. In this sense, this project will evaluate the effect of antifouling coatings on net cage screens by analyzing the abundance and growth of plantigrade larvae and juveniles of this invasive species. In the Chavantes Reservoir (Ipaussu, SP), in three sampling sectors, 36 metal frames were installed in September 2024, each one with three stainless steel meshes: without couting (control), silica and epoxy resin and paint + Lysoglycerophospholipids. Monthly, from October 2024 to March 2025, one frame per sector was removed, and individuals up to 1000 µm were counted and measured using a Zeiss stereomicroscope and Zen 3.3 Lite software. The monthly mean abundance of individuals on the meshes was calculated. Length-frequency histograms allowed us to assess temporal size variation. The non-parametric Kruskal-Wallis and Mann-Whitney tests were used to compare abundance and length among treatments and across months for each treatment. The Kruskal-Wallis test indicated no significant difference between the control and treatments for either abundance ($K = 0.1053$, $p = 0.9483$) or individual length ($K = 3.107$, $p = 0.2115$). No significant temporal difference in the mean abundance of individuals was observed with the data obtained to this moment. However, an increase seems to occur in December, especially on the paint-treated meshes, and in January for the other treatments. The temporal variation in the size distribution of individuals reflects different stages of larval development. The Kruskal-Wallis test indicated a significant difference in individual length across months for all treatments, and the Mann-Whitney test generally showed smaller sizes in November and March. In October and November, smaller organisms were observed, with a maximum size of 600 µm. In subsequent months, more size classes were recorded, with individuals reaching up to 900–1000 µm, indicating intense colonization activity. In March, most individuals were again concentrated in the smaller size ranges, particularly between 200 and 400 µm. The results suggest that colonization by *Limnoperna fortunei* appears to be more pronounced between December and February, as indicated by the higher number of size classes observed during this period. The data obtained thus far do not provide conclusive evidence of any significant effect of the antifouling treatments tested on individuals up to 1000 µm.

Funding Source: Fapesp – Grants 2023/08026-0 and 2024/08842-5.

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VULNERABILITY TO CLIMATE CHANGE OF THE INVASIVE FRESHWATER MUSSEL *Corbicula fluminea*: TEMPERATURE AND NUTRIENT IMPACT ON PHYSIOLOGY AND SURVIVAL

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Keywords: asian clam, nutrient condition, histology, lípid peroxidation, tissue condition index.

The successful establishment of the invasive bivalve *Corbicula fluminea* depend on the existence of lentic habitats with organic matter and a 15-25°C temperature range. Asian clams are sensitive to extreme environmental fluctuations. Abiotic factors (oxygen, pH, nutrients) modulate physiological performance and reproductive success. The present study evaluated mortality rate, Tissue Condition Index, gill tissue integrity and lipid peroxidation of *C. fluminea* across a rage of temperature treatments/nutrient concentration regimes. 150 specimens of *Corbicula fluminea* were collected from the Oeiras stream in the Guadiana River, Portugal. Individuals were acclimated for 10 days at 20°C and then allocated to six experimental treatments (five replicates with five bivalves each) combining temperature (25°C, 28°C, 32°C) with trophic conditions (oligotrophic, eutrophic). Environmental parameters (water temperature, dissolved oxygen, pH, conductivity, nutrients) were monitored daily. After 21 days, the Tissue Condition Index (TCI - ratio of dry soft-tissue mass to shell mass) was measured; Gill histology (samples fixed, embedded in paraffin, sectioned and stained with hematoxylin–eosin); Lipid peroxidation (LPO - thiobarbituric acid–reactive substances assay) determined. Survival was assessed daily. The results show that the survival and physiological performance of *Corbicula fluminea* were strongly shaped by the interaction between temperature and nutrient availability. Mortality was highest at 32°C, particularly under oligotrophic conditions—no individuals survived beyond day 7—whereas under eutrophic conditions survival extended through day 21. These observations are consistent with previous work demonstrating that eutrophication exacerbates the impacts of warming on aquatic biota (Reid et al. 2019; Dodds et al. 2010). The Tissue Condition Index (TCI) mirrored this pattern, reaching its lowest value in the 32 °C oligotrophic treatment (TCI = 0.445), indicative of severe combined thermal and nutritional stress. This finding suggests a synergistic interaction between elevated temperature and nutrient limitation, likely driven by increased metabolic demand in degraded environments. Histological analysis of the gills revealed progressive vacuolization with rising temperatures, culminating in severe structural damage at 32 °C. In contrast, lipid peroxidation (LPO) levels—a proxy for oxidative stress—increased most sharply at moderate temperatures (25 – 28°C) under eutrophic conditions, peaking at 28°C (28.56 TBARS). In the 32°C treatments, LPO values were lower, probably reflecting the high early mortality. These results support the view that the combined pressures of global warming and nutrient over-enrichment pose a significant threat to freshwater fauna (Paerl & Paul 2012; Heisler et al. 2008). Elevated temperatures coupled with low nutrients impair the survival, cellular integrity and overall physiological condition of *C. fluminea*. 32°C represents a critical thermal-tolerance threshold for the species. At 28°C the clams showed significant physiological disturbances and increased oxidative stress, indicating that sub-critical thermal elevations can still induce substantial sublethal damage. Preserving high water-quality standards may enhance the resilience of freshwater communities under climate-change.

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EXPLORING SEASONAL POPULATION DYNAMICS OF INVASIVE *Bulimulus* SNAILS IN FLORIDA CITRUS

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Keywords: *Bulimulus*, snail.

Bulimulus bonariensis is an invasive land snail species that has infested various commercial crops in the southeastern U.S., threatening productivity. In Florida citrus, *B. bonariensis* has been observed clogging irrigation jets, defoliating young trees within individual protective covers, and girdling trees with pre-existing bark damage. Currently, there is limited information on the seasonal population dynamics of these snails, which are important to consider when developing management programs. To explore seasonal population dynamics, experimental traps were deployed at three citrus groves in Florida. Traps were evenly spaced along rows of trees and field edges. Snail count data were collected biweekly from traps at each site from 2023-2025 and plotted to observe seasonal trends in snail activity. To explore within-field spatial distribution, the count data were used to create heat maps in ArcGIS depicting snail distributions at all sites for each sampling date. The count data revealed that snail activity may be correlated with temperature. At one site, populations peaked during the warmer months from May through September but declined and remained relatively inactive during the cooler months from October through April. However, this trend was not consistent across all sites, with some sites exhibiting sporadic year-round fluctuations in activity. Variation in population trends between sites could be due to differences in environmental conditions, management practices, and habitat type. As such, site specific monitoring may be critical for identifying periods of activity and guiding management decisions. The heat maps revealed that snail populations exhibit a clumped distribution within groves and are scarce along field edges. These patterns suggest that management efforts for this species should prioritize areas within groves rather than along edges, and that targeted control may be feasible by identifying snail hotspots through intensive monitoring. The findings of this study provide critical insights into the seasonal population dynamics of *Bulimulus bonariensis*, enhancing our understanding of its complex ecology and guiding the development of effective management programs aimed at mitigating its adverse effects on citrus production.

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FIRST RECORD OF *Perna viridis* IN THE TODOS OS SANTOS BAY, BAHIA, BRAZIL

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Keywords: invasive species, shell morphology, ballast water.

Perna viridis, a bivalve native to the Indo-Pacific and known for its invasive potential, poses a threat to marine biodiversity. While previously reported in southeastern Brazil, records from the northeast remained uncertain. This study confirms the first occurrence of *P. viridis* in Todos os Santos Bay, Bahia, extending its known distribution to northeastern Brazil and underscoring the importance of monitoring non-native marine species. Eight *Perna viridis* specimens were collected near the port of Ilha de Maré in Todos os Santos Bay, Bahia, and taken to the Marine and Coastal Ecology Research Group at the Federal University of Bahia. In the laboratory, specialists identified the mollusks using relevant literature. A comparative analysis was conducted with native Mytilidae species—*Perna perna*, *Mytella strigata*, and *Mytella guyanensis*—which are commonly misidentified as *P. viridis* in northeastern Brazil. Diagnostic traits such as shell color, umbo position, adductor muscle scars, and valve structures were examined. These features confirmed the identity of the specimens. All individuals were measured, photographed, and recorded for further reference. The comparative analysis between *Perna viridis* and the native species *Perna perna* focused on key characteristics, including the bright green coloration on the outer shell, byssus location, and tooth morphology. Notably, *P. perna* has a prominent tooth on the left valve and a corresponding depression on the right valve, whereas *P. viridis* lacks these features. When comparing *P. viridis* to Mytella species, characteristics such as shell orientation (ventrally directed), terminal umbo, and absence of the anterior adductor muscle scar were considered. In contrast, *Mytella* specimens exhibit an anteriorly directed shell face, subterminal umbo, and visible adductor muscle scar. These distinguishing features confirmed the identification of the collected individuals as *P. viridis*. The specimens averaged 8.3 mm ± 0.40 mm in length. Notably, *P. viridis* was found on natural substrates, which is consistent with its ability to adapt to various environments. As a non-native species originating from Southeast Asia, *P. viridis* has recently been recorded in the South Atlantic. Research suggests that its introduction is linked to hull fouling, ballast water discharge, and rafting on marine debris. In Guanabara Bay, *P. viridis* was initially discovered attached to floating debris, and its population is now established, coexisting with native species. The analysis confirmed that the individuals belong to the non-native species *Perna viridis*. The presence of *P. viridis* in Bahia suggests a broad physiological tolerance, facilitating its dispersal into the Todos os Santos Bay. This record extends our understanding of its distribution along the Brazilian coast and highlights the importance of monitoring and research on the ecological impacts of invasive species in marine ecosystems.

Funding Source: No.

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COMPARATIVE STUDY OF INVASIVE POPULATIONS OF *Bulimulus* aff. *bonariensis* (RAFINESQUE, 1833) (BULIMULIDAE) FROM FLORIDA (USA) WITH ARGENTINE ENTITIES

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Keywords: agricultural pest, species complex, origin, morpho-anatomy.

Bulimulus bonariensis (Rafinesque, 1833) is considered a widely distributed species in Argentina. However, according to anatomical and genetic evidence, it is a complex of species of at least eight entities. The aim of this work is to study the anatomy and conchiolar structure of specimens from Florida and to compare them with the entities studied so far in Argentina in order to try to establish a possible argentine origin. Manual collections were completed from two sites: in a research station and a commercial orchard of Polk County, Florida, USA (March/2025). 50 specimens were obtained, the shell morphology was examined, and measurements were taken with digital caliper (total length of the shell; height of the spire, last whorl, penultimate whorl; major, minor and penultimate whorl diameter; length of the parietal space; height and width of the aperture) and a Discriminant Analysis was performed comparing them with specimens from different Argentine provinces. The anatomy in general and especially of the penis complex and the proportions between the sectors that conform it were analyzed (penis sheath, penis, epiphallus and flagellum). Adult individuals showed a narrow and long shell morphology; in general, juveniles do not exhibit the adult appearance, being more rounded at this stage, so they were not included in the DA. The DA separated the individuals from Florida (USA) from the Argentine specimens studied, axis 1 accumulated 92.9% of the variation and the variables that contributed most were the total length of the shell (77.9), the largest (54.5) and smallest diameter (44.7), differentiating graphically the specimens from both countries. From the internal anatomy it was observed that some of the dissected adult specimens have a penile complex similar in appearance and proportions to specimens from the provinces of Corrientes, Santa Fe, and Misiones (Arg.). However, it was also found that juvenile snails with a total length of about 12 mm have a penile complex more similar to specimens from Buenos Aires. On the other hand, at the external level, populations from Florida (USA) were also differentiated by two particularities: the location of the most anterior gonopore on the head, in front of or below the eye-bearing tentacle (in Argentine populations studied the gonopore is located behind) and by the presence of a fold or expansion of the mantle edge at the nuchal level. Anatomical and genetic studies have shown that Argentine *Bulimulus* have a great taxonomic complexity. The presence of populations causing problems in agriculture both in the USA and Argentina are the origin of interest of this study. Due to anatomical similarities, we believe that populations from the USA could originate from Argentina. However, interesting differences have also been found. Future genetic analyses are needed to confirm the origin of these populations.

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GOLDEN MUSSEL WELFARE IN THE LABORATORY: MORTALITY AND BYSSUS FORMATION AT DIFFERENT TEMPERATURES AND SALINITIES OVER A SHORT PERIOD

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

Limnoperna fortunei, native to Asia and introduced to South America in the early 1990s, remains an ecological concern. Transporting and maintaining this mussel under controlled laboratory conditions is crucial for studying its life cycle and preventing its spread. In this experiment, we investigated the relationship between mortality, mobility, and water physicochemical parameters. Adult mussels (240) were kept in the lab for two months, cleaned, and isolated. Four individuals were placed in each experimental unit, consisting of 60 glass containers with 200 mL of water and aeration. Two experiments assessed: salinity (0, 5, 10, 15, 20) and temperature (7, 10, 15, 25, 30, 35 °C), with five replicates each. Controls were set at 25 °C and salinity 0. Mortality and mobility (byssal attachment) were recorded daily for one week without feeding. Data were analyzed using two-way ANOVA (days/ salinity; days/temperature) and Tukey HSD tests (α=0.05) in STATISTICA®demo. Statistical analyses of the first experiment, which evaluated the effects of salinity, revealed significant differences in both mortality and mobility across days ($p<0.001$) and salinity levels ($p<0.001$). Lower salinities (control, 0, 5, 10) exhibited higher survival and mobility, whereas higher salinities (15, 20) resulted in 100% mortality by day 5 and a complete absence of byssal attachment. The second experiment also revealed significant differences for both variables across days ($p<0.001$) and temperatures ($p<0.001$). The extreme temperatures (7, 30, and 35 °C) exhibited the lowest mobility values, while the two highest temperatures (30 and 35 °C) resulted in complete mortality by the second and third days, respectively. Mortality increased and mobility decreased over time, indicating an inverse relationship. These experimental data demonstrate that these two fiscal-chemical factors are limiting factors for the survival and dispersal of the golden mussel. Adults did not survive at salinities >15 or temperatures >30 °C. Therefore, it is concluded that standardized protocols for the transport and laboratory containment of the golden mussel (*L. fortunei*) are necessary. The importance of rapid experimentation in optimizing short-term maintenance conditions when working with this invasive species is crucial for future research.

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SPATIOTEMPORAL DYNAMICS OF *Limnoperna fortunei* (DUNKER, 1857) LARVAE IN A HYDROPOWER RESERVOIR OF THE LOWER IGUAÇU RIVER, BRAZIL: A CONTRIBUTION TO A SUSTAINABLE MANAGEMENT APPROACH

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

Golden mussels cause environmental issues and economic impacts in established areas, resulting in imbalances within these ecosystems. After thirty years of confirmed invasion in South America, practical control actions remain scarce. As a result, this study aims to assess the spatiotemporal dynamics of *Limnoperna fortunei* larvae and their environmental relationships in a hydroelectric power reservoir. During 2023 (February–November), quarterly in situ samplings were conducted across 24 areas along an 11 km stretch downstream from the Baixo Iguaçu Hydroelectric Dam, covering river margins, the main channel, and four reservoir sectors. Samples were collected using plankton nets, motor pumps, and multiparameter probes. A total of 48 samples per event were analyzed under a stereoscopic microscope to assess larval density. Densities (individuals/m³) were log-transformed [log(x+1)] before analysis. Data were subjected to three three-way ANOVAs (sampling periods, river positions, and sectors) and Tukey's HSD tests (α = 0.05) using STATISTICA® demo software to evaluate statistical differences in larval distribution patterns. Based on the analysis of 192 samples, larval density in the monitored areas was observed to range from 0 to 1,108 individuals/m³. When comparing these results with information gathered from 48 bibliographic references spanning approximately 50 years (from October 1971 to November 2023) and covering the spatiotemporal life cycle of *L. fortunei* in different regions worldwide, it was found that the observed density values rank among the ten highest recorded in South America. A two-way ANOVA revealed significant differences (p=0.039) in larval density related to water surface layers and spatiotemporal variations (collection months and river positions) within the studied hydroelectric reservoir. The results highlighted a larval dynamic characterized by significant variations in the surface and subsurface water layers across the reservoir, indicating the presence of larval input hotspots in this segment of the Iguaçu River, as well as a mosaic distribution pattern of golden mussel larval stages. A comprehensive understanding of the life cycle of this mollusk, together with well-established data on the planktonic population dynamics of *L. fortunei*, enhances the effectiveness of control strategies, contributing to the development of sustainable management practices for the species in invaded ecosystems.

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GOLDEN MUSSEL WELFARE IN THE LABORATORY: FEEDING DIET OF POPULATIONS AT DIFFERENT LATITUDES IN SOUTH AMERICA

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

The golden mussel (*Limnoperna fortunei*), a native species to China, has been present in Brazil since late 1998, causing damage to industries and power generation facilities. To contribute to reducing its growth rate, the present study evaluated the species' feeding diet. *Limnoperna fortunei* specimens (n=30) were collected from three latitudes and four localities in South America (one in Ilha das Flores, SE, Brazil; one in Capanema, PR, Brazil; two in Porto Alegre, RS, Brazil). The height (H) and length (L) of the individuals were measured using a digital caliper as described by Oliveira and Oliveira (1974). Subsequently, the animals were weighed, and the meat yield index (MY) was calculated according to Absher and Christo (1993). The digestive tracts were then eviscerated and fixed according to Degraf et al. (2018). Microalgae found in the digestive contents were photographed using a photomicroscope and later identified to the lowest possible taxonomic resolution. In the analyzed material, a diverse range of dietary items was observed, including algae, cyanobacteria, invertebrates such as arthropods and small crustaceans, digested plant material, and various types of organic matter. Differences in the composition and diversity of dietary items were noted among the analyzed *Limnoperna fortunei* populations. Similar food items have also been reported in other regions of Brazil (Molina & Paggi, 2008; Mansur et al., 2012; Sylvester et al., 2005; Molina et al., 2007). These findings demonstrate the species' feeding plasticity and the ecological impact that *L. fortunei* has on plankton communities and nutrient cycling. Its presence may be as significant as that of the invasive zebra mussel (*Dreissena polymorpha*) in Europe and North America. However, the overall ecological effects may vary considerably under different environmental settings (Cataldo et al., 2012). This underscores the importance of expanding dietary studies of *L. fortunei* populations across various regions of South America, particularly in areas at the species' range limits. The analysis of dietary samples revealed a broad diversity of food items, demonstrating that *L. fortunei* does not rely exclusively on photosynthetic organisms. Additionally, dietary variations were observed among populations from different latitudes in South America, suggesting regional influences on feeding behavior.

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DISTRIBUTION AND HABITAT PREFERENCES OF THE INVASIVE SNAIL *Melanoides tuberculata* IN THE PARNAÍBA RIVER BASIN, BRAZIL

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Keywords: ecology, invasive species, pollution.

Freshwater molluscs inhabit diverse environments, and their presence and abundance are influenced by physical, chemical and anthropogenic factors. *Melanoides tuberculata* is an invasive species with notable plasticity and, due to its parthenogenetic reproduction, can colonise various habitats. This study aimed to analyse the spatial distribution and environmental factors associated with the presence of this species in the main rivers of the Parnaíba River Basin, semiarid of Piauí, Brazil. Sampling was conducted in eight rivers belonging to the Parnaíba River Basin between September and October 2022. Three sections of each river (mouth, middle, and headwaters) were surveyed. Molluscs were collected from sediments and macrophytes, along with environmental parameters, using a multiparameter monitor. Continuous variables were standardised and checked for collinearity. The presence of *M. tuberculata* was modelled using binomial generalised linear models with total dissolved solids (TDS), salinity, temperature, and substrate type as explanatory variables. Model validation was performed through AIC and Tjur's pseudo-R^2 analyses. A total of 3,047 *Melanoides tuberculata* individuals were collected. The Pirangi River showed the highest abundance (n = 2,203; $\bar{x}$ = 44 ± 196), while the Piauí River had the lowest (n = 3). No records were found in the Longá, Gurgueia, and Uruçuí Preto Rivers. Middle sections of the rivers had the highest abundance (n = 1,559; $\bar{x}$ = 194 ± 293), followed by headwaters (n = 840; $\bar{x}$ = 105 ± 292) and mouths (n = 648; $\bar{x}$ = 81 ± 293). Environments with muddy and sandy sediments predominated. Regarding substrate type, sediments contained approximately 4.7 times more individuals than macrophytes (2,514; $\bar{x}$ = 34 ± 99). Similarly, muddy substrates had higher abundance (n = 1,477; $\bar{x}$ = 54 ± 149) than sandy ones (n = 257; $\bar{x}$ = 9 ± 19). The GLM explained a significant portion of the variation in *M. tuberculata* occurrence (Tjur's pseudo-R^2 = 0.63), with TDS emerging as the most influential predictor. As TDS values increased, so did the probability of species occurrence (intercept = -3.48; β = 0.03; AIC = 19.7; p = 0.012). This relationship suggests effective establishment in areas with notable anthropogenic activity. The results underscore the ecological resilience of *M. tuberculata*, demonstrating its adaptation to degraded environments with muddy substrates and accumulated organic matter. *Melanoides tuberculata* exhibited wide distribution and a preference for sediment-rich environments with high levels of dissolved solids, showing strong associations with degraded areas. The results highlight the species' invasive potential and its affinity for habitats with higher organic matter concentrations. Given its ecological and sanitary relevance, monitoring and mitigation actions are essential to contain its spread and safeguard aquatic ecosystems in the region.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

Invasive Alien Species

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EDUCATIONAL OUTREACH ON NON-NATIVE MOLLUSKS: CREATION OF THE BOOKLET 'THERE ARE STRANGERS IN OUR CLASS'

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Keywords: exotic species, biological invasions, terrestrial molluscs, limnic molluscs, raising awareness.

