



BARCELONA 4TH - 8TH JULY 2022

Program, Oral Presentations & Posters



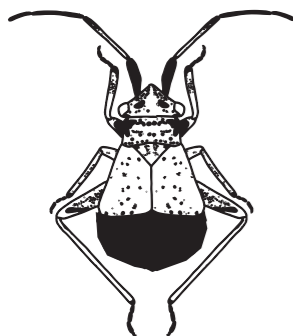
7th IHS ORGANIZING COMMITTEE

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TECHNICAL SECRETARIAT



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Dimorphocoris josephinae Ehanno & J. Ribes, 1994 (Miridae, Orthotylinae). The species is dedicated to Josefina Español, Jordi Ribes's wife. The logo represents a tribute to Jordi Ribes, and, through Josefina Español, to everyone who for love or friendship supports us in our entomological tasks.

Monday 4th July 2022

- 16.00-19.00 **Documentation delivery**
 17.00-19.00 **Welcome cocktail**
 To be held in: Institut d'Estudis Catalans (*Carrer del Carme, 47*)

Tuesday 5th July 2022

- 09.00-09.10 **Welcome**
Organizing Committee
- 09.15-10.30 **Congress opening**
Tom Henry
- 10.45-11.05 **Coffee break**
- 11.10-13.08 **Oral Presentations.** Chairperson: Leticia Nery
- 11.10-11.28 **ID 61 • Vibroacoustic signals of Peloridiidae (Hemiptera: Coleorrhyncha) – structures involved in their production and implications for the phylogenetics of Hemiptera**
Leonidas-Romanos Davranoglou; Hartung, V.
- 11.30-11.48 **ID 21 • Sexual selection and predation drive the repeated evolution of stridulation in arthropods**
Leonidas-Romanos Davranoglou; Taylor, G.K.; Mortimer, B.
- 11.50-12.08 **ID 56 • The functional morphology of heteropteran genitalia elucidated through X-ray microtomography**
Nikolai Tatarnic
- 12.10-12.28 **ID 42 • True bugs (Hemiptera: Heteroptera) in the entomological collection of the Zoology Research Group, University of Silesia in Katowice (DZUS), Poland**
Agnieszka Bugaj-Nawrocka; Taszakowski, A.; Gorczyca, J.; Chłond, D.; Wieczorek, K.
- 12.30-19.00 **Symposium on Gerromorpha in memory of Nils Møller Andersen**
- 12.30-12.48 **ID 14 • Life-history sorting and reference sequence bridging in marine Gerromorpha (Insecta: Heteroptera) with high-throughput sequencing**
Jia Jin Marc Chang; Ip, Y.C.A.; Cheng, L.; Kunning, I.; Mana, R.R.; Wainwright, B.J.; Huang, D.
- 12.50-13.08 **ID 17 • Bugs on the high seas - genes provide clues on *Halobates* (Heteroptera: Gerridae) distribution in the Pacific Ocean**
Lanna Cheng; Leo, S.S.T.; Wang, W.Y.L.; Huang, D.; Chang, J.J.M.; Norris, R.; Sperling, F.A.H.
- 13.15-14.45 **Lunch time**
- 14.50-16.08 **Oral Presentations.** Chairperson: Pablo Varela
- 14.50-15.08 **ID 29 • Phylogeny of Hydrometridae (Heteroptera: Gerromorpha), with establishment of two new subfamilies**
Felipe F.F. Moreira; Polhemus, D.A.; Damgaard, J.; Takiya, D.M.; Cordeiro, I.R.S.
- 15.10-15.28 **ID 44 • Two alternative mechanisms of thrust generation by a midleg stroke in semiaquatic bugs: comparison of leg kinematics in *Gerris latiabdominis* and *Rhagovelia distincta***
Sang Yun Bang; Kim, W.; Park, J.; Khare, V.; Lee, S.-I.; Jablonski, P.G.
- 15.30-15.48 **ID 45 • Size-dependent adaptations for locomotion in Gerridae**
Woojoo Kim; Amauger, J.; Lee, J.H.; Ha, J.; Pham, T.H.; Tran, A.D.; Park, J.; Bang, S.Y.; Lee, S.-I.; Jablonski, P.G.; Kim, H.-Y.
- 15.50-16.08 **ID 51 • An extensive phylogenomic analysis of the Gerridae (Insecta: Heteroptera: Gerromorpha) including the use of old museum specimens**
Michael J. Raupach; Balke, M.; Chang, J.J.M.; Cheng, L.; Deister, F.; Kment, P.; Moreira, F.F.F.; Reynoso-Velasco, D.; Villastrigo, A.; Zettel, H.; Damgaard, J.



16.10-16.28 **Coffee break**

16.30-17.48 **Oral Presentations.** Chairperson: Stephanie Castillo

- 16.30-16.48 **ID 50 • Diversification of the water cricket genus *Velia* (Heteroptera: Gerromorpha: Veliidae) in Eurasia**
Siyang Fu; Berchi, G.M.; Ye, Z.; Bu, W.J.
- 16.50-17.08 **ID 55 • Integrative taxonomy of the water strider *Potamometra* (Hemiptera: Gerridae)**
Chenguang Zheng; Zhu, X.; Bu, W.
- 17.10-17.28 **ID 57 • Transcriptome-based phylogeny of the semi-aquatic bugs (Hemiptera: Heteroptera: Gerromorpha)**
David Armisen; Viala, S.; da Rocha Silva Cordeiro, I.; Crumière, A.J.J.; Hendaoui, E.; Le Bouquin, A.; Duchemin, W.; Santos, E.; Toubiana, W.; Vargas-Lowman, A.; Burguez Floriano, C.F.; Polhemus, D.A.; Wang, Y.H.; Rowe, L.; Moreira, F.F.F.; Khila, A.
- 17.30-17.48 **ID 58 • Origin of evolutionary innovations: from cell and developmental biology to trait utility and diversification**
Abderrahman Khila
- 18.00-19.00 **Discussion time on Gerromorpha Symposium**
Conducted by Felipe Moreira and Lanna Cheng

Wednesday 6th July 2022

09.00-10.58 **Oral Presentations.** Chairperson: Alexander Knudson

- 09.00-09.18 **ID 37 • Systematic revision of the related genera *Neella* Reuter 1908 and *Neoneella* Costa Lima 1942 (Heteroptera: Miridae: Bryocorinae)**
Eugenia Minghetti; Montemayor, S.I.; Dellapé, P.M.
- 09.20-09.38 **ID 39 • Fussy eaters or shrewd operators? Predatory flexibility and selectivity of an ant-eating specialist**
Matthew Bulbert
- 09.40-09.58 **ID 40 • The *signoreti* species complex: final piece of the North American genus *Ambrysus* Stål puzzle (Nepomorpha: Naucoridae: Ambryinae)**
Daniel Reynoso-Velasco
- 10.00-10.18 **ID 28 • Synopsis of the New World Cylapinae (Hemiptera: Heteroptera: Miridae), with a morphology-based cladistic analysis of the tribe Fulviini**
Andrzej Wolski; Henry, T.J.; Taszakowski, A.; Masłowski, A.
- 10.20-10.38 **ID 46 • Phylogenetic revision of *Acanthocephala* Laporte 1833 (Hemiptera: Heteroptera: Coreidae)**
Leoneola Olivera; Melo, M.C.; Dellapé, P.M.
- 10.40-10.58 **ID 36 • Phylogenomic analysis suggests evolutionary convergence of male weapon traits in leaf-footed bugs and allies (Heteroptera: Coreoidea)**
Michael Forthman; Kimball, R.T.; Miller, C.W.

11.00-11.20 **Coffee break**

11.30-13.00 **Poster session**

13.15-14.35 **Lunch time** (Group Photo will be taken after lunch time)

14.40-16.08 **Oral Presentations.** Chairperson: Swapnil Boyane

- 14.40-14.55 **ID 70 • Using combined morphological and molecular datasets to phylogenetically place fossil Reduvidae**
Christiane Weirauch; Heiss, E.; Wedmann S.; Masonick P.
- 14.55-15.08 **ID 15 • Investigating the evolutionary history of the corsairs (Heteroptera: Reduviidae)**
Stephanie Castillo; Weirauch, C.
- 15.10-19.00 **Symposium on Pentatomoidea**
- 15.10-15.28 **ID 20 • A systematic account of Halyini (Heteroptera: Pentatomidae: Pentatominae) with description of two new species from India**
Salini Santhamma; Gracy R.G.; Roca-Cusachs M.; David K.J.
- 15.30-15.48 **ID 10 • 'they're all painted black'-Towards a new Europe-wide key for Cydnidae, with notes on taxonomy and ecology**
Alex Ramsay
- 15.50-16.08 **ID 52 • Ancient rapid radiations may cause the chaos of extant taxonomy at the genus level, a case study of Urostylididae (Heteroptera: Pentatomoidea)**
Yujie Duan; Bu, W.

16.10-16.28 **Coffee break**

16.30-17.58 **Oral Presentations.** Chairperson: Guilherme E.L. López

- 16.30-16.48 **ID 34 • Towards a revision of *Halyomorpha* (Hemiptera: Heteroptera: Pentatomidae): Poorly known relatives of the villain**
Petr Kment; Rider, D.A.; Santhamma, S.; Schwertner, C.F.; Cassis, G.
- 16.50-17.08 **ID 65 • Phylogeny of Phloeidae Amyot & Serville, 1843 (Hemiptera: Pentatomoidea) and its classification within the Pentatomoidea: a morphological approach**
Guilherme E.L. López; Schwertner, C.F.
- 17.10-17.28 **ID 18 • Integrative taxonomy provides fresh insights to systematics of the genus *Coridius* Illiger, (Hemiptera: Heteroptera: Dinidoridae) from India**
Swapnil Boyane; Sen, S.; Darma Rajan, P.; Thunga, P.; Joshi, N.; Ghat, H.
- 17.30-17.58 **ID 77 • Insights into the Pentatomidae Phylogeny: up-to-date revision and preliminary new updated phylogenetic analysis (Pentatomoidea: Pentatomidae)**
Marcos Roca-Cusachs; Genevicius, B.C.; Koehler, S.; Rider, D.A.; Grazia, J.; Cassis, G.; Cheng, M.; Schwertner, C.F.
- 18.00-19.00 **Discussion time on Pentatomoidea Symposium**
Conducted by Marcos Roca-Cusachs and Cristiano Schwertner



Thursday 7th July 2022

09.00-10.58 **Oral Presentations.** Chairperson: Renan Carrenho

- 09.00-09.18 **ID 47 • Invasion process of *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae) in Catalonia and notes on the situation in Spain**
Lucía-Adriana Escudero-Colomar; Roca Cusachs, M.; Tomàs, J.; Pujadas-Rovira, I.; Goula, M.
- 09.20-09.38 Cancelled presentation
- 09.40-09.58 **ID 49 • Untangling the web: Systematics and biogeography of thread-legged assassin bugs (Reduviidae: Emesinae)**
Samantha Standring
- 10.00-10.18 **ID 43 • A project of West European Fauna of Miridae for the 100th anniversary of the Faune de France**
Jean-Claude Streito; Matocq, A.; Chérot, F.; Pagola-Carte, S.; Strauss, G.; Wachmann, E.
- 10.20-10.38 **ID 71 • About the others – those not in your bed. Ecology of Cimicidae**
Steffen Roth; Klaus Reinhardt
- 10.40-10.58 **ID 60 • Morphometrics of *Phymata (P.) chilensis* Handlirsch (Reduviidae: Pymatinae): splitting species**
Pablo S. Varela; Melo, M.C.

11.00-11.20 Coffee break

11.30-13.08 **Oral Presentations.** Chairperson: Jia Jin Marc Chang

- 11.30-11.48 **ID 7 • Integrative approach to the identification and delimitation of the trans-Palearctic *Lygus* species (Heteroptera: Miridae: Mirinae)**
Anna A. Namyatova; Tyts, V.D.; Bolshakova, D.S.
- 11.50-12.08 **ID 8 • Phylogeny of the *Rhinocylapus* complex (Miridae: Cylapinae: Fulviini)**
Veronica Tyts; Namyatova A.; Konstantinov F.
- 12.10-12.28 **ID 26 • Molecular phylogeny of the Family Miridae (Heteroptera: Cimicomorpha) with discussion on divergence date and life history evolution**
Minsuk Oh; Lee, S.; Kim, S.
- 12.30-12.48 **ID 13 • Cleaning out the junk drawer: A phylogeny of the *Teleonemia* Costa generic complex (Hemiptera: Tingidae)**
Alexander Knudson; Simmons, R.; Bowsher, J.; Knodel, J.; Rider, D.
- 12.50-13.08 **ID 35 • Integrating time and space to shed light on the evolution of giant water bugs in the New World (Hemiptera: Belostomatidae: Belostomatini)**
Fabiano Stefanello; Ribeiro, J.R.I.

13.15-14.45 Lunch time

14.50-16.30 **Oral Presentations.** Chairperson: Eugenia Minghetti

- 14.50-15.08 **ID 9 • Quantitative analysis of citizen science data on Heteroptera: example of *Halyomorpha halys* distribution**
Viktor Hartung; Schneider, A.
- 15.10-15.28 **ID 62 • Conspectus of the Lethaeini (Lygaeoidea: Rhyparochromidae) of the Americas**
Renan Carrenho; Dellapé, P.M.; Schwertner, C.F.
- 15.30-15.48 **ID 63 • Hidden life in the interstices: On biology and taxonomy of Dipsocoridae occurring in Central Europe**
Šimon Zeman; Hartung, V.; Kment, P.
- 15.50-16.08 **ID 64 • Heteroptera diversity of the Fernando de Noronha Archipelago, Brazil**
Renan Carrenho; López, G.E.; Rafael, J.A.; Schwertner, C.F.
- 16.10-16.30 **ID 12 • Fieldwork and Phylogenetics: Advancing Miridae Biology and Classification**
Randall T. Schuh

16.30-16.50 **Coffee break**

17.00-18.30 **IHS closing**
Tom Henry

19.30-21.00 **Closing Dinner**
To be held in: Hotel Barceló-Raval (*Rambla del Raval, 17- 21*)

Friday 8th July 2022

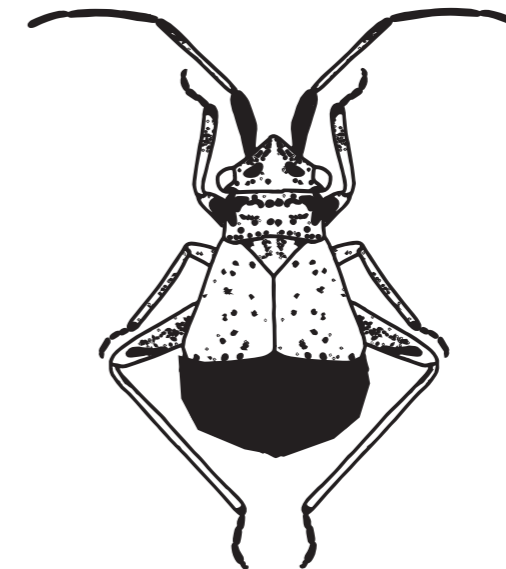
09.00 Picking up at Residència d'Investigadors (*Carrer Hospital, 64*)

10.00 Estimated time to reach sampling area

10.00-13.30 Sampling time

14.00-17.30 **Lunch.** Restaurant "Castellví" (close to the sampling area)

18.00 Picking up back to Residència d'Investigadors (*Carrer Hospital, 64*)



Tuesday, Wednesday and Thursday lunches will be held at *Restaurant Terraccita, C. Montalegre, 5*.
Tuesday, Wednesday and Thursday sessions will be held at *Residència d'Investigadors, C. Hospital, 64*.

In all works, the speaker is the first author.



Abstract ID: 61 • Abstract type: Oral

Tuesday 5th July 2022, 11.10-11.28 h.

VIBROACOUSTIC SIGNALS OF PELORIDIIDAE (HEMIPTERA: COLEORRHYNCHA) – STRUCTURES INVOLVED IN THEIR PRODUCTION AND IMPLICATIONS FOR THE PHYLOGENETICS OF HEMIPTERA

Leonidas-Romanos Davranoglou¹; Viktor Hartung²

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² Senckenberg Research Institute and Museum Frankfurt, Germany, viktor.hartung@senckenberg.de

Communication via substrate vibration is widespread among Hemiptera, having been found in all major suborders. The principal ways of producing vibrational signals are through abdominal tremulation (Heteroptera), tymbals and tymbal-like mechanisms (Cicadomorpha), and snapping organs (Fulgoroidea). It remains to be found whether these structures represent independent developments, or diverged from a shared ancestral vibrational organ. In this context, information on the vibroacoustic structures of Peloridiidae, the only living representatives of Coleorrhyncha, is particularly valuable. We documented the morphology of the vibration-producing organs in several species of Peloridiidae and their fossil relatives for the first time, using state-of-the-art synchrotron microtomography and confocal microscopy. We find that the vibrational organ of Coleorrhyncha is most similar to the heteropteran tergal plate, although we cannot determine whether this represents an ancestral condition, or it is the result of secondary simplification. To test the above hypotheses, we coded the morphological features of all hemipteran vibroacoustic organs as systematic characters, and we analysed them phylogenetically with TNT. When combined with a previously used dataset of 93 characters, Peloridiidae were recovered as the sister group to Auchenorrhyncha. Surprisingly, when vibroacoustic characters were analysed alone, they favoured the sister-group relationship of Peloridiidae to Heteroptera. These contradicting results suggest that the evolution of hemipteran vibroacoustic organs is characterised by high rates of homoplasy, and further character complexes need to be studied to reach definitive conclusions, in addition to much needed developmental and phylogenomic data.

Tuesday 5th July 2022, 11.30-11.48 h.

