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Proceedings of the eighth FORUM HERBULOT 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014)

Axel Hausmann (ed.)

Hausmann, A. (ed.) 2014. Proceedings of the eighth FORUM HERBULOT 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). Spixiana 37 (2): 239–266.

The eighth FORUM HERBULOT 2014 in Schlettau, Germany, focused on modern tools and techniques to accelerate the assessment of global biodiversity without losing accuracy and quality of publications. New studies, projects and results from lepidopteran research were presented in thirty-two lectures. The results of the presentations and discussions were entered in a “Declaration on Accelerated Biodiversity Assessment”.

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Short report and results

Axel Hausmann

Hausmann, A. 2014. Short report and results. Pp. 239–240 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 37 (2).

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Altogether 61 participants from 25 countries were registered for the eighth FORUM HERBULOT (see FORUM HERBULOT 2014, http//www.herbulot.de/) and were welcomed at a “Bavaro-Thuringian Barbecue”. The 32 presentations during six sessions were chaired by Scott Miller (Washington, USA), Axel Hausmann (Munich, Germany), Jeremy deWaard (Guelph, Canada), Pasi Sihvonen (Helsinki, Finland), Catherine Byrne (Hobart, Australia), and Hossein Rajaei (Hamburg, Germany).

The conference started with presentations and break-out discussions on how global biodiversity assessment could be accelerated and improved. Chairman Axel Hausmann presented briefly Claude Herbulot’s strategy of producing a large number of species descriptions. The following keynote talks included contributions of Michael Balke (“Taxonomy: Faster. Better”), Ellinor Michel (“Global Digital Infrastructure for Biological Nomenclature and Taxonomy”), Lyubomir Penev (“Streamlining descriptions of new species identified with barcode data”), Sujeevan Ratnasingham (“The BIN system: Standardizing molecular operational taxonomy in animals”), Jeremy deWaard (“From BINs to Biodiversity: Rapid Arthropod Assessments using DNA Barcodes”), Scott Miller (“DNA barcode enabled ecological research on Geometridae in Papua New Guinea”) and Hermann Staude (“Accelerating the inventory of Lepidoptera early stages and host-plant & other associations, by using citizen-science projects”). The results of the presentations and discussions were entered in a FORUM HERBULOT declaration (see below) reflecting our consensual community position. The seminary sessions of the second and the third day covered also phylogenetic, taxonomic, zoogeographic, faunistic and other topics. FORUM HERBULOT 8 offered pleasant opportunities for collecting in the Ore Mountains during all evenings of the meeting.

Participants expressed their thanks to the organizers and sponsors (e. g. DFG HA 1806/11-1) of Forum Herbulot 8 (2014). The research initiative Forum Herbulot was, once again, generally welcomed and the need for, and the advantages of, close scientific cooperation among geometrid experts were stressed. A proposal to have the next Forum Herbulot 9 in Concepción, Chile, mid-January 2017 was generally appreciated. Chairman Axel Hausmann reported that future venues have been offered by the museums in Stuttgart (Germany) and in South Korea.

The conference was closed after the conference dinner in a restaurant in downtown Chemnitz. Forum Herbulot 8 came to an end with a one-day post-conference trip to Dresden: more than 30 participants visited the Natural History Museum and enjoyed sight-seeing during a guided boat tour on the Elbe river (see footnote below). In the evening, a smaller group attended the opera "Il barbiere di Siviglia" at the famous "Semper-Oper".

Forum Herbulot 2014. Web-page of the International Scientific Community with research focussed on Geometridae. www.herbulot.de [accessed 06-Oct-2014]

A footnote to the report on the post-conference tour to Dresden

Manfred Sommerer

Sommerer, M. 2014. A footnote to the report on the post-conference tour to Dresden. Pp. 240–241 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 37 (2).

