

IOCTX
2025
Conference

The 1st International Online Conference on Taxonomy

3–4 December 2025 | Online

Program and Abstract Book

Organizers



taxonomy

Media Partners



diversity



animals



THE (BIO) DIVERSITY PROJECT



sciforum.net/event/IOCTX2025
ioctx2025@mdpi.com

The 1st International Online Conference on Taxonomy

3–4 December 2025 | Online



Organizing Committee

Conference Chair

Prof. Dr. Mathias Harzhauser

Session Chairs

Dr. Matthias Sipiczki

Dr. Saraj Bahadur

PD Dr. Davit Vasilyan

Scientific Committee

Dr. Edgar Lehr

Dr. Francisco Luis Franco

Dr. Lara Sciscio

Dr. Salomé Fernandes Pinheiro de Almeida

Dr. Slađana Popović

Dr. Stefano Martellos

Dr. Thomas Neubauer

Dr. Xin-Cun Wang

Assoc. Prof. Xiong Xiong

Prof. Jay Richard Stauffer

Prof. Maurizio Biondi

Organised by



Conference Secretariat

Email: ioctx2025@mdpi.com

Table of Contents

Welcome from the Chair	1
Keynote Speakers.....	3
Invited Speakers	4
Program at a Glance	5
IOCTX 2025 Program.....	6
Session 1. Advances in Molecular Systematics	9
Session 2. Microbial Taxonomy.....	15
Session 3. Animal Taxonomy	22
Session 4. Plant Taxonomy	82
Session 5. "Paleotaxonomy".....	108

Welcome from the Chair

Dear colleagues,

It is a pleasure to announce the **1st International Online Conference on Taxonomy (IOCTX 2025)**, proudly organized by the MDPI open-access journal *Taxonomy*. The IOCTX2025 will be held online from 3–4 December 2025. In line with our commitment to fostering collaboration and knowledge exchange, this electronic conference provides a unique platform for researchers to showcase their work, discuss groundbreaking findings, and engage in meaningful conversations with fellow experts.

Conference Overview: This will be a virtual conference held at sciforum.net, a platform developed by MDPI to organize and provide technical support for electronic conferences. The virtual format offers the distinct advantage of eliminating the need for travel and its associated expenses, allowing you to fully immerse yourself in the conference without any logistical constraints.

Key Themes - Sessions of the conference will be organized around the following topics:

- Advances in Molecular Systematics;
- Microbial Taxonomy;
- Animal Taxonomy;
- Plant Taxonomy;
- "Paleotaxonomy".

Conference Format: our conference will exclusively accept abstract submissions. Upon acceptance, we will notify you before the conference via a separate email regarding whether there will be the opportunity to be the selected speaker to give an oral presentation. In addition, we strongly encourage all authors to upload and display their posters on the conference website, enabling attendees to share their insights and feedback with other participants through the Comments Section provided at the bottom of each page.

Free of Charge Participation: we are pleased to inform you that participation in this conference is entirely free of charge for both authors and attendees.

Awards and Opportunities: participants who win the best oral presentation award or best poster award will receive a prize of CHF 200, along with an offer to publish an extended paper, free of charge, in the Special Issue of *Taxonomy*.

We encourage you to explore the conference platform and guidelines provided in advance for a seamless experience. Should you have any queries or require assistance, our dedicated support team is available to ensure your participation is smooth and rewarding.

I hope you will join this e-conference to exchange ideas, begin fruitful collaborations, and make the IOCTX2025 a great success.



Prof. Dr. Mathias Harzhauser
Conference Chair

Geological-Paleontological
Department, Natural History
Museum Vienna, Burgring 7,
1010 Vienna, Austria



taxonomy

an Open Access Journal by MDPI

Taxonomy (ISSN 2673-6500) is an international and interdisciplinary open access journal. It publishes original research articles, review articles, and communications that cover the conception, naming, and classification of groups of organisms, including but not limited to animals, plants, viruses, and microorganisms. It particularly emphasizes the importance and multidisciplinary significance of taxonomy, with contributions which address the implications of all fields for taxonomy, or which improve our understanding of all fields through taxonomic knowledge, especially in relation to the nature, origins, and conservation of biodiversity, at all taxonomic levels.

There is no restriction on the maximum length of the papers. Our aim is to encourage scientists and research groups to publish experimental and theoretical results of research in as much detail as possible. Full experimental details and/or study methods must be provided for research articles so that the results can be reproduced.

Impact Factor: 1.5 (2024); **5-Year Impact Factor:** 1.4 (2024)

Keynote Speakers



Dr. Thomas Neubauer

Bavarian State Collection for Palaeontology and Geology, Munich, Germany

Thomas Neubauer is a conservator for fossil invertebrates at the Bavarian State Collection for Palaeontology and Geology in Munich. He has been Privatdozent at the Ludwig-Maximilians-Universität in Munich since 2024, and he is a member of the Steering Committee of the World Register of Marine Species. His research primarily centers around fossil freshwater mollusks, their evolution, biodiversity, biogeography, paleoecology, taxonomy, and systematics. His current project focuses on developing a novel machine-learning approach to combine extant and fossil data for a unified species delimitation. <https://bspg.snsb.de/sektion-mitarbeiter/thomas-alan-neubauer/?lang=en>.



Prof. Dr. Frank E. Zachos

Natural History Museum Vienna, Burgring 7, 1010 Vienna, Austria, Department of Genetics, University of the Free State, Bloemfontein, South Africa

I studied biology, philosophy and history of science and received my PhD for an evolutionary thesis on roe deer in 2005; in 2009, I got my habilitation for zoology and evolutionary biology, and since 2011 I have been head of the mammal collection at the Natural History Museum Vienna in Austria. Since 2019, I have also been an affiliated professor with the Department of Genetics at the University of the Free State in Bloemfontein, South Africa. I am particularly interested in biodiversity, evolution, systematics and conservation of mammals and birds as well as in history and philosophy of biology, in particular theoretical aspects of taxonomy and the species problem. More information: https://www.nhm.at/en/frank_emmanuel_zachos Photographer: Minitta Kandlbauer.

Invited Speakers



Dr. Lara Sciscio

JURASSICA Museum, Route de Fontenais 21, 2900 Porrentruy, Switzerland, Department of Geosciences, University of Fribourg, Chemin du musée 6, 1700 Fribourg, Switzerland



Prof. Dr. Mushtaq Ahmad

Department of Plant Sciences, Faculty of Biological Sciences, Quaid-i-Azam University (QAU), Islamabad, Pakistan



Prof. Dr. REN Ming-Xun

Hainan University and Hainan Institute of National Park, China, Director of the International Joint Center for Terrestrial Biodiversity around South China Sea of Hainan Province, Haikou, China

Program at a Glance

	Day 1	Day 2
Morning	Session 4. Plant Taxonomy Session 1. Advances in Molecular Systematics*	Session 3. Animal Taxonomy (Part 1)
Afternoon	Session 5. "Paleotaxonomy"	Session 3. Animal Taxonomy (Part 2) Session 2. Microbial Taxonomy

IOCTX 2025 Program

3 December 2025 (Wednesday)

Session 4. Plant Taxonomy Session 1. Advances in Molecular Systematics

Time: 9:00 (CET, Basel) | 3:00 (EST, New York) | 16:00 (CST Asia, Beijing)

CEST Time	Speaker	Title
9:00-9:10	Opening Remark from Conference Chair Prof. Dr. Mathias Harzhauser	
9:10-9:20	Welcome from the Session Chair Dr. Saraj Bahadur	
9:20-9:40	Prof. Dr. REN Ming-Xun Invited Speaker	Karst flora of Hainan Island, China
9:40-10:00	Prof. Dr. Mushtaq Ahmad Invited Speaker	Asian Flora and the Himalayan Biodiversity Hotspot: Integrating Modern Taxonomy with Interdisciplinary Science
10:00-10:15	Mian Muhammad Ahmed Oral Speaker	Integrative Taxonomy of Wild Citrus Germplasm: Linking Molecular and Morphological Evidence to Stress Tolerance
10:15-10:30	Mariette Jackson Oral Speaker	The systematics of <i>Nemesia</i> Vent. (Scrophulariaceae): The current status and New Insights
10:30-10:45	Opeyemi Muideen Mudasiru Oral Speaker	Taxonomic Insights into Nigerian Terminaliinae (Combretaceae) Based on Molecular and Morphological Evidence: Implications for generic circumscription
10:45-10:50	SHIWA CHAUBEY Flash Poster Presenter	Taxonomic Complexity and Ecological Adaptability of <i>Lantana camara</i> L. in India: A Morphological and Molecular Approach
10:50-10:55	Fateme Salmaniabeiat Flash Poster Presenter	Morpho-anatomical taxonomic delimitation of <i>Astragalus bruguieri</i> and <i>A. baba-alliar</i> subsp. <i>Nudicarpus</i>
10:55-11:00	Farzaneh Jafari Flash Poster Presenter	How to classify a species-rich genus
11:00-11:05	Thinhinan Khedim Flash Poster Presenter	Uncovering karyotype and phylogenetic diversity within the North African <i>Allium</i> subgenus <i>Amerallium</i> Traub. Insights on taxonomy and evolution.
11:05-11:10	Khansae Kamal Flash Poster Presenter	First Record of Stranded Holopelagic Sargassum Morphotypes and Associated Fauna on the Moroccan Atlantic Coast
11:10-11:15	RAJENDRA YONZONE Flash Poster Presenter	<i>Cleisostoma linearilobulatum</i> (Seidenfaden & Smitinand) Garay (Orchidaceae): a new record for West Bengal, India
11:15-11:20	Nina Machado Suzigan Flash Poster Presenter	Exploring Knowledge Shortfalls on Legumes in the Tocantins-Araguaia Basin
11:20-11:35	João Carmo Oral Speaker	Two new species of <i>Hexasepalum</i> (Spermacoceae, Rubiaceae) from the "campo rupestre" of Brazil
11:35-11:50	Hattos de Freitas Gomes Oral Speaker	Fabaceae in the Morro do Macaco Environmental Protection Area (EPA), Iporá, Goiás, Brazil

Session 5. "Paleotaxonomy"

Time: 14:00 (CET, Basel) | 8:00 (EST, New York) | 21:00 (CST Asia, Beijing)

CEST Time	Speaker	Title
14:00-14:10	Welcome from the Session Chair Dr. Davit Vasilyan	
14:10-14:40	Dr. Thomas Neubauer Keynote Speaker	Taxonomy in the 21st century: Machine-learning paves the way to bridging paleontology and biology
14:40-15:00	Dr. Lara Sciscio Invited Speaker	Tetrapod Ichnotaxonomy: Preservation, practice, and meaning
15:00-15:15	Diana Osipova Oral Speaker	Hidden species diversity of micro-gastropods from the Late Pleistocene deposits in Taiwan

15:15-15:30	Antonios Isidoros Avrithis Oral Speaker	The plant-insect interactions in a newly discovered Middle Miocene locality in Kos island, Greece
15:30-15:45	Dimitrios Protopapas Oral Speaker	New Paleontological Evidence on <i>Theodoxus micans</i> (Gaudry & Fischer, 1867) from the Megara Basin: A Potential Correlation with the Extant Species <i>Theodoxus meridionalis</i> (R. A. Philippi, 1836)
15:45-16:00	Christos Psarras Oral Speaker	Clearing the Taxonomic Mist: New insights into Neogene Conidae diversity through UV imaging of type specimens
16:00-16:15	Vincenzo Gesualdi Oral Speaker	Revisiting <i>Megalosauripus transjuranicus</i> : new ichnotaxonomical insights from the Plagne tracksite (Tithonian, France) and implications for Late-Jurassic theropod ichnotaxonomy
16:15-16:30	Marcos Vinícius Coelho Oral Speaker	Revisiting the fossil polypterid † <i>Polypterus faraou</i> : taxonomic assessment based on cranial morphology
16:30-16:45	Evangelos Vlachos Oral Speaker	Nomenclature is the scientific language of Taxonomy, and you already know everything about it
16:45-17:00	Paul S Mayer Oral Speaker	Using New Technologies to Classify the Pennsylvanian (307 Million Years Old) Problematic Fossil, <i>Tullimonstrum gregarium</i>
17:00-17:05	Jonathan P. Miller Flash Poster Presenter	Uncovering hidden diversity in Iberian freshwater fossil snails: an integrative approach to <i>Horatia schlosseri</i> (Royo-Gómez, 1922) (Gastropoda: Hydrobiidae)
17:05-17:10	Michael Steenhuyse-Vandevelde Flash Poster Presenter	The morphology, phylogeny, and applications of Oligocene–Miocene <i>Asterigerinoides</i> (Foraminifera)
17:10-17:15	Ingrid M. Veiga Flash Poster Presenter	Taxonomic paleodiversity of the Marizal Formation (Aptian), Tucano Basin (NE Brazil)
17:15-17:20	Eduardo I. Faúndez Flash Poster Presenter	The female of the first Cretaceous velvet water bug <i>Archaeohebrus alius</i> Zhang, Ren & Yao 2024 (Heteroptera: Hebridae)
17:20-17:25	Thales Rodrigues Jardim Barreto Flash Poster Presenter	Taxonomical Review of †Ichthyodectiformes–Actinopterygii, Teleostei—from Cretaceous Period in Brazil
17:25-17:30	Clarice Assumpção Flash Poster Presenter	Taxonomic Review and Anatomical Analysis of Chondrichthyes from the Paraíba–Pernambuco Basin: Itamaracá, Gramame, and Maria Farinha Formations
17:30-17:35	Steven E. Jasinski Flash Poster Presenter	Re-evaluation of the taxonomy of <i>Compsemys</i> : an enigmatic turtle from around the Cretaceous–Paleogene boundary

4 December 2025 (Thursday)

Session 3. Animal Taxonomy (Part 1)

Time: 9:30 (CET, Basel) | 3:30 (EST, New York) | 16:30 (CST Asia, Beijing)

CEST Time	Speaker	Title
9:30-9:40	Welcome from the Conference Chair Prof. Dr. Mathias Harzhauser	
9:40-10:10	Prof. Dr. Frank E. Zachos Keynote Speaker	Of Species and Mountains – Grey areas in taxonomy, how they matter, and why they're here to stay
10:10-10:25	Austin Horenkamp Oral Speaker	Diversity of the squid family Brachioteuthidae in Aotearoa New Zealand and the Southern Ocean
10:25-10:40	Najmudeen Mohamed Theparambil Oral Speaker	Molecular evidence for mislabelling and taxonomic redundancy in public records of COI sequences of the genus <i>Lethrinus</i> (Teleostei: Lethrinidae)
10:40-10:55	M Carmen Cobo Oral Speaker	Integrative Taxonomy as a foundation for understanding host relationships in Solenogastres
10:55-11:10	Marlies Monnens Oral Speaker	Phylogenetic relationships of a new schizorhynch genus refute the monophyly of <i>Schizochilus</i> Boaden, 1963 (Platyhelminthes, Rhabdocoela)
11:10-11:25	Ana Ramos Oral Speaker	Twenty years of taxonomic and ecological research on African marine benthos

11:25-11:30	Rasoul Karamiani Flash Poster Presenter	Taxonomic Synopsis of the Slender Racer Snake Genus <i>Platyceps</i> Blyth, 1860 (Reptilia: Colubridae), from Iran
11:30-11:35	Onika Mabalabala Flash Poster Presenter	Genetic diversity, phylogenetic relationships, and systematics of the species-rich <i>Adeonella</i> genus from two bays along the southern coast of South Africa.
11:35-11:40	Fanny Sieler Flash Poster Presenter	Integrating 3D-imaging with multi-locus phylogenetic analysis to update the diversity of the aegisthid genus <i>Pontostratiotes</i> Brady, 1883 (Copepoda: Harpacticoida)
11:40-11:45	Lais de Mattos Flash Poster Presenter	<i>Apterotonotus albifrons</i> (Otophysi: Gymnotiformes): limitations of pigmentation patterns for the taxonomy of a species complex.
11:45-11:50	Noelia Veronica Guzman Flash Poster Presenter	Exploring Machine Learning for Species Delimitation in the <i>Trimerotropis pallidipennis</i> Complex (Orthoptera: Acrididae)
11:50-11:55	João Victor Couto Flash Poster Presenter	AN INTEGRATIVE ANALYSIS TO RESOLVE TAXONOMIC DEADLOCKS IN ERGASILID COPEPODS IN THE PLANET

Session 3. Animal Taxonomy (Part 2)

Session 2. Microbial Taxonomy

Time: 14:00 (CET, Basel) | 8:00 (EST, New York) | 21:00 (CST Asia, Beijing)

CEST Time	Speaker	Title
14:00-14:15	Júlio César do Carmo Vaz Santos Oral Speaker	Adaptive shifts and diversification of <i>Ferricixius</i> planthoppers in Brazilian caves (Hemiptera: Cixiidae)
14:15-14:30	Maria Eduarda Almeida dos Santos Oral Speaker	Diversity of Calcinea (Porifera, Calcarea) from Heron Island, Great Barrier Reef, Australia: New species and wide distributions
14:30-14:45	Lorena Ailán-Choke Oral Speaker	Integrative taxonomic assessment of <i>Cruzia</i> sp. (Nematoda: Cosmocercoidea, Kathliniidae) from the Argentine black and white tegu lizard: insights into the long-standing Kathliniidae taxonomic puzzle
14:45-15:00	Enrico Lopes Breviglieri Oral Speaker	Phenotypic and vocal differentiation among subspecies of <i>Piculus flavigula</i> (Aves, Picidae) suggest a major taxonomic reassessment
15:00-15:15	Vanessa Yepes-Narvaez Oral Speaker	The taxonomic robustness and complementarity of eDNA metabarcoding provide an effective fish biodiversity assessment in the offshore Colombian Eastern Tropical Pacific
15:15-15:25	Welcome from the Session Chair <i>Dr. Matthias Sipiczki</i>	
15:25-15:40	Farzad Aliramaji Oral Speaker	Unveiling Hidden Diversity: A New <i>Laimaphelenchus</i> Species from Elm Bark in Northern Iran
15:40-15:55	Natalia Bojanić Oral Speaker	Integrated morphometric and DNA metabarcoding assessment of ciliate biodiversity in the Adriatic Sea
15:55-16:10	Ayixon Sánchez-Reyes Oral Speaker	GenoScanner: Rapid Genome-Based Taxonomic Classification Using Phylogenetic Species Concept
16:10-16:15	Ana Milićević Flash Poster Presenter	Unveiling Cyanobacterial Diversity from Serbian Thermal Springs: Molecular Insights
16:15-16:20	Vanessa Vaz Leonel Flash Poster Presenter	Taxonomic characterization of lineages of the genus <i>Ganoderma</i> with emphasis on morphological and molecular analysis
16:20-16:30	Closing Remark from Conference Chair <i>Prof. Dr. Mathias Harzhauser</i>	

Session 1. Advances in Molecular Systematics

sciforum-143367: Taxonomic robustness and complementarity of eDNA metabarcoding provides an effective fish biodiversity assessment in the offshore Colombian Eastern Tropical Pacific

Vanessa Yepes-Narvaez ¹, Joan Lagos-Moreno ², Alejandro Rodríguez-Sánchez ¹, Luis Chasqui-Velasco ¹ and David Alonso-Carvajal ¹

¹ Biodiversity and Ecosystems Program, Marine and Coastal Research Institute - INVEMAR, Santa Marta 470001, Colombia

² Faculty of Sciences, Pontificia Universidad Javeriana, Bogotá 110231, Colombia

Over the last decade, environmental DNA (eDNA) has emerged as a non-invasive and effective tool for characterizing species from water, soil or air samples. The increasing interest in offshore and deep-sea explorations in Colombian oceans, has required the implementation of new technology to improve sampling efforts and data quality in those hard-to access areas.

In this study, we present the promising complementarity of eDNA-metabarcoding in providing accurate taxonomic delimitations fish obtained on board several scientific expeditions along the Colombian Pacific. We filtered 360L of seawater in each 34 sampling stations through 0.2µm capsule filters using peristaltic pumps. Seawater was collected during day and night shifts using oceanographic rosettes in vertical transects (200 to 10m depth). eDNA was preserved and analyzed using 12S-V5 mitochondrial region, followed by high-throughput sequencing. Assignment of molecular operational taxonomic units (MOTUs) were made using OBITools as well as curated reference libraries that included regional voucher sequences.

Results yielded over 20 million DNA sequences, translated into 320 fish ASVs from 71 families, 59 genera and 84 species, most of which were migratory, demersal, meso- and bathypelagic taxa. Families with the greatest species richness belonged to Teleostei families such as Myctophidae, Nomeidae, Scombridae, Coryphaenidae and Istiophoridae. Regarding Elasmobranchii, the most conspicuous families were Carcharhinidae, Alopiidae, Myliobatidae and Rhincodontidae. It is important to mention that another 100 MOTUS could not be identified to species level due to lack of genetic reference databases available in the region.

These results were compared to historical data of fishing activities in the past 20 years, demonstrating that eDNA could match over 90% of the known fish biodiversity surveys in offshore areas while reducing sampling effort and costs. Further research should focus on improving genetic databases and on the implementation of eDNA tools as an alternative that should be embedded in routine monitoring programs.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142629: DNA barcoding of the rare ant *Oxyopomyrmex krueperi* (Hymenoptera: Formicidae) using cox1 marker

Vera Antonova and Stela Lazarova

Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, 2 Yuriy Gagarin Str, 1113 Sofia, Bulgaria

DNA barcode data support species identification, aid in local fauna inventories, and inform the management of protected areas and monitoring of invasive species. As part of the InBuiLT project ("Invertebrate Fauna of Bulgaria and Adjacent Regions – DNA-based Barcoding of Under-represented in Reference Libraries Taxa"), materials from several underrepresented invertebrate groups from Bulgaria and neighboring countries were collected and provided for sequencing. Among the sampled taxa, several rare ant species from Bulgaria were also collected and barcoded. One of them is *Oxyopomyrmex krueperi* Forel, 1911. It is a rare, thermophilous ant species distributed in arid grasslands of north-eastern part of the Mediterranean Basin and the Near East. It is a reported species for Bulgarian myrmecofauna from a single locality near the town of Tzarevo. Here, we present the first DNA barcodes (COI-5P region) for the species, based on four worker ants hand collected in different colonies along the southern Black Sea Coast of Bulgaria near the town of Primorsko. Images, metadata and four DNA sequences (658 bp) were provided the Barcode of Life Data System (BOLD). Bioinformatics analysis retreated three distantly related *Oxyopomyrmex* spp. with approximately 90% identity, confirming the genetic distinctiveness of the species. The phylogenetic relationships based on DNA barcodes with the currently available closest species are discussed. These findings represent the first global molecular record for *O. krueperi* and expand the known range of the genus. The data provide a valuable reference for future taxonomic and phylogenetic studies on Myrmicinae ants from arid and semi-arid regions.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142262: Tetrigidae of Ethiopia: first DNA barcoding and description of three new species

Tarekegn Fite ^{1,2}, Hendrik Devriese ³, Dustin Kulanek ¹, Josip Skejo ⁴, Niko Kasalo ⁵ and Martin Husemann ¹

¹ Staatliches Museum für Naturkunde Karlsruhe, Erbprinzenstraße 13, 76133 Karlsruhe, Germany

² School of Plant Sciences, College of Agriculture and Environmental Sciences, Haramaya University, Haramaya, Oromiya, Ethiopia

³ Royal Belgian Institute of Natural Sciences, Rue Vautier 31, 1040 Brussels, Belgium

⁴ Faculty of Science, University of Zagreb, Department of Biology, Evolution Lab, 10 000 Zagreb, Croatia

⁵ Ruđer Bošković Institute, Division of Molecular Biology, Laboratory of Evolutionary Genetics, Bijenička cesta 54, HR-10000 Zagreb, Croatia

Tetrigidae is a caeliferan family of Orthoptera constituting a diverse and relatively ancient lineage of small Orthopterans, which have their highest diversity in tropical and subtropical areas. However, so far no studies have been conducted on the identification and description of Tetrigidae species in Ethiopia, and even less molecular data is available. Hence, we performed the first DNA barcoding study of species belonging to the genera *Paratettix*, *Leptacrydium*, *Dasyleurotettix*, and *Morphopoides* from Ethiopia. We provide 35 new sequences of the COI gene belonging to six species of these genera. We show that Ethiopian Tetrigidae can be successfully identified using DNA barcodes, even in cryptic genera such as *Paratettix*: species delimitation based on this gene was strongly congruent with the morphological assignments. We report the three species *Dasyleurotettix infaustus* (Walker, 1871), *Morphopoides tessmanni* Günther, 1939, and *M. folipes* (Hancock, 1908) from Ethiopia for the first time. In addition, we describe three new species, which are confirmed both with morphological and genetic data: *Paratettix tanai* **sp. nov.**, *Paratettix geminus* **sp. nov.**, and *Leptacrydium naqamteensis* **sp. nov.** *Paratettix macrostenus* is considered a new synonym of *P. subpustulatus*. Future integrative taxonomic studies, including more material from diverse regions and more comprehensive taxon sampling, need to be performed to understand the diversity of Tetrigidae across Africa.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-136012: Taxonomic relationships within Lake Baikal deep-water scavenger amphipods of the genus *Ommatogammarus* revisited with molecular methods

Polina Drozdova, Ekaterina Telnes and Maxim Timofeyev

Institute of Biology, Irkutsk State University, Irkutsk 664025, Russia

Introduction

Groups of closely related species are often sources of uncertainty in taxonomy. Lake Baikal amphipods (Crustacea: Amphipoda: Gammaroidea) are a perfect example. They comprise over 350 morphological species and subspecies, two conflicting taxonomies and no comprehensive identification key. Here, we concentrate on conflicting views on the composition of the scavenger amphipods of the genus *Ommatogammarus sensu* Takhteew and try to resolve the conflict with molecular data.

Methods

We sequenced the standard barcode sequence, mitochondrial cytochrome c oxidase subunit I 5' fragment, as well as 18S rRNA gene fragment as an additional barcode, in representatives of all subspecies. Three of them were analyzed for the first time. In addition, we performed low coverage whole-genome sequencing for the three most abundant species and assembled full mitochondrial genomes for *Ommatogammarus flavus*, *Ommatogammarus albinus* and *Ommatogammarus carneolus melanophthalmus* to obtain a time-calibrated phylogeny of the genus.

Results

The obtained phylogenies show that the last common ancestor of all species existed about 6 million years ago, and *O. flavus sensu* Takhteew (= *Abludogammarus flavus sensu* Kamaltynov) was the first to split from the rest of the species. Four *O. carneolus* subspecies *sensu* Takhteew (= three *Pretiositus* species + *Eulimnogammarus hyacinthinus* according to Kamaltynov) were close but formed two clusters of related sequences instead of four, while the sequences of 18S fragments were identical between these clusters.