Exotic and invasive species threaten ecosystems by competing with native species, altering habitats, and spreading diseases. The booklet “There Are Strangers in Our Class”—the first volume of the Unwanted Neighbors series—addresses non-native mollusks found in Campos Gerais, Paraná, Brazil. This initiative raises awareness about environmental impacts by combining scientific content with accessible language. The booklet is composed of chapters derived from outreach actions, presented in the form of six informational folders. Each folder describes the concept of exotic or invasive mollusk species and characterizes one species found in the highland region of Campos Gerais, Paraná. The information was collected through field observations and laboratory analyses, a review of the scientific literature to identify and characterize the species, and collaboration with experts and partner institutions to ensure the accuracy and relevance of the data. The chapters characterized three exotic mollusk species (*Bradybaena similaris*, *Limax flavus*, and *Tanychlamys indica*) and three invasive species (*Lissachatina fulica*, *Melanoides tuberculata*, and *Corbicula fluminea*). These species originate from the Asian (4), African (2), and European/Mediterranean (1) continents, with the Trumpet Snail (*Melanoides tuberculata*) exhibiting an Afro-Asian origin. Taxonomically, all studied species belong to distinct phylogenetic families. Five are gastropods, while *Corbicula fluminea* is the only bivalve species included in the study. Combating exotic invasive species is not a task that a single entity can accomplish. The collaboration of researchers, environmental managers, farmers, students, and the public is crucial for the success of control and eradication efforts. A thorough understanding of the ecology and distribution of these species is essential for developing effective management and conservation strategies. The taxonomic diversity of the identified species, representing different classes and families, underscores the complexity of the challenge, necessitating tailored approaches for each case. Public awareness, promoted through educational materials such as this booklet, represents a critical first step toward establishing effective participatory management. The study highlights the presence of exotic and invasive mollusks in the Campos Gerais region. The taxonomic and ecological diversity of these species highlights the need for integrated management strategies that combine scientific research, public policies, and community engagement. Educational materials, such as this booklet, are essential tools for raising awareness and promoting participatory management aimed at conserving native biodiversity.

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Invasive Alien Species

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GOLDEN MUSSEL WELFARE IN THE LABORATORY: NATURAL REPRODUCTION OF *Limnoperna fortunei* (DUNKER, 1857)

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

Knowledge of reproductive biology is essential, as it provides the basis for safe biotechnological inferences. *Limnoperna fortunei* is described as dioecious, reaching sexual maturity at approximately 3 to 4 months, and exhibiting internal sexual dimorphism, evidenced by gonadal coloration. This study aimed to induce spawning and fertilization without chemical agents. Specimens were manually collected from tree trunks, rocks, and artificial structures within the Baixo Iguaçu Hydroelectric Power Plant (UHE) reservoir on the Iguaçu River in Paraná, Brazil. In the laboratory, mussels were cleaned and maintained in tanks with treated water, feeding, and aeration. Five specimens from each batch, representing approximately 300 individuals, showing gonadal maturation were selected for analysis, following Christo et al. (2016). Batches with at least three individuals classified as stages C or PC were subjected to assisted reproduction. Following gamete release and fertilization, samples were collected to monitor the initial developmental stages and photodocument the ontogeny process. Based on the results obtained, individuals measuring between 16 and 27 mm exhibited mature gonads, aligning with the reported size for sexual maturity in *L. fortunei*. Following spawning induction in the laboratory, eggs and embryos were identified, followed by trochophore stages appearing between 8 and 10 hours after fertilization. Subsequently, larvae reached the veliger stage, characterized by the development of the larval shell. As the literature describes, the golden mussel is a dioecious species, with occasional hermaphroditism, reaching sexual maturity at approximately four months. Indirect larval development resulted in trochophore and ciliated veliger larvae around 6 and 24 hours after fertilization. Reproductively, individuals classified as C and PC stages were the most efficient. Rapid sex differentiation based on gonadal coloration facilitated the management of species reproduction. The induction of spawning, fertilization, and larviculture without synthetic chemicals for the golden mussel enables new approaches for developing actions to control the species. These data are fundamental for deepening the understanding of the species' ontogeny and for the proper maintenance of larvae and juveniles in laboratory environments.

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GOLDEN MUSSEL WELFARE IN THE LABORATORY: PHYSIOLOGICAL RESPONSE OF REPRODUCTIVE PARAMETERS IN THE BIVALVE *Limnoperna fortunei* (DUNKER, 1857) EXPOSED TO A SHORT-TERM SALINITY CHALLENGE

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

The golden mussel is an invasive species with high dispersion and reproduction capabilities, causing damage, particularly in hydroelectric plants. Since the use of chemical products does not eliminate it, as they isolate themselves within the valves, the objective of this study was to evaluate the influence of this isolation on the condition index and meat yield over a short period. The bivalves were collected from the Baixo Iguaçu Hydroelectric Reservoir in Paraná, Brazil, and maintained in the laboratory for 30 days before the experiment. To assess the isolation capacity in response to osmotic challenges and reproduction, 48 individuals were exposed to different salinities (0, 2, 4, and 8) for 3 hours, with six replicates per treatment. Half of the animals (n = 24) had a barrier inserted to prevent complete valve closure, while the others did not. Responses were evaluated by Condition Index (CI) and Yield Index (YI). The data were subjected to ANOVAs and Tukey HSD tests (α = 0.05) using the STATISTICA demo software. There was no difference between salinities or between the groups with and without the barrier. The mussels may have employed physiological mechanisms to maintain a high CI and YI. Considering that CI and YI are relative parameters for reproduction, it was observed that the imposed salinity challenges and the condition of mandatory valve opening did not interfere with the reproductive parameters CI and YI. Significant differences may be observed in the evaluated parameters at different times during the reproductive cycle of *L. fortunei* or with prolonged exposure to salinity challenges. A larger barrier could also be tested to further impede the isolation mechanism of the intervalvar tissue from the environment. Understanding the reproductive processes of *L. fortunei* is crucial for developing effective population control strategies. Since the analyzed parameters showed no significant changes under the experimental conditions, we conclude that the salinities tested do not challenge the species' reproduction in the short term. Given the invasive nature of *L. fortunei*, more stringent protocols should be applied to create a real challenge to its reproduction and help manage its population.

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SPATIOTEMPORAL DYNAMICS OF *Limnoperna fortunei* (DUNKER, 1857) RECRUITMENT IN A HYDROPOWER RESERVOIR OF THE LOWER IGUAÇU RIVER, BRAZIL: A CONTRIBUTION TO A SUSTAINABLE MANAGEMENT APPROACH

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

The golden mussel (*Limnoperna fortunei*), native to China, was introduced to the Americas in the 1990s via cargo ships. With planktonic larvae and benthic adults, it causes environmental and economic impacts (Pereira, 2018). This study analyzes the spatiotemporal variation in the recruitment of the species upstream of the Baixo Iguaçu Hydroelectric Plant (UHE) reservoir. Sampling is carried out every three months in the UHE reservoir, located 174 km from the mouth of the Iguaçu River and at the upper boundary of Iguaçu National Park (PNI), Paraná, Brazil. Artificial collectors were installed on both riverbanks, utilizing two monitoring systems: rafts and longlines. For the rafts, wooden collectors were placed horizontally at 1.5 meters; for the longlines, rope collectors were positioned at three depths (1.5, 2.5, and 3.5 meters). Specimen sorting is performed using a stereoscopic microscope, with individuals fixed in 70% ethanol and analyzed following the methodology of Christo (2006). Based on the analysis of wooden and rope collectors from the study area, the movement of adult individuals and the recruitment of *L. fortunei* larvae on the selected substrates were observed. Specimen size was used as the differentiation criterion, with individuals measuring one centimeter or more classified as adults (Darrigran and Damborenea, 2011). The materials used proved satisfactory for analyzing *L. fortunei* population parameters. The data obtained allows for an estimation of the number of individuals settled on each collector over time. Compared to the initial samplings, more individuals were observed on one side of the wooden collectors, with less sediment accumulation. Despite size variation, specimens consistently grouped, demonstrating the gregarious behavior described in the literature (Darrigran and Damborenea, 2009; Darrigran and Damborenea, 2011). For the rope collectors, a higher incidence of individuals was recorded at the shallowest depth compared to the other two depths. The selected test bodies (collectors) proved suitable for analyzing *L. fortunei* population parameters over time and across the selected sampling points. Additionally, the shape and material composition of the test bodies may provide distinct information regarding the species' recruitment patterns.

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LIGHT TRAIL: METHODOLOGY FOR TRACKING THE LAND SLUG *Meghimatium pictum* (STOLICZKA, 1873)

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Keywords: exotic species, biological invasions, terrestrial molluscs, invasive land slug.

Traceability methods for terrestrial molluscs are still scarce. Our objective is to investigate the efficiency of mark-recapture methods, using *Meghimatium pictum* as a model, a slug native to Asia that has established itself in Brazil and affects agricultural products, including strawberries. This research allows us to observe visual evidence of communication between different populations of the invasive species. Thirty slugs were randomly selected in the city of Ponta Grossa, Paraná, Brazil, and injected with a fluorescent polymer that glows under ultraviolet light, in a numerical pattern (position of injections indicating numbers) that allowed their later identification, left to rest for one day (24h), weighed and released. After one day of the slugs' release, recaptures of the marked specimens were monitored for two months, at the end of the day and the beginning of the night, for one hour each. One of the slugs did not survive the polymer injections, but the reason remains unclear, as no damage was caused during the infusion, and the slug was found dead the following day after the resting period. This slug (number 10) was removed from the group and stored in alcohol. Another slug was marked as number 10 and left to rest to recover from the stress for about an hour and a half. Ten of the 30 slugs released were found relatively close to the release area, approximately 10 meters away. While slugs numbers 20 and 30 were easily identifiable (marked with orange polymer) when compared to the other numbers (marked with dark green and light green polymers in different positions of the body), they were more challenging to identify, as the polymer had spread under the skin. Although the experiment demonstrated that slugs can tolerate this marking method (with specimens recaptured 2 months after release) with minimal recovery time, the identification method requires refinement as the polymer migrates into the animal's flesh over time. This could be addressed by using a wider variety of colours for the markings, making it easier to tell which numbers are which. This type of mark-and-recapture process is commonly employed in research involving small fish and shrimp. Gastropods are usually marked with adhesive tags on their shells, which is impossible with slugs. This method is suitable for monitoring the dispersion of *M. pictum* populations and determining habitat size, since these mollusks have a restricted distribution due to the need to stay hydrated. The methodology has shown promise in contributing to identifying transport vectors on a broader scale and their relationship with human activities, such as the movement of food (fruits and vegetables), plants (such as flower pots), and agricultural supplements.

Funding Source: No.

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INVADED WATERS! FIRST RECORD OF THE INVASIVE BIVALVE *Mytilopsis leucophaeata* (CONRAD, 1831) - DARK FALSE MUSSEL, IN THE ESTUARY WATERS OF CACHOEIRA RIVER - SOUTHERN BAHIA, BRAZIL

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Keywords: Dreissenidae, tropical waters, ballast water.

Mytilopsis leucophaeata is native to the Gulf of Mexico, occurring naturally in oligohaline to mesohaline estuaries along the Atlantic coast (USA – Mexico). It was first reported in 2004, in the Northeast region in Brazil, in estuaries adjacent to the Port of Recife - PE. Ten years later, was recorded for the Southeast region, in Lagoa Rodrigo de Freitas - RJ, and from there it reached other nearby lagoon systems. A survey of the benthic macrofauna of Cachoeira River estuary (Ilhéus - BA) was carried out in February 2024. Samples were collected using a van Veen bottom search in the channel and corer on the banks, 12 stations covering the entire estuarine portion. The material present was washed over overlapping sieves with 1.0 and 0.5 mm mesh opening, fixed and preserved in 70% alcohol. Identification was performed with appropriate keys for each group and, when necessary, confirmed by experts. Reference lots are deposited in the Aquatic Invertebrates Collection of Southern Bahia (CIASB). After identification of the invasive species, individuals were quantified and measured. One of the causes of biodiversity loss in Brazil is the arrival of exotic species in the country, accidentally or not. When these species manage to establish local populations, they expand their distribution, threatening native species and altering ecosystems. *Mytilopsis leucophaeata*, Family Dreissenidae, was recorded in the three stations further upstream of the estuary (10 to 12). Salinity was low (maximum of 6), turbidity high (transparency <0.1 m) and total dissolved solids ranging from 83 to 106. pH ranged from 6.17 to 6.64. Depths ranged from 0.9 to 4.7 m. The bottom is composed of metamorphic blocks, to which individuals were attached by the byssus, forming cluster structures, covered with fine, hypoxic sediment. There was no significant differences in average length of individuals among the three stations. The smallest individual recorded measured 0.55 mm (recently recruited) and the largest 28.25 mm. Station 11 had the highest density, 4,300 individuals/m², low when compared to other areas where the species was recorded. Our data suggest that the occupation of the system by *Mytilopsis leucophaeata* is recent - studies carried out in 2021 did not record it in these same stations, but there was already an effective presence of young and adult individuals. This species is considered an ecological and economic threat similar to that of the zebra mussel.

Funding Source: CNPq (BRAZTEM Project - Seasonal model of the functioning of the Estuaries of southern Bahia based on multidisciplinary and multi-scale analysis to identify environmental impacts and effects of climate change. UESC.

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PROVENANCE AND POPULATION STRUCTURE OF A NON-NATIVE NUDIBRANCH IN THE NORTHWEST ATLANTIC

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Keywords: marine invasion, Nudibranchia, phylogenomics, population genomics.

Biological invasions due to anthropogenic activity are of growing concern across the globe and remain understudied in marine systems. The European sea lemon (*Doris pseudoargus*), native to the eastern Atlantic, was first documented in Massachusetts in 2017 and since then has been reported in Connecticut, New Brunswick, New Hampshire, and Nova Scotia. Single gene studies indicate that the invasion originated in northern Europe, but this data lacks fine-scale resolution to determine the precise origin. Additionally, only a single sample from the US was used in previous investigations. Here, we use a 300-gene sequence capture dataset from 35 individuals in the native European range and 10 individuals in the non-native range to elucidate evolutionary origins and investigate spatial genetic structure in *D. pseudoargus*. We integrate both phylogenetic and population genetic approaches to identify the likely origin of this invasion and characterize gene flow across the Atlantic. Currently, we have determined that *D. pseudoargus* is structured into two distinct clusters in its native range - one in the British Isles and another in Scandinavia. Next, we will sequence samples from the non-native range in Canada and the US to place them in this framework and identify the likely origin. We will also compare patterns in single locus data (COI) to the patterns elucidated here with genome-wide data. This work will provide valuable insight and build on our current understanding of marine invasion dynamics, and it will be used in conjunction with ecological models to predict the future invasive range of this species.

Funding Source: No.

Invasive Alien Species

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GOLDEN MUSSEL IS NEVER ALONE: QUALITATIVE ASSESSMENT OF BIODIVERSITY IN LABORATORY MAINTENANCE

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

The golden mussel, an invasive Asian species in Brazilian basins, continues to pose challenges for efficient maintenance and containment under laboratory conditions. Organisms and microorganisms present in the transport water, intervalvar space, and on the mussel surface result in a coexisting fauna in the controlled environment. This study conducted a qualitative analysis of this fauna in maintenance tanks. For biodiversity determination, 1 liter of surface water, 200 mL of bottom water, and 200 mL of mussel wash water were collected over three consecutive days from two tanks housing approximately 3,000 individuals. The samples were filtered through a 30-micron mesh, and 2 mL of the solution was fixed in a 1:1 mixture of distilled water and absolute ethanol (PA) to a final volume of 15 mL and stored at 10.5°C. Qualitative analysis was performed under an optical microscope using 1 ml subsamples. Morphotypes were identified to the lowest taxonomic resolution. This qualitative diversity was compared between the analyzed waters and those associated with the mussels. Analysis identified 20 morphotypes: 11 in surface water (Cyanobacteria 1 and 2, Non-siliceous Algae 1, Diatom, Rotifers 1, 2, and 3, Tecomebas 1, Nematoda, Mite, Nauplius), 19 in bottom water (Cyanobacteria 2, Non-siliceous Algae 1 and 2, Diatom, Rotifers 1, 2, and 3, Tecomebas 1, 2, and 3, Fungal Hyphae, Polychaete, Nematoda, Mite, Nauplius, Crustacean Eggs, Ostracoda, and Copepoda), and 7 associated with mussel encrustation (Non-siliceous Algae 1, Tecomebas 1 and 2, Polychaete, Nematoda, Nauplius, and Copepoda). These results confirm the presence of a self-regulating fauna in the tanks used for maintaining golden mussels. These taxa interact with the residual water, which is not entirely removed from the mussel maintenance reservoirs. It is concluded that a protocol for transporting and conditioning golden mussels (*L. fortunei*) is necessary. In addition, an adequate water containment and treatment system must be established to ensure the daily maintenance of these mollusks, thereby preventing improper management of the accompanying microfauna and the larval stages of this bivalve.

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Poster - 330

MOLECULAR TOOLS FOR RAPID DETECTION AND TRACEABILITY OF THE INVASIVE MUSSEL *Limnoperna fortunei*

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

The golden mussel, an invasive species introduced through shipping vessels, poses environmental and economic challenges in the Americas and Asia. This study aimed to identify molecular signatures among golden mussel populations to understand how they spread across invaded areas. COI gene sequences were obtained from databases and populations collected in different South American river basins. Specimens (n = 20) were collected and fixed from three South American populations: Porto Alegre, Brazil; Iguaçu River, Brazil; and São Francisco River, Brazil. In the laboratory, total DNA and the COI gene fragment were extracted following Ferreira Jr et al. (2024). Sequences were compared, corrected, and aligned as described by Ferreira Jr et al. (2024), and then confirmed. The prospecting of unique polymorphisms (SNPs) was performed using MEGA software (Tamura et al. 2011), through comparison with additional sequences from the NCBI GenBank and BOLD databases. The localization of these sequences and SNPs within the mitochondrial genome was determined by comparing the reference mitogenomes KP756905 and OX104126. Based on alignment analyses of COI gene fragments within the OX104126 mitogenome, these fragments were distributed between loci 9,251 and 9,910. Their distribution revealed partial, non-overlapping regions, with six distinct extension patterns observed across the mitogenome. The position and length of COI gene fragments found in databases may not align with the same polymorphic regions identified in the haplotypes described by Zhan et al. (2012) and Nakano et al. (2015) for *L. fortunei*. This mismatch can hinder the accurate identification of these haplotypes, potentially leading to false positives (Ferreira Jr et al. 2024), and thereby complicating the traceability of dispersal routes and connections of *L. fortunei*. SNP prospecting in the COI gene revealed multiple regions containing polymorphisms, with 48 promising SNPs selected for traceability purposes. These SNPs are located between loci 9,469 and 9,756 of the golden mussel reference mitogenome. The selected SNPs, as well as haplotypes Lfm01, Lfm02, Lfm03, and Lfm04 (Zhan et al. 2012), were identified in the three populations analyzed in this study. The identification of potential molecular markers and the application of single-nucleotide polymorphisms (SNPs) in *L. fortunei* (golden mussel) haplotype analyses may represent a valuable complementary tool for enhancing strategies aimed at controlling the species and elucidating its dispersal pathways across freshwater ecosystems in South America and other invaded regions globally.

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GOLDEN MUSSEL WELFARE IN THE LABORATORY: MAINTENANCE OF *Limnoperna fortunei* (DUNKER, 1857) UNDER CONTROLLED CONDITIONS

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Keywords: exotic species, biological invasions, limnic molluscs, invasive mussel.

Limnoperna fortunei, known as the golden mussel, is a bivalve native to Southeast Asia and belonging to Mytilidae. It exhibits gregarious and encrusting behavior, forming high-density populations in freshwater environments by attaching to solid substrates. Due to the economic damages caused by this species, the present study aimed to develop a protocol for the medium/long-term maintenance in laboratory conditions. Specimens were manually collected every three months from tree trunks, rocks, and artificial structures in the reservoir of the Baixo Iguaçu Hydroelectric Power Plant (UHE Baixo Iguaçu), located in the Iguaçu River, Paraná, Brazil, and transported to the laboratory at the State University of Ponta Grossa. The mussels were cleaned and placed in tanks with treated, neutralized water and continuous aeration in the laboratory. They were fed daily with a liquid food mix under controlled conditions, enabling more detailed long-term studies of their biology. Following a series of collections between 2022 and 2024, the specimens were divided into batches to ensure replication in the laboratory maintenance experiments. In this study, it was possible to maintain golden mussels under controlled laboratory conditions for up to 24 months (727 days), whereas the available literature indicates that the maximum reported laboratory maintenance time for this species is 45 days (Montalto and Ezcurra de Drago 2003; Paolucci et al. 2010; Oliveira et al. 20210; Cordeiro et al. 2015). Six batches were successfully maintained for twelve months, and four batches are currently in the laboratory exhibiting developed gonadal structures and spontaneous release of male and female gametes, indicating good specimen welfare. These findings suggest that it is possible to maintain golden mussels in laboratory conditions for approximately 52.1% of their average lifespan, considering that the species' estimated life expectancy in natural environments is 3.2 years (Darrigran and Damborenea, 2006). The results showed that maintaining *L. fortunei* under controlled laboratory conditions for extended periods enables more in-depth studies of the species without the need for frequent field collections. This approach facilitates research on the golden mussel, particularly regarding its reproductive, physiological, genetic, and chronic ecotoxicological aspects.

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OTHER THEMES

Other themes

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USE AND APPLICATION OF iNATURALIST ON LAND SNAILS FROM ARGENTINA

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Keywords: citizen science, biodiversity, distribution, detection, conservation.

The literature has shown that volunteers to participate in data collection is of great value to biodiversity knowledge on an unprecedented scale. The aim of this work is to evaluate the use and application of the iNaturalist platform in Argentina for land snails, review the quality of the observations, and critically analyze the data of native species and the distribution of exotic species. In the iNaturalist platform, a search was performed for Argentina, where we distinguished observations with pre-validation, and post-validation. Both native and exotic species were analyzed. The observations that were considered of interest were: those that extended the known range of the species, those that could be useful for the detection of exotic species not yet cited for Argentina, those that required collection for identification, those that confirmed the known range in the literature, those that could correspond to new species, misidentifications, cases of interaction with another species and the first images of the animal in life. The results obtained were analyzed and discussed in depth. The terrestrial gastropod search in iNaturalist for Argentina, yielded a total of 3,308 observations for 74 taxa. Exotic species accounted for between 60–63%, and native species 37% to 40%. Of interest for this work were 374 observations, representing 9.97% of the total number of observations analyzed. It was possible to detect the expansion of the range of exotic species such as *Rumina decollata*, *Limacus flavus*, *Bradybaena similaris*, *Deroceras laeve*, *Deroceras reticulatum*, *Deroceras invadens*, *Arion intermedius*, *Milax gagates*, *Limax maximus*, *Vallonia pulchella*, possibly *Laevicaulis alte*, and native species such as *Phyllocaulis soleiformis*, *Drymaeus poecilus* and *Drymaeus papyraceus*. We also recorded species within the known range, a possible case of accidental transfer for *Mesembrinus interpunctus* was detected, and the prediction of the distribution of Megalobulimus lorentzianus was checked. We detected potential new species of *Bulimulus* and *Epiphragmophora*, and we identified species not recorded in Argentina such as *Helix pomatia* and *Mesembrinus gereti*. Citizen science has also proved valuable in learning about the live appearance of species described only by their shells and whose soft parts are unknown. This review has uncovered gaps in knowledge about terrestrial gastropods in Argentina, and we have been able to demonstrate the relevance of citizen science. As its use becomes more widespread, and given the potential it has shown, we believe it could have many other applications in the future. We encourage the scientific community to consult the records the citizen science platforms, as they can provide data to help their research.