Abstract ID: 21 • Abstract type: Oral

SEXUAL SELECTION AND PREDATION DRIVE THE REPEATED EVOLUTION OF STRIDULATION IN ARTHROPODS

Leonidas-Romanos Davranoglou¹; Graham K. Taylor²; Beth Mortimer³

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Acoustic and substrate-borne modes of vibration are among the most widely used forms of signalling in animals. Arthropods display a staggering diversity of vibroacoustic organs and are fundamental to our understanding of the evolution of animal signalling more broadly. The primary mechanism that arthropods use to generate vibroacoustic signals is stridulation, which involves the friction of opposing body parts. Although stridulation is common, its behavioural context and evolutionary drivers are often hard to pinpoint, owing to limited synthesis of empirical observations on species bearing such mechanisms. This is a major knowledge gap, as stridulatory mechanisms can be phylogenetically informative, and are central to our understanding of sensory evolution in arthropods. This is exacerbated by the diversity of the mechanisms involved and the sparsity of their description in the literature, which renders their documentation a challenging task. Here, we conducted the most comprehensive review to date on the systematic distribution and behavioural context of stridulation, using the megadiverse heteropteran insects, as well as four arthropod outgroups (arachnids, myriapods, hemimetabolan insects, and certain other pancrustaceans) as models. We find that stridulatory vibroacoustic signalling has evolved independently at least 84 times and is present in roughly 20% of Heteroptera, representing a remarkable case of convergent evolution. By studying the behavioural context of stridulation across Heteroptera and 189 outgroup lineages, we find that predation pressure and sexual selection are the main behaviours associated with stridulation across arthropods, adding further evidence for their crucial role as drivers of large-scale signalling and morphological innovation in animals. Remarkably, the absence of tympanal ears in the majority of Heteroptera indicates that they typically cannot detect the acoustic component of their stridulatory signals, which demonstrates that the adoption of new signalling modalities is not always correlated with their sensory perception, especially when directed towards interspecific receivers. Furthermore, by mapping their morphology and systematic distribution, we show that stridulatory organs tend to evolve in specific body parts, as they likely originate from cleaning motions and pre-copulatory displays that are shared among most arthropods. Our findings synthesise our understanding of stridulation and stridulatory organs across major arthropod groups, thereby creating the necessary framework for future studies to explore their systematic and behavioural significance, their potential role in sensory evolution and innovation, and the biomechanics involved in this mode of signalling.



Abstract ID: 56 • Abstract type: Oral

Tuesday 5th July 2022, 11.50-12.08 h.

THE FUNCTIONAL MORPHOLOGY OF HETEROPTERAN GENITALIA ELUCIDATED THROUGH X-RAY MICRO TOMOGRAPHY

Nikolai Tatarnic
Western Australian Museum & University of Western Australia, nikolai.tatarnic@museum.wa.gov.au

In this talk I will present examples from ongoing research into heteropteran mating and reproductive morphology using X-ray microtomography (microCT). I will use examples from various taxa to show how this technique is helping extend our knowledge of mating behaviour and genital function, through virtual dissection of reproductive organs and males and females frozen in copula.

Keywords

microCT • genital evolution • sexual selection • mating

Tuesday 5th July 2022, 12.10-12.28 h.

Abstract ID: 42 • Abstract type: Oral

TRUE BUGS (HEMIPTERA: HETEROPTERA) IN THE ENTOMOLOGICAL COLLECTION OF THE ZOOLOGY RESEARCH GROUP, UNIVERSITY OF SILESIA IN KATOWICE (DZUS), POLAND

Agnieszka Bugaj-Nawrocka¹; Artur Taszakowski²; Jacek Gorczyca³; Dominik Chłond⁴; Karina Wieczorek⁵
^{1, 2, 3, 4, 5} Faculty of Natural Sciences, Institute of Biology, Biotechnology and Environmental Protection, University of Silesia in Katowice, Poland

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Information about scientific collections is increasingly available thanks to digitisation funding programs. The digitisation of such resources allows us to verify their value and share these records with other scientists – and they are usually rich in taxa and unique in the world. Moreover, such information significantly enriches local and global knowledge about biodiversity. In the years 2018-2021 the Zoology Research Group, University of Silesia in Katowice, thanks to funds obtained from the European Union (within the Regional Operational Programme of the Voivodeship of Silesia 2014-2020), carried out a project HEMIPTERON Digital Entomological Database for all Hemiptera collections to secure this valuable material in digital form. The digitisation allowed presenting a substantial collection of true bugs (Hemiptera: Heteroptera). The collection counts over 39000 specimens, representing 792 taxa (771 identified to species level), 318 genera and 40 families. DZUS collection preserves 193 type specimens of 84 species (with 23 holotypes). The geographical analysis of the Heteroptera collected shows mainly Eurasian areas, but there is also material from the Americas, Africa, and Australia and Oceania. The database is available at <http://www.hemipteron.us.edu.pl>.

Finance

The material was digitised in the framework of project no. ND-RPSL.02.01.00-24-01DD/17: Digital Database of Entomological Specimens HEMIPTERON (CEBD HEMIPTERON), co-financing from the EU, Priority axis: II. Digital Silesia, Measure: 2.1. Support for the development of digital public services.

Keywords

digitisation • biodiversity • database • collection



Abstract ID: 14 • Abstract type: Oral

Tuesday 5th July 2022, 12.30-12.48 h.

LIFE-HISTORY SORTING AND REFERENCE SEQUENCE BRIDGING IN MARINE GERROMORPHA (INSECTA: HETEROPTERA) WITH HIGH-THROUGHPUT SEQUENCING

Jia Jin Marc Chang¹; Ip, Y.C.A.²; Cheng, L.³; Kunning, I.⁴; Mana, R.R.⁵; Wainwright, B.J.⁶; Huang, D.⁷

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One of the challenges in insect taxonomy is accurate association of larval specimens with adult forms, since immatures can be morphologically distinct from adults. Furthermore, most species descriptions are based on mature adult specimens; some are even based solely on adult males. Biodiversity or survey information collected from females or larvae risks being neglected, especially if no co-occurring males were collected at the same sampling locality. Fortunately, advancements in sequencing technology have greatly increased our DNA barcoding capabilities such that it is now possible for non-experts to sort specimen-rich bulk samples with DNA barcodes rapidly and cost-effectively. We demonstrated this via nanopore barcoding of 757 marine insect specimens, of which 81% were nymphs and half of the localities sampled did not have co-occurring male adults. We successfully associated 738 specimens to nine species of Gerromorpha: *Halobates calyptus* Herring, 1961; *Halobates hayanus* White, 1883; *Halobates maculatus* Schadow, 1922; *Halobates peronis* Herring, 1961; *Halobates proavus* White, 1883; *Halovelia novoguineensis* Andersen, 1989; *Haloveloides papuensis* (Esaki, 1926); *Thetibates serena* (Lansbury, 1992), and an unidentified *Halobates* sp. This improved ability to incorporate information from all life-history stages led to greater precision of species distributional ranges—knowledge that would be crucial for an improved understanding of marine insects. We also highlight two distinct, non-overlapping Gerromorpha COI sequence databases on GenBank that resulted from the use of two different primer sets to amplify different regions of the COI gene. This would inevitably hinder species identification with DNA sequence data. We thus bridged these sequence databases by analysing full-length COI sequences obtained via genome skimming. We hope our efforts will inspire future studies to incorporate DNA-based methods for life-history sorting and enhancing existing genetic resources in insects.

Finance

This research was supported by the National Research Foundation, Prime Minister's Office, Singapore, under the Marine Science R&D Programme (P03, P38 and P47) to D.H., and Ocean Park Conservation Foundation, Hong Kong, to B.J.W.

Keywords

adult-nymph association • biodiversity assessment • *Halobates* • nanopore barcoding • species diversity

Tuesday 5th July 2022, 12.50-13.08 h.

Abstract ID: 17 • Abstract type: Oral

BUGS ON THE HIGH SEAS - GENES PROVIDE CLUES ON *HALOBATES* (HETEROPTERA: GERRIDAE) DISTRIBUTION IN THE PACIFIC OCEAN

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Five species of *Halobates* ocean skaters (*H. germanus*, *H. micans*, *H. sericeus*, *H. sobrinus* and *H. splendens*) are the only insects to live in the high seas. All 5 species occur in the Pacific, and *H. micans* is cosmopolitan and widely distributed between latitudes 40°N and 40°S in the Atlantic. It only occurs within 15°S in the Indian Ocean and is restricted between roughly 15°N and 15°S in the central Pacific where areas beyond its northern and southern boundaries are occupied by *H. sericeus*. *Halobates sobrinus* and *H. splendens* are both confined to the eastern Pacific while *H. germanus* occurs in more coastal waters of the Pacific and Indian Oceans. With no physical barriers on the ocean surface to prevent their movements, it was surprising that each species exhibited a well-defined geographical range. Two studies offered clues to why such patterns were maintained. Phylogenetic and population genetic analyses of *Halobates sericeus* collected from the Pacific Ocean revealed clustering of haplotypes into northern and southern clades that are strongly structured geographically with very limited gene flow between them. The continued presence of two genetically separate populations of this species for tens of thousands of years implies that an unexpected degree of stability of ocean surface physical conditions prevented substantial gene exchange throughout this period. The two *H. sericeus* populations, divided by the range of *H. micans*, now show substantial genetic divergence on the way to vicariant speciation. Gene sequencing and analyses of nearly 400 specimens of *Halobates micans*, *H. sobrinus* and *H. splendens* collected off the coast of the Central and South Pacific Ocean revealed distinct genetic patterns. They have adapted to different current systems as they evolved into their present-day distributions which appear to coincide with past climatic events. *Halobates splendens* now occurs in rich, productive waters of the cold tongue that originated off the coast of South America as the present Peru current. This physical feature came into existence about a million years ago, at the time of increase in genetic diversity and population size of this species. *Halobates sobrinus* and *H. micans* were found to have diversified in the warm, relatively unproductive waters of Central America. Their populations expanded when El Niño effects were especially strong and drove warm currents into the eastern Pacific Ocean where they occurred about 100,000 years ago, coinciding with the time they developed their modern genetic patterns and population sizes. How *Halobates* evolved and became adapted to conquer the high seas remains unknown.

Keywords

ocean insect • *Halobates* • distribution • vicariant speciation • paleo-oceanography



Abstract ID: 29 • Abstract type: Oral

Tuesday 5th July 2022, 14.50-15.08 h.

PHYLOGENY OF HYDROMETRIDAE (HETEROPTERA: GERROMORPHA), WITH ESTABLISHMENT OF TWO NEW SUBFAMILIES

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Representatives of the infraorder Gerromorpha, known as semiaquatic bugs, occupy a wide range of environments, such as humid terrestrial habitats, phytotelmata, habitats marginal to freshwater bodies or their surface, coastal marine habitats, and even the open ocean. Among the eight recognized families of Gerromorpha, Hydrometridae currently includes three subfamilies. Heterocleptinae includes two genera, *Veliometra* Andersen, 1977, with a single species from the Neotropical Region, and *Heterocleptes* Villiers, 1948, with three species from the Afrotropical Region and one species from the Oriental Region. Limnobatodinae includes a single genus, *Limnibatodes* Hussey, 1925, with only one species from the Neotropical Region. Hydrometrinae includes *Bacillometra* Esaki 1927 (one species), *Bacillometroides* Polhemus & Polhemus, 2010 (three species), *Cephalometra* Polhemus & Ferreira, 2018 (one species), *Spelaeometra* Polhemus & Ferreira, 2018 (one species), all from the Neotropical Region; *Chaetometra* Hungerford, 1950 (one species) and *Dolichocephalometra* Hungerford, 1939, from the Marquesas Islands; and *Hydrometra* Latreille, 1797, with about 130 species from all biogeographical regions. Hydrometridae also has a relatively rich fossil record, with 11 genera that are all assigned to extant subfamilies, the oldest of which is dated from the Lower Cretaceous. For the present study, a phylogenetic analysis of Hydrometridae was performed based on 110 morphological characters (68 binary and 42 multistate), all of which are described and coded, and several of which are illustrated in order to facilitate their interpretations. Outgroup taxa represented four families of Gerromorpha and ingroup taxa included eight of the ten recent genera of the family, in addition to two undescribed monotypic genera from Tahiti and Raiatea islands, in French Polynesia. Phylogenetic analyses were performed through heuristic searches with equal weights using TNT 1.5 no taxon limit and by Bayesian Inference using MrBayes 3.2.2. Monophyly of Hydrometridae was not recovered, because *Veliometra* resulted as sister to *Macrovelia hornii* Uhler, 1872 (Macroveliidae), and Hermatobatidae was recovered as sister to the remaining Hydrometridae. Hydrometrinae was not recovered as monophyletic due to the position of *Bacillometra* and *Hydrometra* as sister to Limnobatodinae, being closer to it than to other Hydrometrinae genera. Two new subfamilies are erected to include genera previously allocated in Hydrometrinae; one for *Cephalometra* and *Spelaeometra*, and the other for *Chaetometra*, *Dolichocephalometra*, and the two undescribed Pacific genera. Considering the recent genera, Hydrometrinae now includes only *Bacillometra*, *Hydrometra*, and *Bacillometroides*. Representatives of *Heterocleptes* need to be included in the analyses in order to further test the monophyly of Hydrometridae, and fossil taxa attributed to Hydrometridae need to be thoroughly evaluated in such a phylogenetic context in order to investigate which subfamilies they should be assigned to.

Finance

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Keywords

aquatic insects • classification • semiaquatic bugs • taxonomy

Tuesday 5th July 2022, 15.10-15.28 h.

Abstract ID: 44 • Abstract type: Oral

TWO ALTERNATIVE MECHANISMS OF THRUST GENERATION BY A MIDLEG STROKE IN SEMIAQUATIC BUGS: COMPARISON OF LEG KINEMATICS IN *GERRIS LATIABDOMINIS* AND *RHAGOVELIA DISTINCTA*

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Skating on the water surface is a typical form of locomotion observed in semiaquatic bugs – Gerromorpha – such as water-striders (Gerridae) and water-crickets (Veliidae). While all gerromorphans move on the water surface, the two main groups differ in the mechanism that provides thrust for skating. Gerridae exploits “surface tension” by using the asymmetrically shaped water surface dimples under their middle legs as ‘oars’, pushing the insect forward and creating water surface waves/water vortices moving backward (through hydrodynamic drag). Contrastingly, the genus *Rhagovelia* of Veliidae exploits only the “drag” by inserting their specialized midleg pretarsal fans into the water body and using them as ‘oars’ without creating any significant water surface dimples. Here, we present slow-motion films of *Gerris latiabdominis* to demonstrate how midlegs deform the water surface during a stroke, operating functionally as a ‘virtual oar’. We further present slow-motion films of *Rhagovelia distincta*’s legs during a midleg stroke, providing evidence that the specialized fans penetrate the water surface into the water body, and that midleg dimples are essentially absent during a backward stroke. We also present the midleg morphology responsible for thrust and compare the kinematics of a typical complete midleg’s stroke between *G. latiabdominis* and *R. distincta*. The comparison demonstrates that while *G. latiabdominis* have a single degree of freedom for midleg thrust movement at the coxae, *R. distincta* has more control over their successive joints resulting in distinct angular speeds of different leg sections. We further present a comparison of dynamics of the strides from the analysis of body speed profiles during a stroke, successively discussing the ‘efficiency’ of the two alternative solutions for producing thrust for striding locomotion on the water surface. Based on the results, we suggest that *R. distincta* experiences larger drag resistance (eventually thrust) per unit wetted leg length from its deployment of specialized swimming fans inside of the water body, while *G. latiabdominis* produces smaller thrust per wetted leg length from its ‘virtual oar’ that does not penetrate the water surface. However, because *G. latiabdominis* exploit their relatively longer wetted lengths at a faster speed, covering a larger surface during a stroke, the two species (employing two alternative mechanisms) result in similar final body speed of sliding.

Finance

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3. BK 21 program to the School of Biological Sciences

Keywords

Gerromorpha • *Gerris* • *Rhagovelia* • ecomorphology • kinematics • swimming fan



Abstract ID: 45 • Abstract type: Oral

Tuesday 5th July 2022, 15.30-15.48 h.

SIZE-DEPENDENT ADAPTATIONS FOR LOCOMOTION IN GERRIDAE

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The semi-aquatic insects are good study organisms because their various sizes and basic hydrodynamic mechanisms of locomotion on the water surface are well known. The physics of the water surface can be used to predict the effect of body size on locomotive behavior and morphology used in locomotion in Gerridae. However, existing studies about the detailed mechanism of the locomotion in Gerridae are mostly focused on just several species of mid-sized water striders from two genera (*Gerris*, *Aquarius*) common in Palearctic and Nearctic regions, representing a relatively narrow range of body mass between 10 and 70 mg. It was determined that these small and mid-sized water striders control their midlegs' angular velocity when they jump on the water surface to maximize escape velocity and minimize the delay while preventing the water surface-breaking. Moreover, numerous studies described symmetrical rowing on the surface by these few species of water striders. However, literature and initial observations on the world's largest water strider (with a body mass of up to about 500 mg), *Gigantometra gigas*, suggested that this species uses different modes of jumping and striding. We observed that *G. gigas* individuals break the water surface in their jump, and literature suggested that they stride asymmetrically by stretching one midleg to the front and by rowing with the other midleg and its contralateral hindleg. To determine the mechanisms of locomotion in the large-bodied species, we filmed high-speed movies of jumping and striding of *Gerris latiabdominis*, (12-32 mg); *Aquarius paludum* (35-72 mg); *Ptilomera tigrina*, (83-144 mg); and *G. gigas*, (217-511 mg). We digitized the videos and analyzed the kinematics of the locomotion of these species. We created mathematical models of the hydrodynamics of jumping and sliding in Gerridae on the water surface, and we confirmed their validity by using empirical kinematic data. We then simulated the different modes of jumping (surface un-breaking and breaking jumps) and sliding (symmetric and asymmetric sliding) across the range of leg morphologies and body sizes represented by our empirical data (12-511mg). The jumping model simulated the velocity, height, and delay of jumping; the sliding model simulated the floating possibility, resistance, and deceleration of sliding. The models predict that within the range of body size of 70-80 mg ("threshold body size") the water striders should switch from the "typical" modes of locomotion (surface-tension jumping and symmetrical rowing) to the new modes that are associated with adaptations in legs' morphology. Additionally, we discovered that *A. paludum*, with body size near the "threshold body size", can use both symmetric and asymmetric sliding, suggesting adaptive behavioral plasticity in Gerridae near the theoretical "threshold body size". The model predictions can be tested in future comparative studies.