Conclusions

The genus *Ommatogammarus sensu* Takhteew contains at least three clearly separated species. The relationship within *O. carneolus* containing two lineages needs further investigation, but at the moment we do not have conclusive evidence to recommend splitting this species complex. Importantly, the reassignment of *O. hyacinthinus* to the genus *Eulimnogammarus* is not supported by molecular data.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146913: The systematics of *Nemesia* Vent. (Scrophulariaceae): The current status and New Insights

Mariette Jackson ¹, Hanlie Grobler ¹, Goitseone Sedimo ², Pieter Bester ² and Lize Joubert ¹

¹ Department of Plant Sciences (Botany), Faculty of Natural and Agricultural Sciences, University of the Free State, Bloemfontein, Post Office box 339, Bloemfontein 9300, South Africa

² Foundational Research and Services Division, South African National Biodiversity Institute (SANBI), Pretoria, Private Bag X101, Silverton 0184, South Africa

The genus *Nemesia* Vent. (Scrophulariaceae) comprises about 77 species, the majority of which are endemic to South Africa. *Nemesia* has garnered significant horticultural interest due to its diverse floral shapes, vibrant colours and ease of hybridization and cultivation. The genus was last revised in 1904 by Hiern and the only molecular phylogeny for *Nemesia* was published in 2008 by Datson and others. Datson et al. grouped the 23 included species into five clades highlighting evolutionary relationships and adaptive traits. Their ancestral state reconstruction suggested that multiple transitions occurred between a perennial life history in species occurring in the summer rainfall areas to an annual life form in species adapting to winter rainfall or seasonally dry conditions in the Cape Floristic Region and parts of the Karoo. It was hypothesised that *Nemesia*'s diversification may have been driven by climate change in the Cape Region during the Miocene and Pliocene. Our research aimed to generate a more comprehensive phylogeny incorporating as many *Nemesia* species as possible, to deepen our understanding of the genus's evolutionary history. The Bayesian Inference and Maximum Likelihood phylogenies were generated from gene regions *ITS*, *ETS* and *trnL*-intron, representing 48 species. The phylogeny is divided into two main clades, with five subclades each showing a clear geographic structuring, reflecting adaptations to distinct rainfall regimes. In this paper we discuss the phylogeographic and morphological patterns within the clades and highlight relationships of newly discovered taxa, offering fresh insights into *Nemesia*'s diversification.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

Session 2. Microbial Taxonomy

sciforum-143285: Taxonomic characterization of lineages of the genus *Ganoderma* with emphasis on morphological and molecular analysis

Vanessa Vaz Leonel ¹, Mariana Machado Fidelis Nascimento ² and Juliana Vitoria Messias Bittencourt ²

¹ Graduate Program in Biotechnology, Campus Ponta Grossa, Federal University of Technology – Paraná (UTFPR), Ponta Grossa, Paraná 84017-220, Brazil

² Department of Bioprocess and Biotechnology Engineering, Campus Ponta Grossa, Graduate Program in Biotechnology, Federal University of Technology – Paraná (UTFPR), Ponta Grossa, Paraná 84017-220, Brazil

The genus *Ganoderma*, belonging to the family *Ganodermataceae*, comprises a group of basidiomycete fungi with wide geographic distribution and scientific interest. Despite its ecological relevance and biotechnological potential, its taxonomy remains complex due to high morphological variability among species, influenced by environmental and nutritional factors that directly affect phenotypic characteristics. This study aimed to perform morphological and molecular characterization of eight fungal isolates of *Ganoderma* to support taxonomic identification and provide insights into their phylogenetic relationships. The eight isolates evaluated were cultured in PDA medium, morphologically characterized, and subjected to microscopic observation of hyphal structures. Mycelial growth was evaluated in different media (MEA, PDA, and SDA) and temperatures (18°C, 28°C, and 38°C) to understand the isolates physiological behavior. Subsequently, genomic DNA extraction was performed, according to the protocol by Vicente et al. (2008) and sequencing of the ITS region of ribosomal DNA, used as a marker for molecular fungi identification. Microscopically, all strains presented the trimitic hyphal system, formed by generative, skeletal, and ligative hyphae. These structures, together with colony macromorphology, confirmed generic identity. However, species-level identification was only possible through molecular analysis, which revealed four strains of *G. lucidum*, one of *G. sessile*, one of *G. lingzhi*, and one with ambiguous identity between *G. resinaceum* and *G. sessile*. Physiological analysis showed that medium composition directly influenced development, with some combinations promoting mycelial expansion. The temperature of 28°C favored mycelial growth in most isolates, especially *G. lucidum* and *G. lingzhi*, indicating species-specific physiological profiles. These variations reveal the specific physiological profile of each species. These data show that the traditional approach, based on morphology, is limited in delimiting *Ganoderma* species. The integration of microscopic characteristics, and molecular data, is essential to ensure accurate identification.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-145693: GenoScanner: Rapid Genome-Based Taxonomic Classification Using Phylophenetic Species Concept

Ayixon Sánchez-Reyes^{1,2} and Karel Estrada¹

¹ Department of Molecular Microbiology, Institute of Biotechnology, National Autonomous University of Mexico, Cuernavaca, Morelos 62210, Mexico

² Office of Support for Community Consolidation, Secretariat of Science, Humanities, Technology and Innovation, Mexico 03940, Mexico

Introduction: Accurate and rapid taxonomic classification of microbial genomes is fundamental for microbiology, epidemiology, and biodiversity monitoring. Existing bioinformatic pipelines often require large computational resources and multiple manual steps. **Objective:** We developed GenoScanner, a shell-based, high-speed, and hypothesis-driven pipeline to classify microbial genomes within minutes, integrating genomic analysis, phylogenetic inference, and molecular speciation testing under the Phylophenetic Species Concept. **Methods:** The pipeline compares a query genome against a curated genomic database (nomenclaturally valid genomes), to identify the closest phylogenetic neighbors. Subsequent Average Nucleotide Identity (ANI) estimation and robust phylogenetic reconstruction with JolyTree; provide the basis for Bayesian species delimitation testing using Poisson Tree Processes Models (bPTP default or mPTP optional). This software relies on well-established bioinformatic tools such as NCBI Entrez Direct, BLAST+, and Biopython, among others. The rationale of GenoScanner explicitly evaluates three hypotheses to achieve better taxonomic resolution: 1. Genomic Coherence –via mutational distances and nucleotide identity; 2. Phylogenetic Monophyly – through rapid full-genome tree estimation 3. Molecular Speciation – under probabilistic PTP models. **Results & Advantages:** The proposed framework enables rapid genome classification within minutes, significantly accelerating taxonomic workflows. By integrating genome-based phenetic data like ANI and Mash distance, phylogenomic analysis, and speciation-level evidence, it enhances the resolution and reliability of species assignments. Species delimitation is performed with robust accuracy using the PTP models, and full reproducibility is ensured through a standardized genomic databases. The approach is particularly effective for classifying bacteria, fungi, algae, and protists that are well represented in genomic repositories. These features collectively support diverse applications in molecular systematics, epidemiological monitoring, and biodiversity assessment. **Conclusion:** GenoScanner provides an efficient, reproducible, and conceptually robust framework for genome-based microbial taxonomy. By combining speed, accuracy, and formal species delimitation testing, it serves as a practical tool for both research and surveillance applications. **Availability:** <https://github.com/ayixon/genomescanner>.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142831: Integrated morphometric and DNA metabarcoding assessment of ciliate biodiversity in the Adriatic Sea

Natalia Bojanić, Valjbone Rama Thür, Blanka Milić Roje, Sanda Skejić, Olja Vidjak and Tija Damjanović

Institute of Oceanography and Fisheries, Šetalište I. Meštrovića 63, 21000 Split, Croatia

Ciliates are ecologically important microeukaryotes that transfer energy, remineralise nutrients and regulate microbial communities. Their sensitivity to environmental changes makes them reliable bioindicators of the state of marine ecosystems. Although their taxonomy and ecology are well documented, conventional monitoring methods often overlook cryptic and rare species. Integrative approaches combining morphological and molecular techniques are therefore essential to capture the full spectrum of ciliate diversity. In this study a dual taxonomic approach was used to assess the composition of the ciliate community at a coastal site in the central Adriatic Sea (BioPlan project). Water samples were collected using a Niskin bottle and a 53 µm plankton net. Bulk DNA was extracted by high-throughput sequencing of the nuclear 18S rRNA gene (V4 and V9 regions), in parallel with morphometric identification under a light microscope. The comparative analysis revealed a much better taxonomic resolution of tintinnids by microscopy, suggesting that morphometric identification remains a crucial tool for the detection of ecologically important species in the marine environment. Tintinnid genera such as *Rhabdonella*, *Xystonella*, *Dadayiella*, *Favella* and *Epiplocylis* were confirmed exclusively by microscopic observation. Conversely, metabarcoding proved to be more effective in detecting non-tintinnid ciliates, such as *Spirotontonia*, *Pseudotontonia*, *Bergeriella ovata* (V4), *Metaurostylopsis* and *Mesodinium rubrum* (V9), which were not present in morphological analyses. These discrepancies between approaches likely reflect the limitations of the reference databases, low genetic divergence in the target regions, and potential DNA degradation, particularly in net samples. Our results highlight the limitations of metabarcoding when applied independently and support the use of integrated morpho-molecular protocols in protist biodiversity studies. They also emphasise the importance of expanding curated sequence databases. Understanding the fine taxonomic structure and ecological dynamics of ciliate communities is critical for monitoring ecosystem health and predicting ecological responses to environmental change in marine ecosystems.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-138332: Morpho-Anatomical and Molecular Characterization of Macrofungi from Northern Pakistan: New Insights from Galyat Forests

Laiba Noor

Institute of Botany, University of the Punjab, Lahore

Macrofungi play a significant role in forest ecosystems as decomposers, symbionts and indicators of ecological health, yet their diversity remains understudied in many regions of Pakistan. This study presents a taxonomic investigation of macrofungi collected from Galyat, Khyber Pakhtunkhwa, during the rainy season of August 2023. A total of 12 species, belonging to seven genera and seven families, were identified based on morphological, anatomical and molecular analyses. Among these, two species belong to the phylum Ascomycota, while the remaining ten are classified under Basidiomycota. The identified families include Helvellaceae, Bondarzewiaceae, Cantharellaceae, Geastraceae, Inocybaceae, Mycenaceae, and Thelephoraceae, with Inocybaceae being the most diverse (five species), followed by Helvellaceae (two species). Notably, *Helvella asciatica* and *Xeromphalina cystidiosa* appear to be previously undescribed, while ten species have prior records, including *Cantharellus ravus*, *Geastrum fimbriatum*, *Helvella zhongtiaoensis*, *Heterobasidion linzhiense*, *Inocybe bhurbanensis*, *I. longistipitata*, *I. nitidiuscula*, *I. swatica*, *Pseudosperma quercinum*, and *Thelephora iqbalii*. Morphological descriptions, along with Maximum Likelihood phylogenetic analysis, support the taxonomic placement of selected species. This study enhances the understanding of fungal diversity in Khyber Pakhtunkhwa, Pakistan, and contributes to the taxonomic knowledge of macrofungal species in the region. Understanding fungal diversity is essential for conservation efforts and sustainable ecosystem management, aligning with SDG 15: Life on Land.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147171: Unveiling Cyanobacterial Diversity from Serbian Thermal Springs: Molecular Insights

Ana Milićević ¹, Olga Jakovljević ² and Slađana Popović ²

¹ University of Belgrade, Faculty of Biology, Department of Algology and Mycology, Institute of Botany and Botanical Garden "Jevremovac"

² University of Belgrade, Faculty of Biology, Institute of Botany and Botanical Garden "Jevremovac", Takovska 43, Belgrade, Serbia

Thermal springs represent extreme ecological niches characterized by elevated temperatures and mineral-rich waters, shaping highly specialized microbial communities. Cyanobacteria, as primary producers in these habitats, exhibit remarkable adaptations, yet their diversity and phylogenetic relationships in Serbian geothermal systems remain poorly documented. In this study, we applied a molecular systematics approach based on 16S rRNA gene sequencing to characterize cyanobacterial assemblages from five thermomineral springs in Serbia. Field sampling was conducted during October and November, and all strains were subsequently isolated and cultivated in BG11 medium for several months to ensure stability and purity prior to molecular analysis. The molecular analyses also facilitated the confirmation of morphological identification. *Leptolyngbya* sp. (WUC607) was detected in Niška Banja (38–39 °C), while *Leptolyngbya* sp. (CALU1715) was found in Lopatnica (≈29 °C) and Šarbanovac (30 °C). *Wilmottia* sp. (CCNU0051) was identified in Brestovačka Banja (35 °C). In Vranjska Banja (surface 93 °C), both *Nodosilinea* sp. (PGN35) and *Anabaena variabilis* ("Vasse River Type 3") were found. This study provides molecular characterization of cyanobacterial communities from Serbian thermal springs, enriching a knowledge in thermophilic microorganisms and potentially discovery of new species. The findings emphasize the value of molecular systematics for better understanding evolutionary adaptations to thermomineral environments. Moreover, these thermophilic lineages represent potential candidates for further research on thermal tolerance mechanisms and potential biotechnological applications, such as bioactive compound production.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142922: Unveiling Hidden Diversity: A New *Laimaphelenchus* Species from Elm Bark in Northern Iran

Mohammad Mohammadzamani ¹, Farzad Aliramaji ¹, Abdolhosein Taheri ¹, Kamran Rahnama ¹ and Ebrahim Shokoohi ²

¹ Department of Plant Protection, Faculty of Plant Production, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

² Department of Biochemistry, Microbiology and Biotechnology, University of Limpopo, Private Bag X1106, Sovenga 0727, South Africa

This study aimed to investigate the diversity of nematodes exhibiting various feeding strategies—including fungivorous, bacterivorous, predatory, and insect-associated forms—particularly those linked with bark beetles and Dutch elm disease. Between 2021 and 2023, eighty samples of dried elm bark and associated beetles were collected from Golestan Forest Park, Iran. Nematodes were extracted, fixed, and mounted on permanent microscope slides for morphological examination. Identification was based on morphological and morphometric analyses using standard keys, original species descriptions, and, where needed, molecular data. Fourteen species from ten genera belonging to the superfamilies *Aphelenchoidea* and *Sphaerularioidea* were identified. Among them, one population of *Laimaphelenchus* sp. exhibited a unique combination of morphological characters not found in any previously described species and is therefore proposed as a new species. Key diagnostic features include a body length of 336–446 µm, stylet length of 7–8.5 µm, three lateral lines, an elongated rectangular spermatheca containing sperm, absence of a vulval flap, and a posterior uterine sac measuring 3–4 times the vulval body width. The semi-cylindrical tail terminates in a flat disc with a stalk-like extension bearing four branched tubercles, each ending in a saucer-like structure with fringed, finger-like appendages. Males are present and possess spicules with a short, straight condylus and a blunt-tipped conical rostrum. The combination of these features places the species near *L. patulus*, *L. australis*, *L. phloesini*, and *L. vescus*, but distinct morphological differences support its recognition as a novel taxon within the genus *Laimaphelenchus*.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

Session 3. Animal Taxonomy

***sciforum-143515: Apteronotus albifrons* (Otophysi: Gymnotiformes): limitations of pigmentation patterns for the taxonomy of a species complex**

Lais de Mattos ¹, Marcos Vinícius Coelho ¹, Diogo de Mayrinck ² and Paulo M. Brito ¹

¹ Department of Zoology, Rio de Janeiro State University, Rio de Janeiro 20550-900, Brazil

² Department of Science and Biology Education, Rio de Janeiro State University, Rio de Janeiro 20550-900, Brazil

The Neotropical electric fish *Apteronotus albifrons* is part of a species complex whose synapomorphy is the presence of two clear bands encircling the caudal region throughout their development. These species are very similar, differing mainly in subtle variations in body pigmentation. *A. albifrons* can be recognized by the absence of dark spots on the first clear band and an evenly dark body color. Although its taxonomic validity had not been questioned since its description, until nowadays there is no designated type material for *A. albifrons sensu stricto*, nor a proper diagnosis. We examined specimens previously identified as *A. albifrons* from various ichthyological collections from Brazilian universities. Each specimen was measured, photographed, and assessed with a focus on pigmentation patterns for comparison with other species, such as *Apteronotus caudimaculosus*. Morphological differences were observed among the specimens. However, what drew particular attention was the presence of dark spots on the first clear band in some individuals. Variation in the number and size of the spots was observed among these specimens, even among those collected from the same locality. This variability appears to be unrelated to either body size or geographic distribution. These results suggest that the main characters currently used to distinguish species within this complex may not be as discontinuous as previously thought. Since other studies have identified genetic differences between *A. albifrons sensu stricto* and *A. caudimaculosus*, they are probably distinct taxa whose morphology remains incompletely detailed. Further data are needed beyond pigmentation patterns – such as osteological data – to better understand these issues involving *A. albifrons sensu stricto* and its species complex.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143318: Morphological and genetic variation in *Iguanodectes spilurus* and *I. purusi* (Characiformes, Iguanodectidae) from the Amazon Basin

Luís Ricardo Ribeiro Silva ¹, Lais Reia ¹, Débora Diniz Bezerra ² and Claudio Oliveira ¹

¹ Department of Structural and Functional Biology, Institute of Biosciences, São Paulo State University (UNESP), Botucatu, SP 18618-689, Brazil

² Department of Biological Sciences (DCB), State University of Southwest Bahia (UESB), Jequié, BA 45208-091, Brazil

The family Iguanodectidae comprises small characiform fishes widely distributed across the Amazon Basin, yet species boundaries within some taxa remain poorly understood. In this study, we analyzed specimens of *Iguanodectes purusi*, collected from the Purus River, and *I. spilurus*, from different localities including the Madeira River (Aveiro). Phylogenetic analyses based on molecular markers recovered *I. purusi* nested within the *I. spilurus* (sensu stricto) clade, with extremely low genetic divergence between them (0.005 ± 0.005). Morphological analyses revealed strong similarities between the two taxa, including a complete lateral line with 60–64 perforated scales, eight scales between the lateral line and the dorsal-fin origin, five scales between the lateral line and the pelvic fin, and an anal fin with 32–34 branched rays. General coloration is light, with a silvery stripe along the midline of the body and a dark blotch on the upper caudal-fin lobe. *I. spilurus* is the only species of the genus recorded in the main channel of the Madeira River, whereas the other congeners were found exclusively in terra firme streams. Despite these similarities, *I. purusi* exhibits subtle differences, such as a higher number of predorsal scales (≥ 27 in *I. purusi* vs. ≤ 26 in *I. spilurus*) and more perforated scales on the lateral line (> 65 in *I. purusi* vs. 60–64 in *I. spilurus*). However, these differences may represent geographic (clinal) variation among populations distributed across the Amazon Basin rather than valid species-level differentiation. Our findings highlight the need for taxonomic revisions integrating molecular, morphological, and ecological data to clarify the status of *I. purusi* and to better understand diversity patterns within Iguanodectidae.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143565: Dental Morphology and Taxonomic Assessment of Key Serrasalminae Genera (Actinopterygii: Teleostei: Characiformes)

João Cauzzo Paiva Magalhães, Lais Henriques de Mattos and Paulo Marques Machado Brito

Zoology Department, State University of Rio de Janeiro, Rio de Janeiro 20550-013, Brazil

The family Serrasalminae, which is exclusively Neotropical freshwater Characiformes, comprises 18 South American genera with 105 described species. Most of this species is represented in the fossil record, with one species now extinct. Reviewing the teeth morphology of this family is of great relevance, given the recurrent use of dental morphology in taxonomic classification and in identifying fossil teeth within the family's extinct forms. The goal of this study was to review the dental morphology and taxonomy of the main current representatives of this family. The specimens analyzed are in the ichthyological collection of the State University of Rio de Janeiro (UERJ). The specimens studied (*Metynnis fasciatus* Ahl 1931, *Metynnis guaporensis* Eigenmann 1915, *Myloplus arnoldi* Ahl 1936, and *Pygocentrus nattereri* Kner 1858) were identified using bibliographic references, dissected, and their skeletons prepared using dermestid beetles. The dentary and premaxillary bones were then extracted for detailed analysis. The teeth of *Myloplus arnoldi* and *Metynnis* are molariform, with slightly elevated and convex crowns, asymmetrical cusps, external ones larger and darker (brown) than internal ones (white), broad roots, laterally long and deeply anchored in the dentary, and a wide, smooth surface. These analyses allowed us to identify differences in the heterodonty patterns between the two genera. *Pygocentrus nattereri*'s teeth are caniniform, with long, flat, high crowns, sharp serrated edges, broad conical roots tightly set into the dentary, and a smooth, triangular, whitish surface. In conclusion, this study deepens the discussion on the relationship between dental morphology and taxonomic classification of this family, along with its fossil identification. The data from this study will contribute to a better understanding of morphological-taxonomic relationships, offering a more categorized view of the Serrasalminae dental morphological traits.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143449: COI-Based Phylogenetic Analysis Uncovers Cryptic Speciation and Misidentification in the Genus *Dermogenys* (Teleostei: Zenarchopteridae)

Toji Thomas ^{1,2}, E M Abdussamad ¹ and Badarul Sijad ¹

¹ Finfish Fisheries Division, ICAR- CMFRI (Central Marine Fisheries Research Institute), Kochi- 682018, Kerala, India

² Department of Biosciences, Mangalore University, Mangalagangothri- 574199, Karnataka, India

Introduction

The family Zenarchopteridae, comprising freshwater and brackish water halfbeaks, is restricted to Asia and Oceania and includes five genera: *Dermogenys*, *Hemirhamphodon*, *Nomorhamphus*, *Tondanichthys*, and *Zenarchopterus*. Of the 64 valid species, over half were described after 1950, reflecting considerable taxonomic complexity. The genus *Dermogenys* contains 13 species found in freshwater habitats across South and Southeast Asia. Despite this diversity, molecular studies are limited and indicate the presence of cryptic speciation. This study explores the barcode library for Zenarchopteridae, demonstrates the efficacy of DNA barcoding techniques for differentiating *Dermogenys* species, and the potential thereof in species discovery

Methods

In this study, mitochondrial Cytochrome Oxidase subunit I (COI) gene sequences obtained from publicly available databases were analysed to evaluate species-level diversity and phylogenetic relationships within *Dermogenys*. Maximum Likelihood analysis for reconstructing the phylogenetic tree and mean genetic distances were calculated using MEGA X.

Results

The resulting phylogenetic tree uncovered significant incongruence between morphological identification and genetic clustering. A total of 29 distinct clades were recovered, with *D. siamensis* and *D. collettei* each displaying six different genetic lineages; *D. bispina* and *D. pusilla* showing three; *D. sumatrana* having two; and nine additional clades identified solely as *Dermogenys* sp., indicating cryptic speciation and possible misidentifications. A minimum genetic divergence threshold of approximately 2% in COI sequences, commonly used for species delineation in teleost fishes, supports the presence of cryptic taxa within the group.

Conclusion

All Beloniformes families except Scomberesocidae are recorded from Indian waters. Compared to the well-studied Belonidae and Hemiramphidae, Zenarchopteridae remains understudied, with the genus *Dermogenys* represented by only one species, *D. brachynotopterus*. This study reveals that morphological taxonomy alone is insufficient for species delimitation in *Dermogenys*, highlighting the need for integrative approaches. The findings have important implications for species validation, conservation, and resource management in Southeast Asia.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143579: Does the Brazilian disjunct population of *Embernagra platensis* (Aves, Thraupidae) merit taxonomic status?

Gabriel Augusto Saad Hatanaka and Vagner Cavarzere

Department of Biodiversity and Biostatistics, Institute of Biosciences, São Paulo State University, Botucatu 18618-689, Brazil

Embernagra platensis is a widely distributed South American thraupid comprising four allopatric taxa traditionally treated as subspecies, with documented morphological and vocal variation. Taxonomic boundaries within the group remain uncertain, and anecdotal reports of vocal differences among populations lack quantitative investigation. This study aimed to evaluate the diagnostic potential of acoustic traits for distinguishing *E. platensis* populations, with particular focus on the nominate subspecies *E. p. platensis*, whose range spans Uruguay, central Argentina, eastern Paraguay, and southeastern Brazil, with a conspicuous distribution gap in central São Paulo state. We analyzed 97 recordings sourced from Xeno-Canto and the Macaulay Library, processed in Raven Pro 1.6.5. We measured morphological traits of all 17 specimens at Museu de Zoologia da Universidade de São Paulo with a caliper (0.01 mm), including wing, tail, and tarsus length, as well as bill measurements (length, width, and height). Additionally, we conducted colorimetric plumage analyses. Multivariate analysis of variance (MANOVA) was employed to test for differentiation in continuous variables among populations, supplemented by Student's t-tests for comparisons within populations. Statistical analyses were conducted in R. The disjunct population in northeastern São Paulo, Minas Gerais, Rio de Janeiro, and Espírito Santo states—omitted from current species distribution maps—was investigated for geographic variations. Among the seven variables examined (song duration, maximum, minimum and peak frequencies, 50% and 90% bandwidths, and maximum entropy), no significant differences were detected ($F_{1,2}=0.8$; $p=0.568$). All specimens exhibit uniform coloration across their body: the upperparts, nape, and tail are characterized by olive 2.5Y 4/4, while the underparts display pale olive 2.5Y 6/3, with no discernible differences between populations. Morphometric analyses revealed marginal differences between populations ($F=5.4$; $p=0.011$), except for tarsus length ($p=0.006$), which was larger for the northern population, though with overlapping values. All evidence suggests no morphological or vocal divergence between Brazilian populations.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146157: Immature morphotaxonomy of *Culicoides jacobsoni* Macfie, *Culicoides thurmanae* Wirth and Hubert, and *Culicoides oxystoma* Kieffer (Diptera: Ceratopogonidae)

Ankita Sarkar

Entomology Research Unit, Department of Zoology, The University of Burdwan, West Bengal 713104, India

Morphotaxonomy of immature stages can resolve misidentification, proliferation of cryptic species, and timely and effective management of vector species of *Culicoides* Latreille (Diptera: Ceratopogonidae) at the onset of development. Among 84 valid *Culicoides* species of reported from India, many are unknown as immatures, and some are partially described. *Culicoides jacobsoni* Macfie and *Culicoides oxystoma* Kieffer are two species considered to be proven vectors of the bluetongue virus. In the present investigation, *Culicoides thurmanae* Wirth and Hubert was reported first in India. The surface structures of eggs of *C. jacobsoni* and *C. thurmanae* are newly described and photomicrographed by using Scanning Electron Microscopy (SEM). The gravid females were collected using a UV LED light trap and identified morphologically. The eggs were retrieved by dissecting their abdomens and processed for SEM. Simultaneously, the laboratory-reared oviposited and hatched eggs of *C. oxystoma* were also described. The field-collected engorged females were transferred onto moistened cotton beds for oviposition. Embryonated eggs were then transferred into pre-prepared rearing plates consisting of cattle manure, yeast solution, and nutrient broth solution, allowing for successive egg hatching and rearing of larval instars. The larval instar differentiation and morphometric measurements of four larval instars were newly noted. This investigation also highlights pupal diagnoses across sexes.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143578: Morphological and vocal evidence for the split of eastern *Sittasomus griseicapillus* (Aves, Dendrocolaptidae) subspecies

Valentim Beraldo Rosolen and Vagner Cavarzere

Department of Biodiversity and Biostatistics, Institute of Biosciences, São Paulo State University, Botucatu 18618-689, Brazil

Fourteen names are assigned to the *Sittasomus griseicapillus* complex, yet no taxonomic revision has been conducted. We compared vocalization and morphology of the nominotypic population with those of southeastern South America (*S. g. sylvellus* and *S. g. olivaceus*), assessing potential divergences. Recordings were obtained from databases (WikiAves and Xeno-Canto) and analyzed based on loudsong duration, note number, pace, and minimum and maximum frequencies in Raven Pro 1.6.5. Morphology was compared through body color coding and morphometric analysis of specimens from Museu de Zoologia da Universidade de São Paulo. Using a caliper (0.01 mm), we measured culmen length, width, and height, and tarsus, remiges, and rectrices length. Multivariate analysis of variance (MANOVA) was used to test for differences in traits between populations, followed by Student's *t*-test to assess distinctions within them. Some 38 recordings were examined (*griseicapillus* – 15; *sylvellus* – 23), revealing a statistically significant difference ($F_{1,2} = 3.4$; $p = 0.013$) between populations. Song duration-related traits differed significantly ($p = 0.017$), with mean loudsong duration being shorter in *griseicapillus* (4.2 ± 0.9 s) than in *sylvellus* (5.5 ± 2.1 s), while note number was higher in the former (16.4 ± 5.1) compared to the latter (11.9 ± 5.9). The mean pace of *griseicapillus* was faster (3.9 ± 1.1) than that of the Atlantic population (2.5 ± 1.7). Some 40 specimens were analyzed (*griseicapillus* – 10; *sylvellus* – 28; *olivaceus* – 2). No morphometric differences were found ($F_{1,3} = 0.98$; $p > 0.05$) among the three populations, but body coloration greatly differed. The upperpart and underpart of *griseicapillus* is grayish (2.5Y 4/2) whereas in *sylvellus* and *obsoletus*, these regions are olive-green (5Y 5/6). All populations are reddish brown (2.5 YR4/6 – *griseicapillus*; 2.5YR 3/4 – *sylvellus*) in remiges, rectrices, and uropygium. The significant vocal and morphological differentiation detected suggests that *griseicapillus* and *sylvellus* should be full species.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146637: New molecular data for five dactylogyrid monogenean parasites of freshwater fishes in India and their molecular phylogeny

Km Gazala ¹, Haren Ram Chiary ², Suhani Singh ³, Bindu Sharma ¹ and Anshu Chaudhary ¹

¹ Department of Zoology, Chaudhary Charan Singh University, Meerut- 250004, Uttar Pradesh, India

² Department of Zoology, Kirori Mal College, University of Delhi, Delhi-110007, India

³ Department of Zoology, Meerut College, Meerut-250003, Uttar Pradesh, India

During a study of the monogeneans of three freshwater fishes (*Ompok bimaculatus*, *Chanda nama*, and *Notopterus notopterus*) from the River Ganga, a total of five parasites (*Chandacleidus recurvatus*, *Notopterodiscoides notopterus*, *Spicocleidus namae*, *Thaparocleidus malabaricus*, and *Thaparocleidus octotylus*) of the family Dactylogyridae were characterized molecularly (18S rRNA gene). Our study provides the first 18S molecular data for *Chandacleidus recurvatus*, *Notopterodiscoides notopterus*, *Spicocleidus namae*, *Thaparocleidus malabaricus*, and *Thaparocleidus octotylus*. The present study's phylogenetic analysis for the abovementioned species, developed here, revealed the importance of molecular approaches in the study of monogenean diversity. Although in Indian region, despite the high diversity of monogenean parasites from the freshwater fish hosts, little is known about their genetic diversity. Therefore, an integrative approach further will help to increase the exactitude of genetic diversity and phylogenetic relationships of this group of parasites.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-136911: Phenotypic and vocal differentiation among subspecies of *Piculus flavigula* (Aves, Picidae) suggest a major taxonomic reassessment

Enrico Lopes Breviglieri ¹, Glaucia Del-Rio ², Marco Antonio Rego ², Luís Fábio Silveira ³ and Vagner Aparecido Cavarzere Júnior ⁴

¹ Biodiversity and Biostatistics Department, Botucatu Campus, Institute of Biosciences, Sao Paulo State University, Botucatu 18618-689, Brazil

² Research and Collections, Florida Museum of Natural History, University of Florida, Gainesville, FL 32611, USA

³ Zoology Museum, Sao Paulo Campus, Sao Paulo University, Sao Paulo 04263-000, Brazil

⁴ Biodiversity and Biostatistics Department, Botucatu Campus, Institute of Biosciences, Sao Paulo State University, Botucatu 18618-689, Brazil

Widespread species with visibly variable phenotypes often conceal significant evolutionary diversity. The Yellow-throated Woodpecker *Piculus flavigula* is a Neotropical species distributed across the Amazon and the Atlantic Forests, currently classified into three allopatric subspecies: *P. f. flavigula* (northern Amazonia), *P. f. magnus* (southern Amazonia), and the Atlantic *P. f. erythropis*. Although these groups are diagnosed based on geography and general appearance, their morphological and vocal distinctiveness have not yet been formally evaluated. We assessed phenotypic and acoustic variation using traditional morphometric and vocal traits, combined with automated color pattern segmentation and machine learning-based acoustic analysis. A total of 113 specimens (65 males and 48 females) were measured for wing chord, tail, culmen and tarsus length. Plumage color patterns were analyzed using the R package *recolorize*, which enables segmentation from uncalibrated standardized photographs. Additionally, 117 recordings were analyzed for five acoustic parameters (bandwidth, duration, peak, minimum and maximum frequencies) and further processed through BirdNET, a neural network-based algorithm that extracts 1,024-dimensional feature embeddings. Multivariate statistical tests (MANOVA, LDA) and supervised classification (SVM) were used to assess group separability. We found significant morphometric differences among subspecies, particularly in culmen and tail length (MANOVA $p = 0.016$). While *P. f. erythropis* showed the most distinctive phenotype, including a unique barred ventral pattern and higher peak frequencies ($p = 0.001$), comparisons between *P. f. flavigula* and *P. f. magnus* also revealed consistent, but subtler, differences in tail ($p = 0.022$), culmen ($p = 0.015$), and vocal parameters. These two Amazonian subspecies showed partial overlap in morphological measurements but moderate separation in acoustic space. Classification models based on BirdNET embeddings achieved 86% accuracy in distinguishing vocalizations among groups. These findings support the phenotypic and acoustic distinctiveness of *P. f. erythropis*, while also suggesting divergence between *P. f. flavigula* and *P. f. magnus*, providing robust evidence for a re-evaluation of taxonomic limits within the *Piculus flavigula* species complex.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-137111: A new *Rissoina* species (Gastropoda: Rissoinidae) from the southeastern Pacific

Juan Francisco Araya ¹ and Juan Antonio Aliaga ²

¹ Department of Zoology, Faculty of Zoological and Oceanographic Sciences, Campus Concepción, University of Concepción, Concepción 4070386, Chile

² Department of Chemistry, Faculty of Natural Sciences, Mathematics, and the Environment, Metropolitan Technological University, Santiago 7800003, Chile

