



## **Taxonomy - faster. Better**

**Michael Balke**

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The term “turbo-taxonomy” was recently coined for an approach combining *cox1* sequences, concise morphological descriptions by an expert taxonomist, and high-resolution digital imaging to streamline the formal description of larger numbers of new species. We further developed this approach and demonstrate the functionality of a species-description pipeline by naming 101 new species of hyper diverse New Guinea Trigonopterus weevils in the open-access journal ZooKeys. We conclude that fast track taxonomy will not only increase speed, but also sustainability of global species inventories. It will be of great practical value to all the other disciplines that depend on a usable taxonomy and will change our perception of global biodiversity. While this approach is certainly not suitable for all taxa alike, it is the tool that will help to tackle many hyper diverse groups and pave the road for more sustainable comparative studies. Finally, we will present a proposed large-scale pilot study in Indonesia, and argue that fast track taxonomy and the BIN system will have to work hand in hand to provide objective, sustainable data in such a large framework where it is hopeless to assume that traditional tools will be able to inform stakeholders about the contents of a given area.

## **Global Digital Infrastructure for Biological Nomenclature and Taxonomy**

**Ellinor Michel, Richard L. Pyle & Robert P. Guralnick**

Michel, E., Pyle, R. L. & R. P. Guralnick (2014): Global Digital Infrastructure for Biological Nomenclature and Taxonomy. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The future for interoperable scientific information is digital, yet scientific names, the handles for all biodiversity information, remain without an integrated system tied to published descriptions and museum type specimens. Descriptions and type specimens provide standards for the otherwise fluid concepts of biological taxa. We are working to unify the infrastructures for biological nomenclature across nomenclatural codes (including zoological (ICZN - <http://iczn.org/>), botanical (ICNafp - <http://www.iapt-taxon.org/nomen/main.php>) and bacterial (ICNB) codes) through the Global Names Architecture (GNA). Our initial focus is on animal names, as these comprise the largest component of metazoan biodiversity and ZooBank



(zoobank.org) is the first code-related online nomenclatural registration system. Users are applied scientists in agriculture, medicine, veterinary science and climate change research; biodiversity researchers such as ecologists, physiologists; archives such as museums; the scientific publishing community – in short, all users of scientific names of organisms based on the work of taxonomists.

### **Streamlining descriptions of new species identified with barcode data**

**Lyubomir Penev & Pavel Stoev**

Penev, L. & P. Stoev (2014): Streamlining descriptions of new species identified with barcode data. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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We offer a solution for streamlining of descriptions of new species among the “dark taxa” identified as such with barcode data by establishing a data export and publication workflow between BOLD and Pensoft. Voucher specimens metadata (e.g., occurrences, images, classifications, methodology applied, etc.) that are deemed to represent new taxa (e.g., their BIN numbers do not match a particular taxon concept) could be imported from BOLD into Pensoft’s Writing Tool (PWT) through PWT’s API “at the click of a button”. In this way, the authors will generate a taxonomic manuscript, comprising a number of taxon treatments with their structural elements being automatically filled in.

Authors could then further elaborate the treatments by providing specific epithets, concise morphological description, diagnosis, type specification, or additional taxonomic remarks to complete the taxonomic description in a way to meet the requirements of the biological codes. The manuscript than could be extended further with Introduction, Results and Discussion and other sections to meet the standards of a conventional scholarly publication and then submitted for a community peer-review and publication in the Biodiversity Data Journal (BDJ).

On the day of publication, BDJ will return back to BOLD – either through automated metadata export or through a harvesting mechanism – all data and text of the published paper in machine-readable format, so that these could be linked back to the original BOLD record.

A similar workflow can be established also for data papers describing large data sets. Data paper manuscripts (also known as “barcode data release” papers) can be generated from the metadata descriptors at BOLD and submitted as almost finalized manuscripts into the data paper template of PWT and then to BDJ.

Analogous workflows but based on text file submissions (e.g., RTF) can also be established with ZooKeys and other journals.

### **The BIN system: Standardizing molecular operational taxonomy in animals**



**Sujeewan Ratnasingham**

Ratnasingham, S. (2014): The BIN system: Standardizing molecular operational taxonomy in animals. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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Many animal species are undescribed, and because the identification of known species is often difficult, interim taxonomic nomenclature has often been used in biodiversity analysis. By assigning individuals to operational taxonomic units (OTUs), these methods speed the study of biodiversity. Using DNA barcode data, it is possible for OTU designation can be automated, data can be readily archived, and results can be easily compared among investigations. This BIN system on BOLD exploits these attributes to develop a persistent, species-level taxonomic registry for the animal kingdom based on the analysis of patterns of nucleotide variation in the barcode region of the cytochrome c oxidase I (COI) gene.

**From BINs to Biodiversity: Rapid Arthropod Assessments using DNA Barcodes**

**Jeremy deWaard, Claudia Bertrand, Kara Layton, Angela Telfer & Monica Young**

deWaard, J., Bertrand, C., Layton, K., Telfer, A. & M. Young (2014): From BINs to Biodiversity: Rapid Arthropod Assessments using DNA Barcodes. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The vast majority of animal species in terrestrial ecosystems are arthropods, yet contemporary environmental assessments all but ignore this massive assemblage, and its susceptibility to disturbance is unmeasured. We address this shortfall through a time- and cost-efficient approach for terrestrial arthropod assessments based on DNA barcode analysis of specimens collected by Malaise traps. In a study we conducted in 2012 comparing several standardized techniques, Malaise traps were found to be the most efficient sampling method in terms of capturing the largest proportion of the arthropod assemblage with minimal effort. The material collected by Malaise traps are currently individually sorted, analyzed in a 384-well pipeline, and Sanger-sequenced; this approach permits the link between each barcode record and its source specimen to be maintained, and facilitates the construction of a barcode reference library based on carefully identified specimens. The assignment of taxonomy following analysis is achieved through matches with authoritatively identified records on Barcode of Life Data Systems (BOLD; [www.boldsystems.org](http://www.boldsystems.org)) and by collaborating with taxonomic specialists. This approach is currently employed in several ongoing studies, including a multi-year project inventorying arthropods in all of Canada's 45 National Parks (CNP). The CNP project is



currently running in its third year, and has completed analysis for the first year of field collection. In 2012, 14 sites and 189 weekly malaise samples were processed, to reveal nearly 150,000 specimens, and over 15,000 distinct Barcode Index Numbers (BINs), a reliable proxy for species. Another effective application of this approach involves the early detection of non-indigenous species (NIS) at Canada's ports. The Halifax Port project has analysed 20 weekly samples from a single Malaise trap in the vicinity of the port, and revealed several potential and known NIS, including the recently discovered beech flea weevil (*Orchestes fagi* (L.)). In the near future, this approach will require a shift to Next Generation Sequencing (NGS) to facilitate time- and cost-efficient sequencing of bulk samples. Initial NGS trial runs have resulted in high BIN recovery for bulk samples (>95%), but some analytical biases (such as amplification and body mass bias) require further fine-tuning of protocols. The integration of NGS analyses with DNA barcode reference libraries could ultimately set the global standard for rapid biodiversity assessment, one that finally includes the terrestrial arthropod component.

### **DNA barcode enabled ecological research on Geometridae in Papua New Guinea**

**Scott Miller**

Miller, S. (2014): DNA barcode enabled ecological research on Geometridae in Papua New Guinea. Pp. #### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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We presented examples of the multiple lines of research supported by DNA barcoding of the Geometridae of Papua New Guinea, as part of a large-scale study of insect-plant ecology and biogeography in forests in Papua New Guinea by the Binatang Research Centre. The foundation of the program has been characterization of the insects reared from woody plants, but we are increasingly combining those data with bioassessments of adults using light traps. DNA barcoding provides a rapid and accurate taxonomic framework, which is also instrumental in identifying caterpillars, detecting host-parasitoid interactions, linking historic types with modern specimens, and identifying host plants from caterpillar stomach contents. DNA barcodes add great value to the taxonomic and ecological data, making them useful to a broad range of research enterprises, and allowing linkage with other projects, especially through the BIN system.

### **Accelerating the inventory of Lepidoptera early-stages and host-plant & other associations, by using citizen-science projects**

**Hermann S. Staude**

Staude, H. S. (2014): Accelerating the inventory of Lepidoptera early-stages and host-plant & other associations, by using citizen-science projects. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###



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The ability to identify the early stages of Lepidoptera and knowledge of their host-plant preferences is of fundamental importance in understanding their ecological interactions, biogeography and potential economic impact. In South Africa the early stages (or any part thereof) and host-plant associations are known for less than 10% of the Lepidoptera fauna estimated to be over 10 000 species. Images or illustrations of these early stages are available for only a fraction of the species for which at least some information is available. The advent of modern communication media such as nature websites, online databases, Virtual Museums and social media, as well as the free availability of good digital cameras, has sparked a renewed interest in the smaller fauna by the South African public. This prompted us to find ways of rapidly accelerating the discovery of the early stages of our Lepidoptera by exploiting this growing enthusiasm in the natural history of smaller creatures.