Finance

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Keywords

Gerridae • locomotive behavior • water surface interaction • allometry • fluid dynamics • morphology

Tuesday 5th July 2022, 15.50-16.08 h.

Abstract ID: 51 • Abstract type: Oral

AN EXTENSIVE PHYLOGENOMIC ANALYSIS OF THE GERRIDAE (INSECTA: HETEROPTERA: GERROMORPHA) INCLUDING THE USE OF OLD MUSEUM SPECIMENS

Michael J. Raupach¹; Balke, M.²; Chang, J.J.M.³; Cheng, L.⁴; Deister, F.⁵; Kment, P.⁶; Moreira, F.F.F.⁷; Reynoso-Velasco, D.⁸; Villastrigo, A.⁹; Zettel, H.¹⁰; Damgaard, J.¹¹

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With more than 750 described species, the Gerridae represent one of the largest taxa within the Gerromorpha. Within this family about 70 genera can be found, which are divided into eight subfamilies. Species among others include the naming and well-known genus *Gerris*, the largest known water strider species *Gigantometra gigas*, and the genus *Halobates*, of which five species are the only insects to inhabit the open oceans. Despite their significance within the Gerromorpha, only a few studies analyze the phylogenetic relationships within the Gerridae. Available molecular studies rely on small molecular data sets that are based on only a few short gene fragments or have incomplete taxon selections that lack many important species. Our project aims at a first comprehensive phylogenomic analysis of the Gerridae, considering all relevant and important taxa. The genome skimming approach used allows not only the analysis of freshly collected animals but also the processing of decades-old collection material, enabling the analysis of complete mitochondrial genomes as well as numerous other markers. As part of the presentation, first results will be shown and discussed in the overall context.

Finance

This study is supported by the SNSB-Innovative scheme, funded by the Bayerisches Staatsministerium für Wissenschaft und Kunst to Michael J. Raupach

Keywords

high-throughput sequencing • genome skimming • water striders • mitochondrial genomes • nuclear DNA • museum collections



Abstract ID: 50 • Abstract type: Oral

Tuesday 5th July 2022, 16.30-16.48 h.

DIVERSIFICATION OF THE WATER CRICKET GENUS *VELIA* (HETEROPTERA: GERROMORPHA: VELIIDAE) IN EURASIA

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At present, nearly 1/3 of global biodiversity hotspots are distributed in the Eurasian continent region once covered by the Tethys Sea; these areas are known as the Tethyan transition zone. The Tethyan sea-land changes have affected the origin, dispersal, diversification and extinction of animals in the Tethyan transition zone by changing ecological environment and regional topographies. This study intends to select a semi-aquatic insect group of genus *Velia* Latreille that is widely distributed in the Tethyan transition zone of Eurasia as the research object, including three subgenera and covering more than 70% of the described species. We reconstructed interspecific phylogenetic relationships and chronogram within this genus based on the ultra-conserved element nuclear genome and complete mitochondrial genome data. Our results strongly support that the subgenus *Velia* (*s.s.*), distributed in the western Mediterranean, is more closely related to the *Velia* (*Cesavelia*), distributed in southwestern East Asia. The estimated divergence time (around 21.9 Mya) among the subgenera was largely congruent with the time of aridification of Central Asia in the Miocene. Within the subgenus *Cesavelia*, the taxa distributed in southwest China underwent a rapidly adaptive radiation within 3.5 Mya, which coincided with the uplift of the Hengduan Mountains. This study emphasized that the aridification and mountain uplifting events due to the retreat of the Tethys Sea is an essential driving force for the diversification of this Eurasian water cricket lineage.

Keywords

evolutionary history • Eurasian • *Velia*

Tuesday 5th July 2022, 16.50-17.08 h.

Abstract ID: 55 • Abstract type: Oral

INTEGRATIVE TAXONOMY OF THE WATER STRIDER *POTAMOMETRA* (HEMIPTERA: GERRIDAE)

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The genus *Potamometra* Bianchi, 1896 represents big rheophilic semi-aquatic bugs that typically inhabit middle-altitude mountainous streams. Here, we integrated molecular and morphological data for delimiting species boundaries and understanding the evolutionary history of the genus *Potamometra*. Twenty-seven complete mitochondrial genomes of *Potamometra* were sequenced, with samples representing most of the known geographically distributed locations around the Sichuan Basin. The results of different species delimitation methods (ABGD, bPTP, GMYC and BPP) based on the monolocus or multilocus data strongly supported the existence of two cryptic new species (*Potamometra anderseni* Zheng, Ye & Bu, sp. nov. and *Potamometra zhengi* Zheng, Ye & Bu, sp. nov.) although more entities were found in the tree-based delimitation methods. The two new species were successfully validated using morphological characters within a detailed taxonomic framework. Phylogenetic analyses supported the reciprocal monophyly of the seven highly node-supported clades, which were matched with the five known species and two new taxa. A novel gene arrangement pattern of two trnF (trnF1 and trnF2) genes separated by an intergenic spacer (IGS) was found in all the species except the sister group of *Potamometra berezowskii* Bianchi, 1896 and *Potamometra linnavuorii* Chen, Nieser & Bu, 2016. This gene rearrangement event could be explained by the tandem duplication and random loss (TDRL) model. Our study emphasized that the combination of molecular sequence data, morphological characters and mitochondrial structural information could improve the accuracy of species delimitation.

Keywords

Potamometra • integrative taxonomy • gene rearrangement



Abstract ID: 57 • Abstract type: Oral

Tuesday 5th July 2022, 17.10-17.28 h.

TRANSCRIPTOME-BASED PHYLOGENY OF THE SEMI-AQUATIC BUGS (HEMIPTERA: HETEROPTERA: GERROMORPHA)

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Key innovations enable access to new adaptive zones and are often linked to increased species diversification. As such, they have attracted much attention, yet their concrete consequences on the subsequent evolutionary trajectory and diversification of the bearing lineages remain unclear. The monophyletic group of water striders and relatives (Hemiptera: Heteroptera: Gerronormorpha) represents a group of insects that transitioned to live on the water-air interface and diversified to occupy ponds, puddles, streams, mangroves and even oceans. This lineage offers an excellent model to study the patterns and processes underlying species diversification following the conquest of new adaptive zones. However, such studies require a reliable and comprehensive phylogeny of the infraorder. Based on whole transcriptomic datasets of 97 species and fossil records, we reconstructed a new phylogeny of the Gerronormorpha that resolved inconsistencies and uncovered strong support for previously unknown relationships between some important taxa. Our work reconstructs and dates their phylogeny showing that the initial event of water surface invasion quickly enabled subsequent transitions to new adaptive zones and further diversification of the group multiple times. We also used this phylogeny to reconstruct the ancestral state of a set of adaptations associated with water surface invasion (fluid locomotion, dispersal and transition to saline waters) and sexual dimorphism.

Keywords

adaptation • adaptive zone • key innovation • phylogeny • Gerronormorpha

Tuesday 5th July 2022, 17.30-17.48 h.

Abstract ID: 58 • Abstract type: Oral

ORIGIN OF EVOLUTIONARY INNOVATIONS: FROM CELL AND DEVELOPMENTAL BIOLOGY TO TRAIT UTILITY AND DIVERSIFICATION

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Evolutionary innovations represent lineage-restricted traits that perform new functions allowing access to unexploited ecological opportunities. These traits are widespread, yet we know little about the cellular, molecular and developmental genetic mechanisms underlying their development, or the ecological forces driving their evolution. We study the origin of evolutionary innovations using the propelling fan of *Rhagovelia* as a study system. I will address some aspects of the molecular, cellular and developmental origin of the propelling fan. I will also present results showing how this trait contributes to the functioning of the organism as a whole in challenging environments, and how it may have been associated with a burst of diversification.

Keywords

evolutionary innovation • Gerronormorpha • *Rhagovelia* • evolution • adaptation



Abstract ID: 37 • Abstract type: Oral

Wednesday 6th July 2022, 09.00-09.18 h.

SYSTEMATIC REVISION OF THE RELATED GENERA *NEELLA* REUTER 1908 AND *NEONEELLA* COSTA LIMA 1942 (HETEROPTERA: MIRIDAE: BRYOCORINAE)

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The Miridae, commonly called plant bugs, are the most species-rich family of Heteroptera and one of the 20 most diverse families of insects, with more than 11.300 described species. In the Neotropics there are approximately 560 genera and 3400 species. The Bryocorinae is the fourth-largest subfamily among Miridae, and it is a highly diverse group in terms of feeding habits and morphology, including genitalic structures. A recent phylogenetic analysis recovered its monophyly and recognized five tribes. The Eccritotarsini is the largest tribe, and it is particularly diverse in the Neotropical Region. Although eccritotarsines have been proposed as the sister group of bryocorines, its internal relationships remain unknown. The neotropical genera *Neella* Reuter and *Neoneella* Costa Lima have been relatively little studied, and their species are only known from their original descriptions. According to some authors, they are closely related and constitute the *Neella-Neoneella* complex, in which are also grouped *Adneella* Carvalho, *Paraneella* Carvalho and *Proneella* Carvalho. As part of EM PhD thesis, a systematic revision of this group has been done and a morphological phylogenetic analysis was performed, including 57 terminal taxa -12 of them are new species - combining continuous and discrete characters, with an important number of morphological characters - mainly of male genitalia - that had not been studied before. As a result, the monophyly of the *Neella-Neoneella* complex was rejected, the monophyly of *Neella* was corroborated including 13 known species and four new species, *Neoneella* resulted in a monophyletic group constituted by six species, the monophyly of *Adneella* was also recovered, composed of 14 species - five of them transferred from *Neella* and one new species, the two species of *Proneella* formed a clade, and the monotypic *Paraneella* was recovered as part of a group composed of three eccritotarsine outgroup genera. Also, six new genera were delimited, integrated by species transferred from *Neella* or new species. The 12 new species were described, and the 38 known species were redescribed; all genera and species were diagnosed and keyed. In addition to the phylogenetic analysis, and as there is an absolute lack of knowledge about the biogeographic history of the studied genera, analyses for the identification of areas with highest species richness, areas of endemism and endemic species, and climatically stable areas that may serve or may have served as refugia when regional or global climate conditions change/changed were performed. The identification of refugia was based on an ecological niche modelling approach.

Wednesday 6th July 2022, 09.20-09.38 h.

Abstract ID: 39 • Abstract type: Oral

FUSSY EATERS OR SHREWD OPERATORS? PREDATORY FLEXIBILITY AND SELECTIVITY OF AN ANT-EATING SPECIALIST

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The feather-legged assassin bugs (Reduviidae: Holoptilinae) are ant-eating specialists that are known for their unique prey-luring strategy. They are one of the oldest lineages of assassin bugs and thus are found primarily on old world continents including Africa, Asia and Australia. As their common name suggests the feather-legs are characterised by clusters of feather-like hairs on their hindlegs. The nymphs of the Australian endemic *Ptilocnemus lemur* have been shown to use these 'fluffy' legs to lure ant prey. The current description of the elaborate nymph-ant interactions though, is only part of the story. Here I will illustrate that *P. lemur* adjust their strategy relative to the ant fauna. A possibly more surprising observation is the active ceasing of their predatory sequence, once touched, by what we now deem as antagonistic ant species. The behavioural response is seemingly innate and so strong that it has influence on the distribution of individuals across any given site. This extends to even when the trees have other suitable prey and/or have the ideal bark habitat. The ramifications of these observations are all speculative at this stage, but a bit of speculation never hurt anyone.



Abstract ID: 40 • Abstract type: Oral

Wednesday 6th July 2022, 09.40-09.58 h.

THE *SIGNORETI* SPECIES COMPLEX: FINAL PIECE OF THE NORTH AMERICAN GENUS *AMBRYBUS* STÅL PUZZLE (NEPOMORPHA: NAUCORIDAE: AMBRYSINAE)

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The saucer bug genus *Ambrysus* Stål, the second most species-rich in Naucoridae, is divided into four subgenera, of which only the nominal *Ambrysus* is classified into species complexes. Currently, four complexes have been revised and circumscribed. In the past, Ira La Rivers, the most prolific entomologist working on the group, proposed few characteristics for species inclusion in the *signoreti* complex. Unfortunately, these features have proven to fail in correctly circumscribing the group, as species clearly belonging to other complexes can be considered members of the *signoreti* group based on La Rivers' superficial attributes. For this study, the *A. signoreti* complex, the last complex in the subgenus, was revised and includes 21 species. Besides molecular studies that support the *signoreti* grouping, it has been found that the main feature uniting species in this group is related to the male genitalia; specifically, the presence, in most species, of the endosomal sclerites knob-shaped and covered with conspicuous denticles. A tendency to the reduction or absence of this diagnostic feature of the phallosoma is noticeable in some derived members of the group. Species in this complex are more closely related to the *A. hybridus* complex, a group of nine species present in the Mexican Transition Zone and the area of the North American Cordillera in the western United States. The species in the *A. signoreti* complex are distributed from the southwestern United States south to Costa Rica, with the majority of species present in Mexico, some of which are known to occur exclusively in this country. This study brings an end to the recent efforts to clarify the taxonomy of the genus *Ambrysus*. At the present time, it is fair to say that the taxonomy of this diverse group is well understood and complete. The genus includes 65 species classified into four subgenera: *Ambrysus* (57 spp.), *Dissimilis* (1 sp.), *Grandis* (1 sp.), and *Syncollus* (6 spp.). Furthermore, the nominal subgenus includes 57 species in five complexes: *guttatipennis* (12 spp.), *hybridus* (9 spp.), *pudicus* (11 spp.), *pulchellus* (4 spp.), and *signoreti* (21 spp.). Also, thanks to extensive field work and examination of specimens in multiple entomological collections, the distribution of these species is fairly well understood. Species in the genus *Ambrysus* could have arisen somewhere in Mesoamerica, an area also occupied by species of the genera *Cataractocoris* and *Maculambrysus* and with whom *Ambrysus* shares an immediate common ancestor. The phylogeography of the group is an interesting topic that needs to be investigated to correctly understand the origin and the potential forces leading to the diversification of this North American group of aquatic insects.

Keywords

saucer bugs • taxonomy • distribution • phylogeny

Wednesday 6th July 2022, 10.00-10.18 h.

Abstract ID: 28 • Abstract type: Oral

SYNOPSIS OF THE NEW WORLD CYLAPINAE (HEMIPTERA: HETEROPTERA: MIRIDAE), WITH A MORPHOLOGY-BASED CLADISTIC ANALYSIS OF THE TRIBE FULVIINI

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The Cylapinae are a small (nearly 100 genera with 450 species) but highly morphologically heterogeneous subfamily belonging to the largest heteropteran family Miridae (>11,000 described species). They are distributed primarily in the tropical and subtropical regions with only a few members inhabiting temperate zones. Most cylapines live under the loose bark of dead or dying trees and rotting logs, and on fungi. They are rarely found in collections, with many species known from only the holotype or a handful of specimens. Consequently, the Cylapinae remain one of the most poorly studied mirid groups in terms of their distribution, biology, taxonomy, and morphology as well as the phylogenetic relationships. Our study provides a synoptic review of all 31 New World Cylapinae genera. It includes an illustrated key to genera, generic diagnoses, redescription of selected genera, description of a new genus, color habitus photographs and male and female genitalia, and distributional maps. We also present a first cladistic analysis of the most speciose and morphologically diverse tribe Fulviini as a contribution to the understanding of the ingroup relationship within the tribe and its relationships with other cylapine tribes. The analyses include 51 ingroup and 20 outgroup taxa. Both equal and implied weighting parsimony analyses were conducted using TNT v1.5. These analyses were based solely on morphological characters because sufficient numbers of specimens suitable for molecular studies were not available for most taxa. Over 100 characters obtained from the dorsum, head, pronotum, scutellum, thoracic pleura, hemelytron, legs, and male and female genitalia were analysed. Based on the obtained topologies and the previous phylogenetic hypotheses from different datasets, we discuss the classification of the Cylapinae and the morphological characters supporting its major clades.



Abstract ID: 46 • Abstract type: Oral

Wednesday 6th July 2022, 10.20-10.38 h.

PHYLOGENETIC REVISION OF *ACANTHOCEPHALA* LAPORTE 1833 (HEMIPTERA: HETEROPTERA: COREIDAE)

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The family Coreidae Leach is the most diverse of the five that currently comprise Coreoidea, including around 3.100 species and 519 genera worldwide, of which 158 are exclusively Neotropical. The members of the family are characterized by having robust and oval or elongated body, ranging from 6 to 40 mm in length; the head is smaller than the pronotum; the antenna includes four segments; the membrane of hemelytra has abundant venation; the hind femora are thickened and spiny, mostly in males; the hind tibiae are cylindrical or with foliaceous expansions; they have three lateral trichobothria on abdominal sterna I to VI and two on segment VII; the spermatheca has a single flange; and the nymphs have dorsal abdominal scent glands on terga IV-V and V-VI. The genus *Acanthocephala* Laporte (subfamily Coreinae Leach, tribe Acanthocephalini Stål) currently includes 26 species that are distributed from Canada to Argentina. Its members are characterized by the sharply pointed tylus projecting beyond juga as a compressed plate, the hind femora strongly thickened and spiny and more developed in males, and the hind tibiae have foliaceous expansions in both sexes. Most of the *Acanthocephala* species were described in the 19th century and their identity is unclear, there are many synonymous, and some have only been mentioned in a few works; little is known about their host plants and life cycle, and their distribution is known only from a few records. As part of LO PhD thesis, a systematic revision of this group has been done and a morphological phylogenetic analysis was performed, combining continuous (16) and discrete (100) characters, including 52 terminal taxa, where 14 of them are new species, with a significant number of morphological characters that had not been studied in the Coreidae until now. As a result of this study, five valid names were removed from synonymy and reestablished as valid, 14 new species were described, two species were transferred to the genus *Spilopleura* Stål (new status), and three species were established as nomina dubia. According to these results, the genus *Acanthocephala* is composed of a total of 43 species. Finally, the monophyly of the genus was corroborated, the subgenus *A. (Acanthocephala)* and *A. (Metapodiessa)* Kirkaldy were reestablished as valid names, and three new subgenera were described.