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MUSSELS IN THE FREEZER: THE CRYOPRESERVATION JOURNEY

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Keywords: cryopreservation, *Mytilus*, juveniles.

In Galicia, the farming of the mussel *Mytilus galloprovincialis* holds significant economic, social, and cultural value. However, it heavily relies on the collection of natural seed, making it vulnerable to environmental changes and regulatory restrictions. To address this, we developed cryopreservation protocols that allow the long-term storage of both larvae and juveniles of this species, offering a practical tool for the aquaculture sector. Specimens were obtained from the Marine Science Station of Toralla (ECIMAT). Existing protocols (Heres, 2021) were adapted using a controlled-rate freezing system (Cryologic). Samples were cooled from 4°C to -35°C at a rate of 1°C/min, with a pause at -12°C to induce ice nucleation. We used 0.25 ml straws for larvae and 0.5 ml straws for 40–45-day-old juveniles. Thawing was performed in a seawater bath at 35°C for 6–8 seconds. Cryoprotectants were added and diluted in a single step, with equilibration times adjusted according to larval age. Post-thaw viability was assessed using live-dead fluorescent dyes. For the first time, we successfully cryopreserved fed D-larvae at 72 hpf, achieving a 10% increase in survival compared to unfed larvae (77%± 4.31% vs 84.3±0.96%) compared to the current protocol (Heres, 2021). Pre-freezing feeding improved larval size and normality, contradicting the hypothesis that gut contents increase cryo-damage. Lesions were mainly located in the ciliated velum and digestive region. Survival rates of 63% and 23% were achieved for 40- and 45-day-old juveniles, respectively, using a new cryoprotectant cocktail (12% EG + 0.4 M trehalose), 48 hours post-thawing. This study demonstrates that feeding prior to freezing, combined with protocol optimization, enables successful cryopreservation larval stage from 24 hpf to juveniles over 1 mm in size, marking a significant advance in the cryobiology of complex organisms. This work represents a significant step forward in the relatively unexplored field of organismal cryopreservation, which until now has shown only limited success in a handful of species such as *Caenorhabditis elegans*, *Porites compressa* corals, and embryos of *Drosophila melanogaster*, *Danio rerio*, and shrimp. By achieving the successful cryopreservation of juvenile mussels, organisms over 1 mm in length with structural, metabolic, and tissue complexity comparable to adult individuals, this study expands the range of viable models and marks the first report of whole-organism cryopreservation in a marine bivalve. The proposed goals were achieved by developing and validating cryopreservation protocols for *M. galloprovincialis*, including juveniles. The inclusion of pre-freezing feeding and adjustments to cryoprotectant use significantly improved outcomes, opening new possibilities for genetic resource banking applied to aquaculture and conservation.

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CEPHALOPODS IN THE DIET OF CETACEANS STRANDED ON THE COAST OF RIO GRANDE DO NORTE, BRAZIL: A COMPARISON BETWEEN COASTAL AND OCEANIC ODONTOCETES OF THE FAMILIES DELPHINIDAE AND KOGIIDAE

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Keywords: *Cetacea*, diet, prey-predator, South Western Atlantic Ocean.

Cephalopods, like fish, are the main food items of odontocetes, playing an important role in some oceanic species considered teutophagous. The analysis of cephalopods in the stomach contents of odontocetes has been an important tool for expanding knowledge of the predator-prey relationship. This study aims to compare the occurrence of cephalopods in the stomachs of odontocetes of the Delphinidae and Kogiidae families stranded in Rio Grande do Norte. Five stomachs of cetaceans stranded between 2010 and 2017 were analyzed, corresponding to the species *Tursiops truncatus* (n=2), *Sotalia guianensis* (n=2) and *Kogia sima* (n=1). The samples came from the scientific collection of the Marine Biota Monitoring Laboratory of the State University of Rio Grande do Norte (PCCB-UERN). The stomachs were weighed, and their contents sieved through 400 and 600 µm meshes. After screening, the cephalopod beaks were photographed, counted, measured and identified with the aid of a stereoscopic. Calculations to estimate the size and weight of the cephalopods were based on measurements of the upper hood length (UHL) for octopuses and the upper rostral length (URL) for squids. From the stomachs analyzed, 34 cephalopod specimens were identified by means of 30 upper and 32 lower beaks. The occurrence (FO) and numerical (FN) frequencies corresponded to the species: *Enoploteuthis anapsis* (FO = 40%; FN = 79%), *Octopus vulgaris* (FO = 20%; FN = 6%), *Loligo plei* (FO = 20%; FN = 12%) and *Lolliguncula brevis* (FO = 20%; FN = 3%). The estimated mantle length of the prey varied between 5.7 cm and 12.2 cm, while the weight between 0.24 and 683.72 grams. Specifically, the specimen of *K. sima* presented 20 individuals of *E. anapsis*, with upper beak lengths varying between 0.05 and 0.15 cm, and it was not possible to estimate their size and weight. Among the two specimens of *T. truncatus*, one presented seven specimens also of *E. anapsis* with the length of the upper beak varying between 0.08 and 0.29 cm, while the other presented two *O. vulgaris*, with the mantle length estimated between 11.3 cm and 12.2 cm. On the other hand, in *S. guianensis*, one specimen presented four *L. plei*, with the mantle length varying between 0.09 cm and 0.13 cm, while the other presented one specimen of *L. brevis*, with the mantle length of 5.7 cm. The differences recorded in the cephalopods preyed on by the different odontocetes analyzed show that *S. guianensis* explored coastal zones and *T. truncatus* and *K. sima* demonstrated foraging strategies in deeper areas and further from the coast. The analysis of cephalopods in the stomachs of odontocetes on the coast of Rio Grande do Norte in northeastern Brazil made it possible to highlight the different uses of habitats by the species, demonstrating the importance of cephalopods for teutophagous species such as those of the Kogiidae family.

Funding Source: No.

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FUNCTIONAL MORPHOLOGY OF BIVALVIA FROM THE SALVADOR FORMATION, JATOBÁ BASIN, NORTHEASTERN BRAZIL

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Keywords: Cretaceous, Iridinidae, Berriasian.

The Salvador Formation (Berriasian, Jatobá Basin) comprises a sedimentary setting characterized by three depositional facies: proximal fan delta, distal fan delta, and lacustrine. In bivalves, shell morphology reflects ontogenetic development influenced by environmental conditions, thus supporting functional morphological analyses. This study aims to infer the life habits of these organisms through their functional morphology. The material was collected by the Geological Survey of Brazil (CPRM) near Floresta, Pernambuco, and sent to LAPALMA at UNESP, Bauru. Specimens MCT.I.7192 and MCT.I.7202 are part of the Museu de Ciências da Terra – SGB collection, in Rio de Janeiro. Functional morphology studies the relationship between form and ecological function. In bivalves, shell morphology reflects environmental pressures and is ideal for such analysis due to its conserved structure and preservable shell. This morphology represents a trade-off between developmental constraints and functional demands, with minimal influence from soft anatomy, physiology, or ecological interactions. The specimens were assigned to the freshwater family Iridinidae (Unionida). Neither displays valve ornamentation, likely due to adaptation to deltaic environments and increased burrowing, which smooths the shell surface. The burrowing habit is supported by their compressed shape, thickened anterior region, and well-defined anterior adductor muscle scars. These characteristics are best interpreted as primary morphological traits rather than taphonomic artifacts, given the absence of abrasion or deformation and the well-preserved muscle scars and hinge dentition, indicating minor post-mortem alteration. The morphological differences between MCT.I.7192 and MCT.I.7202 likely reflect habitat variation. In bivalves, dorsal arching correlates with water energy: MCT.I.7192 has a more arched dorsal margin, suggesting adaptation to higher-energy environments, while MCT.I.7202 has a straighter margin and elongated hinge, pointing to low-energy, still or slow-flowing waters. Based on the Salvador Formation facies, MCT.I.7202 likely inhabited distal deltaic or lacustrine facies, whereas MCT.I.7192 was adapted to proximal deltaic zones with stronger currents. The most distinctive trait is their dentition. Both have heterodont dentition beneath the umbo, but MCT.I.7192 also presents taxodont dentition along the hinge. It remains unclear if this combination in MCT.I.7192 has functional adaptive value. From the morphofunctional analysis, it is concluded that both specimens originated in freshwater depositional environments and exhibited shallow burrowing habits. Based on shell morphology, their distribution within the facies of the Salvador Formation are associated with distal deltaic and lacustrine facies for MCT.I.7202 and proximal deltaic for taxon MCT.I.7192.

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COST ACTION SALTAGES: A NEW INTERNATIONAL COLLABORATION NETWORK OF INTEREST TO MALACOLOGISTS

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Keywords: paleontology, cooperation, European Union, funding.

Giant salt deposits have formed in restricted evaporitic basins controlled by dynamic marine gateways throughout the history of the Earth, altering the physical and chemical properties of the ocean, and affecting regional and global climate, and biota. Salt giants mark relatively abrupt and short-lived major water-body disconnection events that affect both the marine and terrestrial realms, with major implications for biodiversity, ecosystem structure and functioning. The European Cooperation in Science and Technology (COST) is a funding organisation for the creation of research networks, called COST Actions. These networks offer an open space for collaboration among scientists across Europe (and beyond) and thereby give impetus to research advancements and innovation. The new COST Action CA23124 Social, biological and climatic impacts of salt ages (SaltAges) aims to bring together scientists working on different regions and time periods to clarify and quantify the biotic impacts of basin restriction across scales and identify overarching patterns. The fossil record of molluscs can offer unique insights into the global biodiversity and macroecological impacts of salt giant formation throughout their appearance, and especially during the Cenozoic. The SaltAges COST Action will run until 2028 and is open for participation to all interested researchers and stakeholders. The topics related to molluscs will be dealt mostly within Working Group 1 (WG1) “Climatic and biological impacts of marine gateway reconfigurations”, whose objectives include evaluating the effects on biodiversity hotspots, biogeography, extinctions, endemism, and repopulation. Additionally, WG4 “Salt Deposition through Earth’s History” will explore the importance of salt cycles for tectonics and climate that lead to the closure of drainage basins through the ages, and WG5 “Education and Public Engagement” will coordinate the training of young researchers as well as the production of an online educational resource and a moving museum exhibition on salt and salt giants. SaltAges is based in Europe, but cooperations with collaborators outside of this area are welcomed and encouraged. The final goal is to establish a global network of scientists, intustry and other interested parties with similar research interests that is going to collaborate in the future.

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REVISING *Zittelia*: A LATE JURASSIC LINK BETWEEN COLOMBELLINIDAE AND CYPRAEIDAE

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Keywords: Gastropoda, Mesozoic, fossil record, caenogastropod radiation.

The Late Jurassic–Early Cretaceous is a crucial period in the evolution of caenogastropods, when stem groups gave rise to crown clades, including Neogastropoda, Tonnoidea and Cypraeoidea (e.g., Bakayeva et al. 2024; Nützel et al. 2025). One such stem group that remains poorly understood, is the extinct family Colombellinidae, which includes the genus *Zittelia*. We re-examined historical type material of *Zittelia* described by Guirand & Ogérien (1865), Gemmellaro (1869), and Zittel (1873), which are stored at the Museum of Geology G. G. Gemmellaro in Palermo, Sicily, Italy, Museum of Confluences in Lyon, France and Bavarian State Collection for Palaeontology and Geology in Munich, Germany. Type series were photographed and measured, and lectotypes with paralectotypes were designated. The taxonomic revision confirmed the validity of eleven species within the genus *Zittelia*, ranging from the Middle Oxfordian to the Tithonian and possibly even Valanginian. The morphological variability among these species indicates a gradual transition from forms more closely resembling species of the genus *Colombellina*—such as *Z. rara* and *Z. oppeli*, which exhibit an oval shell with a higher spire—to cypraeiform species, such as Z. cipraeaeformis. The latter is characterised by a globular shell shape, an inflated last whorl, a narrow, elongated aperture, and a broadened columellar lip—characteristics that strongly resemble those of the cypraeids. This morphological sequence not only strengthens the argument for a phylogenetic relationship between Colombellinidae and Cypraeidae, but also highlights the importance of *Zittelia* as a transitional form. The co-occurrence of *Zittelia* and the earliest cypraeids in the Upper Jurassic–Lowest Cretaceous of Sicily, Italy, may indicate that the Late Jurassic–earliest Cretaceous reefs and associated peri-reefal facies of the Tethys were a centre of diversification of the Colombellinidae and the emergence of the first representatives of Cypraeoidea. The evolution of these groups contributed significantly to the Mesozoic–Cenozoic caenogastropod radiation.

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CHARACTERIZATION OF THE MICROSTRUCTURE AND CRYSTALLOGRAPHY OF CAENOGASTROPODA SHELLS FROM THE NORTHERN COAST OF SÃO PAULO STATE, BRAZIL

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Keywords: mollusks, gastropoda, SEM, XRD, ceramics, biocomposite, materials science.

Mollusk shells consist of a ceramic-polymer biocomposite distributed in overlapping layers. Each layer has a single mineral form, and certain mollusks are capable of producing and overlaying two mineralogies in distinct layers. Its mechanical capacity and potential for use in taxonomic studies has attracted the attention of researchers. Thus, this study aims to characterize the microstructure and crystallography of Caenogastropoda shells from the coast of São Paulo, Brazil. The Caenogastropoda were collected using trawls at four sampling sites in Ubatuba Bay, São Paulo state, Brazil. One specimen per taxon was analyzed using a Scanning Electron Microscope. The periostracum and impurities were removed with NaClO solution (2.0-2.5%) The shells were sectioned with a diamond saw along the body whorl. The face of interest was polished using silicon carbide abrasive powder (meshes 320, 500, 600 and 1000) on a flat glass plate. The tablets were lightly dissolved in CH_3COOH solution (4%, pH 2.3 and temperature 22.6 °C) for 10 min. For crystallography, shell segments were crushed and analyzed in an X-ray diffractometer. Eleven species of Caenogastropoda were identified. All of them had a cross-lamellar microstructure, with the number of layers, the thickness of the layers and the angle between the third-order lamellae varying. With regard to the number of layers, 80% of the groups analyzed had two layers. *Monoplex parthenopeus* and *Siratus senegalensis* were exceptions, showing one and three layers respectively. *Zidona dufresnii* could not be analyzed since no live specimens were collected without damage to the shell. The thickness of each microstructural layer is relatively constant in the cut sections. In 60% of the taxa, the innermost layer was thicker. For *S. senegalensis*, the middle layer is the thickest and for *Strombus pugilis* and *Olivancillaria urceus*, the outermost layer is the thickest. Although *M. parthenopeus* had a single layer, its thickness was greater than 40% of the taxa. The average angle between two consecutive lamellae of the Caenogastropoda shells ranged from approximately 60° to 100°. Using X-ray diffraction analysis, diffractograms were obtained for each Caenogastropoda specimen and their crystallographic phases were identified. The specimens showed diffraction peaks at the same angle values, with intense peaks in the (1 1 1) and (2 0 1) planes. The set of peaks obtained are characteristic of calcium carbonate in orthorhombic form. Thus, the shells of the Caenogastropoda taxa analyzed are aragonitic. The Caenogastropoda studied exhibited a cross-lamellar microstructure with orthorhombic crystallography (aragonite). The number of layers ranged from one to three, with two layers predominating. The innermost layer had the greatest thickness, except for *S. pugilis*, *O. urceus*, *M. parthenopeus* and *S. senegalensis*. The average angle between two consecutive lamellae was between 60° and 100°. This set of data proved to be relevant for taxonomic and taphonomic studies.

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TIME-TRAVELING BIVALVES: *Guiratingia*-BEARING CLASTS AND THE EVOLUTIONARY HISTORY OF THE PARANÁ BASIN

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Keywords: Pachydomidae, Passa Dois Group, resistates, plesiocyprinellinae evolution.

Silicified oolitic carbonate pebbles rich in bivalves—resembling Permian Pachydomidae forms from the Paraná Basin—have been discovered in the Triângulo Mineiro region. These pebbles, eroded from their original geological units and transported by alluvial processes, now form part of the plateau's surface gravel cover (Boggiani et al. 1991). As a result, they are allochthonous and significantly older than the Cretaceous rocks of the Bauru Group that crop out in the area. Pebbles were collected from sites in Ituiutaba (Serra do Corpo Seco, Morro Três Cruzes, Renascer rural settlement) and Monte Alegre de Minas (Vale do Babilônia), in Minas Gerais, Brazil. Pebbles are rounded, centimeter-sized, composed of various lithologies, and contain fossils such as bones, shells, and stromatolites. Only those with shells were selected for this study. Some shells remained attached to the rock, while many were successfully removed. The specimens were identified using specialized literature on Paraná Basin bivalves. Each specimen was measured, photographed, and analyzed, including documentation of valve side (left or right) and articulation. A new species is currently being prepared for formal description. A total of 72 shells have been measured so far (all under 8 mm). Most are disarticulated (86%; n = 62) and include both right (41.7%; n = 30) and left (44.4%; n = 32) valves. The shells display a triangular, blunt cardinal tooth on the right valve, a flattened commissure margin, visible muscle scar striations, and an anteriorly expanded outline; diagnostic features of the Permian genus *Guiratingia* Petri & Fulfaro, 1966 (Simões & Anelli, 1995). This genus is typically found in the ooid grainstone of the Palermo Formation (Guatá Group) in the Guiratinga region of Mato Grosso. *Guiratingia* is the oldest known member of the subfamily Plesiocyprinellinae and the only one documented in pre–Passa Dois Group rocks deposits. It thus represents an early stage in the evolution of the endemic Pachydomidae fauna that radiated during the deposition of the Permian Passa Dois Group (Simões et al. 2018). The remarkably well-preserved shells allow for detailed study of hinge elements and suggest that some previously undescribed specimens from the Teresina and possibly Irati formations (Matos et al. 2017) also belong to *Guiratingia*. Until now, only one species from the Palermo Formation has been formally described—*Guiratingia mendesi* Petri & Fulfaro, 1966. This species predominates among the analyzed pebbles, although at least one additional, undescribed species is also present. In both, the Teresina and Irati formations, *Guiratingia* occurs alongside *Runnegariella fragilis* Simões & Anelli, 1995. These bivalves consistently appear in assemblages of small, anteriorly expanded species preserved in carbonate settings. The findings expand the diversity and stratigraphic range of *Guiratingia*, reinforcing its importance as a link between the Palermo Formation malacofauna and the Passa Dois Group. As the only member of Plesiocyprinellinae present in both units, *Guiratingia* provides critical insights into the subfamily origin. The presence of *Guiratingia*-bearing pebbles far from their source highlights the need to revisit Palermo Formation deposits as a key to understanding this lineage's evolutionary history.

Funding Source: No.

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HOLE IN THE SHELL: METHODOLOGY FOR IDENTIFYING GROUPS OF PREDATORY GASTROPODS IN BIVALVES

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Keywords: taphonomy, drilling gastropods, ecological interactions, drilled shells, predation.

Predatory drilling by Naticidae and Muricidae gastropods in bivalves produces characteristic holes with distinct and identifiable morphologies. The analysis of these structures in modern bivalves reveals predatory behaviors and ecological dynamics, both past and present, contributing to the evolutionary understanding of predator-prey interactions. This study aims to provide an optical methodological approach to characterize and distinguish predatory drill holes made by Naticidae and Muricidae gastropods, based on their morphology. Eighty-two drilled valves (≥ 2 mm) collected from a modern shell bed (Matinhos City) on the Paraná (Brazil) were analyzed. The valves were photographed with scale under a stereo microscope; the internal (dI) and external (dE) diameters of the drill holes were measured (mm) using ImageJ. To distinguish the predatory gastropods (Naticidae or Muricidae) responsible for each hole, the Predatory Drill Hole Difference index (PDHD) was developed, with the equation: PDHD=dE–dI. Based on the calculated indices, gastropods were classified into three categories (ct1 – Naticidae; ct2 – Muricidae; ct3 – Naticidae/Muricidae: uncertainty regarding the predator). The viability of this method was evaluated in STATISTICA using PDHD means and Tukey's test. Of the 82 drilled bivalves, 55 were attributed to predation by Naticidae (ct1), 19 by Muricidae (ct2), and 9 were classified as Naticidae/Muricidae (ct3). Considering that the holes attributed to predation by ct1 exhibited a larger external diameter (dE) than internal diameter (dI) with an inverted-parabolic shape, and ct2 exhibited almost symmetrical dI and dE with an inverted-conical cylindrical shape, it was possible to distinguish the two gastropod taxa. The PDHD values for ct1 ranged from 1.25 mm to 0.13 mm and for ct2 from 0.015 mm to 0.18 mm. In the range of 0.13 to 0.18 mm, an overlap was observed, with holes that were difficult to clearly assign, justifying the Naticidae/Muricidae category (ct3). Thus, the following criteria were established: PDHD > 0.18 mm are ct1; PDHD < 0.13 mm are ct2; PDHD between 0.13–0.18 mm are ct3 in the studied shell bed. Based on the PDHD values, it was possible to associate higher PDHD with ct1 and lower ones with ct2; intermediate values indicated overlap in identification, categorized as ct3 (uncertainty about the predator). Statistical analysis confirmed a significant difference between the three assigned categories, validating this optical method as a tool for preliminary predator identification. However, to reduce the overlap zone and increase the accuracy in identifying shell-drilling gastropods, it is recommended to use complementary analyses, such as Scanning Electron Microscopy (SEM), especially in taphonomic contexts involving interactions between gastropods and bivalves in marine environments. PDHD index proved promising for distinguishing Naticidae and Muricidae drill holes in optical analyses, supporting ecological and taphonomic studies in both current and past environments. Optical analyses, when used alone, require methodological rigor as the absence of defined morphometric parameters can lead to inaccurate interpretations, underestimation, or overestimation of data. In the absence of SEM, the uncertainty zone (ct3) should be recognized, avoiding definitive conclusions based solely on visual observations.

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FRESHWATER BIVALVES, PRESENT AND FOSSILS, FROM RIO GRANDE DO SUL

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Keywords: paleobiology, taphonomy, landscape.