We describe a new species of the genus *Rissoina* d'Orbigny, 1841, from the southeastern Pacific, representing the second species of this genus recorded from the continental coast of Chile. The new species was collected from coarse sand near the port of Caldera, Región de Atacama, northern Chile. The new species is distinguished from other southeastern Pacific *Rissoina* species by the absence of axial ribs, a characteristic brownish-caramel coloration, and a distinctive spiral microsculpture composed of very fine, regularly spaced rows of shallow, elongated, ovate-rectangular depressions separated by irregular cords. The discovery of this previously undocumented micromollusk within a relatively restricted geographic area highlights the need for further taxonomic studies on small-sized mollusks in the region, which represent a significant component of the southeastern Pacific malacofauna.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143469: A Rare Lateral Line Variation in *Cynoglossus quadrilineatus* (Bleeker, 1851): Insights from Morphological and Molecular Analyses

Ameen Ummath ¹, Samrat Kalita ¹ and Sasidharan Venu ²

¹ Department of Ocean Studies and Marine Biology, Pondicherry University, Port Blair, India

² School of Marine Sciences, Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology, Lakeside Campus, Cochin 682016, Kerala, India

The lateral line distribution is an important morphological feature for taxonomic differentiation within the genus *Cynoglossus*. This study documents a rare lateral line anomaly in *Cynoglossus quadrilineatus*, a species typically characterized by two ocular-side lateral lines. A specimen with three well-developed ocular-side lateral lines was discovered in coastal waters near the Andaman and Nicobar Islands, India. Morphological and molecular analyses, including a direct comparison between anomalous and non-anomalous specimens, were conducted to determine whether the anomaly represents a taxonomic feature or a developmental variation. Meristic and morphometric assessments confirmed that the anomalous specimen falls within the diagnostic range of *C. quadrilineatus*. Cytochrome c oxidase I (COI) gene analysis revealed minimal genetic divergence (0.48%) between specimens with two and three ocular-side lateral lines, supporting their conspecificity. These findings suggest that the additional lateral line is a developmental anomaly rather than a species-specific trait, demonstrating that lateral line variations can occur in *C. quadrilineatus*, despite being a critical morphological character in species diagnosis. This conclusion is based on a single individual exhibiting the anomaly, which limits broader generalization and emphasizes the need for additional observations. This study highlights the importance of integrating molecular tools with traditional taxonomy to resolve uncertainties arising from morphological deviations in fish species.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-152723: A revision of the genus *Baltoplana* Karling, 1949 (Rhabdocoela: Schizorhynchia: Cheliplanidae): Phylogenetic Insights and Seven New Species

Jhoe Reyes¹, Marlies Monnens^{1,2}, Laura Vanstraelen¹, Yander L. Diez^{1,3},
Philippe E.H. Jouk^{1,4}, Nathalie J.P. Revis¹, Ernest Schockaert¹ and Tom Artois¹

¹ Centre for Environmental Sciences, Research Group Zoology: Biodiversity and Toxicology, Hasselt University, Agoralaan Gebouw D, B-3590 Diepenbeek, Belgium

² Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Vautierstraat 29, B-1000 Brussels, Belgium

³ Smithsonian Marine Station, 701 Seaway Drive, Fort Pierce, FL 34949, USA

⁴ Royal Zoological Society of Antwerp, Center for Research & Conservation, Koningin Astridplein 20-26, B-2018 Antwerp, Belgium

Schizorhynchia is a taxon of marine free-living platyhelminthes that is generally characterized by having a divided proboscis; however, current taxonomy fails to accurately represent the evolutionary history of species within Schizorhynchia. Here, we present an integrative taxonomic revision and phylogenetic analysis of the genus *Baltoplana* Karling, 1949 (Cheliplanidae). We collected specimens from various locations around the world, including Australia, Brazil, Spain, France, Italy, and the United States. The specimens were extracted from sandy substrates on beaches. After collection, the specimens were placed in 500 mL wide-mouth flasks and processed using the MgCl₂ decantation method. Live specimens were observed under a microscope, and we took photographs, videos, and detailed anatomical drawings to support subsequent species identification. Each observed specimen was fixed in lactophenol and sealed for later observations under differential interference contrast (DIC) microscopy. Phylogenetic work based on newly acquired 18S and 28S rDNA sequences confirms that the family Cheliplanidae is monophyletic, for the first time positions *Baltoplana* within Cheliplanidae, and reveals *Baltoplana* as the sister taxon of *Cheliplana*. We describe seven new species and provide new morphometric data of known species. The new species of *Baltoplana* are mainly distinguished by the shape and size of the (un)armed cirrus, the presence or absence of accessory cirri, and the presence or absence of sclerotized tissue (cap) in the distal region of the male copulatory bulb.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-152725: A taxonomic revision of *Gyratrix hermaphroditus* Ehrenberg, 1831 (Platyhelminthes) using integrative taxonomy

Laura Vanstraelen ¹, Vincent Cuyppers ^{1,2}, Tom Artois ¹, Yander L. Diez ^{1,3}, Philippe Jouk ^{1,4}, Nathalie Revis ¹ and Marlies Monnens ^{1,5}

¹ Hasselt University, Centre for Environmental Sciences, Zoology: Biodiversity and Toxicology, Agoralaan Gebouw D, B-3590 Diepenbeek, Belgium

² KU Leuven, Institute of Philosophy, Kardinaal Mercierplein 2, B-3000 Leuven, Belgium

³ Smithsonian Marine Station, 701 Seaway Drive, Fort Pierce, FL 34949, USA

⁴ Royal Zoological Society of Antwerp, Centre for Research & Conservation, Koningin Astridplein 20-26, B-2018 Antwerp, Belgium

⁵ Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Vautierstraat 29, B-1000 Brussels, Belgium

The microturbellarian flatworm *Gyratrix hermaphroditus* (Kalyptorhynchia: Polycystididae) has long been hypothesised to constitute a vast species complex, a view recently confirmed by molecular evidence. However, to date, the complex has not yet been formally split, as its taxonomy is complicated by multiple nested species hypotheses and by the fact that distinguishing features often consist of very subtle morphological differences in the sclerotised male copulatory organ. Here, building on the existing molecular framework, we present a large integrative effort to resolve the species complex. We add new DNA sequences from specimens collected near the type locality of *G. hermaphroditus*, expand the previously published morphometric dataset with additional measurements and statistical analyses, and use Scanning Electron Microscopy (SEM) to visualise and clarify morphological differences within the complex. As such, we delineate 14 species of *Gyratrix*, originating from freshwater, brackish, and marine habitats across the taxon's global range. Species boundaries are primarily defined by variation in the morphology of the copulatory organ, which is especially evident in the high-resolution SEM images. These morphological differences are robustly supported by molecular and morphometric evidence. Finally, we assess the practical value of our new delineations by testing whether they enable reliable identification of both historical and newly collected specimens in the absence of molecular data.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143513: Adaptive shifts and diversification of *Ferricixius* planthoppers in Brazilian caves (Hemiptera: Cixiidae)

Júlio César do Carmo Vaz Santos ¹ and Rodrigo Lopes Ferreira ²

¹ Center for Studies in Subterranean Biology (Cebs), Department of Ecology and Conservation, Institute of Natural Sciences, Universidade Federal de Lavras, Lavras-MG, Brazil

² Graduate Program in Applied Ecology (PPGECO), Universidade Federal de Lavras (UFLA), Lavras-MG, Brazil

The genus *Ferricixius* Hoch and Ferreira, 2012 was originally described based on a single troglobitic species found in iron-rich caves in southeastern Brazil. Subsequent collections revealed additional species with varying degrees of troglomorphy, including the first epigean/subtroglomorphic species of the genus. More recently, four new species have been discovered in Brazilian caves, exhibiting marked variation in troglomorphic features. These findings make *Ferricixius* a valuable model for investigating processes of subterranean colonization and speciation in tropical cave environments.

The new species are known only from their type localities, located in caves of the Quadrilátero Ferrífero, Minas Gerais – Brazil. Specimens were collected using moistened brushes, transferred to vials containing 96% ethanol for preservation, and later stored in 70% ethanol. Morphological analyses focused on troglomorphic characters (reduction of eyes, wings, and body size) and male genital structures. Descriptions follow the criteria established by Hoch and Ferreira (2012), with adaptations according to Santos et al. (2023).

Four new species of *Ferricixius* are described, representing the first troglobitic species in the genus that still retain functional eyes—indicating that eye reduction does not follow a uniform pattern. Independent variation in the degrees of troglomorphy was observed among species, suggesting environmental influence on selective pressures. Although male genitalia are generally similar among species, they exhibit diagnostic differences that support their separation, suggesting rapid speciation events.

The data suggest multiple subterranean colonization events by a common ancestor, possibly in response to climatic events, followed by rapid adaptive diversification. The discovery highlights the importance of conserving Brazilian caves in the face of increasing threats from mining activities.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-134084: AN INTEGRATIVE ANALYSIS TO RESOLVE TAXONOMIC DEADLOCKS IN ERGASILID COPEPODS IN THE PLANET

João Victor Couto ¹, James P. Bernot ², Geoffrey A. Boxshall ³, Fabiano Paschoal ⁴ and Felipe Bisaggio Pereira ¹

¹ Department of Parasitology, Institute of Biological Sciences, Federal University of Minas Gerais, Belo Horizonte 31270-901, MG, Brazil

² Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT 06269, USA

³ Department of Life Sciences, Natural History Museum, South Kensington, London SW7 5BD, UK

⁴ Department of Microbiology, Immunology and Parasitology, Faculty of Medical Sciences, Rio de Janeiro State University, Rio de Janeiro 20551-030, RJ, Brazil

Ergasilidae is among the most recorded families of parasitic copepods on fish worldwide. Besides its impressive species richness of 281 species, morphological and genetic phylogenies have demonstrated the lack of monophyly in some genera, as well as other taxonomic deadlocks. This scenario highlights the need to conduct new analysis to better understand the evolutionary history of the family and to improve its systematics. The present analysis comprised 31 ergasilid species plus the outgroup, *Hemicyclops tanakai*. A morphological matrix containing 27 characters and an alignment of 18S rDNA genetic sequences were used for phylogenetic reconstruction in BEAST 2.5 using Bayesian Inference. The characters and their states were traced in the tree using Tracer. The integrated tree showed Consistency Index (CI) (homoplasy rate) of 0.55, thus moderately informative. The most informative features (CI>0.60) were the presence of posterolateral processes on cephalosome, segmentation of antennule, terminal armature of antenna and segmentation of leg 4 rami. Species from Neotropical and Ethiopian realms formed distinct lineages, partially supported by morphological traits. Even integrating morphological data, *Ergasilus* maintained its polyphyletic status, indicating that the current morphological diagnosis does not reflect its real evolutionary history. The same occurred for *Neoergasilus*. Giving the present results, at least 5 new genera would be erected to allocate *Ergasilus* spp., but no morphological feature combination appeared to support them. *Paraergasilus* and *Sinergasilus* were monophyletic, supported mainly by morphological traits currently used in their diagnosis. The present results reinforced features that must keep distinguishing genera within the Ergasilidae, but also highlighted others, such as segmentation of rami on leg 4, that could also have taxonomic value. Nonetheless, the poor genetic sampling within the family limited the analysis, highlighting that more sequences must be generated to allow the production of more elucidative results in the future.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143422: Catalogue of the Auchenorrhyncha of the Iberian Peninsula and Macaronesia: A Bibliographic Analysis from Linnaeus to the Present

Dora Aguiñ-Pombo, Mafalda Abreu, Rui Marques, Beatriz Gomes and Cesar Alves

Faculty of Life Sciences, University of Madeira, Campus Universitário da Penteada, 9020-105 Funchal, Madeira, Portugal

The Iberian Peninsula and Macaronesia represent one of the richest regions in the European Union in terms of Auchenorrhyncha diversity and endemism. However, a comprehensive catalogue compiling current knowledge on the distribution and taxonomy of this group is still lacking – a gap that limits both biodiversity conservation efforts and the effective management of vector species in agriculture. This study presents an extensive bibliographic analysis of publications containing primary taxonomic data, from Linnaeus to the present, focusing on the Iberian Peninsula (Andorra, Spain, Portugal, Gibraltar, including Balearic Islands) and the Macaronesian archipelagos (Azores, Canary Islands, Madeira, Cape Verde, Selvagens). Through a thorough review of multiple literature sources, we identified approximately 800 publications with original data on distribution and taxonomy of Auchenorrhyncha covering about 900 species. We compiled a detailed database and evaluated each work in terms of publication type, authorship, country of origin and historical period. This work provides the basis for a forthcoming annotated bibliographic catalogue of the group. The finding offers a solid foundation for future taxonomic, biogeographic, and applied studies on Auchenorrhyncha, and will contribute both conservation strategies and sustainable agricultural management in the region.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143477: Detailed Taxonomic Description and Molecular Confirmation of *Thryssa encrasicholoides* (Clupeiformes: Engraulidae) From the Andaman Islands

Samrat Kalita ¹, Ameen Ummath ¹ and Sasidharan Venu ²

¹ Department of Ocean Studies and Marine Biology, Pondicherry University, Port Blair, India

² School of Marine Sciences, Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology, Lakeside Campus, Cochin 682016, Kerala, India

We provide a detailed taxonomic description of *Thryssa encrasicholoides*, based on five specimens collected from the Andaman Islands, India. The species taxonomic status and distribution have historically been misinterpreted across Indo-West Pacific due to close similarities with *T. baelama*, leading to frequent misidentification. To address this, we performed comprehensive morphological and molecular analyses, targeting the COI gene, to confirm the identity of *T. encrasicholoides*. A 594 bp long sequence was obtained and submitted to GenBank (Accession Number: PV936664). The COI sequence showed high similarity to *T. encrasicholoides* sequences available in the NCBI database. The Neighbour-Joining (NJ) phylogenetic tree revealed that the Andaman isolate clustered in a distinct clade with conspecific sequences from GenBank, thereby confirming its identity. Although *T. encrasicholoides* closely resembles *T. baelama* in having fewer prepelvic scutes and a short upper jaw, it can be distinguished by the presence of weakly developed scutes just behind the isthmus and a blunt posterior tip of the maxilla. By integrating morphological and molecular data, this study clarifies species boundaries, resolves taxonomic ambiguities in Indian marine fishes, and strengthens regional biodiversity records for better conservation and management.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142921: Discovery of a New Fungivorous Nematode, *Deladenus golestanicus*, from Northern Iran: Morphological and Phylogenetic Evidence

Milad Derakhshanfar ¹, Farzad Aliramaji ¹, Abdolhosein Taheri ¹ and Ebrahim Shokoohi ²

¹ Department of Plant Protection, Faculty of Plant Production, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

² Department of Biochemistry, Microbiology and Biotechnology, University of Limpopo, Private Bag X1106, Sovenga 0727, South Africa

A population of a new species of *Deladenus* was recovered from the natural Golestan Forest Park in Golestan Province, northern Iran. This species is characterized by a body length of 450–733 µm, a short stylet measuring 6.0–7.5 µm, seven to eight lateral field incisures, a fusiform median bulb lacking a median chamber, an excretory pore located at the level of the hemizonid and near the terminus of the basal esophageal bulb, and the absence of a posterior uterine sac. The new species closely resembles *D. gilanica* and *D. hyrcanus* but can be distinguished from *D. gilanica* by its longer body length (450–773 vs. 314–422 µm), shorter stylet (6.0–7.5 vs. 7.5–8.0 µm), longer tail (34–58 vs. 27–32 µm), greater vulva–anus distance (20–37 vs. 15–26 µm), and more posteriorly positioned excretory pore (opposite the end of the dorsal esophageal gland). It differs from *D. hyrcanus* in body length (450–773 vs. 718–806 µm), stylet length (6.0–7.5 vs. 7.5–10.0 µm), excretory pore position (near the end of the basal bulb vs. anterior to the basal bulb), and tail length (34–58 vs. 58–72 µm). Additionally, sequences of the small and large subunit ribosomal DNA regions (SSU and LSU D2–D3) were obtained, and phylogenetic analyses were conducted. The proposed new species, *Deladnus golestanicus*, is supported by the morphological and morphometric distinctiveness of the resulting phylogenetic trees.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143119: Diversity of Calcinea (Porifera, Calcarea) from Heron Island, Great Barrier Reef, Australia: New species and wide distributions

Maria Eduarda Almeida dos Santos ¹, Matheus Vieira Lopes ², Michelle Klautau ² and André Padua ¹

¹ Department of Animal Biology, Federal Rural University of Rio de Janeiro/ Biological Sciences and Health Institute, Seropédica 23897-000, Brazil

² Department of Zoology, Federal University of Rio de Janeiro/ Institute of Biology, Rio de Janeiro 21941-599, Brazil

The class Calcarea comprises 831 (8.5%) out of the 9,700 described species of the phylum Porifera. The knowledge on the diversity and distribution of calcareous sponges remains limited due to insufficient sampling and taxonomy specialists. This is also evident in the Great Barrier Reef (GBR), which presents only 25 (9%) out of the 280 calcareous sponges reported for Australia. Therefore, this study seeks to describe the species diversity of the subclass Calcinea from Heron Island, GBR, using integrative taxonomy (morphological and molecular analyses). Among the 19 specimens analysed, 11 species were identified, seven of them being new to science: *Arturia* sp. nov., *Clathrina* sp. nov., *Janusya* sp. nov. 1, *Janusya* sp. nov. 2, *Neoernsta* sp. nov. 1, *Neoernsta* sp. nov. 2, and *Neoernsta* sp. nov. 3. Additionally, four previously known species had their distributions widened within the South Pacific Ocean: *Arturia dubia*, *Clathrina fakaravae*, *Clathrina procumbens*, and *Clathrina* cf. *stipitata*. Some of these species show trans-Pacific distributions. The knowledge on the Calcinea diversity in Heron Island rose from four to 15 species (275%), and from 15 to 26 (73%) in the GBR. Moreover, the endemism of Calcinea in Heron Island is now 53% (8 species), and 46% in the GBR (12 species). This study also documents the first records of the genera *Arturia* and *Neoernsta* in the GBR. These results confirm the underestimation of the diversity of Calcarea in the GBR, evidencing that more studies are needed even in well-studied locations.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143343: Diversity of the squid family Brachioteuthidae in Aotearoa New Zealand and the Southern Ocean

Austin Horenkamp

School of Science, Auckland University of Technology, Auckland 1010, New Zealand

The deep-sea squid family Brachioteuthidae is one of the most systematically unstable cephalopod taxa in need of a global revision. The general lack of adult specimens in research collections, incomplete and inaccurate species descriptions, descriptions based on paralarvae or early juveniles only, and sexual dimorphism have all contributed to the instability of this family. As part of a global revision a local review of the New Zealand and Southern Ocean brachioteuthids is being undertaken using integrative taxonomy. While the family was founded in 1881, Brachioteuthis was only formally reported from New Zealand waters in 2019. In the meantime, four genetically distinct species from around New Zealand have been identified, some of which may represent unnamed/new species. One of these species ('Brachioteuthis sp. Ker 2', sensu Braid & Bolstad 2019) forms a clade with low variation with individuals from the northern Atlantic, which suggests that some brachioteuthids may have very wide geographic ranges. The key morphological characters for specieslevel delimitation include tentacle-club morphology including carpal (fixing) apparatus [when present], skin sculpture (useful in sexual dimorphism cases), arm modifications in males, liver morphology, eye photophore morphology and the general habitus based on shape analysis. This project represents a step forward in the systematic resolution of this complicated family. However, an integrative taxonomic approach will be required to resolve the global systematics of brachioteuthids.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147651: Do male rotifer copulatory organs have systematic value? An integrative analysis of *Asplanchnopus* aff. *multiceps*

Thiago Quintão Araújo ¹, Elizabeth Walsh ², Robert Wallace ³ and Rick Hochberg ¹

¹ Department of Biology, University of Massachusetts Lowell, Lowell, MA 01854, USA

² Department of Biological Sciences, University of Texas at El Paso, El Paso, TX 79968, USA

³ Department of Biology, Ripon College, Ripon, WI 54971, USA

Female monogonont rotifers are among the smallest animals, with many species less than 100 µm in length. Male rotifers are enigmatic; they are only known for relatively few species, are infrequently seen, and are usually smaller than their female counterparts, often lacking a complete gut. Consequently, knowledge of their morphology is scarce, particularly so with respect to the fine details of their copulatory apparatus. In this study, we apply confocal laser scanning microscopy and transmission electron microscopy to study the copulatory (penis) organ of *Asplanchnopus* aff. *multiceps*, for which no data is currently available. Our studies revealed the copulatory organ to be a complex structure with a circumferential ciliated band, a microvillar tip with an actin rich terminal web, and an intricate musculature that functions in protraction and retraction. Two prostate glands and two accessory glands supply the male apparatus. The overall organization of the organ fits into a “type” that characterizes the family Asplanchnidae, with the main exception being the possession of a microvillar tip. Complexity of the organ, which functions purely in attachment to the female and not insertion, is perplexing considering its size (~ 10 µm) and the apparent simplicity of its function. We hypothesize that other male organs are probably equally complex, but their size has limited our knowledge of their anatomy, which might otherwise provide valuable details for both taxonomic studies and a better understanding about the evolution of reproductive structures and behaviors throughout the phylum.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143015: Evidence for the Synonymy of *Laimaphelenchus hyrcanus* with *L. belgradiensis*, two species of nematodes belonging to Aphelenchoididae

Shabnam Naseri ¹, Farzad Aliramaji ¹, Mohammad Esmaeil Agh Atabai ¹ and Ebrahim Shokoohi ²

¹ Department of Plant Protection, Faculty of Plant Production, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

² Department of Biochemistry, Microbiology and Biotechnology, University of Limpopo, Private Bag X1106, Sovenga 0727, South Africa

A population of *Laimaphelenchus* was isolated from the dead bark of a healthy oak tree, a site potentially favorable for fungal growth. This species is morphologically characterized by a body length of 621–796 µm, a stylet measuring 10.5–13 µm, three lateral lines, the presence of a vulval flap, and a post-uterine sac 50–78 µm long (2.2–3.6 times the vulval body width). Males exhibit a four-part tail terminus, a (2+2+2) arrangement of genital papillae, and spicules measuring 18.5–20 µm. Based on morphometric and morphological features, this population closely resembles *L. hyrcanus* and *L. belgradiensis*. However, it differs from the original description of *L. belgradiensis* by having a shorter stylet (10.5–13 µm vs. 13.6–15.2 µm) and a longer post-uterine sac (50–78 µm vs. 17.6–48 µm). In comparison with *L. hyrcanus*, the post-uterine sac is also shorter (50–78 µm vs. 97–152 µm). Previous studies on *Laimaphelenchus* populations from decaying oaks in Iran highlighted variability in post-uterine sac length and its potential limitations for species-level discrimination. A re-evaluation of species boundaries led to a redescription of *L. belgradiensis* and the proposal that *L. hyrcanus* may represent a junior synonym. In the present study, phylogenetic analysis based on the D2–D3 expansion segments of the LSU gene placed this population within a highly supported clade (posterior probability = 1.00), supporting the synonymy—unless additional genomic regions suggest otherwise.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146950: Exploring Machine Learning for Species Delimitation in the *Trimerotropis pallidipennis* Complex (Orthoptera: Acrididae)

Noelia Veronica Guzman

Department of Ecology, Genetics and Evolution, Instituto de Ecología Genética y Evolución de Buenos Aires (IEGEBA), FCEyN, Universidad de Buenos Aires, Buenos Aires 1728, Argentina

The grasshopper *Trimerotropis pallidipennis* (Orthoptera: Acrididae) exemplifies the challenges of species delimitation in widely distributed taxa with low morphological differentiation. This species extends from North to South America, frequently inhabiting high-altitude Andean environments. Although only four species have been formally recognized, cytogenetic and molecular evidence suggest that *T. pallidipennis* represents a complex of multiple evolutionary lineages.

To investigate this, I reanalyzed genome-wide SNP datasets generated through ddRAD-seq using unsupervised machine learning (UML) approaches. Multiple clustering algorithms and dimensionality-reduction methods were implemented to evaluate whether UML can improve species delimitation compared with traditional model-based validation methods.

Those analyses revealed that UML consistently identified lineage-level divergences and signals of admixture, supporting the existence of cryptic diversity within *T. pallidipennis* complex. In contrast to model-based approaches, which tended to oversplit taxa, UML successfully grouped samples according to major evolutionary lineages.

Overall, this study highlights the complexity of species boundaries in the *T. pallidipennis* complex and underscores the importance of integrative frameworks that combine morphology, cytogenetics, and genomic data. By demonstrating the capacity of UML to recover cryptic diversity while avoiding artificial over-partitioning, our findings provide methodological and conceptual advances for species delimitation in complex taxonomic systems.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146652: First Molecular Records and Genetic Links among *Craspedacusta sowerbii* (Cnidaria; Hydrozoa) Populations in Argentina and Brazil

Maria Irene Deserti ^{1,2}, Diego M. A. Guerin ³, Fabian Horacio Acuña ^{1,2} and Sergio Nascimento Stampar ⁴

¹ Institute of Marine and Coastal Research (IIMyC-CONICET); Faculty of Exact and Natural Sciences, National University of Mar del Plata. Deán Funes 3350, B7602AYL Mar del Plata, Buenos Aires, Argentina

² Coiba Scientific Station (Coiba-AIP), Avenida Omar Torrijos Herrera, Ciudad del Saber, Calle. Gustavo Lara, Oficina 145B, Ciudad de Panamá, Panamá

³ School of Philosophy, Faculty of Philosophy and Humanities, National University of Córdoba, France Pavilion, Córdoba 5000, Argentina

⁴ Laboratory of Evolution and Aquatic Diversity (LEDALab), Av. Eng. Luiz Edmundo Carrijo Coube, 14-01, Bauru, São Paulo 17033-360, Brazil

In this study, we present the first molecular records of the freshwater jellyfish *Craspedacusta sowerbii* (Cnidaria, Hydrozoa) for Argentina and Brazil, obtained from specimens collected at Dique Berta Vidal de Battini (San Luis Province), Ariranha do Ivaí (Paraná State), and Videira (Santa Catarina State), respectively. These results are highly relevant, as previous reports in both countries are scarce and lack genetic confirmation.

The phylogenetic analysis, based on the mitochondrial COI marker, showed that the Argentine sequences form a well-supported clade together with Brazilian samples from Paraná, suggesting a biogeographic connection and genetic cohesion among these groups. These samples also integrate into a broader lineage that includes records from Chile, Japan, Italy, and Canada, reaffirming the cosmopolitan nature and invasive potential of *C. sowerbii*.

The differences observed between the Santa Catarina and Paraná populations could be attributed to several factors: geographic barriers and distinct hydrographic basins that limited direct genetic exchange. The genetic proximity among Argentina, Paraná, and Chile may reflect both historical dispersal and human-mediated colonization. In contrast, the genetic divergence observed in the Santa Catarina population could be explained not only by its isolation due to natural barriers but also by following a dispersal route different from Paraná and Argentina, which has kept it more genetically separated.

These preliminary results should be interpreted with caution, as they are based on a single marker and a limited number of samples. However, given the ecological impact of the species, monitoring its presence is crucial to understanding potential alterations in local communities. This context highlights the importance of expanding molecular and ecological studies, integrating hydrological and anthropogenic information, which will guide management strategies that respect regional conservation practices.

This study represents an essential starting point for understanding the genetic structure, dispersal pathways, and potential ecological impact of *C. sowerbii* in local freshwater ecosystems.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-129127: four species of Digeneans (Trematoda, Opecoelidae) of the gilthead seabream *Sparus aurata* (teleostei, Sparidae) off the Algerian coast in the Mediterranean Sea

Fatima Zohra Sarah Zedam

Biodiversity and Environment: Interactions-Genomes (LBEIG). University of Science and Technology Houari Boumediene USTHB

A study was conducted between May 2020 and April 2022, in an attempt to investigate the diversity of digeneans infecting the digestive tract of the gilthead sea bream *Sparus aurata* (Linnaeus, 1758) (Sparidae) off the Algerian coast. Four species belonging to the family Opecoelidae Ozaki, 1925 were collected: *Macvicaria obovata* (Molin, 1859) Bartoli, Bray & Gibson, 1989; *Macvicaria maillardi* Bartoli, Bray & Gibson, 1989; Bartoli & Gibson, 2007; *Macvicaria maamouriae* Antar, Georgieva, Gargouri & Kostadinova, 2015 and *Allopodocotyle pedicellata* (Stossich, 1887) Pritchard, 1966. Algeria is a new geographical record for *M. obovata* and *A. pedicellata*, whereas *M. maillardi* has already been reported on the Algerian coast, but not from its type host *S. aurata*. We provide a redescription of these species based on newly collected specimens which were identified using only morphological features such as the distribution of vitelline follicles and, uterus, the position and shape of the cirrus-sac, and the presence or absence of the metraterm.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146271: Genetic Divergence and Phylogeographic Structuring in *Lethrinus* (Osteichthyes: Lethrinidae): Evidence of Species Complexes and Regional Lineages

Badarul Sijad and Theparambil Mohamed Najmudeen

ICAR-Central Marine Fisheries Research Institute, Kochi, Kerala, India

Introduction:

The emperors (*Lethrinus*, Osteichthyes: Lethrinidae) are ecologically and commercially important reef fishes distributed across the Indo-Pacific. Species delimitation remains problematic due to morphological similarity, synonymy, and broad ranges. DNA barcoding using cytochrome oxidase I (COI) offers a powerful tool for exploring genetic divergence, phylogeographic structure, and potential species complexes. This study analyses COI sequences of *Lethrinus* to evaluate intra- and interspecific variability and highlight taxonomic ambiguities.

Methods:

COI sequences representing multiple *Lethrinus* species were retrieved from GenBank, spanning the Indo-Pacific (Indonesia, Philippines, China, Malaysia, Australia, Japan, India, Mozambique, South Africa, Madagascar, Seychelles, Mauritius, Myanmar, Saudi Arabia, Israel, Pakistan, Fiji, Micronesia, and French Polynesia). Sequences were aligned in BioEdit and trimmed to a 648 bp fragment. Phylogenetic reconstruction was performed in MEGA7 using Maximum Likelihood (ML) with the best-fit substitution model and 1,000 bootstrap replicates. Pairwise genetic divergence was calculated in MEGA7 using the Kimura-2-Parameter (K2P) model.

Results:

Intraspecific distances were low across validated species (0.0–0.005), consistent with species-level cohesion. Interspecific distances ranged from 0.083 to 0.204, supporting a clear barcode gap. However, unusually low divergence occurred among *L. ornatus*, *L. obsoletus*, *L. lentjan*, and *L. harak* (0.082–0.098), indicating a potential species complex. By contrast, *L. genivittatus* (0.150–0.204 vs congeners) and *L. olivaceus* (0.146–0.202 vs congeners) were well differentiated. The ML tree supported these findings, showing distinct clades for Red Sea/Arabian Gulf populations of *L. lentjan* and *L. nebulosus* relative to Indo-Pacific counterparts, as well as regional structuring in *L. harak*, *L. rubrioperculatus*, and *L. olivaceus*.