This presentation reported on the creation of a citizen-science project aimed at visually recording the 'caterpillar – host-plant – adult' associations of African Lepidoptera, which culminated in the formation of the now active Caterpillar Rearing Group under the auspices of The Lepidopterists' Society of Africa.

In the first eighteen months the project has yielded some spectacular results: Number of valid entries received: 1168. Number of species for which we now have the minimum criteria: 725. Number of host-plant associations new to science: 568. Minimum number of species never reared before: 214.

### **DNA barcoding and DNA metabarcoding as tools for rapid inventory and high-throughput identification of Lepidoptera species in Amazonia**

**Rodolphe Rougerie, Thibaud Decaëns, David C. Lees, Carlos Lopez-Vaamonde, Shadi Shokrala & Mehrdad Hajibabaei**

Rougerie, R., Decaëns, T., Lees, D. C., Lopez-Vaamonde, C., Shokrala, S. & M. Hajibabaei (2014): DNA barcoding and DNA metabarcoding as tools for rapid inventory and high-throughput identification of Lepidoptera species in Amazonia. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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In the fields of ecology and conservation biology, when information requiring species-level identification is needed, many groups of living organisms are generally excluded de facto from the studies, merely because of the lack of access to the scarce specific taxonomic expertise and because of the largely unexplored and overwhelming diversity of some taxa, in particular in the species-rich inter-tropical regions. In French Guiana, we used standard Sanger-based DNA barcoding to document this relatively unknown tropical Lepidopteran fauna, revealing an outstanding local diversity. Our efforts resulted in the assembly of a large DNA barcode library



comprising expert-identified species when possible as well as a large portion of unidentified species only characterized to date by their Barcode Index Number (BIN) in BOLD. As an alternative approach and to demonstrate the usefulness of DNA barcode libraries, we carried out a community ecology study in Brazilian and Colombian Amazonia where we used a DNA metabarcoding approach to identify bulk samples of Saturniidae and Sphingidae moths along a gradient of land-uses. This study used Next Generation Sequencing technology (454 Roche) to expedite the process of sequencing a large number of samples (ca. 1700) in many collecting sites (54).

### **The flowchart of taxonomy – right pieces in the right order**

**Mari Kekkonen**

Kekkonen, M. (2014): The flowchart of taxonomy – right pieces in the right order. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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#### Challenge

Numerous insect groups include a great amount of unknown species, and many of them lack present-day taxonomic expert. One such group is the Australian Hypertrophinae (Gelechioidea: Depressariidae) with 51 described and tens of undescribed species. Very little is known about these endemic moths, mainly due to their insufficient taxonomy. To be able to gather knowledge on hypertrophines, their species boundaries need to be defined, phylogenetic relationships studied, and newly discovered species described. However, their small size, somewhat cryptic wing patterns, and the lack of present-day experts pose a considerable challenge.

#### Solution

A flowchart of taxonomy was recently presented to describe the workflow of the study of the Hypertrophinae (Kekkonen 2014). The flowchart includes four steps, starting from the phylogenetic analyses concentrating on the hierarchical level above the focal group (for further details, see Heikkilä et al. 2013). The next phase introduces DNA barcode-based delineation of putative species (i.e., operational taxonomic units, OTUs) (for further details, see Kekkonen & Hebert 2014), and the third part returns to the phylogenetics, but this time, at the level of the focal group. The last step includes the validation of OTUs based on all available data (e.g., morphological characters, nuclear loci), and subsequent association of type specimens with defined species by applying DNA barcodes.

#### Reason

A rationale behind the flowchart of taxonomy is to choose the most suitable source of data and the set of methods for each phase. The flowchart presents a viewpoint where initial boundaries of putative species are formed based on DNA barcodes. This approach offers many benefits



when compared to generally used ‘morpho grouping’. As initial species delineation forms a distinct phase with one source of data and is based on specified delineation methods, it is repeatable and more objective. Furthermore, with a group including tens of unknown species, the total duration of taxonomic work is considerably shorter and the taxonomic accuracy is improved as many cryptic species are discovered in the beginning. Although single-locus mtDNA poses possible problems especially with recently diverged species, these drawbacks will most likely be revealed in the validation phase.

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### **With or without speed-limit? How to assess 3000 Emerald species (Lepidoptera, Geometridae, Geometrinae)**

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Hausmann, A., Staude, H. S., Dieterle, C. & A. Moser (2014): With or without speed-limit? How to assess 3000 Emerald species (Lepidoptera, Geometridae, Geometrinae). Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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So far, 2225 Emerald species (subfamily Geometrinae) have been described worldwide. Based on the material studied in various collections and on the accumulation curve of DNA Barcode clusters (Barcode Index Numbers, "BIN"s, cf. Ratnasingham & Hebert 2013) in the international Barcode of Life project we estimate the total species number to exceed 3000 species. We studied the material from major collecting projects in the Neotropical and Afrotropical regions, e.g. in Ethiopia, Tanzania, South Africa, Ghana, Cameroun, Mali, Brazil, Peru, Ecuador, Colombia and Costa Rica. Our integrative taxonomic approach combines information from DNA barcoding with classical morphological methods. Preliminary results and accumulation curves suggest the total species number of the subfamily Geometrinae to increase from 458 to more than 750 in the Neotropical region (currently available: 2450 DNA barcodes clustering to 557 BINs) and from 633 to more than 1000 in Africa (currently available: 2510 DNA barcodes clustering to 676 BINs). The first research focus was laid on the the revision of the African species of the genera *Pingasa*, *Prasinocyma* and *Victoria*, and the



Neotropical species of the genera *Lophochorista*, *Oospila*, *Nemoria* and *Lissochlora*. The Natural History museums of Munich, London and Pretoria (ZSM, NHM, NFI; "Afroemeralds Project") initiated an integrated assessment of all type specimens of Geometrinae including DNA barcoding, genitalia dissection, digital photography and accurate databasing to rapidly achieve an objective, close-to-complete knowledge of the Geometrinae fauna of the whole African continent. Furthermore, representatives of all BIN-clusters on the barcode of Life Datasystems (BOLD) are submitted to genitalia dissection.

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doi:10.1371/journal.pone.0066213

### **DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artifact of tropical under-sampling**

**Carlos Lopez-Vaamonde, David C. Lees, Akito Kawahara, Rodolphe Rougerie, Issei Ohshima, Atsushi Kawakita, Olivier Bouteleux & Jurate De Prins**

Lopez-Vaamonde, C., Lees, D. C., Kawahara, A., Rougerie, R., Ohshima, I., Kawakita, A., Bouteleux O. & J. De Prins (2014): DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artifact of tropical under-sampling. Pp. #### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ####

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With thousands of undescribed tropical Lepidoptera species and alarming rates of deforestation, developing methods that allow rapid biodiversity assessment is crucial to quantify levels of endemism and identify areas of high conservation value. DNA barcoding has been shown to be an efficient tool to speed up the identification of known species and the discovery of new ones. Barcodes can be used as proxy for clustering unidentified specimens into operational units and estimate levels of diversity within and between sites. This approach can be used to carry out rapid biodiversity assessments of hyperdiverse, mostly undescribed, insect fauna in tropical areas. Here we use DNA barcode data to quantify species richness of Gracillariidae leaf-mining moths of several sites in French Guiana and Ecuador.

Field surveys in six French Guianan (Figure 1) and one Ecuadorian sites produced 516 gracillariid specimens that were DNA barcoded to facilitate identification and to match larvae inside leaf-mines with adults. We obtained 485 barcodes (372 adults and 104 larvae). Species delineation from sequence data was approximated using Automatic-Barcode-Gap-Discovery and Refined-Single-Linkage-Analysis through the Barcode Index Number system, and the proportion of described/undescribed species was estimated after comparison with types. The total number of candidate species ranged from 142 (ABGD) to 151 (BINs). For Nouragues we obtained 108 BINs. 64 BINs (59.3%) are represented by singletons. 33% of specimens were





identified down to genus level. We were able to assign 17 species names to 38 specimens. Strikingly, at least 85% of the species collected as adults were found to be undescribed. Nearly all barcodes were novel to BOLD. The results from both our molecular and morphological analyses indicate that most of the gracillariid fauna in the studied region is unknown and undescribed. The estimated lower bound of species richness of Gracillariidae for Nouragues ranged from 240 species (Chao1) to 260 species (ACE). Our results show that DNA barcoding allows researchers to overcome the taxonomic impediment and carry out rapid biodiversity assessments in poorly documented regions (Lees et al 2013).

