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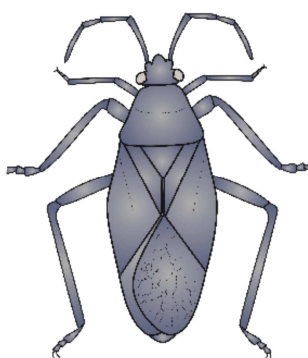
UNLP | Facultad de Ciencias Naturales y Museo

2018
VOL. 3, NÚM. 1, SUPLEMENTO RESÚMENES

PROCEEDINGS OF THE SIXTH QUADRENNIAL MEETING OF THE
INTERNATIONAL HETEROPTERISTS' SOCIETY
(3rd- 7th December 2018, Museo de La Plata, Argentina)



**PROCEEDINGS OF THE SIXTH QUADRENNIAL MEETING OF
THE INTERNATIONAL HETEROPTERISTS' SOCIETY**



3RD – 7TH DECEMBER 2018, MUSEO DE LA PLATA, ARGENTINA

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Heteropteran Phylogeny: What do we know?

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Phylogenetic relationships in the Heteroptera and their relationship to the classification of the group are reviewed. Major contributions to understanding the Heteropteran tree of life using cladistic methods over the last 40 years are emphasized. Most studies, using morphological and molecular data, support the monophyly of the seven infraorders as reviewed by Štys and Kerzhner in 1975. Varied schemes of relationships among infraorders are reviewed, indicating support by the preponderance of data for the hypothesis (Nepomorpha (Gerromorpha (Dipsocoromorpha + Enicocephalomorpha) (Leptopodomorpha (Cimicomorpha + Pentatomomorpha))). Multiple Nepomorpha schemes support Nepoidea as sister to other true water bugs, but other relationships within the infraorder remain unsettled. The early hypothesis of Andersen for relationships within Gerromorpha receives continued support with the exception of veliid paraphyly. Dipsocoromorpha are undergoing a descriptive and phylogenetic revolution at the moment, whereas Enicocephalomorpha classification has been little influenced by cladistic methods. Leptopodomorpha, well represented in the fossil record, have been repeatedly corroborated as the sister group of Terheteroptera (Cimicomorpha + Pentatomomorpha), forming the Geoheteroptera. Most studies corroborate cimicomorphan monophyly; significant questions concerning relationships with the group are discussed. The relationship Aradoidea + Trichophora is highly corroborated. Most studies recognize the trichophoran superfamilies Idiostoloidea, Pentatomoidea, Pyrrhocoroidea, Coreoidea, and Lygaeoidea, but many details require further study and clarification. Fossil evidence offers varying amounts of evidence across the infraorders concerning ages, diversity, and relationships. Possibly most perplexing is the Jurassic record for fossil families such as Pachymeridiidae, Probascaniidae, and Protocoridae, known primarily from Western Europe. These, some of the oldest heteropteran fossils, have been assigned to the Trichophora by many authors, imputing great age to the group, but without evidence for their possession of any of the defining characters seen in the Recent fauna.

ORAL CONFERENCES

Niche shift of the invasive pest *Bagrada* bug: a global threat to agricultural systems from now to the future

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It has been widely accepted that an accelerated global warming is in fact happening. Substantial alterations are expected in the near future on biological composition, phenology, and species range, affecting species interactions and ecosystems processes. The painted bug, *Bagrada hilaris* (Burmeister, 1935) is native to eastern Africa, Middle East, and South Asia. Currently, the painted bug spread out to other continents, as Europe and America. *Bagrada hilaris* is an invasive species and its distribution has increased every year towards warm and dry regions. It is considered a pest crop, causing damage mainly on Brassicaceae. Our aim was to estimate the potential worldwide distribution using models based on occurrence data of *B. hilaris*, and also to predict the future potential distribution using different scenarios on global warming. Two database were built for *B. hilaris*, one for native distribution, and a second for invasion records. Both were compiled from primary literature and the Global Biodiversity Information Facility. We used ecological niche modelling (ENM) on the native dataset to access the potential worldwide distribution of the species in current climate scenario. The native model failed to predict the invasive occurrence in USA and Chile. Therefore, we investigated niche shifting comparing the range of environmental variables for both native and invasion datasets using the Wilcox tests and boxplot graphics. We merged native and invasion datasets to predict species distribution in the current and two different future climate scenarios. Environmental layers were gathered from Ecoclimate public dataset, and six uncorrelated layers were selected. According to the ENMs the painted bug presents high suitability to invade most part of continental Europe, Australia, USA (South, Midwest and Northeast), and southern South America. The modeled future scenarios are quite similar to the current one, slightly increasing environmental suitability on warm and dry areas. The climate niche of *B. hilaris* has shifted on invaded continents relative to native range. It indicates a significant realized niche plasticity, or rapid evolution. The unfilled observed geographic range may occur as a result of a non-equilibrium situation, such as recent colonization of a landscape. Once the invasion records are increasing every year, we expect from now to the future these environmental suitable areas free of painted bugs become invaded. Brassicaceae crops are grown and traded across the world, so we warn high-suitable countries to this global threat not only for their agricultural but also their natural systems.

Phenotyping of *Trissolcus basalis* strains, Egg Parasitoids of Pentatomidae, in context of Augmentative and/or Classical Biological Control

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The Family of Pentatomidae (Heteroptera) encompasses numerous species which are considered as significant or even major pests for various crops. With regard to societal expectations and environmental policy towards the reduction of pesticides in France (Ecophyto Plan) and Europe, the development of biological control strategies is required. In France, such initiatives are currently implemented against two native pests, *Nezara viridula* (Linnaeus, 1758) and *Eurydema spp.* (Laporte, 1833), as well as the exotic Black Marmorated Stink Bug (BMSB), *Halyomorpha halys* (Stal, 1855). In this context, DNA-Barcoding approaches were used to characterize the natural biodiversity of their egg parasitoids. Furthermore, we started to evaluate the biology of potential BCA candidates with a particular emphasis on the possibility of mass production, a key for parameter for augmentation or even classical biological control. Using a cross-rearing experiment, we thus more precisely compare how fresh eggs of *N. viridula* and frozen eggs of *H. halys* can influence the phenotype of a *Trissolcus basalis* (Wollaston, 1858) strain. *A posteriori*, we evidenced complex results. While the development in BMSB seems to improve some physiological traits with regard to *N. viridula*, the opposite trend is observed for some behavioural traits. Moreover, a transgenerational effect was observed, the development of the mother's parasitoid influencing the phenotype of this latter. In conclusion, if frozen eggs of BMSB can be used as a substitution host for the routine rearing of our *Trissolcus* strain, some vigilance must be kept to maintain a high productivity in the rearing and the efficiency towards the targeted pest.

Comparative phylogeographies of five widespread species in East Asia (Insecta: Hemiptera: Heteroptera)

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The phylogeographic patterns of five widespread East Asian heteropteran species including *Acanthocoris scaber* (Coreidae), *Amphiareus obscuriceps* (Anthocoridae), *Gerris latiabdominis* (Gerridae), *Halyomorpha halys* (Pentatomidae) and *Microvelia douglasi* (Veliidae) have been

studied based on the combined molecular and distribution data. The results indicate that phylogeographic structures of native populations in the mainland of East Asia of two invasive species *A. obscuriceps* and *H. halys* exhibit homogeneous structures and possess strongly dispersal abilities. The deeply genetic divergence between island and mainland populations for the two invasive species might be due to the Pleistocene sea level fluctuation and repeated exposure and submergence of land bridges. In contrast, the heterogeneous phylogeographic structures are found in the three non-invasive species, *A. scaber*, *G. latiabdominis* and *M. douglasi*, in East Asia, which possess moderately dispersal abilities. The coincident lineages of southwestern China for these three species are probable shaped by the isolations of Hengduan mountains and local environmental adaptations. The demographic dynamics of these five widespread species in East Asia all exhibit "pre-LGM expansion mode" and are in accord with common conclusions from East Asian vertebrates, which is distinctly different from "post-LGM expansion mode" of organisms in Western Europe and North America in North Hemisphere. We suggest that the unique demographic history of East Asian organisms may underwent a relatively long and mild climate since the Pleistocene, and also may be due to most area of East Asia was not covered by large-scale ice sheets since the LGM.

Hidden diversity in Discocephalinae (Pentatomidae)

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Discocephalinae groups about 80 genera occurring mainly in the Neotropical Region, whose real diversity remains to be described. The subfamily is divided into two tribes, Discocephalini and Ochlerini, differentiated especially by the general coloration and the tarsal structure of the females. The discocephalines feed on phloem, and the best studied species are related to phytosanitary issues in cacao, coconut and palm trees plantations. Aspects of discocephaline biology, behavior, and ecology are little known, and there are few studies describing maternal care and trophobiosis with ants, and reports associating the discocephalines with litter in forests. These are among the many challenging and fascinating subjects in the study of Discocephalinae.

Funding: CNPq 307204/2015-4

Cladistic analysis and character evolution of the thread-legged bugs of the tribe Metapterini Stål, 1859 (Hemiptera, Reduviidae, Emesinae) based on morphological characters

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Metapterini Stål, 1859 is a worldwide tribe of Emesinae, with 28 genera and approximately 280 described species. Wing polymorphism is common, with a large proportion of genera with micropterous and apterous individuals; besides some genera are associated to spider's webs. The first phylogenetic hypothesis for the tribe was proposed by Wygodzinsky (1966) and it put forward Deliastini as the sister-group of Metapterini, based on the reduction of the eye size and the loss of M-CU cross vein on the hind wing, but this hypothesis was never tested with cladistic approaches. Recent studies analyzing characters' sets of male and female genitalia, and prolegs, suggested that Metapterini might be paraphyletic. In this study a morphological data set that includes external morphological characters, detailed features of the prolegs, and the genitalia of both sexes for Metapterini was analyzed cladistically for the first time: 132 characters and 53 terminals, comprising 24 genera-level taxa, 41 species of Metapterini and 12 outgroups, was examined and included in the analysis. The analyses were conducted in TNT using parsimony as optimality criterion, with characters under equal weights and implied weighting; the analyses implemented sectorial searches combined with ratchet and tree-drifting algorithms. As a result, Metapterini was recovered as paraphyletic by the inclusion of *Bergemesa*, *Stalemesa* and *Palacus*, assigned to Deliastini, as sister-group to the Barce group. *Gardena* (Emesini) is recovered as sister-group of Metapterini+Deliastini as suggested by Wygodzinsky (1966). The close relationship of the exclusively Neotropical genera *Ghilianella*, *Ghinallelia*, *Emesella* and *Liaghinella*, was previously suggested due to genitalic and proleg characters and confirmed in this study. Based on these results, we synonymize Deliastini with Metapterini *sensu nov.* Ancestral state reconstruction of wing polymorphism indicates that males and females were fully winged in the ancestor of Metapterini *sensu nov.* with several evolutionary transitions to male and female apterous and brachypterous groups, within the clade. The asymmetric male genitalia appear several times in Emesinae and within Metapterini, the asymmetry in the phallus occurs in two structures: in the dorsal phallosclerite at its apex or at the lateral regions, and on the endosoma, in which the endosomal sclerites are arranged in an asymmetrical pattern. The ancestral reconstruction shows an ancestor with symmetric male genitalia and two independent emergences of asymmetric male genitalia.

Paraguay: overlooked and under collected: results of collecting expeditions in 2016 and 2017 – Pentatomoidea (Hemiptera: Heteroptera)

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Historically, Paraguay has been poorly collected for Heteroptera (and perhaps other insect orders) and is not well represented in revisionary and faunal studies. This is a report on the results of two collecting trips, one each in 2016 and 2017 for a total of five weeks. One hundred and fifty-eight species of Pentatomoidea were collected. Of these, 118 were identified to species and 54 (46%) had not been reported previously from Paraguay. In addition, 40 species could not be identified to species and many of these are probably not known from Paraguay. The families collected (and number of species in each) were as follows: Pentatomidae (102), Thyreocoridae (20), Cydnidae (18), Scutelleridae (17), and Megarididae (1). The families Acanthosomatidae, Canopidae, Dinidoridae, and Tessaratomidae were not represented in any of my collections, but probably occur in Paraguay. There are six ecoregions in Paraguay. The Atlantic Forest in the eastern part of the country, Dry Chaco in the west, and Humid Chaco in the central and southern part of the country constitute the majority of the land area. There are small areas of Pantanal and Cerrados in the north and Mesopotamia Grasslands in the south. The areas sampled on collecting trips were primarily the Atlantic Forest and Humid Chaco regions. Total number of species collected per ecoregion and number collected only in that ecoregion, respectively, were Atlantic Forest (107, 43); Humid Chaco (85, 23), Cerrados (39, 16), Dry Chaco (13, 9); and the Mesopotamia Grasslands (6, 0). Collecting in the Dry Chaco was difficult with temperatures approaching 46°C and swarms of mosquitoes and we were not able to run lights in this area, but 69% of the 13 species collected there were found only in that region, suggesting that further collecting in this area is warranted. Beating and/or sweeping was the most productive collecting method (88 species), followed by lights (72 species) and fish carrion butterfly traps (22 species). There were a few species found exclusively on their host plants, specifically *Agonosoma* and *Chelycoris* species on *Croton* spp. and *Semilliserdia aciculate* Fortes and *Grazia* and *Marghita crepuscula* Ruckes on bamboo at night. Cydnidae and Chlorocorini are groups primarily collected at light, while broad-headed discocephalines were exclusively beaten from woody vegetation and Thyreocoridae were mainly collected sweeping. These results suggest that Paraguay offers an excellent opportunity for collecting and expanding our knowledge of Pentatomoidea and other groups and should be a focus of continued faunal studies.

Rostrum Length versus Stylet Penetration Potential

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Stink bugs (Hemiptera: Pentatomidae) and related species continue to plague cotton (*Gossypium hirsutum* L. [Malvales: Malvaceae]) and other high value crops worldwide. Stink bugs utilize their stylets (housed within the rostrum) to feed upon cotton bolls and transmit pathogens that cause seed and boll rot of cotton. Stylet penetration potential of stink bugs is influenced by species and recent observations indicated a phenomenon where stink bugs with shorter rostra yielded deeper stylet penetration estimates. The objective of this study was to elucidate the relationship between rostrum length and known stylet penetration estimates for two pairs of pentatomid species: *Chinavia hilaris* (Say) versus *Euschistus servus* (Say), and *Oebalus pugnax* (F.) versus *Piezodorus guildinii* Westwood. For each species, individual rostral segments were measured to yield total lengths, and measurements were compared against known stylet penetration estimates. *Chinavia hilaris* and *P. guildinii* possessed longer rostra than *E. servus* and *O. pugnax*, respectively, yet *E. servus* and *O. pugnax* yielded deeper stylet penetration estimates. Deeper stylet penetration by species with shorter rostra can be attributed to differences in the lengths of rostral segments 1 and 2 between species. *Euschistus servus* and *O. pugnax* each had significantly longer rostral segments 1 and 2 than *C. hilaris* and *P. guildinii*, respectively. Also, the cumulative lengths of rostral segments 1 and 2 comprised a higher overall proportion of the entire rostrum length in *E. servus* and *O. pugnax* versus *C. hilaris* and *P. guildinii*, respectively. Rostral segments 1 and 2 are instrumental in the feeding mechanics of these phytophagous species, and it is clear that longer lengths for said segments and their role in stylet penetration model calculations override the presumption that total rostrum length equates to stylet penetration potential. This newly discovered phenomenon contributes to the general knowledge base of feeding mechanics and factors influencing stylet penetration potential among differing stink bug species.