Conclusion:

The COI-based phylogeny and distance analysis reveal both robust species separations and zones of ambiguity within *Lethrinus*. The *ornatus-obsoletus-lentjan-harak* group appears as a taxonomic complex requiring integrative revision, while deep geographic structuring in several widespread species suggests historical isolation and potential cryptic diversity. These results underscore the need for combined morphological, multilocus, and ecological approaches to refine species boundaries and better understand the evolutionary biogeography of Indo-Pacific emperors.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143623: Genetic diversity, phylogenetic relationships, and systematics of the species-rich *Adeonella* genus from two bays along the southern coast of South Africa

Onika Mabalabala ¹, Melissa Kay Boonzaaer-Davids ², Courtney-Ann Puckree-Padua ¹ and Jyothi Kara ¹

¹ Department of Conservation and Marine science, Faculty of Applied Sciences, District six campus, Cape Peninsula University of Technology, Cape Town, South Africa 7925, South Africa

² Fisheries Management Branch: Abalone Scientist Production: Inshore Resources Research, Department Forestry, Fisheries and the Environment (DFFE), Cape Town, South Africa 8001, South Africa

The study of bryozoans in South Africa is still in its early stages, but molecular techniques offer significant research potential. Bryozoans are crucial bioindicators of changing environments, and understanding their evolutionary history and taxonomic richness is essential. Bryozoans, like many invertebrates, serve as important bioindicators, reflecting the impact of changing environments. Globally, 45 *Adeonella* species are recognized, with 28 species (62%) considered endemic to South Africa. Recent studies indicate that the genera *Adeonella* and *Laminopora* require revision: *Adeonella* is polyphyletic, while *Laminopora* forms a paraphyletic clade with some *Adeonella* species. Both genera are predominantly found in South Africa. Due to cryptic speciation and morphological variability, validating adeonid species is needed for biodiversity research and for understanding the distribution and phylogenetic patterns. 30 samples of South African adeonellid species collected within False Bay and Algoa were used for this study, where five species (*A. pluscula*, *A. conspicua*, *A. Guttata* and *L. jellyae* and an unnamed *Adeonella* sp.) were identified. Three of these species are considered endemic to South Africa. Four of the five species identified in this study were found in both False Bay and Algoa Bay, which are approximately 600 km apart. This widespread occurrence and the potential reasons for their dispersion may be attributed to the influence of the Agulhas Current, which could be responsible for pushing larvae downward along the southeast coast and facilitating their movement as seen in other marine invertebrates like crustaceans and annelids. DNA extraction and PCR were conducted. Poor sequences were produced; however, troubleshooting is underway to ensure quality sequences.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143506: Genus *Amphinema* Haeckel, 1879 (Cnidaria, Hydrozoa): a brief taxonomic review with the description of a new species?

Jorge L. Llorente-Vega ¹ and Cristina Cedeño-Posso ²

¹ Grupo de investigación en Biotecnología-GRUBIODEQ, Facultad de Ciencias Básicas, Universidad de Córdoba, Montería, Colombia

² Programa de Biodiversidad y Ecosistemas Marinos, Línea de Inventarios, Taxonomía y Biología de Especies, Instituto de Investigaciones Marinas y Costeras, Santa Marta, Colombia

The genus *Amphinema* comprises a group of hydrozoans within the order Anthoathecata, currently consisting of 20 species, 19 of which have detailed morphological descriptions of their medusoid stage (Schuchert et al., 2025). The hydromedusae of this genus exhibit a combination of distinctive diagnostic features, including an apical projection, two hollow and opposite marginal tentacles, numerous rudimentary marginal warts or bulbs, a manubrium with four simple lips, absence of a gastric peduncle, and gonads located in adradial, interrarial, or perrarial positions, which occasionally extend along the radial canals (Bouillon, 1999; Bouillon et al., 2006; Fuentes et al., 2012; Schuchert & Collins, 2021). As part of a systematic review of the hydromedusae of Colombia, the morphological characteristics of 56 specimens collected from two coastal sites in the department of Córdoba (Colombia) were analyzed and compared with the diagnostic traits of the nominal species of the genus *Amphinema*. Based on these analyses, a synthesis of the diagnostic features of the reviewed species is presented, along with the morphological description of a potential new species to science. This taxon differs primarily in the shape and anatomy of the umbrella, apical projection, “gonads”, mouth, and lips. Given the high morphological plasticity observed within this group, it is proposed that molecular analyses be conducted to support the taxonomic identification. Documenting the diversity of hydromedusae contributes significantly to understanding the country’s marine biodiversity and provides a foundation for future studies on aspects such as ecology, phylogeny, and biogeography.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143574: How many species are there within *Chamaeza campanisona* (Aves, Formicariidae)?

Lucas Romero and Vagner Cavarzere

Department of Biodiversity and Biostatistics, Institute of Biosciences, São Paulo State University, Botucatu 18618-689, Brazil

Chamaeza campanisona is a species complex with cryptic diversity and currently has 12 recognized subspecies, predominantly distributed along altitudinal and longitudinal gradients in the Andes. Within the Atlantic Forest, two subspecies are currently recognized. Given the limited taxonomic studies of this genus, we investigated vocal variation among Atlantic Forest populations of this species complex. We analyzed 183 recordings obtained from the Macaulay Library, WikiAves, and Xeno-Canto databases and examined 56 specimens housed at the Museu de Zoologia da Universidade de São Paulo. Vocalizations were analyzed using Raven Pro 1.6.5. Comparison between populations were made with a Multivariate analysis of variance (MANOVA) within the R environment. The following measurements were analyzed: bill height, width and length, tarsus, tail, and wing length. Statistical analysis was not conducted due to the limited sample size (only one specimen from the northeastern Brazilian population). Plumage coloration was color-coded and compared across specimens. All examined *C. campanisona* specimens exhibited a distinct black patch on the front, whereas the single specimen from northeastern Brazil lacked this trait. The loudsongs typically consist of rapid series of short-spaced notes, with population-specific variation particularly in pace and in the presence of a terminal series of slowed, descending grunting notes. Our analyses revealed two distinct loudsong patterns: a southern variant occurring from southeastern Paraguay and northeastern Argentina north to Bahia state in Brazil, and a pattern restricted to Ceará state, northeastern Brazil. MANOVA revealed significant differences between populations ($p = 0.001$). Specifically, song duration varied significantly, whereas maximum entropy differed across populations ($p = 0.001$). The southern vocal type corresponds to *C. campanisona*, whereas the northeastern population represents a morphologically and vocally diagnosable unrecognized taxon, which requires formal description once more detailed information on other northeastern specimens are made available.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147486: Integrating 3D-imaging with multi-locus phylogenetic analysis to update the diversity of the aegisthid genus *Pontostratiotes* Brady, 1883 (Copepoda: Harpacticoida)

Fanny Sieler¹, Sahar Khodami², Martin Husemann³ and Nancy Fabiola Mercado-Salas¹

¹ Section Crustacea, Leibniz Institute for the Analysis of Biodiversity Change (LIB), 20146 Hamburg, Germany

² Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB), 26382 Wilhelmshaven, Germany

³ State Museum of Natural History Karlsruhe, 76133 Karlsruhe, Germany

The hyperbenthic zone, the transition between pelagial and benthos, is known as an environment of unique interactions with endemic species. Taxa inhabiting the marine benthic and hyperbenthic zone are often deemed as having the most plesiomorphic characters, making the study of hyperbenthic species essential to understanding the evolutionary history of several taxa, among them copepods. One copepod family whose representatives are found especially within deep-sea hyperbenthic communities is the Aegisthidae Giesbrecht, 1893, which, together with the family Rometidae Seifried & Schminke, 2003, is considered the sister group to all remaining Harpacticoida. Whilst efforts have been made to unravel phylogenetic relationships within Aegisthidae, the monophyly of the hyperbenthic genus *Pontostratiotes* Brady, 1883 has yet to be tested across specimens from both the Pacific and the Atlantic Ocean. Here, we apply an integrative approach, combining the inference of a phylogenetic tree, including the gene fragment of mitochondrial cytochrome oxidase c subunit I, as well as nuclear sequences of 18S and 28S, with high-resolution imaging techniques – confocal laser scanning microscopy and synchrotron radiation-based microcomputed tomography – for detailed morphology documentation. The *Pontostratiotes* specimens analyzed were collected during expeditions across the North Atlantic Ocean (IceAGE, IceAGE 3, IceDivA, IceDivA 2). Our analyses, including the molecular data available, which originate almost exclusively from Pacific samples, recovered the subfamily Pontostratiotinae, including all members of *Pontostratiotes*, as monophyletic. Four of the nine resulting species clusters of *Pontostratiotes* specimens examined in this study were assigned to valid species, while five previously undescribed lineages were provided with molecular barcodes and morphological descriptions. The examination of spatial records of the genus lead to the assumption of a near-worldwide distribution. As closely related benthic harpacticoid copepods are seldomly found in multiple samples across greater distances, abundant specimens of *Pontostratiotes* could be a good proxy to understand the connectivity of North Atlantic communities.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143317: Integrative taxonomic assessment of *Cruzia* sp. (Nematoda: Cosmocercoidea, Kathlaniidae) from the Argentine black and white tegu lizard: insights into the long-standing Kathlaniidae taxonomic puzzle

Lorena Allán-Choke ¹, Nahuel Fernando Galloso ¹, Gloria Maria Lacerda ², Gustavo Carmo Macedo ², Cynthia Gonzalez ¹ and Felipe B. Pereira ³

¹ Center for Applied Ecology of the Littoral (CECOAL), National Scientific and Technical Research Council (CONICET), Corrientes s 3400, Argentina

² Graduate Program in Parasitology, Institute of Biological Science, Federal University of Minas Gerais, Belo Horizonte 31270-901, Brazil

³ Department of Parasitology, Institute of Biological Science, Federal University of Minas Gerais, Belo Horizonte 31270-901, Brazil

Kathlaniidae (Ascaridomorpha: Cosmocercoidea) represents a diverse family of intestinal nematodes parasitic in all classes of vertebrates worldwide, except Aves. However, our knowledge on the systematic and molecular phylogeny of this family is unclear and complicated. The phylogenetic relationships between its subfamilies Kathlaniinae, Oxyascaridinae and Cruzeinae are still under debate. Moreover, the systematic position of the genus *Cruzia* (Cruziinae) within Kathlaniidae remains unclear. This work aimed to characterize morphologically and genetically specimens of *Cruzia* sp., evaluate the phylogenetic position of this genus within the Kathlaniidae, the phylogenetic relationships of this family with other taxa of Cosmocercoidea and the status of Cruzeinae as a subfamily. During a parasitological survey carried out in December 2024, specimens of *Cruzia* sp. were collected in the intestine of *Salvator merianae* (Squamata: Teiidae) from Corrientes (Argentina) and characterized using morphological (light and scanning electron microscopy) and molecular (sequencing of partial fragments of 18S rDNA, and COI mtDNA) methods. Phylogenies were reconstructed based on Bayesian inference. The morphological analysis indicated the presence of 15–16 teeth per row in the pharynx, equatorial vulva in females, 11 pairs of cloacal papillae in males, arranged as follows: 3 precloacal, 3 paracloacal, 5 postcloacal, and a minute precloacal unpaired, and spicule length less than 1mm. Such combination of morphological features seems to be unique when compared with that of other congeners, suggesting a possible new taxon. In the phylogenetic reconstructions based on 18S rDNA and COI mtDNA, *Cruzia* sp. formed an independent lineage, sister to a group formed by *C. americana* and *C. tentaculata*. Kathlaniidae was paraphyletic, because Cruzeinae formed a separate lineage from other kathlaniids and closely related to the cosmocercid *Cosmocerca* (Cosmocercidae, Cosmocercoidea). Based on these results we suggest that Cruzeinae should be elevated to family.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142713: Integrative Taxonomic Delimitation of Stonefishes (Perciformes: Synanceiidae) from the Kerala Coast, India

CS Anagha

Department of Marine Biology, Microbiology and Biochemistry, Cochin University of Science and Technology (CUSAT), Kochi 682016, India

Stonefishes (Family: Synanceiidae) are venomous, benthic marine fishes with cryptic morphology and unresolved taxonomy. Despite their ecological and medical significance, they are poorly documented in Indian waters, particularly along the Kerala coast. This study employed an integrative approach, combining morphological and mitochondrial DNA analyses, to clarify species boundaries. Specimens were collected as bycatch from trawl landings at Munambam, Kalamukku, and Sakthikulangara (January–April 2025). Forty-seven morphometric measurements and five meristic counts were recorded per specimen. Mitochondrial DNA was extracted from muscle tissue, and the cytochrome c oxidase subunit I (COI) gene was amplified via PCR. Sequences were aligned, and phylogenetic relationships were inferred using the Maximum Likelihood method. Eight species were identified—*Apistus carinatus*, *Inimicus didactylus*, *I. sinensis*, *Choridactylus multibarbus*, *Minous monodactylus*, *M. inermis*, *M. trachycephalus*, and *M. dempsterae*. Morphological identifications were confirmed through DNA barcoding, with COI-based phylogeny revealing eight distinct clades and interspecific genetic divergence of 4.1–24.6% (mean: 19%). Distinct length–weight relationships were established for *M. inermis* and *M. dempsterae*. This first integrative taxonomic account of Synanceiidae from the Kerala coast demonstrates the value of combining classical and molecular tools for delineating cryptic marine species and provides a foundation for accurate biodiversity assessment, ecological monitoring, and conservation planning.

Author Affiliation:

C.S. ANAGHA, Fishery Biology and Taxonomy Laboratory, Department of Marine Biology, Microbiology and Biochemistry, School of Marine Sciences, Cochin University of Science and Technology, Kochi, Kerala, India.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143499: Integrative Taxonomy as a foundation for understanding host relationships in Solenogastres

Franziska S Bergmeier¹ and M Carmen Cobo²

¹ Systematic Zoology, Ludwig-Maximilians-Universität München, Munich, Germany

² Département Systematique et Evolution, Museum National d'Histoire Naturelle, Paris, France Department of Invertebrate Zoology, National Museum of Natural History - Smithsonian Institution, Washington, DC, USA

Solenogastres (Mollusca, Aplacophora) are small, worm-shaped marine molluscs that are often overlooked in biodiversity studies, despite their widespread distribution across all oceans and depths. Many species exhibit intimate ecological relationships with other invertebrates, particularly colonial cnidarians but also sponges, which they use as hosts and food sources. Ecological associations often drive adaptation and speciation. For instance, species that rely on obligate symbiosis tend to have smaller populations, limited dispersal, and fragmented habitats, making them more vulnerable to environmental stress and extinction. Thus, studying associations in Solenogastres is essential to understand their evolution and resilience. Moreover, corals and sponges are vital components of benthic ecosystems and are highly sensitive to environmental changes. However, due to challenging taxonomy and historically limited sampling, the nature and specificity of these interactions remain poorly documented. This mirrors a broader lack of data on the biogeography and species documentation of solenogasters. Therefore, building a robust taxonomic framework for Solenogastres is critical, not only to resolve their diversity, but to illuminate the ecological and evolutionary implications of their symbiotic lifestyles. Here, we present a synthesis of what is currently known about solenogaster-host relationships, based on an extensive literature review, alongside preliminary results from ongoing morphological and molecular studies. Our integrative approach combines ecological observations with molecular and morphological approaches to improve species delimitation and host identification. This work lays the foundation for a more comprehensive understanding of Solenogastres ecology and evolution in a changing ocean.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143286: Integrative Taxonomy of a New Species of *Hoplias* Gill (Characiformes: Erythrinidae) from the Upper Paraná River Basin, Brazil

José Vitor Costa ¹ and Fernando Carvalho ²

¹ Department of Biological Sciences, Institute of Biosciences, Letters and Exact Sciences (IBILCE), São José do Rio Preto Campus, São Paulo State University (UNESP), São José do Rio Preto, 15054-000, Brazil

² Três Lagoas Campus (CPTL), Federal University of Mato Grosso do Sul (UFMS), Três Lagoas, 79613-000, Brazil

Hoplias Gill has long been considered taxonomically challenging among Neotropical freshwater fishes, particularly due to the presence of cryptic species within the *H. malabaricus* complex, which exhibits extensive morphological overlap among lineages of many Neotropical drainages. In this study, an integrative approach combining morphological and molecular data was employed to describe a new taxon from the upper Paraná River basin, Brazil. A total of 22 specimens were analyzed using morphometric and meristic assessments, along with mitochondrial COI gene sequencing. Species delimitation was performed through multiple methods, including genetic distance analysis on the BOLD Systems platform, Automatic Partitioning (ASAP), Generalized Mixed Yule Coalescent (GMYC), and Poisson Tree Processes (PTP). Phylogenetic trees were reconstructed using Bayesian inference. *Hoplias* sp. n. presents distinct diagnostic characters among congeners: 36–37 perforated lateral-line scales (vs. 37–43), 13–15 predorsal scales (vs. 15–19), 37–38 total vertebrae (vs. 39–45), and a rectilinear arrangement of scales at the base of the caudal fin. Molecularly, it forms a distinct clade with minimum K2P genetic distances of 3.7% from its closest relative (*H. aur*), exceeding the commonly accepted 2–3% threshold for species delimitation. All applied methods consistently recovered the new taxon as an independent evolutionary unit: ASAP (nine groups; $p = 8.79 \times 10^{-3}$), GMYC (nine entities; $p = 0.0007$), and PTP (support = 0.999). The convergence of morphological and molecular evidence strongly supports the recognition of *Hoplias* sp. n. as a valid new species for the upper Paraná River basin. These findings enhance our understanding of the genus diversity and underscore the power of integrative taxonomy in resolving cryptic species complexes among Neotropical fishes, thereby helping to reduce the Linnean shortfall.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143462: Karyotypic and Phylogenetic Assessment of an Individual of *Mazama cita sanctaemartae* Allen, 1915, From The Colombian Caribbean

Juan Daniel Jaramillo Hernández ¹, Eluzai Dinai Pinto Sandoval ¹, Pedro Peres ¹,
Héctor Ramírez Chavez ², Sergio Alcides Solari Torres ³ and José Mauricio Barbanti Duarte ¹

¹ Deer Research and Conservation Center (NUPECCE), School of Agriculture and Veterinarian Sciences, São Paulo State University (UNESP), Jaboticabal, Brazil

² Department of Biological Sciences, Faculty of Exact and Natural Sciences, University of Caldas. Manizales, Colombia

³ Mammalogy Group & Theriological Collection, Institute of Biology, University of Antioquia, Medellín, Colombia

The taxonomic classification of the genus *Mazama* Rafinesque, 1817, has been widely debated due to homoplastic morphological characters. Although six species have been described in Colombia based on morphology, integrative analyses combining genetic and morphological data are still lacking. This study aimed to analyze the species originally described as *Mazama cita sanctaemartae* Allen, 1915, and to characterize its phylogenetic and cytogenetic relationships. To achieve this, fibroblast cultures were established from the skin tissue of a recently collected specimen (ID: T467) seized from illegal wildlife trafficking in Barbosa, Antioquia, which exhibited morphological traits consistent with gray brocket deers from Colombian Caribbean. Chromosomal preparations were obtained, and Giemsa-stained karyotypes were analyzed. In addition, a phylogenetic analysis was performed using a 660 bp fragment of the mitochondrial Cytochrome B (CytB) gene from individual T467, in comparison with other gray brocket deer from different genera: *Subulo*, *Passalites*, and *Bisbalus*. Cytogenetic analysis revealed a diploid number ($2n$) = 66 and a fundamental number (FN) = 69, showing chromosomal similarities with the karyotype of *Bisbalus citus* from northwestern Venezuela. Phylogenetic reconstruction using Bayesian inference placed individual T467 within the *Bisbalus* clade. Thus, the karyotypic and phylogenetic analyzes of our study suggest that all Colombian individuals assessed may belong to the genus *Bisbalus*. The cytogenetic results may be further complemented with molecular cytogenetic techniques and chromosome painting to identify specific chromosomal rearrangements. This study provides preliminary insights into the cytogenetic and phylogenetic identity of gray brocket deer from the Colombian Caribbean, contributing to clarifying their taxonomic status and informing future conservation and management strategies.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143284: Lineage diversity and craniofacial disparity of Navajini (Apterontidae, Gymnotiformes) in deep river channels of tropical South America

Jonathan Allen and James Albert

Department of Biology, University of Louisiana at Lafayette, Lafayette, Louisiana, 70503, USA

The Navajini, a clade of Neotropical electric fishes within the family Apterontidae, exhibit exceptional craniofacial diversity that reflects a dynamic interplay of evolutionary forces. This study examines the morphological, ecological, and developmental drivers of phenotypic diversification in this group, which includes some of the most specialized skull morphologies among South American freshwater fishes. We integrate 3D geometric morphometrics, high-resolution micro-computed tomography (micro-CT), and multivariate statistical analyses within a robust phylogenetic comparative framework to assess patterns of skull shape evolution across the clade. Ancestral state reconstruction and tests for phylogenetic signal reveal that key cranial traits such as lower jaw elongation, opercle morphology, and maxilla orientation are not randomly distributed but instead show significant phylogenetic structure and ecological relevance. Morphological disparity is strongly influenced by sexual dimorphism in certain lineages, particularly those exhibiting hypertrophied male traits, while other groups display more conservative, modular cranial architectures. We find that access to novel regions of morphospace has been facilitated by shifts in feeding ecology and developmental modularity, enabling trophic specialization and repeated convergent evolution among ecologically similar taxa. These findings support a model in which cranial evolution is shaped by both adaptive responses to ecological opportunity and intrinsic developmental constraints. Overall, this work sheds light on the mechanisms generating phenotypic diversity in Apterontidae and contributes to a broader understanding of how ecological and evolutionary processes interact to shape morphological evolution in Neotropical freshwater fishes.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143425: Molecular evidence for mislabelling and taxonomic redundancy in public records of COI sequences of the genus *Lethrinus* (Teleostei: Lethrinidae)

Najmudeen Mohamed Theparambil, Badarul Sijad and Shoba Joe Kizhakudan

Finfish Fisheries Division, ICAR-Central Marine Fisheries Research Institute, Ernakulam North PO, Kochi, Pin 682018, India

Public DNA barcode databases such as GenBank and BOLD are invaluable tools for taxonomic and biodiversity research. However, inconsistencies in species identification and labelling can undermine their reliability, particularly for morphologically similar taxa like *Lethrinus*, a diverse genus of reef-associated fishes of family Lethrinidae prevalent throughout the Indo-Pacific. This study examines the consistency of species-level identifications in public COI sequence data of *Lethrinus* using molecular phylogenetic evidence. Over 200 COI sequences, representing more than 30 nominal species of the genus *Lethrinus*, were retrieved from GenBank and BOLD and used to construct a maximum likelihood (ML) tree in MEGA X. Sequences were annotated by species name and country of origin to detect taxonomic conflicts and potential mislabelling. *Lutjanus argentimaculatus* was included as an outgroup. The ML tree revealed several instances of taxonomic redundancy and probable misidentification. Sequences labelled as *Lethrinus atkinsoni* appeared in at least four divergent clades, with representatives from Indonesia, Australia, and the Philippines failing to cluster together—indicating either cryptic diversity or mislabelling. Likewise, *L. obsoletus* sequences from Micronesia and Australia were found in multiple, non-monophyletic lineages. Unresolved entries such as *Lethrinus* sp. (e.g., BOLD:AAC1547 from Mozambique and JN311945 from Australia) were placed within established species clades, suggesting unclear or incomplete identifications. Additionally, overlapping clades between nominal species—such as *L. rubrioperculatus* and *L. conchylatus*, or *L. olivaceus* and *L. genivittatus*—raised questions regarding the validity of current species boundaries. These results demonstrate notable taxonomic inconsistencies within public COI records of the genus *Lethrinus*. This underscores the urgent need for rigorous database curation, voucher-backed identifications, and integrative taxonomic frameworks combining morphology, molecular data, and geographic context to ensure accurate species delimitation and dependable molecular reference libraries.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143572: Morphological And Vocal Divergence In Disjunct Populations Of Three Endemic Atlantic Forest Rhynchocyclidae Species

Renan Teixeira da Silva and Vagner Cavarzere

Department of Biodiversity and Biostatistics, Institute of Biosciences, São Paulo State University, Botucatu 18618-689, Brazil

Recent taxonomic studies of Neotropical suboscine passerines have demonstrated the importance of integrative approaches, particularly for cryptic species complexes where traditional morphological characters show limited diagnostic value. Our investigation focused on three challenging *Hemitriccus* species (*H. mirandae*, *H. furcatus*, and *H. nidipendulus*) with disjunct distributions across Brazil. We combined bioacoustic analysis using convolutional neural networks (CNN) with comprehensive morphological examination of 35 voucher specimens from the Museu de Zoologia da Universidade de São Paulo. Detailed morphometric analysis included six measurements: culmen length, width and height, tarsus, wing, and tail length. Multivariate analysis of variance (MANOVA) was used to assess differences among populations, while Student's t-tests were applied to evaluate pairwise population differences. Plumage coloration was assessed using standardized color catalogs. *Hemitriccus mirandae* specimens exhibited pale yellow underparts (2.5Y 8/4) becoming lighter posteriorly, contrasting with their uniform greenish-olive dorsum (49-Greenish Olive); *H. furcatus* showed more complex plumage with the gray chest (N 6/0) grading to a light gray abdomen (10Y 8/6), and upperparts featuring a brownish head (23-Raw Umber) transitioning to greenish-olive body (49-Greenish Olive); *H. nidipendulus* displayed distinctive gray underparts (N 6/0) with prominent yellowish streaking (157-Sulfur Yellow) and consistent greenish-olive (49-Greenish Olive) upperparts. Statistical analysis revealed significant morphological differentiation between *H. nidipendulus* subspecies ($F_{1,1} = 5.9$, $p = 0.005$), primarily driven by wing and tail dimensions ($p = 0.001$ and $p = 0.003$, respectively). However, the lack of corresponding plumage differences and the moderate (70-80%) classification accuracy of vocal signatures from CNN analysis suggest these may represent intraspecific variation rather than species-level divergence. These findings support the synonymization of *H. n. paulistus* with *H. n. nidipendulus*, while highlighting the need for additional sampling to clarify the taxonomic status of *H. mirandae* and *H. furcatus* populations.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143587: Morphological and vocal divergences suggest a rearrangement in the taxonomy of eastern populations of *Cnemotriccus fuscatus* (Aves, Tyrannidae)

Melissa Pessoa Osaku and Vagner Cavarzere

Department of Biodiversity and Biostatistics, Institute of Biosciences, São Paulo State University, Botucatu 18618-689, Brazil

Cnemotriccus fuscatus comprises a complex of seven subspecies that have not undergone thorough taxonomic revision. We aimed to evaluate the morphological and vocal characters of two eastern South American subspecies—*C. f. fuscatus* and *C. f. bimaculatus*—to assess their taxonomic status. Specimens from the Museu de Zoologia da Universidade de São Paulo were examined and color-coded, while vocal recordings were obtained from the Macaulay Library and Xeno-canto databases. Morphometric measurements—including wing chord, tail length, tarsus length, and bill dimensions—were taken from 13 *fuscatus* and 23 *bimaculatus* specimens using a precision caliper. Additionally, 51 recordings of the nominotypic taxon and 53 of *bimaculatus* were analyzed for loudsong duration, note number, pace, maximum entropy, and frequency ranges using Raven Pro 1.6.5. Statistical analyses were conducted in R, employing a Multivariate Analysis of Variance (MANOVA). Both populations display a predominantly brownish (10YR 3/4 for *bimaculatus* and 2.5Y 3/3 for *fuscatus*) plumage, but *fuscatus* exhibits a yellowish-olive (5Y 8/6) belly, contrasting with the buff (5Y 8/3) or whitish (8/N) underparts of *bimaculatus*. While no significant morphometric differences were found ($F_{1,1} = 0.7$; $p = 0.547$), bioacoustic divergence was highly significant ($F_{1,7} = 26.1$; $p = 0.001$). Three variables—duration and maximum frequency and entropy—were correlated. Among the remaining parameters, *bimaculatus* exhibited more notes ($t = 2.8$; $p = 0.005$), faster pace ($t = 10.7$; $p = 0.001$), and broader bandwidth ($t = 3.3$; $p = 0.001$) compared to *fuscatus*. On average, *fuscatus* produced 6.8 ± 4.2 notes per song at a pace of 3.8 ± 0.7 , with a bandwidth of 975.3 ± 162.4 Hz, whereas *bimaculatus* averaged 9.6 ± 6.0 notes, pace of 5.9 ± 1.1 , and bandwidth of $1,149.5 \pm 339.6$ Hz. Despite overlap, the vocal differences, alongside morphological analysis, strongly support elevating these taxa to full species.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-129133: Morphological data & first record of *Lecithocladium excisum* (rudolphi, 1819) (Digenea; Hemiuridae) in the new host *Capros aper* (linnaeus, 1758) (Caproidae) off the Algerian coast in the Mediterranean sea

Fatima Zohra Sarah Zedam

Biodiversity and Environment: Interactions-Genomes (LBEIG). University of Science and Technology Houari Boumediene USTHB

This study contributes to the knowledge of Digenean diversity by documenting newly recorded species in Algerian waters, either through new host associations or from previously unreported localities.

The trematode *Lecithocladium excisum* (Rudolphi, 1819), originally described from *Scomber scombrus* Linnaeus, 1758 (Scombridae) off Rimini, Italy, is a cosmopolitan species widely distributed across tropical and temperate marine environments. It has been reported from the same host in the Atlantic Ocean and in various parts of the Mediterranean Sea, including the Turkish coast.