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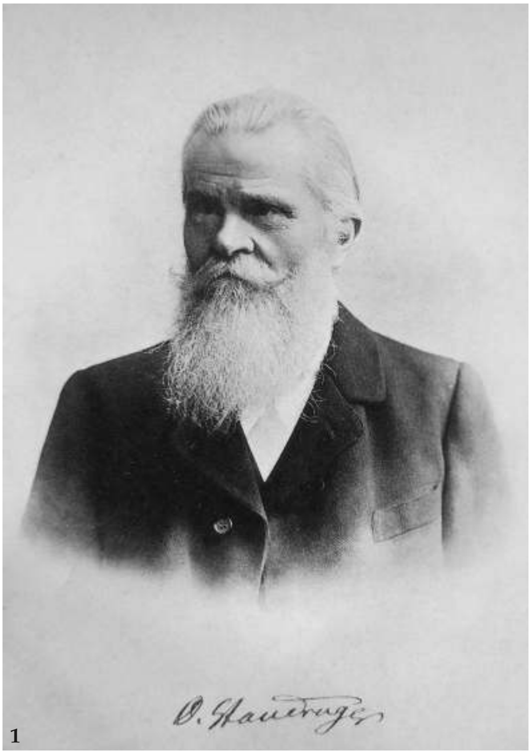
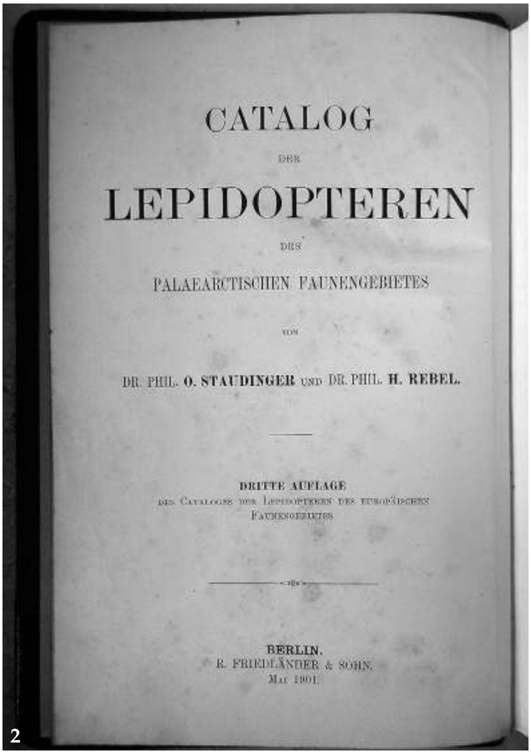
The cruise on the river went from the centre of Dresden (Elbterrassen) down to the Loschwitz bridge, famous as the "Blue Miracle" (Blaues Wunder). Built in 1893, the middle part of this steel bridge spans almost 150 m without intermediate pylon – at that time an amazing technical achievement. The colour


1


2

CATALOG
DER
LEPIDOPTEREN
DES
PALAEARCTISCHEN FAUNENGEBIETES
VON
DR. PHIL. O. STAUDINGER UND DR. PHIL. H. REBEL.

DRITTE AUFLAGE
DES CATALOGES DER LEPIDOPTEREN DES EUROPÄISCHEN
FAUNENGEBIETES

BERLIN.
R. FRIEDLÄNDER & SOHN.
MAI 1901.

Figs 1–2. Portrait of Dr. O. Staudinger and title page of the "Catalog" (3rd ed., 1901).

was light blue. Connecting the formerly suburban areas of Loschwitz and Blasewitz, this bridge has, in a way, a historical relation to entomology: Dr. Otto Staudinger and Andreas Bang-Haas, the owners of the well-known firm Staudinger & Bang-Haas (cf. Figs 1–3) trading in Lepidoptera from remote and exciting parts especially of the palaearctic region, had their homes at Blasewitz-Dresden. Staudinger's "Catalog der Lepidopteren des palaearctischen Faunengebietes" (3rd ed. together with Rebel, 1901) is known to most lepidopterists. The major part of the important Staudinger collection with many type specimens is housed at the Museum of the Humboldt University of Berlin. A part of Staudinger's collection came, however, together with the collection of Bang-Haas, to the Museum in Dresden (Senckenberg Museum für Tierkunde) and was shown to the participants of FORUM HERBULOT 8 by Matthias Nuss.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Auswahlsendungen von besseren Arten bereitwilligst.

Dr. O. Staudinger & A. Bang-Haas
Blasewitz-Dresden.

Fig. 3 Advertisement of the firm Staudinger & Bang-Haas, printed at the end of the book K. Lampert, Die Großschmetterlinge und ihre Raupen Mitteleuropas, Verlag J. F. Schreiber, Esslingen/München 1907.

Conference Materials FORUM HERBULOT 2014

FORUM HERBULOT 2014 statement on accelerated biodiversity assessment (Community Consensus Position)

Forum Herbulot

FORUM HERBULOT 2014. FORUM HERBULOT 2014 statement on accelerated biodiversity assessment (Community Consensus Position). Pp. 241–242 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 37 (2).