Wednesday 6th July 2022, 10.40-10.58 h.

Abstract ID: 36 • Abstract type: Oral

PHYLOGENOMIC ANALYSIS SUGGESTS EVOLUTIONARY CONVERGENCE OF MALE WEAPON TRAITS IN LEAF-FOOTED BUGS AND ALLIES (HETEROPTERA: COREOIDEA)

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The incredible diversity of exaggerated traits, such as sexually selected weapons in males of many animal species, has captivated biological researchers for centuries. Insect weaponry can have multiple functions (e.g., male-male competition and/or anti-predator defense), and once evolved, these traits are predicted to be maintained due to their selective advantage. However, phylogenetic studies in several groups of vertebrate taxa have found evidence of a bias towards losses of exaggerated traits. Understanding the macroevolutionary patterns of exaggerated trait evolution for any group is necessary to begin understanding why such important traits become lost. We focus on the Coreoidea (Hemiptera: Heteroptera), a charismatic group of insects where males of many species have exaggerated hind legs that are often used in contests over access to mates. The hind legs may be variously comprised of a few to many spines or tubercles on various surfaces, compressed expansions, and distinctive curvatures. Here, we provide the first rigorous study on the evolution of the striking hind legs in this group. We use a large multilocus dataset comprised of ultraconserved element loci for 248 taxa and infer evolutionary transitions among character states using ancestral state estimation to answer the following questions: 1) when did various weapon traits evolve in the Coreoidea, 2) did all traits evolve once or multiple times, and 3) if traits are convergently evolved, are there more derived trait gains than losses? Our results, based on maximum likelihood and multispecies coalescent approaches, suggest that the last common ancestor of the superfamily exhibited non-exaggerated weapons, with derived traits arising at various times in the Coreoidea. Furthermore, all characters studied are convergently evolved, with several traits involving the metafemoral processes and tibial expansions exhibiting more losses than gains. Thus, our study suggests that the costs involved in developing and maintaining weapon traits can often lead to their losses.



Abstract ID: 70 • Abstract type: Oral

Wednesday 6th July 2022, 14.40-14.55 h.

USING COMBINED MORPHOLOGICAL AND MOLECULAR DATASETS TO PHYLOGENETICALLY PLACE FOSSIL REDUVIOIDEA

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The fossil record of Reduvidae is limited to ~35 described species recovered from fairly young deposits (Eocene, Oligocene, and Miocene). Emesinae are best represented (13 spp.), followed by Holoptilinae (3 spp.), Triatominae (2 spp.), Harpactorinae (3 spp.), Reduviinae (2 spp.), and Centrocnemidinae (2 spp.), while subfamilial placement of the remaining fossil taxa is uncertain. None of these fossil taxa were included in phylogenetic analyses to assess their placement. In addition, placing fossils based on robust combined morphological and molecular datasets (as opposed to morphological only) has no tradition within Heteroptera. We here present two separate studies focusing on a fossil species of the reduviid subfamily Harpactorinae from the Eocene Messel Pit and a second species from Cretaceous Burmese amber that we recognize as part of the Reduvidae, but that lacks synapomorphies of either Pachynomidae or Reduviidae. We use combined molecular and morphological analyses to phylogenetically place both the harpactorine and reduvioid fossil species.

Wednesday 6th July 2022, 14.55-15.08 h.

Abstract ID: 15 • Abstract type: Oral

INVESTIGATING THE EVOLUTIONARY HISTORY OF THE CORSAIRS (HETEROPTERA: REDUVIIDAE)

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The corsair bugs (Reduviidae: Peiratinae) are a medium-sized subfamily of assassin bugs with over 340 described species worldwide. Individuals in the subfamily exhibit putative aposematic color patterns, several of which occur in different genera suggesting a complex evolutionary history of color patterns in the group. Along with their striking appearance, corsair bugs are unique among reduviids in having asymmetric male genitalia and an accordingly modified mating position. Our objectives are to infer the first robust phylogenetic hypothesis across Peiratinae using nuclear, mitochondrial, and anchored hybrid enrichment loci and to use this hypothesis to reconstruct the ancestral character state of color patterns and male and female genitalic characters while comprehensively documenting the unique phenotypic diversity in this group.

Keywords

Reduviidae • phylogenetics



Abstract ID: 20 • Abstract type: Oral

Wednesday 6th July 2022, 15.10-15.28 h.

A SYSTEMATIC ACCOUNT OF HALYINI (HETEROPTERA: PENTATOMIDAE: PENTATOMINAE) WITH DESCRIPTIONS OF TWO NEW SPECIES FROM INDIA

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The tribe Halyini is one of the most diverse and species rich tribes of Pentatominae, comprising nearly 433 species in 91 genera. It is represented by 66 species in 18 genera from India. Members of Halyini are medium to large in size with somewhat flattened body and are known for phenotypic plasticity in most of the external morphological characters. Body colouration usually varies from dark grey to black, mostly with mosaics of ochraceous and brown; head usually elongate with bucculae rounded, antennae with number of segments varying from three to five, though most genera have five-segmented antennae; lateral margins of head and pronotum often with denticles/serrations; humeri variable; scutellum subtriangular; legs with femora armed or unarmed, foretibiae sometimes dilated; base of the abdominal venter unarmed and venter of abdomen may or may not be sulcate. Most of the members are inhabitants of tree bark, camouflaging bark of trees, probably a form of crypsis to hide from natural enemies. Comparative studies on the variations of male postabdominal structures viz., genital capsule, paramere and phallus of Halyini from India were undertaken primarily based on specimens collected from India and also from published literature, excluding *Asyla* Walker, *Nevisanus* Distant and *Orthoschizops* Spinola. Two new species in Halyini are described here, *Dalpada veenae* Salini, sp. nov. from Arunachal Pradesh and *Meridindia arjuni* Salini, sp. nov. from Karnataka. *D. veenae* is similar to *D. neoclavata* Rider in external colouration and morphology but can be differentiated by the presence of a broad crown of paramere whereas it is acuminate in the latter. *M. arjuni* can be separated from other described species of *Meridindia* based on the angulate dorsal margin of the parameral crown. *Dalpada mcdonaldii* Azim & Shafee, 1983 is proposed as a junior subjective synonym of *Eupaleopada concinna* (Westwood, 1837) based on examination of the original description. DNA barcode sequences of ten species of Halyini in six genera were obtained and accession numbers generated. Preliminary phylogenetic analysis using 24 mt-COI sequences of Halyini belonging to 13 genera and 22 species employing Maximum likelihood method using General Time Reversible model revealed the monophyly of *Meridindia*, *Halys*, *Neohalys*, *Parabrochymena* and *Erthesina* whereas *Dalpada* was found to be polyphyletic.

Finance

This work is financially supported by the Science and Engineering Research Board (SERB), Department of Science and Technology, Government of India (CRG/2019/001619).

Keywords

Dalpada • postabdominal structures • *Meridindia*

Wednesday 6th July 2022, 15.30-15.48 h.

Abstract ID: 10 • Abstract type: Oral

'THEY'RE ALL PAINTED BLACK'-TOWARDS A NEW EUROPE-WIDE KEY FOR CYDNIDAE, WITH NOTES ON TAXONOMY AND ECOLOGY

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The European species of Cydnidae comprise nearly 60 species, including some rare imports to Europe; however, they have historically been regarded as a 'difficult' group, and males are often required for accurate identification. This is compounded by the rarity and low detection rate for some species known from just a handful of museum specimens, and so reliable reference specimens are scarce. Keys exist for the European fauna, most notably Stichel (1955-1962) which covers all Europe, with regional faunas covered by Fuente (1972) for Iberia and Vidal (1950) for the Mediterranean, but in many cases are now outdated due to taxonomic changes and new species, or cover only part of the known fauna, and even at the family level current taxonomic issues include correct placement of Thyreocoridae. Recent studies by Magnien (2006) on *Ochetostethus* Fieber have only served to underline how poorly understood the European fauna is, with species collected in the 19th century showing as 'new to' certain countries. Some species groups, such as the recent revision of *Canthophorus* Mulsant & Rey (Gapon, 2018) have had more modern treatment, and ongoing revisions have rendered earlier checklists obsolete due to generic level changes. An overview is provided of all known European species, including those recently recorded in Europe, with known ecology and host plant family preferences. Many genera of Cydnidae in Europe are specific on certain plant families, a factor which appears to have been ignored in modern taxonomic revisions and could be a useful tool in resolving many taxonomic issues and even locating very rare species. Additional notes are provided on identification and taxonomic issues. Habitat preferences for each species are illustrated where these are known.

Keywords

Cydnidae • Europe • taxonomy • host plant families • habitat



Abstract ID: 52 • Abstract type: Oral

Wednesday 6th July 2022, 15.50-16.08 h.

ANCIENT RAPID RADIATIONS MAY CAUSE THE CHAOS OF EXTANT TAXONOMY AT THE GENUS LEVEL, A CASE STUDY OF UROSTYLIDIDAE (HETEROPTERA: PENTATOMOIDEA)

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Urostylididae is a moderately species-rich family within the Pentatomoidea (Heteroptera: Pentatomomorpha), occurring in southern and eastern Asia. All species are phytophagous, feeding on the sap of various trees and shrubs. The monophyly of, and the relationships among genera of Urostylididae, have not been truly investigated thus far. Herein, we present the first molecular phylogeny of Urostylididae based on complete mitogenome and nuclear ribosomal genes from almost all genera and representative species, using maximum likelihood analysis and Bayesian inference. All phylogenetic results produced overall consistent topological relationships, indicating that the three most species-rich genera, *Urolabida*, *Urochela*, and *Urostylis*, were polyphyletic groups and further split into several lineages in different locations of the trees. For three monotypic genera, *Chelurotropella* and *Urochela wui* Yang formed a steady sister group and nested in a lineage of some species of *Urochela* in all the trees; *Cobbenicoris* was a stable sister group to *Urostylis fici* Ren, but its position was variable in different trees; *Urochellus* either formed a sister group with *Urostylis cuneata* (Ren) or with some species of two or more genera. *Tessaromerus* with one species was a constant sister group with *Urostylis tricarinata* Maa, but its position was variable in different trees. The above results did not support the taxonomy at genus level of Urostylididae, showing the currently recognized genera of Urostylididae unreliable. Furthermore, our results also suggested that some topological incongruence occurred among the trees resulting from different analytical methods and data sets, mainly distributed among internal nodes with short branch lengths and low support values. Given the suggestions of Quartet Sampling method and the interpretation of branch patterns, Urostylididae did undergo rapid radiations after their first divergence, resulting in the presence of incomplete lineage sorting and introgression in our data sets, which made our phylogenetic analyses more sensitive to the type of data or the method employed. Moreover, rapid radiations may also explain the chaos of taxonomy at the genus level of Urostylididae, as the pervasive morphological convergence during rapid radiations poses a challenge to the establishment of higher-level groups that are both monophyletic and diagnosable. Our divergence time estimates indicate that Urostylididae experienced ancient rapid radiations during the Early Cretaceous (115.3-102.5 Ma). The temporal overlap of rapid diversification between Urostylididae and their host plants proposes potential coevolution between these two groups or rapid diversification in Urostylididae induced by the radiations of their host plants. Our results also suggest that the origin of Urostylididae arose in 187.3 Ma during the Early Jurassic, implying that Urostylididae were already present before their host plants and have probably had different ancestral hosts, which further illustrates that host plant shifts can lead to a burst of diversification driven by their arrival in a new adaptive zone.

Wednesday 6th July 2022, 16.30-16.48 h.

Abstract ID: 34 • Abstract type: Oral

TOWARDS A REVISION OF *HALYOMORPHA* (HEMIPTERA: HETEROPTERA: PENTATOMIDAE): POORLY KNOWN RELATIVES OF THE VILLAIN

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The East Asian brown marmorated stink bug, *Halyomorpha halys* (Stål), is a notorious invasive pest species of significant economic importance, having spread throughout North America, the Euro-Mediterranean region, and Chile. It is intensively studied, with dozens of papers published annually. However, nearly all of this research seems oblivious of the fact that *H. halys* is merely one of the 36 valid species recognized within the genus *Halyomorpha* Mayr. Some of the species from SE Asia are morphologically very similar to *H. halys*, and examination of the male genitalia is a prerequisite for their correct identification. Lack of knowledge of the species limits of *Halyomorpha* species has already led to false reports of *H. halys* in India and *H. picus* in Egypt. This also precludes the use of a citizen science approach for correctly identifying SE Asian species of *Halyomorpha*. As most of the species are inadequately described (25 of them being published prior to 1950), lacking necessary details of the male genitalia, the genus is in urgent need of a modern revision. Our preliminary results already identify important nomenclatural and taxonomic problems in the genus that require resolution. The double misidentification of the type species has already been solved by the fixation of *H. halys* as the type species by the action of the first revising author. The genus in its present concept is certainly not monophyletic, as there are several misplaced taxa to be moved in or out of *Halyomorpha*, e.g., the mysterious *Aurungabada singularis* Distant, currently placed in the Tessaratomidae, which is however a teneral specimen of *H. picus*. The remaining species of *Halyomorpha* form a morphologically heterogeneous assemblage and the relationships among the African, Asian and Oceanian species require a phylogenetic analysis. The goal of the project is to determine specific and generic limits in *Halyomorpha* and related genera of Cappaeini, using an integrative approach. It will be achieved by fulfilment of the following objectives: i) morphological and molecular characterization of described taxa by acquiring research materials in various collections as well as based on their primary types; ii) development of diagnostic tools including generation of DNA sequences and illustrated keys; iii) phylogenetic analysis of species using morphological and molecular characters, to determine the generic limits and relationships of the genus-groups of the *Halyomorpha* complex. The research on *H. halys* will result in: i) clarification of its southern limit, resulting in enhanced understanding of its current distribution and predictive models, and ii) generation of a sound taxonomic baseline for further analysis of biological and ecological data of *H. halys* and related species, and new perspectives on *Halyomorpha* research.

Keywords

Pentatomidae • *Halyomorpha* • taxonomy • revision



Abstract ID: 65 • Abstract type: Oral

Wednesday 6th July 2022, 16.50-17.08 h.

PHYLOGENY OF PHLOEIDAE AMYOT & SERVILLE, 1843 (HEMIPTERA: PENTATOMOIDEA) AND ITS CLASSIFICATION WITHIN THE PENTATOMOIDEA: A MORPHOLOGICAL APPROACH

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The family Phloeidae includes three species known as Neotropical bark-bugs, distributed mainly in Brazil: *Phloea corticata* (Drury, 1773), *Phloea subquadrata* Spinola, 1837 and *Phloeophana longirostris* (Spinola, 1837). The monotypic genus *Serbana borneensis* Distant, 1806, found only in Borneo, was originally described as a phloeid, a classification supported and followed by many authors until today. More recently, *S. borneensis* was regarded as a subfamily within the Pentatomidae, hypothesized as the sister-group to all other pentatomids, as Serbaninae. Nonetheless, evidence for the Phloeidae classification within Pentatomoidea is still inadequate.

We perform a phylogenetic analysis of Phloeidae using published and original morphological data to unveil its relationship with other pentatomoid families, and test whether the additional data impact the classification of *Serbana* as well. To accomplish these goals, the ingroup taxa include species from the families Acanthosomatidae (4 spp.), Cydnidae (4 spp.), Cyrtocoridae (2 spp.), Dinidoridae (4 spp.), Pentatomidae (39 spp.), Scutelleridae (5 spp.), and Tessaratomidae (2 spp.), as well as the 3 species included in Phloeidae and *Serbana*; outgroup taxa included species of Coreidae, Lygaeidae, Pyrrhocoridae, and Urostylididae. Original morphological data were compiled and coded based on the study of specimens, focusing mainly on the reinterpretation of the genitalia from males and females.

Finance

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Keywords

neotropical bark bugs • female genitalia • insect morphology • phylogenetic systematics

Wednesday 6th July 2022, 17.10-17.28 h.

Abstract ID: 18 • Abstract type: Oral

INTEGRATIVE TAXONOMY PROVIDES FRESH INSIGHTS TO SYSTEMATICS OF THE GENUS *CORIDIUS* ILLIGER, (HEMIPTERA: HETEROPTERA: DINIDORIDAE) FROM INDIA

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In recent decades the integration of molecular approaches in traditional taxonomy for species discovery has increased. It is a reliable approach, especially when some taxa contain cryptic species posing difficulties in identification. The hemipteran genus *Coridius* (Heteroptera: Dinidoridae) is composed of phytophagous terrestrial bugs with 35 species distributed in the Afrotropical (20 species) and Indo-Malayan regions (15 species). This genus is taxonomically complex due to a wide range of intraspecific differences and poor taxonomic treatments. In this paper, we present, taxonomic revision of the Indian *Coridius*, with an improved sampling from Northeast India. We sequenced the mitochondrial Cytochrome c oxidase subunit 1 (COI) and 16s to reconstruct phylogenetic relationships within *Coridius*, using both maximum likelihood (ML) and Bayesian inference (BI). We employed the Bayesian implementation of Poisson tree process (bPTP) to further assess species boundaries and delimit operational taxonomic units (OTUs). Our analysis supported the establishment of two new species. Further it revealed seven distinct lineages within *Coridius chinensis*. Linear discriminant analysis (LDA) of general body morphology indicated substantial overlap in the *Coridius chinensis* groups and clustered *Coridius* sp. nov 1, *Coridius nepalensis* and *Coridius fuscus*. *Coridius nigriventris*, which was formerly synonymized with *Coridius nepalensis*, is also reinstated in this study.