Lecithocladium excisum exhibits a euryxenous host specificity, infecting a wide range of teleost fishes across multiple families such as Stromateidae, Carangidae, Mullidae, Scombridae, Triglidae, Sparidae, Pristigasteridae, Bothidae, and Nemipteridae. In the present study, *L. excisum* is reported for the first time in Algerian waters, parasitizing a new host species, *Capros aper* (Linnaeus, 1758), from the family Caproidae Bonaparte, 1835. Morphological data are provided to support this new host and locality record, enriching the parasitological inventory of Mediterranean marine fishes.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143241: New *Astyanax* Baird & Girard from the Madeira and Tapajós River drainages, Southern Amazon (Characiformes: Acestrorhamphidae)

Letícia Paes Esteves and Fernando Rogério de Carvalho

Department of Zoology, Federal University of Mato Grosso do Sul, Três Lagoas Campus, Três Lagoas, 79613-000, Brazil

Astyanax Baird & Girard, 1854 is the most widely distributed genus of Acestrorhamphidae, occurring from the West Texas Gulf to Central Argentina. Out of the 120 valid species currently recognized, around 15 occur in the Amazon basin. A possible new species was registered in streams of the Aripuanã River basin (= Madeira River basin) and Juruena River basin (= Tapajós River basin). For the new taxon, morphological, meristic, and coloration characters of 42 specimens were analyzed. *Astyanax* sp. n. differs from all its congeners by the following combination of characters: two humeral spots, the first vertically elongated and the second approximately rounded, beginning on the dark longitudinal stripe; maxilla toothless or with 1 tooth; premaxilla with two tooth rows: outer row with 4 or 5, tricuspid, inner row with 4 or 5, heptacuspids; dentary with 4 teeth, penta- to hexacuspids; complete lateral line, extending to the end of the caudal peduncle, with 34 to 37 perforated scales; 12 to 15 circumpeduncular scales; 6 or 7 transverse scale rows above the lateral line; 5 or 6 below; anal fin with 22 to 27 branched rays. Males of the new species show a straight anal fin and a bony hook on the distal segments of the last unbranched ray. The record of the new taxon highlights the importance of sampling headwaters of Amazonian drainages, which harbor significant undescribed species diversity, especially small-sized ones, in areas subject to anthropogenic impacts (e.g., extensive agriculture). The description of this new species expands the known diversity of *Astyanax* and contributes to reducing the Linnean shortfall of Neotropical ichthyofauna.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147303: New country record of globally threatened *Uperodon assamensis* (Amphibia: Microhylidae) from Bangladesh, with an updated global distribution and taxonomic analysis

Najmul Hasan ^{1,2}, Harij Uddin ^{1,2}, Md. Rafiqul Islam ³, Md. Asir Uddin ³, Md Habib Ullah ^{2,4}, Konok Roy ⁵, Erich Köck ⁶, Christoph Andrijczuk ⁷, Mohammad Abdul Wahed Chowdhury ^{1,2,3,4} and Ibrahim Khalil Al Haidar ^{1,2,3,4}

¹ Eco-climate Lab, Department of Zoology, University of Chittagong, Chattogram 4331, Bangladesh

² Animal Immunization Lab, Department of Zoology, University of Chittagong, Chattogram 4331, Bangladesh

³ Venom Research Centre, Chittagong Medical College, Chattogram 4203, Bangladesh

⁴ Department of Zoology, University of Chittagong, Chattogram 4331, Bangladesh

⁵ Forensic Lab, Wildlife Crime Control Unit, Bangladesh Forest Department, Dhaka 1207, Bangladesh

⁶ Independent Researcher, Quellengasse 15, 4072 Alkoven, Austria

⁷ Department of Surgery, Evidensia Veterinary Clinic for Small Animals, Kabels Stieg 41, 22850 Norderstedt, Germany

We report a new country record of *Uperodon assamensis* (a globally threatened species, previously considered endemic to India), with its taxonomic description from south-central Bangladesh. The newly recorded specimen was identified by having a distinct yellowish dorsal vertebral stripe, an absent or non-visible tympanum, rounded and moderately large choanae, absence of vomerine teeth, an oval tongue with rounded tips and papillae, and a distinct supratympanic fold that extends from the eyes' posterior corner to the supra-axillary region. The boxplot of the morphometric measurements of the type specimens from distant geo-locations reveals substantial variability in snout-vent length, head width, head depth, tibia length, and axillary-groin distance. In contrast, the eye diameter, internarial distance, eye nostril distance, and eye to snout distance show less variability. Besides this, we compiled its known occurrence records and confirmed the current global distribution in three South Asian countries: India, Nepal, and Bangladesh. This study contributes to understanding the geographic distribution of *U. assamensis* and intraspecific morphological and morphometric diversity, highlighting the importance of continued field surveys in uncovering the biodiversity of underexplored regions in South Asia.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143497: Notes on the diversity and conservation of three threatened subtidal octocorals of the highly urbanised coastal regions of Mumbai, Arabian Sea

Ramvilas Ghosh A ¹, Pradip Patade ² and Ranjeet Kutty ³

¹ Faculty of Ocean Science and Technology, Kerala University of Fisheries and Ocean Studies, Kochi, India

² Coastal Conservation Foundation, Mumbai, India

³ Department of Aquatic Environment Management, Kerala University of Fisheries and Ocean Studies, Kochi, India

Here, we formally redescribe *Menella indica* Gray, 1870, a century after its original description from Back Bay, Mumbai, India. We also report *Pseudopterogorgia fredericki* Williams & Vennam, 2001, a species common along Mumbai's rocky shores and *Echinogorgia* sp., a potential new species and more elusive sub-tidal inhabitant of the region. Using an integrative taxonomic approach, we provide descriptive notes and detailed illustrations of external morphology and sclerites of the three species. A phylogenetic tree based on sequences (12 newly generated) of a single mitochondrial marker (mtMutS) was also constructed to examine the systematic position and evolutionary relationship of the three species among similar Indo-Pacific taxa. The white, unbranched specimen matches the original description of *M. indica* Gray, 1870, with distinguishable sclerites in the form of rooted leaf-scales mostly in the calyx and surface layer. Similarly, the external morphology and sclerite structure (mostly spindles and scaphoids) match the original description of *Pseudopterogorgia fredericki* Williams & Vennam, 2001, described from St. Mary Isles, Karnataka, India. However, Williams & Vennam stated that there are no sclerites in the polyps, whereas the specimens examined here have flattened rods on the polyps. *Echinogorgia* sp. colonies are small, grow in one plane, with non-anastomosing branches, and thornscales and tuberculate spindles as the major type of sclerites. The phylogenetic tree recovers all sequences of the genus *Pseudopterogorgia*, including *P. fredericki*, and genera *Echinogorgia* and *Menella*, including *Echinogorgia* sp. and *M. indica* within the family Gorgoniidae and Paramuriceidae, respectively. We further discuss the conservation status of the three species based on the International Union for Conservation of Nature (IUCN) methodology and classify the species into specific Red List categories. Major threats to species in the region include coastal zone reclamation and development, pollution, and climate change.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143102: On the Taxonomy and Holotype of *Rhachidelus brazili* Boulenger, 1908 (Serpentes: Dipsadidae)

Giovanna Lissa Cambuí-Milhomens and Nathalie Citelli

Zoology Department, Darcy Ribeiro Campus, University of Brasilia, Brasilia - 70910-900, Brazil

Rhachidelus Boulenger, 1908, is a monotypic snake genus belonging to the tribe Pseudoboini and the family Dipsadidae, distributed only in South America. The genus and the species were described by Boulenger (1908) based on a single male specimen from the state of São Paulo, Brazil, sent at the time by Vital Brazil, a physician and public health officer. In the description, Boulenger was succinct, basing it on data from scalation (number of ventrals, subcaudals, supralabials, infralabials, and postoculars), coloration, biometry, and scale topography. In the present study, based on data collected from 11 new specimens, we propose an emended diagnosis for the species, as well as track its holotype. *Rhachidelus brazili* can be differentiated from other species of the tribe Pseudoboini by the combination of the following characters: (1) midbody dorsal scales in 25 rows; (2) smooth dorsal scales with two apical pits; (3) enlarged vertebral row; (4) mixed subcaudals (single and divided); (5) single cloacal scale; (6) divided nasal scales; (7) one preocular; (8) two postoculars; (9) two or three preventrals; (10) darkened dorsum; (11) dorsal coloration invading the lateral sides of the ventral scales. In addition, we tracked the holotype of *Rhachidelus brazili*, since in the description, Boulenger (1908) did not assign a registration number to the specimen, only mentioning that it would be deposited at the British Museum of Natural History, in London. Through contact with the curatorship of the institution's Reptile Collection and through photographs, it was possible to identify the label with the name of Vital Brazil, indicating that it is the only individual sent by him and used by Boulenger to describe the genus and the species. With this, it becomes possible to officially link registration number 1946.1.9.35 to the holotype of *Rhachidelus brazili*.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143103: Osteological intraspecific variation in Taxonomy: a look into the green iguana

Vieno Rosa ¹, Marcos Vinícius Coelho ² and Camila Cupello ³

¹ Postgraduate Program in Ecology and Evolution (PPGEE), Rio de Janeiro State University (UERJ), Rio de Janeiro, 20550-900, Brazil

² Department of Zoology, Rio de Janeiro State University (UERJ), Rio de Janeiro, 20550-900, Brazil

³ Department of Archaeology, Rio de Janeiro State University (UERJ), Rio de Janeiro, 20550-900, Brazil

Taxonomy studies of extant taxa generally focus on external morphology, often ignoring all intraspecific variation. Thus, possibly creating morphospecies that do not correspond to valid taxonomic units. Additionally, osteological studies are often neglected, which could provide a lot of new information regarding morphological traits. Hence, studying not only osteology but also intraspecific variation in skeletal structures could be of great value for species description and separation. To better assess the relevance of intraspecific osteological variation for taxonomy, here we analyze this variation in the skeleton of nine specimens of *Iguana iguana*. We observed considerable individual variability in skull bones, including differences in shape and proportions; in the atlas vertebra, which either presented or lacked a neural spine; variation in the number of ribs; and, most notably, in caudal vertebrae morphotypes. The caudal vertebrae displayed significant variation among individuals, comprising seven distinct morphotypes that exhibited a consistent sequential pattern while also differing in count and presence. As a result, no specimen shared the same caudal vertebral pattern as another. We conclude that a species may present substantial variation in different osteological complexes. Therefore, evaluating intraspecific variation may help prevent the overestimation of the number of existing species. Moreover, understanding the estimated degree of variation in a determined extant taxon could be extrapolated to its fossil representatives. The present study thus highlights the importance of incorporating osteological individual variation into taxonomic analyses.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-152722: Phylogenetic relationships of a new schizorhynch genus refute the monophyly of *Schizochilus* Boaden, 1963 (Platyhelminthes, Rhabdocoela)

Yander L. Diez ^{1,2}, Marlies Monnens ^{2,3}, Sam Hermans ², Jhoe Reyes ², Holly Sweat ¹ and Tom Artois ²

¹ Smithsonian Marine Station, 701 Seaway Drive, Fort Pierce, Florida 34949, United States

² Hasselt University, Centre for Environmental Sciences, Research Group Zoology: Biodiversity and Toxicology, Agoralaan Gebouw D, B-3590 Diepenbeek, Belgium

³ Royal Belgian Institute of Natural Sciences, OD Taxonomy and Phylogeny, Vautierstraat 29, B-1000 Brussels, Belgium

Rhabdocoel flatworms constitute one of the most ecologically diverse and speciose groups of microturbellarians (Platyhelminthes). Within this clade, Schizorhynchia, a monophyletic group of nearly 200 species worldwide, remains taxonomically challenging, with a poorly resolved phylogeny and a classification that does not accurately reflect the taxon's evolutionary history. In this contribution, we describe a new schizorhynch genus from Cuba and the southeastern coast of the United States, integrating morphological data with new molecular phylogenetic evidence. Species of this new genus exhibit a *conjuncta-duplex* type male copulatory organ, which terminates in a sclerotised cap and comprises a prostate vesicle, cirrus, and stylet. The female system features an elaborate bursa that proximally opens to the digestive parenchyma through an internal pore. The three new species described here are primarily distinguished by differences in bursa morphology and stylet length. Morphologically, members of this new genus most closely resemble species of *Schizochilus* Boaden, 1963, yet molecular evidence clearly separates them in the phylogeny. Our analyses further demonstrate that the current concept of *Schizochilus* is non-monophyletic, splitting it into two distinct lineages. To resolve this, we here propose to transfer two previously described species to the new genus and hypothesize that several additional species of *Schizochilus* will ultimately require reassignment once molecular data become available.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-145818: Redescription and first molecular characterization of *Spauligodon oxkutzcabensis* (Chitwood, 1938) from lizards in Brazil

Glória Maria Cardoso Lacerda ¹, João Antonio de Araujo-Filho ², Samuel Cardozo Ribeiro ³ and Felipe Bisaggio Pereira ⁴

¹ Postgraduate Program in Parasitology, Institute of Biological Sciences, Department of Parasitology, Federal University of Minas Gerais, Pampulha Campus, Belo Horizonte, CEP 31270-901, Brazil

² Center for Biological and Health Sciences, Regional University of Cariri, Campos Sales, CEP 63150-000, Brazil

³ Laboratory of Biology and Ecology of Wild Animals, Institute for Educator Training, Federal University of Cariri, Brejo Santo, CEP 63260-000, Brazil

⁴ Helminth Ecology and Taxonomy Laboratory, Department of Parasitology, Institute of Biological Sciences, Federal University of Minas Gerais, Pampulha Campus, Belo Horizonte, CEP 31270-901, Brazil

The genus *Spauligodon* Skrjabin, Schikhobalova, Lagodovskaja, 1960 has a wide global distribution and comprises 52 species, of which 12 are reported in the Neotropical Region, parasitizing mostly reptiles. In Brazil, there are records of only one species, namely *Spauligodon oxkutzcabensis* (Chitwood, 1938), which is an abundant parasite in lizards of the family Phyllodactylidae. The original description of *S. oxkutzcabensis* was based on the analysis of a restricted set of morphological and morphometric characteristics, with limited taxonomic detail. This study provides a detailed redescription of *S. oxkutzcabensis*, including the first observations using scanning electron microscopy (SEM), as well as the first genetic characterization of the species. During a parasitological survey carried out in May 2024, in the municipality of Mauriti, State of Ceará, Brazil, specimens of *Spauligodon* were found in the intestine of *Phyllorhynchus periosus* (Squamata: Phyllodactylidae). The nematodes were identified as *S. oxkutzcabensis* based on the presence of well-developed lateral wings in males, three pairs of papillae in the posterior region, with the last pair not supported by the caudal wing, and the presence and number of spines on the tail of female specimens. The nematodes were characterized morphologically by light microscopy and SEM. The parasites were also subjected to molecular analysis, with the amplification and sequencing of partial fragments of the 18S and 28S rDNA genes. Based on the, it was possible to provide a more comprehensive morphological description, such as the location of the nerve ring, males with a tripartite lateral wing in the region where it begins in the esophagus, and females with elongated muscular ovijector, characteristics not observed before. This improves the specific diagnosis of *S. oxkutzcabensis* (Chitwood, 1938), which was supplemented by molecular data, contributing to knowledge about species variability and the general taxonomy of members of the genus *Spauligodon* in the Neotropical region.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146884: Shedding light on the hidden larvae of *Benthescymus laciniatus* Rathbun, 1906 (Decapoda, Dendrobranchiata): An integrative taxonomic approach

Rita F. T. Pires ^{1,2}, Cátia Bartilotti ^{1,3}, Clara Lopes ^{1,2}, Jorge Lobo-Arteaga ^{1,3}

¹ Portuguese Institute for the Sea and Atmosphere (IPMA), Sea and Marine Resource Department, Av. Doutor Alfredo Magalhães Ramalho 6, 1495-165 Algés, Portugal

² Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), Terminal de Cruzeiros de Leixões. Av. General Norton de Matos s/n 4450-208 Matosinhos, Portugal

³ Marine and Environmental Sciences Centre (MARE), ARNET – Aquatic Research Network Associate Laboratory, Universidade NOVA de Lisboa, Campus de Caparica, 2829-516 Caparica, Portugal

Advancing the current knowledge about deep-sea shrimps is challenging considering the difficulty in sampling organisms and the damaged state in which they arrive at the surface after collection. Thus, several aspects of their biology and ecology remain unknown or poorly understood, despite the importance of many species to worldwide fisheries. Integrative taxonomic approaches, merging morphological and DNA barcoding analyses, have been useful to obtain more information about these crustaceans. The family Benthescymidae, which includes benthopelagic species inhabiting depths of 500 to 2000 m, remains among the least understood, since information available for both larvae and adults is scarce. The taxonomy of the family has been phylogenetically reviewed in recent years, as in the case of *Benthescymus* now considered a paraphyletic genus with two species – *Benthescymus crenatus* and *Benthescymus laciniatus*. Previously described species of the genus were reassigned to new and distinct genera within the family Benthescymidae. The present study provides an extension of a previous work in which we reported the first description of the decapodid stage of *B. laciniatus* using integrative taxonomy, by adding the first description of zoeal stages of the species. Specimens were collected in the neuston layer (surface of the water column) during a sea survey in the Madeira-Tore geological complex in the north-eastern Atlantic. Several morphological characters distinguished the individuals from closely related taxa described in the literature, especially regarding the abdominal spines and the telson shape. The morphology of the sampled larval stages is discussed and compared with the available knowledge for Benthescymidae shrimps, adding new knowledge for future taxonomic studies and clarifying older larval descriptions. Insights into the larval ecology of the species are provided, with a focus on its adaptations to a neustonic lifestyle.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143549: Taxonomic revision of the species *Hoplias malabaricus* Bloch, 1794 (Characiformes: Erythrinidae) from the Restinga de Jurubatiba National Park, Rio de Janeiro, Brazil

Luísa Andrade Mendes ¹, Paulo Brito ², Thiago de Paula ³ and Diogo Mayrinck ¹

¹ Department of Science and Biology Education, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

² Department of Zoology, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

³ Department of Genetics, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

The Restinga de Jurubatiba National Park, is located in the northern coast of Rio de Janeiro state, and presents eighteen coastal lagoons with a wide range of environmental conditions, specially salinity levels and geographic orientation relative to the shoreline. This diversity makes the region an ideal setting for ecological and evolutionary studies. *Hoplias malabaricus* is a fish widely distributed throughout South America, being considered a taxonomic complex due to the difficulty in delineating its lineages, representing one of the main challenges for Neotropical ichthyofauna taxonomy. To revise this complex, we collected 22 individuals from six lagoons in the Restinga de Jurubatiba National Park, whose selection was mainly based on the variations of the salinity levels. Comparative anatomical analyses were performed with specimens of the *Hoplias malabaricus* complex from other basins from South and Central America. Furthermore, we extracted and sequenced the mitochondrial COI gene and compared them with data from BOLD and GENBANK databases. We observed significant osteological variation among the species within the species complex, especially the mandibular symphysis shaped like a “lock,” a lateral ethmoid with a slender process projecting ventrolaterally, and a huge jugular depression on the lateral surface of the braincase. Molecular analyses indicated genetic divergences of approximately 7.7% compared to the species from the Rio Doce group (MG) and 8.3% relative to *H. malabaricus sensu stricto* from the North-Northeast of Brazil, confirming considerable differences within the complex. The analyses revealed significant novel anatomical and molecular differences in the collected individuals. The combined approach of anatomical and genetic analysis is essential to clarify the taxonomy and to understand the evolution and distribution of species within the complex *Hoplias malabaricus*.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143606: Taxonomic Survey of Ascidians (Tunicata: Ascidiacea) in the Parque Natural Municipal Marinho Recife de Fora Natural, Porto Seguro, Bahia, Brazil

Emily Rios da Silva, Paulo Cezar Azevedo da Silva and Luis Felipe Skinner

Marine Benthic Ecology and Dynamic Lab, Science Department, Teacher Formation Faculty, Rio de Janeiro State University (UERJ), City of São Gonçalo 24435-005 Brazil

Ascidians (Ascidiacea) are sessile marine invertebrates found in coastal and reef environments, occurring in both solitary and colonial forms. Despite their ecological relevance as filter feeders and bioindicators, their diversity in tropical reef environments from Southwest Atlantic remains poorly understood. This study presents a taxonomic survey of ascidians from the Parque Natural Municipal Marinho Recife de Fora (PNMRF), a marine reef protected area located on the southern coast of Bahia, recognized as the third largest center of marine biodiversity in Brazil. Sampling was conducted through free diving and manual collection on coralline substrates. Specimens were fixed in 4% formalin and preserved in 70% ethanol for subsequent morphological analysis, based on external, internal, and larval characteristics, with the support of specialized taxonomic literature for the Atlantic. A total of 21 species were identified, with a predominance of the genus *Didemnum*. Among the recorded taxa, highlights include new records for the Brazilian coast, including representatives of *Diplosoma*, the possible range expansion of non-native species such as *Pyura gangelion* and *Styela canopus*, and the distribution extension of native species such as *Eudistoma recifensis* and *Polycarpa spongiabilis*. These results underscore the still underexplored richness of ascidians in reef environments and provide essential data to support taxonomic studies, biological monitoring, and conservation strategies in PNMRF and other tropical coastal ecosystems.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142427: Taxonomic Synopsis of the genus Slender racer snake *Platyceps* Blyth, 1860 (Reptilia: Colubridae) from Iran

Rasoul Karamiani

Department of Biology, Faculty of Science, Razi University, 6714967346 Kermanshah, Iran

The genus slender racer snake *Platyceps* Blyth, 1860 with about 33 valid species, is distributed in northern and northeastern Africa, southern and southeastern Europe, Central Asia, southwestern Asia, to India; Among colubrid non-venomous snakes, the genus *Platyceps* is distinguished by such characteristics as: high speed in movement, round pupils, loreal scales present, the uppermost scale in front of the eye is connected to the frontal scale, seven or more upper labials scales, 19 dorsal scales smooth or slightly serrated. Five species of this genus occur on Iranian Plateau as follows: *Platyceps karelini* (Brandt, 1838), *P. mintonorum* (Mertens 1969), *P. najadum* (Eichwald, 1831), *P. rhodorachis* (Jan, 1863), and *P. schmidtleri* (Schätti & McCarthy, 2001). Based on morphological and molecular characteristics, the taxonomic status of the subspecies *P. k. mintonorum* and *P. n. schmidtleri* was changed to full species. The data used for the distribution maps were based on all available bibliographic records, and personal field observations. The results showed that among the five species located in Iran, *P. rhodorachis* has the most widespread distribution and habitat diversity, and *P. mintonorum* has a very limited distribution in the border of Iran and Afghanistan and Pakistan.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143577: Taxonomy and systematics of *Gymnorhamphichthys* (Rhamphichthyidae: Gymnotiformes)

Eric Bruschi Haddad and James Albert

Department of Biology, University of Louisiana at Lafayette, 411 E St Mary Blvd, 70503, Lafayette, LA, United States

The ability to delimit species and clades is essential to understand their ecology, evolutionary history, and assess their conservation need. *Gymnorhamphichthys*, known as Sand knifefishes, is a genus of South American weakly electric fishes. The clade has five valid species, most of which have broad geographic distributions with substantial phenotypic variation. These variations resulted in a convoluted taxonomic history, lack of clear diagnostic features and misidentification. Since older taxonomic methodologies failed to distinguish between possible pseudo cryptic species, we expect newer methodologies such as micro-computed tomography, 3D morphometrics and multi loci molecular sequences to allow us to elucidate patterns of diversity within this clade. Data was collected from specimens in museums across North America (ANSP, FMNH, UF, USNM), Brazil (INPA, MZUSP, MNRJ, DZUFMG, LBP, PUC-Minas) and Europe (MHNG). Non-destructive microtomography allowed for character search, osteological description, and species delimitation. Phylogenetic tree was created combining both molecular and morphological matrix following maximum likelihood and posterior Bayesian analysis. Preliminary results support the five valid species already described with external and internal characters, molecular data, and ecological traits. Two possible new species from Guyana and Trombetas region are being evaluated. Results from this research will clarify the alpha taxonomy of *Gymnorhamphichthys*, addressing a major gap in the field of neotropical freshwater fishes and permit future studies such as how intraspecific variation can be transformed into interspecific differences, evolutionary and biogeography trends of Neotropical freshwater fishes and morphological evolution.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147170: Taxonomy of Demospongiae from the Indo-Pacific shallow waters

Gabrielle Czyzewski ¹, Cristiana Castello Branco ^{2,3} and Camilla Alves Souto ^{3,4}

¹ School of Natural Sciences and Mathematics, Department of Marine Science, Galloway Campus, Stockton University, Galloway, NJ 08205, United States of America

² Department of Invertebrates, National Museum - Federal University of Rio de Janeiro, Rio de Janeiro (RJ) 20941-160, Brazil

³ National Museum of Natural History, Smithsonian Institution, Washington D.C., United States

⁴ School of Natural Sciences and Mathematics, Department of Marine Science, Galloway Campus, Stockton University, Galloway, NJ 08205, United States of America

The shallow waters of the Indo-Pacific Ocean are known for harboring an immense biodiversity of organisms, specifically sponges (Porifera). An expedition conducted by the National Institute of Health (NIH) collected six species of sponges with potential medicinal properties from Thailand and Papua New Guinea. This project aims to identify, classify and describe those specimens, so that their names can be linked to the biomedical compounds described by the NIH. All samples were deposited at the Smithsonian National Museum of Natural History, and identifications followed standardized taxonomic protocols. To date, the classification of four specimens has been narrowed down to a lower taxonomic level. Three specimens were identified in the order Axinellida: Specimen 1 is a Raspailiidae, with a smooth, paper-like surface and massive shape, it presents oxeas, styles and subtylostyles; specimen 2 is an Axinellidae, with a smooth, massive cylindrical shape, it has oxeas, raphidiform oxeas, and very rare styles; and specimen 3 is an Axinellidae that has a dichotomous branching body-shape, with worm-like strongyles and styles. The fourth specimen was identified in the genus *Wigginsia* (family Acarnidae, order Poecilosclerida) by having choansomal tyloles and acanthostrongyles. All sponges will be identified to the lowest taxonomic unit possible and new species will be named and described. The next step to improve species identification and describe morphological details is to obtain images of spicules under a scanning electron microscope.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147437: Taxonomy of Hyalonema (Porifera, Hexactinellida, Amphidiscosida) from Campos Basin (off Rio de Janeiro, Brazil)

Julie Maia, Eduardo Hajdu and Cristiana Castello-Branco

¹ Department of Invertebrates, National Museum - Federal University of Rio de Janeiro, Rio de Janeiro (RJ) 20941-160, Brazil

² Smithsonian Institution, National Museum of Natural History, Department of Invertebrate Zoology, 10th and Constitution Ave NW, Washington, D.C. 20560, USA

Sponges are one of the most representative and abundant benthic groups, with records to different environments and depths. Regarding their diversity, around 450 marine species are described to the Brazilian Economic Exclusively Zone (EEZ), with only 17 of them belonging to the class Hexactinellida. These sponges are found in cold and deep waters, and remain poorly studied due to the high costs and logistical challenges of sampling. This study aims to describe hexactinellid species of the family Hyalonematidae, sampled in the Southwestern Atlantic (Campos Basin, off Rio de Janeiro state), and deposited at the Museu Nacional (MNRJ-UFRJ), in Rio de Janeiro, Brazil. The three specimens analyzed here belong to *Hyalonema*. This genus encompasses 100 species described worldwide, which are classified in 12 subgenera. In Brazil, four species have been recorded to date: *H. (Coscinonema) schmidtii*; *H. (Cyliconema) conqueror*; *H. (Cyliconemaoida) alucia*; and *H. (Prionema) dufresnei*. Among the specimens examined, two potentially new species are being described, one *H. (Corynonema)* sp. and one *H. (Cyliconema)* sp.. Notably, the former represents the first record of this subgenus to the Atlantic Ocean. *Hyalonema (Cyliconema)* sp. is characterized by acanthophorae in its basalia, pinnular pentactines in the dermalia and atrialia, diactins, hexactins, and pentactins in the choanosome, as well as amphidisc microscleres (macro-, meso-, and microamphidiscs). In turn, *H. (Corynonema)* sp., presents basalia with acanthophorae, pinnular pentactins and hexactins in its dermalia and atrialia, diactins, pentactins and hexactins in the choanosome, together with amphidisc microscleres (macro-, meso- and microamphidiscs) and microhexactins. The uniqueness of the samples, the potential discovery of new species, and the first Atlantic record of the subgenus highlight the need for further taxonomic studies on the group, which appears to be markedly understudied in the SW Atlantic.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143552: The taxonomic status of *Phalloceros uai* (Poeciliidae: Cyprinodontiformes) in the Quadrilátero Ferrífero, Brazil

Eric Bruschi Haddad ¹, Tatiana Moura Barroca ² and Fábio Vieira ³

¹ School of Biological Sciences, University of Louisiana at Lafayette, Lafayette, LA 70501, USA

² Development Foundation, Federal University of Minas Gerais, Belo Horizonte, MG 31270-901, Brazil

³ Department of Zoology, Institute of Biological Sciences, Federal University of Minas Gerais, Belo Horizonte, MG 31270-901, Brazil

The genus *Phalloceros* Eigenmann, 1907 is one of the 27 valid and described of the Poeciliidae family, representing 22 small size species distributed in South America. Among the species, *Phalloceros uai* Lucinda, 2008 is an endemic species to the Rio das Velhas basin, diagnosed autapomorphically by a distinctive large square lateral spot in larger specimens. However, subsequent studies have reported its occurrence in adjacent sub-basins, such as Piracicaba and Santo Antônio basins, and noted the presence of various phenotypes. Given these discrepancies in current understanding of its geographic distribution, morphological and genetic recognition, and the paucity of natural history data, this study aimed to assess the taxonomic status of *Phalloceros uai* specimens from the Quadrilátero Ferrífero using an integrative taxonomic approach. Specimens were collected between 2018 and 2021 from four localities across the upper Doce and São Francisco River basins. Morphological measurements included total and standard length, height, and gonopodium length in males. Osteological structures were examined via diaphanization and compared to the holotype, and molecular analyses were conducted using COI gene. Stomach content and gonads analyses were performed on randomly selected individuals. We identified six distinct lateral spot phenotypes, five divergent from the original diagnosis. No significant differences were observed in diet, reproductive characteristics, size, or gonopodium structure among specimens of varying phenotypes, sexes, or populations. Genetic sequences showed less than 2% divergence among *Phalloceros uai* sequences. Females exhibited viviparity and superfetation. The species' diet primarily consisted of autochthonous animal items. In conclusion, the studied populations did not present sufficient morphological or molecular distinctions to warrant species differentiation, aligning with the diagnosis of *Phalloceros uai*, despite partial deviations from the large square lateral spot autapomorphy. Therefore, we recommend expanding the diagnosis of *Phalloceros uai* to include the phenotypic and geographic variation found in this work.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143500: Twenty years of taxonomic and ecological research on African marine benthos

Ana Ramos ^{1,2}, Amanda Luna ^{1,2}, Francisco Rocha ¹, Sidi M.M. Moctar ³, Henar Antolínez ^{1,2},
Eva García-Isarch ⁴, Eli Muñoz ⁴, Susana S. de Matos-Pita ², Belén Calero ⁴, Keider Neves ²,
Josep Suárez ², Hiba Mrich ^{1,2}, Javier Costas ¹, Alán Rey ¹, Sara Castillo ^{1,2}, Marta Gil ^{2,5}, Fran Ramil ¹