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FORUM HERBULOT is a research initiative, founded in the year of 2000, with approx. 150 members from 42 countries. Most are renowned experts in Lepidopterology (with a main focus on the largest family, Geometridae). During the 8th congress of the FORUM HERBULOT, held between June 30th and July 5th at the Nature Conservation Centre of the Ore Mountains in Schlettau, Germany, attendants joined a general discussion of the topic "How to accelerate the inventory of biodiversity" and decided to publish the following declaration:

(1) FORUM HERBULOT (FH) highlights that global biodiversity assessment needs to be accelerated, through
- extensive sampling projects, especially in tropical and subtropical regions where a large part of Lepidopteran diversity remains undescribed,
- species descriptions and
- interim-assessments and characterization of diversity (e. g. DNA Barcoding, collection management, databasing)

To achieve this goal we urge national and international funding agencies, as well as decision-makers to provide substantial support and financial resources to projects involving sampling, DNA barcoding, and taxonomic research. WE NEED TO consider that mankind is facing, within the next few years, its biggest environmental crisis ever, i. e. the definitive and irreversible loss of a considerable part of biodiversity on earth. Species on Earth are disappearing at an alarming rate and it will soon be too late to perform research on (and subsequent conservation of) life's most precious heritage: biodiversity. FH urgently asks national and international authorities to endorse and support biodiversity research by adopting collecting/exportation regulations in fact facilitating, rather than obstructing, research on biodiversity, along the lines of Article 8a of the Nagoya Protocol on Access and Benefit Sharing.

(2) FH highlights the need of formally described species within the universally adopted Linnean system, but also recognizes the urgent need to develop and integrate the use of interim DNA-

based systems to characterize species. Such an interim system can be generated, for instance, by the use of DNA barcoding, and of automatically assigned Barcode Index Numbers (BIN), in the Barcode of Life Datasystems (BOLD). Therefore we welcome:

- the forthcoming online documentation of BIN history in BOLD
- DNA barcoding programs focusing on unnamed species (suspected to be new) in collections
- projects of DNA barcoding of type specimens. National funding agencies and decision-makers should commit themselves quickly to provide substantial support and financial resources to generate DNA-barcodes for all type specimens deposited in their national collections.

(3) FH acknowledges the advantages of modern tools for species descriptions, and supports/encourages:

- electronic publication of species descriptions linked to online databases
- development of interfaces linking DNA barcode data (e. g. BOLD), online publishing tools and other online databases (e. g. GenBank, GBIF, EOL, etc.)
- registration in Zoobank as a standard for all new nomenclatural acts
- DNA barcoding of holotypes as best practice for all newly described species.

(4) FH recommends, for species descriptions, the following minimum quality standards (in addition to the minimum requirements of the Code):

- information on wing pattern
- internal morphological features (usually genitalia)
- genetics (preferably the standard DNA barcode, i. e. the 5' 658 bp of the COI gene) if available
- differential diagnosis from the closest related species. FH encourages careful and thorough differential diagnoses, as well as full bibliographic references to the original descriptions of all mentioned species names in taxonomic publications whenever possible.

(5) Common resource data: FH supports the Bouchout Declaration (http://bouchoutdeclaration.org/) for open access to biodiversity data and thus strongly encourages opening for free use the online access to key biodiversity data including sequences (along with access numbers on BOLD and GenBank/EMBL/DDBJ published in the original descriptions), taxonomic names, descriptions, occurrence data, images, ecological dates, habitats, biological traits and data.

The Forum Herbulot, 3 July 2014, Schlettau (Germany)

Claude Herbulot – his way of accelerating biodiversity assessment

Axel Hausmann

Hausmann, A. 2014. Claude Herbulot – his way of accelerating biodiversity assessment. P. 242 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 37 (2).