Phylogenomic analysis of the Coreoidea (Hemiptera: Heteroptera) demonstrates non-monophyly of the families Coreidae and Alydidae

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The application of next-generation sequencing technologies (NGS) allows phylogeneticists to amass a wealth of genomic data from non-model species for phylogenetic resolution at various temporal scales. However, phylogenetic inference for many lineages dominated by non-model species have not yet benefited from NGS. One such lineage, whose phylogenetic relationships remain uncertain, is the diverse, agriculturally important, and charismatic Coreoidea (Hemiptera: Heteroptera). Given the lack of consensus on higher-level relationships and the importance of a robust phylogeny for evolutionary hypothesis testing, we use a large multilocus dataset comprised of hundreds of ultraconserved element (UCE) loci to infer the phylogeny of Coreoidea (excluding Stenocephalidae and Hyocephalidae), with particular emphasis on the largest families, Coreidae and Alydidae. We generated three datasets by including UCE alignments that contained at least 50%, 60%, or 70% of the total taxa, and inferred the phylogeny using maximum likelihood and summary coalescent methods. Twenty-six external morphological features previously used in relatively comprehensive phylogenetic analyses of coreoids were also re-evaluated within our molecular phylogenetic framework. We recovered 439–970 loci per species (16–36% of UCE loci targeted) and combined this with previously generated UCE data for 12 taxa (Kieran et al., in revision). Our 50%, 60%, and 70% taxon-complete matrices included 855, 504, and 284 UCE loci, respectively. All datasets, regardless of analytical approach, yielded topologically similar and strongly supported trees, with the exception of outgroup relationships and the position of Hydarinae. We recovered a monophyletic Coreoidea, with Rhopalidae highly supported as the sister group to Alydidae + Coreidae. Neither Alydidae nor Coreidae were monophyletic; the coreid subfamilies, Hydarinae and Pseudophloeinae, were consistently recovered as more closely related to Alydidae than to the other coreid subfamilies. Coreinae were paraphyletic with respect to Meropachyinae. In general, most morphological traits examined were homoplastic with a number of clades defined by few, if any, synapomorphies. Our results demonstrate the utility of phylogenomic approaches for resolving long-standing problems in phylogenetics and highlight that novel insights may come from such approaches. Additionally, we demonstrate that currently used morphological traits in coreoids, and possibly other groups, may need to be re-evaluated.

The brown marmorated stink bug (*Halyomorpha halys*) invasion in France: city bug or country bug?

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The invasion of *Halyomorpha halys* (Brown Marmorated Stink Bug, BMSB or HH), an Asian origin pentatomid, is now well established in France but remains very poorly documented. The lack of real interest of the public authorities, despite the reality of a threat elsewhere considered (in most European countries including Italy and now in Spain) and documented, the lack of natural knowledge and interest of insects in France are responsible for a very bad knowledge of how to install this species in France. The existence of an urban entomology program (CITYBugs) will make it possible to compensate for this obvious disinterest. It is motivated by the political will to manage cities towards a growing greening, even a real desire to reintroduce biodiversity in cities, including nature inspired urbanization. This program is supported by two permanent citizen inventories managed by INRA and MNHN / INPN (citizen science). The city of Paris, particularly affected by this invasion, wants to be a pioneer of this urban renewal, as part of the ecological transition. We present the first advances of this program, first intended to understand the urban ecology of HH, while comparing it with rural or quasi-natural situations in South of France. One of the objectives is also to establish rational management of populations of this species that can be used in cities that are or will be affected by the problem of this disconcerting species. The similarity of HH with other native species, complicates the situation and more than 10 % of the reports concern these species, mainly the nebulous stink bug, *Rhaphigaster nebulosa*, which in addition to a resemblance, seeks to return to the houses in the fall, sometimes as a group, just like HH. In addition, the American bug *Leptoglossus occidentalis* (Coreidae) is also invasive now in France.

Developmental and functional roles in the evolution of stink bug genitalia

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Male genitalia are among the most variable structures across animals with internal fertilization. The equivalent structures in females are considered more conserved. Yet, little is known about the mechanisms underlying these intersexual differences. One hypothesis is that male genital diversification is mostly determined by functional demands; male genitals would be composed of different subunits, representing targets of independent selective pressures that have more degrees of freedom to change. On the other hand, female genitals may be more evolutionarily constrained if their components are more integrated due to developmental limitations. Here, we determine the roles of functional morphology and development in shaping the evolution of male and female genitalia of pentatomids in a coevolutionary framework. We quantify the variation in both structures using geometric morphometrics and test between different models of modularity that represent two alternative scenarios. The first is a scenario where traits originated from a single structure in immatures evolve as semi-independent modules (developmental modularity). The second is a scenario where functionally integrated components evolve jointly and independently of the other components (functional modularity). We show that male and female genitalia, in spite of coevolving and being functionally complementary, are shaped by different factors. While male genital evolution is shaped exclusively by functional demands, female genitalia evolution is mostly determined by developmental constraints. We provide novel quantitative evidence of a persistent selective process favoring a mosaic modular architecture of genitalia in broad evolutionary scales. We also propose that functional diversity, in the absence of any type of constraints, may be a great facilitator of genital diversification.

Pentatominae checklist of the Neotropical Region (Hemiptera: Heteroptera: Pentatomidae)

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The family Pentatomidae encompasses a monophyletic group of true bugs (Grazia *et al.* 2008), representing the fourth largest family within Heteroptera and one of the most diverse groups of hemimetabolous insects. The pentatomids are known as stink bugs and green bugs, and contain about 940 genera and more than 4,900 species in the world (Rider *et al.* 2018). Nine (Grazia *et al.* 2008) or ten subfamilies (Rider *et al.* 2018) are recognized, half of them with restricted distribution. The Pentatominae is the most diverse subfamily in the Pentatomidae, containing 660 genera and 3,484 species (Rider *et al.* 2018). Its members occur worldwide. The classification within this

subfamily has been chaotic at best. The number of tribes recognized has varied dramatically from worker to worker and from eight to over 40 (Schuh and Slater 1995, Rider *et al.* 2018). Besides catalogs and checklists of some countries of the Neotropics have being published, including Pentatomidae (i.e. Argentina, Colombia, Venezuela, Puerto Rico) we assembled a checklist of Neotropical Region, Mexican Transition Zone, Andean Region, and South America Transition Zone (*sensu* Morrone 2002). Our main goal is to answer the following questions: 1. What are the current tribal and genus classification of the Pentatominae species found in the Neotropical region? 2. How many tribes, genera and species there are: World, America, Neotropics/Andean? 3. How many endemics in the Neotropical region? 4. How many genera and species are introduced to the Neotropics from other regions? 5. How many genera and species are shared between Neotropics and other biogeographical regions? 6. How many genera and species are shared between America North of Mexico and Neotropics? Also we provide the knowledge about the distribution of each species: number of genera, species and endemics per country; the number of records (countries), species and endemics per tribe and genus; the number of countries and species per author; and finally, the accumulation of species over time. The total number of species in the Neotropical region (Mexico+NT+AN) are 816 spp. being endemics in the Neotropics 696 spp.

Phylogenetic analysis of the strangest lacebug subfamily Vianaidinae (Heteroptera, Tingidae)

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Vianaidinae (Heteroptera, Tingidae) is a small group endemic to South America. Their morphology is highly modified and specialized and their presence in entomological collections is unusual. The group is currently composed by ten species, nine extant and one fossil. Six species are known from coleopteroid forms: *Anommatocoris coibensis*, *A. coleopteratus*, *A. minutissimus*, *A. zeteki*, and *Thaumamannia manni*, *T. vanderdrifti*. The three remaining extant species have fully-developed hemelytra: *A. bolivianus*, *Pterovianaida duckensis* and *P. melchiori*. The fossil species, *Vianagrama goldmani*, was described from amber in the late Cretaceous of New Jersey presenting remarkably different features. The coleopteroid forms were frequently found on soil or even associated with ants or ants' nests whereas the

macropterous forms in soil but in understory vegetation as *Anommatocoris bolivianus*, or on light traps indicating an active flight pattern, different from most tingids. In this study we present a phylogenetic analysis aiming to understand the phylogenetic relationships within Vianaidinae. Besides the nine known extant species, nine new species are also included in the analysis as well as two outgroups (*Cantacader quinquecostatus* and *Phatnoma marmorata*). A total of 32 morphological characters were analyzed based on external morphology. Only extant species were included in the analyses as the fossil material is not well preserved and most of the characters included in the analyses could not be observed. Five characters were included from the specialized literature while 27 were proposed as new. The parsimony analysis was conducted on TNT 1.5, using implicit enumeration. All characters were equally weighted and multistate characters were considered non-additive. Bremer was the support measure chosen. The analysis resulted in six equally parsimonious trees of 59 steps (CI = 0.66; RI = 0.87), and a consensus tree of 62 steps (CI = 0.62; RI = 0.85). The results indicate that all known genera are monophyletic, two of the new species are included in the genus *Thaumamannia*, five in *Anommatocoris* and two are recovered as a monophyletic clade constituting a new genus. *Thaumamannia* is the sister group of *Pterovianaida* and the new genus of *Anommatocoris*. The highest Bremer support value was in the *Anommatocoris* clade (Br = 7), followed by the *Pterovianaida* clade (Br = 3), the new genus clade (Br=2) and the *Thaumamannia* clade (Br = 1). Characters related to the thoracic scent gland support the most basal clade ((*Pterovianaida* + *Thaumamannia*) + (New genus + *Anommatocoris*)).

Systematics of Peloridiidae (Hemiptera: Coleorrhyncha) – an integrative approach

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Specimens of 21 species of Peloridiidae, a poorly studied hemipteran family of controversial systematic affinities, were collected in Australia, Chile and New Zealand. Their fine morphology, host plant ecology and bioacoustics were investigated, uncovering many previously unknown features. These data, along with some earlier information on cytogenetics or symbiont biology, were used in a phylogenetic analysis with 9 outgroup taxa from Sternorrhyncha, Auchenorrhyncha and Heteroptera. The hypothesis on intrafamilial systematics of the family delivered by the analysis coincides well with two previously published studies, except for the position of the genus *Peloridium* (although its placing is supported by some new data on molecular phylogenetics). Still, bioacoustic and behavioral data, although incomplete,

can change the position of the genus in the tree topology when integrated into the analysis. Among possible sister groups of Peloridiidae, Auchenorrhyncha received most support, although the characters supporting this grouping are not unambiguous and cytogenetic data strongly favors Heteroptera as the sister group of Peloridiidae. Generally, the necessity of an analysis on a much broader scale and with a richer outgroup sampling, integrating the new data set with the previously published ones, is obvious for clarification of the systematics of Peloridiidae/Coleorrhyncha.

Scanning electron microscopy as a tool for the systematics of Dipsocoromorpha

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Dipsocoromorpha, with little more than 400 described species, might include hundreds or even thousands of yet undescribed taxa and thus the highest cryptic diversity within the Heteroptera. Research on these bugs is challenging due to their cryptic habits, small size, wing polymorphism and paucity of systematic characters aside from their remarkable male genitalia. A good character should allow reliable recognition of conspecifics among different wing forms and sexes. In this study, scanning electron microscopy was applied to search for new systematic characters. The magnifications available with this method allow conclusions on the functions of minute structures and thus might lead to a deeper understanding of the character in question. Some preliminary results of the study are presented here, with examples of potentially useful characters such as the structure of the antenna, sclerotization of the abdominal tergites, labial sensilla etc.

Revision and Phylogeny of the Bryocorinae Genus *Caulotops* (Hemiptera: Heteroptera: Miridae)

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The previous concept of the plant bug genus *Caulotops* Bergroth as a widespread Neotropical genus of eccritotarsine Miridae that feed mostly on *Agave* spp. (Asparagaceae: Agavoideae), with the type of the genus (*Caulotops platensis* Berg) known only from Argentina, but with the majority of taxa occurring in North and Central America, is investigated. Study of the known U.S. and Mexican species and large amount of borrowed material, including that collected by Joseph Schaffner in Mexico, indicated that none of these taxa are congeneric with the disjunct Argentine type species. We, therefore, revised and analyzed in a phylogenetic context the species and generic limits of this diverse taxon. Based on our morphologically based phylogenetic analysis, *Caulotops* from Argentina is considered a monotypic lineage distinct from the species from Central and North America that were previously placed in *Caulotops* and are known to specialize on agaves and related Asparagaceae. Further, the northern hemisphere taxa comprise four distinct lineages, each of which is treated as a new genus. Herein we discuss the distinctive features of each taxon and their included species, distribution, unique morphology, and phylogenetic relationships with closely related Eccritotarsini.

On the status of the Heteroptera types deposited in the Museu Nacional, Quinta da Boa Vista, Rio de Janeiro

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On September 2, 2018, a fire tragically swept through the Museu Nacional in Rio de Janeiro, destroying all of the entomological holdings in the main building, including the entire Heteroptera collection that contained more than 900 primary types. By far the largest family represented was the Miridae with 747 holotypes comprised almost entirely of species described by the late Dr. José C. M. Carvalho, followed by 76 Tingidae all described by Dr. Oscar Monte, and 42 Reduviidae described largely by Dr. Peter Wygodzinsky. Prior to this great tragedy, we had developed a detailed list of 929 primary types, which included the original combination, author (s), date of description, page number, sex, verbatim label data, and a comprehensive bibliography. Because of various circumstances, publication of the list was delayed, and, subsequently, with the advent of new-generation camera equipment, a project to create high-quality color photographs of all types ensued. In this paper, we present an overview of the types known to have been deposited in the Museu Nacional, how many were photographed, and how many were lent out (and, therefore, saved). We now are stepping up our efforts to complete the type list with photographs of nearly all of the lost types by early 2019, which, eventually, will be made available online. Although we have some records of borrowed material, all official paperwork documenting loans was destroyed; thus, we put out a request to you, our colleagues,

to send us reports on what you have on loan, especially primary types, so that they also can be photographed and included in this important publication.

Assassins of the little red dot: species diversity and natural history of reduviids in Singapore

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Singapore is a highly urbanized tropical island that has already lost 95% of its original vegetation and less than 10% of its remaining green areas are primary forests. Despite its state of development and small size, Singapore still hosts an exemplary diversity of assassin bugs found in the Oriental Region. The first species checklist of assassin bugs for the city-state is generated here based on museum specimens, fieldwork and literature sources to provide a preliminary assessment of the local diversity. An online annotated identification key is constructed together with online species pages to help improve local taxonomic resources. In addition, the gathering of much-needed natural history data in the form of behavioral displays and dietary prey via NGS barcodes provides useful insights towards the ecological interactions and roles the assassin bugs play in the Oriental tropical rainforests.

The hemimetaboly of a museum and field explorations in Southeast Asia

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The Lee Kong Chian Natural History Museum, formerly known as the Raffles Museum of Biodiversity Research, re-opened its doors officially in a newly constructed facility in April 2015. While the inherited entomological collection is modest, the new lease of life has provided exciting opportunities for growth and collection-building. In our quest to pursue, develop and support biodiversity research, we have partnered with regional institutions to conduct field surveys in Singapore and neighboring countries. I share here a brief summary of recently concluded field work and field techniques in Southeast Asian tropical rainforests that may yield useful information for fellow heteropterists.

Phylogeny of the plant bug subfamily Mirinae (Hemiptera: Heteroptera: Cimicomorpha: Miridae) based on total-evidence

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The subfamily Mirinae is one of the largest groups in Heteroptera, with more than 4,100 described species worldwide. However, the monophyly and generic relationships of each group within the subfamily Mirinae have not been understood, due to the lack of phylogenetic analysis. In this talk, the first comprehensive phylogenetic analyses of the most diverse subfamily are presented based on a total of 85 morphological characters and molecular data (COI, 16S, 18S and 28S). Main results obtained in this study include monophyly of the tribe Mecistoscelini, paraphyly of the tribe Stenodemini, and polyphyly of the largest tribe Mirini. Major questions such as the relationships among the main clades and the evolution of important characters in each group are discussed.