¹ University of Vigo, Vigo, Spain

² EcoAfrik Platform, Nigrán, Spain

³ Mauritanian Institute of Oceanographic Research, Mauritania

⁴ Spanish Institute of Oceanography, Spain

⁵ Institute of Marine Research, Bergen, Norway

Over the last two decades, a team of Spanish researchers has developed the ECOAFRIK project, which aims to study the biodiversity and benthic habitats from African seas. The group has taken advantage of the opportunity provided by several international bottom-trawling surveys (13 surveys, 1600 stations) carried out in northwest Africa to acquire large collections and biological and environmental data. This has improved our knowledge about the biodiversity and distribution of vulnerable marine ecosystems, mainly in deep-sea waters of the CCLME region. As results of our extensive taxonomic and ecological research more than 12 taxa —already identified (as Decapoda, Bivalvia, Gastropoda, Cephalopoda, Hydrozoa, Ophiuroidea, Holothuroidea, Scleractinia, Pycnogonida, Pennatuloidae), or currently under study (other Octocorallia groups, Actinaria and Porifera)— we have described 20 new species, and produced six PhD thesis (plus five in preparation), 20 Bachelor and Master Degree Dissertations, 65 scientific papers and more than 80 communications in international forums. A monographic volume published by Springer offered a characterization of the benthic biodiversity and main deep-sea ecosystems off Mauritania. This knowledge represented the basis of the proposal to establish the first deep-water MPA network in Africa. The current team, associated in the EcoAfrik scientific Platform includes professors, senior and postdoctoral researchers, as well as PhD and master's students. The team has a high degree of specialization in taxonomic research, teaching, knowledge transfer, training, advice and dissemination in the field of biodiversity and marine habitats.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147858: Ultrastructural characterization of *Tricholeiperia leiperi* in new host *Desmodus* in the Restinga in Rio de Janeiro, Brazil

Beatriz Elise Andrade Silva ¹, Marcione de Oliveira Brito ², Daniele Santoro ², Cibele Rodrigues Bonvicino ² and Eduardo José Lopes Torres ³

¹ Romero Lascasas Porto Helminthology Laboratory, Department of Microbiology, Immunology, and Parasitology, State University of Rio de Janeiro, Rio de Janeiro 20550-170, Brasil

² Laboratory of Biology and Parasitology of Wild Mammals Reservoirs, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro 21040-900, Brasil

³ Romero Lascasas Porto Helminthology Laboratory, Department of Microbiology, Immunology, and Parasitology, State University of Rio de Janeiro, Rio de Janeiro 20550-170, Brasil

Bats are members of the mammalian fauna, known for their high species richness and diversity, and play a crucial role as reservoirs of emerging and reemerging zoonotic pathogens. Thirty-five bat species have been reported in the coastal ecoregion of Restinga, in the state of Rio de Janeiro. *Trachops cirrhosus* is a carnivore/insectivore, feeding primarily on insects, lizards, and frogs. *Desmodus rotundus* is a hematophagous bat, feeding on the blood of other mammals (domestic and wild). Nematodes of the genus *Tricholeiperia* have been reported in bats of the families Noctilionidae and Phyllostomidae. The objective of this study is to contribute to the detailed ultrastructure of *T. leiperi* by performing a detailed characterization using scanning electron and confocal microscopy, in addition to reporting parasitism in *D. rotundus* for the first time. A total of 11 *T. cirrhosus* and 33 *D. rotundus* specimens were captured over five nights using mist nets. After euthanasia, the recovered helminths were preserved in 70% ethanol and subsequently examined for their morphological characteristics. Eight *T. cirrhosus* specimens were parasitized by *T. leiperi*, while only two *D. rotundus* specimens were parasitized. The helminths were identified through morphological and morphometric taxonomic characteristics, such as the shape of the cephalic vesicle, the presence of cervical papillae, the division at the distal end of the spicules, the size and arrangement of the bursa rays, the conspicuous vulva flap, and the presence of tubercles on the tip of the female's tail. The observed morphological characteristics involve the species *T. leiperi* previously described in *T. cirrhosus*, and this is the first report of *T. leiperi* in *D. rotundus*. This finding highlights the importance of studying parasite biodiversity in hosts across different biomes, particularly in heavily impacted ecosystems such as Restinga.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143468: Use of DNA Barcoding as an Auxiliary Investigative Tool Reveals High Hidden Diversity in the Genus *Hypomasticus* (Characiformes, Anostomidae)

Ian Solon B. Ito ¹, Lenice Souza-Shibatta ² and José Luís Oliván Birindelli ²

¹ Postgraduate Program in Biological Sciences, Department of Animal and Plant Biology, State University of Londrina, Londrina, Paraná, Rodovia Celso Garcia Cid, PR-445, km 380, Caixa Postal 10.001, 86057-970, Brazil

² Department of Animal and Plant Biology, State University of Londrina, Londrina, Paraná, Rodovia Celso Garcia Cid, PR-445, km 380, Caixa Postal 10.001, 86057-970, Brazil

Characiformes represent the largest order of fishes in the Neotropical region. Among the most diverse families within the group is Anostomidae, which includes 148 species across 17 genera, including *Hypomasticus*—a recently revalidated genus comprising 17 valid species, although its composition and diagnosis remain uncertain. This study aimed to investigate the species composition of the genus using DNA barcoding. Tissue samples were collected from various river basins where the genus occurs across South America, ranging from coastal drainages of the Guiana Shield, rivers of the Amazonian Shield, to Brazilian coastal drainages. A ~640 bp fragment of the mitochondrial gene Cytochrome c Oxidase I (COI) was amplified and sequenced for molecular analyses. All available sequences from online repositories were also included. The data were used to construct a phylogenetic tree to visualize species relationships and apply species delimitation analyses. Species delimitation was performed using three mitochondrial DNA-based approaches: ASAP, GMYC, and PTP. The use of DNA barcoding as a taxonomic investigative tool revealed the existence of seven undescribed species—four from Amazonian basins and three from Brazilian coastal drainages—representing a 41.18% increase in species richness for the genus. The analyses highlight the great utility of DNA barcoding as an investigative tool in the family Anostomidae, particularly within *Hypomasticus*, and demonstrate how the genus's hidden diversity underscore the need for a more comprehensive taxonomic revision.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147648: Using an integrative morphological approach to species delimitation in a marine gastrotrich (Gastrotricha: Macrodasysida)

Thiago Quintão Araújo¹ and Rick Hochberg²

¹ Department of Biology, University of Massachusetts Lowell, Lowell, MA 01854, USA

² Department of Biology, University of Massachusetts Lowell, Lowell, MA, USA 01854

Gastrotricha is a group of microscopic animals that are often overlooked in ecological surveys, despite their worldwide distribution across all oceans on Earth. The apparent incongruence between widespread distribution of microscopic animals and their life history is known as the “meiofauna paradox”. This concept has been investigated in many meiofaunal groups and recent studies provide new insights revealing that the restricted distribution of these organisms is more common than was previously thought based on molecular diversity and muscular organization. The use of integrative morphological methods has been used in the past decades to increase the accuracy of species delimitation. In the present study we discovered a new species of the genus *Kryptodasys* (Macrodasysida: Macrodasysidae) from Capron Shoal, Florida, USA. For species delimitation, we used traditional light microscopy and Confocal Laser Scanning Microscopy (CLSM). The specimens of the new species show a unique reproductive apparatus and for the first time in the group, a muscular complex dedicated to the seminal vesicle is described. Also, a complex caudal organ composed of two compartments were observed. The complete muscular analysis added important novelties to the knowledge of muscular architecture of Macrodasysida group and to the phylum.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

Session 4. Plant Taxonomy

sciforum-143516: *Cleisostoma linearilobulatum* (Seidenfaden & Smitinand) Garay (Orchidaceae): a new record for West Bengal, India
RAJENDRA YONZONE Department of Botany, Victoria Institution (College), 78-B, APC Road, Kolkata – 700009, West Bengal, India
E-mail: yonzonebiosystematics@gmail.com

DR. Rajendra Yonzone

Department of Botany, Victoria Institution College, Kolkata, West Bengal, India

Abstract

Introduction: Orchidaceae is one of the largest groups of angiospermic plants with world-wide distribution except hot desert and cool polar regions and it is found in three different habitats viz., i. Saprophytic, ii. Terrestrial and iii. Epiphytic.

Method: selective and periodical field survey covering entire west Bengal. because orchids are blooming almost throughout the region. Specimens collection, photographs taken in the habitat, drawing and dissection, mounting and herbarium preparation and identification.

Result: finding diversity, endemic, new record, new species, new variety etc.

Conclusion: Whole orchidaceae family faced extreme threat in nature. Therefore, *in situ* conservation is highly emphasized.

During a field survey for the orchid flora of West Bengal, the author collected blooming orchid species from Darjeeling Himalaya and collected species was identified as *Cleisostoma linearilobulatum* (Seidenfaden & Smitinand) Garay with the help of available literature of King & Pantling 1898, Tang & Wang 1951, Yonzone *et al.* 2012, Pearce & Cribb 2002, and it was not recorded earlier from West Bengal. Therefore, *Cleisostoma linearilobulatum* (Seidenfaden & Smitinand) Garay, is a new record of its occurrence for the state of West Bengal, India. Taxonomic description, exact existence, flowering month, habitat photographs have been provided for its easy identification in the fields.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147688: Exploring Knowledge Shortfalls on Legumes in the Tocantins-Araguaia Basin

Nina Machado Suzigan ¹, Rafael Barbosa Pinto ² and José Alexandre Felizola Diniz-Filho ¹

¹ Universidade Federal de Goiás

² Universidade Estadual de Goiás

Knowledge shortfalls remain a major barrier to understanding global biodiversity, especially in tropical hotspots such as the Brazilian Cerrado. Among these, the Darwinian shortfall—the lack of molecular and phylogenetic data—limits evolutionary and ecological inference and hampers conservation planning. The Tocantins-Araguaia Basin, a highly diverse region within the Cerrado, harbors numerous species of Fabaceae, one of the most diverse and ecologically relevant angiosperm families. However, the extent of molecular data coverage for these taxa remains poorly characterized. We compiled a list of Fabaceae species occurring in the Tocantins-Araguaia Basin using GBIF, SiBBr, speciesLink, and BIEN, filtered through Re flora nomenclature. Molecular data availability was assessed from BOLD Systems and NCBI, considering sequences, annotated genes, and genome assemblies. Phylogenetic representation was mapped onto the Legume Phylogeny Working Group (2017) tree, with species insertions performed in R using ape and visualized with ggtree. A total of 1,423 valid Fabaceae species were identified. Molecular coverage is uneven: the most common markers are ITS, ITS2, matK, rbcL, and rbcLa, but most species are represented by only one or none. Subfamilies such as Papilionoideae are relatively well covered, while Detarioideae and Dialioideae show significant data gaps. NCBI searches revealed a strong asymmetry, with few species having extensive nucleotide data or annotated genes, and complete genomes are extremely rare. These findings demonstrate that Darwinian shortfalls are not randomly distributed but phylogenetically structured, with data concentrated in a few economically important clades. This bias reduces the representativeness of phylogenies and limits conservation prioritization based on evolutionary distinctiveness. By identifying patterns of molecular data scarcity in Fabaceae of the Tocantins-Araguaia Basin, this study provides a framework for guiding future sequencing efforts and conservation strategies. Expanding molecular coverage will be crucial to strengthen biodiversity assessments in the Cerrado.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147532: Integrative Taxonomy of Wild Citrus Germplasm: Linking Molecular and Morphological Evidence to Stress Tolerance

Muhammad Asim ¹, Mian Muhammad Ahmed ², Ayaz Ahmad ², Muhammad Saud Khan ², Syeda Maira Hamid ² and Pan Zhiyong ³

¹ National Key Laboratory for Germplasm Innovation and Utilization of Horticultural Crops, Huazhong Agricultural University, Wuhan, 430070, Hubei, China

² College of Life Science and Technology, Tarim University, Alar, Xinjiang, 843300, China

³ National Key Laboratory for Germplasm Innovation & Utilization of Horticultural Crops, Huazhong Agricultural University, Shizhishan Street, Hongshan District, Wuhan, Hubei, 430070, China

Integrative taxonomy offers a powerful approach to clarify species boundaries and enhance the utility of wild germplasm in breeding programs. The genus *Citrus* and its wild relatives harbor rich genetic diversity with the potential to enhance crop resilience under climatic stress. Yet, frequent hybridization, polyploidy, and overlapping morphological traits have created taxonomic ambiguities that constrain their systematic use. This study integrates molecular and morphological evidence to resolve classification challenges and identify lineages associated with stress tolerance traits. Morphological characterization employed key descriptors such as leaf morphology, fruit architecture, and reproductive traits, while molecular analyses utilized chloroplast and nuclear DNA markers together with genome-wide SNP data. Phylogenetic reconstructions provided improved resolution of taxonomic relationships, revealing distinct clades that correspond with adaptations to salinity, drought, and temperature extremes. Comparative analyses further highlighted taxonomic groups enriched for allelic variants associated with stress-responsive pathways. By resolving taxonomic uncertainties, this integrative framework strengthens the use of wild *Citrus* germplasm in breeding climate-resilient varieties, advancing sustainable fruit production and food security.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147048: The Genus *Buddleja* L. (Scrophulariaceae): Taxonomic Complexity, Diversity, and Cultural Relevance in Mexico

Alexis Josué Sánchez-Lara ¹, Carmen Zepeda-Gómez ¹, Hugo López-Camarillo ² and Armando Sunny ³

¹ Laboratory of Aquatic Plants, Faculty of Sciences, Universidad Autónoma del Estado de México, Campus El Cerrillo, Supermanzana Carretera Km 15.5, Piedras Blancas, 50200 Toluca de Lerdo, Mexico

² Departament of Evolutionary Biology, Facultad de Ciencias, Universidad Nacional Autónoma de México. Investigación Científica, C.U., Alcaldía Coyoacán, C.P. 04510. Ciudad de México, México.

³ Center for Research in Applied Biological Sciences (CICBA), Faculty of Sciences, Universidad Autónoma del Estado de México, Carretera Toluca–Ixtlahuaca Km 14.5, San Cayetano de Morelos, 50200 Toluca de Lerdo, Mexico

The genus *Buddleja* L., described by Linnaeus in 1737 in honor of Adam Buddle, has experienced multiple taxonomic reclassifications, being placed in Loganiaceae, Buddlejaceae, and currently Scrophulariaceae. Despite its ecological and cultural relevance, species delimitation and classification remain contentious, reflecting persistent challenges in defining morphological and molecular boundaries. Estimates of species richness range from 100 to 150 taxa, with *Plants of the World Online* recognizing 111 accepted species, nearly half distributed in the Americas. In Mexico, 14 species are reported, including *Buddleja cordata* Kunth (tepozán), a tree of notable cultural and medicinal importance. We reviewed classical taxonomic literature, modern systematic studies, botanical databases (e.g., POWO), and ethnobotanical records to synthesize historical classifications, nomenclatural variants, species richness estimates, and cultural associations. Our analysis confirms that *Buddleja* is a taxonomically complex genus, characterized by wide morphological variation in vegetative and reproductive traits, further complicated by dioecy and hybridization. Mexican species exhibit multiple vernacular names, reflecting their strong cultural recognition. While *B. cordata* is widely employed in traditional medicine for renal, digestive, and inflammatory conditions, other taxa are valued for ornamental and ecological functions. Overall, *Buddleja* exemplifies broader challenges for plant taxonomy in the 21st century. Addressing these complexities is essential not only for biodiversity conservation and ecological restoration, but also for the preservation of traditional ecological knowledge.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147665: Two new species of *Hexasepalum* (Spermacoceae, Rubiaceae) from the “campo rupestre” of Brazil

João Carmo ¹, Roberto Salas ², Elsa Cabral ² and Andrea Fader ³

¹ Department of Plant Biology, Institute of Biology, State University of Campinas – UNICAMP, Campinas, São Paulo 13083-970, Brazil

² Institute of Botany from the Northeast – IBONE, National University of the Northeast (UNNE – CONICET), Corrientes 3400, Argentina

³ Center for Applied Ecology of the Coast – CECOAL, National University of the Northeast (UNNE – CONICET), Corrientes 3400, Argentina

The “campo rupestre” is a montane vegetation mosaic associated with rocky outcrops, with outstanding levels of endemism. *Hexasepalum* Bartl. ex DC. is nested in the Spermacoceae, the largest predominantly herbaceous tribe in the Rubiaceae. The genus, with 14 accepted species, is distributed mostly in the Americas. Brazil is home to eight species, occurring mainly in the Caatinga and Cerrado (including the “campo rupestre”) domains. The analysis of specimens collected in the “campo rupestre” of Bahia (NE Brazil) and Minas Gerais (SE Brazil) has revealed that these are new to science. *Hexasepalum bacigalupoe* Cabaña Fader & E.L.Cabral sp. nov. is mostly similar to *Hexasepalum apiculatum* (Willd.) Delprete & J.H.Kirkbr., but differs by the 3–5-fimbriate stipular sheath (vs 7–9-fimbriate in *H. apiculatum*) and mericarps with flat ventral faces (vs with two depressions). *Hexasepalum motaviananum* Cabaña Fader, J.A.M.Carmo & R.M. Salas sp. nov. is similar to *Hexasepalum zappiae* E.L.Cabral & Cabaña Fader, but differs by the ovate leaves (vs linear leaves in *H. zappiae*), 6–7(8)-lobed calyx (vs 4–5-lobed calyx), and the ventral surface of the seed with a “Y”-shaped groove, delimited by an apical fold, without apical grooves (vs ventral side of the seed without a Y-shaped groove nor apical fold, with 3–5 apical grooves). The new species are described and illustrated. We comment on their distribution, habitat, and taxonomy. We also provide an updated key to the species of *Hexasepalum*. *Hexasepalum bacigalupoe* and *H. motaviananum* are preliminarily assessed as Endangered and Critically Endangered, respectively, underscoring the crucial importance of conserving the “campo rupestre.”



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-126098: A new species of *Jacaratia* (Caricaceae) from the Brazilian drylands, with nomenclatural notes on the South American *J. corumbensis*

Earl Celestino de Oliveira Chagas and James Lucas da Costa-Lima

Departamento de Biociências, Universidade Federal Rural do Semi-Árido, Mossoró, 59625-900, Brazil

Caricaceae Dumort. (the papaya family) is primarily known for its edible fruit-bearing species, including the genera *Carica* L., *Jacaratia* A.DC., and *Vasconcellea* A.St.-Hil. These genera are economically and ecologically important, providing food, traditional medicine, and ecological services in their native habitats. In this study, we describe a new species within the genus *Jacaratia*, locally economically important and segregated from *J. corumbensis* Kuntze, named *Jacaratia guazoubira* E.C.O.Chagas & Costa-Lima sp. nov. Both *Jacaratia corumbensis* and the newly described *J. guazoubira* are found within the Seasonally Dry Tropical Forests and Woodlands biome of South America, particularly on sedimentary soils. *Jacaratia corumbensis* occurs in dry and semideciduous forests in the central region of South America, spanning Argentina, Bolivia, Brazil, and Paraguay, within the Bosque Seco Chiquitano, Gran Chaco, and Pantanal ecoregions. In contrast, *J. guazoubira* is restricted to the caatinga vegetation and dry forests of northeastern Brazil and adjacent areas, including the Caatinga ecoregion and the edges of the Cerrado. Morphologically, these two species can be distinguished by a series of reproductive characters, including sessile staminate flowers in *J. guazoubira* (vs. pedicellate in *J. corumbensis*), corolla tube 5–7 mm long (vs. 10–12 mm), reflexed corolla lobes (vs. suberect to patent), pistillate inflorescences with 5–8 flowers (vs. solitary), hypopodium 2.5–3 mm long (vs. 7–30 mm), closely spaced bracteoles (vs. sparsely distributed), pentagonal-fusiform fruits (vs. ellipsoid to pyriform), 5 greenish longitudinal ribs (vs. 8–10 cream or pinkish to reddish), and seeds with tuberculate (vs. smooth) sarcotesta. Additionally, we discuss the potential uses of these species in human and animal nutrition, their roles in landscaping, and their conservation implications. To stabilize the nomenclature and taxonomy of this group, we also designate lectotypes for *J. corumbensis* and its synonyms.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143603: Between extinction and uncertainty: Nomenclature revision of genus *Dalea* L. (Papilionoideae, Fabaceae) in Cajamarca, Peru

Ivan Luis Fernandez-De la Cruz ^{1,2}, Javier Javier ^{1,2}, Joaquina Albán-Castillo ^{1,2} and Briggitthe Melchor-Castro ^{1,3,4}

¹ Department of Ethnobotany and Economic Botany, Museum of Natural History, Lima 15072, Peru

² Faculty of Biological Sciences, National University of San Marcos, Lima 15081, Peru

³ School of Biological Sciences, University of Edinburgh, Edinburgh EH9 3JW, The United Kingdom

⁴ Acience Division, Royal Botanic Garden Edinburgh, Edinburgh EH3 5LR, The United Kingdom

Dalea L. is the only genus from the Amorphaeae tribe distributed in the Peruvian Andes, where most of its species are endemic and endangered. The centre of diversity is within northern and central Andes mountain ranges converging with the Huancabamba Depression, a hotspot for cryptic plant diversity located in Cajamarca. Despite taxonomic studies conducted 40 years ago, morphological delimitations remain ambiguous due to phenotypic plasticity and the lack of type specimens, particularly among endemic taxa. This study aimed to assess morphological differentiation and carry out a nomenclatural revision of *Dalea* L. (13 species and 8 varieties) from the Cajamarcan Andes. As a result, we identifies 16 species in Cajamarca, based on distinctive morphological characters, including in stipule type; leaflet shape, pubescence density and number; inflorescence type; bract morphology; length of calyx distal tooth relative to its tube; number of glands per intercostal margin of the calyx; and fruit morphology. Nomenclatural changes were proposed for certain infraspecific taxa through their elevation to species rank, establishing: *D. sericophylla* Ulbr., *D. cutervoana* Szyszyl. and *D. microphylla* Kunth. The remainig varieties were reduced to synonymy under their respective species. Additionally, lectotypifications were carried out for the species *D. myriadenia* Ulbr., *D. sericophylla* Ulbr. and *D. weberbaueri* Ulbr., due to the loss of their holotypes which had been deposited at the Berlin Herbarium.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147067: Challenges in using *Chara contraria* A.Braun ex Kützing oospores as taxonomic markers

Vanja Milovanović¹, Jasmina Šinžar Sekulić², Gordana Subakov Simić¹ and Ivana Trbojević¹

¹ Department of Algology and Mycology, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Takovska 43, 11000 Belgrade, Serbia

² Department of Plant Ecology and Phytogeography, Institute of Botany and Botanical Garden "Jevremovac", Faculty of Biology, University of Belgrade, Takovska 43, 11000 Belgrade, Serbia

Chara contraria A.Braun ex Kützing is an endangered charophyte species in Serbia, widely recognized for its highly variable thallus morphology, which often hinders precise and reliable identification, leading to misidentification. Oospores, resistant reproductive structures, had already been used as promising taxonomic markers for delineation of several charophyte species in Serbia. However, the oospores of this highly variable species have not been examined in Serbia before. In this study, we aimed to describe *C. contraria* oospores and to explore their usefulness as taxonomic parameters. A total number of 537 *C. contraria* oosporangia containing mature oospores were collected from the individuals from various localities in Serbia. The oosporangia were left in 30% hydrogen peroxide for up to 10 minutes, after which the spiral cells and coronula were removed, and the oospores were prepared for further analysis. First, visual inspection was performed, based on the general appearance of the oospores and the appearance of their apical and basal poles. The oospores were photographed and a standard set of quantitative characteristics was measured. Analyzed oospore specimens were subjected to K-means clustering, an unsupervised machine learning procedure, to determine the potential existence of homogeneous subgroups within them and further investigate their variability. The oospores of *C. contraria* ranged in color from dark brown to black and showed considerable variability in their general appearance. K-means cluster analysis further confirmed the observed qualitative variability, by identifying 3 clusters. The parameters that contributed most to the separation into clusters were oospore height, length, and the isopolarity index. Our results suggest that the application of *C. contraria* oospores as taxonomic parameters is limited by pronounced variability of both qualitative and quantitative characteristics. Integrating molecular and morphological approaches is recommended to enhance the reliability of taxonomic assessments.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-144542: Exploring Chiococceae (Rubiaceae) in Mexico: Morphology, Diversity, and Endemism Uncovered

Alejandro Torres-Montufar

Department of Biological Sciences, FESC-UNAM, Faculty of Higher Studies Cuautitlan, National Autonomous University of Mexico, Cuautitlan 54714, Mexico

This study aims to provide the first comprehensive checklist and analysis of the Chiococceae tribe in Mexico, based on more than 4,000 herbarium specimens and georeferenced occurrence records cross-validated from online repositories. A total of 28 species across nine genera were recorded, including two endemic genera (*Coutaportia* and *Nernstia*) and 14 species restricted to the country. Approximately half of the Chiococceae species occurring in Mexico are endemic, underscoring the country as a centre of diversity for the tribe. Distribution patterns show a strong concentration in the tropical south, particularly in Chiapas (17 species; 5 endemic), Veracruz (14 species; 4 endemic), and Oaxaca (14 species; 6 endemic). Diagnostic combinations of reproductive traits—such as corolla form, size, and symmetry; fruit texture and dehiscence; and seed morphology—proved valuable for distinguishing genera. However, persistent taxonomic challenges remain at both generic (e.g., *Asemnantha*/*Chiococca*, *Coutaportia*/*Lorencea*, *Solenandra*/*Exostema*) and species levels (e.g., *Chiococca alba*), highlighting the need for further systematic research. Overall, this work establishes a baseline for future taxonomic, ecological, and conservation studies on Chiococceae in Mexico.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147213: Fabaceae in the Morro do Macaco Environmental Protection Area (EPA), Iporá, Goiás, Brazil

Hattos de Freitas Gomes, Isabella Vitória Araújo Santos, Paulo César de Oliveira, Kawayne Costa Silva and Rafael Barbosa Pinto

Laboratório de Botânica; Instituto Acadêmico de Ciências da Saúde e Biológicas; Universidade Estadual de Goiás

The Fabaceae is one of the most diverse and ecologically important angiosperm families, widely used in human activities and strongly represented in the Brazilian Cerrado. The Cerrado, the world's most diverse savanna, is severely threatened by anthropogenic pressures. Despite its high richness, large portions of its flora remain poorly studied. This study focuses on the floristic survey of Fabaceae in the Morro do Macaco EPA, located in Iporá, Goiás (Brazil), aiming to provide baseline taxonomic data to support ecological, molecular, and conservation research. Fieldwork was conducted through periodic collections following traditional methods. Fertile specimens were collected, prepared as herbarium vouchers, and identified using specialized literature, virtual herbaria, and consultation with experts. So far, 35 species belonging to 21 genera and three subfamilies (Cercidoioideae, Caesalpinoioideae, and Papilionoioideae) have been recorded. Caesalpinoioideae (including mimosoid clade) was the most diverse, with 18 species, followed by Papilionoioideae with 16 species, and Cercidoioideae with two species (*Bauhinia brevipes* and *Bauhinia unguolata*). The most species-rich genus was *Chamaecrista* (five spp.), followed by *Centrosema* and *Mimosa* (four spp. each). *Inga* and *Senegalia* were represented by three species each. These results highlight the high taxonomic diversity of legumes within this relatively small conservation unit of the Cerrado and a relatively short survey. Our findings reinforce the importance of regional floristic inventories as essential tools for conservation planning, since they provide critical information for biodiversity assessments. The Morro do Macaco EPA harbors a significant richness of Fabaceae, supporting its role as a priority area for the preservation of Cerrado flora, despite historical anthropogenic impacts and limited local conservation support. Future efforts will expand this baseline by assessing endemism and conservation status and producing a photographic guide.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142704: First Record of Stranded Holopelagic Sargassum Morphotypes and Associated Fauna on the Moroccan Atlantic Coast

Khansae Kamal ¹, Khaoula Khaya ¹, Zahira Belattmania ¹, Abdellatif Chaouti ¹, Joao Neiva ²,
Aschwin Hillebrand Engelen ², Valérie Stiger-Pouvreau ³, Ester A. Serrão ² and Brahim Sabour ¹

¹ Phycology, Blue Biodiversity and Biotechnology RU, LB2VE URL CNRST n°10, Faculty of Sciences, University Chouaib Doukkali, PO Box 20, 24000 El Jadida, Morocco

² Centre of Marine Sciences, CCMAR/CIMAR-LA, Campus de Gambelas, Universidade do Algarve, 8005-139 Faro, Portugal

³ Univ Brest, CNRS, IRD, Ifremer, LEMAR, IUEM, 29280 Plouzané, France

In early 2024, a large influx of holopelagic *Sargassum* were discovered drifting along the Atlantic coast of Morocco, marking the first recorded occurrence of these drifting macroalgae in the region. This event revealed a striking morphological diversity within the drifted biomass, with three distinct morphotypes identified: *Sargassum natans* morphotypes I and VIII, and *Sargassum fluitans* morphotype III. The biomass density reached 10 ± 3 ind/m², with *S. natans VIII* dominating at 58%. Alongside the algal masses, a diverse associated fauna was observed, including hydroids and crustaceans, highlighting the role of *Sargassum* mats as transient pelagic habitats. The diversity of morphotypes observed reflects complex dispersal dynamics and potentially multiple origins or developmental pathways, possibly shaped by environmental drivers. The arrival of these forms following the Nelson storm underscores the influence of extreme hydrometeorological events in facilitating long-distance transport from the tropical Atlantic to the North Atlantic coast of Africa. As climate change continues to intensify such events, the frequency and morphotype variability of holopelagic *Sargassum* blooms are likely to increase. This study highlights the importance of monitoring not just biomass but also morphological variability, which can influence ecological impact and inform future coastal management strategies.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-135731: How to classify a species-rich genus

Farzaneh Jafari

Department of Biology, Faculty of Basic Sciences, Lorestan University, Khorramabad, P.O. Box 6815144316, Iran

Species-rich genera with various circumscriptions are always a source of controversy. The controversy over which taxonomic level the taxa belong to? Which characters help botanists to classify taxa in natural groups? The taxa show diversity in life form, leaf shape, and texture, flower shape and pieces of flowers. Genetic diversity and accommodation make some genera rich, like the genus *Silene*. *Silene* with currently 870 species is one of large genus. It grows from temperate to arctic zone in northern hemisphere. The three central diversities are discerned for it: SW Asia, the Mediterranean area, and Central Asia. Several species have been shown to be polyploid. For using the rich- species genus as a model in genetic, ecological, and evolutionary study, it is necessary to classify the genus.