The diversity of freshwater bivalves from Rio Grande do Sul is relatively well known, with more than 40 species living in the Rio Uruguay and South/Southeast Atlantic basins. Fossils in this region are little known and sometimes omitted from literature review, but at least two fossiliferous sites are recognized. However, no study tested the representativeness of fossil species composition and relative abundance to present-day, basin level communities. The Camaquã River drain an area largely dominated by high topographic and geological variation, with little accommodation space available for long-term sedimentation all except two sectors throughout it curse. On the opposite, several Quaternary deposits are associated with most rivers from the Ibicuí Basin. The geology from the Ibicuí Basin is constituted mostly by Paleozoic and Mesozoic sedimentary units. All present-day and fossil sites were analyzed together using multivariate analysis (Principal Coordinate Analysis) based on Jaccard distance. At each locality, abundance of shells from each species were computed as 0 (zero, absent), 1 (if only one shell was found), 2 (2 to 9 shells), and 3 (more than 10 shells). Considering that shells first accumulate in riverbanks, here we evaluate the presence and relative abundance of shells from families Hyriidae, Mycetopodidae and Corbiculidae present in seasonally-exposed bars of rivers Ibicuí da Armada, Santa Maria, Toropi and Ibicuí (Ibicuí Basin), Touro Passo (an affluent from Uruguay River), and Camaquã River, and compared with known fossiliferous Quaternary deposits of Rio Grande do Sul (Touro Passo Formation and Sanga da Cruz site). *Anodontites trapesialis*, several *Diplodon* species and *Corbicula fluminea* and *C. largillierti* were widespread in the studied area, mainly in the Ibicuí Basin. Species indicated as threatened were present at some sampling sites, including *Leila blainvilliana* (one site) and *Fossula fossiculifera* (two sites). *Cyanocyclas limosa*, a native corbiculid species abundant at the fossil site (Touro Passo Formation), was not recorded in present-day bars. *Monocondylaea*, *Mycetopoda* and *Castalia* occurred only in rivers from Ibicuí basin. The ordination showed that the three set of sites (Camaquã basin, Touro Passo – Fossil, Ibicuí basin) are significantly different, based on PERMANOVA ($F=2,98$, $P<0,0001$). In the ordination space (scatterplot), the two sites appear more closely related to samples from the Ibicuí basin, probably because of the higher richness present, and relatively high abundance of species from genus *Anodontites* and *Diplodon*, rare in the Camaquã basin. In the ordination space (scatterplot), the two sites appear more closely related to samples from the Ibicuí basin, probably because of the higher richness present, and relatively high abundance of species from genus *Anodontites* and *Diplodon*, rare in the Camaquã basin. Further analysis should include minute shells of gastropods such as *Heleobia* and *Potamolithus*, that are present as fossils in the Touro Passo Formation, and whose shells are relatively robust.

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FAILED PREDATION AND SHELL REPAIR DAMAGE PRESERVED IN *Pachycymbiola brasiliana* LAMARCK, 1811 (GASTROPODA, VOLUTIDAE) SHELLS FROM SOUTHERN BRAZIL

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Keywords: bioerosion traces, *Caedichnus*, durophagous predation.

Predation is the effectiveness or unsuccessful attempt to consume living organisms. In shelled-animals, prey effectiveness can be identified by typical bioerosion traces. The repaired shell injury is a common sign of unsuccessful attacks (predatory failure), but can also result from other ecological processes. This study aims to report the ichnogenus *Caedichnus* in *P. brasiliana* for the first time; characterize two morphologies of these traces; evaluate shell effectiveness against durophagous predation. A total of 1,225 *P. brasiliana* shells were collected from a natural shell accumulation at Cassino Beach, southern Brazil. Each specimen was measured using a digital caliper (±0.01 mm), and the presence or absence of repair scars was recorded. The traces were identified at the ichnogenus level and described using current classification criteria and descriptors commonly used for failed predation, such as scalloped damage and embayed breakage. Although modern traces are not formally named following ichnotaxonomic rules, we used established ichnotaxa for comparison due to the temporal mixing of the sample. Repair frequency (RF) was calculated to evaluate shell resistance against durophagous predation. Fracture-shaped bioerosion traces identified as *Caedichnus* were found, indicating durophagous predation, likely from cutting and peeling attacks. Two morphologies were recognized: scalloped damage and embayed breakage, both interpreted as variants of failed predation events. Repair scars associated with these morphologies suggest survival after attack. Puncture-type repairs were rare. Secondary traces attributed to *Caulostrepsis*, likely produced by Spionidae polychaetes, were observed in 15.1% of the shells bearing *Caedichnus* scars, suggesting that repaired areas may facilitate post-attack colonization by sclerobionts. Scalloped scars had higher repair frequency, indicating more frequent survival, possibly due to less lethal damage or thicker shell areas. The sample was dominated by large specimens (mean shell size = 91.08 mm), suggesting that adult individuals may be more resilient to predation. A clear disparity in repair frequency was observed between scalloped and embayed morphologies, with the latter being more commonly lethal. Embayed breakage may be attributed to durophagous vertebrates like *Caretta caretta*, while scalloped scars may result from failed decapod attacks or even self-inflicted damage during feeding. The frequent presence of repair scars and sclerobionts supports the hypothesis that *P. brasiliana* experiences repeated interactions with predators and colonizers. These traces document complex ecological interactions and highlight predation as a key driver in the evolutionary history of gastropods, shaping shell morphology and behavior over time. Predation traces of *Caedichnus* were identified in two morphologies: scalloped damage and embayed breakage. The high frequency of scalloped scars suggests *P. brasiliana* shells are effective against crushing predation (decapods). Embayed damage points to vertebrate predators (turtles). This is the first record of *Caedichnus* in *P. brasiliana* and adds to the few known occurrences of this ichnogenus in the Southern Hemisphere. Associations with *Caulostrepsis* suggest repair scars may also promote sclerobiont colonization.

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FROM BIOCONSTRUCTORS TO BIOERODERS: VERMETID GASTROPODS AND THE FIRST RECORD OF *Renichnus* IN THE SOUTH ATLANTIC

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Keywords: Gastropoda, Vermetidae, bioerosion, ichnology.

Vermetid gastropods are ecologically important marine molluscs, especially in tropical and subtropical coastal zones, where they act as reef builders. As bioengineering, their calcareous shells serve as substrates for reef formation and substrate stabilization, contributing to paleoenvironmental interpretations. However, their role as bioerosion agents remains poorly documented. This study aims to report, for the first time, bioerosion traces produced by vermetid gastropods along the Brazilian coast. Samples were located in the MORG molluscan collection (Oceanographic Museum, FURG) during routine curatorial review. Shells of gastropods presenting bioerosion traces were selected, cleaned, and analyzed using scanning electron microscopy (SEM) for detailed morphological characterization. Vermetid shell fragments associated with the substrates were also examined. Identification of the ichnogenus followed diagnostic criteria (Mayoral, 1987; Verde et al., 2022), focusing on morphology, arrangement, and overlapping patterns. The bioerosion traces identified as *Renichnus* represent the first record of this ichnogenus in the South Atlantic. These traces were found on gastropod shells (*Crepidula* sp.) collected along the coast of São Paulo state, Brazil. Characterized by crescent-shaped depressions arranged in irregular rows, they are attributed to the attachment behavior of *Petaloconchus varians* (d'Orbigny, 1841), a widely distributed vermetid along the Brazilian coast. This discovery expands the paleobiogeographic distribution of *Renichnus* sp., previously known only from fossil records in the North Atlantic. It also emphasizes the dual ecological role of vermetids as both reef builders and bioerosion agents. The study contributes to the understanding of sclerobiont interactions in modern tropical-subtropical environments and reinforces the need for further research on bioerosion processes in South Atlantic coastal systems. This study documents the first occurrence of *Renichnus* in the South Atlantic, produced by *Petaloconchus varians*. The findings expand the known distribution of this ichnogenus and highlight the dual ecological role of vermetids as both bioconstructors and bioeroders. These results enhance the understanding of bioerosion processes and offer valuable data for paleoecological interpretations in tropical and subtropical marine environments.

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Achatina fulica: MALACOLOGICAL SURVEILLANCE OF THE GIANT AFRICAN SNAIL IN RESPONSE TO EOSINOPHILIC MENINGITIS CASES IN PARÁ STATE, BRAZIL

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Keywords: terrestrial gastropods, One Health, giant african snail, *Angiostrongylus cantonensis*.

The mollusk *Achatina fulica* (Bowdich, 1822), currently found in all Brazilian states, offers a risk to human health due to its ability to host the parasite *Angiostrongylus cantonensis* (Chen, 1935), the etiological agent of Eosinophilic Meningitis. In 2021, two cases of this disease were reported in Pará state. Following these reports, the Evandro Chagas Institute was requested by the Pará State Health Department to conduct a malacological investigation. Specimens were collected in October and November 2021 at and around the patients' residences, through active search and manual collection, over a 30-minute period. The collection sites were georeferenced, and the *A. fulica* samples were sent to the Malacology Laboratory (LABMAL) at the Evandro Chagas Institute (IEC) for proper storage and to be later sent to the National Reference Laboratory for Schistosomiasis - Malacology (LRNEM) at the Oswaldo Cruz Institute/FIOCRUZ in Rio de Janeiro, where morphomolecular analyses were performed to detect and identify nematode larvae, if present. This is the first report of a malacological investigation in response to the occurrence of eosinophilic meningitis cases in Pará. The investigation led to the collection of 56 *A. fulica* specimens in two cities: Ananindeua and Belém. Laboratory examination was possible on 24 of them (24/56; 42.9%). Analyses conducted at LRNEM detected the presence of *A. cantonensis* larvae in specimens from both collection sites. As naturally infected mollusks were found at the investigated locations, the disease was considered autochthonous. The patients had neither interacted with each other nor shared the same environment, and the cases were not considered related. Malacological investigation, when combined with clinical diagnosis, should be encouraged, as the detection of infected vectors in the patient's environment can be crucial in reaffirming the disease diagnosis and guiding clinical decision-making. The current scenario of eosinophilic meningitis caused by *A. cantonensis* in Brazil may still be underestimated. Worldwide, *A. fulica* has contributed to the spread of *A. cantonensis* and, consequently, of this zoonosis, increasing the risk of human exposure. The findings of this study underscore the need to strengthen malacological surveillance in Pará state, particularly regarding the monitoring of *A. fulica* as a vector of eosinophilic meningitis. Surveillance strategies that consider human, animal, and environmental health under the One Health approach emerge as a crucial tool for identifying and assessing risk areas for this disease. This integrated perspective also enables the monitoring of host populations and vectors, generating essential data on the local epidemiological scenario to support the planning and implementation of surveillance actions by health authorities.

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IMPORTANCE OF PUBLIC PARKS IN THE EPIDEMIOLOGY OF WATERBORNE AND TERRESTRIAL DISEASES IN THE CITY OF SÃO PAULO: THE EXPERIENCE AT ACLIMAÇÃO PARK, SÃO PAULO, SP, BRAZIL

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Keywords: public parks, mollusks, gastropods limnics, waterborne, helminthiases, parasitology.

Public parks can pose risks in the transmission of waterborne and terrestrial helminthiases, with mollusks of various species acting as vectors. Thus, the present study investigated in 2024 the occurrence of limnic gastropods and their possible helminth fauna of medical-veterinary importance in the lake of Aclimação Park, Municipality of São Paulo. The lake has a diverse fauna of wild and migratory aquatic birds, fish, amphibians, and reptiles, contributes to the drainage of the Pedra Azul stream basin, and receives rainwater from the region, being subject to pollution from clandestine domestic sewage. Areas on the shore where park users can access the water body were researched. Limnic gastropods collected included *Pomacea* cf. *canaliculata* (Lamarck, 1804), *Melanoides tuberculatus* (Müller, 1774), *Pseudosuccinea columella* (Say, 1817), *Stenophysa marmorata* (Guilding, 1828), and *Omalonyx convexus* (Martens, 1835). The collected specimens were subjected to a parasitological test involving light exposure to detect larval forms of trematodes, where only one specimen of *P.* cf. *canaliculata* released *Cercaria lutzi* (Ruiz, 1943), of veterinary importance. A parasitological test using the modified Rugai technique for nematode larvae was also performed, resulting in negative for Metastrongylidae in all specimens collected. The species collected are potential intermediate hosts of the nematode *Angiostrongylus cantonensis*, the cause of neuroangiostrongyliasis, and the helminths *Fasciola hepatica* and *Clonorchis sinensis*, which cause hepatic fascioliasis and abdominal clonorchiasis, respectively, parasitic diseases of medical and veterinary importance. The presence of these gastropods, the inflow of polluted external waters into the lake, and user contact with the lake water characterize a risk for the transmission of these helminthiases to humans and other animals. In this case, it was recommended to restrict user access to the lake shores through landscaped vegetative barriers and warning signs to prevent direct contact with the water and animals living there due to the associated health risks. The results of this study demonstrate the need for aquatic malacological monitoring and surveillance of public areas and parks with water bodies accessible to users, with seasonal mollusk collections at established points, minimizing possible risks related to the transmission of helminthiases.

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MALACOLOGICAL SURVEILLANCE IN THE DIAGNOSIS OF FATAL MENINGOENCEPHALITIS CAUSED BY *Angiostrongylus cantonensis* IN A BLACK-FACED SPIDER MONKEY (*Ateles chamek*): A ONE HEALTH PERSPECTIVE

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Keywords: One Health, zoonosis, mollusks, malacological survellance, nematode, *Angiostrongylus cantonensis*.

Angiostrongylus cantonensis is a neurotropic nematode of the Metastrongyloidea family. Its definitive hosts are rodents, and intermediate hosts are gastropods; humans and other mammals may serve as accidental hosts. While infections in Brazil have only been reported since 2007, data on non-human primates are scarce. In May 2023, an 11-month-old captive-born male *Ateles chamek* at Sorocaba Zoo (São Paulo, Brazil) developed acute tetraplegia, anorexia, urinary retention, and nystagmus. Despite supportive treatment, the animal died. A necropsy revealed hemorrhagic and inflammatory lesions in the brain and cerebellum. Larvae consistent with Angiostrongylidae were found in nervous tissue and pulmonary arterioles. Molecular diagnosis by qPCR confirmed *A. cantonensis* (Cq = 17.48). In response, environmental surveillance was initiated in September 2023. Terrestrial and limnic mollusks were collected from multiple zoo locations, especially areas previously inhabited by the monkey. A total of 171 mollusks (living and shells) were collected. Terrestrial species included *Subulina octona* (69 specimens), *Bradybaena similaris* (37), *Leptinaria concentrica* (27), and *Leptinaria unilamellata* (8). Limnic species included *Physa acuta* (16 specimens, 12 living and 4 shells), *Lymnaea columella* (7 specimens, 3 living and 4 shells), *Stenophysa marmorata* (5 specimens, 4 living and 1 shell), and *Depanotrema cimex* (only 2 shells). Parasitological analysis revealed metastrongylid larvae in terrestrial species, especially *S. octona* (286 larvae), *B. similaris* (38), and *L. concentrica* (16). All limnic species tested negative. qPCR confirmed the larvae as *A. cantonensis* (Cq range: 25.26–32.04). Rodent feces from the area also tested positive for *A. cantonensis* by qPCR (Cq = 24.33). To confirm viability, 15 L3 larvae from *S. octona* were inoculated into a Wistar rat, resulting in the recovery of 10 adult worms (8 females, 2 males) after 67 days, thereby confirming the complete biological cycle of *A. cantonensis* at the zoo. GIS mapping showed that the detection sites were in close proximity (<40 m) to urban households and near eight schools, the nearest only 200 m away. This highlights the public health risk associated with parasite circulation in urbanized environments. This report documents the first confirmed case of fatal angiostrongyliasis in *Ateles chamek*, underscoring its vulnerability and the broader implications for One Health. The involvement of multiple disciplines - animal health, environmental monitoring, epidemiology, and laboratory diagnostics - enabled not only the resolution of the case but also the implementation of preventive and educational actions aimed at protecting both animal and human populations.

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SCHISTOSOMAL AND MOLLUSCICIDAL ACTIVITY OF ANTARCTIC MACROALGAE *Palmaria decipiens* (REINSCH) R. W. RICKER, 1987 (RHODOPHYTA, PALMARIALES)

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Keywords: schistosomiasis, *Biomphalaria glabrata*, marine natural products, extremophilic macroalgae, bioactive metabolites.

Antarctic is characterized by extreme climate conditions, which favors the production of secondary metabolites by native species and consequently making them a good source of bioactive compounds. As good producers of secondary metabolites, marine macroalgae have been largely used in bioprospection studies, thus, the present study aim to evaluate the activity of the red seaweed *Palmaria decipiens* in *Schistosoma mansoni* cercarie and *Biomphalaria glabrata* embryos for potential use in schistosomiasis. Polar and nonpolar extracts were obtained from *P. decipiens* through supercritical CO_2 (EFS-CO_2) followed by ethanol extraction. Embryos and cercarie were exposed to ethanol, EFS-CO_2 and EFS-CO_2/ethanol at 100 ug/mL and 50 ug/mL. Cercariae were analyzed in steriomicroscope at 15, 30, 60 and 120 minutes after exposure. Embryos at blastulae and veliger stage were exposed for 24h and transferred to 24 well culture plates with reconstituted water for 7 days for analysis. Supercritical CO_2 (EFS-CO_2) extraction is effective for non polar compounds. In the present study, 10 g of *P. decipiens* were extracted with EFS-CO_2 yielding 28 mg. The residual mass of 9.35 g was extracted with ethanol resulting in a final mass of 24 mg. The ethanol extract was enriched in polar compounds. Chemical characterization of the extracts was performed through High Performance Liquid Chromatography (HPLC) showing a high chemical diversity. The assessment of biological activity showed that the extracts affected the viability and motility of *S. mansoni* cercariae with 100 ug/mL. This concentration also caused malformation and mortality in *B. glabrata* embryos at both stages analyzed. At 50 ug/mL, no effects were observed for both models. The partial results obtained indicated that macroalgae *P. decipiens* is a good source of compounds for use in schistosomiasis control, especially for the development of products for the environmental controle of the disease, given the optimal activity on embryos and cercariae.

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NANOTECHNOLOGY-BASED STRATEGY FOR SCHISTOSOMIASIS CONTROL: BIOGENIC SILVER NANOPARTICLES AS NEXT-GENERATION MOLLUSCICIDES AND CERCARICIDES

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Keywords: *Schistosoma mansoni*, freshwater snails, tropical disease.

Schistosomiasis is a neglected tropical disease caused by *Schistosoma mansoni* Sambon, 1907, transmitted via contact with freshwater containing cercariae released by Biomphalaria snails (Preston, 1910). Nanotechnology-based approaches offer promising alternatives for developing molluscicides and cercaricides. This study evaluated biogenic silver nanoparticles (AgNPs), synthesized using the extremophile fungus *Aspergillus tubingensis* Mosseray, 1934 (AgNP-AT), against adult and embryos of *Biomphalaria glabrata* (Say, 1818), and *S. mansoni* cercariae for potential environmental disease control. Toxicity assays were conducted on adult snails, embryos of *B. glabrata* at the blastulae, gastrulae, trochophore, and veliger stages, and *S. mansoni* cercariae. Organisms were exposed to five or more serial concentrations of AgNP-AT, with three experimental replicates. Negative and positive controls were maintained under identical conditions. Mortality was the endpoint, and median lethal concentration values (LC_{50}) were determined. AgNP-AT were characterized as spherical particles with an average diameter of 35 ± 10 nm and a zeta potential of –30 mV, indicating good stability. AgNP-AT showed potent cercaricidal activity, with an LC_{50} of 0.003 mg L^{-1} after 2 hours of exposure, highlighting their potential for interrupting transmission of this larval stage of the parasitic worms. Sensitivity among *B. glabrata* developmental stages varied: blastulae (LC_{50} = 0.13 mg L^{-1}) and gastrulae (LC_{50} = 0.15 mg L^{-1}) were the most sensitive, followed by veliger (LC_{50} = 0.25 mg L^{-1}) and trochophore (LC_{50} = 0.38 mg L^{-1}). Adult snails were comparatively least sensitive, with an LC_{50} of 1.9 mg L^{-1}. The enhanced sensitivity of embryos suggests higher vulnerability during early developmental stages. The presence of a biomolecular corona on the AgNP-AT surface likely regulates silver ion release, reducing nonspecific toxicity and improving environmental safety. These findings underscore the selective effectiveness of AgNP-AT and their advantage over conventional synthetic compounds, which often pose higher ecotoxicological risks. Compared to silver nitrate ($AgNO_3$), previously tested, AgNP-AT demonstrated lower overall toxicity to non-target aquatic organisms, confirming their suitability for integrated host control strategies. The World Health Organization emphasizes snail control as a primary strategy for schistosomiasis mitigation. Our findings demonstrate the effectiveness of AgNP-AT against both *B. glabrata* and *S. mansoni*, with particularly high sensitivity observed in the parasite's cercariae. The low effective concentrations required, combined with reduced environmental toxicity, support the potential application of AgNP-AT in developing eco-friendly alternatives to synthetic molluscicides and cercaricides for integrated disease management.

Funding Source: This work was supported by the São Paulo Research Foundation (FAPESP, Grant #2020/03883- 4) and Butantan Foundation.

Parasitology

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SURVEILLANCE OF *Angiostrongylus* spp. LARVAE IN *Achatina fulica* COLLECTED IN URBAN AREAS OF BELÉM AND MOSQUEIRO DISTRICT, PARÁ, BRAZIL

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Keywords: *Angiostrongylus* spp., *Achatina fulica*, laboratory diagnosis, Baermann-Moraes, helminths.

Angiostrongylus spp. are parasitic nematodes that cause cerebral and abdominal angiostrongyliasis in humans. Transmission occurs through the ingestion of L3 larvae present in infected mollusks, such as *Achatina fulica*. This exotic species is widely distributed in Brazil due to its high reproductive capacity. This Study aimed to monitor *A. fulica* in Belém and Mosqueiro district to identify potential risk areas for angiostrongyliasis. Specimens of *A. fulica* were collected from 24 locations in the municipality of Belém and 3 locations in Mosqueiro district, during surveillance activities of the Malacological Department at Evandro Chagas Institute, in 2023. The mollusks were processed using the modified Baermann-Moraes technique, which involves artificial digestion of the tissues followed by sedimentation analysis for the presence of larvae. The sedimented material was examined under a stereoscopic microscope. Mollusks were found in 15 of the 27 surveyed locations, including 12 in Belém and 3 in Mosqueiro. Among these, 7 sites tested positive for *Angiostrongylus* spp. larvae, while 8 were negative. The detection of larvae in urban and peri-urban areas highlights the potential risk of human exposure, especially in regions with poor sanitation and frequent presence of *A. fulica*. The results reinforce the importance of routine malacological surveillance to identify and control areas at risk for angiostrongyliasis transmission. This study also supports the relevance of implementing laboratory techniques capable of detecting early environmental circulation of zoonotic parasites, contributing to public health strategies in the state of Pará and helping prevent the spread of parasitic diseases through informed interventions. The identification of positive samples in both Belém and Mosqueiro reinforces the necessity of continuous environmental monitoring. These results contribute to the development of public health strategies aimed at controlling parasitic diseases, especially in urban areas with known circulation of mollusks capable of hosting zoonotic parasites.