#### References

Lees, D.C., Kawahara, A. Y., Bouteleux, O., I. Ohshima, A. Kawakita, R. Rougerie, De Prins, J., Lopez-Vaamonde, C. (2013). DNA barcoding reveals a largely unknown fauna of Gracillariidae leaf-mining moths in the Neotropics. *Molecular Ecology Resources*, 14 (2): 286-296

#### **Using DNA barcoding as a tool to describe moth community patterns in Lopé and Ivindo National Parks, Gabon**

**Sylvain Delabye, Thibaud Decaëns, Sandrine Bayendi, Stephan Ntie, Philippe Le Gall, Carlos Lopez Vaamonde, Nicolas Moulin, David Sebag, Rodolphe Rougerie & the Ecotrop team**

Delabye, S., Decaëns, T., Bayendi, S., Ntie, S., Le Gall, P., Lopez Vaamonde, C., Moulin, N., Sebag D., Rougerie, R. & Ecotrop team (2014): Using DNA barcoding as a tool to describe moth community patterns in Lopé and Ivindo National Parks, Gabon. Pp. #### in Hausmann, A. (ed.): *Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014)*. – Spixiana ####

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The existence of a taxonomic shortfall has been stressed as an important constraint for invertebrate biodiversity studies, especially in tropical countries where natural communities are more diverse and less studied. Here, we used DNA barcoding to achieve a rapid description of moth communities in two contrasted ecosystems of central Gabon: the rainforest of Ipassa research station (November 2009), and the savannah/forest patchwork near La Lopé (November 2009, March 2011). Specimens collected at light-trap were subsequently sorted by morphospecies, of which up to four individuals were selected and processed through DNA barcoding. The diversity and composition of the communities are described using Barcode Index Numbers (BINs) as operational taxonomic units considered here as proxy for species. Family-level assignment was carried out using morphology and/or existing DNA barcode libraries in BOLD (the Barcode of Life Data System, [www.boldsystems.org](http://www.boldsystems.org)).

A total of 3307 DNA barcodes were obtained from the 3387 specimens collected, representing 1305 BINs and 22 families, of which the most represented are Noctuidae, Erebidae and Geometridae. We found 733 singletons (i.e. 56% of the total BINs number), suggesting a high proportion of rare species in communities and/or a significant level of under-sampling, which is



a classical limit in most tropical arthropod surveys. Observed richness was of 807 and 713 BINs in Ipassa and La Lopé, respectively, but richness estimators indicate that up to 1700 and 1440 species could occur in both sites. Accordingly, sampling coverage ranged from 65 to 75% (in Ipassa and La Lopé, respectively). When comparing composition among sites (2009 dataset), we found a 66% BINs turnover, suggesting a strong spatial structuring due to geographical distance and/or contrasted environmental conditions. Likewise, turnover was of 68% between two sampling periods in La Lopé, indicating that communities could also be strongly structured according to seasonal cycle.

This study represents a first step in the description of moth diversity in ecosystems of Gabon. In 2012, 2013 and 2014, sampling was intensified by involving students of the ECOTROP field school and by diversifying collecting methods. A total of 3000 additional individuals were sampled and their DNA barcodes will be sequenced in the next few months, which hopefully will strengthen and refine the description of community patterns in Lopé National Park.

**The importance of the traditional taxonomy in the exploration of the real biodiversity of Lepidoptera. A study case: the Nolini (Lepidoptera, Nolinae, Noctuoidea) fauna of Eurasia**

**Gyula M. László, Gabor Ronkay & László Ronkay**

László, G. M., Ronkay, G. & L. Ronkay (2014): The importance of the traditional taxonomy in the exploration of the real biodiversity of Lepidoptera. A study case: the Nolini (Lepidoptera, Nolinae, Noctuoidea) fauna of Eurasia. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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After more than 200 years of the birth of the descriptive science taxonomy, the exploration of the real biodiversity of Lepidoptera is still far not complete. The ratio of the undiscovered taxa strongly depends on the popularity of the given Lepidoptera group: usually the larger, spectacular groups are better explored than the small, less conspicuous ones, there are, however, several new discoveries even in the most popular groups.

Our research team started the taxonomic work on the rather neglected Noctuoidea tribe Nolini (Nolidae) in 2002, in collaboration with Mr. T.J. Witt and the Museum Witt, Munich, based on recently collected material from the Himalayas, Indochina, the Philippines and the Indonesian Archipelago. After the detailed examination of all historical Nolini types preserved in large European museums, we could continue the work on the vast material harboured in these institutions that has resulted in the discovery of an unexpectedly large number of new taxa.

The history of the descriptions of Nolini species is demonstrated on the following diagram:

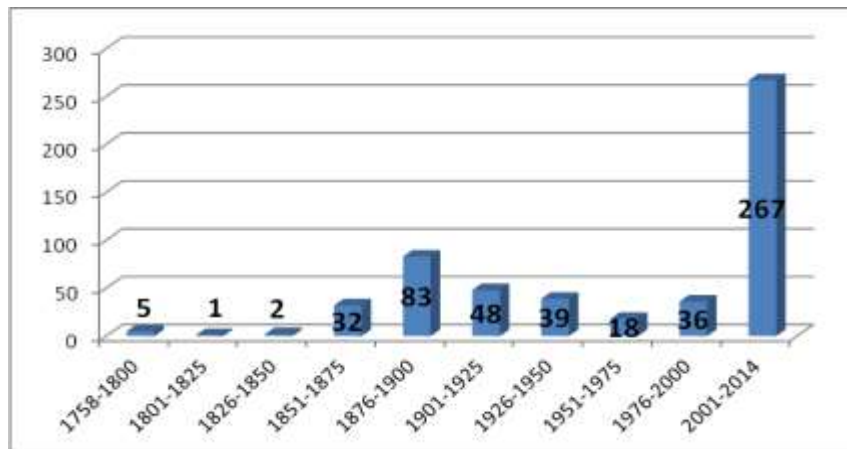


Fig. 1. The numbers of valid taxa (species and subspecies) have been described since 1758.

The big leap in the number of new species described in the last 14 years, thanks above all to Dr J. Holloway (Natural History Museum, London) and the present research group, is due to the increase of the available material from less explored areas and the thorough morpho-taxonomic studies. In many groups of Nolini, according to the new results, a number of (sometimes 4-5) externally undistinguishable species may occur sympatrically in a given area (the best example is the genus *Manoba* Walker, 1864), which can be properly separated and identified only by the careful examination of the morphological structures of their genitalia. The study of the relevant specific (distinctive) characters of the externally very similar species often requires a careful preparation technique and a coherent mounting process. This work is often difficult and time-consuming due to the small size of the animals.

The steep rising tendency of the last decades predicts a continuation of further discoveries and descriptions of numerous new taxa, especially from the hot spots of South East Asia and the Indonesian Archipelago. Actually, the known Nolini fauna of Eurasia has been doubled in the last fifteen years and the case is similar for the African Nolini (Hacker et al 2012). Such results may demonstrate the predictions for the rate of the known/unknown species of the recent fauna and insist the re-thinking of its consequences.

The Lepidoptera taxonomists and morphotaxonomy in the 21st century still have a decisive role in the exploration of the real biodiversity of the Earth. Without getting at least close to the complete knowledge of the fauna of a given region or the species content of a taxonomic unit it is simply too early to establish ecological, biogeographical, phylogenetic etc. statements and conclusions on the, in fact poorly known, subjects of the investigations. Our sample case for the Nolini could be applicable for a number of other groups of Lepidoptera. Thus, for instance, all digital databasing projects must consider the newest taxonomical revisions and follow the increase of the described fauna instead of using the 20-50 years old stock of information, otherwise they will be out of date already in the moment of their birth. This is our responsibility and taxonomists still have a lot of things to do in order to accelerate our activity in a highly co-operative manner, because the increasing destruction of the habitats of insects all over the world will give us less and less opportunity to get acquainted the real biodiversity of Planet Earth.



Hacker, H.H., Schreier, H-P. & Goater, B. (2012): Revision of the tribe Nolini of Africa and the Western Palaearctic Region (Lepidoptera, Noctuoidea, Noctuidae, Nolinae) – *Esperiana* 17: 1-614.

### **Land in sight? – exploring the global geometrid diversity hotspot**

**Gunnar Brehm**

Brehm, G. (2014): Land in sight? – exploring the global geometrid diversity hotspot. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – *Spixiana* ###

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The tropical Andes are known as the global diversity hotspot of geometrid moths. Diversity has been investigated along a forested elevational gradient (ca. 1000-3000 m) in south-eastern Ecuador since 1999. Surprisingly, diversity is constantly very high at all elevations. There is a constant species turnover, subfamily composition changes with elevation, and assemblages become phylogenetically more clustered at higher elevations. Recent sampling and systematic barcoding reveals that species richness in the area is much higher than previously thought and microhabitats play an important role. Biodiversity in the area is endangered by ongoing extensive forest destruction.