Phylogeny reconstruction could be one way to find natural groups. To this end, a comprehensive sampling of *Silene* and allied genera in the tribe *Sileneae* was provided. Two common and very useful markers, nrDNA ITS and cpDNA rps16, were used. All 44 sections recognized by Chowdhuri (1957) covered the entire geographical range of the genus. The analyses were performed with STACEY v.1.2.5 as implemented in BEAST v.2.5.1.

Nuclear and chloroplast tree topologies were congruent. The polyploidy in some taxa can distort the phylogeny and classification of the species-rich genus. Different accommodation to different habitat also can make the phylogeny and classification unclear. These led us to face limitations for defining the diagnostic morphological characters of subgrouping.

To get rid of these limitations and define subgrouping, a broad sense was used. Three subgenera, *Lychnis*, *Behenantha*, and *Silene*, and 35 sections were recognized for the genus. However, one section has uncertain placement.

Here, *Silene* sects. *Auriculatae*, *Physolychnis*, *Sclerocalycinae*, *Silene*, and *Siphonomorpha* are each defined in a broad sense. The next step, phylogeny using more loci, will be reconstructed to discover the natural subgrouping of these sections.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-153610: Integrating Phytochemical Profiling and DNA Barcoding to Explore Medicinal Potential in Selected *Dendrobium* Species

Ravewish Takham ^{1,2}, Natapol Pornputtapong ^{2,3}, Pantamith Rattanakrajang ^{1,2}, Chayapol Tungphatthong ^{1,2}, Boonchoo Sritularak ^{1,4}, Ranganathan Babujanarthanam ⁵ and Suchada Sukrong ^{1,2,6}

¹ Department of Pharmacognosy and Pharmaceutical Botany, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand

² Center of Excellence in DNA Barcoding of Thai Medicinal Plants, Chulalongkorn University, Bangkok 10330, Thailand

³ Department of Biochemistry and Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University Bangkok, 10330, Thailand

⁴ Center of Excellence in Natural Products for Ageing and Chronic Diseases, Chulalongkorn University, Bangkok 10330, Thailand

⁵ Nano and Energy Bioscience Laboratory, Department of Biotechnology, Thiruvalluvar University, Serkkadu, Vellore, 632115, Tamil Nadu, India

⁶ Chulalongkorn School of Integrated Innovation, Chulalongkorn University, Bangkok 10330, Thailand

The extensive morphological variation and broad distribution of *Dendrobium* species often hinder accurate identification, leading to potential misapplication and supply challenges in medicinal use. This study aimed to investigate the correlation between phytochemical composition and DNA barcoding markers based on ITS and *matK* to improve identification in twenty-one medicinal *Dendrobium* species. Phytochemical data compiled from databases were analyzed through hierarchical clustering to construct a chemical dendrogram. Seven chemical clusters were identified, characterized by key structural compounds such as bisbibenzyls, fluorenones, flavonols, phenanthrenes, and 9,10-dihydrophenanthrenes. Each chemical cluster revealed characteristic profiles of major and minor compounds among *Dendrobium* species. The ITS-based phylogenetic tree proved more reliable than *matK* for distinguishing *Dendrobium* sections. Correlation analysis between the phytochemical dendrogram and the ITS-based phylogenetic tree using the Fowlkes–Mallows Index (FMI) yielded a value of 0.5536, reflecting a noteworthy correlation that highlights the underlying relationship between chemical and genetic clustering. A strong correlation was observed when a phylogenetic clade contained a single chemical cluster. This pattern was evident in clades E and F, which were associated with chemical cluster 7. Cluster 7 comprised eight species, representing the largest group among all clusters. This integrative approach provides a framework for chemical forecasting and supports the authentication and sustainable utilization of *Dendrobium* resources in traditional medicine.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146379: Karst flora of Hainan Island, China

Ming-Xun Ren ¹ and Shao-Jun Ling ²

¹ Hainan University

² School of Ecology, Hainan University

Hainan Island, locating at south China and the north edge of tropical Asia, is an island with an area of 34,000 km². Hainan Island harbors vast rainforests with high levels of biodiversity, with more than 5000 vascular plants among which ~ 500 are endemic to this island. Such rich biodiversity is mainly due to its high mountains, spatial-temporal dynamics in rainfalls associated with monsoons, and habitat heterogeneity caused by different types of soils and rocks. About 400 km² of karst (limestone landscape) were found on Hainan Island, largely distributed at the west and south part of this mountainous island. Totally about 1500 vascular plants in 181 families (750 genera) can be found in karst regions on Hainan Island, of which 65 species are Hainan-endemic. The karst flora on this island is largely pantropical, with some belong to temperate zone. There are 27 plant species on Hainan's karst regions are included into national or provincial protection lists as endangered or rare species.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146164: Morpho-anatomical taxonomic delimitation of *Astragalus bruguieri* and *A. baba-alliar* subsp. *nudicarpus*

Fateme Salmaniabeiat¹ and Mohammad Reza Parishani²

¹ Dept. of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran

² Department of Biology, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran

Astragalus (Fabaceae) includes many closely related species that are often difficult to distinguish. Within section *Poterion*, *A. bruguieri* and *A. baba-alliar* subsp. *nudicarpus* are morphologically similar, and the latter has sometimes been treated as a variety of the former. This study aimed to clarify their taxonomic boundaries using morpho-anatomical evidence and identify reliable diagnostic traits. 45 populations were sampled from natural habitats in western and southwestern Iran. Plant specimens were identified using comprehensive floras and herbarium references. For morphometric analyses, at least ten mature individuals per site were measured with three replicates per organ. Transverse sections of stems and leaflets were prepared, double-stained with methylene blue and carmine alum, and examined under a light microscope; the epidermis was further stained with fuchsin. Data were analyzed using NTSYS software, with PCoA and the Mantel test. *A. bruguieri* grows as short shrubs (mean 50 cm), whereas subsp. *nudicarpus* reaches nearly three times this height and bears smaller stipules (1–2 mm vs. 5–6 mm). In *A. bruguieri*, leaflets are glabrous and ovaries pubescent, while traits are reversed in the subspecies. Their distribution patterns also differ: *A. bruguieri* occurs across several Middle Eastern countries at lower elevations on calcareous soils, whereas subsp. *nudicarpus* is restricted to Iran and prefers higher elevations with light soils, indicating distinct though overlapping phytogeographical regions. Anatomically, vascular bundles in stems are smaller in *A. bruguieri* (50–60 μm vs. up to 80 μm), and its leaflets have more lateral veins (4–5 vs. 2). In subsp. *nudicarpus*, epidermal cell number and stomatal density reach up to 250 cells and 20 stomata per mm^2 , both considerably lower in *A. bruguieri*. This study highlights the importance of morpho-anatomical traits in distinguishing closely related *Astragalus* taxa. However, the taxonomic position of subsp. *nudicarpus* requires further investigation, including molecular phylogenetic analyses.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-144540: Rarity and Endemism in *Coutaportla* Urb.: An Updated Taxonomic Perspective (Chiococceae, Rubiaceae)

Alejandro Torres-Montufar

Department of Biological Sciences, FESC-UNAM, Faculty of Higher Studies Cuautitlan, National Autonomous University of Mexico, Cuautitlan 54714, Mexico

Coutaportla Urb. occurs from northern Mexico to parts of Guatemala and Honduras, bearing tetramerous or pentamerous flowers and capsules that dehisce loculicidally. The delimitation of the genus has been controversial since *Lorencea* was segregated; however, both molecular and morphological evidence reject this separation, supporting the recognition of five species within *Coutaportla*. This study provides an updated taxonomic treatment that incorporates newly described species, identification keys, distribution maps, and detailed descriptions. A thorough review of taxonomic literature and protologues was conducted, complemented by the examination of herbarium specimens (including types) and consultation of online collections to refine species descriptions and distribution data. The genus comprises five species, four endemic to Mexico and one extending into Central America. Three of these are known only from their type localities. Species occur in a variety of environments, ranging from arid and temperate to tropical-humid zones. Diagnostic features include ovary placentation (subapical, median, basal), along with floral and foliar characters. Morphological evidence supports synonymising *Lorencea* with *Coutaportla*. The genus is highlighted as a subendemic Mexican element, with most species having restricted ranges and requiring conservation attention.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-144536: Reassessing *Mexocarpus*: Molecular and Morphological Evidence from Mesoamerican *Palicourea* (Rubiaceae)

Alejandro Torres-Montufar and Eduardo Lazcano-Flores

Department of Biological Sciences, FESC-UNAM, Faculty of Higher Studies Cuautitlan, National Autonomous University of Mexico, Cuautitlan 54714, Mexico

Within Rubiaceae, one of the most taxonomically problematic assemblages is the Psychotria–Palicourea complex, largely due to its high species richness, unstable generic boundaries, and marked morphological variability. The genus *Mexocarpus* was originally established to accommodate *Palicourea tetragona*, distinguished by its pyrenes bearing prominent ridges—an unusual trait compared to other members of *Palicourea*. This taxon occurs from southern Mexico to Central America and, apart from its distinctive pyrenes, is characterised by elongated white flowers with nocturnal anthesis and fruits that become tetragonal when dry. The species was first described under *Cephaelis*, later transferred to *Palicourea*, and subsequently placed in *Mexocarpus*. However, this last reassignment has been contested by some authors, who argue that pyrene morphology is too variable to justify generic separation. To clarify the phylogenetic position of *Mexocarpus tetragonus*, we performed phylogenetic analyses using two nuclear DNA markers (ETS and ITS) and one plastid marker (trnL–F) under Maximum Likelihood and Bayesian inference. The resulting molecular phylogeny indicates that *M. tetragonus* lacks phylogenetic support for generic distinction, forming an unresolved clade with *P. tomentosa* and *P. faxlucens*. Furthermore, comparative morphological assessments with closely related taxa demonstrate that pyrene characters are highly variable and show overlapping variation, rendering them unsuitable as diagnostic features for defining a separate genus. Based on combined molecular and morphological evidence, we therefore recommend treating *Mexocarpus* as a synonym of *Palicourea*.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-115193: Taxonomic Complexity and Ecological Adaptability of *Lantana camara* L. in India: A Morphological and Molecular Approach

Shiwa Chaubey

CSIR-NBRI, Lucknow, Uttar Pradesh 226001, India

Lantana camara L., a species native to tropical and subtropical regions, is known for its high morphological plasticity, which complicates both its identification and control. This study aims to review the taxonomic heterogeneity of *L. camara* in India, with a special focus on its spatial distribution, ecological adaptability, and morphological polymorphism.

Introduction:

Belonging to the family Verbenaceae, *L. camara* is widely recognized for its ornamental and medicinal applications. However, due to its invasive nature, it poses significant threats to native ecosystems. Effective management of this species requires a thorough taxonomic understanding.

Methods:

Field surveys were conducted from 2021 to 2023 across diverse biogeographical zones, including the Western Ghats, Gangetic Plains, and Himalayan Terai. Morphological traits such as leaf shape, flower color, and fruiting habits were recorded. Molecular identification was performed using ITS2 and matK DNA barcodes. Spatial distribution was mapped using GIS tools.

Results:

The study revealed substantial phenotypic variation among *L. camara* populations, corresponding to regional climatic and edaphic conditions. Five distinct morphotypes were identified, although morphological boundaries between them were often ambiguous. Molecular analyses supported the presence of cryptic diversity within the *L. camara* complex. The species was most invasive in disturbed habitats, particularly in semi-arid and tropical zones.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142290: Taxonomic contribution on genus *Dactylorhiza* (Orchidaceae) from flora of Iran

Elham Hatami

Department of Biology, Faculty of Science, Razi university, Kermanshah, 6714414971, Iran

The generic name *Dactylorhiza* was first introduced by Necker in 1790, later on in 1935, Nevski officially re-established the name and distinguished it from the genus *Orchis* by characteristics such as palmate tuberoids (vs. ovoid or globose), cauline leaves (vs. basal, rosette-forming), herbaceous leafy bracts (vs. scale-like), and the usual number of chromosomes $2n = 40$ (vs. $2n = 36, 42$). *Dactylorhiza* is known for its very high propensity of hybridization and morphological variability, so some taxonomic concepts are difficult to apply in practice only based on morphology. The number of *Dactylorhiza* species varies from 660 to over 720 names depending on the authors. In general, members of this genus occupy a wide range of habitats, usually humid, from the slopes of dunes to alpine meadows, including swamps, peatbogs, and various types of forest in Eurasia, Northern Africa, and North America. Some species of this genus are particularly noteworthy as ornamental and medicinal plants, with their underground parts (tubers) used to produce salep. Due to importance of this genus in the context of ornamental and medicinal uses and conservation priorities in flora of Iran and because of dispersed and inconsistent information in previous references, the present study focuses on organizing and updating the taxonomic information on *Dactylorhiza* species distributed in Iran. Based on our investigation on relative literatures and herbarium samples, it was revealed that in southwest Asia, flora of Iran encompasses four species and four subspecies of this genus including *D. iberica*, *D. romana* (subsp. *georgica*), *D. umbrosa* (subsp. *knorringiana*, subsp. *longibracteata*, subsp. *ochroleuca*), and *D. lancibracteata*. These species are geographically distributed in Hyrcanian district and Irano-Turanian region in north, northwest and west of Iran, although, *D. iberica* and *D. umbrosa* have been additionally reported from center and south of Iran. *Dactylorhiza lancibracteata* was recently synonymized with *D. urvilleana*. In Flora Iranica, Renz (2008) noted that *D. cuneata* may be found in the Azerbaijani mountains of the westernmost part of Iran, but, until now, this species has not been recorded from Iran. Following the footsteps of Renz in Iran, Kreutz and Spencer (2011) mentioned the presence of *D. flavescence* in northwest of Iran but he could not find this species during his trip, thus, thus, it is not confirmed yet that *D. flavescence* is distributed in Iran.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-117252: Taxonomic Insights into Nigerian Terminaliinae (Combretaceae) Based on Molecular and Morphological Evidence: Implications for generic circumscription

Opeyemi Muideen Mudasiru ¹, Abiodun Emmanuel Ayodele ² and Tikam Singh Rana ³

¹ Department of Pure and Applied Botany, Federal University of Agriculture Abeokuta, Nigeria

² Department of Botany, University of Ibadan, Nigeria

³ Molecular Systematics Laboratory, Plant Diversity, Systematics and Herbarium Division, CSIR-National Botanical Research Institute, Rana Pratap Marg, Lucknow, Uttar Pradesh, India

The circumscription of the subtribe Terminaliinae (Combretaceae) has been a subject of controversy. Its generic phylogeny has also not been clearly elucidated. In this study, the taxonomic position of the Nigerian Terminaliinae taxa was revised based on the morphology and combined analyses of molecular markers to document taxonomic information on classification of Terminaliinae and ascertain the morphological and phylogenetic relationships among the members. Phylogenetic relationships were inferred using three DNA regions: ITS, *rbcL* and *trnH-psbA* sequences, while the morphological studies included the analysis of macromorphological and micromorphological features of all Terminaliinae species in Nigeria. The findings support the inclusion of *Anogeissus leiocarpus* in *Terminalia* while also retaining the *Conocarpus* and *Pteleopsis* species within Terminaliinae. The relationships between *Terminalia* and other Terminaliinae taxa remain unresolved based on only one molecular marker. The phylogenetic studies showed that *trnH-psbA* has better species discrimination efficiency than *rbcL* and ITS genes due to its highly variable nature. Transition/transversion bias test corroborated this finding as *trnH-psbA* showed higher bias (2.714) than *rbcL* (2.225) and ITS (2.126). The outcomes from the morphological studies indicated significant differences between *Anogeissus*, *Conocarpus*, *Pteleopsis* and *Terminalia*. However, the seed shape, inflorescence position, number of petals, stamens and fruit-wings, extrafloral nectaries, epidermal cells shape and anticlinal walls are useful characters for the identification of some Terminaliinae species. The morphometric analysis and molecular data suggest that *Anogeissus* and *Terminalia* could have evolved from a common ancestor. Accumulation of morphological differences and acceleration of the evolution of *Anogeissus* and *Terminalia* were more intensive than in other Terminaliinae species and this could probably be synchronized with adaptation to different climatic conditions. The phylogenetic relationships between the taxa were best resolved with Maximum Likelihood (ML) and Neighbour-joining (NJ) in combination with nrDNA ITS and chloroplast (*rbcL* and *trnH-psbA*) genes, phylogenetic trees constructed with combined ITS, *rbcL* and *trnH-psbA* revealed monophyletic nature of origin for the three genera: *Anogeissus*, *Pteleopsis* and *Terminalia*, while *Conocarpus* serves as a sister group to all remaining genera and species in the subtribe Terminaliinae. Bootstrap support and Bayesian posterior probability were found to be higher in *trnH-psbA* topologies than that of *rbcL* and ITS. The dendrogram and phylogeny of Terminaliinae revealed nested grouping of the *Anogeissus* species within *Terminalia*, and we suggest that all genera of Terminaliinae, with the exception of *Conocarpus* and *Pteleopsis* should be included in an expanded circumscription of *Terminalia*. Morphological and molecular trees revealed congruence in the number of main clades resolved and an indented dichotomous key was produced for easy identification of species.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-133546: Taxonomic remarks on genus *Ramaliella* (Scorzonerinae, Cichorieae, Asteraceae) from flora of Iran

Elham Hatami

Department of Biology, Faculty of Science, Razi University, Kermanshah, Iran. Post code: 6714414971

Based on the recent comprehensive taxonomic reassessment of subtribe Scorzonnerinae (Cichorieae, Asteraceae) using molecular, morphological and carpological data, the genus *Scorzonera* s.l. was divided into six distinct genera. Each of the species belonging to these new genera received new combination names in accordance with the international plant nomenclature rules. *Ramaliella* with seven species in the world is one of these new genera. This genus comprised the species that were previously belonged to section *Intricatae* of *Scorzonera* subg. *Scorzonera*. The name *Ramaliella* was derived from the fact that most of the species belonging to this genus have semi-shrub to cushion-like or in another word brushwood habit (rāmālia: brushwood). Morphologically, members of this genus are characterized by possessing subshrub or cushion-like vegetative form, numerous intricately or divaricately branched stems, few numbers of filiform basal leaves, reduced and curved cauline leaves, terminal capitula with 3-12 florets, and pollen with 24 lacunae. Furthermore, previous karyological studies on this genus represented the basic chromosome number of $n=7$ and also presence of different ploidy ($2n$, $3n$, $4n$, $6n$) and aneuploidy ($3n-1$) levels. In general, the species belonging to this genus are geographically distributed in southwest Asia with high species richness in the eastern and southern regions of the Irano-Turanian region. Among these regions, Iran has high species diversity, including five species such as *R. tortuosissima*, *R. microcalathia*, *R. intricata*, *R. koelopinioides*, and *R. longipapposa*. Members of this genus are mainly found in steppes or semi-desert areas in the east and south of Iran, representing that the species can tolerate semi-dry or dry climate. Among the species distributed in Iran, *R. intricata* and *R. microcalathia* are endemic to Iran. Moreover, *R. longipapposa* and *R. koelopinioides* are considered as rare species since they were observed in Khalij-Omani region in south of Iran only with limited numbers of individuals. Moreover, for defining the species delimitation in this genus based on morphological characters, we used traits such as cushion- or not cushion-like life form, the thickness of inflorescence peduncle relative to the stem, density of hairs on the stems, length of capitula, achene and pappus.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146861: Towards a comprehensive taxonomic revision of *Nemesia* Vent. (Scrophulariaceae, Hemimerideae)

Stoffel Petrus (Pieter) Bester¹, Mariëtte Jackson² and Lize Joubert²

¹ South African National Biodiversity Institute (SANBI), Foundational Research and Services Division, National Herbarium (PRE), Private Bag X101, Silverton, 0184, South Africa

² Department of Plant Sciences, Faculty of Natural and Agricultural Sciences, University of the Free State, P.O. Box 339, Bloemfontein, 9300, South Africa

The tribe Hemimerideae (Scrophulariaceae) is the earliest branching lineage of the family, with *Nemesia* as one of its most diverse and horticulturally significant genera. The genus currently comprises 77 species of annuals and perennials, all endemic to southern Africa, with greatest diversity in the Cape Floristic Region and Succulent Karoo, and additional species in Namibia, Zimbabwe, and Mozambique. South Africa is the centre of endemism, with many species restricted to the winter rainfall region. Since Hiern's 1904 revision, several species have been described, notably by Steiner (1994–2010), yet many remain inadequately treated, underscoring the need for a comprehensive revision.

Nemesia is characterized by zygomorphic, bilabiate flowers, usually with a single spur (versus paired spurs in *Diascia*), and fruit as a laterally compressed capsule. Floral diversity and annual life history underpin its wide horticultural use in bedding, containers, and hybrid breeding. The genus also provides insight into evolutionary processes in southern Africa. One species (*N. micrantha*) is extinct, and 14% are of conservation concern. The only published molecular phylogeny (Datson et al. 2008) indicated multiple life-history shifts between perennials of summer rainfall areas and annuals of winter rainfall regions, with diversification linked to Miocene–Pliocene climatic shifts.

Our recent phylogenetic analyses of 48 species using nuclear (ITS, ETS) and plastid (*trnL* intron) markers reveal two major lineages and five geographically structured subclades, also incorporating provisionally recognized taxa. These results, combined with morphological and distributional evidence, establish the framework for a full taxonomic revision to describe new taxa, update species circumscriptions, refine identification keys and maps, and expand herbarium and molecular resources.

This presentation provides an overview of *Nemesia*, highlighting key morphological traits and phylogenetic evidence guiding the ongoing revision.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-126093: Two new combinations in *Oxossia* (Passifloraceae s.l., Turneroideae)

James Lucas da Costa-Lima and Earl Celestino de Oliveira Chagas

Departamento de Biociências, Universidade Federal Rural do Semi-Árido, Mossoró, 59625-900, Brazil

Recently, a new genus segregated from *Turnera* L. (Passifloraceae s.l., Turneroideae) was described to accommodate a group of species that are phylogenetically well-supported. This new genus, *Oxossia* L.Rocha, was established to reflect these evolutionary distinctions within the subfamily Turneroideae. Although *Oxossia* does not present clear autapomorphies, it appears to be morphologically cohesive and can be recognized by a combination of characters that support its recognition as a separate evolutionary lineage. These diagnostic features include conspicuous stipules, flowers arranged in congested inflorescences, typically white corollas, pilose styles and stamens, and stamens that are basi-dorsiventrally adnate to the floral tube. Concomitantly with the establishment of *Oxossia*, we describe two species from northeastern Brazil, *Turnera acangatinga* Costa-Lima & E.C.O.Chagas and *T. ibateguara* Costa-Lima & E.C.O.Chagas, which exhibit morphological traits consistent with the circumscription of this new genus. Both species present unique reproductive characters that align them with the diagnostic features of *Oxossia*, including distinctive floral structures that set them apart from typical *Turnera* species. To update the taxonomy of this group and reflect the currently accepted circumscription, we followed the criteria of the International Code of Nomenclature for algae, fungi, and plants, and formally propose the transfer of these species to *Oxossia*. This results in the new combinations *Oxossia acangatinga* (Costa-Lima & E.C.O.Chagas) Costa-Lima & E.C.O.Chagas comb. nov. and *O. ibateguara* (Costa-Lima & E.C.O.Chagas) Costa-Lima & E.C.O.Chagas comb. nov.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143589: Uncovering karyotype and phylogenetic diversity within the North African *Allium* subgenus *Amerallium* Traub: Insights on taxonomy and evolution

Thinhinan Khedim ¹, Hana Zakkoumi ², Imene Boussalem ^{2,3}, Nabila Abdi ² and Imene Laouar ²

¹ Laboratory of Biology and Physiology of Organisms (LBPO-TAMAYOUZ), Department of Biology and Physiology of Organisms, Faculty of Biological Sciences, University of Sciences and Technology Houari Boumediene, Algiers, El Alia, BAB-EZZOUAR, ALGIERS, POB 32

² Laboratory of Biology and Physiology of Organisms (LBPO-TAMAYOUZ), Department of Biology and Physiology of Organisms, Faculty of Biological Sciences, University of Sciences and Technology Houari Boumediene, Algiers, El Alia, BAB-EZZOUAR, ALGIERS, POB 32

³ Faculty of Medical sciences, Department of Pharmacy, Bejaia, Algeria

The *Allium* subgenus *Amerallium* Traub encompasses a diverse and ancient lineage of approximately 140 species distributed disjunctly across the Mediterranean Basin, North America, and Western Asia. Phylogenetic and cytogenetic evidence supports its origin in the Old World, with North American taxa sharing a conserved base chromosome number ($x = 7$), unlike the broader variation observed in Old World taxa ($x = 7-11$). Despite its evolutionary significance, the North African representatives of this subgenus remain insufficiently studied, and their taxonomic boundaries are often unclear. This study focuses on elucidating the chromosomal diversity and phylogenetic structure of *Amerallium* species in Algeria, with the aim of clarifying species delimitations and identifying key evolutionary processes. A total of 80 wild populations belonging to six taxa (*A. subhirsutum*, *A. subvillosum*, *A. roseum*, *A. odoratissimum*, *A. triquetrum*, and *A. chamaemoly*) were sampled along an environmental gradient from coastal to arid regions in northern Algeria. Karyotype analyses uncovered a high degree of variation, with six distinct cytotypes ($2n = 14, 16, 18, 22, 28, 32$) corresponding to four basic chromosome numbers ($x = 7, 8, 9, 11$). Polyploid forms were limited to $x = 7$ and $x = 8$. Significant disparities in karyotype asymmetry indices were detected, particularly among polyploids. Molecular phylogenies based on ITS rDNA and chloroplast sequences (*trnL-trnF*, *trnD-trnT*) resolved a distinct North African clade, clearly separated from other Old and New World lineages. These findings emphasize the unique evolutionary trajectory of North African *Allium* species and underscore the role of chromosomal dynamics, particularly polyploidy and dysploidy, in their diversification. Further genomic investigations are needed to fully understand the origins and complexity of this lineage.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143210: New Paleontological Evidence on *Theodoxus micans* (Gaudry & Fischer, 1867) from the Megara Basin: A Potential Correlation with the Extant Species *Theodoxus meridionalis* (R. A. Philippi, 1836)

Dimitrios Protopapas and Efterpi Koskeridou

Department of Geology and Geoenvironment, National and Kapodistrian University of Athens, Athens, Greece

The Megara Basin in Greece, located east of the Corinthian Gulf and bordered by the Alkyonides Gulf to the north and the Saronic Gulf to the south, comprises Neogene-Quaternary formations rich in marine and lacustrine fossil mollusks. Shell morphology of *T. micans* closely resembles that of both fossil and extant taxa, notably *Theodoxus meridionalis*, a species widely distributed throughout the Mediterranean region, including Greece. However, substantial intraspecific variability in shell shape and coloration among *Theodoxus* species complicates taxonomic assignments. Conversely, the operculum has been recognized as a potentially more reliable feature for species-level differentiation. Our research draws on material from the historical collection of the Museum of Geology and Paleontology at the National and Kapodistrian University of Athens (NKUA), which includes fossil specimens and sediment samples from sites such as Alepochori and the Mauratza Ravine. This material consists of both bulk fossiliferous sediments and previously sorted fossils from the 20th-century research. We discovered opercula, which were identified as belonging to *T. micans*. These were found alongside *T. micans* shells and other species such as *Lymnaea megarensis* Gaudry, 1867, but no other *Theodoxus* species. Comparative analysis with extant and fossil material from other localities—where *T. micans* has been reported—yielded no prior operculum descriptions. Our findings suggest that *T. micans* may be conspecific with or closely related to *T. meridionalis*. These results contribute to the ongoing taxonomic and systematic reassessment of this fossil taxon.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

Session 5. "Paleotaxonomy"

sciforum-143475: Tetrapod Ichnotaxonomy: Preservation, practice, and meaning

Lara Sciscio ^{1,2}

¹ Jurassica Museum, Rte de Fontenais 21, 2900, Porrentruy, Switzerland

² Department of Geosciences, University Fribourg, Chemin du Musée 6, 1700, Fribourg, Switzerland

Ichnotaxonomy is the naming and classification of trace fossils based on their morphological features, which incorporate tracemaker anatomy, behaviour, and substrate. Unlike traditional taxonomy, it is a parataxonomic system whereby ichnotaxa are named independently of the animal that produced them. Tetrapod ichnotaxonomy was established by Edward Hitchcock, who applied Linnaean binomial nomenclature to the naming of dinosaur tracks. Today, ichnotaxonomy follows rules established by the International Code of Zoological Nomenclature.

Historically, tetrapod ichnotaxonomy has struggled with inconsistent descriptive standards, nomenclatural issues, a legacy of producer-focused naming, and a reliance on qualitative methods. Efforts have been made to standardise tetrapod ichnotaxonomy, especially since the vertebrate ichnology “renaissance”, and several scholars have provided guidelines to streamline the practice, and for its greater utility in palaeobiological and palaeoecological studies. Nonetheless, subjective interpretation is common, and the incorporation of quantitative methods is not consistent. A conceptual divide concerns preservation bias and the definition of “preservation” in tetrapod ichnology. Preservation can relate to anatomical fidelity (morphological preservation) and thus be diagnostic for ichnotaxonomy, while an alternative view defines preservation in terms of post-formation modification. This perspective treats formation variation from foot–sediment interaction and behaviour as distinct from taphonomic loss. These approaches differ on when taphonomy begins.