Funding Source: Evandro Chagas Institute / Brazilian Ministry of Health.

REPRODUCTION

Reproduction

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FIRST RECORD OF BROODING BEHAVIOUR IN *Acanthochitona pygmaea* (PILSBRY, 1893)

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Keywords: Acanthochitonidae, egg hull, chiton reproduction.

Brooding behaviour is widespread among molluscs and has evolved independently across multiple lineages. So far, 42 chiton species are known to hold developing embryos. While brooding is not uncommon, documented cases remain scarce; as many species of chitons are rare or poorly studied, it is likely an unobserved behaviour in many more species. Here, we present the first record of brooding in *Acanthochitona pygmaea* and describe the egg hull morphology. Over the past four years, fresh specimens were collected during multiple field trips along the Brazilian coast, across different seasons. Among approximately 2,000 polyplacophoran specimens of multiple species from the Brazilian coasts—both fresh and from existing collections—we observed brooding behavior in a single specimen of *A. pygmaea*. This individual was collected by hand in the intertidal at Praia do Leão, Fernando de Noronha, Pernambuco, Brazil (03°52'18''S, 32°26'13''W), and examined under a stereomicroscope. The specimen was preserved in 96% ethanol and is housed in the malacological collection of IBUFRJ 23637. The examined specimen carrying eggs exhibited notable differences compared to others collected on the same day and at the same location. One significant difference was a markedly enlarged girdle on both sides, likely to accommodate the developing embryos. Approximately 90 eggs were found distributed equally in both sides of the pallial cavity. The eggs measure around 150 µm in diameter. This discovery represents the first documented instance of egg-carrying behavior in a member of the family Acanthochitonidae. The next steps will involve a more detailed examination and analysis of the egg hull to describe their morphology, as this structure is also an important taxonomic characteristic. Further studies on species with unknown life histories should be pursued, as species with different dispersal strategies have different potential ranges and conservation needs. This first record of brooding behavior in *Acanthochitona* provides new insights into the reproductive strategies of Acanthochitonidae and expands our understanding of brooding within Polyplacophora. The morphological adaptations observed and the presence of eggs highlight the importance of continued field and microscopic investigations. Further analyses of egg morphology may also offer valuable taxonomic information, contributing to future studies on chiton diversity and evolution.

Funding Source: CAPES, FAPERJ, CNPq, Senckenberg Fellowship program, SOSA, SBMa.

Reproduction

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GENETIC MIXING AMONG INVASIVE ANDROGENETIC *Corbicula* CLAMS IN WESTERN EUROPE

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Keywords: reproduction, invasive alien species, genetic mixing, hybridization, freshwater clams.

The genus *Corbicula* includes estuarine and freshwater clams native to Asia, Australia, Africa, and the Middle East. It comprises both sexual and asexual lineages, the latter reproducing clonally via androgenesis—a rare form of reproduction involving hermaphroditism and exclusive paternal nuclear inheritance. While sexual lineages remain restricted to native areas, androgenetic lineages have colonized freshwater ecosystems globally. This study examines the role of genetic mixing in facilitating their invasive success. Specimens were collected from rivers in France, Belgium, and the Netherlands and genetically characterized using Oxford Nanopore Technologies (ONT) amplicon sequencing of mitochondrial (COI) and nuclear markers (alpha-amylase, calmodulin, beta-tubulin). Amplicon reads were processed with amplicon_sorter, and haplotypes in heterozygous individuals were phased using HairSplitter. Haplowebs, created with HaplowebMaker, were used to define genetic pools. Genome sizes and ploidy levels were assessed by flow cytometry or Feulgen Image Analysis Densitometry. To explore genome composition in hybrids, one individual was sequenced on an ONT PromethION 2 platform. Genome size and heterozygosity of this hybrid genome were estimated with GenomeScope, assembly performed using Flye, and phasing with HairSplitter. Among 200 sequenced clams, three mitochondrial lineages (A/R, B, and Rlc) were identified. However, haplowebs based on the nuclear markers revealed a single genetic pool, indicating extensive allele sharing across the samples and suggesting widespread genetic mixing. In particular, individuals from the Waal River (Netherlands) were predominantly hybrids, carrying alleles from the invasive A/R and C/S lineages, as well as previously unrecorded alleles likely originating from the native range. Genome sizes range from 3.6 to 5.1 pg, suggesting the presence of polyploids among our samples. Whole-genome sequencing of one hybrid individual yielded a 4.7 Gb genome with a high heterozygosity (2.7%). These initial findings demonstrate that, despite their ability to reproduce clonally, *Corbicula* androgenetic lineages continue to exchange genes. Ongoing comparative genome analyses will help clarify how reproductive strategy, genetic mixing, and polyploidy interact to support long-term persistence and invasion of androgenetic *Corbicula* lineages. This study confirms the prevalence of genetic exchanges among androgenetic *Corbicula* lineages from Western Europe. Our initial findings suggest that a mixed reproduction mode combining androgenesis with genetic mixing may be one of several factors underpinning the ecological success of invasive *Corbicula* clams, alongside other life history traits. A comparative study between invasive and native populations is currently underway to further investigate the putative link between androgenesis and invasion success.

Funding Source: This study was supported by Fonds de la Recherche Scientifique - FNRS (research grant 1.E.108.24F to Dina Mae Rañises).

TAXONOMY AND SYSTEMATICS

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IMPROVING THE TAXONOMY OF *Mytilopsis* (BIVALVIA, DREISSENIDAE): RECENT ADVANCES AND MAJOR GAPS

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Keywords: estuarine bivalve, integrative taxonomy, invasive species.

The estuarine bivalves *Mytilopsis* currently comprise seven extant species (MolluscaBase), in addition to several extinct ones. The extant species were originally described from the West Atlantic (*M. leucophaeata*; *M. sallei*), East Atlantic (all from Africa: *M. africana*; *M. lacustris*; *M. ornata*) and East Pacific (*M. adamsi*; *M. trautwineana*). Two of them (*M. leucophaeata* and *M. sallei*) are historically associated to anthropic introductions worldwide, causing severe ecological and economic problems. Based on a literature survey (Scholar Google and Web of Science), we explore the recent advances and major gaps in the taxonomy of *Mytilopsis*, with emphasis on the genetic results that elucidated some aspects of this troublesome genus. Most genetic studies comprised the mitochondrial gene COI (cytochrome c oxidase subunit I), with a few adding data on the nuclear 28S gene. The taxonomy of *M. leucophaeata* is advanced after the adoption of molecular tools: there are two genetic lineages that possibly represent distinct species, one confirmed from Florida, USA (native) to South America (invasive), the other from Chesapeake Bay (native) to northeastern USA, Europe and Caspian Sea (invasive). The inclusion of additional localities and the refinement of population genetics will be essential to test the validity of these lineages as separate species. Contrastingly, the taxonomy of *M. sallei* is currently chaotic: three cryptic species are known, one confirmed from Florida, USA (possibly native), southeastern Brazil and Asia (invasive), another from Brazil (probably invasive) and the other from East Mexico (native). Much more sampling in the Caribbean is required in order to discover additional species in the complex *M. sallei*, and to refine the range of each species. None of the other *Mytilopsis* species have available DNA sequences, precluding the knowledge whether the East Pacific and African species are valid or merely represent old introductions. We argue for the necessity of more partnerships in order to increase the number of studied sites and species, in addition to a complete anatomical investigation of *Mytilopsis*, aiming to identify diagnostic features for each species. With a robust species delimitation, we will gain benefits for the conservation of species in their natural ranges, as well as improve mitigation actions for those in introduced sites.

Funding Source: No.

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PHYLOGENETIC ANALYSES USING CONCHOLOGICAL AND MOLECULAR DATA OF SPECIES FROM THE *Megalobulimus oblongus* COMPLEX

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Keywords: complex oblongus, phylogeny, analysis.

The phylogenetic analysis of conchological characters included 33 species, 21 of which *Megalobulimus*, and was done using the Tree analysis using New Technology (TNT) software parsimony Most of the material analyzed was sourced from the Malacology Collection of the Museum of Zoology of the University of São Paulo (MZSP), supplemented by images from other reference collections. For the molecular analysis, genetic sequences available in GenBank were used along with sequences newly obtained from MZSP specimens, using the mitochondrial COI barcoding marker. The Bayesian inference analysis was done using the MrBayes plugin in the Geneious software. The conchological analysis revealed the formation of inconsistent clades, suggesting that shell characters alone are not sufficient for accurately delimiting the species within the oblongus complex. The overlapping shell features among taxa hinder the precise classification based solely on conchological characteristics. Furthermore, inconsistencies were also observed in some clades composed of species external to the complex, although a few expected groupings were successfully confirmed, such as *M. lopesi* and *M. pergranulatus* indicating some degree of phylogenetic signal in shell traits. In contrast, the molecular analysis demonstrated a clearer pattern of geographic separation within *M. oblongus*, with better-defined regional clades. However, several of these molecular groupings did not correspond well with the traditionally accepted species boundaries, revealing a degree of incongruence between morphological and genetic data. Notably, some subspecies of *M. oblongus* previously proposed by Bequaert (1948) were supported by the molecular evidence. Although still preliminary, these findings provide valuable insights into the complexity, diversity, and taxonomic structure of the oblongus species complex. The analyses presented are part of an ongoing research project, and current limitations are being addressed. The results highlight the need to incorporate anatomical data into the analyses to achieve a more comprehensive and informative morphoanatomical approach. From a molecular perspective, the results highlight the importance of including genetic sequences from individuals from a wider geographic range, particularly for species of the oblongus complex, other molecular markers will be included.

Funding Source: CAPES.

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NATIVE NO MORE: *Thaisella mariae* (NEOGASTROPODA: MURICIDAE) REVEALED AS AN EXOTIC SPECIES IN BRAZIL THROUGH INTEGRATIVE TAXONOMY

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Keywords: Rapaninae, morphology, DNA, West Atlantic, Indo-Pacific.

Thaisella mariae (Lange-de-Morretes, 1954) is a muricid species considered endemic from Brazil, occurring in estuarine areas with a disjoint distribution from Bahia to Paraná states. However, the high variability of shell phenotypes, limited morpho-anatomical data, and uncertainties regarding its distribution continue to obscure its taxonomic understanding. Therefore, the taxonomy of *T. mariae* was revised through an integrative approach, combining detailed morphological analysis and mitochondrial COI gene data. Specimens preserved in ethanol from the MZSP and NHMUK malacological collections were dissected under a stereomicroscope. Radulae and shell ultrastructure were examined via SEM. DNA was extracted using a silica-membrane commercial kit, with quality assessed by a Nanodrop spectrophotometer. The mitochondrial COI marker was amplified for specimens from two states (São Paulo and Paraná), using 'universal' primers. PCR products were purified and sequenced by Macrogen Inc. (Korea). A phylogenetic analysis was conducted including GenBank sequences of other species from Rapaninae. The sequences were aligned in Geneious Prime using the MUSCLE plugin. A Bayesian inference was conducted using the MrBayes software. The specimens identified as *Thaisella mariae*, including the type material analyzed, exhibit morpho-anatomical features consistent with those of the types and topotypes of *Indothais malayensis*, a species from the Indo-Pacific. Notable features include the shell with spines that, when present, may be either short or long and apically curved; the interior of the outer lip typically displaying three to five brown spiral bands; a penis bearing an external flap from which the apical penile flagellum retracts; a sperm ingesting gland composed of multiple chambers; and the presence of an exophageal gland located near the duct of the gland of Leiblein. The DNA sequences of *T. mariae* and *I. malayensis* cluster together within a single clade. All Brazilian specimens form a monophyletic group with *I. malayensis* and *Indothais javanica* (the latter interpreted here as GenBank misidentifications attributed to *I. malayensis*), which is sister to Indothais wutingi. Therefore, this investigation revealed that *T. mariae* corresponds to an exotic species from the Indo-Pacific on the Brazilian coast. Consequently, *Indothais malayensis* is synonymized with *T. mariae*, which is herein reassigned to *Indothais mariae* (comb. nov.). Our findings clarify that the observed disjoint distribution coincides with two of the largest port terminals in Brazil. Given the high port activity in these regions, it is likely that the introduction of *I. mariae* into Brazil occurred via interoceanic shipping. These results emphasize the importance of integrative approaches, combining morphological and molecular data, for accurate taxonomic delimitation in widely distributed, morphologically variable taxa. The findings advance the taxonomic understanding of this group of rapanines and underscores to the increasing introduction of exotic species along the Brazilian coast, an issue linked to anthropogenic vectors such as maritime transport, highlighting the essential role of taxonomy in monitoring and interpreting biodiversity changes.

Funding Source: CAPES; FAPESP.

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THE GREAT TREASURE OF THE GREATER CAUCASUS: NEW SPECIES OF OPEN-COILED SUBTERRANEAN FRESHWATER SNAIL FROM FAMILY HYDROBIIDAE

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Keywords: groundwater snails, minute shell, endemism, integrative taxonomy, cave tauna.

The Caucasus is home to enormous biodiversity, some of which is hidden from our eyes deep underground. Stygobiotic microgastropods of the family Hydrobiidae are widespread in this region, but we still know very little about their true diversity. In this study we would like to present a new species of the genus *Caucasopsis* with a bizarre open coiled shell. The material for this study consisted of 18 molluscs and about 20 empty shells collected on 15 and 18 September 2022 from Lakada Cave in Samegrelo, Western Georgia. The material was sampled from a clay pit at a depth of approximately 3 m using a sieve attached to a 2 m long handle. The study was carried out using morphological (dissection, SEM) and molecular taxonomic techniques, including one mitochondrial and two nuclear molecular markers. The species is distinguished by a high conic openly coiling shell, which can reach a maximum height of 4 mm. Concurrently, the mollusc shells within the population exhibit varying degrees of openness in shell structure. Despite the fact that the mollusc has such an expressive shell, which is not characteristic for any of the known genera of hydrobiids from the Caucasus, the female sexual reproductive shows many features of similarity with members of the genus *Caucasopsis*. The female genitalia is characterized by a large bursa copulatrix, a small coiled oviduct and a single seminal receptacle. The characteristics of the operculum and radula of the mollusc are also consistent with the diagnosis of the genus. Molecular data also confirm that the new species belongs to the genus *Caucasopsis*. It is important to note the significant role of the integrative approach employed in this study for the description of this species. In the absence of molecular and internal structure data, this snail would most likely have been erroneously described as a monotypic genus. This finding indicates that within the same genus there can be considerable diversity in shell shape, for example in the genus *Caucasopsis* the shell shape varies from planispiral to conical, including open-coiled forms. However, the possible adaptive advantages of a shell of this shape remain a mystery to us and are the subject of further research.

Funding Source: This study was partially funded by the Russian Scientific Fund (project No. 25-24-00006).

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EXTERNAL ANATOMY OF *Ommastrephes bartramii* (CEPHALOPODA: OMMASTREPHIDAE) FROM THE MALACOLOGY COLLECTION OF THE MUSEUM OF ZOOLOGY OF THE UNIVERSITY OF SÃO PAULO (MZUSP)

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Keywords: taxonomy, anatomy systematic, morfology, morfometric.

The squid species of the family Ommastrephidae Steenstrup, 1875 include 22 economically important species. One of the most commonly fished is *Ommastrephes bartramii*. In 2020, cephalopod fishing generated 10.2 billion dollars, with one-third coming from this family. This project aims to compile data on the external anatomy of *O. bartramii*, using specimens from the Museum of Zoology of USP to produce anatomical plates for better understanding of the group. In the methodology, drawings of the external anatomy of *Ommastrephes bartramii* specimens were created using Photoshop based on a photo taken with a cellphone. For structures such as the tentacular club, hectocotylus, and suckers, photos were taken with the aid of a camera lucida connected to stereomicroscope to ensure greater precision in anatomical details. The drawings were made using specimens suitable for recording, and anatomical plates were created showing dorsal, ventral, tentacle, and hectocotylus views. For comparison, the plates will be accompanied by photos of the individuals. Analyzing the morphological characters of studied specimens plates and photos, we confirm that the specimens they indeed belong to the species *Ommastrephes bartramii*, displaying all its apomorphiesfeatures: two rows of suckers, violet coloration with a darker stripe in the middle of the mantle, and a blue spot near the eyes. This contrasts with a recent 2020 study that used a molecular approach to analyze the four *Ommastrephes* species and their distribution, suggesting that the only species of the genus in South America is *Ommastrephes cylindraceus*. This highlights the importance of anatomical studies on cephalopods, a field with limited research, especially regarding oceanic squids, which are challenging to collect and, consequently, less studied. The specimens showed significant size variation, even among adults, possibly due to high water temperatures accelerating the growth of marine animals. The plates produced in this study can be used to create illustrated identification guides for oceanic squids. With the completion of the anatomical study of external features. we gained a better understanding of the anatomy of *Ommastrephes bartramii* occurring in Brazil adn its size variation. This also highlights the importance of anatomical studies for species comprehension, wich can be replaced added to molecular analysis. Further collections and studies will be necessary to determine whether only one *Ommastrephes* species occurs in Brazil.

Funding Source: No.

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DEALING WITH A BIG PUZZLE: THE HIDDEN DIVERSITY OF THE SPECIES COMPLEX *Happia vitrina* THROUGH MOLECULAR ANALYSIS

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Keywords: *Happia*, Scolodontidae, cryptic species, molecular analysis.

The genus *Happia* is widely distributed throughout Brazil and includes terrestrial snails with discoidal shells and conserved morphology, hindering specific delimitation. Within the genus, *Happia vitrina* stands out due to its wide distribution and low morphological variation, suggesting a cryptic species complex, as indicated in the literature. The objective of the study is to test the monophyly of the complex *H. vitrina* and identify possible cryptic lineages. The analysis included samples from museum lots identified as *H. vitrina* and deposited in representative collections of terrestrial snails from Brazil. For the genetic analysis, the mitochondrial COI gene was amplified from 25 specimens (19 of *H. vitrina*, six of other scolodontids), representing five Brazilian states and 12 municipalities. GenBank sequences from other species of Scolodontidae were included as outgroups. Molecular analyses were performed using the MEGA7 software, based on the Maximum Likelihood criterion, with statistical support obtained through bootstrap. Species delimitation was carried out using the ASAP software, employing the K2P genetic distance model, based on the genetic distance matrices generated from the data. Molecular analyses based on the COI region indicated that individuals traditionally grouped under the name *Happia vitrina* do not form a monophyletic clade. The molecular tree recovered several distinct and well-supported lineages, often associated with clear geographic separations. Within the *H. vitrina* complex, the first partition of the ASAP analysis identified 14 distinct species, almost all represented by singletons, except for one species represented by six sequences (all from the municipality of Rio de Janeiro, specifically from the Tijuca National Park). Specimens from the Serra do Mar mountain range and nearby urban areas, for example, formed a reasonably cohesive clade, although with moderate statistical support. Specimens from Ceará and Pará grouped into distinct lineages, suggesting historical isolation and significant genetic divergence. The degree of divergence between these lineages is consistent with interspecific values observed within Stylommatophora. The results confirm that *Happia vitrina* (sensu lato) includes multiple independent lineages, representing a cryptic species complex. The absence of monophyly and the geographical correspondence between the clades justify the taxonomic revision of the group. Such evidence highlights the value of molecular methods in systematics and warns for the underestimation of biodiversity in regions of high ecological complexity.

Funding Source: CAPES (Fundação Coordenação de Aperfeiçoamento de Pessoal de Nível Superior).

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HARNESSING THE POTENTIAL OF HIGH-THROUGHPUT PHENOTYPING FOR THE SYSTEMATICS AND EVOLUTION OF GASTROPODA

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Keywords: imaging, high-throughput phenotyping, systematics, evolution, Gastropoda.

Despite major advances in imaging technologies over the past 25 years, few malacological studies have leveraged 3D shell models for systematics and evolutionary research. A likely explanation lies in the still relatively high cost and time investment required to acquire and reconstruct multiple specimens—often dozens—necessary for robust statistical analyses. This has limited the application of 3D approaches in large-scale comparative or evolutionary studies of gastropods. Using custom-designed sample holders produced by 3D printing and compatible with the EasyTom S automatic loader, we enabled the simultaneous scanning of multiple specimens. Acquisition was semi-automated through tailored macros. To illustrate scan quality and biological insight, we present a case study on internal shell remodeling across diverse Neogastropoda groups, including both extant and fossil species. This setup allows for efficient, repeatable high-throughput scanning adapted to morphological studies in systematics and evolutionary biology. The protocol includes mounting specimens in holders, configuring acquisition settings in Xact, scanning, reconstructing 3D models, and saving outputs. Over 1,000 specimens were digitized in less than three weeks, averaging 70 scans per day. The complete workflow (from mounting the specimens to saving the 3D models) of a batch CT-Scan of 60 specimens required approximately 12.5 hours, hence the full processing time averaged 12 minutes per specimen. Scanning costs were reduced to under 2 euros per specimen, marking a significant improvement over traditional methods. In our exploratory analysis of various neogastropod families (e.g., Conidae, Conorbidae, Columbellidae, Cystiscidae), we identified repeated patterns of internal shell remodeling. These patterns show striking convergences across clades and can be chronologically calibrated using fossil data. This highlights the potential of high-throughput 3D phenotyping to uncover overlooked or cryptic morphological traits relevant for phylogenetics and to bridge the gap between extant and extinct biodiversity. This study demonstrates that high-throughput, non-invasive 3D phenotyping is now accessible, affordable, and highly informative for malacological research. By streamlining acquisition and reconstruction workflows, we enable the rapid generation of large-scale morphological datasets. Our findings reveal convergent patterns in internal shell architecture and highlight the value of 3D morphology in understanding evolutionary trends across time and taxa within the Gastropoda.

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WHAT DO THE CAVES OF SERRA DOS CARAJÁS REVEAL ABOUT GASTROPOD BIODIVERSITY IN NORTHERN BRAZIL

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Keywords: biodiversity, Carajás, caves, Gastropoda, subterranean.