### **Spatial and temporal pattern of species richness and abundance of macromoths including Geometridae in Mt. Jirisan National Park, South Korea**

**Sei-Woong Choi & Jeong-Seop An**

Choi, S.-W. & J.-S. An (2014): Spatial and temporal pattern of species richness and abundance of macromoths including Geometridae in Mt. Jirisan National Park, South Korea. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – *Spixiana* ###

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We sampled macromoths from 2005 to 2013 at eleven sites in Mt. Jirisan National Park (JNP), the oldest and largest national park in South Korea, to address the following questions: (1) what is the total macromoth species richness of JNP and can the total moth species richness be estimated after 9-years? (2) What is the proportion of moth families and is this pattern of family dominance similar to that seen in other areas? (3) What are the yearly patterns of macromoth and geometrid species richness and abundances? In total, 46,452 individuals belonging to 1,185 species of 21 families of macrolepidoptera were collected. The proportions of dominant



families were similar to those reported in temperate and tropical moth fauna studies: Geometridae was the most species-rich taxon, followed by Noctuidae, Erebidae, Notodontidae, Drepanidae, and Sphingidae. Yearly change of species richness and abundance of all macromoths was 502 species ( $\pm 68.34$ ) and 5161 individuals ( $\pm 1349.9$ ). Yearly change of species richness and abundance of Geometrid moths was 173 species ( $\pm 20.17$ ) and 2328 individuals ( $\pm 772.9$ ). Overall species richness and abundance for all macromoths and geometrids were similar, but the elevational pattern of geometrid species richness was different from the total species richness. Species richness and abundance of four dominant subfamilies of the Geometridae declined as elevation increased.

### **Current Research on Australian Geometridae – redefining the Tasmanian ‘Archiearinae’ and the blitzing of Australia’s remote fauna**

**Catherine Byrne & Abbey Throssell**

Byrne, C. & A. Throssell (2014): Current Research on Australian Geometridae – redefining the Tasmanian ‘Archiearinae’ and the blitzing of Australia’s remote fauna. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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Two areas of research on the Australian Geometridae are reported in this presentation. Firstly we highlight recent work on the Tasmanian representatives Archiearinae, which describes and discusses for the first time all life cycle stages of all species, their biology and clarifies the phylogenetic position of these enigmatic taxa. Secondly the principal author presents findings on Australian Geometridae collected in six surveys of Australian flora and fauna in remote areas of Australia.

The Archiearinae have traditionally been considered a basally derived sub-family in the Geometridae. This phylogenetic position and the monophyly of the group have been contradicted recently on morphological (Young 2006, 2008) and molecular studies (Young 2006, Yamomota & Sota 2007, Sihvonen et al. 2011). The Tasmanian representatives of the amphipolar Archiearinae consist of five species and two undescribed species of the genera *Acalyphes* Turner and *Dirce* L. B. Prout. Young (2006) found that the superficial similarities of these taxa with the world fauna, the Holarctic *Archiearis* Hübner, Palaeartic *Leucobrephos* Grote fauna and the Neotropical *Lachnocephala* Fletcher and *Archiearides* Fletcher that led to these moths being treated under the Archiearinae are most likely convergent adaptations to a cold environment and similar biology. All are diurnal geometrids with rather stout, highly melanised, hairy bodies, relatively small eyes and brightly coloured hindwings in some species. These adaptations are a recurring theme in alpine moths. It is probable, therefore, that *Acalyphes* and *Dirce* have been misplaced into the Archiearinae. These genera are most likely ennomine with close links to the Australian Nacophorini from the molecular and morphological evidence (Young 2006, 2008).

Several morphological characters have been used to corroborate a primitive phylogenetic position for the Archiearinae. Unlike most geometrids, Holarctic archiearines lack an accessory



tympanum and have a very narrow fenestra media (Minet 1983). Pupal characters, have also been used to substantiate a basally derived status for *Archiearis*. This is discussed comprehensively in Young (2006) The combination of unusual features, diurnal habit, absence of secondary tympanum and pupal autapomorphies may indicate that the Holarctic archiearines, rather than being a sister group to the Geometridae is a derived group within the family. This is certainly supported by molecular evidence (Young 2006, Yamomota & Sota 2007, Sihvonen et al. 2011).

Recent research on the iconic Tasmanian alpine genera *Acalyphes* and *Dirce* clarifies the phylogenetic position and nomenclature of these Tasmanian endemics, describes comprehensively all stages of the life-cycle and provides previously unpublished information on their biology, ecology and distribution. Eggs, larvae and adults are all illustrated.

Bush Blitz is a national species discovery project funded by the Federal Department of Sustainability, Environment, Water, Population and Communities with support from corporate sponsors. The main aims of this project are the collection of new species and the surveying of remote areas in Australia that are poorly known for their biodiversity. Australia has a rich geometrid fauna of around 1300 known species with at least one third of the fauna still new or undescribed. The southern Australian geometrid fauna is highly endemic and entire groups such as the Oenochrominae s. str. are mainly only found in Australia. Much is yet to be learned about the biology of the Australian Geometridae. The Bush Blitz surveys have enriched our knowledge of the Australian Geometridae by adding new species, rare species and new records to our state museum collections and to the Atlas of Living Australia (<http://www.ala.org.au/>). Systematics on the Geometridae has benefited from this project from financial support given to research describing new species collected on Bush Blitz Surveys.

Selected major findings for the Geometridae from seven Bush Blitz surveys, three in Western Australia (WA) and four in Tasmania, in which Geometridae were a target group are as follows:

1) 2009 – WA semi-arid wheatbelt area in southwest WA

56 species (25 genera)

The percentage of undescribed species collected was very high at 70% and consisted of 39 unidentified Geometridae with eight new to science. The genus *Dichromodes* Guenée was particularly diverse with 15 new species and 4 new to science. *Dichromodes* is the largest Australian genus of Geometridae with 70 described species and around 100 new or undescribed species. It is arguably one of the most unresolved genera taxonomically because of the large number of undescribed species in the genus and the likelihood of many synonyms due to the cryptic colour and wing patterns of specimens. They are particularly diverse in the semi-arid interior of Australia.

2) WA Sept 2011 Credo Reserve, Eastern Goldfields

20 new or undescribed species of geometrids in 18 genera were collected, including three in the Oenochrominae that were most likely new to science:

One male specimen only of an extremely rare species of the Oenochrominae s. l., *Taxeotis lechrioschema* Turner was collected. This species has not been collected since F. Walker took the first specimens in Merredin, WA, in September and October 1938, and, to date, the species has only been known from these five specimens all designated as types by A. J. Turner in the same year.



### 3) Tasmania 2014 Flinders Island

35 species of Geometridae in 41 genera with five new species.

The results from this survey have not been fully documented but this remote area of Tasmania was notable for the number of new records for the state. Rare species collected were *Casbia oenias* (Meyrick), *Chrysolarentia ptochopis* (Turner) and *Epyaxa agelasta* (Turner). One species of *Dichromodes* collected is most likely new to science. In addition a species of the Hepialidae rarely collected in Tasmania, *Fraus nanus* (Herrich-Schäffer) was also collected.

Four generic revisions of Geometridae including descriptions of new species collected in Bush Blitz surveys, funded through the Bush Blitz Project, are being conducted by the primary author have been.

- Redescription of *Omoplatica* Turner (Geometridae: Oenochrominae s. str.) from the semi-arid interior of Western Australia, with description of three new species and re-description of the type species, all endemic to WA. All species in this genus are rare apart from one species which is commonly collected in the semi-arid interior of WA. The type species is only known from eight specimens from two collecting trips in the wheat-belt of WA. One undescribed species is only known from one location and another from three specimens from two locations again from the wheatbelt in WA. The remaining new species a large showy moth was collected in spring on a Bush Blitz expedition and is reasonably well-represented in collections.

- Redescription of *Lipogy auctororum* Warren (Geometridae: Boarmiini) with the description of two new species, and redescription of three species.

- Redescription of *Nisista* Walker (Geometridae: Nacophorini) with the description of five new species and the redescription of three species.

- Redescription of *Scioglyptis* Guest (Geometridae: Boarmiini) with the description of four new species and the redescription of six species.