Heteroptera of the Socotra Archipelago

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Socotra Archipelago is situated in the western part of the Arabian Sea and consists of the main Socotra Island (3,625 km²), two smaller islands of Samha (41 km²) and Darsa (10 km²), and the more detached Abd el Kuri (133 km²) which lies about 100 km southwest of the main island. All four islands are closer to east Africa (232 km) than to the Arabian Peninsula (351 km). The archipelago is of continental origin in east Gondwana. Socotra lies within boundaries of the monsoonal precipitation regime and harbours diverse vegetation from coastal mangroves, salt-marshes and sand dunes through sparse bush, woodland and succulent vegetation on slopes of mid elevations to cloudy evergreen forests high in the Hagher Mts. (1200–1550 m a.s.l.). There are about 843 species of vascular plants, including 15 genera and 311 species (i.e. 37%) regarded as endemic. Until recently 61 species of Heteroptera were recorded from the Socotra Island, classified in 52 genera and 22 families. Of this number, 1 genus (*Socantestia*) and 16 species (i.e. 26%) were considered endemic. Based on the recently acquired material the knowledge of Heteroptera of Socotra Archipelago has substantially increased. We currently register 209 species in 158 genera and 31 families, with high proportion of endemics – 12

genera and 61 species (i.e. 29%). Among the plant feeding Miridae and Tingidae the endemism reaches 52%. First data on host plants of the phytophagous Heteroptera are given; some species seem polyphagous, but some of the endemic Tingidae and Miridae were found to be associated with a single endemic plant taxon. First cases of probable adaptive radiations are documented in Miridae (e.g., seven endemic genera of Orthotylinae, *Volumnus* – 5 endemics, *Isometopus* – 3 endemics) and Tingidae (*Cysteochila* – 2 endemics on *Cissus*). From a zoogeographical point of view, most of the collected taxa represent the following elements: Eremian (Saharo-Sindian) element, followed by the Afrotropical (mainly in mountain forests) and Mediterranean (mostly in costal regions); minority of species has relations to Indian fauna.

An update on the phylogeny and classification of Phylinae, a hyperdiverse subfamily of plant bugs (Heteroptera: Miridae)

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Phylinae is the second largest subfamily of the hyperdiverse family Miridae containing ca. 40% of total family diversity. Phylogenetic studies of this group have long been hampered by its large size and uniformity in many morphological traits. Menard et al. (2014) analyzed extensive molecular and morphological datasets and provided a robust phylogenetic framework of phylinae interrelationships. This work resulted in the substantially revised suprageneric classification of the subfamily (Schuh & Menard, 2013) but left many genera incertae sedis due to inevitably incomplete taxon sampling. Aiming to get a better understanding of interrelationships within the subfamily, we updated the phylogeny of Phylinae by including molecular (COI, 16S, 18S, and 28S) and morphological (114 characters) data for 65 predominantly Palaearctic species. A total of 198 terminal taxa were included in our dataset and analyzed in MP, RAxML and Bayesian frameworks. Based on the obtained topologies we discuss the classification of the subfamily and morphological support of the major clades.

Integrative species delimitation in Nearctic ambush bugs (Heteroptera: Reduviidae): Insights from geometric morphometrics, molecules, and ecological associations

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Biodiversity cannot be accurately assessed without a resolved understanding of species boundaries. Species delimitation, the process of identifying species-level diversity and defining tangible boundaries between taxa, is central to this understanding and a fundamental component of evolutionary biology. Defining species as consistently and objectively as possible is crucial when classifying polymorphic taxa in which boundaries are less apparent. Ambush bugs, *Phymata* Latreille (Heteroptera: Reduviidae), represent a diverse assemblage (~109 spp.) of predatory true bugs in which species delimitation is confounded by intraspecific polymorphism, subtle interspecific differences, and sexual dimorphism. Recent phylogenetic research on Phymatinae has revealed that several widespread species are actually para- or polyphyletic. To improve understanding of bug biodiversity on the Tree of Life, *Phymata* taxonomy must first be revised and the crux involves identifying species boundaries within this genus. In this study, we focused our attention on a Nearctic group comprised of 11 closely related species and numerous subspecies. We used molecular species delimitation approaches, geometric morphometrics of the pronotum, and ecological host plant association data to tease apart the true evolutionary lineages and delimit species. Results from this integrative study provide a new, more objective foundation for the taxonomic revision of the group, which in turn, could bare important implications for evolutionary and ecological research that include these insects in their study systems.

An online catalog of Heteroptera from Argentina and Uruguay

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The rapid advances in cyber-infrastructure, bioinformatics, digital photography and information technologies contribute to an easy access to taxonomic knowledge and allow the generation of information at an incommensurate scale in accordance to the needs of the biodiversity crisis. Basic taxonomic knowledge, such as taxonomic literature, catalogs of scientific names, records of specimens, location of type specimens in biological collections, and interactive keys of various groups of organisms are now available through the Internet. However, up to now there is no single web portal that gathers information about the knowledge about the entomological biodiversity from Argentina. Here, we present a new web portal, which hosts author databases that provide lists of species/catalogs of insect names of different taxonomic groups, their distribution in Argentina, images, synonyms, most relevant literature, host plants, economic importance, conservation status, and/or sanitary relevance. Each catalog uses the software *Taxonian*, and can be viewed on cell phones and tablets, and can also be downloaded on personal computers and will serve as an identification guide in the field. Likewise, the new web portal will provide different global statistics referring to diversity, economic importance, conservation status, sanitary relevance and distribution of the set of catalogs included, and in addition, individual searches can be made among all the hosted ones.

We believe that having a site where the information of a set of insect catalogs converges, added to certain quality standards, as well as the possibility of constructing emergent statistics and searches of the whole, will constitute a very valuable and unprecedented tool for the knowledge of the insects' fauna from Argentina. We have developed one catalog about the Heteroptera from Argentina and Uruguay corresponding to 23 families (Reduviidae, Tingidae, Pentatomidae, Acanthosomatidae, Scutelleridae, Tessaratomidae, Dinidoridae, Megarididae, Largidae, Pyrrhocoridae, Coreidae, Rhopalidae, Berytidae, Blissidae, Colobathristidae, Cymidae, Geocoridae, Lygaeidae, Ninidae, Oxycarenidae, Pachygronthidae, Piesmatidae, and Rhyparochromidae). The catalog was compiled by our team through our own field work and from the available scientific literature. It contains more than 1,000 species, and it is in constant development, as updates are programmed to be every three months. In the future we will be adding more families to complete the inventory of the Heteroptera from Argentina and Uruguay.

Ecological niche modeling of *Gargaphia decoris*, potential biological control agent of *Solanum mauritianum* a problematic invasive alien plant

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Solanum mauritianum Scopoli is a perennial tree native to South America. It has invaded conservation areas, agricultural lands, forestry plantations and riverine habitats in Australia, the Cook Islands, Fiji, India, Kenya, Madagascar, New Caledonia, New Zealand, Papua New Guinea, Sri Lanka, South Africa, St Helena, Swaziland, Uganda and parts of the United States, including California, Hawaii and Florida. *Gargaphia decoris* Drake 1931 is a Tingidae native to Argentina and Brazil that has been introduced for the biological control of *S. mauritianum* in South Africa in 1999 and in New Zealand in 2009 after years of exhaustive laboratory tests and risk analyses. It was selected as biological control agent of this plant because it causes extensive foliar damage, it has a narrow potential host range and has exhibited very strong feeding and oviposition preferences for *S. mauritianum* in choice tests in the laboratory. In South Africa it has caused extensive damage to *S. mauritianum* during population outbreaks but it has been deemed an inefficient agent due to its sporadic fluctuations in population, in New Zealand its performance has been better being effective and constant through time. Originally cold winter temperatures were considered the cause for the low densities though currently predation is also considered a major feature constraining *G. decoris* populations. Ecological niche models (ENM) assesses the ecological requirements of a species based on its known occurrences and allows its distribution to be projected on different regions or on future climatological reconstructions. For Biological control studies this methodology can be of great help to recognize areas where an invasive species is present and a potential control agent has chances to successfully be introduced. Such information can be very valuable to determine the extent, cost and probability

of success of monitoring and control programmes. Hence, ENM is an important tool when defining strategies for the biological control of invasive species. This study aims to identify areas where *S. mauritanum* is considered a problematic invader and where suitable climatic conditions are found for the introduction of *Gargaphia decoris* as biological control agent; to investigate climate niche dynamics of *G. decoris* in the areas where it has been successfully introduced; and to generate a worldwide ecological niche model of *G. decoris* for future climates (period 2050) considering that most probably *S. mauritanum* will continue invading new regions in the future.

Morphological and genetic diversity of the green-belly stink bugs *Dichelops* spp. (Heteroptera: Pentatomidae)

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The green-belly stink bugs *Dichelops* spp. (Hemiptera: Heteroptera: Pentatomidae) are considered emergent pests in different cultivated plants in Brazil. The species *Dichelops furcatus* (Fabricius) and *Dichelops melacanthus* (Dallas) are morphologically similar, and the characteristics used for their recognition are mostly those of male and female genitalia. Such characteristics may exhibit within species variation, sometimes overlapping between them. These factors make the identification of these species difficult for non-specialists, and even the boundaries between those species may be questioned. To date, no quantitative analysis testing these morphological traits were carried out. Based on wide sampling of *Dichelops* spp., the goal of this study was to test the limits between *D. furcatus* and *D. melacanthus* using morphological and molecular data. Morphological discontinuities between the species were assessed through geometric morphometrics techniques of morphological structures (head, pronotum, scutellum, external male and female genitalia), while DNA data included the mitochondrial genes COI and 16S. Morphological data showed almost no signals of species separation; pronotum, head and scutellum were strongly overlapping, whereas male and female genitalia were partially overlapping. These results agree with previous comparative studies that show that male and female genital traits are the most rapidly evolving in pentatomids. In contrast, we found high genetic divergence between species, supporting the existence of two separate lineages and corroborating the taxonomic delimitation of these two species.

APOIO: FAPESP, CAPES, CNPq.

Disentangling the Australian *Lygus*-complex taxonomy using the comparative morphological and molecular phylogenetics approaches

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Lygus-complex is one of the most difficult groups within Mirinae. Currently it includes around 50 genera known from around the world and this number is growing. The genera are similar to each other externally and poorly defined. No revision or phylogenetic analysis for this complex exists to date. *Lygus*-complex is worldwide distributed, and fauna of tropical areas and Australia is far from being completely known. Before this project, five genera and nine species from this group have been known from Australia. As a result of the present work, two more genera, *Diomocoris* Eyles, 1999 and *Micromimetes* Eyles, 1999, and four species new to science have been added to this list. *Taylorilygus nebulosus* (Poppius, 1914), distributed throughout the continent, was transferred to *Diomocoris*. It has considerable variation in color and size, although, the structures of male and female genitalia are almost identical in all specimens examined. Four new species have been described for *Micromimetes*. Three genera, *Taylorilygus* Leston, 1952, *Diomocoris* and *Micromimetes*, are very similar to each other, distinguished mostly based on the male and female genitalia. The comparative morphological approach combined with the molecular-based phylogeny has been used to test whether those genera should be treated separately or there are any evidences for synonymy. The phylogenetic analysis is based on four markers: COI, 16S, 18S and 28S. We have added 21 genera from the *Lygus*-complex and representatives from all the Mirinae tribes. The analysis shows that the *Lygus*-complex is non-monophyletic and includes other Mirini genera with high support. *Micromimetes* and *Taylorilygus* form a clade with *Filicicoris* Namyatova & Cassis, 2016 with high support. *Diomocoris* is closer related to *Apolygus* China, 1941, *Neolygus communis* Knight, 1916 and *Ommatodema* Poppius, 1911. Specimens of *Diomocoris nebulosus* from the different Australian states were added to the analysis, no noticeable genetic variation has been found in this work.

***Leptoglossus clypealis* (Heidemann) (Heteroptera, Coreidae) a potential global invader: use of ecological niche modeling to predict possible current and future worldwide distributions**

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Leptoglossus clypealis (Heidemann) (Heteroptera, Coreidae), is a phytophagous true bug, native to the central and southern United States and northern Mexico. In the recent years it has rapidly expanded its distribution to the middle of United States toward to the east coast, and from the southeastern of Canada to south of Mexico. It has been reported feeding on several crops, most of them with economic importance like *Helianthus sp.* (sunflower), *Phaseolus vulgaris* L. (beans), *Pistacia vera* L. (pistachio), *Prunus dulcis* (Mill.) D. A. Webb (almond) and *Solanum tuberosum* L. (potato). It represents a serious agricultural problem and currently it has pest status. Within this genus there is another species with similar characteristics that has been considered for a long time a major pest, *L. occidentalis*, and that has become a highly successful worldwide invader. The recognition of possible susceptible areas to be invaded is an important step to establish suitable management programs such as the development of biological control solutions, or of strategies for understanding invasion pathways and preventing new accidental introductions. The identification of areas climatically suitable for the establishment of invasive species offers a great opportunity for preventing or slowing invasions. These areas can be recognized through the development of ecological niche models (ENM), which identify the climatological requirements of a species based on its known distribution and allows the recognition of similar conditions on different regions or time periods. Thus, the information provided by ENM should be considered when defining strategies for the containment of invasive species. The aims of the present study are: to compare the climatic niche of *L. clypealis* and *L. occidentalis* in order to determine if a similar pattern of expansion could be expected in *L. clypealis*; to identify climatically suitable areas for the establishment of *L. clypealis* worldwide; to explore if *L. clypealis* occurs in regions where the climatic conditions are different to the ones in its native range to evaluate if it could be expected its establishment in regions with different climates; to generate ecological niche models projected to future climate reconstructions (period 2050).

The Genus *Leptoscelis* Laporte (Coreidae: Anisoscelini) and the species within the genus

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The phylogenetic position of the genus *Leptoscelis* Laporte is discussed. Species that are currently in the genus are delineated and revealed along with key characteristics. Three new species are introduced and pathways to possible splitting of the genus are also given.

Heteroptera research in Southeast Asia: What has been done and current gaps

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Southeast Asia is well-known for its biodiversity due to its complex geological history. However, unlike vertebrates, aquatic macroinvertebrates had been a lesser concern for the scientific community. A milestone was the publication of “Fauna Malesiana” authored by Chen, Nieser, and Zettel in 2005. Our research network centered around the Natural History Museum Vienna and the Ateneo de Manila University has been exerting efforts on updating the state of water bug fauna, especially in the Philippines, Thailand, and Cambodia. Due to the intense efforts of Zettel and colleagues, the Philippines has a comparably well-studied aquatic Heteroptera fauna. However, several new species have been still being discovered recently. One of those is for instance *Aphelocheirus freitagii* Zettel & Pangantihon, 2010 featured by the Taxonomy in Action campaign of the global BioNet initiative. Also ‘Aqua Palawana’ launched in 2004 to promote biodiversity research in the Greater Palawan region produced several publications increasing the number of species accounts known in the area. In this paper, we present the most recent efforts done to update the species accounts in Cambodia and in the Philippines. The Cambodia expedition provided the first comprehensive checklist of the 41 aquatic heteropteran species of the country with two new discoveries, *Microvelia (Picaultia) falcata* Zettel *et al.* 2017 and *Ranatra cardamomensis* Zettel *et al.* 2017. In the Philippines, the aquatic bugs with coastal and marine association were reviewed in a recently published paper under the lead of Pangantihon. The Mindoro water bug survey (currently prepared by Pelingen *et al.*) revealed one new *Pseudovelina* sp. among 30 species, some of which are new records of Gerromorphan and Nepomorphan species from the island and during expeditions to Mindanao two new *Microvelia* spp. (currently being studied for formal description) were discovered. In all these projects, foreign and local scientists, junior researchers, conservationists, and local communities were encouraged to participate. However, more sampling efforts should still be done in the region to update species list and to further understand Heteroptera Systematics and Zoogeography.