Keywords

species delimitation • *Coridius* • cryptic species



Abstract ID: 77 • Abstract type: Oral

Wednesday 6th July 2022, 17.30-17.58 h.

INSIGHTS INTO THE PENTATOMIDAE PHYLOGENY: UP-TO-DATE REVISION AND PRELIMINARY NEW UPDATED PHYLOGENETIC ANALYSIS (PENTATOMOIDEA: PENTATOMIDAE)

Marcos Roca-Cusachs¹; Genevcius, B.C.²; Koehler, S.³; Rider, D.A.⁴; Grazia, J.⁵; Cassis, G.⁶; Cheng, M.⁷; Schwertner, C.F.⁸

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Pentatomidae is one of the largest families within the Heteroptera and contains many species of economic importance, either by being plant pests or by their usefulness as biological control agents. After the excision (and acceptance) of cyrtocorids from the pentatomids resulting in an independent family (probably more related to family Dinidoridae based on previous results), the family is currently subdivided into 9 subfamilies. However the results obtained so far indicate that the current subdivisions lack coherence; subfamily, tribal and generic groupings need severe reconsideration and reinterpretation.

In this talk, we present what is known so far regarding the existing phylogenies of the family (either partially or in a superfamily context) and reanalyze the latest phylogeny of the family with the inclusion of a broader spectrum of samples, including many groups that had not been included. Results are explored including the whole dataset, and posteriorly, just with the inclusion of selected taxa.

Problems and restrictions on the markers, taxon sampling, and methodologies are presented, as well as the proposal of new lines of research that might help elucidate the systematics of the group.

Keywords

Pentatomoidea • Pentatomidae • phylogeny • systematics • classification

Thursday 7th July 2022, 09.00-09.18 h.

Abstract ID: 47 • Abstract type: Oral

INVASION PROCESS OF *HALYOMORPHA HALYS* (STÅL) (HEMIPTERA: PENTATOMIDAE) IN CATALUNYA AND NOTES ON THE SITUATION IN SPAIN

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The invasive brown marmorated stink bug (BMSB) *Halyomorpha halys* (Stål) was first recorded in Spain, in Catalonia, in 2016. Data treated in this work come from a citizen science project named Hh Wanted launched on the Spanish naturalists' website Natusfera and other data sources, together with results from traps baited with a commercial aggregation pheromone, installed to check the activity of the species in urban environments. From 2016 to 2021, 1130 valid records were compiled from the Hh Wanted project and other sources. The BMSB is present in the four provinces of Catalonia (Barcelona, Girona, Lleida, and Tarragona) and, until the end of 2020, the presence of BMSB increased exponentially in municipalities of Barcelona and Girona provinces although this trend broke in 2021. ANOVA showed that citizen reports were significantly higher in October, related to BMSB overwintering behavior inside buildings. In urban green areas, significantly more immatures and adults were captured in June and September, respectively. BMSB was found on 35 new host plant species. From June to October, the species was detected in crops, primarily on nectarine and apple, followed by lucerne, fig, pear, bean, hazelnut, olive, tomato, eggplant, grape, citrus, pepper, walnut, and artichoke. The citizen science project found that BMSB was also reported in eight other Spanish provinces (Cáceres, Castelló, Gipuzkoa, Madrid, Pamplona, Sevilla, València and Bizkaya).

Keywords

Halyomorpha halys • BMSB • invasive species • Catalonia



Cancelled presentation

Thursday 7th July 2022, 09.20-09.38 h.

Thursday 7th July 2022, 09.40-09.58 h.

Abstract ID: 49 • Abstract type: Oral.

UNTANGLING THE WEB: SYSTEMATICS AND BIOGEOGRAPHY OF THREAD-LEGGED ASSASSIN BUGS (REDUVIIDAE: EMESINAE)

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Emesinae sensu lato (Hemiptera: Reduviidae: Emesinae, Saicinae, and Visayanocorinae) are the only hemipterans known to prey on spiders in their web and do so using complex predation strategies. Potentially due to this unexplored niche, Emesinae are species rich, with over 950 species in 95 genera. Emesinae additionally differ from other Reduviidae in having several cosmopolitan genera spread across three tribes as well as a number of endemic island species. Though several authors suggested that these genera are not cosmopolitan and are in need of revision, preliminary results support their monophyly, as well as suggest a relatively young age for the subfamily. This suggests that dispersal, rather than vicariance, led to their wide range. Using a combined analysis of Sanger sequencing (175 ingroup taxa) and Anchored Hybrid Enrichment data (12 taxa), we generated a phylogenetic hypothesis and determined relationships between subfamilies, tribes and genera. In addition, we estimated divergence times and biogeographic patterns within the clade.



Abstract ID: 43 • Abstract type: Oral

Thursday 7th July 2022, 10.00-10.18 h.

A PROJECT OF WEST EUROPEAN FAUNA OF MIRIDAE FOR THE 100TH ANNIVERSARY OF THE FAUNE DE FRANCE

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«Faune de France» is a series of books created in 1921 with the main purpose to give tools to naturalists to identify and study animals of France. Most of the later volumes deal with fauna of West European regions. Books are written in French but in most of the later volumes keys are bilingual French/English. 103 volumes have been published since 1921, 100 years ago. Invertebrates represent 95%, insects 71%. Heteroptera with 15 volumes (nearly 15%) is a very well-studied group thanks especially to Jean Péricart who is the author of ten of them. 45 European families of Heteroptera (of 49 reported in Western Europe) have been studied to date in the series. The “Faune de France” on Miridae by Wagner E. & Weber H.H. was published in 1964, and although it was an exceptional work at the time and is still in use, it needs to be completely reviewed: the taxonomy of this huge family has been deeply modified, synonymies have been established and new species described, the keys are often outdated and unusable and the iconography needs to be improved significantly. For all these reasons the authors decided to rewrite the book. They chose to write a fauna not restricted to France but of Western Europe (France and neighbouring countries, including Spain and Italy but excluding Greece and the Balkans). It will deal with more than 820 species and subspecies in 5 volumes estimated to 500 pages each. Most of the species will be illustrated by photographs of habitus and genitalia from G. Strauss and E. Wachmann works. The first volume is expected to be published at the end of 2023 and the last one at the end of 2027.

Keywords

Faune de France • Miridae • books • Europe

Thursday 7th July 2022, 10.20-10.38 h.

Abstract ID: 71 • Abstract type: Oral

ABOUT THE OTHERS – THOSE NOT IN YOUR BED. ECOLOGY OF CIMICIDAE

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There are over 100 species of Cimicidae on a global scale. But only the two species that are parasites on humans, *Cimex lectularius* and *C. hemipterus*, are extensively investigated with regards to their behavior and ecology. Here we present some ecological and behavioral information about other bed bug species. We briefly summarize the long term research on *Cimex (Oeciacus) vicarius* by the Charles R. Brown lab, probably the third best studied cimicid species. Moreover, we show our own research from several bed bug species (e.g. *Paracimex borneensis*, *Hesperocimex sonorensis*, *Primicimex cavernis*, *Propicimex tuomatiani*) ranging from more anecdotal behavioral observations to distribution and population genetic studies.



Abstract ID: 60 • Abstract type: Oral

Thursday 7th July 2022, 10.40-10.58 h.

MORPHOMETRICS OF *PHYMATA (P.) CHILENSIS* HANDLIRSCH (REDUVIIDAE: PHYMATINAE): SPLITTING SPECIES

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The subfamily Phymatinae Laporte includes a particular group of reduviids commonly called “ambush bugs”. They are cryptic species, some with strong sexual dimorphism and unusual reproductive behaviors. The taxonomy of the group is complex; they show many polytypical and polymorphic species and are also widely distributed. With the exception of recent studies on some Nearctic species, specific delimitation usually is restricted to a few morphological features, mainly the pronotum, and coloration characters based on a limited number of specimens are unable to establish clear differences between inter and intraspecific variations. *Phymata (P.) chilensis* Handlirsch includes six subspecies from southern South America, most of them from Argentina. These subspecies were described on the basis of the development and shape of the pronotal lateral angles from a few individuals and with a particular distribution (that posteriorly widely overlap); the frontal process length, the shape of connexiva and the coloration pattern. This approach considers that the pronotum and the connexiva are determining and variable, respectively (approach widely extended into the genera). We propose to analyze the original hypothesis classification (sensu Kormilev) using Geometric Morphometry on both the pronotum and connexiva. The results obtained suggest a greater importance of the connexiva for the delimitation of subspecies. We decided to elevate *P. chilensis monrosi* to species level, leaving *P. chilensis* made up of two apparently distinct groups: one including *P. chilensis cordobensis* and *P. chilensis chilensis*, and the other including *P. chilensis pampeana* and *P. chilensis uruguayensis*; *P. chilensis brasiliensis* was defined based on a single individual and was excluded from the analysis and we consider that it requires a separate review. We propose that a molecular analysis would be necessary to confirm the identity of these two groups and redefine *P. chilensis* species.

Finance

UNLP N905

Keywords

Reduviidae • *Phymata* • geometric morphometry

Thursday 7th July 2022, 11.30-10.48 h.

Abstract ID: 7 • Abstract type: Oral

INTEGRATIVE APPROACH TO THE IDENTIFICATION AND DELIMITATION OF THE TRANS-PALEARCTIC *LYGUS* SPECIES (HETEROPTERA: MIRIDAE: MIRINAE)

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Lygus is one of the most challenging genera within Miridae. It is very abundant in the Holarctic, and some species are pests and widely distributed over large areas of this region. The species are very similar to each other externally and in genitalia and possess significant intraspecific polymorphism. The taxonomic studies have been performed for the Nearctic and Palearctic faunas; however, there are still many inconsistencies and errors in the species identifications. Molecular studies also showed that *Lygus* species in the Nearctic cannot be separated using a single marker, including barcoding region of the cytochrome c oxidase subunit 1 (COI). We have performed an integrative study on the species delimitation of the trans-Palearctic *Lygus* species; they are *L. gemellatus*, *L. pratensis*, *L. punctatus*, *L. rugulipennis* and *L. wagneri*. We have checked all the morphological characters published by the previous authors and have found that only punctuation on hemelytron, spicule in vesica and coloration can be helpful in species separation. We have performed principal component analysis using different body measurements of those five species. The result shows that most species pairs have significant differences in body size and shape. There are only two exceptions, i.e. *L. wagneri* – *L. punctatus* pair and *L. rugulipennis* – *L. gemellatus* pair. We have compared COI and 16S rRNA for 91 Palearctic specimens, and have found that the representatives of the trans-Palearctic species can be separated using those sequences, except for *L. wagneri* and *L. pratensis*, which do not have differences in those markers. The phylogenetic analyses based on each of those markers and combined dataset for Palearctic representatives demonstrate that all specimens split into two well supported clades. The first of them includes *Lygus rugulipennis*, *L. punctatus* and Nearctic species, and the second clade includes *L. gemellatus*, *L. pratensis* and *L. wagneri*. This is also confirmed by the phylogenetic analysis based on COI for 28 species from the Holarctic. The species delimitation analyses (ABGD, GMYC, PTP, BPP) performed on Palearctic representatives differ in the results depending on the type of analysis and dataset. However, *L. gemellatus*, *L. pratensis*, *L. wagneri* and *L. rugulipennis* have never been assigned to a separate species each.

Finance

The research was supported by the Russian Foundation Grant 20-14-00097.

Keywords

integrative taxonomy • haplotype network • taxonomy • PCA • mitochondria markers • plant bugs



Abstract ID: 8 • Abstract type: Oral

Thursday 7th July 2022, 11.50-12.08 h.

PHYLOGENY OF THE *RHINOCYLAPUS* COMPLEX (MIRIDAE: CYLAPINAE: FULVIINI)

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Cylapinae is a mainly tropical subfamily, one of the smallest in the plant bug family Miridae. It currently comprises five tribes: Bothriomirini, Cylapini, Fulviini, Rhinomirini and Vanniini, with its representatives mostly living in cryptic habitats such as litter and under the bark of trees. Over the last decade numerous works on this taxon appeared; however many species remain undescribed and biological data are lacking for most of the taxa. Molecular-based phylogeny of only one tribe Rhinomirini has been published (Namyatova and Cassis, 2019); in that work the *Rhinocylapus* complex and *Rhinomiriella* were transferred to Fulviini, and Rhinomirini were limited to the *Rhinomiris* complex. That phylogeny was based on molecular and morphological data, and included the molecular data for representatives of all Cylapinae tribes. The *Rhinocylapus* complex includes eight genera and 24 species, and the phylogeny published by Namyatova and Cassis (2019) demonstrated the monophyly of this group. *Punctifulvius* was shown to be a sister group to the remaining taxa within the *Rhinocylapus* complex. However, that study included the molecular data (COI, 16S rRNA, 18S rRNA, and 28S rRNA) for only four representatives from this clade and the relationships between other genera within the *Rhinocylapus* complex remained unknown. Therefore, the main aim of our study was to resolve the relationships within this group based on more molecular and morphological data. For the present study, we expanded the morphological matrix and obtained molecular data on the same four markers for six more specimens of the *Rhinocylapus* complex. The topologies were constructed using methods of parsimony, maximum likelihood, and Bayesian inference based on morphological only, molecular only and total-evidence datasets. As a result, we confirmed the main results of the previous study and refined the diagnosis of the *Rhinocylapus* complex. We also demonstrated that *Rhinocylapus*, *Tatupa* and *Proamblia* are more closely related to each other, rather than to *Mycetocylapus*. We also confirmed that the previously described genus *Tatupa* Tyts et al. represents a separate genus. However, the position of other genera, *Yamatofulvius*, *Rhinocylapoides*, *Rhinocylapidius* as well as monophyly of *Rhinocylapus* remain questionable.

Finance

This research was supported by the Russian Foundation for Basic Research (grant 20-04-01040 A).

Thursday 7th July 2022, 12.10-12.28 h.

Abstract ID: 26 • Abstract type: Oral

MOLECULAR PHYLOGENY OF THE FAMILY MIRIDAE (HETEROPTERA: CIMICOMORPHA) WITH DISCUSSION ON DIVERGENCE DATE AND LIFE HISTORY EVOLUTION

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Miridae, a group of plant bugs, is the most diverse of the heteropteran families, comprising more than 11,700 species. Their high morphological and ecological diversity has made phylogenetic definitions of Miridae and their subordinate group the subject of frequent debate. In this work, we present a more rational phylogenetic tree of plant bugs, based on multigene phylogeny with denser taxon sampling and more gene loci. In addition, we estimated the most recent common ancestor of Miridae, with emphasis on their diet and habitat features, and also estimated divergence date of Miridae and its subordinate groups. We expect our result can provide reasonable insights into mirid phylogeny and evolution.

Keywords

Cimicomorpha • Miridae • phylogeny • divergence date



Abstract ID: 13 • Abstract type: Oral

Thursday 7th July 2022, 12.30-12.48 h.

CLEANING OUT THE JUNK DRAWER: A PHYLOGENY OF THE *TELEONEMIA* COSTA GENERIC COMPLEX (HEMIPTERA: TINGIDAE)

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The *Teleonemia* Costa generic complex is distributed throughout the Western Hemisphere. It is characterized by the presence of the following attributes; general tan to brown or red-brown coloration, apically rounded antenniferous tubercles, setose antennae that end in moderately elongate or obclavate distiflagellomeres, vertically reflexed paranota, three uniseriate pronotal carinae, well developed ostiolar peritremes, coxae with setae on distal margins; subcostal area of each hemelytra with one to four rows of areolae and pygophore with two basal depressions. Separation of the included genera, *Alveotingis* Osborn & Drake, *Eurypharsa* Stål, *Hesperotingis* Parshley, *Melanorhopala* Stål, and *Teleonemia* have historically relied on antennal morphology and the width of the costal areas of the hemelytra; however, the generic boundaries of most included genera have been modified through subsequent description of taxa during the past century. A phylogenetic analysis was undertaken to better define the generic boundaries within the complex. A 98-character multistate character matrix with 150 taxa was created in Mesquite 3.7 and analyzed in PAUP* 4.0 using non additive parsimony analysis. Characters were treated unordered and without weights. We performed a heuristic search with 1000 random replications, with one starting tree per replication. Our results indicate that several genera of the complex, *Teleonemia*, *Hesperotingis*, and *Melanorhopala*, are not monophyletic and need to be redefined in order to proceed with generic revisions. We also propose several new genera to accommodate phylogenetic incongruence and stabilize the current classification of the *Teleonemia* generic complex.

Keywords

Tingidae • morphology • Cimicomorpha • Miroidea • phylogenetics

Thursday 7th July 2022, 12.50-13.08 h.