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### **On the Phylogeny and Systematics of the tribe Larentiini (Lepidoptera: Geometridae)**



**Andro Truuverk & Erki Õunap**

Truuverk, A. & E. Õunap (2014): On the Phylogeny and Systematics of the tribe Larentiini (Lepidoptera: Geometridae). Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schletttau, 30 June – 4 July 2014). – Spixiana ###

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Hereby we concentrated on resolving the phylogeny of tribe Larentiini and its relationships with other tribes from the subfamily Larentiinae. In total, 63 species from 22 tribes were included into the analysis. 12 species from 10 genera belonged to the tribe Larentiini according to the recent classification. Sequence data from one mitochondrial and eight nuclear genes were used: cytochrome oxidase subunit 1 (COI), 28S rRNA (expansion segments D1 & D2), elongation factor 1 alpha (EF-1 $\alpha$ ), ribosomal protein S5 (RpS5), carbamoylphosphate synthase domain protein (CAD), cytosolic malate dehydrogenase (MDH), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), isocitrate dehydrogenase (IDH) and wingless (WGL). The total length of the data matrix was 7264 bp. Our results demonstrate that the tribe Larentiini within its current limits is not monophyletic. Indeed, majority of the studied larentiine genera formed a well-supported monophyletic lineage together with *Larentia*, the type genus of the tribe. However, three genera were placed into different sub-lineages of the subfamily Larentiinae.

**Molecular and morphological phylogenies in geometroid lepidopterans (Insecta: Lepidoptera: Geometriformes) – discordant or concordant**

**Evgeny A. Beljaev**

Beljaev, E.A. (2014): Molecular and morphological phylogenies in geometroid lepidopterans (Insecta: Lepidoptera: Geometriformes) – discordant or concordant. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schletttau, 30 June – 4 July 2014). – Spixiana ###

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Comparative analysis of modern morphological and molecular phylogenies in geometroid lepidopterans is made. This group includes a number of mainly nocturnal macrolepidopteran families – Cimeliidae, Sematuridae, Epicopeiidae, Drepanidae, Uraniidae and Geometridae, which were united in series Geometriformes by Kuznetzov and Stekolnikov (2001). This series corresponds to the drepanoid/geometroid assemblage plus superfamily Cimelioidea following Minet and Scoble (1998). Geometriformes are one of the largest taxonomic groups in Lepidoptera, numbering nearly 25 thousand described species. Numerous questions about relationships of geometroid lepidopterans at all taxonomic levels are still far from solved.







	1	2	3	4	5	6	7	8	9
1.	Yamamoto & Sota 2007	29	3/ 10%	23/ 79%	3/ 10%	27	2/ 7%	23/ 86%	2/ 7%
2.	Sihvonen & al. 2011	67	14/ 21%	33/ 49%	20/ 30%	42	11/ 26%	25/ 60%	6/ 14%
3.	Regier & al. 2009	23	2/ 9%	12/ 52%	9/ 39%	14	2/ 14%	11/ 79 %	1/ 7%
4.	Mutanen & al. 2010	25	3/ 12 %	12/ 48%	10/ 40%	16	2/ 12%	11/ 69%	3/ 19%

Note. Percentages are rounded to whole numbers.

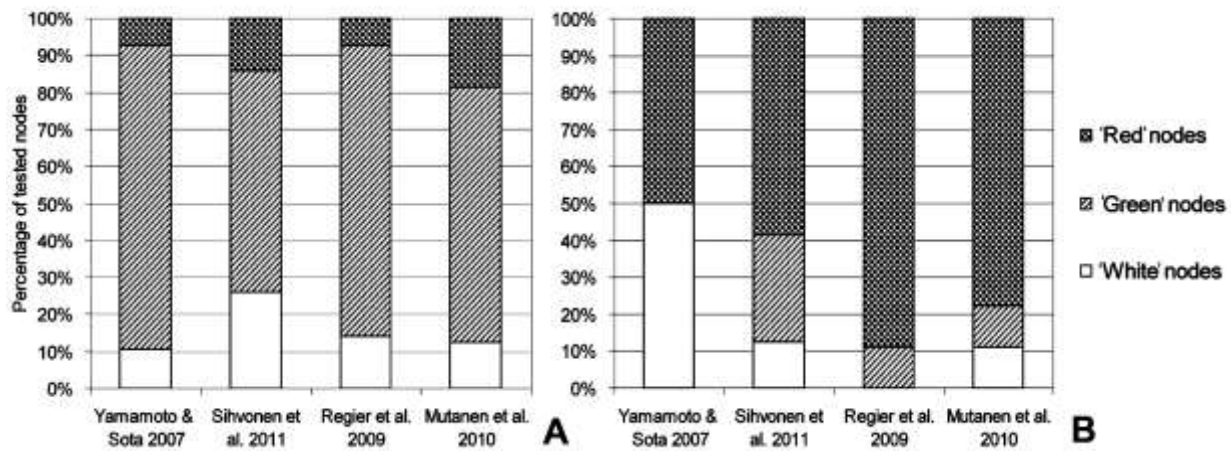


Fig. 1. Percentage of 'white', 'green' and 'red' resolved nodes (A) and unresolved nodes (B) in phylogenies by Yamamoto & Sota (2007), Sihvonen & al. (2011), Regier & al. (2009) and Mutanen & al. (2010).

As can be seen from Table 1 (columns 3, 4), 'red' nodes account for 30 – 40 % of the phylogenies and their percentage is comparable with the share of 'green' nodes, which account for 48 – 52 % of all tested nodes. The only exception is the phylogeny by Yamamoto & Sota (2007) with 10% of the nodes being 'red' and 79% being 'green'. This ratio indicates low concordance between the morphological and molecular phylogenetic data and calls into question the results of one or both studies.

However, if we exclude the nodes with bootstrap support values less than 50 from our calculations, the results will look quite differently. The rate of 'red' nodes drops to 7 – 19 % and becomes much less than the ratio of 'green' nodes, which account for 60 – 86 % of all tested nodes excluding the nodes in the 'grey' area (Table 1, columns 8 and 9; Fig. 1A.). Percentage of 'white', 'green' and 'red' nodes with bootstrap support values less than 50 is illustrated on Fig. 1B. It is clear that 'red' nodes are absolutely predominant in this area.

In the phylogeny by Sihvonen & al. (2011), the rate of 'green' nodes is comparatively low – only 60% of all tested nodes with bootstrap support values 50 and more, and the share of 'red' nodes reaches almost one-fourth of 'green' nodes (24%). This is a result of a large percentage of morphologically unresolved 'white' nodes, which account for 26% of all nodes outside of the



'grey' area. However, I expect that most of them could reflect true phylogenetic relationships, taking into account appearance of moths and their superficial morphology.

Thus, modern morphological and molecular phylogenies of the geometroid lepidopterans demonstrate rather good concordance when tree nodes have high bootstrap support values (at least when more than 50). The exceptions are rare and require targeted research using both – molecular and morphological approaches. Discrepancies between molecular and morphological phylogenies within the area of nodes with low bootstrap support values can not be used as the argument for rejection of relationships established on the basis of morphological criteria and for revision of taxonomic systems.

Noteworthy, this concordance was attained for phylogenies reconstructed by entirely different ways: by formal quantitative methods for molecular data and by logic analysis for morphological data. This indicates that morphological data are consistent with logic construction of phylogenetic trees, which requires the preliminary selection (a priori weighting) of characters based on the previous knowledge about the probability and probable directions of certain morphological transformations. This corresponds to the informal subjective nature of morphological character as hypotheses about similarity or difference between the homologous morphostructures of different organisms. Also, only the combination of functional-morphological method, manual cladistic technology and historical understanding of apomorphy, provides maximal concordance between the morphological and molecular phylogenies.

The area of nodes with low bootstrap support values in molecular phylogenies generally more or less coincides with taxonomic groups which are also difficult for morphological phylogenetic analysis. Obviously, this coincidence is not accidental and results from the loss of clearness of the 'phylogenetic signal' at both levels of the organization of organisms or from the peculiarities of divergence on the early stages of the 'maturing' of taxa. However, within this area of molecular phylogenies, nodes established morphologically appear to be more reliable than branching pattern in the molecular trees.

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**Molecular and morphological investigations suggest family level for the little known *Pseudobiston pinratanai* Inoue, 1994**

**Hossein Rajaei, Carola Greve, Harald Letsch, Dieter Stüning, Niklas Wahlberg, Joël Minet & Bernhard Misof**

Rajaei, H., Greve, C., Letsch, H., Stüning, D., Wahlberg, N., Minet, J. & B. Misof (2014): Molecular and morphological investigations suggest family level for the little known *Pseudobiston pinratanai* Inoue, 1994. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schleittau, 30 June – 4 July 2014). – Spixiana ###

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After the description of *Pseudobiston pinratanai* Inoue, 1994 within the Geometridae, the family placement of this enigmatic, oriental species has been questioned by different authors. Although a complete lack of abdominal tympanal organs strongly suggested a non-geometrid taxon, the other morphological characters of *P. pinratanai* were initially considered poorly informative with regard to any tentative family assignment. Then, in order to elucidate this systematic position, we used a large molecular dataset (sequences of eight genes including one mitochondrial gene (COI) and seven nuclear genes: EF-1 $\alpha$ , Wingless, RpS5, MDH, GAPDH, CAD and IDH) taking into account *P. pinratanai* and 111 other species, mostly members of various macroheteroceran families. All phylogenetic analyses (Maximum likelihood, Parsimony and Bayesian inference) revealed a strongly supported sister-group relationship between *Pseudobiston* and the Epicopeiidae, suggesting that the former would deserve its own family (new taxon in prep.). This hypothesis could be supported by following synapomorphies of Pseudobistonidae+Epicopeiidae: I) strongly reduction or absence of ocelli; II) relatively short tibia of hindleg; III) vertical flexion zone across the metepimeron; IV) a broad furco-epimeral bands on metathorax; V) posterior foramen in dorsal position of euphragma; VI)



anterolateral processes of the second sternum arched in lateral view; VII) juxta of male genitalia, possess a pair of long, sclerotized excrescences.