The Serra dos Carajás region, located in southeastern Pará state, houses one of the main speleological provinces in Brazil, with over than 1,500 registered subterranean cavities. Gastropods represent one of the most prominent groups in Brazilian caves overall, including troglophilic, troglobitic, and accidental species, though still largely unstudied in northern Brazil. This ongoing study aims to investigate the diversity of terrestrial gastropods associated with caves in Serra dos Carajás. Specimens, including both dry shells and live animals, were collected during multiple field expeditions conducted between 2021 and 2023 and are currently housed in the scientific collection of the Laboratório de Estudos Subterrâneos (LES) at UFSCar, São Carlos, Brazil. Species identification, as well as ongoing photographic documentation and detailed image processing, are being performed using taxonomic publications and iconographic resources. To date, 10 morphospecies have been recorded, distributed among six genera (*Scolodonta*, *Systrophia*, *Leptinaria*, *Dysopeas*, *Cyclodontina*, and *Obeliscus*), with three species formally identified so far: *Systrophia siolii*, *Leptinaria parana* and *Leptinaria unilamellata*. The first two species are endemic to Pará state, while the latter species is widespread in the neotropics. Notably, the shells of the studied specimens exhibited thinner walls and often reduced sculpture, typical of ferruginous environments with low calcium and nutrient availability and high hydric variability. Within the available material and in the context of the scarcely surveyed Pará state, there seems to be significant potential for the discovery of new species, reinforced by the nature of the subterranean environments in Serra dos Carajás. Despite the recognized ecological importance of the region, research efforts remain limited and primarily focused on environmental licensing services, resulting in significant gaps in the understanding of subterranean ecosystems and highlighting the need for further biodiversity studies. We hope this study will contribute to the expansion of knowledge on Brazilian terrestrial gastropods and cave-dwelling invertebrate faunas in general. Furthermore, we aim to produce an illustrated field guide of shells from the Carajás region, which should promote citizen science initiatives and foster the environmental awareness of the public in understanding and preserving the subterranean fauna.

Funding Source: TCCE ICMBio/Vale number 02/2020 (BT LFS); TCCE ICMBio/Vale number 01/2018 (PJ JEG); CNPq (Productivity Grant MEB, 310378/2017-6); FAPESP (2019/19520-0, Regular Grant MEB).

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FAMILIAR FACES, HIDDEN IDENTITIES: UNMASKING UNDESCRIBED NUDIBRANCHS FROM EAST TIMOR

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Keywords: seaslug, *Thecacera*, *Nembrotha*, morphology, phylogeny.

Nudibranchs, the vibrant jewels of the sea, dazzle divers with vivid colors and striking forms, and they are iconic reef creatures featured in many guides. Yet, some frequently photographed species remain scientific mysteries—misidentified or still undescribed. This study highlights three such enigmatic species from the family Polyceridae, collected across vibrant reef sites in East Timor, a lesser-known hotspot within the Coral Triangle. Using integrative taxonomy, we combined species delimitation analyses (ASAP, ABGD, bPTP, GMYC) with molecular phylogenetics (Bayesian Inference and Maximum Likelihood) based on two mitochondrial (COI, 16S rRNA) and one nuclear marker (H3) to examine evolutionary relationships. External morphology was assessed through photographs of living animals and stereomicroscope observations. Internal anatomy was studied via dissections. Key structures (radulae, labial cuticles, jaws, spicules and penises) were isolated, cleaned, dried with hexamethyldisilazane (except radulae), and examined under a scanning electron microscope for detailed analysis. Our results clearly demonstrate that the three new species described in this study are distinct from their closest relatives and can be readily identified by their unique external features and vivid color patterns. These nudibranchs have been widely photographed and featured in field guides and online platforms, yet remained scientifically unnamed until now. By formally describing them, we not only resolve longstanding taxonomic confusion but also contribute to a more accurate understanding of marine biodiversity. Furthermore, our findings reveal a remarkable new color morph of *Nembrotha purpureolineata* O'Donoghue, 1924 and provide compelling molecular and morphological evidence for two additional, putative new species—one belonging to the genus *Thecacera* and another to *Nembrotha*. These discoveries not only enrich our understanding of nudibranch diversity but also remind us that even the ocean's most familiar faces can hold untold secrets. It is noteworthy that the help of the Dreamers Dive Academy was essential throughout the campaign in East Timor and without their support, these beauties would surely remain unknown to the rest of the world.

Funding Source: No.

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UNCOVERING CRYPTIC DIVERSITY IN *Thuridilla* BERGH, 1872 (MOLLUSCA, SACOGLOSSA) SEA SLUGS FROM EAST TIMOR WITH THE DESCRIPTION OF A NEW SPECIES

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Keywords: Heterobranchia, phylogenetics, new species.

The sacoglossan genus *Thuridilla* Bergh, 1872 exhibits remarkable diversity and varied patterns of coloration, although its true species richness remains underestimated due to its cryptic morphology. Understanding this hidden diversity is crucial for accurate biodiversity assessments. The present contribution aims to analyze *Thuridilla* species from East Timor through integrative taxonomy in a global phylogenetic context, revealing possible cryptic species and formally describing a new taxon. Fourteen *Thuridilla* specimens were collected along the coast of East Timor during July and August 2023. Molecular analyses were performed based on the sequencing of two mitochondrial (COI and 16S rRNA) and one nuclear (H3) genetic markers. Bayesian Inference and Maximum Likelihood analyses were used to construct the phylogenetic tree and three species delimitation methods (ABGD, bPTP and GMYC) were applied, using both new and previously available data from Genbank. The morphological study was performed on specimens belonging to the undescribed species referred to as *Thuridilla* sp. nov. 06. In addition, haplotype networks were inferred using PopART to explore the genetic evolutionary patterns within the populations in this new species. The molecular analyses revealed the presence of 8 species of *Thuridilla* distributed in East Timor, four of which belong to the *Thuridilla gracilis* species complex, including the new species described herein, and two more still undescribed. This newly described species externally resembles *Thuridilla ratna* (Marcus, 1965) in its black and white/yellowish striped body color pattern but differs in the pattern of coloration of the rhinophores, which consists of a broad white band followed by a narrower orange stripe and ending in a dark-colored tip. It is distributed across the Indo-Pacific Ocean, particularly along the southeastern coast of Africa and the Malay Archipelago, which contributes to the increase in the known diversity of the genus *Thuridilla* in the Indo-Pacific. Through integrative taxonomy, a new species was described, and several undescribed lineages were identified from the coast of East Timor. These findings emphasize the importance of combining molecular and morphological approaches to accurately document species richness in cryptic marine groups.

Funding Source: No.

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OCEAN SPECIES DISCOVERIES - A NOVEL PEER-REVIEWED PUBLICATION SERIES FOR MARINE INVERTEBRATE SPECIES DESCRIPTIONS

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Keywords: new species, alpha taxonomy, marine invertebrates, Mollusca, Senckenberg Ocean Species Alliance.

Marine invertebrate taxonomy faces a critical bottleneck, with numerous species remaining undescribed due to limited taxonomic capacity. The Ocean Species Discoveries publication series addresses this challenge by streamlining the description process for new species. The overarching aim is to accelerate species documentation, enhance taxonomic efficiency, and provide a collaborative, replicable model for expanding work on describing biodiversity internationally. Ocean Species Discoveries integrates concise, high-quality species descriptions from all marine phyla into multi-taxon publications. Each individual description follows a structured template and includes morphological descriptions, high-resolution imaging, and DNA barcoding where applicable. Contributions originate through work funded within the Senckenberg Ocean Species Alliance and independent submissions by external collaborators. Each species description is attributed to the contributing individual(s) as the taxonomic authority. Authorship of the paper is shared by all contributors, who are listed in alphabetical order. The co-authors therefore can include additional contributors, for example those who provided additional intellectual contributions such as observations and specimens, but who are not named as a taxonomic authority for any species. Two Ocean Species Discoveries publications to date resulted in the description of 25 new marine invertebrate species, 2 re-descriptions, and 3 new genera across diverse taxa, including molluscs, as well as arthropods, annelids, and echinoderms. Community participation was integral, with local researchers contributing to specimen collection, analysis, and dissemination of findings. The initiative also highlighted challenges, such as the need for consistent funding and the importance of integrating traditional taxonomic knowledge with modern techniques. Overall, this model showcased a scalable and effective framework for accelerating marine species discovery and description, with potential applications in many understudied ecosystems. It is well known that numerous species remain undescribed because the effort/reward ratio is not favourable for single species descriptions in an academic career. But large-scale publications with many co-authors have been successfully used to accelerate the description of fungal species already, and the Ocean Species Discoveries project demonstrates that such collaboration is also viable in marine invertebrates. The benefits of participating in a large co-authored publication include a lower effort and higher reward, and an increased citation rate for all. There is an advantage to the whole community in generating (relatively) highly cited papers about pure alpha taxonomy. The Ocean Species Discoveries publications promote high-quality integrative taxonomy and provide a platform to name and describe species that would otherwise languish on the shelf. Taxonomy as a discipline usually feels no sense of urgency, as the academic reward is low. However, conservation and protection of species are dramatically enhanced when species have a name, which is increasingly a pressing concern in times of rapid biodiversity loss. Contributions are welcome.

Funding Source: The Senckenberg Ocean Species Alliance project was funded by a generous philanthropic donation.

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DIVERSITY AND TAXONOMY OF "LOWER" HETEROBRANCHIA AND PYRAMIDELLIDAE GASTROPODS IN NORWAY

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Keywords: Heterobranchia, Pyramidellidae, Norway.

The "lower" Heterobranchia sensu lato and Pyramidelloidea represent paraphyletic assemblages of families and genera with unresolved taxonomy and phylogeny. They consist of small, shelled gastropods spanning 16 families—nine are represented in Norway ("lower" Heterobranchia: Acteonidae, Cimidae, Mathilididae, Murchisonellidae, Omalogyridae, Rissoellidae, Tjaernoeiidae, Xylodisculidae; Pyramidelloidea: Pyramidellidae). These gastropods are studied for the first time in Norway using an integrative approach combining DNA analysis, shell morphology, and anatomical traits. Samples were obtained from museum collections and fieldwork involving snorkelling and SCUBA in habitats like mussel beds, serpulid worm aggregations, kelp forests, seagrass meadows, mud and sand flats, coralline algae (maerl), and areas with biofouling in harbours and marinas. Additional samples were obtained by inspecting potential hosts like echinoderms and bivalves, where pyramidellids are ectoparasites. Furthermore, dredging and grab sampling of soft-bottom habitats (1–800 m depth) was carried out from the shore and on-board research vessels. To date, 147 specimens have been barcoded for the cytochrome c oxidase subunit I gene (COI). Preliminary Bayesian phylogenetic inference and an Assemble Species by Automatic Partitioning (ASAP) species delimitation analysis were performed. The preliminary results based on the 147 specimens barcoded yielded 28 candidate species, namely nine "lower Heterobranchia" and 19 Pyramidellidae. Currently there are 14 species of "lower" Heterobranchia and 52 of Pyramidellidae cited in Norway, but identification of species has been mostly based on shell characters and only in few cases anatomical traits. In the Pyramidellidae the use of shells alone is responsible for pervasive taxonomic problems at species and genus level worldwide, and most likely in Norway the situation is no different. For example, several species have been recorded only once and others are of doubtful occurrence in the country (e.g., *Odostomia plicata*, *Turbonilla lactea*). Species composition and relationships among the "lower" Heterobranchia are still poorly understood, but they remain of considerable interest, because this group is the link between the species-rich crown group of Heterobranchia – the Euthyneura, and the Heterobranchia sister group – the Caenogastropoda. Therefore, better understanding of the diversity of this group in Norway not only contributes to enhance knowledge of local biodiversity but also generates new data to resolve the phylogenetic relationships of these snails. To date nine species of "lower Heterobranchia" and 19 Pyramidellidae have been recognized through DNA barcoding. Additional specimens are in the pipeline to be sequenced and ongoing fieldwork across various Norwegian counties and unexplored habitats is expected to yield further diversity. All lineages will undergo detailed morphological characterization using electron microscopy to examine shell traits and possibly anatomical characters.

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REVISITING *Orthoyoldia solenoides* (DALL, 1881) (BIVALVIA: PROTOBRANCHIA): SYSTEMATICS, GROSS ANATOMY AND GEOGRAPHIC DISTRIBUTION

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Keywords: taxonomy, biodiversity, Brazil, deep-sea, Yoldiidae.

Protobranchia is a subclass of Bivalvia characterized by its anatomy highly adapted for deposit-feeding habits. *Orthoyoldia solenoides* (Dall, 1881) is an infaunal protobranch species occurring from the continental shelf to bathyal zones from Gulf of Mexico, Caribbean, Suriname and North of Brazil. Like many marine protobranch species, it remains poorly studied. This study aims to provide a detailed anatomical description and to expand its geographical distribution. Specimens analyzed in this study were preserved in 70% alcohol and stored in the collection of the Museum of Zoology at the Universidade de São Paulo and in the Biological Institute at the Universidade Federal do Rio de Janeiro. The anatomical sections acted in accordance with the pattern established for the group, including the removal of one of the valves to analyse the details of the mantle lobe and the structures of the pallial cavity, followed by the removal of the digestive gland and adjacent tissues to access the internal anatomy. These features were documented using a Nikon D3200 DSLR camera coupled with a Carl Zeiss stereoscopic microscope. *Orthoyoldia solenoides* is characterized by long inhalant and exhalant siphons, fused to form a complete tube. The inhalant siphon is thick and striated, with an anterior end forming two lateral folds, whereas the exhalant siphon is thin and smooth. The anterior adductor muscle is larger than the posterior one. The ctenidium is small and narrow, nearly rectangular but forming an arch between the base of the siphon and the visceral mass. The proboscis extends posteriorly and forms a spiral at its tip when retracted. The lamellar palp exhibits diagonal striations oriented towards the mouth. A well-developed anterior marginal sensory organ is located at the anterior edge of the mantle. The digestive tract loops after the stomach before continuing its course to the anus. The shell is white, thin, inequilateral, oblong, gaping at both ends, lacking a carina or a distinctive rostrum, umbones are inconspicuous and slightly opisthogyrous. The hinge is taxodont, with a large resilifer. The structures observed in *O. solenoides* align with those documented in the literature for the family Yoldiidae, reinforcing the idea that there is a high level of conservatism among various Protobranchia groups. This study also broadens the known distribution of *O. solenoides* to include locations such as the mouth of the Amazon River, off Espirito Santo state and the Campos Basin, Rio de Janeiro state. Despite significant efforts to elucidate the systematics of Brazilian deep-sea protobranchs, the present report of *O. solenoides* highlights the gap in research regarding deep-sea protobranch bivalves in Brazilian waters. We hope to enhance the understanding of this group and contribute to a more comprehensive understanding of evolutionary patterns and ecosystem dynamics in deep marine environments.

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MICROSHELLS OF GASTROPODA (MOLLUSCA) FROM THE COAST OF PERNAMBUCO (PE), NORTHEASTERN BRAZIL

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Keywords: gastropoda, reef, intertidal, microshells.

Microshells are adult forms of tiny mollusk groups that have a maximum size of 10 mm. They are poorly studied in Brazil and are represented with greater diversity in the Gastropoda class. This study analyzes taxonomic aspects, community structure, and distribution in the Boa Viagem reef area (PE), to expand geographical distribution records and knowledge of micromollusk biodiversity. The study analyzed the micromollusk species collection from the LABMAR (ICB/UPE) reference collection of previous monitoring studies and epifauna analysis of the Mollusca phylum from the arenitic reefs at Boa Viagem beach (8° 03' 14" S; 34° 52' 50" W), conducted during low tide in microhabitats: submerged in tide pools (depth of 1.0 m), reef lateral side and upper the reef, manual collection. In the laboratory, organisms were sorted, measured, quantified, identified with specialized bibliography, and photographed using a digital stereomicroscope. Zonation analysis considered species occurrence frequency in microhabitats. Quantitative data were organized in tables. Eleven gastropod micromollusk species were identified, belonging to nine families: *Eullithideum affine* (C.B. Adams, 1850), *Parviturbo rehderi* Pilsbry & McGinty, 1945, *Parvanachis obesa* (C.B. Adams, 1845), *Pyrgocythara cinctella* (Pfeiffer, 1840), *Schwartziella bryerea* (Montagu, 1803), *Bittiolum varium* (Pfeiffer, 1840), *Vitreolina arcuata* (C.B. Adams, 1850), *Calliostoma sapidum* Dall, 1881, *Zebinella striatocostata* (Orbigny, 1842), *Boonea jadisi* (Olsson & McGinty, 1958), *Boonea seminuda* (C.B. Adams, 1839). The Phasianellidae and Columbellidae families were the most representative, with *E. affine* and *P. obesa* considered constant species with 90% occurrence frequency in tide pools, characteristic species occurring throughout the reef extension in all microhabitats. The other species showed restricted distribution to the submerged microhabitat in tide pools and are considered rare (F<30%) in the study area. Species with high resistance can distribute across the entire emerged reef area, generally with greater activity during low tide while searching for food. These results agree with studies conducted in Pernambuco's intertidal zone, indicating that tide pools in reefs and the lower level of beach rocks, with greater wetness, present higher biodiversity, associated with algae, when compared to emerged microhabitats. Micromollusks find suitable substrate in algae that are abundant in submerged environments, with available food, which may explain their restricted occurrence in these locations. Organisms that cannot withstand desiccation remain in sheltered areas away from direct sunlight, despite significant differences in temperature and salinity occurring in tide pools. Distribution limits of micromollusks are determined by tolerance to long exposure periods. It is verified that species are located in submerged areas during low tide. The high biodiversity of microgastropods in tide pools compared to low occurrence in emerged microhabitats can be explained by the small size of specimens, constant wetness, algae occurrence, constituting the predominant factor in species distribution.

Funding Source: PIBIC CNPq / UPE.

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TAXONOMY AND ZONATION OF FISSURELLIDAE (MOLLUSCA, GASTROPODA) IN THE SANDY REEFS GAIBÚ BEACH (PE) BRAZIL

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Keywords: Gastropoda, reef, intertidal, Fissurellidae.

The family Fissurellidae comprises marine gastropods characterized by a limpet-shaped shell with an apical fissure related to excretion and gas exchange. They inhabit rocky substrates in the intertidal zone, attached by a ventral muscular foot. This study aims to answer questions about the taxonomic aspects, community structure, and distribution in the reef area, contributing to expanding geographical distribution records and knowledge of biodiversity. The collection was carried out in Gaibú (8°17'15"S; 35°02'00"W) in December/ 2024. On the reef, the distance between low tide and high tide is 115 m, characterizing the mid-littoral. Transects were delineated in the east-west direction, from the limit of the breaking waves (rough mode) to the limit with the sandy beach (calm mode). Environmental parameters were measured: water and air temperature, salinity, insolation and air relative humidity. The collected specimens were transported in seawater to the Marine Biology Laboratory (LABMAR, UPE) and preserved in 10% saline formalin. The organisms were sorted, measured, and identified according to specialized literature and quantified. The data were organized into tables. Families that adopted limpet-shaped morphology demonstrate excellent adaptation to the environmental conditions of the intertidal region. The family Fissurellidae in the reef area of Gaibú Beach presents a diverse composition, with a predominance of the genera *Fissurella* and *Diodora*. Thirteen species were identified: *Fissurella itapema* (Ihering, 1927); *Fissurella nimbosa* (Linnaeus, 1758); *Fissurella barbadensis* (Gmelin, 1791); *Lottia subrugosa* (d'Orbigny, 1841); *Lottia abrolhosensis* (Petuch, 1979); *Diodora fluviana* (Dall, 1889); *Diodora sayi* (Dall, 1889); *Diodora dysoni* (Reeve, 1850); *Diodora listeri* (d'Orbigny, 1853); *Diodora cayenensis* (Lamarck, 1822); *Lucapina sowerbii* (Soweby, 1835); *Lucapina suffusa* (Reeve, 1850); *Lucapina aegis* (Reeve, 1850). A total of 153 individuals of *F. itapema* were collected, being considered constant with a 62% occurrence frequency and the characteristic species occurring throughout the transect, with greater abundance in the calm mode near the sandy beach (95 individuals). The other species are considered rare (F<10%) being absent in the rough mode, near the breaking waves. The microhabitats in the reef area offer, according to their physical characteristics, variable degrees of protection, demonstrated by the occurrence of species in specific locations. On emergent substrates, the distribution limits of the mollusks are determined by their tolerance to long periods of exposure. It is observed that most species are fixed on rocks in exposed situations and under stones and corals. Confirming studies conducted on biodiversity in the intertidal zone of Pernambuco, F. itapema remains as the characteristic species of the family Fissurellidae, while Lottia subrugosa, considered constant, showed a significant decrease in occurrence, with nine individuals recorded. Climate changes in the rainfall regime, sunlight, and relative humidity were determinants for the distribution of organisms in the study area and the trend for a decrease in species abundance when compared to previous studies. *F. itapema* demonstrated high ecological valence being predominant both in abundance and in distribution in the microhabitats and the frequency of the other species confirmed the studies in which they were considered rare.

Funding Source: PIBIC CNPq / UPE.

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BEYOND BEACHES AND RESORTS: MOLLUSCAN BIODIVERSITY AND SAMPLING GAPS IN CANCÚN, MÉXICO

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Keywords: marine, continental, urbanization, protected natural area, tourism.

Mollusks play a crucial role in aquatic and terrestrial ecosystems, yet their diversity in southeast México remains largely understudied compared to other regions of the country. Cancún, as an internationally recognized tourist hub, has undergone rapid urbanization and coastal development, which may significantly impact local molluscan biodiversity. This study aims to assess molluscan diversity across different habitats in Cancún, ranging from cenotes and tropical forest to urban and marine environments. Random sampling was conducted in coastal, freshwater, and urban terrestrial environments throughout Cancún. Specimens were directly observed or collected using timed direct sampling, sediment sieving, and quadrat sampling along transects at selected sites. Samples were processed partially in situ and in the laboratory, where taxonomic identification was performed using conchological characteristics and species accumulation curves, for the Protected Natural Área “Parque Kabah” was generated. Other specimens from the National Collection of Mollusks (CNMO) as well as online records for preserved specimens recorded in the Global Biodiversity Information Facility (GBIF), digital collections and cited in the literature were included in the study. More than 175 molluscan taxa were recorded across marine, freshwater, and terrestrial ecosystems. The recorded species belong to four classes: Bivalvia, Cephalopoda, Gastropoda and Polyplacophora. With 19 terrestrial superfamilies and 25 families, Cancún harbors the highest land snail diversity recorded in the state of Quintana Roo, and likely in the Yucatán Peninsula. Additionally, one species of the family Spiraxidae was identified for the first time outside its type locality, and a marine species of the family Zebinidae was recorded for the first time in the Mexican Caribbean. Despite human disturbances, some native species persist in urban green spaces, while new records of non-native and invasive species were recorded in several sites, posing potential ecological risks. This work provides valuable baseline data for biodiversity conservation in rapidly developing tourist destinations. It represents one of the first integrative studies of the malacofauna in the city, and the first for non-marine mollusks in Cancun's history, filling a critical knowledge gap in the region.