Abstract ID: 35 • Abstract type: Oral

INTEGRATING TIME AND SPACE TO SHED LIGHT ON THE EVOLUTION OF GIANT WATER BUGS IN THE NEW WORLD (HEMIPTERA: BELOSTOMATIDAE: BELOSTOMATINI)

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Belostomatini is a highly diverse lineage of giant water bugs (Belostomatidae) with 81 species distributed exclusively throughout the New World, being most abundant in the Neotropical region. Three genera are recognized in this tribe: *Abedus* Stål, with 12 species predominantly North American; *Weberiella* De Carlo, a monotypic genus constituted by *W. rhomboides* (Menke) restricted to Amazonia; and *Belostoma* Latreille, including 68 species distributed throughout southern Argentina and Chile to southern Canada classified into 16 species groups. Here, we propose the first dated phylogenetic hypothesis for the species of Belostomatini combining morphological and molecular datasets with a comprehensive taxonomy sampling, about 90% of the species diversity. The sampling included 71 species of Belostomatini representing the three genera plus 10 species including the other five genera of Belostomatidae as outgroups. The complete dataset includes data from five nuclear and mitochondrial gene fragments (COI, 16S, 18S, 28S, and H3), which sum up to 3173 aligned characters, plus 94 morphological characters from external morphology and male genitalia. The combined dataset was analyzed under Bayesian Inference. Then, we used an uncorrelated log-normal relaxed clock model to estimate divergence times among the lineages of Belostomatini using a node-dating scheme under a birth-death diversification model. For these analyses, four fossil calibration points were addressed based on giant water bug fossils available. Our phylogenetic analyses using the combined dataset recovered the three genera as monophyletic; *Abedus* as the sister of *Weberiella* + *Belostoma*; for *Belostoma*, three subgenera are recognized: *Belostoma* (*Microbelostoma*) subgen. nov., *Belostoma* (*Perthostoma*) stat. nov., and *Belostoma* s. str. These subgenera can be distinguished by the morphology of male genitalia, especially the gonopore and paramere. The phylogenetic results were critical for the first comprehensive reevaluation of the generic limits and for the subgeneric classification in *Belostoma*. The differentiation of major clades within *Belostoma* and *Abedus* was estimated to split between the Paleocene and the Eocene (62–37 Mya), a time interval within approximately 25 Mya, a period when the number of lineages of Belostomatidae increased significantly. The preferred DEC model under AIC estimation has estimated the Amazon region played the most important role in the early diversification of Belostomatini, with subsequent cladogenetic events to the northern and southern portion of the ancestral distribution, and more recent expansion of range distribution of the species in different lineages, potentially facilitated by warm climate conditions during the Cenozoic.

Finance

Coordination for the Improvement of Higher Education Personnel—Brazil (CAPES)—Finance Code 001

Keywords

biogeography • morphology • systematics



Abstract ID: 9 • Abstract type: Oral

Thursday 7th July 2022, 14.50-15.08 h.

QUANTITATIVE ANALYSIS OF CITIZEN SCIENCE DATA ON HETEROPTERA: EXAMPLE OF *HALYOMORPHA HALYS* DISTRIBUTION

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Citizen science platforms such as iNaturalist.org are getting more and more popular, with tens of thousands of nature aficionados worldwide contributing new photos day by day. Although the users of such platforms often lack taxonomic expertise, the sheer number of their contributions provides a valuable resource for research, since thousands of “amateurs” can access so many regions and habitats with such a regularity that a few hundred taxonomists cannot match. Many professionals already employ citizen science data in their research – however, this research is still mostly qualitative, pertaining to new records of species and distribution shift ranges. Here, we demonstrate that the immense amount of data collected by citizen scientists also has much potential for quantitative approaches. Citizen science data on *Halyomorpha halys* distribution allows us e. g. to test the hypothesis of this subtropical species’ spread in Germany via cities – the so-called “warmth island hopping”. We compare its distribution with that of the local pentatomids *Palomena prasina* and *Rhaphigaster nebulosa*, the results supporting the city-mediated distribution of *H. halys*. We hope that this and some additional examples will inspire heteropterists to approach more sophisticated questions using citizen-science data.

Finance

Applying for the DAAD (German academic Exchange) congress travel grant; to get it, a confirmation of acceptance of the proposed topic by the organizers is needed.

Keywords

Heteroptera • citizen science • *Halyomorpha halys* • distribution pattern • quantitative analysis • GIS

Thursday 7th July 2022, 15.10-15.28 h.

Abstract ID: 62 • Abstract type: Oral

CONSPECTUS OF THE LETHAEINI (LYGAEOIDEA: RHYPAROCHROMIDAE) OF THE AMERICAS

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The most diverse family in Lygaeoidea is Rhyparochromidae with over 2,000 described species and hundreds still unknown, especially for the Neotropical region, where only few specialists are dedicated to the taxonomy of the group. With significant representation in the tropical and subtropical region, Lethaeini is one of the most diverse tribes within the family, with 41 genera and more than 190 species worldwide. Currently Lethaeini is considered a monophyletic tribe based on the following apomorphies: linear position of the trichobothria in the fifth abdominal sternite, Y chromosome loss, extreme modification of sperm reservoir, and development of iridescent areas in the head. The latter character allows to divide Lethaeini into two distinguishable groups: species with one or two iridescent spots in the head. Here, we present a conspectus of the Lethaeini in the Americas, with keys to genera and species. In this compilation, information about 54 species in 13 genera and updated distribution maps are presented, with several new records from Brazil. Although the tribe is considered monophyletic, it has never been properly tested. We also highlight the following questions about the group: 1) do the American genera and the current generic classification represent monophyletic groups?; 2) are the genera with one or two iridescent spots natural groups?; and 3) what are the relationships between the American genera? These questions are addressed based on a preliminary analysis of a morphological phylogenetic analysis, with 54 terminals and 52 characters. The ingroup terminals include 38 species from the Neotropical and Nearctic regions, and 12 species from the Afrotropical, Australian, Indomalayan and Palearctic regions; outgroup taxa include species belonging to four other Rhyparochromidae tribes.



Abstract ID: 63 • Abstract type: Oral

Thursday 7th July 2022, 15.30-15.48 h.

HIDDEN LIFE IN THE INTERSTICES: ON BIOLOGY AND TAXONOMY OF DIPSOCORIDAE OCCURRING IN CENTRAL EUROPE

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Dipsocoridae (Heteroptera: Dipsocoromorpha) is a small family of true bugs, inhabiting interstitial spaces in riverbanks (*Cryptostemma* spp.) or various bogs and fens (*Pachycoleus* spp.). So far, five species have been reported from Central Europe (*Cryptostemma alienum*, *C. carpathicum*, *Pachycoleus pusillimus*, *P. waltli*, *Alpagut* cf. *medius*), but due to their cryptic lifestyle, only few details about their biology are known. In this study, *Cryptostemma remanei* is reported for the first time from several countries in Central Europe. Observations on hunting behaviour, microhabitat preferences and ability to survive under water are provided for *P. pusillimus* and *C. remanei*. Furthermore, SEM pictures of ultrastructures located on the rostrum and antennae of the two species are presented. In the further course of this project, we aim to revise the distribution of *C. alienum* and *C. remanei* in Central Europe, assess their taxonomic validity using DNA barcoding and provide deeper insight into the biology of selected species of Dipsocoridae, possibly including mating behaviour and differences in preferred microhabitats.

Keywords

Dipsocoromorpha • interstices • ultrastructure • feeding biology • microhabitat

Thursday 7th July 2022, 15.50-16.08 h.

Abstract ID: 64 • Abstract type: Oral

HETEROPTERA DIVERSITY OF THE FERNANDO DE NORONHA ARCHIPELAGO, BRAZIL

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The Fernando de Noronha Archipelago has a volcanic origin, estimated at 12.0 to 1.5 million years old, never connected to the continent. It is a Brazilian National Park located 360 km from the northeastern coastline of Brazil, with a total land area of 18.4km². The archipelago has a harsh environment, lacking a permanent source of freshwater, with low vegetation diversity and a shallow soil that has poor capacity for water retention. The dominant vegetation is primarily represented by bushes and herbs, with several introduced plant species. Fernando de Noronha is poorly collected concerning insects in general, and until recently only two works on Heteroptera fauna of the archipelago were published: one in 1957 by JC Carvalho and J Becker on Miridae, and the other in 1962 by M Alvarenga, which includes records of true bugs of different families. During the period 2019-2020, expeditions led by one of the co-authors (JAR), focused on Hexapoda in general, increased the number of insects collected in the archipelago. Here, we present detailed information on the Heteroptera diversity from approximately 200 specimens collected during these expeditions using a wide range of sampling methods. The number of true bug species has doubled since 1962. Among the families collected are included Anthocoridae (2 spp.), Berytidae (1 sp.), Cydnidae (1 sp.), Lygaeidae (2 sp.), Miridae (4 spp.), Nabidae (1 sp.), Pentatomidae (2 spp.), Rhopalidae (2 spp.), Rhyparochromidae (4 spp.), Thyreocoridae (1 sp.), Tingidae (1 sp.) and Veliidae (1 sp.). Most of the true bugs were collected using sweep net, light and Malaise traps. We also compare the new records with previous data published, and discuss the potential processes that may have driven the occupation of the archipelago.



Abstract ID: 12 • Abstract type: Oral

Thursday 7th July 2022, 16.10-16.30 h.

Abstract ID: 6 • Abstract type: Poster

FIELDWORK AND PHYLOGENETICS: ADVANCING MIRIDAE BIOLOGY AND CLASSIFICATION

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The creation of a database-driven catalog of the Miridae has allowed for the preparation of species accumulation curves as of 2011 which show that the Miridae faunas of the Palearctic and Nearctic are much more diverse than those of the southern continental areas. Data from the catalog also allow us to plot levels of host specificity which indicate that most Miridae with known hosts feed on a single plant species, with much smaller numbers feeding on two or more host species; most of these host data still come from the Northern Hemisphere fauna. In this presentation I will provide a somewhat personal history of how our knowledge of diversity in the Miridae—particularly for the large and widespread subfamily Phylinae—has developed and the significant changes that have occurred concerning regional diversity, host utilization, and biogeographic patterns from what was known a half century ago. Upon joining the staff of the American Museum of Natural History in 1974 I was faced with designing a field/research program that would augment the small existing collection of the institution while also advancing our knowledge of overall Miridae diversity and relationships. Over a period of nearly 30 years I spent approximately 1.5 years in the field in Western North America, South Africa, and Australia, participated with colleagues in the collection of more than 150,000 Miridae specimens, and secured authoritative identification of >2500 host vouchers. These efforts provided core background information for revisions of more than 25 large genera and numerous smaller groups, including the description of ~500 new species of Miridae: Phylinae, for the first time documenting the great diversity and host associations of the Australian fauna and improving knowledge of classification, diversity, and host associations for Western North American and South African faunas. Phylogenetic analyses, produced in collaboration with colleagues, culminated in a revised classification of Phylinae with 9 tribes and 9 subtribes, and the postulation of multiple origins of myrmecomorphy and fleshy parempodia, radical departures from the single origin per subfamily of these two diagnostic features in the 3-tribe system for Phylinae in Carvalho's World Catalog of the 1950s. Phylogenetic analysis also supported the existence of transantarctic distributional patterns in the Phylinae, an idea that was previously unimaginable because of the paucity of knowledge for the Australian fauna.

Keywords

Phylinae • host plants • myrmecomorphy • transantarctic distributions

TOTAL-EVIDENCE PHYLOGENY OF THE PREDATORY PLANT BUG SUBFAMILY DERAEOCORINAE (HEMIPTERA: CIMICOMORPHA: MIRIDAE)

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The predatory subfamily Deraeocorinae is one of the large groups in the plant bug; however, the monophyly of this subfamily and its tribal relationships are still veiled. The first comprehensive phylogenetic analyses based on the 86 morphological characters and molecular data (COI, 16S, 18S and 28S) were performed i) to test the monophyly of the Deraeocorinae; ii) to hypothesize the monophyly and the relationship of the tribes; and iii) to test the monophyly of the nominate tribe and genus (*Deraeocorini*, and *Deraeocoris*). In this poster presentation, the preferred topology based on the morphological and molecular data is presented. The major questions such as the monophyly and the tribal relationship are provided with the brief discussion.

Keywords

Heteroptera • Deraeocorinae • Miridae • Phylogeny



Abstract ID: 11 • Abstract type: **Poster**

PRIORITY AREAS FOR THE CONSERVATION OF SEMIAQUATIC BUGS (HETEROPTERA: GERROMORPHA) IN ALAGOAS AND SERGIPE STATES, NORTHEASTERN BRAZIL

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Semiaquatic bugs (Heteroptera: Gerronormorpha) are distributed throughout the world and occupy a wide variety of habitats. The diversity of these insects in Brazil is relatively well studied, but there are still large knowledge gaps in certain areas, especially in the northeastern portion of the country. Recently, a series of collections was carried out in two states in this region, Alagoas and Sergipe, where the Gerronormorpha fauna was practically unexplored. As a result, a total of 40 species were reported in both states, with 35 new records for Alagoas and 31 for Sergipe. With the aim of evaluating the areas in the two states that harbor the greatest potential richness of Gerronormorpha species and contributing to the definition of priority areas for their conservation, potential distribution models for 11 species of the infraorder were generated. Such models use species occurrence records and allow inferring ecological aspects and, thus, predicting which geographic areas are suitable for them. The models were then generated in the software R, using occurrence records, a set of environmental variables (climatic, hydrographic, landscape data), pixels of approximately 1km² and the package modelR. Given the models generated, a greater concentration of potential richness and priority for the conservation of Gerronormorpha can be seen in two areas of Alagoas and Sergipe, both in the Atlantic Forest. This has a more adequate rainfall regime for the establishment of gerronormorphan populations than the Caatinga, the other biome in the region with semiarid characteristics. Despite this, there is a predominance of pasture areas, sugarcane plantations and exposed soil in the region, with high forest fragmentation, except for the two full protection conservation units, where the vegetation is more pristine. In addition, there are hotspots of high potential richness in the region that are currently completely unprotected, especially in forest fragments in northern Ibateguara and São José da Laje municipalities, and in the transition to the Caatinga in northwestern Chã Preta municipality. The region is dominated by areas of pasture, agriculture and exposed soils, with elevated fragmentation of the forest remnants. The vast majority of conservation units in the area are for sustainable use, not full protection, and of minute size, except for Pratagy Environmental Protection Area, which covers lands in Maceió, Messias and Rio Largo municipalities (Alagoas). Noteworthy, however, are the two full protection conservation units in this area, Serra de Itabaiana National Park and Mata do Junco Wildlife Refuge. In view of this panorama, it is fundamental to maintain and effectively protect the conservation units that already exist in the two priority areas, in addition to creating new ones, especially in the corridor along the Tabuleiros Costeiros. Such actions can preserve a high richness of Gerronormorpha and, potentially, also of other insects and aquatic organisms that may present similar environmental requirements.

Finance

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Keywords

aquatic insects • Atlantic forest • Caatinga • species distribution modeling

Abstract ID: 16 • Abstract type: **Poster**

RHYPAROCHROMIDAE OF MADAGASCAR (HETEROPTERA, LYGAEOIDEA)

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The Heteroptera fauna of Madagascar has been studied by several authors since the 19th century but among them the Rhyparochromidae fauna of the island is less researched. We studied Madagascan Rhyparochromidae specimens in collections of several European museums (like Brno, Berlin, Brussels, Cardiff, Helsinki, Innsbruck, London, Paris, Prague, Stockholm, Tervuren, Vienna) and one American museum (San Francisco). 71 species of Rhyparochromidae belonging to 9 tribes were found in Madagascar until 2021. During our investigation, we found at least 30 additional taxa (undescribed ones and already described taxa that weren't formerly known from the island). We detected among them 5 new Antillocorini and 3 Plinthisini species (these tribes were unknown on Madagascar). Furthermore, we found a number of undescribed and unpublished taxa in each native tribe known from the country.

Finance

This study was supported by EFOP-3.6.3-VEKOP-16-2017-00008 project.

Keywords

Lygaeoidea • Rhyparochromidae • Madagascar • new species



Abstract ID: 22 • Abstract type: **Poster**

POSTEMBRYONIC DEVELOPMENT OF THE STRIDULATORY APPARATUS OF THE SELECTED SPECIES BELONGING TO THE GENUS *PLATYMERIS* LAPORTE, 1833 (HETEROPTERA: REDUVIIDAE: REDUVIINAE)

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The stridulatory apparatus of assassin bugs consists of two parts: stridulitrum and plectrum. In Reduviidae, the stridulitrum has a structure of a groove in the prosternum and the plectrum is represented by the apical part of the third visible labial segment. During our studies we have found the stridulatory organs both in adults and nymphs of all development stages and investigated the morphology of this apparatus, using scanning electron microscope (SEM). Within the genus *Platymeris* the imagines as well as all nymphal stages of *P. biguttatus* L., *P. rhadamanthus* Gerst., and their hybrid were studied. The specimens used in our studies have been bred in the insectarium of the Zoology Research Team, the University of Silesia in Katowice, Poland. Morphological analysis of all five immature stages shows that the stridulitrum (regardless of the instar) is narrow and elongated. However, the ratio of length to width increases during development. Our studies also show, that the slight variations in the structure of the nymph stridulitrum may be useful in distinguishing these species from each other (including the hybrids), but plectrum cannot be a significant diagnostic feature.

Keywords

stridulatory apparatus • stridulation • *Platymeris* • Reduviidae

Abstract ID: 23 • Abstract type: **Poster**

MORPHOLOGY OF THE STRIDULATORY APPARATUS OF SELECTED SPECIES, REPRESENTING ALL SUBFAMILIES OF REDUVIIDAE LATREILLE, 1807

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The stridulatory apparatus of assassin bugs consists of a groove in the prosternum (stridulitrum) and the tip of the rostrum (plectrum). The stridulitrum, the morphological structure of which is based on the presence of transverse ridges is the most widely distributed among assassin bugs, while the plectrum consists of two sclerotized tubercles. All individuals used during our studies, representing all the known subfamilies, were examined using a scanning electron microscope (SEM). Our preliminary results show visible differences in the structure of the stridulation apparatus among selected subfamilies. However, the common feature of the investigated species is the presence of transverse ridges. The degree of sclerotization of the plectrum varies. The next stages of our research will include investigating the morphology of the stridulatory apparatus in representatives of all 25 known subfamilies, selected in terms of food specialization or lack thereof. Additionally, our studies will include an examination of the sensilla associated with the stridulatory apparatus.