**Enigmatic cycad moths of Africa: a holistic approach to examine their systematic position (Lepidoptera: Geometridae)**

**Pasi Sihvonen, Hermann S. Staude & M. Mutanen**

Sihvonen, P., Staude, H. S. & M. Mutanen (2014): Enigmatic cycad moths of Africa: a holistic approach to examine their systematic position (Lepidoptera: Geometridae). Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schleittau, 30 June – 4 July 2014). – Spixiana ###

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The systematic position and hierarchical level of the moth taxon Diptychini Janse, 1933 (the cycad moths) have remained controversial and largely uninvestigated (Lepidoptera: Geometridae). The uncertainty is partially due to their unique morphological, biological and behavioural characteristics. To examine these questions, comprehensive molecular analyses of eight genes, representing over 100 Geometroidea taxa, were carried out in a global context. Data matrices were analysed and phylogenetic trees were constructed using model-based methods (Bayesian inference). The molecular results were placed in a larger framework through extensive morphological examinations. We demonstrate that the Diptychini belong to the Geometridae subfamily Ennominae, pinpoint its more exact position within the subfamily, and identify its potential relative taxa. The results and their significance are discussed in the global context.

**Recent advances on the knowledge of Geometrid moths of Ethiopia**

**Andrea Sciarretta, Axel Hausmann & Francesco Parisi**

Sciarretta, A., Hausmann, A. & F. Parisi (2014): Recent advances on the knowledge of Geometrid moths of Ethiopia. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schleittau, 30 June – 4 July 2014). – Spixiana ###

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Due to the geographical position and orogenic history of Eastern Africa, Ethiopia constitutes a unique arrange of natural habitats characterized by extremely different climatic and environmental conditions. The Ethiopian highlands contribute to more than 50% of the land area with Afromontane vegetation and, due to its isolation from other mountain systems of



Africa, it has been acting over millions of years as a real "laboratory of evolution", thus leading to a high percentage of endemic plants and animals.

Despite this, the knowledge of Lepidopteran biodiversity in the country is very scarce and this is particularly true for the family Geometridae. So far, 90 taxa have been described from Ethiopia of which 79 are currently accepted as valid at species rank. A rough estimate based on the study of collection material involving both morphology and DNA barcoding suggests the number of Ethiopian geometrid species to exceed 500 species. So far, no comprehensive study on the fauna of this country has been published.

The studies of the authors are based on thousands of Ethiopian geometrid moths in their collections, offering a good starting point for reviewing the historical descriptions and for providing additional data. The first focus was laid on the subfamily Geometrinae, so far revealing more than 90 species which were assessed in an integrative taxonomic approach combining classical morphological and molecular (DNA Barcoding) methods. Particularly significant is the case of the genus *Prasinocyma*, with 44 species currently identified for the fauna of Ethiopia, of which at least 26 are new for science.

#### **A complex diversity of taxa behind one species: *Lophophelma luteipes* Felder, 1875**

**Claude Tautel**

Tautel, C. (2014): A complex diversity of taxa behind one species: *Lophophelma luteipes* Felder, 1875. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schletttau, 30 June – 4 July 2014). – Spixiana ###

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The Asian Geometrid moth *Lophophelma luteipes* Felder, 1875 (Geometrinae) has been considered (e.g. by Holloway, 1996) a rather homogeneous species with the similar but different species *L. ruficosta* (S. India) and another not yet named one in Sulawesi. Barcoding results (in BOLD) of a number of specimens yielded, however, at least four different BINs. As many specimens as possible were examined and genitalia slides were made of specimens from N.W. and N.E. India, Sri Lanka, N. and S. Thailand, Cambodia, N. and S. Vietnam, Hong Kong, Mainland Malaysia and Sabah, N. and W. Sumatra, Palawan, Jawa, and Sulawesi. The morphological structures in the genitalia turn out to be surprisingly diverse and group, grosso modo, in two very distinct pattern groups which are also correlated to differences in the coloration of the wing undersides. Morphological and genetic differences in both groups point to a wide diversity of taxa (on species or subspecies level) behind *L. luteipes* as currently understood. The fact that both groups occur sympatrically in Vietnam, Malaysia (Borneo), Sumatra, and Java is an interesting biogeographical feature. Since the unique holotype of *L. luteipes* is a female, it seems important to study also the morphology of the female genitalia of representative specimens from all involved regions, what was not yet completely possible. Pictures of specimens (habitus and underside) from all regions involved, of genitalia slides, and maps of distribution were presented. Publication is planned for early 2015.



**Advances in the knowledge of the larentiine fauna of southern Italy by DNA barcoding  
(Lepidoptera, Geometridae)**

**Stefano Scalercio, Marco Infusino & Axel Hausmann**

Scalercio, S., Infusino, M. & A. Hausmann (2014): Advances in the knowledge of the larentiine fauna of southern Italy by DNA barcoding (Lepidoptera, Geometridae). Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The lepidopteran fauna of southern Italy receives growing interest due to its peculiar biogeography and its ecological vulnerability. In this area several species have their southernmost distributional boundary and are prone to climate changes. Many populations will be submitted to an immediate threat due to climate warming expected for the next decades. Other species have their northernmost distributional boundary here and may colonize Europe northwards as a consequence of increasing mean temperatures during the next decades. Along the Italian peninsula the populations of several species were reproductively isolated from the other European populations and sometimes diverge consistently from a genetic point of view. Recent studies on DNA barcoding in southern Italy resolved various taxonomic questions on Larentiinae (Lepidoptera Geometridae), and strongly improved the knowledge of its fauna.

*Hydriomena sanfilensis* (Stauder, 1915) was raised to species rank from synonymy (Hausmann & Viidalepp 2012). The nearest species is *Hydriomena impluviata* (Denis & Schiffermüller, 1775) at a genetic distance (COI, barcode region) of 4.0%. This species is endemic to southern Italy. Through DNA Barcoding we have been able to identify a larva, found in a spun leaf of *Rosa canina*, as *H. sanfilensis*, which is the first record of a host-plant for this species. *Nebula carlae* Hausmann, 2011 from central and southern Italy was described as an allopatric sister species of *Nebula achromaria* (la Harpe, 1853) at 3.2% genetic distance. Similarly, *Coenotephria antonii* Hausmann, 2011 was recently separated from *Coenotephria topheata* (Denis & Schiffermüller, 1775) and supposed to be its central and southern Italian vicariant. However, both species were recently found to occur sympatrically (though appearing rather asynchronously) in central and southern Italy, genetically diverging by 6.6%.

For the fauna of Sicily and southern Calabria, barcoding analysis allowed a correct identification of *Eupithecia cocciferata*, previously identified as *E. lentiscata*, and they allowed to certainly attribute some Sicilian specimens to *Triphosa dubitata* (Linnaeus, 1758) which had been attributed to *Triphosa tauteli* Leraut, 2008, previously. DNA barcoding allows us also to carry out correct specific attributions of specimens belonging to taxonomically 'complicated' species such as *Xanthorhoe disjunctaria* (la Harpe, 1860), *Coenotephria ablutaria* (Boisduval, 1840), *Epirrita christyi* (Allen, 1906), *Eupithecia linariata* (Denis & Schiffermüller, 1775).





Furthermore, new questions arose from DNA barcoding analyses. Further studies are required to examine the taxonomic status of Italian populations of *Colostygia sericeata* (Schwingenschuss, 1926), currently validated as *C. sericeata* subsp. *holli* (Prout, 1938), and to investigate the genetic difference (2.5%) between European and southern Italian populations of *Lampropteryx suffumata* (Denis & Schiffermüller, 1775), a genetically very homogeneous species all over the rest of Europe, Altai mountains and North America.