Classification of the Cryphocricinae Montandon (Hemiptera: Heteroptera: Naucoridae): Reconsiderations based on molecular phylogenetics

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Currently, the classification of the subfamily Cryphocricinae (Heteroptera: Naucoridae) includes 117 species in three tribes and seven genera: Ambrycini (*Ambrysus*, *Carvalhoiella*, *Hygropetrocoris*, *Picrops*), Cataractocorini (*Cataractocoris*), and Cryphocricini (*Cryphocricos*, *Procryphocricos*). The phylogenetic relationships among species in Cryphocricinae were examined using Maximum-likelihood and Bayesian inference methodologies and a molecular dataset of 2.4k bp of DNA sequences from mitochondrial genes encoding COI and COII, and nuclear genes 18S rRNA and 28S rRNA. Data from 98 species representing all five subfamilies in Naucoridae were included, together with an outgroup species in the family Belostomatidae. Eighty-four species of Cryphocricinae were included and represent all seven genera in the subfamily. The resulting phylogeny shows that as currently recognized, Cryphocricinae is not monophyletic, since species of *Cryphocricos* appear closely related to those in *Limnocoris* (Limnocorinae). This clade is sister to a group including ((*Macrocoris* (*Hygropetrocoris* + *Carvalhoiella*)) + (*Picrops* (*Pelocoris* (*Procryphocricos* (*Ambrysus* in part (*Ambrysus* in part + *Cataractocoris*)))))). Relevant information based on this phylogenetic hypothesis suggests that the species-rich genus *Ambrysus* is not monophyletic. All the North American species in this genus, and few from South America, are closely related to the Mesoamerican genus *Cataractocoris*; sister to this clade is the rest of South American species of *Ambrysus*. Additionally, the genus *Procryphocricos* is not closely related to *Cryphocricos* as originally thought. The genera *Pelocoris* (New World) and *Macrocoris* (Africa), both in Naucorinae, appear not to be closely related; instead, *Pelocoris* is related to other genera in the New World. In light of the results herein presented, a new classification of the genera previously included in *Cryphocricinae* is proposed. The subfamily Cryphocricinae only includes species in the genus *Cryphocricos* and it is closely related to Limnocorinae. The subfamily Ambrycinae *stat. rev.* is resurrected and the relationships among its tribes are: (Carvalhoiellini *trib. nov.* (Picropsini *trib. nov.* (Pelocorini *trib. nov.* (Procryphocricini *trib. nov.* (Australambrycini *trib. nov.* + Ambrycini); where Carvalhoiellini (*Carvalhoiella* + *Hygropetrocoris*), Picropsini (*Picrops*), Pelocorini (*Pelocoris*), Procryphocricini (*Procryphocricos*), Australambrycini (*Australambrysus gen. nov.*), and Ambrycini (*Ambrysus sensu stricto* + *Cataractocoris*). The species in Ambrycinae apparently are more closely related to species in the African genus *Macrocoris* than to other species from genera distributed in the New World (*Interocoris*, *Cryphocricos*, *Limnocoris*).

Coevolution between male and female genitalia in *Belostoma angustum* Lauck, 1964 (Nepomorpha, Belostomatidae): disentangling size and shape

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Continuous sexual selection and natural selection through a lock-and-key mechanism might drive the variation in the genitalia of male animals. All aforementioned mechanisms are known to predict coevolution of male and female genital morphology. *Belostoma angustum*, a cryptic species, is known to have subtle continuous variation in the male genitalia of its members. Phallosoma with dorsal arms (PHA + DA) and ventral diverticulum (VD) are assumed to be intromittent male genital traits in this species that interact with the female genital chamber. Here, we evaluated the existence of variation after disentangling the size from the shape of male genitalia in *B. angustum*. Body and genitalia dimensions and photographs of PHA + DA, VD and lateral views of the right paramere (PAR) (the non-intromittent part) were obtained. Semi- and landmarks were used to capture phenotypic variation, by eliminating all non-shape variation with a generalised least-squares Procrustes superimposition. The male and female specimens collected from the same location or immediate vicinity were grouped, and 12 groups originating from 12 locations were used to conduct 2B-PLS analyses. Group structures were also taken into account by adopting a multilevel approach. The male and female genital traits had similarly shallow static allometry slopes (Mann-Whitney *U*-test, $P = 0.1000$), as well as the measure of point dispersion around the allometric line, CV' (Mann-Whitney *U*-test, $P = 0.2000$). Similarly, the standard error of the estimate (SEE) of intromittent sexual traits and PAR in males was not significantly higher than SEE of genital traits in females (Mann-Whitney *U*-test, $P = 0.2000$). Correlation between the pooled within-locality covariance matrix of symmetric component of PHA + DA and female genital chamber was significant (r -PLS = 0.37, $P < 0.05$), as well as that between PHA + DA and male body dimensions (r -PLS = 0.36, $P < 0.05$), even after allometry controlling. Specimens with lower PLS shape scores bear PHA + DA that are narrower, with the outer margins of DA poorly curved, whereas specimens with higher PLS shape scores have slightly shorter DA that have their outer margins also strongly curved. Lower shape scores are associated with narrower and especially shorter and narrower female genital chambers. Similar shallow allometric curves among sexes and the correlation between intromittent male parts and female genital chamber, as well as male dimensions, suggest in part the existence of a lock-and-key mechanism driving the coevolution of the size and shape of those traits.

Molecular phylogeny of the stink bug family Pentatomidae (Hemiptera: Heteroptera)

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Family Pentatomidae has a worldwide distribution, and is one of the largest groups within the Heteroptera. The family is subdivided into 10 different lineages (subfamilies): Aphylinae, Asopinae, Cyrtocorinae, Discocephalinae, Edessinae, Pentatominae, Phyllocephalinae, Podopinae, Serbaninae and Stiroarsinae, however the phylogenetic study within the family including subfamily level relationships still remain unstudied. In this talk, molecular data of COI, 16S RNA, 28S RNA, and 18S RNA genes with a sampling of around 200 species are used to test their monophylies and relationships. Based on the results, we discuss Pentatomidae classification and its reinterpretation based on their evolutionary lineages and morphological features.

The evolution of host specialization in bedbugs (Cimicidae)

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All 100+ bedbug species (Cimicidae) are obligate blood-sucking parasites but the evolutionary trajectory of blood-sucking and hosts are unknown. We constructed a new, fossil-dated, molecular phylogeny that estimates that ancestral Cimicidae evolved ca. 115 MYA as hematophagous specialists on an unidentified host (bats evolved ca. 50 MY later), switching to bats and birds several times thereafter. Humans were independently colonized three times, always from host specialist lineages that extended into host generalists. Our phylogeny rejects the idea that the divergence of the two current urban pests (*Cimex lectularius* and *C. hemipterus*) was associated with the divergence of *Homo sapiens* and *H. erectus*.

Systematics of Cappaeini (Heteroptera: Pentatomidae: Pentatominae) with description of two new species of *Halyomorpha* Mayr from India

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The tribe Cappaeini is represented by 24 genera and 151 species from the world (Rider *et al.*, 2018). They are usually brown to dark brown, characterized by triangular or subtriangular head, straight mandibular plates subequal to clypeus, smooth anterolateral margins of pronotum, simple humeri without any spines/tubercles (except in *Homalagonia* Jakovlev), smooth ventrite III, lacking median longitudinal spine or tubercle and elongate peritreme. Currently, this tribe comprises 11 species in 4 genera namely *Cappaea* Ellenrieder, *Halyomorpha* Mayr, *Tolumnia* Stål and *Homalagonia* in India. Among these, *Halyomorpha* is cosmopolitan in distribution with six described species from India. Fortunately, the brown marmorated stink bug, *Halyomorpha halys* (Stål), native to East Asia, an alien invasive pest of several economically important crops, is not yet recorded from India; though Nikam and More (2016) quoted its presence in Maharashtra, which is likely to be a misidentification. The external genitalia of all species of *Halyomorpha* except *H. illuminata* Distant from India, is studied and illustrated. Two species of *Halyomorpha*, *H. shivaprakashai* sp.n. from Tripura and *H. savandurga* sp.n. from Karnataka are described herein. Apart from this, the colour variability associated with various population of *H. picus* (Fabricius) from India is also studied. *Tolumnia* is represented by five species namely *T. antennata* Distant, *T. basalis* (Dallas), *T. latipes* (Dallas), *T. maxima* Distant and *T. immaculata* Distant. Examination of postabdominal structures of the species of *Tolumnia*, collected from various parts of India revealed that *T. basalis* is restricted to southern part of India though various previous literature mentioned it as *T. latipes*, which was originally described from Tenasserim by Dallas (1851). Hence all the previous literatures mentioning *T. latipes* from southern part of India may essentially refer to *T. basalis*. *T. maxima*, originally described from Tenasserim and Myitta (Myanmar), is recorded for the first time from India (Tripura). Recently Kaur *et al.* (2017) reported this species from India (Uttarakhand and Himachal Pradesh), but their illustrations and description are not in conformity with the original description of *T. maxima*. Male and female genitalia of *Cappaea taprobanensis* (Dallas) were also studied and illustrated. Phylogenetic relationships between 4 genera and 13 species of Cappaeini were analysed using morphological characters by Tree analysis using new Technology (TNT) (Goloboff, 2008) and unambiguous, nonhomoplasious synapomorphies were mapped using Winclada (Nixon (2002)). Statistical support for nodes were calculated using TNT.

Phylogeny of the stink bug family Pentatomidae (Hemiptera, Pentatomoidea) based on molecular markers and morphology

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The Pentatomidae (stink bugs) stands out within true bugs as the third most diverse family, with nearly 5,000 species. They exhibit a plethora of morphological and behavioral peculiarities that make the group ideal models to approach broad macro-evolutionary questions and to test hypotheses on longstanding morphological puzzles. However, comparative studies as such are hampered by the lack of a phylogenetic hypothesis to the family. Here, we conduct a series of phylogenetic analyses including a comprehensive sample of in-group and out-group taxa, focusing on the “catch-all” subfamily Pentatominae. We used three molecular markers and 72 morphological characters, analyzed in combination and separately, aiming to: i) test the monophyly of Pentatomidae; ii) identify evolutionary lineages within the family; iii) test the hypothesis that Pentatominae is not monophyletic. Our analyses were overall robust, corroborating the monophyly of Pentatomidae and subfamilies Asopinae, Discocephalinae, Edessinae, and the polyphyly of the Pentatominae. Furthermore, several groups proposed in the taxonomic literature were supported as monophyletic, including some recognized subfamilies tribes within Pentatominae. We show that the combination of morphological and molecular characters provided results with strongest support levels. A few specific relationships were poorly resolved, and we briefly discuss the reasons and future directions to improve our results. A phylogenetic classification derived from the analysis will be presented.

A phylogeny for the Saucer Bugs (Naucoridae)

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The family Naucoridae is currently represented by 407 species in 39 genera and 5 subfamilies. This classification scheme has been followed for many decades and is based mostly on gross morphological characters without consideration of a phylogeny. Creation of a meaningful phylogeny using morphology is made particularly problematic because of pervasive convergence in many of the characters. Throughout the past 20 years, I have collected as many species and genera as possible worldwide with the objective of amassing enough taxa to produce a molecular-based phylogeny of the family. As a result, I have now constructed a preliminary phylogeny and will propose a new evolutionarily meaningful classification for the

family. All five subfamilies, 37 of the 39 genera, and 202 species were included in maximum likelihood (ML) and Bayesian inference analyses to determine relationships among taxa. Outgroup sampling comprised four species of Naucoroidea (one Potamocoridae and three Aphelocheiridae), one other Nepomorpha (Belostomatidae), and one Pentatomomorpha (Coreidae). Two nuclear genes (18s and 28s) and two mitochondrial protein-coding genes (COI and COII) were sequenced, resulting in 2,444 aligned nucleotides. ML and Bayesian analyses resulted in similar topologies, with ML supported by slightly higher bootstrap values. A new classification with more than five subfamilies is proposed here. Only one previously recognized subfamily is retained without change (Limnocoidea). Additional sequencing is continuing; thus, this preliminary phylogeny and classification are subject to change.

Identification key to the species of adult *Belostoma* Latreille from the Amazon region (Hemiptera: Heteroptera: Belostomatidae)

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The genus *Belostoma* Latreille, 1807, comprises 70 species occurring mostly in the Neotropical Region. The Amazon encompasses the single largest remaining tropical rainforest in the world. For the Brazilian Amazon, 25 species of *Belostoma* were recognized recently. Here, we examined 124 specimens from Invertebrate Collection of Instituto Nacional de Pesquisas da Amazônia (INPA), Manaus; 40 specimens from Museo Javeriano de Historia Natural "Lorezo Uribe, S.J." (MPUJ) and 28 specimens from the Universidad Nacional de Colombia (UNC), Bogotá. Additionally, we also examine some specimens housed in the Museu de Zoologia of the Universidade de São Paulo (MZUSP), São Paulo and Instituto Oswaldo Cruz (IOC), Rio de Janeiro. Almost all Amazon countries were represented in the examined collections, except Venezuela and Ecuador. From the examined material and previous distributional records, we recognized 34 species occurring in the Amazon region. We proposed an identification key to adult *Belostoma* based on characters previously described, such as body size, pilosity of the laterotergites and sternites, the shape of eyes and body, segments of the rostrum, aspects of the prosternal keel and ventral diverticulum of the male genitalia, and also new characters. The new set of characters include morphological information of the male genitalia, tarsal claws and arolium, mouthparts, wing knob, and Drückknopf system, all of them using scanning electron microscopy. This study provides the first key for giant water bugs from Amazon and it represents a considerable advance on the biodiversity and taxonomic knowledge of *Belostoma*. Furthermore, it will contribute to future systematics and biogeographical studies of this fauna.

Ten years of Heteroptera barcoding at CBGP: outputs and prospects

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The INRA research unit CBGP (Centre for Biology and Management of Population) aims to characterize the biodiversity, focusing on pests and beneficial organisms for crops. In the last ten years many species of arthropods important for agriculture have been characterized using COI barcodes, including quarantine and invasive species. Indeed, many true bug species have become major pests in Europe due to pesticide reduction, especially on fruit and vegetable crops. In addition, several alien species have become invasive, including *Halyomorpha halys*, *Corythucha arcuata*, and others may threaten cultures if they are introduced such as *Megacopta cribraria* or *Bagrada hilaris*. The promotion of alternatives to chemical plant protection encourages the use of predatory true bugs as biocontrol agents. In this context, several barcoding projects of Heteroptera have been achieved, while some other are in progress. Barcodes were first obtained through classical PCR and Sanger sequencing but are now generated through two-step PCR and Miseq sequencing. Multiple quality controls are implemented including i) a non-destructive DNA extraction that allows vouchering and morphological re-examination by a taxonomist; ii) a bioinformatic pipeline that discards non-coding sequences, contaminants and numts through BLAST comparison and phylogenetic inferences. A database (Arthemis DB@se: <http://arthemisdb.supagro.inra.fr/DefaultInfo.aspx?Page=Home>) focusing on pests and their natural enemies is continually implemented. Until now 2060 sequences of Heteroptera belonging to 343 species from 34 families were obtained. For many genera, the analysis of standard COI barcodes reveals taxonomic problems such as putative cryptic species (e. g. *Orius*, *Macrolophus*). In some cases, closely related species (e. g. *Lygus*, *Nabis*, *Eurydema*, *Arocatus*) have identical COI sequences, suggesting either potential introgression or taxonomic issues (synonyms).

Revisiting sticky assassins and relatives: evolutionary history and diversification of Harpactorinae sensu latu (Insecta: Hemiptera: Reduviidae)

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Harpactorinae sensu latu (“Harpactorinae” + Bactrodinae) are the most speciose subfamily-level clade among Reduvidae. Most species are characterized by close associations with living

plant tissue including flowers, and the group displays diverse predatory and anti-predation strategies. Recent phylogenetic analyses have generated testable hypotheses on relationships among tribes and genus groups, but critical nodes have remained poorly supported, and published datasets lacked taxon sampling to test evolutionary hypotheses across the group. We here use a supermatrix combining legacy datasets with phylogenomic sampling for selected taxa to generate the most comprehensive molecular phylogenetic hypothesis for Harpactorinae sensu lato to date. Previously proposed hypotheses on relationships among early diverging lineages within the group are corroborated with high branch support. Estimated divergence dates based on revised fossil calibrations and models are similar to previous estimates. Diversification rate analyses suggest rate shifts within the Harpactorinae sensu lato. Ancestral state reconstructions of morphological (e.g., aposematism, egg batch type) and lifestyle (e.g., predatory strategy, oviposition site) traits attempt to determine transitions that may be associated with these rate shifts.