The need to separate formational from post-formational variation to combat ichnotaxonomic inflation is illustrated by several case studies in the literature, including ongoing reassessments of historically oversplit ichnotaxa and morphometric analyses of conservative track morphologies. By defining and assessing preservation, applying standardised methods, and considering ichnotaxonomic decisions within morphological, sedimentological, and behavioural contexts, tetrapod ichnology can be holistic, ensuring that what we name aligns with what we can know.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143274: Taxonomic Review and Anatomical Analysis of Chondrichthyes from the Paraíba-Pernambuco Basin: Itamaracá, Gramame, and Maria Farinha Formations

Clarice Assumpção¹, Camila Cupello² and Paulo Brito¹

¹ Department of Zoology / Roberto Alcântara Gomes Institute of Biology / Rio de Janeiro State University. Rua São Francisco Xavier, 524, Maracanã, Rio de Janeiro 20550-013, RJ – Brazil

² Department of Archaeology / Rio de Janeiro State University. Rua São Francisco Xavier, 524, Maracanã, Rio de Janeiro 20550-013, RJ – Brazil

The Paraíba-Pernambuco Basin, located between Recife and Mamanguape, northeastern Brazil, is notable for its remarkable Mesozoic chondrichthyan fauna and its critical role in the geological evolution of the South Atlantic. Geological evidence indicates that this basin was among the last regions to separate during the fragmentation of Gondwana. The fossil assemblages preserved in this area hold global significance for paleontological research, particularly in relation to the evolution and paleobiogeography of elasmobranchs throughout the Cretaceous. This study aims to provide an anatomical and taxonomic redescription of the chondrichthyes from the Paraíba-Pernambuco Basin, based on dentition and its morphological variations. A total of 128 fossil chondrichthyan teeth from the Itamaracá (Campanian–Maastrichtian), Gramame (Maastrichtian), and Maria Farinha (Paleocene) formations, housed in scientific collections at Brazilian universities, were examined, some of which had been described in earlier studies. Anatomical and taxonomic assessments were conducted based on criteria such as main cusp angulation, accessory cusps number, crown shape and size, presence of serrations, and overall proportions. Additionally, morphological comparisons with living species were employed to infer the original tooth position within the jaw. The morphological analyses enabled the identification of the specimens and the reconstruction of their jaw positioning, thereby enhancing the understanding of elasmobranch jaw architecture. Taxonomic revisions included the reclassification of *Notidanus microdon* as *Hexanchus microdon*, *Odontaspis tingitana* as *Carcharias tingitana*, and the reassignment of all previously identified *Lamna* species to the genus *Cretolamna*. Notably, *Ptychodus whipplei* was recorded for the first time in the Itamaracá Formation, extending its known geographic distribution. The findings underscore the value of integrating fossil and living morphological data to refine taxonomic identifications. Moreover, the Paraíba-Pernambuco Basin is reaffirmed as a key fossil locality for elucidating elasmobranch diversity and biogeography during the Mesozoic. This study contributes valuable insights for future taxonomic and paleoecological investigations in the region.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143068: Taxonomical Review of Ichthyodectiformes -Actinopterygii Teleostei- from Cretaceous of Brazil

Thales Rodrigues Jardim Barreto ¹, Diogo de Mayrinck ¹ and Paulo Marques Machado Brito ²

¹ LICTAE- Laboratory of Applied Ichthyology: Anatomy and Evolution, IBRAG - Roberto Alcântara Gomes Institute of Biology, UERJ - Rio de Janeiro State University, Rio de Janeiro Cep 20550-900, Brazil

² Zoology Department, IBRAG - Roberto Alcântara Gomes Institute of Biology, UERJ - Rio de Janeiro State University, Rio de Janeiro Cep 20550-900, Brazil

The Ichthyodectiformes are a fossil teleostean lineage known from the Middle Jurassic to Early Cenozoic, found in marine and freshwater sediments on every continent. The clade is supported by five synapomorphies and currently known from over 30 valid species. However, most fossils are poorly preserved or incomplete, and therefore, the synapomorphies for the group are hard to identify or even homoplastic in many teleostean lineages. This identification problem is recognized, and many authors highlight a combination of characteristic anatomic aspects to identify the group, like the distinctive "bulldog-like" head shape. In Brazil, the Ichthyodectiformes are represented by six valid nominal genera (*Saurocephalus*, *Chiromystus*, *Itaparica*, *Ogunichthys*, *Cladocycclus*, *Cladocynodon*) temporally distributed in the Cretaceous, exclusively on the northeastern sedimentary basins (Araçuaia, Parnaíba, Recôncavo-Tucano-Jatobá, Sergipe-Alagoas). Despite these known forms, to this day, there's no comparative anatomical work between the Brazilian species. This work aims to conduct the comparative anatomical and phylogenetic study of the Cretaceous species from Brazil to better understand the order's interrelationship, based on the data available for the taxa in question. The specimens were reviewed by comparative anatomy and analyzed using the program PAUP* 4.0a169, based on the last data matrix to test the intrarelationships of Ichthyodectiformes. Based on the anatomical review, characters for the taxa were updated. Compared to the previous results, our analysis resulted in a large polytomy, with no clear affinities for *Cladocynodon araripensis*, and the relationship between Ichthyodectiformes from Brazil remains unclear. The available material in the collections was insufficient to elucidate the relationships of the Brazilian species. Only the synapomorphies of teeth in a single series and a ventrally enlarged coracoid could be verified in every taxon. A larger sampling effort is recommended to elucidate the phylogeny.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142790: A fossil of the austral tree fern genus *Lophosoria* (Dicksoniaceae) from mid-Cretaceous Myanmar amber

Chunxiang Li ¹, Junxian Li^{Ma} ² and Junye Ma ³

¹ Key Laboratory of Palaeobiology and Petroleum Stratigraphy, Nanjing Institute of Geology and Palaeontology, Chinese Academy of Sciences (NIGPAS), Nanjing 210008, China

² College of Animal Science and Technology, Southwest University (Rongchang Campus), Chongqing 402460, China

³ Department of Micropaleontology, NIGPAS, Nanjing 210008, China

The occurrence of taxa typically associated with Gondwana, in what is now the Northern Hemisphere, remains an intriguing subject in paleobiogeography. We describe an unusual tree fern from mid-Cretaceous amber in Myanmar, classified in the genus *Lophosoria* (Dicksoniaceae, Cyatheales). Its classification within the extant genus *Lophosoria* is supported by distinctive morphological features of the fertile pinnule, notably its unique flanged spores. Currently, *Lophosoria* is restricted to the Neotropics and southern South America, with prior paleopalynological and megafossil data indicating its exclusive presence in the Southern Hemisphere, particularly in Eastern Australia, the Falkland Plateau, South America, and the Antarctic Peninsula, suggesting a Gondwanan origin. The identification of the new species in mid-Cretaceous Northern Hemisphere deposits marks the genus's earliest confirmed occurrence in this region, broadening our understanding of its historical distribution and early evolution. This discovery contributes to the recognized diversity of *Lophosoria*, which has largely been based on spore fossils linked to the genus *Cyatheacidites*. We also discuss the paleobiogeographic and paleoclimatic implications for the evolutionary history of *Lophosoria*.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-141668: Revisiting the fossil polypterid †*Polypterus faraou*. taxonomic assessment based on cranial morphology

Marcos Vinícius Coelho ¹, Diogo Mayrinck ², Andossa Likius ³, Paulo M. Brito ¹, Olga Otero ⁴ and
Camila Cupello ⁵

¹ Department of Zoology, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

² Laboratory of Applied Ichthyology: Anatomy and Evolution (LICTAE), Department of Biological Sciences Education, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

³ Department of Paleontology, University of N'Djamena, N'Djamena, BP 1117, Chad

⁴ UMR 7262 PALEVOPRIM CNRS, University of Poitiers, Poitiers, 86000, France

⁵ Department of Archaeology, University of the State of Rio de Janeiro, Rio de Janeiro, 20550-900, Brazil

Polypterus is an African freshwater fish genus comprising 13 extant species and three fossil species, including †*P. faraou*, which is based on a single articulated specimen from the Late Miocene (~7 Ma) of Chad. Recently, †*P. faraou* has been suggested to be conspecific with *P. bichir*, as its meristic values fall within the expected range of variation for *P. bichir*, which entirely encompasses the diagnoses of both taxa. In this study, we use X-ray tomography and three-dimensional reconstructions to generate new data on the cranial anatomy of †*P. faraou* and compare it with *P. bichir* in order to test the validity of the fossil species. Owing to the fossil's exceptional preservation, all cranial regions and the pectoral girdle were described, either fully or partially. Regarding meristic characters, we corroborate that †*P. faraou* indeed falls within the range expected for *P. bichir*. However, we were able to distinguish the two species based on features of the opercular region and posterior ceratohyal morphology. Accordingly, we propose an emended diagnosis for †*P. faraou*, characterized by a proportionally longer ventral process of the preopercle, a higher subopercle that extends well beyond the mid-height of the opercle, an opercle with a more triangular outline, and a rounded posterior ceratohyal. Although these species show few morphological differences, we present here the first cranial osteological diagnosis for this genus, highlighting its importance for advancing the understanding of cranial morphology in polypterids.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142602: Using New Technologies to Classify the Pennsylvanian (307 Million Years Old) Problematica Fossil, *Tullimonstrum gregarium*

Paul S Mayer¹, Victoria E McCoy², Jacob J Potter² and Jack Wittry¹

¹ Geology Department, Field Museum of Natural History, Chicago, Illinois, 60605, USA

² Department of Geosciences, University of Wisconsin-Milwaukee, Milwaukee, Wisconsin, 53211, USA

Tullimonstrum gregarium is an enigmatic soft-bodied fossil from the Pennsylvanian Mazon Creek Lagerstätte of Northern Illinois. It was originally described by Richardson (1966), as problematica, but listed as a worm-like animal in the title. Since this initial description, researchers have struggled to classify the 30-cm-long fossil. Cladistic analyses have placed it with the clade uniting vertebrates, molluscs, annelids, and nemerteas.

Recently, these fossils have been subject to renewed testing and analysis. McCoy et al. (2016) assigned it to the Agnathans based on identifying a notochord, gill pouches, and w-shaped myomeres. They further supported this assignment with synchrotron analysis of trace element enrichment in the fossil. A vertebrate assignment was indicated by the discovery of melanosomes structures in the eyes using SEM (Clements et al. 2016). In situ Raman microspectroscopy showed evidence that the structural tissue, made of proteins not chitin, a strong evidence for a vertebrate assignment (McCoy et al. 2020).

Mikami et al. (2023) examined surface features on the fossils using a 3-D laser scanner, conducted x-ray microcomputed tomography scans of the teeth-like structures, and suggested that some features in the head represent preserved segments; they argued that the combination of features they observed is most consistent with a non-vertebrate chordate classification.

The use of new technologies and innovative methods to classify *Tullimonstrum gregarium* has resulted in new ideas about its origin, but researchers still disagree on its identity and even on its morphology. However, research continues, including a current investigation of its structural tissues using scanning electron microscopy, and each project provides new data that brings us closer to a final answer to this mystery.

References

1. Clements T, Dolocan A, Martin P, Purnell MA, Vinther J, Gabbott SE. The eyes of *Tullimonstrum* reveal a vertebrate affinity. *Nature*. 2016 Apr 28;532(7600):500-3. doi: 10.1038/nature17647.
2. McCoy VE, Saupe EE, Lamsdell JC, Tarhan LG, McMahon S, Lidgard S, Mayer P, Whalen CD, Soriano C, Finney L, Vogt S, Clark EG, Anderson RP, Petermann H, Locatelli ER, Briggs DE. The 'Tully monster' is a vertebrate. *Nature*. 2016 Apr 28;532(7600):496-9. doi:10.1038/nature16992. Epub 2016 Mar 16. PMID: 26982721.
3. McCoy VE, Wiemann J, Lamsdell JC, Whalen CD, Lidgard S, Mayer P, Petermann H, Briggs DEG. Chemical signatures of soft tissues distinguish between vertebrates and invertebrates from the Carboniferous Mazon Creek Lagerstätte of Illinois. *Geobiology*. 2020 Sep;18(5):560-565. doi:10.1111/gbi.12397. Epub 2020 Apr 28. PMID: 32347003.
4. Mikami T, Ikeda T, Muramiya Y, Hirasawa T, Iwasaki W. Three-dimensional anatomy of the Tully monster casts doubt on its presumed vertebrate affinities. *Palaeontology*. 2023 66: e12646. doi.org/10.1111/pala.12646.
5. Richardson, ES Jr. Wormlike Fossil from the Pennsylvanian of Illinois. *Science*. 1966 151, 75-76. doi:10.1126/science.151.3706.75.b.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-142583: Clearing the Taxonomic Mist: New insights into Neogene Conidae diversity through UV imaging of type specimens

Christos Psarras

National and Kapodistrian University of Athens, Faculty of Geology and Geoenvironment, Department of Historical Geology-Paleontology, Athens, Greece

Fossils of the family Conidae (predatory marine gastropods) present persistent taxonomic challenges due to limited morphological variability between species and the often-overlooked potential of shell colour patterns. Consequently, certain historical classifications from the 19th century, many of which remain in use today, include ambiguous or potentially redundant taxa. During a Short-Term Scientific Mission to the Museo Regionale di Scienze Naturali di Torino (Italy), I studied over 180 Neogene Conidae specimens, including the 35 type specimens originally described by Federico Sacco, hosted in the Museum. Sacco's many named varieties, known for their taxonomic uncertainty, were also partially assessed. Ultraviolet (UV) light imaging was used to reveal residual shell colour patterns that are not visible under natural light. Preliminary results display that some species or varieties likely represent multiple distinct taxa, while some varieties are distinct species. For example, *Conus (Kalloconus) berghausi* (Michelotti, 1847), including the neotype and Sacco's varieties, appears to encompass at least three separate species. UV imaging proved particularly useful in detecting consistent colour pattern elements that support species delimitation. This initial assessment illustrates the potential of combining UV imaging with classical morphological approaches to refine the taxonomy of Neogene Conidae. Further detailed study of Sacco's broader collection may yield additional taxonomic insights and contribute to a more stable framework for interpreting fossil cone snail diversity.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143489: Hidden species diversity of micro-gastropods from the Late Pleistocene deposits in Taiwan

Diana Osipova ^{1,2,3} and Chien-Hsiang Lin ¹

¹ Biodiversity Research Center, Academia Sinica, No. 128, Academia Road, Sec. 2, Nankang, Taipei 11529, Taiwan

² School of Life Science, National Taiwan Normal University, Heping E. Rd, Da'an, Taipei 106308 Taiwan

³ Biodiversity Program, Taiwan International Graduate Program, Academia Sinica and National Taiwan Normal University, Taipei 115201, Taiwan

Taiwan, with its rich biodiversity since the Neogene period, has been the subject of extensive paleontological research; however, studies of its molluscan fossil fauna remain outdated. Contemporary gastropod diversity in the surrounding waters is considerably higher than that reflected in Quaternary deposits, suggesting that certain Pleistocene gastropod groups may have been undersampled or overlooked. To evaluate potential gaps in the Pleistocene mollusk record, we examined bulk sediment samples from two strata of the Toukoshan Formation (northern Taiwan) and the Szekou Formation (southern Taiwan). We focused on small gastropods (5 mm), which may have been neglected in previous investigations. Specimens were sorted, identified to the lowest possible taxonomic level, and compared with both fossil and modern reference collections. We identified more than 150 taxa previously unreported from the Taiwanese Pleistocene record. These include representatives of Patellogastropoda; Vetigastropoda (≥ 4 families, 1 newly recorded family); Neomphaliones; Caenogastropoda (≥ 9 families, 5 newly recorded); and Heterobranchia (≥ 5 families, 4 newly recorded, and 1 newly recorded order). Several taxa represent their first occurrence as fossils, thereby extending their known geological ranges. Notable findings include pelagic Littorinimorpha and Pteropoda, as well as Cephalaspidea specimens potentially representing new species. Our results reveal a substantially richer and more diverse Pleistocene molluscan assemblage than previously recognized in Taiwan. These findings improve assessments of Late Pleistocene species richness, facilitate comparisons with the modern Indo–West Pacific fauna, and contribute to understanding the timing of lineage appearances in the region. The expanded fossil inventory will also enhance future paleoecological and biogeographical reconstructions, shedding light on the processes underlying the establishment of present-day Indo–West Pacific marine biodiversity.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-140357: Nomenclature is the scientific language of Taxonomy, and you already know everything about it

Evangelos Vlachos

Museo Paleontologico Egidio Feruglio and CONICET (National Scientific and Technical Research Council), Av. Fontana 140, 9100 Trelew, Chubut Province, Argentina

Nomenclature and Taxonomy are often considered boring topics of research, whereas even some researchers consider Nomenclature not to be a scientific discipline at all. Others believe that Taxonomy needs a major image change to attract interest from modern scientific audiences. In this contribution, I rebrand Nomenclature and Taxonomy as parts of the same scientific discipline, following Schneider's (2009) scheme. Furthermore, I focus on the role of taxonomists in promoting the importance of nomenclature and taxonomy to younger scientific audiences and teaching these techniques in a way that supports the entire discipline. My own experience with Nomenclature and Taxonomy teaching is that it usually focuses on the most complicated and confusing exceptions where the Code did not work, instead of focusing on teaching the main part of the discipline that does work well. Even in those cases, teachers present it with excessive terminology and complex terms that may discourage the student or young researcher. Here, I propose a new, simple method for teaching the key concepts of nomenclature and taxonomy – availability, validity, homonymy, synonymy, coordination, and spelling – using analogies that people are familiar with their daily lives: how a computer archives its files. With this analogy, the teacher can deliver the main concepts of nomenclature and taxonomy in a few minutes.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143502: On the morphology, phylogeny and applications of Oligocene-Miocene *Asterigerinoides* (Foraminifera)

Michael Steenhuyse-Vandeveldel and Robert Speijer

Department of Earth & Environmental Sciences, KU Leuven, Celestijnenlaan 200E, Heverlee, Belgium

Asterigerinoides guerichi guerichi (Franke 1912) is a well-known benthic foraminifer from the Chattian (upper Oligocene) of the North Sea Basin. The base of this classic Chattian is marked by an extensive bloom of *A. g. guerichi*, historically the 'Asterigerina Horizon' (recently the 'Asterigerinoides guerichi guerichi acme event'). Despite its wide usage for stratigraphic purposes, the taxonomy and paleoecology of *Asterigerinoides* are quite obscure.

This study aims at identifying ecological traits, such as feeding strategies, which can elucidate the prolific abundance of *A. g. guerichi* during the Chattian and of *A. guerichi staeschei* during the Miocene, while simultaneously providing more insight into the phylogenetic relationships between *A. g. guerichi*, *A. g. staeschei* and *Asterigerinoides frankei* (mostly referred to as *Asterigerina frankei*) through literature study and comparison with collection material. We compared the morphology of *A. g. guerichi*, *A. g. staeschei* and *A. frankei* through optical microscopy and SEM, highlighting different features of these species. Ultimately, we also aim at achieving a revised taxonomy of *Asterigerinoides* and an improved utilization of *A. g. guerichi* as a stratigraphic marker.

Our observations on the morphological features in the three *Asterigerinoides* (sub)species, such as the equally biconvex test and teeth-like granules near the aperture, point towards a shallow marine habitat and epibenthic lifestyle with an endosymbiotic and potentially multitrophic feeding strategy. Stable isotope analyses are ongoing to evaluate these paleoecological interpretations towards paleotemperatures and possible vital effects caused by photosymbionts. The presence of keel pores, slit-like apertures surrounded by teeth-like granules and similar arrangements of secondary chambers observed in *A. frankei*, as well as *A. g. guerichi* and *A. g. staeschei*, led us to conclude that *A. frankei* is a member of the genus *Asterigerinoides* rather than *Asterigerina*. The insights presented here will improve our understanding of these species and their use as biostratigraphic markers.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147225: Re-evaluation of the taxonomy of *Compsemys*: an enigmatic turtle from around the Cretaceous-Paleogene boundary

Steven E. Jasinski

Department of Environmental Science and Sustainability, Harrisburg University, Harrisburg, Pennsylvania 17101-2208, United States

Compsemys is an enigmatic turtle first described over 150 years ago. Its taxonomic placement has been in flux, with many of its referred species being removed. For the last three decades or so, *Compsemys victa* has been the only accepted North American species. New fossil specimens collected from the Paleocene of North America suggest a re-evaluation of its taxonomy is in order, calling into question the long-held belief that only one species of *Compsemys* is valid in North America. Paleocene specimens are far more complete than the holotype of *C. victa* but have all been referred to this species based on similar surface sculpturing. Differences between Cretaceous and Paleocene fossil material suggest multiple species of *Compsemys* are valid. In addition to the genotypic species *C. victa*, two Paleocene species (*Compsemys puercensis* and *C. torrejonensis*) are valid based on morphological differences of the carapace and plastron, particularly aspects of scute sulci (such as that of the humerals, pectorals, femorals, and vertebrae), the neurals, and some aspects of the shapes of the plastral lobes. North American *Compsemys* survived the Cretaceous-Paleogene mass extinction. Rather than being a monospecific genus, this taxonomic re-evaluation of *Compsemys* shows it became more diverse during the early Paleocene, at least in the American southwest, perhaps exploiting the loss of numerous other taxa during the K-Pg mass extinction event. Not only does this re-interpretation of *Compsemys* taxonomy suggest an increase in diversity of North American compsemysids but also leads to the possibility of anagenesis within the genus during the Late Cretaceous and Paleocene, at least in the American southwest.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-139735: Revisiting *Megalosauripus transjuranicus*: new ichnotaxonomical insights from the Plagne tracksite (Tithonian, France) and implications on Late Jurassic theropod ichnotaxonomy

Vincenzo Gesualdi ¹, Lara Scicio ^{2,3}, Alessandro Riga ⁴, Christian Meyer ^{5,6}, Diego Castanera ⁷, Jean-David Moreau ^{8,9}, Emmanuel Fara ¹⁰, Isacco Alberti ^{11,12}, Matteo Belvedere ¹¹

¹ Department of Earth Sciences, University of Florence, Florence, via G. la Pira 4, 50121, Italy

² JURASSICA Museum, Porrentruy, Route de Fontenais 21, CH-2900, Switzerland

³ Department of Geosciences, Fribourg, University of Fribourg, Chem. du Musée 4, 1700, Switzerland

⁴ Department of Biology, University of Florence, Florence, Via Madonna del Piano, 6, 50019, Italy

⁵ Department of Environmental Sciences, Basel, University of Basel, Bernoullistr. 32, 4056, Switzerland

⁶ Museo de Historia Natural Alcide d'Orbigny Cochabamba, Avenida Potosi N-1458, Bolivia

⁷ Grupo Aragosaurus-IUCA, Facultad de Ciencias, Zaragoza, Universidad de Zaragoza, C. de Menéndez Pelayo, 24, 50009, Spain

⁸ Université Bourgogne Europe, Dijon, CNRS, Biogéosciences UMR 6282, 21000, France

⁹ Université Paris-Saclay, Orsay, CNRS, GEOPS, 91405, France

¹⁰ Université Bourgogne Europe, CNRS, Biogéosciences UMR 6282, 21000 Dijon, France

¹¹ Dipartimento di Scienze della Terra, Università degli Studi di Firenze, via G. la Pira 4, 50121 Firenze, Italy

¹² NBFC, National Biodiversity Future Center, Palermo, Italy

The Jura region (France and Switzerland) is a key area for studying Late Jurassic (Kimmeridgian–Tithonian) dinosaur tracks. Cyclical fluctuations in sea level during this period exposed the Jura carbonate platform, creating land bridges that facilitated the dispersal of vertebrates and the formation of track-bearing surfaces. As a result, there are numerous tracksites in both countries. They exhibit well-preserved tracks with strong morphological similarities and possible ichnotaxonomical affinities. Dinosaur ichnotaxonomy is based primarily on morphological rather than behavioural characteristics, and in many studies the correct attribution of footprints to specific ichnotaxa has been problematic. In this study, we propose the classification of the Plagne theropod tracks in *Megalosauripus transjuranicus* through a quantitative approach, using two landmark-based analyses: Geometric Morphometrics (GM) and Whole-Track Analysis (WTA). Our results reveal clear clustering in morphospace for GM and morphological overlap in the WTA, supporting this attribution. Utilizing a dataset including other Jurassic theropod ichnotaxa, new ichnotaxonomical affinities have been revealed. This study records the presence of *M. transjuranicus* in the French Jura and highlights the utility of this approach in ichnotaxonomical identification. Furthermore, it extends the known stratigraphic range of *Megalosauripus transjuranicus* into the Tithonian in France and up to the Berriasian in Spain, suggesting a longer persistence than previously documented for large theropods in these areas.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-146929: Taxonomic paleodiversity of the Marizal Formation (Aptian), Tucano Basin (NE Brazil)

Ingrid M. Veiga ^{1,2} and Paulo M. Brito ²

¹ Department of Ecology, Rio de Janeiro State University, Rio de Janeiro 20550-900, Brazil

² Department of Zoology, Rio de Janeiro State University, Rio de Janeiro 20550-900, Brazil

The Amargosa Bed is a fossiliferous stratigraphic marker within the Marizal Formation, cropping out throughout the Tucano Basin in Northeastern Brazil. The fossil record of this unit was first reported during the 1960's and 1970's and is currently comprised by remains of dinocysts (*Subtilisphaera* sp.), pollen (Schizaeaceae and Matoniaceae), plants (e.g., Bennettitales), invertebrates (e.g., caridean shrimps), vertebrates (Ophiopsidae, Amiidae, Aspidorynchidae, Cladocyclidae, Chanidae, and Clupavidae), as well as ichnofossils. These taxa are mostly indicative of a freshwater ecosystem. In light of continued excavation work, several new remains (35 scale impressions and approximately 200 articulated fish remains) have been retrieved and are currently being studied in order to assess their taxonomic identity and significance. So far, morphological approaches have shown the existence of three scale morphotypes unlike those present in the previously described fish taxa – which were reevaluated and redescribed in detail. In the same sense, the articulated remains, still under study, can be assigned to at least four morphotypes with distinct proportions and morphological characteristics that hint at possible new taxa for the Amargosa Bed. These new findings, although still preliminary, highlight the biological paleodiversity of the unit – which likely comprises a higher number of taxa and ecological actors than previously thought.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-147382: The female of the first Cretaceous velvet water bug *Archaeohebrus alius* Zhang, Ren & Yao 2024 (Heteroptera: Hebridae)

Eduardo I. Faúndez ^{1,2} and Sofía Araya-Lobos ^{1,3}

¹ Cape Horn International Center (CHIC), Av. Bulnes 01890, 6350000, Punta Arenas, Chile

² Entomology Laboratory, NINFA Center for Arthropod Research, 6200000 Punta Arenas, Chile

³ Ingeniería en Recursos Naturales Renovables, Facultad de Recursos Naturales, Universidad Católica de Temuco, P.O. Box 15-D, Temuco, Chile

Recently, the first Cretaceous velvet water bug (Heteroptera: Hebridae), *Archaeohebrus alius* Zhang, Ren & Yao 2024 was described from Myanmar amber, based on a one male specimen. In the present contribution, we report the finding of the first female of this species, based on one specimen collected in the same area. The amber piece containing the studied fossil originated from Noije Bum, near Tanai Village Hukawng Valley, Kachin State, northern Myanmar. It is dated as the earliest Cenomanian, mid-Cretaceous (98.79 ± 0.62 Ma). The female studied has an elongated body (2.28 times longer than wide) with a subtriangular head and hexagonal pronotum. The hemelytra are fully developed, bearing 3 closed cells and almost reaching the end of the abdomen. Finally the external genitalia has an 8th abdominal segment strongly concave towards the middle; the 9th abdominal segment is elongated, and looks subtrapezoid in lateral view; the valvifer 1 is well developed, and has isosceles triangle shaped in lateral view; the valvula 3 are visible and well developed, subrectangular in lateral view; and the ovipositor is well esclerotized and resting inside the valves. In general, the female looks similar to the male, but is a little more slender, with the head and pronotum more stylized. This dimorphism has been observed in other modern Hebridae. In addition to the diagnostic characters shared with the male, the genitalia details observed in the female support the placement of this species in Hebridae.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-143310: The plant-insect interactions in a newly discovered Middle Miocene locality in Kos island, Greece

Antonios Isidoros Avrithis

Department of Natural Sciences, The Open University, Walton Hall, Kents Hill, Milton Keynes MK7 6AA, United Kingdom

The Middle Miocene represents a critical interval in the history of European angiosperms and insects particularly in the Mediterranean region, where climate change influenced these communities as the few unevenly dispersed data indicate. Here, we present new findings from the island of Kos, Greece, where a rich assemblage of fossilized angiosperm leaves from the Middle Miocene provides novel data of plant-insect interactions at this transitional time interval. Palaeobotanical analysis confirms multiple angiosperm morphotypes, likely belonging to both deciduous and evergreen lineages. These fossils exhibit a diverse array of insect-mediated damage types (DTs), including margin feeding, hole feeding, skeletonization, mining, and galling structures.

Using the established Labandeira DT classification framework, I documented over 10 discrete damage types, indicating a high level of functional feeding group diversity. Interactions' relative richness and diversity is different among different leaf morphospecies although *Quercus* and *Acer*, which are some of the most common leaf elements found in the assemblage, exhibiting highest diversity on DTs.

This study is the first to document such detailed insect-plant interaction data from the Miocene of Greece and contributes a new regional data point to the research on Cenozoic plant-insect associations. The diversity and specificity of the interactions observed underscore the ecological complexity of Miocene forests in the Aegean region. These results offer new insight into the vegetational and insect community dynamics of the region and support the use of trace fossil evidence as a proxy for reconstructing ancient insect diversity.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

sciforum-144210: Uncovering hidden diversity in Iberian freshwater fossil snails: an integrative approach to *Horatia schlosseri* (Royo-Gómez, 1922) (Gastropoda: Hydrobiidae)

Jonathan P. Miller ¹, Julio Talavan Serna ² and Diana Delicado ¹

¹ Museo Nacional de Ciencias Naturales – CSIC

² Independent Researcher

The classification of Hydrobiidae Stimpson, 1865, a diverse family of freshwater gastropods, is hindered by their minute size and simplified shell morphology, resulting in a lack of diagnostic features in fossils. This leads to taxonomic ambiguities and the concealment of cryptic diversity, as seen in *Horatia schlosseri* (Royo-Gómez, 1922), a species frequently reassigned without consistent analysis. An integrative taxonomic approach is thus essential for accurate fossil identification and systematic resolution. To assess morphological variation within *H. schlosseri*, we applied geometric morphometrics (GM), analyzing shell shape across 163 specimens from eight Iberian localities. These included syntypes of *H. schlosseri*, type material of *Horatia klecakiana* (type species of *Horatia*), and paratypes of the similar genus *Tarraconia*. Shells were digitized with 18 landmarks/semi-landmarks and analyzed using Procrustes superimposition, Linear Discriminant Analysis (LDA), and ANOSIM. GM analysis revealed four distinct morphotypes within the *H. schlosseri* complex. Specimens from Alcalá del Júcar, previously attributed to *H. schlosseri*, clustered statistically with *Tarraconia* (ANOSIM $p > 0.05$) and were reassigned as *Tarraconia* sp. 1, further supported by the presence of a diagnostic varix. Two new cryptic species were also identified: *Horatia* sp. 1 (La Hontanilla Spring, Cuenca) and *Horatia* sp. 2 (Concud, Teruel), both from localities historically linked to *H. schlosseri*. Our results highlight the limitations of traditional morphological methods in Hydrobiidae systematics and emphasize the value of GM in revealing cryptic diversity. This study underscores the need for a comprehensive revision of Iberian caenogastropod fossils using integrative, quantitative approaches.



© 2025 by the author(s). Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<http://creativecommons.org/licenses/by/4.0/>).

MDPI AG
Grosspeteranlage 5
4052 Basel
Switzerland
Tel.: +41 61 683 77 34

Taxonomy Editorial Office
E-mail: taxonomy@mdpi.com
www.mdpi.com/journal/taxonomy



Disclaimer/Publishers' Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.