### **Palyadini Systematics, state-of-the-art**

#### **Glauca Marconato**

Marconato, G. (2014): Palyadini Systematics, state-of-the-art. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schleittau, 30 June – 4 July 2014). – Spixiana ###

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Palyadini, a tribe of Ennominae, are characterized by the absence of frenulum and retinaculum and the presence of golden scales composing metallic points and lines in the wings at the dorsal view. 115 valid species are distributed in the Neotropics from Argentina to the southern United States. Palyadini currently comprises six genera: *Palyas*, *Phrygionis*, *Pityeja*, *Argyrotope*, *Opisthoxia* and *Ophtalmoblysis*. In 1994, Scoble has reviewed two genera *Phrygionis* Hübner and *Pityeja* Walker; and in 1995, the same author has reviewed the tribe at genus level, and described or synonymized genera. The largest genus *Opisthoxia* Hübner with almost 90 species remained untreated. Currently, the phylogeny of the tribe is analysed in an integrated approach combining morphological and molecular characters. The challenge was to find sufficient (fresh) material, and some taxa are very rare in museums (some of them being potential synonyms). In the genus *Opisthoxia*, which is supposed to harbor many cryptic species, species delimitation is particularly difficult because of great similarity and insufficient number of valuable differential features in morphology. Therefore DNA barcodes were chosen as an additional character set for supporting species delineation (identifying synonyms and cryptic species) and, consequently, warranting a robust phylogenetic analysis.

### **Family ranking in Lepidoptera communities in southwestern Africa: are Geometridae statistically important?**

#### **Wolfram Mey**

Mey, W. (2014): Family ranking in Lepidoptera communities in southwestern Africa: are Geometridae statistically important?. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schleittau, 30 June – 4 July 2014). – Spixiana ###

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Lepidoptera are one of the mega-diverse orders of insects. There are no Lepidoptera taxonomists who are able to work on all or most groups. The huge number of existing species needs specialisation. Today, taxonomic work is done by entomologists, who are specialists of a superfamily, a single family or even a single genus. Fieldwork being performed by these specialists follows the same pattern: they usually collect specimens from their groups and disregard the rest. This kind of specialisation, unfortunately, has the disadvantage of preventing a general view on local Lepidoptera communities and of ignoring ecological contexts.

Right from the beginning of the faunistic exploration of southwestern Africa (Namibia, western RSA) a holistic approach was applied towards the collecting and processing methodology. By using automatic light traps the entire spectrum of Lepidoptera was sampled and subsequently studied. All individuals of a sample were counted and sorted to species, which were identified at first to family level, later to morphospecies and species levels. In this way frequency and abundance distribution of species were preserved, which is an intrinsic source of data included in each sample.

Most of the results were published in Mey (2011). These data are used here to analyse and demonstrate the statistical rank of the Geometridae as one family among many others in Lepidoptera communities of about 40 localities distributed in the major biomes of southwestern Africa.

The Geometridae is one of the most dominant families in southwestern Africa concerning species and specimens numbers. The family belongs to the Macrolepidoptera, and in this group it takes the second rank in species numbers. At the time of analyzing the light trap catches the Noctuidae was recognised as the largest family and consequently took the first rank. Today, the Noctuidae are split into several families, and future analyses will probably demonstrate, that all families in the Noctuoidea superfamily fall behind Geometridae taking rank two or less.

When considering the whole Lepidoptera spectrum Gelechiidae and Pyralidae: Phycititinae of the Microlepidoptera are similarly speciose and even occupy the first rank sometimes.

In Savanna and Nama-Karoo localities in Namibia and RSA Geometridae species make up about 8.5 % of the total Lepidoptera fauna. The percentage rises to 14 % in Succulent Karoo and 24 % in Fynbos localities.

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Mey, W. (2011): Basic pattern of Lepidoptera diversity in southwestern Africa. – *Esperiana* Memoir 6, 320 pp

Biome	localities	total species number			Geometridae species number		
		min.	max.	mean	min.	max.	mean
Savanna	14	93	382	219	7	42	20
Nama-Karoo	13	63	158	108	2	19	9
Desert	8	13	95	39	0	11	3
Succulent-Karoo	5	82	135	112	8	24	15



Fynbos	6	71	266	123	16	64	30
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Table 1: Portions of Geometridae in light trap samples taken in five biomes in southwestern Africa

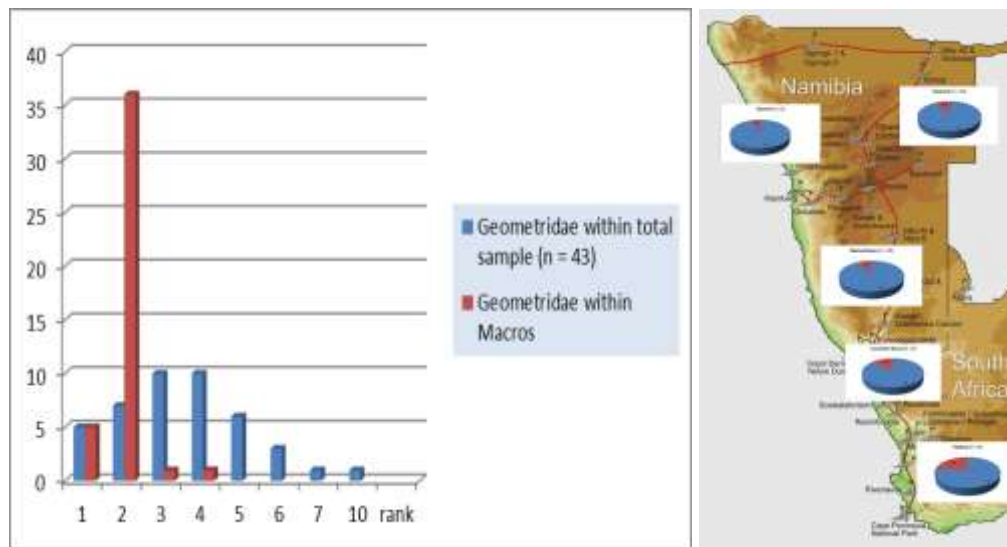


Figure 1: Rank-abundance plot of Geometridae in light trap samples. - Fig.2: Map of southwestern Africa (BIOTA Project area) depicting the proportion (%) of Geometridae species in light trap samples taken in five different biomes.

### **The Geometridae of the Amanos mountains in southern Turkey - with a review of the historical exploration**

**Feza Can Cengiz & Axel Hausmann**

Can Cengiz, F. & A. Hausmann (2014): The Geometridae of the Amanos mountains in southern Turkey - with a review of the historical exploration. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The Amanos mountains in the east Mediterranean Region of Turkey arise sharply from sea level up to 2240 m (Mıgır Peak) and are situated from Kahramanmaraş to Hatay province measuring approx. 200 km in length and 25 km in width. Its topographical, geological and geomorphological features supported a high rate of endemism and a large number of still ongoing speciation events. Therefore, the Amanos Mountains can be regarded as a 'laboratory of evolution' and thus are an ideal model for case studies in research of evolution biology,



biogeography and the effects of biotic and abiotic factors on biodiversity (e.g. effects of climatic change). The Amanos mountains are one of the least damaged natural ecosystems of Turkey. The range is located at the intersection point of three different phytogeographic vegetation zones, i.e. the Euro-Siberian, the Irano-Turanian and the Mediterranean zone.

The biodiversity of the Amanos mountains is notably rich as a consequence of the above mentioned geological and climatic diversity. Many reptiles, mammals, freshwater fishes, butterflies and plants were described as endemic species and subspecies. However, there is no comprehensive and no recent study on the moths of this mountain range. An ongoing project will investigate the biodiversity of moths of the Amanos Mountains, their habitats, vertical and horizontal distribution, abundance, host-plants and (potential) pest status by combining morphological and molecular methods.

**Contribution to an understanding of the early stages (egg, larva) of *Lythria sanguinaria* (Duponchel, 1842) with reference to two species in the Rhodometrini Agenjo, 1952 (Geometridae: Sterrhinae) (data from central Spain)**

**Gareth Edward King**

King, G. E. (2014): Contribution to an understanding of the early stages (egg, larva) of *Lythria sanguinaria* (Duponchel, 1842) with reference to two species in the Rhodometrini Agenjo, 1952 (Geometridae: Sterrhinae) (data from central Spain). Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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Data obtained ex females (foothills of Sistema Central, central Spain, 720m) under captive conditions produced images of egg deposition with strategies employed in a similar fashion to both *Rhodometra sacraria* (L., 1767) and *Casilda consecraria* (Staudinger, 1871), images were also provided of larvae in L1 and L5. Host plant data coincide with that of *Lythria cruentaria* (Hufnagel, 1767) which also feeds on *Rumex acetosella* (Polygonaceae). Larval habitus at a general level both in terms of morphology (L5) and resting position in relation to the substrate also coincides with *Rhodometra sacraria*. Initial analyses of larval chaetotaxy (L5) suggest only three SV setae on the anterior surface of A6 pro-leg, interestingly the anal pro-leg (A10) places the CD2 seta below the level of the L2 seta, a Sterrhine larval synapomorphy already recognised in the 1950s when the Lythriini Herbulot, 1962 were still considered larentiines.