Molecular phylogenetics of Pentatomoidea, with emphasis on Scutelleridae

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Pentatomoidea, as the third largest group of Heteroptera (Hemiptera), riches in species number and varies in morphology. Nearly all pentatomoid species are phytophagous (except for Asopinae) and many of them are agricultural pests with different damage degree. Scutelleridae is one of the representative one. However, due to lack of obvious synapomorphies and the failure to apply rigorous phylogenetic methods, the higher classification of Scutelleridae has been disputed for more than 150 years. Here we reconstructed a phylogeny of Scutelleridae based on complete sequences of 18S and 28S nuclear rDNAs and all 13 protein-coding genes of the mitochondrial genome, with the sampled taxa covering all of the currently recognized subfamilies. The monophyly of Scutelleridae was confirmed by the congruence of the results of analyses conducted using Bayesian inference, maximum likelihood and maximum parsimony. The phylogenetic relationships among subfamilies were well resolved for the first time. Furthermore, time-divergence studies estimated that the time of origin of Scutelleridae was in the Early Cretaceous (142.1–122.8 Ma), after the origin of the angiosperms. The diversification between the extant subfamilies of Scutelleridae and within the subfamilies occurred from the late Palaeocene to the late Miocene, simultaneously with the rise of the major groups of angiosperms and other phytophagous insects.

Evolutionary history of the true water bugs (Hemiptera: Heteroptera: Nepomorpha) reveal heterogeneous diversification rates associated with arising palaeoecological niche opportunities

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Climate fluctuations and tectonic reconfigurations associated with environmental changes play large roles in determining patterns of adaptation and diversification, but studies documenting how such drivers have shaped the evolutionary history and diversification dynamics for limnic organisms during the Mesozoicum are relatively scarce. Members of the heteropteran infraorder Nepomorpha, or aquatic bugs, are ideal for testing the effects of these determinants on their diversification pulses because most species are confined to aquatic environments during their entire life, the group has a relatively mature taxonomy, and is well represented in the fossil records. We investigated the evolution of Nepomorpha based on phylogenetic analyses of morphological and molecular characters sampled from 120 taxa representing all 13 families and about 40% of recognized genera and found our results to be largely congruent with the established morphological phylogenetic relationship. A timescale analysis indicated that Nepomorpha began to diversify in the latest Permian (approximately 255 mya), and diversification analyses suggested that arising palaeoecological opportunities probably promoted lineage diversification.

The first three authors contributed equally to this study.

Functional analyses of three melanin pathway genes (*pale*, *yellow*, *aaNAT*) in hemimetabolous insect, *Platymeris biguttatus* (Linnaeus)

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Insect pigmentation is one of the most distinctive and variable features. It plays indispensable roles in behavioral, physiological, and reproductive processes. Functional analysis in *Drosophila* shed light on basic information about genes that regulate pigmentation, such as *DDC*, *yellow*, *tan* and *ebony*. Most supplementary pigmentation studies have been carried out in holometabolous insects, such as *Tribolium*, *Heliconius*, *Monochamus* and *Aedes*. In contrast, researches that performed in hemimetabolous insects are few. These results suggest that the melanin pathway plays a conserved role in insects. Both *Oncopeltus* and *Platymeris* belong to hemiptera, but *Oncopeltus* is Lygaeidae, *Platymeris* is Reduviidae. They have different feeding

habits, *Oncopeltus* is phytophagous, while *Platyperis* is feeding on other insects. Therefore, it is essential to supplement more pigmentation studies in hemimetabolous insects. In this study, we use RNAi to examine three essential genes in this pathway: *pale*, *yellow* and *aaNAT*. Our results suggest that in *Platyperis* the black pigmentation is solely generated from the melanin pathway. Also, down regulation of *yellow* cause brown phenotype with highly mortality. Interestingly, *aaNAT* RNAi induced totally black pigmentation. Overall, the mechanism of pigmentation is generally used across the insect lineages, while the evolution of related genes involves frequent divergent and convergent changes.

Taxonomic study of Triatominae subfamily (Heteroptera, Reduviidae)

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Triatominae (Heteroptera: Reduviidae) is a special subfamily of Reduviidae whose members are hematophagous. The Triatominae includes about 150 species, with nearly straight rostrum, a flexible membranous connection between third and fourth segment allowing upward pointed when feeding. Most species occur exclusively in the New World, and only two genera are recorded in the Old World. Several are the vectors of Chagas disease by carrying *Trypanosoma cruzi*. In this study, we examined about 90 species and discovered six new species including five species in the old world. To some extent, it implies that species of triatomines in the old word need more study. Besides, male genitalia of nearly 80 species were dissected and digital micrographs are provided for the pygophore, parameres, and phallus of the male in the study. According to combining morphological data and molecular data, our study supports that 1) It is unnecessary to build Lishcosteusini, 2) *Triatoma* and *Panstrongylus* are not monophyletic. 3) *Rhodnius* is divided into at least two groups in genital morphology.

POSTER PRESENTATIONS

Taxonomic Study of the Genus *Sadoletus* Distant, 1903 from the Oriental Region (Heteroptera: Lygaeoidea: Heterogastridae)

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The genus *Sadoletus* Distant of the heteropteran family Heterogastridae Stål comprises 11 species (Slater, 1964; Ban & Ishikawa, 2013). Most species feed on *Ficus* seeds and are attracted to artificial light. Their general habit is myrmecophily. Distant (1903) established the genus *Sadoletus* to accommodate a single species, *S. validus* (type species) from India, and then he described *S. corvus* from Borneo (Distant, 1908) and *S. pallescens* from India (Distant, 1909). Bergroth (1918) described 6 species from Philippines. To date, 9 species have been described from the Oriental Region (Slater, 1964). Afterwards, several studies on *Sadoletus* have been conducted from the surrounding areas of the Oriental Region such as Japan and China (Hidaka, 1959; Zheng & Zou, 1981; Ban & Ishikawa, 2013; Gao & Rédei, 2017). However, there has been no comprehensive work on the taxonomy of *Sadoletus* from the Oriental Region. In this study, Oriental species of *Sadoletus* are revised and 14 species are recognized. Three species are newly described: *S. laosensis* and *S. subpellucidus* from Laos and *S. melasmus* from Thailand. One is an undescribed species: *S. sp. 1* from Borneo. Furthermore, one species, *S. ryukyuensis* Ban & Ishikawa is newly recorded from Taiwan and Thailand. Moreover, a species previously known as *S. valdezi* from Japan, which is newly recognized from Taiwan, may be different from true "*S. valdezi*" described originally from Philippines.

Illustrated key for the genera of the Mecocephala Group (Heteroptera: Pentatomidae: Carpocorini)

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Currently, Carpocorini is the taxon that comprises the highest number of genera described and reviewed in Pentatominae. Despite the lack of studies on intergeneric and tribal

phylogenetic relationships, several genus groups were proposed in Carpochorini, based mainly on morphological similarity and taxonomic history. Among these, the Mecocephala group is one of the most diverse, bringing together 41 species in 12 genera of similar habitus (*Mecocephala* Dallas, 1851, *Tibraca* Stål, 1860, *Ogmocoris* Mayr, 1864, *Glypompis* Berg, 1891, *Hypatropis* Bergroth, 1897, *Paramecocephala* Benvegnú, 1968, *Paratibraca* Campos & Grazia, 1995, *Parahypatropis* Grazia & Fernandes, 1996, *Amauromelpia* Fernandes & Grazia, 1998, *Luridocimex* Grazia, Fernandes & Schwertner, 1998, *Stysiana* Grazia, Fernandes & Schwertner, 1999 and *Pedinonotus* Fernandes & Grazia, 2002), distributed in the Neotropical region. Preliminary phylogenetic hypotheses have already suggested the group, mainly by characters of general morphology. However, these hypotheses are questionable based on misinterpretation of morphological characters, sub-sampling of taxa and outdated methodology. Thereby, a phylogenetic study with robust methodology and broad taxonomic sampling is necessary to better define inter and intrageneric relations. In addition, several species of the group are reported as pests of cultivated plants and have shown evidence of distributional expansion. For example, *Tibraca limbativentris*, popularly known as stem rice stink bug, is considered an important pest causing diseases and losses in rice paddy fields. The group also needs an updated view of its economic importance and its geographic expansion potential, due to the recent descriptions of new taxa that have been increasing the composition of the group. In this work, we present an illustrated dichotomous key to identify the genera of the Mecocephala group, with a brief comparative diagnosis of each one of them, proposing new taxa. In addition, information on associated plants available in the literature and labels and geographical distribution are also provided. Specimens of all genera were examined and the type-species were photographed and/or illustrated. Most of the images were taken from the type material. New distribution records and associated host plants are provided.

***Macrolophus melanotoma* (Heteroptera Miridae): new aspects to understand this little-known species**

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Macrolophus melanotoma (Hemiptera: Miridae) was considered a real species since 2007 only, after the revision of the taxonomic status of *M. caliginosus* and the distinction of two different species (*M. melanotoma* and *M. pygmaeus*). While *M. pygmaeus* is quite well known and used as biological control, *M. melanotoma* has been poorly studied. In the Mediterranean basin, *M. melanotoma* appears closely associated to *Dittrichia viscosa*, a common ruderal plant. In order to understand whether *D. viscosa* and *M. melanotoma* could respectively act as a bank plant and a native biocontrol agent for neighbouring horticultural crops, we investigated the relative attractivities of both *D. viscosa* and tomato plants for *M. melanotoma* as well as the

feeding behaviour of the Miridae. Four specific results are highlighted: (1) A high affinity of *M. melanotoma* towards *D. viscosa* was evidenced, this affinity being partly explained by easily extractable plant compounds. (2) A close association between *M. melanotoma* and *D. viscosa* was found, *M. melanotoma* being able to complete its life cycle on *D. viscosa* without any prey. (3) In non-choice conditions, *M. melanotoma* is however able to lay eggs on tomato plants and the offspring successfully develop. (4) Complementarily, *M. melanotoma* also behaved as generalist and probably opportunistic predator as it is able to prey on various arthropods (Tetranychus eggs, Whiteflies, Aphids and Ephestia kuehniella eggs). Taken as a whole, this study contributes to a better understanding of the *M. melanotoma* ecology. From an applied perspective in biological control, the *D. viscosa* – *M. melanotoma* association does not probably simply act as a plant bank towards neighbouring crops. Based on the exploitation of attractive and/or repellent natural compounds, new strategies may however be planned.

***Podisus* Herrich-Schaeffer 1851, the taxonomic dumping ground of Asopinae (Heteroptera: Pentatomidae): actual knowledge and perspectives**

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Asopinae is the only group of Pentatomidae with predatory behavior, feeding mainly on larvae of Lepidoptera and Coleoptera, acting as biological controllers in natural and modified areas. *Podisus* is the most diverse genus of predatory stink bugs, comprising 32 valid species and two *incertae sedis*, distributed in the Nearctic (five species) and the Neotropic (29 species). Species of *Podisus* have been studied in the Americas for at least eight decades and some of them are considered the most important agents in biological control programs, mainly *Podisus maculiventris* (Say) in North America and *P. nigrispinus* (Dallas), *P. sagitta* (Fabricius) and *P. distinctus* Stål in Central and South America. Most studies on the genus focus on applied fields, with little attention given to the systematics of *Podisus*. The identification keys found in the literature oftentimes contain errors, and the lack of information about the species result in several taxonomic problems. The diagnosis of *Podisus* comprises a set of characteristics shared with other genera without any putative homology exclusive to *Podisus* species, and both somatic and genital morphology is quite variable, making doubtful the classification of several species in the genus. Currently five groups of species are recognized based only on variations of the pronotum. *Podisus* can be considered a dumping ground in Asopinae, since the species have been included in the genus due the lack of diagnostic characters found in the remaining asopine genera. In order to solve these problems, we are gathering as much information as possible about *Podisus* species: analyzing holotypes, original descriptions and examining specimens deposited in institutions from all over the world. Our preliminary results have revealed taxonomic problems such as erroneous synonyms, and the recognition of new species. In addition, we are describing the morphology of eggs and nymphs of five *Podisus* species and

also of other genera of Asopinae. So far, we accessed material from at least ten institutions, gathering 29 of the 32 species included in the genus. Based on general and genital morphology we reorganized *Podisus* in 11 species groups, as a starting point for a morphological phylogeny. At present, we are working on the revision of *Podisus*, with description of new taxa, description of immature and character search for a phylogenetic analysis including all possible species of *Podisus* and supposedly related genera.

Does sampling time influence the diversity of light-attracted true bugs (Insecta: Heteroptera) in Atlantic Forest?

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Light traps are widely used and very efficient method used to survey flying insects at population and community levels. This method is also applied in insect conservation studies and arthropod monitoring programs to detect long-term changes in the diversity. Little is known about the period of time for collecting insects by light trap and its differences in diversity, especially in unusual groups. The importance of better understanding of the method used is also relevant to have a cost efficient sampling and fieldwork. One group of insects highly attracted by light trap is Heteroptera, however few studies have used standardized period of time, and usually as complementary in exhaustive samplings. Experimental fieldwork was delineated to answer the following question: does the period of time influence richness and abundance of true bugs collected using light trap? Sampling was done using a trap made with sheet (2 m x 2 m) over a 500 w mixed lamp, in a patch of the Atlantic Forest in southeastern Brazil (Jundiá municipality, São Paulo state). Each collect event started at the sunset and 6 hours' period, with the light turned on at approximately 30 minutes before the sunset and turned off at the end of the sampling time. All true bugs were collected and storage separately at each hour, totaling 6 samplings per night. In a total of 120 hours of light trapping, 1.425 specimens were collected, representing 114 species among 13 families. Miridae family represented 89% of total abundance and 63% of the species richness. The results did not clearly differ between families. There was no significant difference in either species richness or abundance between the period of time of sampling, suggesting that potential differences between time did not affect the diversity during the samplings. True bugs might respond to climate, environmental conditions and their inherent behavior, as others groups of insects, thus the activity may vary by environmental factors and their behavioral phase. Nevertheless, standardized light trap can be a useful tool in true bugs diversity studies, especially for monitoring studies or ecological approaches. Moreover, mirids as the most abundant and rich group, could be used as an interesting group for future studies.

First notes on the female genitalia of *Eurystethus microlobatus* Ruckes, 1966 (Pentatomidae: Discocephalinae: Discocephalini)

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The genital morphology is widely used as a source of characters for phylogenetic studies and taxonomic delimitation. Since *Eurystethus* Mayr, 1864 was described it was poorly studied. Authors have focused on the external morphology, and the work by Becker in 1966 was the only one that gave some attention to the ectodermal genital ducts of the two species described by her. *E. (Hispidisoma) microlobatus* Ruckes, 1966 was described from single male specimen, so the female morphology is yet unknown. Years later the species was found in Serra do Cipó, Minas Gerais State, Brazil, feeding on *Psittacantus robustus* Mart. (Loranthaceae) and trophobiotic with ant species of *Camponotus* and *Cephalotes*. We here describe and illustrate the female genital plates and ectodermal genital ducts of *E. microlobatus* comparing it with Becker's *E. goianensis* and *E. deplanatus*. Genital plates of the species are densely setose with long and yellow setae, sparsely black punctured and marked with black spots. Gonocoxites VIII are subtrapezoidal with rounded angles, as large as laterotergites VIII. Laterotergites VIII are rounded with a black spiracle at base partially hidden by an inner deflection of laterotergites IX. Laterotergites IX are drop-like, short, not surpassing laterotergites VIII. Segment X partially visible, flat and rounded. The three species differ in plates shape and black marks. Internally we found the *capsula seminalis* globose with claw-like projections at base. Distal and proximal flanges usually of same length, but in *E. microlobatus* the distal flange is almost absent. *Pars intermedialis* medially large, 1.5x longer than *capsula seminalis*. *Ductus receptaculi* narrow and long before the vesicular area. Vesicular area large, fusiform. Medial tube of the vesicular area dilated in the basal portion. Species differ in the number and shape of projections of *capsula seminalis*: two in *E. microlobatus*, one thinner than the other; three in *E. deplanatus*, one larger than the other two; and four in *E. goianensis*, equal in size. Despite this few variations, further investigations and more taxa sampling are necessary to find characters that help us to elucidate the relationships between the subgenera and species of *Eurystethus* in future studies.