Keywords

stridulatory apparatus • stridulation • Reduviidae • morphology



Abstract ID: 24 • Abstract type: **Poster**

A REVIEW OF *OXYCARENUS* (LYGAEOIDEA: OXYCARENIDAE), EXCLUDING THE AFROTROPICAL SPECIES

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Although several of them are serious pests, the non-Afrotropical species of *Oxycarenus* Fieber, 1837, the largest genus of Oxycarenidae, has never been reviewed. Currently 54 species are known in the genus, but only 16 of them are not endemic to the Afrotropical Region. The African fauna was reviewed by Samy (1969). Our investigations concluded that three of the described Asian species should be synonymized, and two species described by Montrouzier should be declared as incertae sedis; additionally, *O. heraldus* Distant, 1903 should be restored as a valid species. Three undescribed species, all from the Papuan Subregion, were also recognized. One species should be transferred into the subgenus *Euoxycarenus* Samy, 1969, and a new subgenus should be established for the Palaearctic *Oxycarenus modestus* (Fallén, 1829), currently placed in the subgenus *Pseudoxycarenus* Samy, 1969, endemic to the Afrotropical Region (not considering Walker's doubtful record from "Hindustan"). A key has been compiled for the Palaearctic, Oriental and Pacific species, and several new country records are provided.

Finance

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Keywords

Oxycarenus • revision • new species • new synonym • Lygaeoidea

Abstract ID: 25 • Abstract type: **Poster**

THE HETEROPTEROFAUNA OF ITALY, AN UPDATE

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As part of the "Checklist delle specie della fauna italiana" project, which listed the whole Italian fauna, Faraci and Rizzotti Vlach (1995) published the booklet on Heteroptera. A new project, updated "Checklist of the Italian Fauna" was launched in 2020; we here present the results regarding the Heteroptera. Each co-author dealt with a part of the Checklist: Cianferoni with Dipsocoromorpha, Gerromorpha, Nepomorpha and Leptopodomorpha, Carapezza with Microphysidae and Miridae, Faraci with the remaining Cimicomorpha and Pentatomomorpha. Only data published before November 2020 were included. The systematic order at family level is that adopted in the CHPR (Aukema & Rieger, 1995-2006 [and subsequent updates]) except Lygaeidae s.l. which are divided into families as proposed by Henry (1997) according to phylogenetic studies. In 1995, 1398 species group taxa were listed, including 81 whose presence in Italy needed confirmation; in detail: 5 Dipsocoromorpha, 33 Gerromorpha, 58 Nepomorpha (6 of which doubtful), 31 Leptopodomorpha, 730 (59) Cimicomorpha and 541 (16) Pentatomomorpha. The updated checklist lists 1395 species (45 of which still need to be confirmed if belonging to Italian fauna): 5 Dipsocoromorpha, 32 Gerromorpha, 54 Nepomorpha (1 of which doubtful), 32 Leptopodomorpha, 730 (32) Cimicomorpha and 542 (12) Pentatomomorpha. Although the total number remains almost identical, decreasing by 3 taxa, actually numerous changes occurred and the additions almost completely compensated for all the deletions made. Out of 48 families whose representatives are currently found in Italy, the most speciose is by far Miridae, with 496 (21) taxa; out of 509 (45) taxa in the former checklist, 26 were deleted as the result of misidentifications or referred to areas no longer belonging to Italy and 21 were synonymised with other taxa already belonging to the Italian fauna while 34 taxa were added. Thaumastocoridae is a new entry, with the alien *Thaumastocoris peregrinus* Carpintero & Dellapé (2006) which is more or less present everywhere its host plants (*Eucalyptus*) are widespread. The distribution is detailed in 4 macro-areas: the mainland, divided into 2 areas (the continental North and the Apennine peninsula), plus Sicily and Sardinia, each including surrounding smaller islands. As expected, diversity in the northern regions, contiguous to continental Europe, is greater with as many as 1071 (49) taxa recorded while it is reduced in Sardinia with just 557 (38); southern regions and Sicily have intermediate values. Overall, 44 endemites and 12 subendemites are recorded; 14 of these are exclusive to Sardinia (some shared with neighbouring Corsica) and only 1 is recorded in all the macro-areas. The most significant additions are those of alien entities, now totalling 23 taxa, 10 of which are cryptogenic. The families with more allochthonous elements are Tingidae (6), Reduviidae (4) and Lygaeidae (3). Four alien species (*Corythauma ayyari*, *Corythucha ciliata*, *Leptoglossus occidentalis*, *Halyomorpha halys*) show high spreading capabilities being already found in the 4 macro-areas.

Keywords

Heteroptera • Dipsocoromorpha • Gerromorpha • Nepomorpha • Leptopodomorpha • Cimicomorpha • Pentatomomorpha • Italy • faunistics



Abstract ID: 27 • Abstract type: **Poster**

COMPARATIVE STUDIES OF SENSORY ORGANS ON THE LEGS OF REPRESENTATIVES OF PLANT BUGS (HEMIPTERA: HETEROPTERA MIRIDAE)

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The plant bugs (Miridae) belonging to the infraorder Cimicomorpha and superfamily Miroidea, are one of the most species-rich families of insects, with more than 11,300 described species (Schuh and Weirauch, 2020). In accordance with the most recent literature (Wolski and Henry, 2015; Schuh and Weirauch, 2020), seven subfamilies are recognized within the Miridae: Bryocorinae, Cylapinae, Deraeocorinae, Isometopinae, Mirinae, Orthotylinae, and Phylinae. Plant bugs ranging in size from less than 2 mm to about 15 mm, are among the most delicate of all Heteroptera. The family Miridae is poorly studied in terms of sensory organs. A limited number of studies have been published about the sensilla of mirids, and they were focused mainly on the sensilla on mouthparts and the antennae. Almost all of these studies were conducted on specimens of only one plant bug subfamily (Mirinae). Although some of the sensory structures on the legs of mirids are significant taxonomic characteristics (trichobothria, parempodia), there were no studies that would describe in detail the ultrastructure and morphology of these and other sensory structures on the legs of mirids. This study presents the results of morphological analyses of sensory organs on all three pairs of legs of representatives of all seven subfamilies belonging to Miridae. A detailed morphological structure has been described based on micrographs of legs covered with gold obtained with a scanning electron microscope (SEM). Sensilla observed on legs were divided into morphological types and subtypes. In this study, we provide information about the occurrence of each type and subtype of sensillum in studied taxa and their arrangement on the legs. We also discuss the possible function of each type of sensillum and differences in morphology and arrangement of sensilla between taxa.

Keywords

Miridae • morphology • sensilla • SEM

Abstract ID: 30 • Abstract type: **Poster**

AREAS OF ENDEMISM IN COLOMBIA BASED ON DISTRIBUTION OF GERROMORPHAN SPECIES

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The identification of biogeographic patterns has been important both for historical biogeography and for conservation. Within these patterns, endemic areas are included, which are defined by the congruence of the distribution areas of two or more species, and are considered a key step for biogeographic regionalization. However, there are few biogeographical studies involving insects, and especially the suborder Gerromorpha in Colombia, even when current studies on biodiversity suggest that groups of organisms, such as the species of the Gerridae and Veliidae families, gain importance in the evaluation of aquatic ecosystems as indicator agents of water quality and therefore key elements to conserve these ecosystems. In this context, the identification of patterns not only allows us to have elements for conservation, but also to analyze the biogeographic history of a region, since these areas represent a biota with a single historical product of tectonic and climatic events. According to the above, an endemism analysis of Gerromorpha species distributed only in Colombia was carried out, to establish areas of endemism, and thus generate inputs for a biogeographic regionalization for the country. To determine the areas, a data set of 480 records belonging to 4 families was constructed, distributed as follows: Gerridae (9 genera, 19 species), Hydrometridae (1 genus, 3 species), Mesoveliidae (1 genus, 1 species), Veliidae (10 genera, 47 species), for a total of 21 genera and 71 species, considering the valid species for the country, based on the bibliographic review and records obtained from nine entomological collections. The endemism analysis was implemented through the NDM/VNDM program using three different grid sizes. 25 areas of endemism were identified in Colombia with 21 endemic species belonging to the genera *Altavelia*, *Hydrometra*, *Microvelia*, *Potamobates* and *Rhagovelia*. In the overlapping pattern of the 12 consensus areas, we identified six generalized areas that we propose to be named as: South-occidental of Colombia, North of Colombia, North of the Western cordillera of Colombia, Center Pacific of Colombia, North Pacific of Colombia and South of the Central Cordillera of Colombia. Our results highlight the importance of the Colombian mountain ranges and the Pebas system to understand the distribution patterns of skater bugs in the Neotropical region. This is possible thanks to the availability of a resolved taxonomy that can reduce the Wallacean deficiencies in studies of biogeography conservation.

Finance

Vicerrectoría de Extensión y de Investigación, Dirección de Investigaciones, Universidad Pedagógica y Tecnológica de Colombia.

Keywords

biogeography • distribution • conservation • Neotropics • patterns



Abstract ID: 31 • Abstract type: **Poster**

CAPUTELLA, A NEW GENUS OF SUBFAMILY ECTRICHODIINAE (HETEROPTERA: REDUVIIDAE) FROM MADAGASCAR

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The fauna of Reduviidae of Madagascar is very rich and diverse, but only some subfamilies or tribes of assassin bugs are well known or partially studied and described (Villiers, 1950, 1964, 1968, 1971, 1975, 1979; Forthman et al., 2016). Among the better known are representatives of the subfamily Ectrichodiinae. According to the World Catalogue of Maldonado Capriles (1990), and the latest research (Forthman et al., 2016) over 120 genera and over 730 species of Ectrichodiinae are known so far in the world fauna of assassin bugs, and among them, nine genera and 73 species are known from Madagascar. During the examination of undetermined materials from Madagascar, deposited in the collection of the Muséum national d'Histoire naturelle in Paris, remarkable and very distinctive specimens belonging to Ectrichodiinae were found. Examination of these specimens shows that they belong to a new undescribed genus and two new species. These specimens could not be placed in any known genera and will be described as the genus *Caputella* gen. nov., which is named after an unusually large head.

Keywords

Reduviidae • Ectrichodiinae • new genus • new species • Madagascar • Heteroptera

Abstract ID: 32 • Abstract type: **Poster**

DESCRIPTION OF THE IMMATURE STAGES OF *DISTIROGASTER TARSALIS* (SIGNORET, 1860) (HETEROPTERA: REDUVIIDAE: ECTRICHODIINAE)

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The genus *Distirogaster* Horváth, 1914 is distributed exclusively on Madagascar and it is the largest (in terms of body size) known genus of Ectrichodiinae on the Island. Among the numerous specimens of the above-mentioned genus, deposited in the Muséum national d'Histoire naturelle, Paris, France we have found a large number of all five immature stages, belonging to *Distirogaster tarsalis* (Signoret, 1860). The main goal of our research is to describe the morphology of each developmental stage using the stereoscopic microscope as well as SEM techniques. The description was based on about 60 specimens of immature stages of *D. tarsalis* deposited in the MNHN.

Keywords

Reduviidae • Ectrichodiinae • Heteroptera • Madagascar • nymphs • description • SEM



Abstract ID: 33 • Abstract type: Poster

**DESCRIPTION OF THE IMMATURE STAGES OF *DIASPIDIUS SCAPHA* (DRURY, 1782)
(HETEROPTERA: REDUVIIDAE: HARPACTORINAE)**

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The genus *Diaspidius* Westwood, 1857 is a large (in terms of the body size) genus belonging to the subfamily Harpactorinae. Within the genus, five species have been described so far, and all of them are distributed exclusively in Africa as well as on small islands around the continent. During our studies, among the numerous specimens of *Diaspidius* deposited in the Royal Museum for Central Africa, Tervuren, Belgium, we have found specimens representing three immature stages belonging to the species *Diaspidius scapha* (Drury, 1782). The main goal of our research is to describe the morphology of three developmental stages (nymphs of II, III and V instars) of the above-mentioned species, using the stereoscopic microscope as well as SEM techniques. The description was based on about 25 specimens of immature stages of *D. scapha* deposited in the MRAC.

Keywords

Heteroptera • Reduviidae • Harpactorinae • description • nymph • SEM

Abstract ID: 38 • Abstract type: Poster

**DESCRIPTION OF THE IMMATURE STAGES OF *PSYTTALA HORRIDA* (STÅL, 1865) (HETEROPTERA:
REDUVIIDAE: REDUVIINAE)**

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The representatives of the genus *Psytala* Stål, 1859, are the largest known representatives of the subfamily Reduviidae (in terms of body size). Six species (according to Maldonado, 1990), distributed exclusively in Africa, have been described so far. Since individuals of *Psytala horrida* (Stål, 1865) (commonly called the horrid king assassin bug or giant spiny assassin bug) are breeding in our laboratory, and we have also found the immature specimens in the collection of the Muséum national d'Histoire naturelle, Paris, France, we decided to analyse the morphology of those specimens and describe the nymphs of each instar. For this purpose, we used a stereoscopic microscope and SEM techniques. Our studies allowed us to describe the development of wing buds, spike-like processes present on the body, fossula spongiosa, as well as present the distribution and morphological types of sensilla found on the body of the nymphs. The descriptions were based on about 40 specimens of immature stages of the above-mentioned species.

Finance

not applicable

Keywords

development of nymphs • SEM techniques • Reduviidae • morphology



Abstract ID: 41 • Abstract type: **Poster**

IS *EURYDEMA CYANEA* (FIEBER, 1837) (HETEROPTERA, PENTATOMIDAE, STRACHIINI) A GOOD SPECIES OR AN ALTITUDE VARIANT OF *EURYDEMA DOMINULUS* (SCOPOLI, 1763)?

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Reduction of insecticide and pesticide policies and the development of organic agriculture have led to an increase in damage caused by phytophagous true bugs for the last ten years. This is the case of cabbage bugs represented by several *Eurydema* species in Europe, especially in organic crops. In this context and with the aim of developing and integrating innovative methods for control of true bugs in vegetable crops, integrative taxonomy including barcoding proved to be the most relevant approach to characterise species of the genus *Eurydema*. The use of barcoding with the standard COI gene fragment (658 bp) revealed several unsuspected inconsistencies in that well-known genus. Among them, the specific status of *E. cyanea* and *E. dominulus* was questioned. Since its description, the specific status of *E. cyanea* has been well established. This taxon can be easily recognised by its unique entirely blue metallic dorsum while *E. dominulus* is red with black patches. *E. cyanea* is a mountainous species endemic to the Pyrenees and reported from France and Spain. *E. dominulus* is a Palearctic species widely distributed from France to Japan and Korea. Both species distributions overlap in the Pyrenees to the extent that these two pentatomids occur in the same humid biotopes, sometimes in mixtures. Barcodes of *E. cyanea* and *E. dominulus* from France and Europe are strictly identical and the use of other molecular markers (Cytb, 28S and ITS) confirms that result. However, there is some genetic variability up to 2% in *E. dominulus* comparing western European specimens (from France, Spain, Belgium and Germany) to specimens from Korea and China. In addition, we carried out morphological studies on genitalia as well as a preliminary study of morphometry with homologous points (landmarks) on 11 specimens of each species and did not find any significant difference. Matings between *E. dominulus* and *E. cyanea* were also observed both in the field and in the lab. A female of *E. dominulus* mating in the field with a male of *E. cyanea* was collected and laid living eggs in the lab. All descendants from this egg-laying reared to adults had a phenotype of *E. dominulus*. These preliminary results may question the taxonomic status of the species *E. cyanea* that could potentially be a high altitude-related colour variation of *E. dominulus*. Further studies involving a larger number of samples as well as sufficient controlled crosses over several generations would allow to conclude whether both species are interbreeding or not.

Keywords

Eurydema cyanea • integrative taxonomy • barcoding • *Eurydema dominulus*

Abstract ID: 53 • Abstract type: **Poster**

PHYLOGENETIC RELATIONSHIPS INSIDE RIFFLE BUGS (*RHAGOVELIA ANGUSTIPES* COMPLEX, VELIIDAE) COMBINING: MORPHOLOGY AND MORPHOMETRICS

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The *Rhagovelia angustipes* complex is a group of riffle bugs found in the surface film of freshwater, and marine aquatic ecosystems (Andersen, 1982; Moreira, 2015). This complex has been extensively studied in the Neotropical region (Bacon, 1956; Polhemus, 1997; Padilla-Gil & Moreira, 2013; Moreira, 2015), however, have presented problems in taxonomy due to high intra-specific variability (Galindo-Malagón et al. 2021), and until the moment no hypothesis has been proposed on the internal relationships of this complex. Our objective was testing the morphological variability of the species belonging to the *R. angustipes* complex in order to adequately distinguish the biological species that have been identified by means of traditional taxonomy. We analyzed variation of the characters and performed a phylogenetic analysis of a combined matrix of linear measurements, geometric configurations, and discrete characters. We studied specimens from six entomological collections and selected wingless males to avoid the effects of changes in shape because of sexual dimorphism, in total, 114 individuals belonging to 14 defined species were included, and analyzed the variation of characters and performed a phylogenetic analysis of a combined matrix of linear measurements, geomètric configurations, and discrete characters. We found that the linear characters of head length, metanotum length, femur width, and geometric morphometry of the head, anterior tibia, posterior femur, and abdomen are important in delimiting the species of the complex, as evidenced mainly in morphologically close species such as *R. tantilla*, *R. angustipes* and *R. molanoi*. In the phylogenetic reconstruction we found that the relations of the salina group were recovered for three of the four species evaluated (*R. nuqui*, *R. plumbea* and *R. tintipan*), with the exception of the species *R. colombiana* which was found to be more closely related to the species *R. calceola* and *R. calopa*. In the case of the bisignata and hambletoni groups, these could not be recovered in the phylogenetic reconstruction from the variables evaluated. This is why it is necessary to evaluate other characters that allow us to establish the internal relationships of the species of the complex. Furthermore, morphometric techniques proved to be an important tool in the taxonomic resolution of species complexes.