Funding Source: No.

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LIVING IN THE DISC: DISCOVERY OF EULIMID SNAILS ENDOPARASITIC IN OPHIUROIDS (CAENOGASTROPODA: VANIKOROIDEA)

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Keywords: Eulimidae, endoparasites, molecular phylogeny, Ophiuroidea.

Eulimid gastropods are parasites of all five extant classes of echinoderms: Asteroidea, Ophiuroidea, Echinoidea, Holothuroidea and Crinoidea. Temporary parasites, permanent ectoparasites and permanent endoparasites can individually occur in the five classes and hence the associations can be grouped into 15 different categories, all of which have been documented except for endoparasites in the Ophiuroidea. Here, we report for the first time on two endoparasitic eulimid species from ophiuroids. The first endoparasitic species (sp. A) was found from the amphiurid brittle star *Amphiura capensis*, inhabiting the intertidal zone of South Africa. Another species (sp. B) was recently captured from the gorgonocephalid basket star *Astroglymma sculptum* at a shallow subtidal site in Japan. Morphological observation was conducted under a stereomicroscope and a SEM; phylogenetic positions were assessed based on six gene sequences (nuclear 28S, 18S and H3, and mitochondrial 16S, 12S and COI) using Bayesian inference and maximum likelihood approaches. The two species exhibit different ecological traits in the disc of their hosts. The species A from South Africa lives in the bursa, a sac-like pouch on each side of the arms with genitorespiratory functions, while the Japanese sp. B forms a gall on the digestive gland. They also show conchological differences. The former is characterized by a tiny globose shell up to 1.8 mm in length and a brown brunt apex, while the latter bears a much larger (>5 mm) globose shell with a colorless, pointed or mucronate apex. The molecular phylogenetic reconstruction did not support a close affinity of the two species. Rather, they belonged to distant clades of ophiuroid parasites. The South African sp. A clustered with the temporary parasites of the genera *Pyramielloides*, *Eulima* and *Hemiliostraca*, while the Japanese sp. B with the temporary parasites and ectoparasites of *Fusceulimoides* and *Stilapex*. These results conform with the following, previously suggested trends: (1) closely related eulimids exploit hosts of the same echinoderm class, whereas (2) each host class is parasitized by more than one eulimid clade, which often exhibit independent evolutionary shifts to endoparasites. The radiation of eulimid gastropods has involved remarkable diversification into 15 categories (three types of parasitism and five classes of host echinoderms). The combination of endoparasitism in Ophiuroidea was the last of the 15 categories that had not been observed before, whereas the two new species seem to have independent origins of this mode of life. These findings further compliment the extraordinarily high ecological diversity of the family.

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TAXONOMY, MORPHOLOGY, AND DISTRIBUTION OF THE CHITONS (MOLLUSCA: POLYPLACOPHORA) COLLECTED BY THE BRAZILIAN ANTARCTIC EXPEDITIONS

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Keywords: Polyplacophora, Antarctica, morphology, taxonomy, distribution.

The Southern Ocean hosts a rich diversity of organisms, which have been intensively collected since the XIX century. When the scientific activities of the Brazilian Antarctic Program (PROANTAR) began, many mollusks were obtained from 1982 to 1988, triggering studies on the taxonomy and anatomy, mostly on bivalves; now, those of the Polyplacophora are under investigations, aiming to identify and describe its species, also recording their geographic and bathymetric distributions. In the Antarctic environment, the animals came from 10 bottom samples collected in the South Shetlands Islands; other three samples were from the Magellan Region. Initially, they were separated into morphotypes and for each individual the characteristics of the plates and girdle were examined under a stereomicroscope. Detailed photographs were taken using a coupled camera, illustrating the color and ornamentation of the plates and the arrangement of the girdle's spicules or scales. These and the radula were extracted from the soft parts to be observed more thoroughly by the Scanning Electron Microscopy (SEM). Data on depth and geographic position were compiled to plot the distribution of each species. Twenty-eight individuals were examined, 23 from the South Shetlands, and five from the Magellan Region. Four morphotypes were recognized and two of them could be further identified at the specific level: *Callochiton bouveti* Thiele, 1906 (Callochitonidae), that is the most abundant in the material (13 specimens), and *Nuttallochiton mirandus* (Thiele, 1906) (Mopaliidae), with nine individuals. The later exhibits distinctive features, including a sinuous ornamentation on the anterior margin of the cephalic plate and radial striations/riblets on the central areas of all the plates. Its girdle and plates have a predominantly pink coloration. It is known as being widely distributed in the Antarctic region; in the South Shetlands it was collected from 96 to 280 meters depth. *Callochiton bouveti* has plates with distinct lateral, pleural, and jugal areas, each one decorated with varied granules and vertical striations. This is also a characteristic Antarctic species; it was collected from 96 to 275 meters depth. The animals from the Magellan Region are larger, reaching up about 60 mm in length, appearing to be of *Plaxiphora aurata* (Spalowsky, 1795) (Mopaliidae). In the Southern Ocean, there are about 17 species of chitons, which belong to only six families; there, five species are known as being typically Antarctic, one of them *N. mirandus*. The present work contributes to a better illustration and characterization of these molluscs. The examined animals will be deposited in the Museum of Biological Diversity (MDBio) of UNICAMP, also improving its molluscan collection.

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A COMPARATIVE STUDY BETWEEN TWO SPECIES OF CAUDOFOVEATA (MOLLUSCA): DISCOVERING NEW ANATOMICAL PATTERNS THROUGH HISTOLOGY

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Keywords: Aplacophora, anatomy, malacology, histology, Brazil.

A rich diversity of Caudofoveata has been discovered in the southwestern Atlantic, with two species - *Falcidens australocaudatus* Passos et al., 2016 and *F. amiae* Passos et al., 2022 (Chaetodermatidae)- characterized as very distinct, the first bearing a long tail, the latter having a stoutish body without externally perceptible divisions. Here, they are compared through histology, aiming to verify if they have a correspondingly distinctiveness in their tissues and organs. After collection, the specimens were fixed in 4% formaldehyde and then preserved in 70% alcohol. They were dehydrated in an increasing series of ethanol and embedded in methyl methacrylate resin (Historesin®). A retraction microtome was used to obtain histological sections of 5 µm thickness; microtomization was performed through transversal planes in some specimens, and for others parassagittal and sagittal sections were obtained. These sections from a total of nine specimens of *F. australocaudatus* and ten of *F. amiae* were stained with toluidine blue. A microscope with a coupled a digital camera was used for observations and to take pictures of the best whole sections or of specific organs and structures. In both species, the body can be described as divided in three regions: an anterior, a median, and a posterior. The anterior region holds the ganglia, the buccal cavity, the esophagous, and the anterior part of the stomach; in *F. australocaudatus* this anterior region is separated from the medium region by a well-developed transverse septum (not visible in *F. amiae*). The median is divided in two parts in *F. australocaudatus*, the most anterior bearing the posterior part of the stomach, the digestive gland and the gonad, while the posterior region is tapered as a tail, that has a developed musculature, the gonoducts, and the intestine; in *F. amiae*, all these organs are spread throughout the length of the median region. The digestive gland in *F. amiae* is fused with the posterior part of the stomach, while in *F. australocaudatus* they are separated; in the former a gastric shield is not visible. A ventral, spacious blood sinus is present in the medium region in both species. The posterior region holds the pericardial cavity and its associated organs, and the pallial cavity with its pair of gills. The organs were observed and compared according to their component tissues. Some structures already described could also be confirmed, like the existence of two pairs of teeth in *F. amiae*, and one in *F. australocaudatus*; a complex radular musculature is observed in both species. Comparisons with other caudofoveate species is difficult, as these data are not available in such detail. The study revealed that the organs of *Falcidens australocaudatus* and *F. amiae* have a distinct distribution in the median region and different tissue organization, suggesting that the condition in *F. amiae* is derived, requiring future phylogenetic analyses. Chaetodermatidae is known for its morphological diversity and debated monophyly. This work demonstrates that the internal structure of Caudofoveata is not uniform, and may be useful in the taxonomy of the group.

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INTEGRATING TRADITIONAL AND GEOMETRIC MORPHOMETRICS TO RESOLVE *Donax* (BIVALVIA: DONACIDAE) TAXONOMY IN BRAZILIAN WATERS

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Keywords: Northeastern Brazil, new species, taxonomy.

The genus *Donax* comprises approximately 90 described bivalve species, four of which occur along the Brazilian coast. Specimens collected in Aracaju, Sergipe (northeastern Brazil), had previously been identified only to the genus level. In this study, we present the first taxonomic investigation of *Donax* species from the Sergipe coast and describe a new species, *Donax* sp. nov. We combined conchological analysis with geometric morphometrics to compare *Donax* sp. nov. with congeners, particularly *Donax gemmula* from southeastern Brazil, due to their morphological similarities. We distributed eight landmarks and 80 semilandmarks along the inner surface of the left valve and performed a Principal Component Analysis (PCA) to assess morphological variation. A Procrustes ANOVA tested for shape and size differences among populations, while a multivariate regression evaluated shape-size allometry. Finally, k-means clustering identified groups of specimens with similar morphologies, which were then compared to their original populations. Conchological analysis revealed two morphotypes along the Sergipe coast: one clearly identifiable as *D. gemmula* and a second, distinct form exhibiting significant morphological divergence from all known *Donax* species. The putative new species is characterized by a larger size, a lower height-length ratio, and a trapezoidal shape with a slightly concave ventral margin, contrasting with the smaller, more globose morphology of *D. gemmula*. Morphometric results statistically supported conchological findings. Procrustes ANOVA confirmed that species identity significantly influenced both shape and size ($p < 0.01$ and 0.005, respectively), explaining 2.85% of shape and 4.59% of size variation. Multivariate regression indicated allometry ($p < 0.0001$), with size accounting for 6.9% of shape variation. K-means clustering (silhouette score = 0.294) segregated most *Donax* sp. nov. specimens from two Sergipe populations, while grouping *D. gemmula* from the southeast with a third northeastern population. Our findings provide the second record of *D. gemmula* in northeastern Brazil, supporting its continuous distribution along the Brazilian coast. We successfully distinguish two *Donax* species in Sergipe, clarifying the distribution of *D. gemmula* and proposing a new species. These results significantly advance the understanding of *Donax* taxonomy and biogeography in Brazil.

Funding Source: No.

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FIRST PHYLOGENY OF THE FAMILY CEPOLIDAE: A CARIBBEAN GROUP OF ENDEMIC MOLLUSCS

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Keywords: taxonomy, systematics, Stylommatophora, Cuba, *Polymita*.

Molluscs are highly diverse, with over 120,000 described species. Among them, Helicoidea land snails, particularly the Cepolidae family, show taxonomic controversies. Cepolidae is most diverse in Cuba, hosting 10 of its 17 genera. Despite this, phylogenetic relationships remain unclear. This study aims to clarify Cepolidae taxonomy through integrative morphological and molecular analyses, generating genetic data for 14 genera for the first time and evaluating relationships within Helicoidea. This study conducted an integrative phylogenetic analysis of Cepolidae land snails using both morphological and molecular data. Morphological analysis included 39 species from 19 genera and 40 shell, jaw, radula, reproductive, and ecological characters. *Labyrinthus leprieurii* was selected as the outgroup. For molecular analysis, 51 specimens were sequenced for four genes (COI, 16S, 28S, H3). Phylogenies were reconstructed using maximum likelihood and Bayesian inference. Species delimitation was performed using ASAP. Cladistic analyses were conducted with TNT under various weighting schemes, and support was evaluated using jackknife resampling. This study addresses the systematics of the family Cepolidae, a highly diverse yet poorly studied group of terrestrial gastropods. Based on anatomical observations of 54 species and molecular data from 53 individuals representing 15 genera, the monophyly of the family is supported, although intergeneric relationships remain weakly resolved due to low branch support, largely attributed to degraded DNA from museum specimens. Notably, the genus *Suavita* is confirmed as part of Cepolidae, contradicting earlier placements in Sagdidae and Thysanophoridae. *Suavita* shares morphological synapomorphies such as the auxiliary copulatory organ and shell traits with *Setipellis* and *Jeanneretia*, suggesting close phylogenetic ties. The *Setipellis-Guladentia-Jeanneretia* clade shows clearer relationships, with *Setipellis* exhibiting reduced reproductive structures. Biogeographical data suggest that geographic isolation, especially in calcareous mountainous regions, has driven speciation in this group. In the Western Caribbean clade, *Dialeuca* shows unique reproductive reduction and is restricted to Jamaica. *Eurycampta*, while generally consistent, shows unexpected placement of *E. exdeflexa* with *Coryda*, suggesting homoplasy. The Eastern Caribbean clade includes genera such as *Plagioptycha*, *Polymita*, and *Euclastaria*, with evidence of cryptic species complexes (*Jeanneretia parraiana*, *Euclastaria euclasta*). Biogeographic divergence patterns are evident, often linked to topography and habitat specialization. Some taxa (*Cepolis*, *Coryda*) require further study due to limited molecular data. Overall, this study provides the first phylogenetic framework for Cepolidae, revealing biogeographic structuring driven by insular isolation and altitudinal gradients. However, further molecular work with broader taxon sampling and higher-quality DNA is essential to resolve remaining uncertainties. The family Cepolidae comprises 17 genera, now including *Suavita*, forming a monophyletic group characterized by shared reproductive traits. Despite limited sequencing success, sufficient molecular data enabled the first phylogeny, identifying three main clades. Low resolution in some branches reflects missing data from unsampled species. This study highlights the need to resolve the taxonomic homonymy with fishes to improve clarity and access to information across both unrelated animal groups.

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SEA GODDESSES IN DISGUISE: TWO NEW SPECIES OF CHROMODORIDIDAE (GASTROPODA, NUDIBRANCHIA) FROM NEW CALEDONIA, SOUTHWEST PACIFIC

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Keywords: integrative taxonomy, sea slugs, marine biodiversity, Southwest Pacific.

Chromodorididae nudibranchs are known for their vibrant coloration and soft, typically elongated bodies. With 397 described species, Chromodorididae is the most speciose family within Nudibranchia, but many species remain undescribed. In this study, we present molecular and morphological data for two new species of Chromodorididae from New Caledonia, in the Southwest Pacific Ocean. Unidentified chromodoridid specimens were collected in Koumac and Nouméa, 2018–2022, photographed, and preserved in 96% ethanol. Body length, mantle shape and color, rhinophore and gill shape, and internal morphology were analyzed and described. For molecular analysis, DNA was extracted from four specimens, and sequences of COI, 16S rRNA, and H3 were obtained. Sequences of additional species were downloaded from GenBank, including representatives of different chromodoridid genera such as *Chromodoris* (31), *Hypselodoris* (72), *Goniobranchus* (2), and *Dorisprismatica* (3), including their type species. Sequences were aligned using MAFFT. The evolutionary model and maximum likelihood trees were estimated with IQ-TREE based on the best partition scheme. Bayesian inference was performed using MrBayes. Phylogenetic trees based on concatenated COI, 16S rRNA, and H3 sequences placed the four sequenced specimens into two clades. Three specimens formed a new clade within the genus *Hypselodoris*, which also included '*Goniobranchus*' sp. 47 from French Polynesia. This clade is part of a larger group that includes *Hypselodoris lacuna* Gosliner & Johnson, 2018 from the Philippines, *Hypselodoris krakatoa* Gosliner & Johnson, 1999 from Madagascar, among other species. Externally, *Hypselodoris* sp. from New Caledonia is clearly distinct from all other species in the genus due to its cryptic beige coloration, including the rhinophores and gill, and its fibrous, reticulated mantle pattern. In smaller specimens, the mantle is less fibrous and features a dorsal white longitudinal line with blue spots. Internally, *Hypselodoris* sp. has the typical features of the genus, including unicuspid jaw rodlets, a radula with numerous teeth per row, bicuspid lateral teeth, and a reproductive system with a short vagina and a very small seminal receptacle. The other chromodorid specimen from New Caledonia formed a distinct clade within the genus *Chromodoris*. *Chromodoris* sp. exhibits a translucent yellowish mantle covered by a cream mesh with circular spots and a small red gill. Internally, the radula is very small, with a low number of teeth and an unusual multicuspid innermost lateral tooth. The prostate is well differentiated, and the seminal receptacle is as large as the bursa copulatrix. At first glance, *Hypselodoris* sp. and *Chromodoris* sp. do not resemble typical members of their genera. The discovery of a *Hypselodoris* species with a fibrous, cryptically colored mantle expands the characterization of the genus. Similarly, *Chromodoris* sp. possesses a unique radula, featuring a large, spoon-shaped first lateral tooth. These findings highlight the morphological plasticity within Chromodorididae, which can lead to misidentifications when relying solely on external and radular traits.

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REDESCRIPTION AND GEOGRAPHICAL DISTRIBUTION OF *Leiostracus vittatus* (SPIX, 1827) (GASTROPODA: STYLOMMATOPHORA: SIMPULOPSIDAE)

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Keywords: Bahia State, internal anatomy, land snails.

There is growing evidence that land snails' shells may be ineffective in distinguishing species, leading to underestimation of species diversity. Conversely, shell polymorphisms may lead to taxonomic inflation when differences in shell color patterns are interpreted as evidence of interspecific variation. In this sense, the search for additional operational criteria is essential to assess species limits, and consequently species diversity, for a great number of land snail taxa in Brazil. Herein, we present the first anatomical description of *Leiostracus vittatus*. The specimens analyzed were collected in the municipalities of Igrapiúna and Uruçuca, Southern Bahia, Brazil. For the anatomical study, adult specimens were dissected immersed in 70% ethanol, under a stereoscopic microscope, and the anatomical structures were drawn under a camera lucida. The specimens were deposited at the Prof. Maury Pinto de Oliveira Malacological Museum. A distribution map was constructed with QGIS 3.22.10, based on our original occurrence records and records available at the online biodiversity database iNaturalist. Taxonomic attribution in iNaturalist was verified by checking the correspondence of the shell traits of the specimens in the images with species diagnosis. Revisiting species known only by shells, with the aim of providing new diagnostic traits, is essential for the proper knowledge of the diversity of terrestrial gastropods in Brazil. Herein, we provided the first anatomical description of *L. vittatus*, offering new operational criteria for further *Leiostracus* species delimitation. The genital system of *L. vittatus* is characterized by ovotestis with three or four branches of enlarged digitiform acini. Albumen gland elongated. Spermoviduct, bursa copulatrix and penial complex with approximately the same length. Spermatheca well-differentiated. Bursa sac lying on the concave face of the spermoviduct. Prostate with tubular-acini, in the columellar surface of the spermoviduct. Penial complex long, club-shaped, penis with a sheath. Flagellum present. Genital atrium short. The pallial system is characterized by primary ureter along the rectal side of the kidney up to the top of the pallial cavity. Secondary ureter wide and slender, parallel along the left side of the rectum. Kidney elongated, triangular. Pericardial cavity on the left side of the kidney, at the columellar margin of the pallial cavity. Pulmonary vein oblique, converging to the pneumostome region along with the ureter and rectum. The available data in the literature on the geographic distribution of *L. vittatus* indicates its occurrence for the states of Bahia and Pernambuco. No information is available on specific occurrence localities. The specimens herein analyzed were collected at Igrapiúna and Uruçuca municipalities, Atlantic Forest, Southern Bahia. Additionally, we compiled occurrence records available in iNaturalist for the municipalities of Ibirapitanga, Itanagra, Jussari and Maraú (Bahia, Brazil). *Leiostracus vittatus* presents shell color polymorphism which may easily lead to taxonomic errors when the shell is the only source of information available for species determination. Future studies on the anatomy of additional specimens and color morphs will help elucidating intraspecific variability in shell and anatomical traits. Herein, we didn't find any records of the species for Pernambuco state, which may indicate the need for collection efforts at this locality.

Funding Source: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES).

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MORPHOLOGICAL AND ANATOMICAL REDESCRIPTION OF *Mendicula transversa* (PAYNE & J. A. ALLEN, 1991), A MINUTE BIVALVE OF THE SUBFAMILY AXINOPSIDINAE (THYASIRIDAE)

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Keywords: Thyasiridae, taxonomy, deep sea bivalves, *Mendicula transversa*.

The family Thyasiridae comprises deep-sea bivalves that remain poorly known in the southwestern Atlantic, especially those of the subfamily Axinopsidinae, that has species bearing shells with minute sizes (~1 mm in length) and few distinctive characteristics. The occurrence of one of these species – *Mendicula transversa* (Payne & J. A. Allen, 1991) – is here confirmed from the Brazilian coast, with a redescription of its shell and soft parts. The holotype deposited in the British Museum (Natural History) (No. 1990033) were analyzed and compared with samples more recently obtained in the Campos and Santos basins, southeastern Brazil, from depths of 75 to 416 meters. The conchological analysis was carried out through light and scanning electron microscopies (SEM). The chemical composition of concretions deposited on the outer surface of the valves was investigated by energy-dispersive spectroscopy (EDS). For the anatomical study, resin embedded specimens were microtomized and then observed by conventional histological techniques. The shell of the specimens from the Brazilian coast are small, thin, with a maximum length of 1,07 mm and height 0,85 mm; subequilateral, with beaks displaced posterior to midline, length greater than height; in the posterior surface, there is a marked submarginal sulcus forming a flat, descending postero-dorsal margin; the outer surface bears just a fine sculpture and the EDS analysis showed that its deposits are composed by mainly manganese (Mn), oxygen (O) and iron (Fe); the hinge plate is thin, having a triangular to oval shaped pseudotooth. The holotype is here illustrated for the first time and its features matches with those of the Brazilian specimens. The soft parts exhibit typical characters of thyasirids, such as the presence of an elongated foot and a visceral with lateral pouches; the gills bear only the inner demibranch, that is characteristic of axinopsidines, and their filaments have not elongated abfrontal surfaces, suggesting bacterial symbionts are lacking. *Mendicula transversa* is known as widely distributed in the Atlantic Ocean, from 508 to 5223 meters depth; here in Brazil it was found in samples from shallower waters. Its shape, longer than high and with a descending posterior flat margin, is characteristic of a species of *Mendicula*. The absence of irregular granules on the hinge, that are found on species of *Adontorhina*, prevents its transfer to this genus, as recently proposed. The Atlantic deep waters hold an interesting biodiversity, which is still little investigated regarding many groups of bivalves. Morphology and anatomy studies enable a more comprehensive understanding of the diagnostic taxonomic characteristics necessary for the identification and classification of a deep-sea species, such as *M. transversa*. In this way, the contribution of this study to the knowledge and conservation of deep-sea benthic fauna along the Brazilian coast is emphasized.