Wing shape and chromatic variation in *Triatoma rubrovaria* (Blanchard, 1843) (Heteroptera: Reduviidae) from Argentina, Brazil, and Uruguay

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Chagas disease is caused by *Trypanosoma cruzi* (Chagas, 1909) (Kinetoplastida: Trypanosomatidae) and transmitted by the infected feces of Triatominae (Heteroptera: Reduviidae). This subfamily includes 153 species grouped into five tribes and 18 genera. *Triatoma rubrovaria* (Blanchard, 1843) is widely distributed in Uruguay, northeastern Argentina, and several municipalities in southern Brazil. Individuals are found primarily among rocks and can be naturally infected by *T. cruzi*. *Triatoma rubrovaria* is considered sylvatic and rarely found in human dwellings, however, recent reports demonstrate an increase in the occurrence of such species in domestic environments. This work aims to analyze and compare the polymorphism of *Triatoma rubrovaria* using the geometric morphometry of the wings and the chromatic patterns of the pronotum. We analyzed specimens from the Triatomines Collection of the Instituto Oswaldo Cruz, Rio de Janeiro, Brazil; the Museum für Naturkunde, Berlin, Germany; and insects collected in different locations of Rio Grande do Sul State, Brazil. The pronotum of *T. rubrovaria* presents chromatic polymorphism, with the anterior lobe varying from brown to black, posterior lobe orange yellow to red, collar brown to black, sometimes with a pair of red to orange lateral spots. Our results corroborate with the color patterns described in the literature, to which we add 12 new chromatic polymorphisms, and the pronotum entirely black is the main pattern in southern Brazil. Besides the chromatic polymorphism, it was possible to observe a high variation of the wing form between adult specimens from Argentina, Brazil, and Uruguay. The wings of specimens recently collected in Rio Grande do Sul State present a different wing form when compared to the oldest specimen of *T. rubrovaria* collected in southern Brazil (1859) and deposited in the Museum für Naturkunde. These results show that there are changes in wing form through time and suggest that the variation is correlated with the geographical distribution of the species.

Taxonomic revision of *Macropygium* Spinola, 1837 (Pentatomidae: Discocephalinae: Ochlerini)

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Macropygium is a monotypic genus with a large distribution in South America. Since its description the genus didn't have other morphological or taxonomic studies, though the existence of more than one species has been suggested based in the observation of differences in the male genitalia. We analyzed about 900 specimens of different locations, and observed in detail the general morphology of the body, external and internal genitalia. Besides the type species *Macropygium reticulare* (Fabricius) we identified three other morphotypes as putative new species. They are separated mainly by pygophore morphology: the conical projection of the ventral rim is single pointed in *M. reticulare* and *M. sp. 1* while these species differ in the shape

of the segment X, oval in *M. reticulare* and more wide and setose in *M. sp. 1. Macropygium sp. 2* and *M. sp. 3* have the conical projection apically forked, the segment X truncated at base and acute at apex. The greatest difference between *M. sp. 2* and *M. sp. 3* is the four-segmented antennae in the latter. Female genital plates are very similar between the four species, so most differences are in the internal genitalia.

Cladistic analysis of Spartocerini Amyot & Serville, 1843 (Hemiptera, Heteroptera, Coreidae)

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Spartocerini (Hemiptera, Coreidae, Coreinae) currently includes six genera, *Euagona* Dallas (3), *Eubule* Stål (13), *Menenotus* Laporte (2), *Molchina* Amyot & Serville (6), *Sephina* Amyot & Serville (24), and *Spartocera* Laporte (18), distributed in the Nearctic and Neotropical regions. Published works on the tribe include taxonomic revisions, catalogs and faunal lists, however, there are no phylogenetic hypotheses for the relations among genera neither about its monophyly. A cladistic analysis was performed to test the monophyly of Spartocerini and its intergeneric relations. The analysis was performed with implied weights, under Mirande's script, with 56 terminal taxa and 115 discrete and unordered morphological characters. The TNT software was used to perform the analyses and the characters polarized by the external group comparison method. The relative Bremer values, as well as the Fit of the topology and the characters, were obtained with the same software. The 11 K values established by the method obtained eight distinct topologies, with the ninth K value (K = 28.015) chosen as the best hypothesis, resulting from the larger sums of SPRdif. The monophyly of Spartocerini was not corroborated, since the tribe formed two distinct clades. *Molchina* is the sister group of Mictini, while the other members of the tribe, *Spartocera*, *Sephina*, *Eubule*, *Euagona*, and *Menenotus*, formed a distinct clade, having as sister group *Madura* + *Discogaster*. Actually, the position of *Molchina* within Spartocerini has been controversial in the literature, as its position has varied within Coreinae. The analysis also suggests the paraphyly of both *Eubule* and *Sephina*, and the polyphyly of *Spartocera*. No synapomorphies were found for Spartocerini, and many of the diagnostic characters mentioned in the literature are homoplasious. This is a first contribution to the systematics of Spartocerini, based on cladistic methodology.

Species distribution modeling to evaluate the impact of climate change on the distribution of *Nysius simulans* (Stål) (Heteroptera: Lygaeoidea: Orsillinae)

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The subfamily Orsillinae comprises about 30 genera and 250 species, separated into four tribes. In the Neotropics, three tribes, nine genera and about 46 species are known. Many Orsillinae, such as species of the genus *Nysius*, are agriculturally important. In South America, *N. simulans*, a widespread species known from Argentina, Brazil, Paraguay, Peru, and Uruguay, has been implicated as a pest of soybeans. The first record of *N. simulans* associated with soybeans comes from Buenos Aires Province, Argentina. *Nysius simulans* also has been recorded on soybeans in Paraná and Rio Grande do Sul, Brazil. Software such as Maxent enables one to identify areas where a species is likely to occur. Species distribution-modeling analysis can be used for evaluating the impact of climate change on the distribution of species. The results of our work are intended to show the impact of future climate change on the distribution of *N. simulans* in South America, indicating areas where this species can expand its distribution. In this study, we used 81 site records of *N. simulans* in the South America. We used raster with 2.5-minute resolution representing 19 bioclimatic variables. The analysis comprised the default settings of Maxent, as well as 20% random test percentage, the pre-1940 records as test sample, and the locations that did not showed significant autocorrelation as test sample. We modeled the impact of climate change on *N. simulans* distribution using the climate projections for the year 2050. There are high-impact climate areas in northern and northeastern Argentina, southern Brazil, northern and western Uruguay, the central regions of Argentina, and central Chile. Many provinces where *N. simulans* could occur are strategically important to avoid its colonization into new areas of South America, which may impact soybean crops in the future. Economically important populations of *Nysius* species develop when the seed supply of the preferred host becomes insufficient for a large population and the bug's movement to a new host, often one of agricultural importance. We proposed that the mean temperature of the driest quarter (BIO9) could be an important explanatory variable. The largest populations occur in Rio Grande do Sul during periods of drought. From the reproductive period of the soybean crop, the abundance of *N. simulans* increased, and the largest population was observed between the second half of February and the first half of March. Only adults were found on the soybean plants.

Argentinean pentatomoids (Heteroptera: Pentatomoidea) of economic importance

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The superfamily Pentatomoidea comprises about 7,000 species worldwide belonging to 15 families, of which eight are represented in Argentina, with more than 140 genera and 400 species. Pentatomoidea includes mainly phytophagous bugs, except the pentatomid subfamily Asopinae that have predacious habits. The knowledge about the economic importance of Argentinean pentatomoids is fragmented, and only refers to isolated species in each particular crop. In this contribution, we provide an integral vision on the distribution, host plants and biology to the economic important and less important species of Pentatomoidea in Argentina. The family Pentatomidae is one of the most diverse groups within Heteroptera, with about 94 genera and 254 species recorded in Argentina. The phytophagous pentatomids of economic importance belong to the subfamilies Edessinae, with some pest species in the genus *Edessa*, and Pentatominae, which contains the majority of species that are pests of crops. Edessines feed on Solanaceae and are pests of tomato and potato, although are found them on soybean, strawberry, sunflower, cotton, and alfalfa too. The pest species of Pentatominae injure a wide range of plants, from vegetables to trees. Among them, *Nezara viridula*, *Piezodorus guildinii*, *Euschistus heros*, and *Dichelops furcatus* attack grain, legumes, and vegetables. Several species of *Oebalus*, *Mormidea*, and *Tibraca* are major pests of Gramineae, particularly rice and wheat. Thyreocoridae is represented with three genera and 61 species in Argentina. Among them, species of *Galgupha* feed on potato, citrus, rice, sorghum, corn and yerba mate. Although several species of thyreochorids feed on cultivated plants, there are no records of damage by these bugs. Some species are cited as secondary pests of gardens and garden flowers. The family Cydnidae comprises ten genera and 28 species in Argentina. These bugs are chiefly root-feeders in nymphal and adult's stages; for example, *Scaptocoris castaneus* feed on roots of alfalfa, tomato, cotton and kidney bean. Scutellerids, represented in Argentina for 13 genera and 24 species, are generalist phytophagous that feed on Euphorbiaceae, Poaceae, Myrtaceae, and Malvaceae, although they are not crop pests. Acanthosomatidae is represented in Argentina by 14 genera and 20 species. Most of the species are found in the Andean Patagonia, associated with native trees and shrubs such as *Nothofagus* and *Luma* species, and with several species of berries. The families Dinidoridae, Megarididae, and Tessaratomidae comprise only one genus and less than three species each in Argentina, and there are no records of damage from Neotropical species.

Sexual dimorphism in hind legs of *Belostoma angustum* Lauck (Insecta, Heteroptera, Belostomatidae) may be related to paternal care

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Structures involved with the sexual selection and those associated with parental care are often dimorphic. Females of *Belostoma angustum* lay eggs on the hemelytra of their mates, where eggs are brooded until hatch. Males utilise their hind legs to carry, aerate, and protect the eggs. Taking into account the covariance between variables, we fitted a series of structural equation models and evaluated the existence of sexual dimorphism, by exploring whether the relationship between the body size and hind legs, and between the shape and centroid size (CS) of hemelytrum and hind legs are identical among males and females (multigroup analysis). We also tested whether hind legs, head, body, and right hemelytrum dimensions could show sexual size dimorphism in their intercepts biased towards males as a selective response for paternal care. We landmarked the right hemelytrum of 78 males and 60 females to capture its phenotypic variation. Also, we carried out modularity tests among different parts of the hemelytrum. After controlling for the effect of size, models using males fit better than those with females. By separately imposing equality constraints on relationships and intercepts, the multigroup analysis showed that neither the shape of hemelytrum nor its centroid size is significantly related to the head, the largest width of hemelytra (LWH) and the inner margin of median and hind leg variables. Instead, the size-related differences in inner margin of hind tibiae are mediated by the total body length (TBL) ($b = 0.27$, $P < 0.001$), whereas size-related differences in inner margin of hind femora are mediated by LWH ($b = 0.62$, $P = 0.008$) only in the model 2. Those fixed parameters in the constrained model 2 significantly improved model fit if estimated freely ($\chi^2_{diff} = 29.51$, $df = 12$, $P = 0.0033$; $\Delta CFI = 0.010$). Specifically, the influence of both TBL and LWH is more positive in males and not significant in females when estimated freely. Our findings suggest that sexual dimorphism in the allometric relationships between body and median and hind legs may be related to a balance between sexual selection and viability costs. The absence of modularity in both male and female hemelytra further indirectly supports this conclusion. The intercepts of LWH and interocular space in males are higher than in females ($\chi^2_{diff} = 67.37$, $df = 12$, $P < 0.001$; $\Delta CFI = 0.032$), and such a sexual dimorphism may be related to the sexual role reversal in *B. angustum*.

The oldest chinch bug Blissidae (Hemiptera, Heteroptera) from the Eocene Oise amber

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Oise amber, also called Paris amber, has been discovered in Lowermost Eocene (Ypresian, 53- 55Ma) lignitic sands of Oise Department in the early 90's. A large amount of this highly fossiliferous amber is now housed in the collection of the Muséum National d'Histoire Naturelle in Paris (MNHN) with more than 24,000 inclusions. Investigations in Oise amber is highly valuable for insect studies, being among the first fossiliferous deposits from the post K-Pg boundary. Hemiptera is one of the dominant orders in number of specimens and diversity. We described a new Blissidae *nov. gen, nov. sp.* using regular imaging methods and fluorescence microscopy to enhance description and facilitate taxonomic assignation. This fossil is the oldest undoubtful Blissidae. Eocene Oise amber is one of the most diverse outcrop for Heteroptera palaeodiversity, including the oldest Piesmatidae and Thaumatoscoridae, Miridae and Reduviidae representatives.

Associations between Harpactorinae (Reduviidae) and plants: a fact possibly more common than recorded

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Reduviidae is the second largest family of true bugs (Hemiptera, Heteroptera), while its subfamily Harpactorinae contains the greatest number of genera and species. In the New World, Harpactorinae contains two tribes: Apiomerini and Harpactorini. Almost all reduviids are predators. However, several observations have shown that certain reduviids, particularly members of the tribe Harpactorini may be associated with particular plants. These generalist predators frequently live on a particular plant species, not only as adults but sometimes also as immature instars. Besides seeking prey, these species apparently became adapted to visiting these plants species exclusively. In addition to hosting the arthropod prey species the assassin bugs feed on, these plants provide additional resources such as sugary or proteinaceous secretions produced in extrafloral nectaries or other structures. Yet, members of tribe Apiomerini, such as species of *Apiomerus* collect plant resins with their forelegs that may facilitate prey capture in immature and adults. In females, this resin is particularly important during oviposition. The second author have added recent observations on various species of

Reduviidae, mostly Harpactorini, in Argentina (Misiones), associated to some plants as well as the occurrence of use of nectar as alimentary source by them, which will be cited here. The observations correspond to visitors of the family Apocynaceae (Asclepiadoideae), which attract floral visitors using colors and aroma of the flowers, as well as a reward in nectar. A total of 13 species of Asclepiadoideae were recorded as being visited by 15 species of Reduviids, most of the latter visiting flowers, alternating the capture of preys with nectarivory. The absence of pollinia in legs was observed too. *Notocyrtus dorsalis* (Harpactorini) was observed feeding only with nectar, without any observation of predatory events by this species. The oviposition on leaves of *Oxypetalum erianthum* by *Harpactor angulosus* (Harpactorini) was also observed. Likewise, the oviposition and stalking of prey in leaves of *Macrosepis elliptica* by *Bactrodes* (Bactrodinae) was recorded. These observations reinforce that the associations between Reduviidae, mainly those belonging to Harpactorinae subfamily, and plants is probably a fact more common than have been recognized and must be recorded and more thoroughly studied.