Keywords

Integrative taxonomy • traditional morphometrics • geometric morphometrics • Gerromorpha



Abstract ID: 54 • Abstract type: **Poster**

PHYLOGENETIC RELATIONSHIPS WITHIN EUTRICHOPHORA AND PYRRHOCOROIDEA (HEMIPTERA: HETEROPTERA) INFERRED FROM THE MORPHOLOGY OF METATHORACIC SCENT EFFERENT SYSTEM, ABDOMINAL VENTRITES AND TRICHOBOTHRIA

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Eutrichophora forms a diverse, well-supported clade within pentatomomorphan true bugs, consisting of the superfamilies Coreoidea, Lygaeoidea and Pyrrhocoroidea. However, the precise phylogenetic relationships among these taxa are unclear. Previous studies proposed four mutually conflicting hypotheses, each supported by several molecular and/or morphological datasets. In our study, we focused on the comparative morphology of the external structures of the scent efferent system of metathoracic glands, including the microstructure of the metathoracic spiracle opening, and abdominal ventrites including their sensory organs (trichobothria). A cladistic analysis of 23 characters supported Pyrrhocoroidea as a sister-group to a clade consisting of Coreoidea + Lygaeoidea. Hyocephalidae were supported as the most basal group within the Coreoidea. Within the previously poorly studied Pyrrhocoroidea (of which we examined 64 genera, i.e. 90%), Larginae, Physopeltinae and Pyrrhocoridae were each well-supported as monophyletic but their relationships to each other and their internal phylogenies remained largely unresolved. In particular, no synapomorphies were found to support the monophyly of Larginae or any of its currently recognised tribes. Future studies of additional morphological (e.g., male and female terminalia, mouthparts, and wing venation) and molecular characters are therefore necessary to better understand the evolution of the Pyrrhocoroidea.

Keywords

Eutrichophora • Coreoidea • Lygaeoidea • Pyrrhocoroidea • morphology • phylogeny

Abstract ID: 59 • Abstract type: **Poster**

PHYLOGENY AND EVOLUTION OF BIG-EYED BUGS - REVIEW OF KNOWLEDGE AND RECENT ADVANCES (HETEROPTERA: LYGAEOIDEA: GEOCORIDAE)

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The lygaeoid true bug family Geocoridae, commonly known as big-eyed bugs, is a moderately species-rich but peculiar taxon both in terms of appearance and feeding habits. The family currently comprises nearly 290 species of 30 valid genera divided into 5 subfamilies, from which the nominotypical subfamily Geocorinae is the largest. Geocorid true bugs are distributed throughout terrestrial biomes of warm to moderate climate, and inhabit even extreme habitats, e.g. deserts and high mountains. Representatives of the family can be readily distinguished from other lygaeoids based on their large, kidney-shaped, often stylate eyes and the curved median portions of the intersegmental sutures between abdominal tergites 4/5 and 5/6 (Henry 1997). Due to their predaceous feeding habits (their prey mostly consists of aphids and thrips) multiple species became subjects of biocontrol research (Sweet 2000, Kóbor 2020). The relatively high proportion of flightless, short-winged members of limited dispersal ability makes them ideal candidates for studying faunagenetic processes. Both directions of research require a solid identification which is impeded by the taxonomic uncertainties and misconceptions resulting from superficial descriptions and diagnoses. Furthermore, phylogenetic relationships within the family are virtually unexplored. In the course of a review of the literature concerning the taxonomy and systematics of Geocoridae the following key areas of study were identified: 1) exploration of the relationships within the family; 2) revisiting the tribal classification of the subfamily Geocorinae proposed and elaborated by Montandon (1907, 1913) and Parshley (1921); 3) taxonomic revisions of the genera of Geocorinae with an emphasis on *Geocoris* and *Germalus*. All of these topics require a redefinition of the diagnostic characters of taxa at different ranks because it became apparent that the taxonomic errors and confusions can be attributed to the peculiar appearance of these bugs: a high number of descriptions and diagnoses, even among the more recent ones, are restricted to pigmentation patterns and easy-to-observe exoskeletal characters e.g., the general arrangement and gross morphology of the head, pronotum or hemelytra. A thorough study of materials from several collections and recent field collecting combined with novel morphological explorations of other heteropteran taxa resulted in revised definitions of the following key character systems: 1) head and appendages, 2) meso- and metathoracic wings, 3) exoskeletal structures of metathoracic scent efferent apparatus, 4) abdomen (sutures of tergites 4/5-5/6, abdominal trichobothria). A study of these character systems along with additional characters of smaller importance not only allow well-founded redefinitions of taxa at different ranks, but also enabled morphology-based phylogenetic reconstructions which provided support for previous systematic hypotheses, e.g. the non-monophyly of the genus *Geocoris*, or the presence of distinct evolutionary lineages within subfamily Geocorinae.

Keywords

Lygaeoidea • Geocoridae • big-eyed bugs • taxonomic revision • morphology • phylogeny



Abstract ID: 67 • Abstract type: **Poster**

FOSSILS SUPPORT IN CONSTRUCTING PHYLOGENY: A CASE STUDY IN ISOMETOPINAE (HEMIPTERA: CIMICOMORPHA: MIRIDAE)

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Currently, most phylogenetic analyses are based on sampling of extant groups, due to the fact that in many groups the fossil is rare and few fossils clearly provide the characters used for analysis; therefore, there have been few phylogenetic studies using fossils, and no study to understand how fossils affect the phylogenetic analysis, at least in Heteroptera. The plant bug subfamily Isometopinae provides the benefit for the comparison between the phylogenetic results, accommodating the relatively many fossil taxa described in amber inclusions and containing the fossil tribe (Electromyiommini). In this poster, we present the phylogenies of the Isometopinae based on 105 morphological characters: i) a single parsimonious tree for the fossils and extant taxa, ii) the Bayesian inference topology for the fossils and extant taxa, and iii) the parsimonious trees for the extant taxa only under the different weighting levels, showing the critical conflict. Brief discussions on the monophyly and the tribal relationships based on the preferred topology are presented

Keywords

Heteroptera • fossil • Isometopinae • Miridae • phylogeny

Abstract ID: 68 • Abstract type: **Poster**

MOLECULAR PHYLOGENY OF NABIDAE (HETEROPTERA: CIMICOMORPHA): INSIGHT INTO THE RELATIONSHIPS AND THE EVOLUTIONARY HISTORY

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Nabidae also commonly known as 'damsel bugs' is a small predatory family of Heteroptera with approximately two subfamilies, 20 genera and 500 species worldwide. This family and nabid members are well defined based on morphological characters (e.g., the presence of Ekblom's organ and scutellum trichobothria); however, internal relationships are still unclear and controversial. Particularly, there has been no consensus of the generic and subgeneric concepts which were presented and used by the previous authors. In this presentation, the first phylogenetic analysis is presented based on the molecular data. The major issues, the monophyly of the Nabidae and its subgroups, and the tribal and generic relationships are briefly presented and discussed. Additionally, an evolutionary history based on the divergence time estimation using molecular dating is presented.

Keywords

Heteroptera • Nabidae • phylogeny • molecular • evolution



Abstract ID: 69 • Abstract type: Poster

THE GUESTS FROM THE PAST: INTRODUCTION OF THE RECENTLY DESCRIBED AND THE UNDESCRIBED FOSSIL MIRIDS (HETEROPTERA: CIMICOMORPHA)

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Describing fossils is important not only to explore the ancient morphology and the relationships among both ancestors and extant groups, but also to provide the fundamental data used for the various analyses such as molecular dating. The largest family Miridae also has a high proportion of described fossils to date, apart from the undescribed fossils. Among the fossils, the amber fossils in general show the morphology in a high quality, which facilitates deeper relevant research. In this presentation, several mirid fossils which have been studied and undescribed are presented including the recently described species, *Electromyiomma herczeki*. The brief taxonomic information of the studied fossils is also provided.

Keywords

Heteroptera • Miridae • taxonomy • fossils • amber

Abstract ID: 72 • Abstract type: Poster

TESTIS FOLLICLES IN THE MIRIDAE: IS THERE ANY PHYLOGENETIC SIGNAL?

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The number of testicular follicles and ovarioles provides valuable data for taxonomy and phylogeny of insects. Among true bugs, the number of follicles per testis varies from one to eight, with seven follicles being modal and probably the ancestral state in Heteroptera in general (found in over 36% of studied species). The number of ovarioles per ovary varies from two to 24 and the number seven clearly prevails being found in 48% of studied species. Although data are available for all infraorders except Enicocephalomorpha, more than 60% of studied species belong to the Cimicomorpha. The number of follicles (and, to a lesser extent, ovarioles) has been extensively used as a potentially important character for the higher-level taxonomy and phylogeny of the family Miridae. In total, data on ca. 300 species (less than 3%) are currently available. Eight subfamilies and 39 tribes are generally recognized within the Miridae, and data for many of these taxa are clearly insufficient due to sampling bias. Available data for better-studied taxa shows a stable pattern of follicle numbers at the tribal and sometimes subfamily levels. In Dicyphini, a sister clade to the remaining Bryocorinae, the presence of a single follicle per testis was documented for all 27 examined species from four genera. The same appears to be true for the monotypical tribe Felisacini (two species examined). The modal number of one was observed in the small tribe Bryocorini. Seven examined species of Monaloniini have either one or three follicles per testis, while the largest tribe Ecritotarsini remains almost unexamined. Forty-three examined species of the largest tribe Orthotylini (Orthotyliinae) have two follicles per testis. In the tribe Halticini (Orthotyliinae), the follicle number ranges from one to three. Almost all species (>50) of the large and diverse tribe Phylini (Phylinae) have a remarkably stable follicle number of three. The modal number for the tribe Pilophorini is also three but only four species from the genus *Pilophorus* were studied to date. In the tribe Deraeocorini (Deraeocorinae), the follicle number ranges from one to eight and no apparent pattern could be established at this point. Among the Mirinae, the largest and the best-studied plant bug tribe (>70 species examined), Mirini unequivocally show seven follicles. Stenodemini, the second well-examined tribe (>30 species), which forms a sister clade to all other tribes of the family, also have the modal number of seven. However, stenodemines demonstrate an exceptionally high diversity of follicle numbers ranging from one to eight. Various authors documented contrastingly different numbers for different species of the genus *Stenodema* (from three to seven). These and some other patterns will be discussed during the talk.

Finance

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Abstract ID: 73 • Abstract type: **Poster**

TRUE BUGS UNDER MASTODON LEGS – THE FIRST FOSSIL HETEROPTERA RECORDS IN BULGARIA

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The first fossil Heteroptera of Miocene age and also the first fossil Naucoridae and Largidae discovered in Bulgaria are reported. The fossils were discovered in a diatomite complex from the middle Miocene in the Rhodope mountains. The presence of Largidae family suggests a warm-temperate to subtropical climate at this time, warmer than the present one in the Rhodope mountains. This fact well corresponds to the paleofloristic composition, which is closest to the present day “evergreen broadleaved forest” and “mixed semi-evergreen forest” of Southeast Asia and distinguishes Satovcha Basin from other Middle Miocene-age deposits on the Balkans.

Keywords

Heteroptera • Middle Miocene • Rhodope mountains • diatomitic clays • Balkan Peninsula

Abstract ID: 74 • Abstract type: **Poster**

NEW DATA ON THE KARYOTYPE AND THE MALE REPRODUCTIVE SYSTEM OF THREE INVASIVE ALIEN TRUE BUGS (HETEROPTERA)

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Invasive alien species (IAS) are considered as the second major threat for European biodiversity. Very often the problems caused by IAS and the analysis of their impact are the reason some of their biological peculiarities are largely neglected. Here the first results of karyological studies of three of the most important IAS true bugs in Europe – *Corythucha arcuata* (Tingidae), *Leptoglossus occidentalis* (Coreidae) and *Halyomorpha halys* (Pentatomidae) are presented. The karyotype of *H. halys* was determined as $2n=12+XY$ (male). The testes were covered with a red membrane and it was difficult to distinguish the follicles in the testis. The colorless ovaries consisted of 7 ovarioles each. The karyotype of *L. occidentalis* was determined as $2n=18+2m+X$ (male). The testes were very large, covered with a red membrane and with 7 follicles each. Females of this species were not examined. The testes of the third species *C. arcuata* had two elongated follicles per testis and the karyotype of this species was found to be the same as in the majority of the lace bugs examined – $2n=12+XY$. Information about the distribution of the AT- and GC-repeats in the heterochromatin of these species is discussed. All these species could be serious pests in various European countries and threatened habitats and any additional information about them could be important.

Finance

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Abstract ID: • Abstract type: **Poster**

HETEROPTERAN TYPE SPECIMENS (HEMIPTERA, HETEROPTERA) IN THE JORDI RIBES' COLLECTION, DEPOSITED IN THE CENTRE DE RECURSOS DE BIODIVERSITAT ANIMAL

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The Faculty of Biology of the University of Barcelona lodges the CRBA (Center of Animal Biology Resources), which is responsible for the preservation of important animal collections. Among them outstands Jordi Ribes's Heteropteran collection, one of the largest and most significant personal collections of Iberian and Macaronesian True bugs, consisting of 27,851 specimens belonging to 2,991 species and subspecies. They belong mainly to Palearctic taxa, with a high representation of Iberian and Macaronesian endemics from many families, but the number of taxa from other bioregions is not negligible. The collection information was digitalized and can be consulted in the online database of the CRBA website (<https://www.ub.edu/portal/web/crba>). In addition, either J. Ribes also left a large number of Ibero-Macaronesian, Palearctic, Ethiopian, Neotropical and Oriental specimens unstudied, in the form of prepared specimens, or unprepared stored in boxes protected with loose cotton plates. The total number of unprepared specimens is countless.

In the whole of the J. Ribes collection stand out 187 type specimens. Among these, there are 44 species and 1 subspecies described by J. Ribes as author or co-author, out of the 59 taxa described by him, of which 51 are currently valid.

In the present work, we fully catalogue the 45 type specimens described by Ribes, providing the following information: name of the taxon, the author's name and year of description, bibliographic reference and page containing the original description, list of all type specimens, all of them identified with the CRBA collection code, and the details on location, date of capture and the author of the same. Moreover, the picture on dorsal habitus of all 45 type specimens are included. Per families, distribution of J. Ribes' described species type specimens is as follows: Anthocoridae (1), Artheneidae (1), Lygaeidae (1), Microphysidae (2), Miridae (29), Pentatomidae (2), Reduviidae (3), Rhypariochromidae (2), Tingidae (4). By biographic areas, 25 are Iberobaleaic species, 15 are Macaronesian, 3 are Paleotropical and 2 are Asian (Indonesia | Iran).

Moreover, we list also the 152 type specimens from species not described by Ribes, received from his numerous colleagues and friends. In this case, a code indicating which type are preserved in the CRBA collection (allotype, holotype, etc.) is only given. Distribution of these types per families is as follows: Aradidae (2), Artheneidae (1), Belostomatidae (1), Berytidae (1), Corixidae (1), Cydnidae (2), Cymidae (1), Lygaeidae (3), Miridae (87), Nabidae (1), Pentatomidae (8), Piesmatidae (1), Plataspidae (1), Reduviidae (5), Rhopalidae (2), Rhyparochromidae (11), Saldidae (2), Scutelleridae (2), Tingidae (17), Veliidae (3). In the list, 35 different names appear as donors, which witnesses the very good personal reports that J. Ribes kept with all Heteropterists, mainly those working in Europe.

Keywords

Type specimens • Jordi Ribes • collection • taxonomy

Abstract ID: • Abstract type: **Poster**

THE TYPE SPECIMENS OF HETEROPTERA (HEMIPTERA) DEPOSITED AT THE MUSEO NACIONAL DE CIENCIAS NATURALES, MADRID

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The Museo Nacional de Ciencias Naturales (MNCN, Madrid) is responsible for the preservation of important animal collections. Among them outstands Heteropteran collection, one of the largest and most significant collections of Iberian and Macaronesian True bugs, consisting of ca. 60.000 specimens belonging ca. 3000 species and subspecies. They belong mainly to Palearctic taxa, with a high representation of Iberian and Macaronesian endemics from many families, but the number of taxa from other bioregions is not negligible. In addition, a large number of Ibero-Macaronesian, Palearctic, Ethiopian, Neotropical and Oriental specimens unstudied, in the form of prepared specimens, are also preserved.

In the whole of the MNCN Heteroptera collection stand out 112 type specimens, which we fully catalogue in the present work. For each type specimen, the following information is provided: original name with author and year of publication, current placement of the nominal taxon, and if necessary the reference to its synonymy, reference of description, original type status, number and sex of types, and type locality as given in the original description, information about the primary type, if necessary including reference to lectotype designation, type locality according to the labels, including country and if changed, current name of the locality, and information on secondary types. Moreover, some types in the Entomology collection of the MNCN bear two different numbers: "MNCN Cat. Tipos No." identifies with one number all specimens of a type series housed in the MNCN. "MNCN_Ent ..." is the individual number for each specimen. The catalogue is systematically arranged until family level, and alphabetically for genera and species.

Moreover, the picture on dorsal habitus of all type specimens are included. Per families, distribution of the MNCN collection described species type specimens is as follows: Alydidae (1), Anthocoridae (1), Aphelocheiridae (3), Aradidae (1), Ceratocombidae (1), Coreidae (8), Cydnidae (3), Largidae (2), Lygaeidae (5), Miridae (16), Ochteridae (1), Pentatomidae (15), Plataspidae (3), Reduviidae (28), Rhopalidae (2), Rhyparochromidae (3), Saldidae (1), Tessaratomidae (1), Tingidae (14), Urostylididae (1), Veliidae (1). By biogeographic areas, 25% are Iberobaleaic species, 7% are Macaronesian, 50% are Paleotropical, 7% are Neotropical, and the remaining 14% belong to other biogeographic areas. In the list, 33 different names appear as authors, of which three names stand out: García Varela, who contributes with 23 new species mainly from the paleotropics, Bolívar who contributes with 13 type species mainly from the Iberobaleaic fauna, and Horváth, with 11 type species from several biogeographic areas.

Keywords

Type specimens • entomology collection • taxonomy • Natural History Museum



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