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FIRST MORPHOANATOMIC STUDY OF *Mycetopoda soleniformis* (ORBIGNY, 1835)

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Keywords: freshwater mussels, Mycetopodidae, anatomy, systematics.

Mycetopodidae is a family of freshwater mussels vastly spread through South America. *Mycetopoda soleniformis* is a representative of the family found mainly in the Amazon Basin. Only the anatomy of the soft parts in the mantle cavity is known. This work aims to study the internal morphoanatomy of the soft parts, especially the stomach and better understand diagnostic characters in the family. The valves were separated from the body with a stylus, used to detach the adductor muscles. With the help of stereomicroscope attached to camara lucida, the inhalant and exhalant openings were drawn. A small incision was made on the ligament between both openings, allowing the complete removal of the left mantle lobe and exposing the mantle cavity. An incision on the left side of the mouth was made with a scissor. The incision continually followed the extension and shape of the esophagus and stomach. A transversal cut on the posterior end of the dorsal hood was made until the whole esophagus and stomach roof could be opened like a lid. The inhalant opening is covered by tentacles with brownish ends, while the exhalant opening lacks tentacles, but the third fold of the mantle is corrugated. Only the internal fold of the mantle is involved in the fusion between the openings (type A mantle fusion). The external demibranchia present septa varying in length, alternating through thick and thin septa. There are around 19 filaments between septa. The labial palp is elongated, as is the whole body, but also high, semilunar in shape, different from the great length and small height of the palps in *Mycetopodella falcata*. The esophagus is very close to the adductor muscle, and positioned above it in a way that makes it hard to detach the muscle from the shell without damaging the structure of the esophagus. The stomach entrance is short compared to that of *Mycetopodella falcata* and narrow. The anterior fold rises considerably at the entrance of the stomach, where it is wrinkled, and then gradually rises to the stomach roof. The stomach floor is typical of Mycetopodidae, classified as type IV. Noteworthy is the great width of the stomach, resulting in a large dorsal hood. The anterior pouch is positioned in the middle of the stomach length and does not project anteriorly. Both pouches have oval depressions. The minor typhlosole is narrow. The overall morphology of the stomach resembles that of Mycetopoda legumen. The soft parts of *Mycetopoda soleniformis* assessed in the study show the general characteristics expected in Mycetopodidae. The results are the first morphoanatomic study of the soft parts of *Mycetopoda soleniformis*. The length of the labial palp compared to the branchia, the orientation and length of the esophagus, the depth of the anterior fold and width of the dorsal hood are some characters related to *M. legumen*, but differs from *M. falcata*. These might suggest characters of value in the generic diagnose of the subfamily Mycetopodinae.

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FRESHWATER MUSSELS IN PARAGUAY: EXPLORING A STILL LITTLE-KNOWN BIODIVERSITY

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Keywords: Bivalvia, Neotropical region, freshwater ecosystems, species rinchess, biogeography.

Paraguay is part of one of the most important hydrographic systems in South America (La Plata Basin). However, its freshwater mussel diversity (Unionida) remains poorly documented. The organisms play key ecological roles as water filters and bioindicators. This study aims to update the taxonomic and geographic knowledge of Paraguay's freshwater mussels, generating key information to support the development of effective strategies for their conservation and management. The review was conducted through the examination of specimens from national and foreign scientific collections, the compilation of bibliographic records, and the results of recent field campaigns. Species identification was based on morphological characteristics, following taxonomic references for Neotropical freshwater mussels. Occurrence records were analyzed geographically to assess distribution patterns, and taxonomic revisions were performed to validate species and genera, addressing historical classification challenges. Species belonging to the families Mycetopodidae Gray, 1870, Hyriidae Swainson, 1840, and Etheriidae Deshayes, 1838, were identified, comprising eight genera and 33 valid species for the country. The recorded genera include *Anodontites* (seven species), *Fossula* (one species), *Mycetopoda* (two species), *Monocondylaea* (four species), *Lamproscapha* (one species), *Leila* (two species), *Haasica* (one species), *Castalia* (two species), *Diplodon* (seven species), *Rhipidodonta* (five species), and *Bartlettia* (one species). Most occurrence records are concentrated in the Paraguay and Paraná rivers and tributaries, whereas large areas of the national territory, particularly minor tributaries, show limited sampling efforts. Taxonomic difficulties, especially within the genus *Diplodon*, hinders the reveal of the real diversity of freshwater mussels in Paraguay. The presence of invasive exotic species such as *Corbicula fluminea* and *Limnoperna fortunei*, and the habitat modification, pose additional challenges for understanding and conserving this group. This analysis highlights the urgent need to strengthen systematic research, expand sampling efforts in underexplored areas, and update taxonomic classifications through morphological and genetic studies. Improving taxonomic and geographic knowledge of Paraguay's freshwater mussels is essential for designing effective conservation strategies to safeguard aquatic biodiversity in the country.

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ISOLATED BEAUTY: NUDIBRANCH DIVERSITY FROM GOUGH ISLAND, SOUTH ATLANTIC OCEAN

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Keywords: Gastropoda, sea slugs, Nudibranchia, isolation, biogeography.

Gough Island, located in the South Atlantic Ocean approximately 2,700 km from Africa and 3,200 km from South America, is one of the most remote places on Earth. It has been the subject of few marine invertebrate surveys, and its nudibranch fauna is poorly documented, with only one species, *Tritoniopsis brucei* Eliot, 1905, recorded. This study conducts an integrative taxonomic assessment of Nudibranchia collected during the 2014 Darwin Plus expedition. Between January and February 2014, scuba dives were conducted at multiple sites around Gough Island, resulting in the collection and photography of 14 nudibranch specimens. DNA was extracted using a standard kit, amplified with traditional primers, and sequenced. Sequences were edited in Geneious R7, and mitochondrial genes COI and 16S were analyzed. Phylogenetic analyses using RAxML and MrBayes included additional sequences from GenBank and BOLD. Specimens were dissected under a stereomicroscope to examine mantle structures, rhinophores, and gills. Coloration was assessed from live photographs. Jaws and radulae were prepared for SEM, and reproductive systems were dissected and illustrated with a camera lucida. Based on external morphology, nine distinct morphotypes were preliminarily identified, belonging to the suborders Cladobranchia and Doridina. Phylogenetic analysis of concatenated COI and 16S genes revealed that one specimen, identified initially as *Myrella challengeriana* (Bergh, 1884) (Tritoniidae), did not cluster with any recognized genus. Instead, it formed a polytomy with *Myrella*, *Tritonia*, and *Candiella*. Morphologically, this specimen also differed from *Tritoniopsis brucei*, particularly in gill arrangement, coloration, and rhinophore shape. One specimen of *Kaloplocamus* clustered with an undescribed species from South Africa, while another, initially identified as *Holoplocamus papposus*, grouped within the *Limacia* genus but formed a distinct clade. Molecular data for *Holoplocamus* are not available in public databases. The comparison of radular morphology revealed similarities with *Limacia*, including a hook-shaped first lateral tooth and rectangular marginal teeth. The remaining six morphotypes are under analysis to confirm their identification. Nudibranch diversity on Gough Island is greater than previously recorded. Given the island's isolation, it is not surprising that its fauna can show biogeographic affinities with different regions of the South Atlantic, as exemplified by *Kaloplocamus* sp. Ongoing work includes the analysis of the remaining morphotypes with species delimitation analyses combining molecular and morphological data.

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FIRST ANATOMICAL CHARACTERIZATION OF *Comoropeas vulgare* (MORELET, 1888) AND *Comoropeas avenaceum* (MORELET, 1881) (ACHATINIDAE, PETRIOLINAE) FROM COMORO ISLANDS

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Keywords: Grande Comoro, Anjouan, reproductive system, pallial system, Subulinidae.

Achatinidae (ex Subulinidae) is a group of pantropical taxa for which there is little information on fundamental biological attributes, including anatomy, life history, and distribution. The last comprehensive revision for the set of genera previously recognized as Stenogyrinae, in the early 19th century, and later as Subulinidae, in the 1950s, was entirely based on shell characteristics and remains to this day the main reference for taxonomists working on this group. The malacological collection of the Muséum National d'Histoire Naturelle de Paris houses an impressive assemblage of Achatinidae snails from Comoro Islands, collected during recent years (2002 and 2009) and preserved in ethanol, allowing for the anatomical characterization of the species. Specimens of *C. vulgare* from Grande Comore (lot NG52: Grande Comore, Ntsimimnapanga lieu dit "Shihafune" Fôret semipervirante de montagne) and *C. avenaceum* from Anjoan (lot ND15: Comores, Anjouan. Valée de la Mro oua Bouénidouani) were dissected under a stereomicroscope equipped with camera lucida. The reproductive and pallial systems of both species were dissected immersed in ethanol and simultaneously drawn for anatomical characterization. The description of practically all species of Subulinidae (except for a few more recently described species) has been based only on shell characteristics. Nonetheless, this family is relatively well represented in museums and malacological collections. In this sense, the reexamination of the species, with the objective of expanding their descriptions, can be carried out through the analysis of wet material deposited in collections. Herein we revisited the species *C. avenaceum* and *C. vulgare* providing anatomical descriptions for both species. The anatomy of the reproductive system of *C. avenaceum* is characterized as follows: albumen gland elongated. Spermatheca complex well-defined, compact. Prostate long, occupying the external face of the spermoviduct. Bursa copulatrix round, lying at the transition between the spermoviduct and the free oviduct. Penial complex cylindrical, muscular, long, about the same length of the free-oviduct + vagina. Vas deferens enters the epiphallus terminally. Transition between epiphalus and phallus well-marked. Verge of the epiphallus-phallus transition round and wide. The reproductive system of *C. vulgare* is characterized as follows: albumen gland compact, rounded. Spermatheca complex well-defined, compact, sinuous. Prostate with large, rounded acini, occupying the columellar face of the spermoviduct. Bursa copulatrix rounded, exceptionally wide, lying at the transition between the spermoviduct and the free-oviduct. Penial complex cylindrical, muscular, long, about the same length as the free oviduct + vagina. Phallus constricted at the base. Vas deferens enters the epiphallus terminally. Transition between epiphalus and phallus well-marked. Verge of the epiphallus-phallus transition round and wide. Vagina long. Genital atrium short. Information on the anatomy of the soft parts of the species previously ascribed to Subulinidae (now Achatinidae) is scarce and mostly restricted to the type species of some genera. Most of ex-subulinid genera remains characterized by shell morphology. This is the case for *Comoropeas*, for which we provide the first anatomical characterization. Our results provide new operational criteria for *Comoropeas* species delimitation and for the differential diagnosis of the genus.

Funding Source: No.

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FIRST ANATOMICAL CHARACTERIZATION OF *Petriola simpularia* (MORELET, 1851) (ACHATINIDAE, PETRIOLINAE) FROM COMORO ISLANDS

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Keywords: reproductive system, taxonomic impediment, ovoviviparity, Subulinidae.

Achatinidae (ex-Subulinidae) is a taxonomically neglected group of pantropical snails. Almost all ex-subulinid species were described based on the shell morphology and remain characterized by a few conchological traits. Anatomical features are not generally used for species delimitation, despite the inefficiency of shell traits as operational criteria being demonstrated for several land snail taxa. The scarcity of revisions and taxonomists dedicated to this family makes taxonomic impediment a major problem. The malacological collection of the Muséum National d'Histoire Naturelle de Paris houses an impressive assemblage of Achatinidae snails from Comoro Islands, collected during recent years (2002 and 2009) and preserved in ethanol, allowing for the anatomical characterization of the species. Specimens of *Petriola simpularia* from Mayotte were dissected under a stereomicroscope equipped with camera lucida. The reproductive and pallial systems of the specimens were dissected immersed in ethanol and simultaneously drawn for anatomical characterization. Herein we revisited the species *P. simpularia*, providing an anatomical description of this species. The anatomy of the reproductive system of *P. simpularia* is characterized as follows: Albumen gland longer than wider. Prostate with large, rounded acini, occupying the proximal portion of the spermoviduct, near the transition between the spermoviduct and the free oviduct. Bursa copulatrix round, lying at the transition between the spermoviduct and the free oviduct. Bursa copulatrix duct very long. Penial complex cylindrical, muscular, shorter than the free oviduct. Vagina short. Flagellum absent. Vas deferens enters the epiphallus terminally. Transition between epiphalus and phallus well-marked. Distal portion of the phllus round. Pallus constricted at the base. During the anatomical dissections, we observed the presence of free embryos (without eggshells) inside the spermoviduct, evidencing that *P. simpularia* is an ovoviviparous species. Information on anatomy is available for about 3.6 % of ex-subulinid species. Considering the wide body of evidence that the shell characteristics of terrestrial gastropods may be insufficient as characters for species distinction, it is likely that the diversity of achatinid (ex-subulinid) species is underestimated. Thus, studies that propose integrative methodologies for the delimitation of species are needed.

Funding Source: No.

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MORPHOLOGICAL VARIATION IN *Spirula spirula* SHELL SHAPE

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Keywords: Cephalopoda, morphology, *Spirula*, natural history collections.

Spirula spirula is a small mesopelagic cephalopod with an internal, chambered, calcareous shell. Shells vary in the diameter of the shell whorl and the tightness of coiling. Past research has demonstrated variation in overall shell shape, but whether this variation is due to population differences, species differences, or sexual dimorphism remains unknown. Multiple species of *Spriula* have been described, but molecular data suggests a single species with a worldwide distribution. Whole animals are rarely encountered or collected, but their shells are commonly found on beaches and in natural science collections. We used undamaged dry shells from the Mollusk collection at the Delaware Museum of Nature and Science to test for differences in shell shape in specimens collected from the North Atlantic and the South Pacific Oceans. We used both landmark-based geometric morphology and traditional morphometrics on a polar coordinate system to analyze specimens with a similar number of total segments and a fully intact first segment to confidently set repeatable landmarks. Preliminary results based on specimens collected from the east coast of Florida, USA show that most useable shells had between 28 – 33 chambers, and that shells with only minimal damage at the origin could be used for these analyses. In addition, the distance between the whorls at the free end of the shell is variable. Variation at this location may indicate differences in overall growth rate, sexual dimorphism, or simply natural within-population variation. Analysis of larger specimens from around the world indicates that the whorl diameter stops increasing in shells with >40 chambers. This change may indicate the onset of maturity or end of life. A more complete understanding of within-population variation in overall shell shape and coiling is necessary before shell morphology can be used as a species-level indicator. Natural history collections provide opportunities for basic research that would otherwise be difficult to conduct.

Funding Source: No.

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ANALYSIS OF THE POTENTIAL OF MOLECULAR MARKERS IN THE DIFFERENTIATION AND RECONSTRUCTION OF EVOLUTIONARY RELATIONSHIPS OF SPECIES IN THE GENUS *Biomphalaria* PRESTON, 1910

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Keywords: *Biomphalaria*, relationships, coi, ITS.

The genus *Biomphalaria* includes intermediate hosts of *Schistosoma mansoni*. Morphological characteristics alone do not always allow for the differentiation of cryptic species, posing challenges to taxonomic identification and highlighting the importance of complementary molecular methodologies. This study aims to evaluate genetic divergence of the *Biomphalaria* using coi and ITS1 markers, and to delimit Operational Taxonomic Units (OTUs), with the goal of identifying potential cryptic species and distinct genetic lineages. A database was constructed using public sequences obtained from GenBank, as well as DNA from snails in the collection of the Medical Malacology Collection at Fiocruz-MG (CMM-Fiocruz) and the Museum of Southwestern Biology (UNM). Partial regions of the coi gene and the ITS1 spacer region were amplified and sequenced. The sequences were aligned using the MAFFT program, and phylogenetic relationships were reconstructed through maximum likelihood and Bayesian inference. Approximately 7.0% of the analyzed coi sequences suggest the need for taxonomic revision based on the integration of morphological, molecular (PCR/RFLP), and phylogenetic data. Specimens as *B. straminea* and *B. kuhniana* from the CMM-Fiocruz, as well as *B. sudanica* and *B. choanomphala* from the UNM collection, exhibited incongruent groupings with their original identifications. Phylogenetic analyses formed well-supported clusters for most species, except for the cryptic pairs *B. choanomphala*/*B. sudanica*, *B. straminea*/*B. kuhniana*, *B. cousini*/*B. amazonica*, and *B. peregrina*/*B. oligoza*. Some of these clusters align with previous findings in the literature, which have pointed out not only morphological limitations in distinguishing between these species but also the existence of extremely similar morphology in certain pairs, such as *B. straminea* and *B. kuhniana*, which can be virtually indistinguishable based solely on internal organ morphology. Additionally, our analyses reinforce the hypothesis that African species of *Biomphalaria* are closely related to *B. glabrata*, corroborating the theory that an ancestral form resembling *B. glabrata* colonized Africa. This affinity is evidenced by both the relative positioning of these species in the reconstructed phylogenies and the low diversity observed among African species compared to their Neotropical counterparts. Our data support the hypothesis that *B. glabrata* is more closely related to African species than to those from Latin America. The presence of cryptic species within the genus emphasizes the importance of integrative approaches for accurate identification. The next steps, we intend to sequence the ITS2 marker and conduct genomic analyses via RAD-seq to enhance taxonomic resolution and obtaining a more thorough understanding of the evolutionary processes this genus.

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TAXONOMIC BONANZA OF NEW *Bothriembryon* (MOLLUSCA: BOTHRIEMBRYONTIDAE) LAND SNAIL SPECIES IN A GLOBAL BIODIVERSITY HOTSPOT SHAPED BY ARIDIFICATION

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Keywords: endemism, native fauna, biogeography, cryptic species, *Bothriembryon*.

The Australian land snail genus *Bothriembryon* Pilsbry,1894 is largely confined to the south-west corner of Western Australia. Fifty-seven extant and eight fossil *Bothriembryon* species are currently recognised. A comprehensive phylogenetic analysis was recently undertaken to reconstruct the relationships of the group using mitochondrial and nuclear DNA sequences. The work revealed numerous putatively new species clades. Funding was made available through BHP Social Investment Fund to describe up to thirty species through rapid taxonomical methodologies. All the genetically identified phylogenetic clades were tagged to existing taxonomic types. Ten clades without types, unknown taxa, we examined in detail morphologically and geographically to ascertain probability of novelty. Each taxon accepted as new was imaged in multiple aspects in with a Canon 6D, mounted in a remote controlled WeMacro focus stacker via Helicon Remote and acquired into Helicon Focus for focus stacking. Images were then mounted as plates in Adobe Photoshop and or sized in ImageJ software. The species were mapped in Qgis mapping software and holotypes flagged in the map. We describe a total of ten new species, three from the Geraldton Sandplains (GES), one from the Jarrah Forrest (JAF), two from the Avon Wheatbelt (AVW), three from Coolgardie (COO) and one from the Malee (MAL) IBRA (Interim Biogeographic Regionalisation for Australia) bioregions. All species are presented with full illustrations of their shells in five angles of the teleoconch and with detailed imaging of the protoconch. A standardised measurement schedule is presented and discussed to formalise good measurement protocols that have been too loosely defined in the past. The measurements of all species are presented and compared in diagnosis. A genetic diagnosis is presented based on genetic uniqueness. This first 1/3rd of the total undescribed species identified in the phylogenetic papers has laid the foundation for the next twenty species description over the next couple of years. A comprehensive phylogenetic analysis of the genus *Bothriembryon* has revealed numerous novel clades. Thirty clades were identified that offered potential for being described. Recently funding became available to described them. The first alpha taxonomic paper describing ten new *Bothriembryon* species from Western Australian is in final preparation for submission with full illustrations of the shells, maps as well as morphological and genetical diagnoses.

Funding Source: BHP Social Investment Fund.

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MOLECULAR PHYLOGENY AND POPULATION GENETIC STRUCTURE OF MANILA CLAM *Ruditapes philippinarum*

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Keywords: genetic structure, *Ruditapes philippinarum*.

Manila (Asari) clam *Ruditapes philippinarum* is a commercially important bivalve species primarily distributed in East Asia. However, in Japan, due to a decline in catches since the 1980s, individuals from China and Korea were introduced anthropogenically. The genetic characteristics of this species are assumed to be complex due to the interplay between natural and anthropogenic dispersal. This study conducted genetic analysis to evaluate the population genetic structure of *R. philippinarum*. Samples included individuals from Japan, as well as from China, South Korea, France, and the United Kingdom. Samples from Japan were collected from 36 locations, while those from South Korea and France were obtained from 2 locations each, and samples from China and the United Kingdom were obtained from 1 location each. A total of 312 samples, including outgroup individuals, were used for the analysis. Genetic analysis was performed using RAD-seq, and phylogenetic and STRUCTURE analyses were conducted based on the SNPs obtained. This species was genetically divided into two major groups: the Japan group and the China-Korea group. In the Japanese archipelago, it was observed that populations belonging to the Japan group are widely distributed throughout northeastern Japan, particularly along the Pacific coasts of Hokkaido and the Tohoku region. These areas are characterized by having little to no documented history of anthropogenic introductions of *R. philippinarum*, suggesting that the genetic structure may reflect the native distribution. In contrast, in other regions where long-term and repeated anthropogenic introductions have taken place, individuals classified as belonging to the China-Korea group, as well as individuals likely to represent hybrids between the China-Korea and Japan groups, were found to be widely and frequently distributed. The existence of two dispersal routes may have facilitated the genetic differentiation of this species. In Japan, where *R. philippinarum* has been experiencing a marked decline, it will be necessary to promote the resource management and conservation of the "Japan group" populations, which possess unique genetic characteristics adapted to the Japanese environment, in order to sustain the species' population.

Funding Source: No.

Workshop

TAXONOMIC CATALOG OF THE BRAZILIAN FAUNA (TCBF): UPDATING NON-NATIVE AND INVASIVE MOLLUSCS IN BRAZIL

Coordinator:

FABRIZIO MARCONDES MACHADO – Universidade Estadual de Campinas, Brazil

Created in 2015 by a team of over 500 zoologists, the TCBF is a bilingual, open-access government platform (http://fauna.jbrj.gov.br) that allows specialists from various metazoan groups to perform real-time taxonomic updates. Specifically for Mollusca, more than 50 taxonomists are currently responsible for compiling the list of mollusk species in Brazil. Recently, around 6,000 updates were made to the platform, with 3,634 species listed for the Brazilian territory – for the first time, it was possible to provide a tangible answer to one of the most basic questions in Brazilian malacology: how many species of Mollusca are there in Brazil? Now, this cohesive group of malacologists will focus on developing the first comprehensive checklist of all potential exotic and invasive mollusks within the national territory. Following this important meeting (GT), a manuscript will be prepared to make these new findings available to the scientific community.

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