Presentation of the superfamily Pentatomoidea preliminary catalog of Spain (Acanthosomatidae, Cydnidae, Pentatomidae, Plataspidae, Scutelleridae, Thyreocoridae)

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Pentatomoidea is a well-defined superfamily with six families included within the Spanish fauna: Acanthosomatidae, Cydnidae, Pentatomidae, Plataspidae, Scutelleridae, and Thyreocoridae, bringing together 80 genera and 197 species. The members of this group have a wide range of eating habits and habitat selection, which is the reason why they are present in most of the terrestrial ecosystems. Some of the species are of economic importance because they may become crop pests or, on the contrary, they can be useful as pest predators, like the members of the subfamily Asopinae. There are no precedents for an exhaustive catalogue of the Heteroptera in the Spanish area besides some old incomplete checklists. To prepare this Poster more than 300 published papers dealing with the superfamily Pentatomoidea have been reviewed, in order to set up the first catalog of the Pentatomoidea from Spain, including the Balearic Islands and the Canary Islands. Moreover, in order to alleviate the lack of bibliographic information resulting from some less sampled areas it was useful to supplement this information with occurrence data from verified photo-sharing websites. The records of Pentatomoidea species were assembled to build a comprehensive species distribution data set, and thus the Pentatomoidea assemblages in each geographic area considered were stated. The richness of taxa belonging to different biogeographic categories was mapped for the Spanish provinces,

revealing patterns of species segregation. In addition, a hierarchical clustering approach yielded a general view of Spanish Pentatomoidea biocenoses associations.

Survey of the aquatic and semiaquatic bugs (Heteroptera: Gerromorpha & Nepomorpha) from Marambaia Island, Rio de Janeiro State, Brazil

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Marambaia Island (23°02'S, 43°35'W, 23°04'S, 44°00'W) is located on the southern coast of Rio de Janeiro State, Brazil. It is an important and preserved area of Atlantic Forest, with a phytophysognomy composed of areas of coastal Atlantic rainforest and restinga. The island is managed by the Brazilian Navy, which helps in the preservation of the area. Despite its relevance, only one species of aquatic or semiaquatic bug (Heteroptera: Gerromorpha & Nepomorpha) was recorded from the region: *Hydrometra argentina* Berg, 1879. In the present study, monthly collections were carried out in three rivers of the island: Rio Marambaia, Rio Sebastopol, and Rio da Praia João Manoel. At each sampling station, manual collections were carried out on six types of substrates: sand, fixed rocks, loose rocks, submerged leaf litter, floating leaf litter, and moss. In the Rio Marambaia, due to its extension, collections were carried out in four different stations separated from each other by a distance of 200 m, whereas only one station was selected in the other rivers. Five excursions were carried out between May and September 2018. A total of 340 specimens were collected, distributed in five families: Gerridae, Mesoveliidae, Veliidae (Gerromorpha), Belostomatidae, and Notonectidae (Nepomorpha). Among the Gerridae, the species identified were *Brachymetra albinervis* (Amyot & Serville, 1843) (n = 169), *Halobatopsis platensis* (Berg, 1879) (n = 16), *Tachygerris adamsoni* (Drake, 1942) (n = 2), *Limnogonus aduncus* Drake & Harris, 1933 (n = 6), and *L. ignotus* Drake & Harris, 1934 (n = 2). Two species of Veliidae were recorded, namely *Microvelia pulchella* Westwood, 1834 (n = 40) and *Rhagovelia itatiaiana* Drake, 1953 (n = 52), whereas one Mesoveliidae was represented in the samples: *Mesovelia mulsanti* White, 1879 (n = 2). Finally, two species of Nepomorpha were found: *Buena platycnemis* (Fieber, 1851) (Notonectidae, n = 50) and *Lethocerus annulipes* (Herrich-Schäffer, 1845) (Belostomatidae, n = 1). Despite intensive collections, no specimens of *Hydrometra argentina*, previously reported from the island, have been found yet.

Catalogue of genera of Assassin-bugs (Hemiptera: Heteroptera: Reduviidae) of the Rio Grande do Sul State, Brazil

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Assassin bugs (Reduviidae) are the second largest group within Heteroptera, with 25 subfamilies and more than 7000 species distributed around the world. They have a characteristic predatory habit, morphology quite diverse and several feeding and behavioral habits; besides, they are of economic importance as potential agents of biological control and in public health, being vectors of diseases. Despite of the importance and diversity of this family, at least in Brazil, faunistic studies and up-to-date revisions are scarce; with research efforts mostly about the subfamily of medical importance (Triatominae). Rio Grande do Sul (RS) is located at the south of Brazil, sharing borders with Uruguay and Argentina, presents subtropical climate and it is composed by two of the most threatened biomes: Mata Atlântica and Pampa. The Brazilian Fauna Taxonomic Catalog (2018) register in Brazil about 18 subfamilies and 121 genera, and for RS eight subfamilies and near to 28 genera, but the majority records without specific geographic distribution. Here, we examined about 1200 specimens deposited in the most important entomological collections of the state: (MCNZ) Museu de Ciências Naturais, Fundação Zoobotânica do Rio Grande do Sul; (MCTP) Pontificia Universidade Católica do Rio Grande do Sul, Museu de Ciências; (MGAP) Museu Anchieta de Ciências Naturais; (UFRG) Universidade Federal do Rio Grande do Sul, Instituto de Biociências; and (FURG) Coleção entomológica da Universidade Federal de Rio Grande; and we provide the first catalogue of Reduviidae genera for RS/Brazil with taxonomic information, diagnosis, distribution within RS and Brazil, comments and examined material for each genus. Besides, macrofotografies of habitus in dorsal and lateral view, taxonomic key for the genera of Reduviidae that occur in RS and distribution maps are provided. We record 55 genera and 11 subfamilies of Reduviidae for Rio Grande do Sul state, as follow: Bactrodinae (1 genus); Ectrichodiinae (7 genera); Emesinae (9 genera); Hammacerinae (1 genus); Harpactorinae (18 genera); Peiratinae (5 genera); Phymatinae (2 genera); Reduviinae (4 genera); Saicinae (1 genus); Stenopodainae (7 genera) and Triatominae (2 genera).

New record of *Brontocoris tabidus* (Hemiptera: Pentatomidae) attacking larvae of *Heteroperreyia hubrichi* (Hymenoptera: Pergidae)

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Brazilian peppertree (*Schinus terebinthifolia* Raddi, Anacardiaceae) is a Neotropical species whose native range extends along the Atlantic coast of Brazil, west to north-eastern Argentina and adjacent Paraguay and Uruguay. This species has been introduced to many countries around the world as an ornamental. Currently, Brazilian peppertree is one of the most aggressive and widespread invasive species in Florida, Hawaii, and Texas (USA). A potentially host-specific species is the defoliating sawfly, *Heteroperreyia hubrichi* Malaise (Hymenoptera: Pergidae), which has been intensively studied as a biological control candidate of Brazilian peppertree. This species is known to occur in southern Brazil and northeastern Argentina feeding on the leaves of *S. terebinthifolia* and on the closely related species *S. weinmannifolia* Engl. Like other members of the Pergidae sawfly family, this species is known to produce cytotoxic peptides. Additional host specificity studies with *H. hubrichi* have been delayed because of the potential for poisoning native wildlife and domesticated animals that may consume the insect larvae. However, given the restricted host range of *H. hubrichi*, the utilization of this species as a biological control agent for *S. terebinthifolia*, is being reconsidered. During 2017-18, while conducting surveys of plant use under natural conditions in the native range of *S. terebinthifolia* in Argentina and Brazil, nymphs and adults of the stink bug *Brontocoris tabidus* (Signoret) (Hemiptera: Pentatomidae) were found attacking *H. hubrichi* larvae feeding on *S. terebinthifolia* leaves in Misiones Province, Argentina. In March 2018, while surveying for natural enemies of *S. terebinthifolia* in southern Brazil, *B. tabidus* adults were also found attacking *Heteroperreyia* n.sp. larvae feeding on *S. terebinthifolia*. The genus *Brontocoris* includes only two species, *Brontocoris nigrolimbatus* (Spinola) from Chile, Uruguay and Argentina; and *B. tabidus* from Chile, Brazil, Paraguay and Argentina. In Brazil, *B. tabidus* is a generalist predator that naturally controls defoliating Lepidoptera caterpillars in Eucalyptus plantations. Among the many prey used by this species, *B. tabidus* is known to prey on another leaf-feeding sawfly, *Haplostegus nigricrus* Conde (Hymenoptera: Pergidae), this one feeding on *Psidium guajava* (Myrtaceae). The predation by *B. tabidus* on *Heteroperreyia* species constitutes a new record. If *H. hubrichi* is approved for the biological control of Brazilian peppertree in the US, predation by similar members of the Pentatomidae in the invaded range may decrease its performance against *S. terebinthifolia*.

A new apterous Blissidae (Hemiptera: Heteroptera: Lygaeoidea) from Ecuador and the first blissid with a tymbal-like organ

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The worldwide distributed family Blissidae, includes species that feed exclusively on the sap of monocots. According to Lygaeoidea SpeciesFile, the family comprehends 421 species

and 28 subspecies in 54 genera. Nineteen genera occur in the Western Hemisphere, and excepting the cosmopolitan genus *Ischnodemus* Fieber, the other 18 are restricted to the Western Hemisphere. Many blissids are fully macropterous or submacropterous, but also many taxa present some degree of forewing reduction or modification, and several micropterous and only one apterous form are known. Among the six micropterous genera from the Western Hemisphere the genera *Aulacoblissus* Slater known from Venezuela, *Barrerablissus* Brailovsky from Ecuador, *Heteroblissus* Barber from Argentina and Brazil, *Napoblissus* Brailovsky & Barrera from Ecuador, and *Wheelerodemus* Henry & Sweet from USA are monotypic; and the genus *Praetorblissus* Slater includes six species from Mexico, Costa Rica, Peru and Bolivia. All these species, excepting *P. wilcoxae*, present a micropterous condition. The genus *Howdenoblissus* Štys, described to accommodate the new species *H. slateri*, known from a single female from Colombia, constitute the first apterous species in the Lygaeoidea. In this contribution, a new genus and a new apterous species from the Ecuadorian mountain rainforest is described. The apterous condition in this new species, with only small protuberances representing forewings is similar, but more extreme, to the "neotenous apterism" exhibited in *Howdenoblissus*. We also recorded the male drumming inside leaf sheaths of bamboo. The low frequency sound emitted, the up and down vibration of abdomen observed in the field, and the fused first two tergites that are folded on both sides of the middle line are consistent with a tymbal mechanism. Tymbal organ have been reported in several families of Heteroptera, but in Lygaeoidea it was only observed in a very few species. This constitute the first record in the Blissidae. Digital photographs of the adults, and main characters including the male genitalia are provided, as well as oscillograms of the low frequency vibrational song.

A new species of *Paraneella* Carvalho, 1954 (Heteroptera: Miridae) from México

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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 family of insects, with more than 11.130 described species, or about 25% of the true bugs. Plant bugs are found in most zoogeographic regions of the world, in the Neotropics there are approximately 561 genera and 3400 species. The family is currently divided in seven subfamilies. Among them, the Brycorinae, representing the fourth-largest subfamily of the Miridae, are a highly diverse group in terms of feeding habits, external morphology and thoracic, pretarsal and genitalic structures, that comprise 200 genera worldwide within five tribes. Comparatively little taxonomic attention has been focused in this subfamily in the last 50 years; most of the recent taxonomic work consist of isolated descriptions of species and genera or regional treatments of Asian and Australian fauna. The Eccritotarsini is the largest tribe and are particularly diverse in the Neotropical Region, where 70 genera and 452 species are known. Its species are recognized by the swollen femoral trichobothrial bases, the fleshy

pulvilli attached to the inner surface of the claw, the asymmetrical parempodia, the dilated tarsi, the greatly reduced metathoracic scent gland opening, the single closed membranal cell, and the strongly developed male genitalia. The monotypic genus *Paraneella* Carvalho 1954 is related with the genera *Neella* Reuter 1908 and *Neoneella* Costa Lima 1942. It is characterized by the structure and length of the first antennal segment, the shape and pubescence of posterior femora, and the very small and flat scutellum. The only species described until now, *Paraneella amazonica*, is based on a single female from Itacoai River in Amazonas (Brazil). During the study of specimens from Instituto de Biología de la UNAM, within the context of the doctoral thesis project of the first author, a new species of *Paraneella* from Mexico was identified, that is herein described including morphological and male and female genitalic characters.

Two New Species of *Acanthocephala* Laporte (Hemiptera: Coreidae) from Bolivia and Colombia

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The Coreidae or leaf-footed bugs are a diverse group that includes the larger terrestrial Heteroptera of striking colors and frequently collected. They present a cosmopolitan distribution, showing greater diversity in tropical and subtropical areas. These insects are phytophagous, and many have a specific association with particular plants, being some of them important agricultural pests. The family contains 519 genera with about 3,098 species worldwide, of which 158 genera are found in the Neotropical region. The genus *Acanthocephala* Laporte belongs to the Acanthocephalini, and includes 26 species distributed from Canada to Argentina. Species of *Acanthocephala* are among the largest coreids from America, reaching lengths up to 34 mm, and some of them have been reported as regular pests of crops. They can be recognized by the sharply pointed tylus projecting beyond juga as a compressed plate, the strongly incrassate and dorsally spined or tuberculate hind femora in males, and the sinuate or toothed expanded hind tibiae in both sexes. Most of the species were described in the 19th century and there is confusion about the identity of most of them. Little is known about their host plants, immature stages, and their distribution is inferred from a very few records. The knowledge about the South American species is really poor. According to the literature, there are 15 species recorded from this region, but this number is far from the real diversity from the Neotropics. Recently, Brailovsky studied the Mexican fauna and highlighted the need for a taxonomic revision of the group. Within the context of the doctoral thesis project of the first author, the phylogenetic revision of the genus *Acanthocephala* and related genera is being carried out. In this contribution we describe two new species of *Acanthocephala* from Bolivia and Colombia.

The taxonomic value of the female genitalia in *Euschistus* (*Euschistus*) Dallas, 1851

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Euschistus Dallas, 1851, popularly known as brown stink bugs, is the largest genus within Carpororini, currently comprises 67 species, distributed in 3 subgenera. This genus is restricted to the New World, and some species are important pest for several crop plants. Regarding the nominal subgenus (54 species). Empirical groupings are being proposed within the subgenus *Euschistus*, i.e. the groups *crenator*, *strennus* and *sulcatus*. These groupings are based on general morphology as well as external male genitalia, not including female genitalia information to distinguish the taxa. There is little knowledge dealing with the female genitalia of *Euschistus*. Stål inferred a group of species based on external morphology and geographical distribution. Here we explored both internal and external genitalia of the group suggested by Stål, evaluating seven taxa: *Euschistus ictericus* (Linnaeus), *E. variolarius* (Palisot de Beauvois), *E. latimarginatus* (Zimmer), *E. inflatus* (Van Duzee), *E. servus servus* (Say) *E. servus euschistoides* (Vollenhoven), and *Euschistus tristigmus* (Say), aiming search for structures with taxonomic value, and also summarize the knowledge of female genitalia of *Euschistus* (*Euschistus*). Except for *E. tristigmus*, the analyzed species share some characteristics on the genital plates: posterior margin of gonocoxites VIII concave, posterior margin of laterotergites IX surpassing the band that unites dorsally the laterotergites VIII, apex of segment VII not reaching the posterior margin of laterotergites IX. The internal genitalia present ductus receptaculi proximalis at least twice longer than vesicular area, conical pars intermedialis, and globose capsula seminalis. *Euschistus tristigmus* presents laterotergites VII with slightly concavity on the postero-lateral region and the ductus receptaculi proximalis shorter than vesicular area. Female genitalic features are strongly variable within *Euschistus* (*Euschistus*). Besides the shape of the genital plates, we highlight variation on capsula seminalis (e.g. elliptical), pars intermedialis (e.g. cup-like, cylindrical) and ductus receptaculi varying on length and form. These variations may provide valuable information to distinguish the species. Female genital features, both external and internal, seems to be conserved within those empirical groups of species in the subgenus *Euschistus*. This reinforces the hypothesis of a possible evolutionary relation among these species, and demonstrates the taxonomic value of female genitalic morphology. Although the female genital features differ from the remaining species of the subgenus, only a phylogenetic analysis will corroborate with an evolutionary relation hypothesis among these species. We suggest that, in order to elucidate the relationships between the groups within *Euschistus*, data on female genitalia should be included in future studies.