**Unexpected feature of geometrid species composition (Lepidoptera: Geometridae) on the small islands in the Peter the Great Gulf (Sea of Japan, south of Russian Far East)**

**Evgeny A. Beljaev**



Beljaev, E.A. (2014): Unexpected feature of geometrid species composition (Lepidoptera: Geometridae) on the small islands in the Peter the Great Gulf (Sea of Japan, south of Russian Far East). Pp. #### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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Unexpected feature of agrolological structure of the moths' species assemblages on four small shelf islands in the Peter the Great Gulf (Sea of Japan, south of Russian Far East) is discussed. Before the geometrid fauna, also as nocturnal lepidopterofauna as whole, on these islands was almost unknown. Details ate published in Beljaev (2013).

The study was conducted according to standard entomological procedures of insect collecting and chorological analysis of local faunas. Materials were obtained during the author's field studies in 1997 and in 2012 on the Rikord Island (area 5.0 sq. km), on the Bolshoi Pelis Island (area 3.1 sq. km) and on the Furugelm Island (area 1.9 sq. km); also literature data was infolded for the Askold Island (area 14.6 sq. km). For comparison three neighboring continental geometrid faunas were taken (2006, 2009). Table of species is published in Beljaev (2013). Statistical analysis was performed using the detrended correspondence analysis (Hill, Gauch, 1980). Typification of areas was made following the principles by Gorodkov, modified for geometrids by Beljaev (2011).

Table 1. Number and proportion (%) of geometrid species from different arealogical groups in local faunas in Primorskii region.

Arealogical group	Ask.	Rick.	B.P.	Fur.	Laz.	Lit.	Razd.	Prim.
Widespread	49/34,5%	26/32,9%	18/32,7%	31/28,9%	104/33,8%	92/29,9%	96/30,6%	154/28,9%
Central Palaearctic – Far Eastern	15/10,6%	4/5,1%	8/14,6%	10/9,5%	30/9,7%	21/6,8%	43/13,6%	65/12,3%
East Asian	76/53,5%	44/55,7%	29/52,7%	65/60,7%	166/53,9%	190/61,7%	169/53,8%	302/56,6%
Far Eastern	2/1,4%	2/2,5%	0/0%	0/0%	5/1,6%	1/0,3%	3/1,0%	5/0,9%
East Asian – Indo-Malayan	0/0%	3/3,8%	0/0%	1/0,9%	3/1,0%	4/1,3%	3/1,0%	7/1,3%
Total	142/100%	79/100%	55/100%	107/100%	308/100%	308/100%	314/100%	533/100%

Legend. Territories: Ask. – the Askold Islands, Rick. – the Ricord Islands, B.P. – the Bolshoi Pelis Islands, Fur. – the Furugelm Islands, Laz. – Lazovsky Nature Reserve, Lit. – Litovka Mountain, Razd. – Razdolnaya river, Prim. – Primorskii region. Arealogical groups: Widespread – the species with broad Palaearctic or Holarctic ranges; Central Palaearctic–Far Eastern – the species with ranges covering east of Central Asia, South Siberia, Mongolia, North-East China and countries around the Sea of Japan; Far Eastern – the species with ranges covering most northeastern Pacific Asia south to the lands around northern part of the Sea of Japan; East Asian – species with ranges covering the extratropical China (except west) and territories neighboring to the Sea of Japan; the species with ranges covering subtropical and tropical zones of East, South and Southeast Asia.



As a result, it was found that geometrid fauna demonstrates high degree of patchiness between the islands and species richness at times lesser than in neighboring continental localities. Nevertheless, a high similarity of agrological structure of the moths inhabited the islands and the continental localities was explored (Table 1, Fig. 1).

This is unexpected because of low species richness of geometrids on the islands and their mosaic distribution between them, being original current climatic conditions on the islands and their separation from mainland at beginning of Holocene in different climatic epoch (Markov, 1983).

According to the classic views of the theory of island biogeography, richness and composition of biota on islands depend on the balance of rate of foreign colonization and rate of extinction of resident populations. On the example of small islands of the Baltic Sea (the Southwestern Archipelago off the coast of Finland) Nieminen and Hanski (1998) showed that structure of population and migration of nocturnal Lepidoptera on these islands meet this assumption. Besides, these authors shown the mixed nature of populations of moths on the small islands, included both resident populations and continental-island metapopulations supported by flow of migrants from the mainland coast.

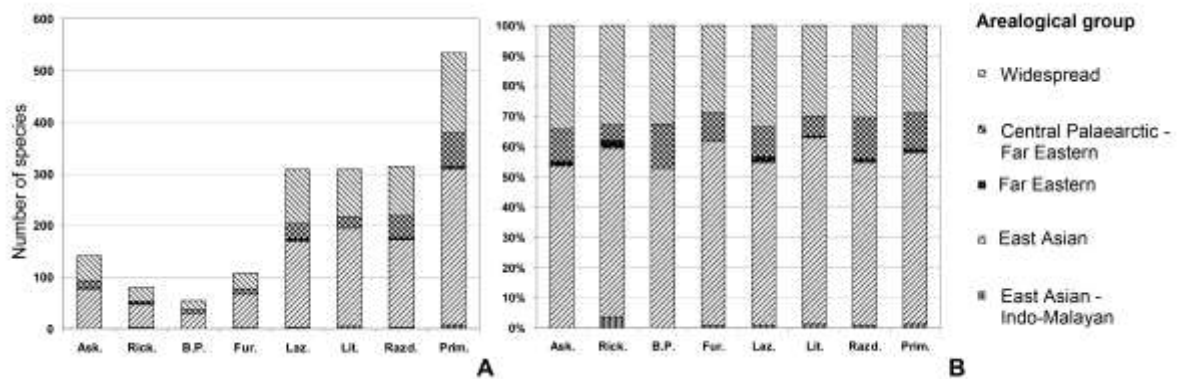


Fig. 1. Major species of geometrid moths on the islands and in the continental local faunas in Primorskii region. A – number of species, B – the share (%) of species. Notations see Table 1.

Taking into account results obtained by Nieminen and Hanski (1998), the agrological structure on the small islands in the Peter the Great Gulf could be explained by assuming that the moths on the islands represented mainly by resident populations, which occasionally, but regularly over long time intervals, are replenished by random immigrants from mainland. This random immigration could align the areological structure of moths between islands and mainland. This model could explain both a high degree of patchiness of the species composition of the moths on the islands, as well as a high degree of compliance of their areological structure to neighboring continental localities. However, this hypothesis assumes an equivalence of distribution of migratory ability of moths in large areological groups, which requires special research.

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## **Charissa, subgenus Pterygnophos: little-known geometrid moths from Central Asia**

**Laura Marrero Palma & Sven Erlacher**

Marrero Palma, L. & S. Erlacher (2014): *Charissa*, subgenus *Pterygnophos*: little-known geometrid moths from Central Asia. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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*Charissa* Curtis, 1826 is a species-rich genus within the Ennominae. Most of them occur in the Palearctic region. Externally they resemble each other due to their adaptation to rocks. Therefore they are generally considered to be hardly determinable. For that reason it is often necessary to analyze their genitalia, but even then, differences between species are sometimes difficult to find.

Within the genus *Charissa* Curtis, 1826 the subgenus *Pterygnophos* Wehrli, 1951 was taxonomically revised. *Pterygnophos* was originally proposed as a subgenus of *Gnophos* Treitschke, 1825, but now transferred to the genus *Charissa*. The species of that subgenus occur in Southeast Asia, Mongolia and South Siberia. There has been no revision of that group for 60 years. As a result of the recent work one species from Mongolia was considered as new. Three species have to be transferred from *Gnophos* Treitschke, 1825 to *Charissa*, and three new synonyms were recognized. Now the subgenus *Pterygnophos* comprises four species in total which are presented in detail.

## **Phylogeny and classification of Timandrini and related groups - preliminary results**



### **Erki Õunap**

Õunap, E. (2014): Phylogeny and classification of Timandrini and related groups - preliminary results. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The geometrid subfamily Sterrhinae comprises two clades, which informally have been named ‘Sterrhini lineage’ and ‘Timandrini lineage’. The latter comprises the tribes Cosymbiini, Timandrini, Rhodometrini and Lythriini. However, morphological data indicate that placements of several genera in these tribes may need revision. In the current study, generic composition of tribes placed into ‘Timandrini lineage’ was revised using molecular phylogenetic approach. The results demonstrate that Timandrini and Cosymbiini in the current sense are paraphyletic. Moreover, genera *Pseudosterrha*, *Chlorerythra* and *Traminda* form a separate lineage that does not fit within any of the currently recognized tribes.