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Claude Herbulot (1908–2006) published descriptions of close to 800 valid geometrid species. Only three taxonomists ever described more geometrid species than him (Prout 3591 species, Warren 2282 species, Walker 1027 species). All of them used "short-description-methods" that would not be accepted by today's peer-reviewed journals and reviewers. Current requirements and high standards for species descriptions, as well as lacking funds for taxonomy lead to a deceleration of species description rates. So far, some 23000 geometrid species have been described, but research on unidentified collection material and results from the global DNA barcoding campaign suggest that there are more than 40000 species on earth. However, no living taxonomist is author of more than 300 geometrid species descriptions and nowadays worldwide description rates dropped below 100 per year for this family. At this pace, another 200 years may be needed for describing the remainder of species. Forum Herbulot 2014 offers the scientific platform for discussing how modern methods allow adjusting our standards and description practice to achieve an acceleration of biodiversity assessment. One of these tools is DNA barcoding which has provided genetic assessment for 20000 geometrid species in just eight years. The results of the discussions are published in the "Forum Herbulot 2014 statement on accelerated biodiversity assessment".

Taxonomy – faster. Better

Michael Balke

Balke, M. 2014. Taxonomy – faster. Better. P. 243 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 37 (2).

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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* Fauvel, 1862 weevils in the open-access journal ZooKeys (Riedel et al. 2013). 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.

Riedel, A., Sagata, K., Surbakti, S., Tänzler, R. & Balke, M. 2013. One hundred and one new species of *Trigonopterus* weevils from New Guinea. ZooKeys 280: 1. doi:10.3897/zookeys.280.3906

Global digital infrastructure for biological nomenclature and taxonomy

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

Michel, E., Pyle, R. L. & Guralnick, R. P. 2014. Global digital infrastructure for biological nomenclature and taxonomy. P. 243 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 37 (2).

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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 2014, http://iczn.org/), botanical (ICNafp 2014, 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 2014, http://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.

ICNafp 2014. International Code of Nomenclature for algae, fungi and plants. http://www.iapt-taxon.org/nomen/main.php/ [accessed 06-Oct-2014]

ICZN 2014. International Commission on Zoological Nomenclature. http://iczn.org/ [accessed 06-Oct-2014]

ZooBank 2014. The Official Registry of Zoological Nomenclature. http://zoobank.org/ [accessed 06-Oct-2014]

Streamlining descriptions of new species identified with barcode data

Lyubomir Penev & Pavel Stoev

Penev, L. & Stoev, P. 2014. Streamlining descriptions of new species identified with barcode data. P. 244 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 37 (2).

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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 then 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

Sujeevan Ratnasingham

Ratnasingham, S. 2014. The BIN system: standardizing molecular operational taxonomy in animals. P. 244 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 37 (2).

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The Barcode Index Number (BIN) system is an algorithmic system that registers operational taxonomic units (OTUs) based on DNA barcodes in the Barcode of Life Data System. It has been designed and developed to address the large number of unrecognized animal species on the planet. By assigning individuals to presumptive species this system speeds investigations into the patterning of biodiversity and enable studies that would otherwise be impossible. Although OTUs have conventionally been separated through their morphological divergence, DNA-based delineations have important advantages. OTU designation can be automated, data can be readily archived, and results can be easily compared among investigations. The BIN system exploits these attributes and provides 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. The algorithmic methods utilized are designed to restructure registered OTUs, merging in some cases and splitting in others, when new data supports it. Such dynamism, although challenging at times to work with, reflects conventional taxonomic processes, is necessary to accurately illuminate dark taxa. Aside from a pragmatic role in biodiversity assessments, BINs aid revisionary taxonomy by flagging possible cases of synonymy, and by collating geographical information, descriptive metadata, and images for specimens that are likely to belong to the same species, even if it is undescribed. With over 300 000 registered OTUs and associated web pages now available, the BIN system continues to evolve with new functionality including detailed audit trails and community annotations.

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. & Young, M. 2014. From BINs to biodiversity: rapid arthropod assessments using DNA barcodes. P. 245 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 37 (2).

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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 2014, 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 150000 specimens, and over 15000 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* (Linnaeus, 1758)). 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.

BOLD 2014. Barcode of Life Data Systems. http//www.boldsystems.org/ [accessed 06-Oct-2014]

DNA barcode enabled ecological research on Geometridae in Papua New Guinea

Scott E. Miller

Miller, S. E. 2014. DNA barcode enabled ecological research on Geometridae in Papua New Guinea. Pp. 245–246 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 37 (2).