A new genus of Neotropical Veliinae, with four new species from Colombia (Heteroptera: Gerromorpha: Veliidae)

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The subfamily Veliinae (Heteroptera: Gerromorpha: Veliidae) is represented in the Neotropical Region by the genera *Oiovelia*, *Paravelia*, *Platyvelia*, *Steinovelia*, *Stridulivelia*, and *Veloidea*. *Paravelia* differs from *Platyvelia* and *Steinovelia* in the position of the tubercles on the thoracic sternites, which are absent or located centrally, and from *Stridulivelia* by the absence of stridulatory structures on the hind femur and dorsal connexiva, and further absence of transverse lateral sulci on the abdominal sternites. There are 61 valid species of *Paravelia*, recorded from the Neotropical Region, with the exception of *P. taipiensis* from the Marquesas Islands. *Paravelia* is similar to *Oiovelia*, from which it differs by the shape of tarsomere III, with the lateral margins usually parallel in the former, whereas the lateral margins diverge in the latter. *Paravelia* is probably not monophyletic, and a robust phylogenetic analysis is necessary to delimit genera within Neotropical Veliinae and establish the relationships among them. Previous students of Neotropical Veliidae have long recognized the distinctive attributes of a subgroup of *Paravelia* species occurring in the Andes, which were treated in part as the *inveruglas* group. Species conforming to this group possess the following putative synapomorphies: development of prominent setal tufts or sclerotized wing-like processes on the male proctiger; elongate body shapes, with length-to-width ratios ranging from ~3.0–4.5; and a uniformly blackish forewing coloration, lacking pale markings of any sort. To the above can also be added: antennae with segment I longest; very long and slender legs in relation to the body, with the length of hind leg exceeding that of the body; and the terminal female abdomen with tergite VIII deflected downward. We propose a new genus for the species of *Paravelia* possessing the above character states, namely *P. boliviana*; *P. columbiensis*; *P. daza*; *P. flavomarginata* [= *P. amoena*]; *P. inveruglas*; *P. osborniana*; and *P. willei*. In addition, we describe four species of the new genus from the Colombian departments of Boyacá, Antioquia, Norte de Santander, and Quindío. Ecologically, the members of the new genus occur at high elevations in the Andes (between 1500 and 3600 m), and possess semi-terrestrial habits that are notably different from other species held in *Paravelia*. All of the included species have very long legs in relation to the size of their bodies, which appear to aid in terrestrial locomotion.

Aquatic and semiaquatic bugs (Heteroptera: Gerromorpha & Nepomorpha) from Tolu viejo Municipality, Sucre Department, Caribbean region of Colombia

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Colombia is located in the tropical South America and considered one of the megadiverse countries of the world, which together contain 70% of the global biodiversity. Five geographic regions are recognized in the country: Caribbean, Andean, Pacific, Orinoquia, and Amazonia. Sucre Department, in the Caribbean region, is divided into five subregions: La Mojana, Montes de Maria, Morrosquillo, Sabanas, and San Jorge. This department shows a considerable number of ecosystems, including mangroves, swamps, and savannas, among others. Tolu viejo Municipality is part of the Montes de Maria subregion and has different landscapes, such as plains, foothills, hills, and mountains reaching altitudes slightly above 1,000 m. Over 300 species of aquatic and semiaquatic bugs (Heteroptera: Gerromorpha & Nepomorpha) have been recorded from Colombia, but many areas of the country remain largely unexplored, including Sucre Department, where only 15 genera and 21 species have been reported so far. We present here a survey of the aquatic and semiaquatic bugs from four streams (Pechilín, Bobo, Camarón, and Macaján) located in Tolu viejo Municipality, which is an important contribution to our knowledge of the diversity of these insects in the dry tropical forests of Sucre Department and the Colombian Caribbean. Representatives of 8 families, 20 genera, and 32 species have been collected, increasing the diversity known from the region by 109.5%. Out of the sampled species, *Curicta montei* De Carlo, 1961, *Martarega hondurensis* Bare, 1932, *Microvelia mimula* White, 1879 and *Ovatametra obesa* Kenaga, 1942 are recorded for the first time from Colombia. In addition, *Buena platycnemis* (Fieber, 1851) *Centrocorisa kollari* (Fieber, 1851), *Martarega pacifica* Manzano, Nieser & Caicedo, 1995, *Mesovelia amoena* Uhler, 1894, *Mesoveloidea williamsi* Hungerford, 1929, *Platyvelia brachialis* (Stål, 1860), *Ranatra parvula* Kuitert, 1949, and *Tenagobia incerta* Lundblad, 1928 are reported for the first time from the Colombian Caribbean region. Furthermore, *Gelastocoris flavus flavus* (Guérin-Méneville, 1835), *Gelastocoris hungerfordi* Melin, 1929, *Gelastocoris major* Montandon, 1910, *Hydrometra caraiba* Guérin-Méneville, 1857, *Limnogonus hyalinus* (Fabricius, 1803), *Mesovelia mulsanti* (White, 1879), *Microvelia longipes* Uhler, 1894, *Microvelia panamensis* Champion, 1898, *Microvelia pulchella* Westwood, 1834, *Rheumatobates bergrothi* Meinert, 1895, and *Trepobates taylori* (Kirkaldy, 1899) are newly recorded from Sucre Department. Finally, additional records are presented for *Brachymetra albinervus* (Amyot & Serville, 1843), *Limnogonus aduncus* Drake & Harris, 1933, *Rhagovelia calopa* Drake & Harris, 1927, *Rhagovelia elegans* Uhler, 1894, *Rhagovelia tenuipes* Champion, 1898, *Tachygerris opacus* (Champion, 1898), *Telmatometra ujhelyii* Esaki, 1926, *Trepobates panamensis* Drake & Hottes, 1952, and *Trepobates trepidus* Drake & Harris, 1928.

New records of semiaquatic bugs (Hemiptera: Heteroptera: Gerromorpha) from Vale do Ribeira, southern Brazil

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The suborder Heteroptera (Insecta: Hemiptera) includes a majority of terrestrial species, but also several that occupy aquatic environments. Gerromorpha is an infraorder of Heteroptera represented almost entirely by semiaquatic bugs. They are predators, playing an important role on aquatic ecosystems, and can be used as indicators of biological quality. The eight Gerromorphan families include about 160 genera and 2,100 extant species. Vale do Ribeira is a region encompassing areas from southeastern São Paulo and northeastern Paraná states, including the Ribeira de Iguape River Basin and the Estuarine Lagoon Complex of Iguape-Cananéia-Paranaguá. It extends through 2,830,666 hectares and 31 municipalities (22 in São Paulo and nine in Paraná). The region's forests are highly preserved and ecologically diverse, representing about 21% of the remaining Brazilian Atlantic Forest. However, very little is known about the diversity and distribution of the aquatic fauna of Vale do Ribeira, where studies are scarce. The current study presents new records of Gerromorpha from the region, based on material collected from January to June of 2013. Only two species of Gerromorpha had been previously recorded from Vale do Ribeira (municipalities of Barra do Turvo, Cananéia, and Iporanga), namely *Rhagovelia occulcata* Drake, 1959 and *R. trepida* Bacon, 1948. Here, we record seven species for the first time from the region: *Mesovelia bila* Jaczewski, 1928; *Microvelia nelsoni* Moreira, Barbosa & Ribeiro, 2012; *M. venustatis* Drake & Harris, 1933; *Paravelia bilobata* Rodrigues, Moreira, Nieser, Chen & Melo, 2014; *R. plaumanni* Polhemus, 1997; *R. robusta* Gould, 1931; and *R. zela* Drake, 1959. Specimens of *R. occulcata* and *R. trepida* were also collected in localities of Vale do Ribeira not yet reported in the literature.

Review of the genus *Mecidea* Dallas in the Americas (Hemiptera: Pentatomidae: Mecideini)

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The genus *Mecidea* Dallas includes 17 species found in all biogeographic regions except for the Australian region, associated with xeromorphic environments. In the American Continent, 4 species are known: *M. major* Sailer and *M. minor* Ruckes mostly known from Central and North America (Costa Rica, Honduras, Mexico, Nicarágua, South and Southwest of the USA), *M. longula* Stål, Central and North America (Caribbean and Florida in the USA), and

M. pampeana Sailer, from South America (Argentina and Uruguay). Recently, a species of *Mecidea* was discovered in Brazil, collected from localities within Caatinga and Cerrado ecorregions, States of Goiás and Pernambuco. This species is very similar to *M. major* and *M. pallida* (from the Afrotropical region), but characteristics such as larger size, shape of the dorsal and ventral rim of pygophore, and shape of the paramere, support that it represents a new species. This paper presents a review of the *Mecidea* spp. that occur in the American continent, highlighting diagnostic characters of each species. We also present detailed comparative analysis of the male genitalia of *M. major*, *M. pallida* and the new species, discussing on their status as valid species. Updated distribution maps will be provided.

Unraveling the identity of the ambush bug *Phymata (P.) chilensis* Handlirsh (Hemiptera: Reduviidae: Phymatinae)

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The Phymatinae Laporte subfamily includes a peculiar group of reduvids commonly called “ambush bugs” by the way they capture their preys. They are cryptic species that stand on herbs and flowers waiting for insects that come to feed. Some species show strong sexual dimorphism and unusual reproductive behaviors. The taxonomy of the group is complex, 13 species are polytypical, many polymorphic and also widely distributed. The species delimitation is restricted to a few morphologic and coloring characters, the descriptions usually have been made on the basis a few specimens without considering the intraespecific variability. *Phymata* Latreille, 1802 includes about 108 species that are grouped in four subgenera of mainly Nearctic and Neotropical distribution, the subgenus *Phymata* is the most diverse with 103 species. *Phymata (P.) chilensis* Handlirsch includes six subspecies from southern South America, most of them from Argentina. These subspecies were described on the basis of differences in the shape and development of the lateral angles of the pronotum, studying a few specimens with particular distributions, that after analyzing many specimens, overlapped. The objective of this work is to review the identity of the subspecies of *Phymata (P.) chilensis*. We comparatively studied the morphology of the shape and height of lateral angles of pronotum (measurements, angles and proportions); the male genitalia and the distributional patterns; these variables were analyzed by multivariate statistical analysis techniques. In order to reinforced our results, we proposed to apply a geometric morphometry analysis using MorphoJ software, and the Niche Distributional Modelling.

Taxonomic key of Ochlerini (Pentatomidae: Discocephalinae) genera – a new taxonomic treatise of an enigmatic group of Pentatomidae

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Ochlerini is a tribe within the subfamily Discocephalinae. A phytophagous group, endemic to the Neotropics. A key of the tribe was last produced by Rolston in 1992 where he recognized 28 genera, 9 of which were new. Twenty-six years later, a few genera have been described and the tribe itself was tested as monophyletic but a revised taxonomic key of the tribe remains elusive. The absence of a new key may be a consequence of the tribe itself exhibiting strong cryptic making it difficult for systematists to identify characters needed in constructing a key; and subsequent authors would have to re-examine *Ochlerus*, a paraphyletic genus composed of ~ 18 species. Currently, Campos and his colleagues have tackled this seemingly difficult genus, yielding several new genera. In this current treatise of Ochlerini, we provide a key to all 39 genera, including 3 undescribed genera from the *Ochlerus*-species complex, *Xynocoris*, *Ocellatocoris*, *Parastalius*, *Stapecolis*, *Smiliforstonia*, and *Hondocoris*; re-examine characters of male and female terminalia; and include new information on nomenclature and distribution.

Systematics and character evolution of *Ascra*, a new genus within Edessinae

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Ascra is a recently created genus of Edessinae in 2015. Most of its biodiversity is concentrated in Central America, particularly Mexico. Considered a basal genus in Edessinae by the lack of humeral angles. *Ascra* can be recognized by the body densely punctuated; tumid pronotum; proctiger extending or surpassing the posterior plane; and moderate to extensive tumidness on the dorsal surface of the proctiger. There are currently 14 species, six published and eight unpublished. Despite the extensive taxonomic work achieved for *Ascra*, its monophyly has not been examined. Therefore, we intend to test the monophyly of all 14 species using phylogenetic analyses in PAUP 4.0; and discuss the morphological evolution of the proctiger and metasternal process.

Biogeography and diversification of Holarctic water striders: Cenozoic temperature variation, habitat shifting and multiple intercontinental dispersals

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It is now rare to find a semi-aquatic organism group with which to vigorously test whether their diversification model and distribution pattern are closely related to the Cenozoic temperature variation. This hypothesis is explored for water striders of the genera *Aquarius* Schellenberg, *Gerris* Fabricius and *Limnopus* Stål, which comprise a monophyletic clade with primarily Holarctic distribution. We sample almost 90% of the currently recognized *Aquarius*, *Gerris* and *Limnopus* species. Five DNA fragments from 62 species are used to reconstruct a phylogram. Divergence time is estimated using Bayesian relaxed-clock method and three fossil calibrations. We investigate diversification dynamics, biogeography and ancestral state reconstruction by using maximum-likelihood, Bayesian and parsimony approaches. Our results showed that the crown of the three genera originated and underwent an initial diversification in Asia at 72 Ma (HPD: 59–86 Ma) in the Late Cretaceous, subsequently expanding into other regions via dispersal. The Bering Land Bridge was the major migration route between Eurasia and North America but was interrupted before the early Oligocene (34 Ma). Ancestors most likely used lentic habitats, and a minimum of two independent shifts to lotic habitats occurred in the initial diversification. Cenozoic temperature variation regulated the evolutionary history of Holarctic water striders of the genera *Aquarius*, *Gerris* and *Limnopus*. Temperature warming during Stage I (52–66 Ma) was associated with the disappearance of shallow lentic habitats; this phenomenon forced certain lentic lineages to colonize new lotic habitats and promoted the diversification of lineages. Temperature cooling during Stage II (after 34 Ma) was associated with the fragmentation of water habitats of the "mixed-mesophytic" belt, resulting in the extinction of historical taxa and influencing close lineages that shaped the present disjunct Eurasian–North American distribution.

The first two authors contributed equally to this study.

Pattern of endemism of Miridae (Insecta: Hemiptera) in China is conserved by mountain regions with high ambient energy, topographical heterogeneity and climatic stability

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Aim: Effectively identifying conservation priorities and detecting the mechanisms underlying the pattern of endemism are vital for studying and protecting the endemism of species. We studied the plant insects, Miridae, to delimitate the hotspots and areas of endemism and investigated the environmental correlates underlying the richness patterns. **Methods:** Based on long-term field work and well-documented taxonomic studies, we digitized and assembled a map of richness and endemism for Miridae in China. We identified both hotspots and areas of endemism by combining grid-based and Geographic Information System (GIS) analysis methods. We used a complementary algorithm and neighborhood statistics for hotspots, and the Endemicity Analysis (EA) and the Geographical Interpolation of Endemism (GIE) for areas of endemism. The potential environmental drivers of richness patterns were tested by three models: an ordinary least square (OLS), a simultaneous autoregressive regression (SAR) and hierarchical partitioning (HP). **Results:** We identified six hotspots and four areas of endemism. Most of these areas were located in mountain regions of southwestern China. The results from three statistical models suggest that the Net Primary Productivity (NPP), the Elevation Range (ER) and the Glacial-interglacial Mean Annual Temperature (V_{MAT}) were potential drivers of richness patterns of endemic species, while ER and V_{MAT} had minor influences on the richness of all species and nonendemic species. **Main conclusions:** Our results suggest that mountain regions conserve the endemism of Miridae in China. The species richness patterns revealed that the ambient energy, topographical heterogeneity and climatic stability were potential explanations of the driving mechanism the pattern of endemism, which provide the support to identify conservation priorities for endemism.

The first two authors contributed equally to this study.

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