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DNA barcoding of the Geometridae of Papua New Guinea provides a framework for multiple lines of systematic and ecological research, as part of a large-scale study of insect-plant ecology and biogeography in forests in Papua New Guinea by the Binatang Research Centre (Novotny et al. 2010). 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 (Pagi et al. in preparation). DNA barcoding provides a rapid and accurate taxonomic framework, which is also instrumental in analysis of phylogeographic patterns (Craft et al. 2010), identifying caterpillars (Miller et al. 2013), detecting host-parasitoid interactions (Hrcek et al. 2013), linking historic types with modern specimens (Holloway et al. 2008), identifying host plants from caterpillar stomach contents (Erickson et al. in preparation), and phylogeny (Segar et al. in preparation, including additional genes). 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 (Ratnasingham & Hebert 2013).

This work is highly collaborative, and has been supported by the USA and Czech National Science Foundations, USA National Institutes of Health, Moore Foundation, Genome Canada, Natural History Museum (London), Biodiversity Institute of Ontario, PNG National Agriculture Research Institute, University of Minnesota, and many other funders and collaborators.

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Miller, S. E., Hrcek, J., Novotny, V., Weiblen, G. D. & Hebert, P. D. N. 2013. DNA barcodes of caterpillars (Lepidoptera) from Papua New Guinea. Proceedings of the Entomological Society of Washington 115: 107–109.

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Ratnasingham, S. & Hebert, P. D. N. 2013. A DNA-based registry for all animal species: the Barcode Index Number (BIN) system. PloS ONE 8(7): e66213.

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

Hermann S. Staude

Staude, H. S. 2014. Accelerating the inventory of Lepidoptera early stages and host-plant and other associations by using citizen science projects. P. 246 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 37 (2).

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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. & Hajibabaei, M. 2014. DNA barcoding and DNA metabarcoding as tools for rapid inventory and high-throughput identification of Lepidoptera species in Amazonia. P. 247 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 37 (2).

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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 intertropical 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. 247–248 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 37 (2).

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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. 2014). 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.

Heikkilä, M., Mutanen, M., Kekkonen, M. & Kaila, L. 2014. Morphology reinforces proposed molecular phylogenetic affinities: a revised classification for Gelechioidea (Lepidoptera). Cladistics 30 (6): 563–589. http://dx.doi.org/10.1111/cla.12064

Kekkonen, M. 2014. Taxon delineation in gelechioid moths: from phylogenetics to DNA barcoding. 60 pp., PhD thesis, University of Helsinki. http://urn.fi/URN:ISBN:978-952-10-9895-6

– – & Hebert, P. D. N. 2014. DNA barcode-based delineation of putative species: efficient start for taxonomic workflows. Molecular Ecology Resources 14: 706–715. http://dx.doi.org/10.1111/1755-0998.12233

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

Axel Hausmann, Hermann S. Staude, Clarissa Dieterle & Alfred Moser

Hausmann, A., Staude, H. S., Dieterle, C. & Moser, A. 2014. With or without speed-limit? How to assess 3000 Emerald species (Lepidoptera, Geometridae, Geometrinae). P. 248 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 37 (2).

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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* Moore, 1887, *Prasinocyma* Warren, 1897 and *Victoria* Warren, 1897, and the Neotropical species of the genera *Lophochorista* Warren, 1904, *Oospila* Warren, 1897, *Nemoria* Hübner, 1818 and *Lissochlora* Warren, 1900. 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.

Ratnasingham, S. & Hebert, P. D. N. 2013. A DNA-based registry for all animal species: the Barcode Index Number (BIN) system. PLoS ONE 8(7): e66213. doi:10.1371/journal.pone.0066213

DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artefact 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. & De Prins, J. 2014. DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artifact of tropical under-sampling. P. 249 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 37 (2).

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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 (Fig. 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).

Lees, D. C., Kawahara, A. Y., Rougerie, R., Ohshima, I., Kawakita, A., Bouteleux, O., 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

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Delabye, S., Decaëns, T., Bayendi, S., Ntie, S., Le Gall, P., Lopez Vaamonde, C., Moulin, N., Sebag, D., Rougerie, R. & the Ecotrop team. 2014. Using DNA barcoding as a tool to describe moth community patterns in Lopé and Ivindo National Parks, Gabon. Pp. 249–250 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 37 (2).

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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 (BOLD 2014, 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 undersampling, 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.

BOLD 2014. Barcode of Life Data Systems. http//www.boldsystems.org/ [accessed 06-Oct-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

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László, G. M., Ronkay, G. & Ronkay, L. 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. 250–251 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 37 (2).

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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 in Figure 1.

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.

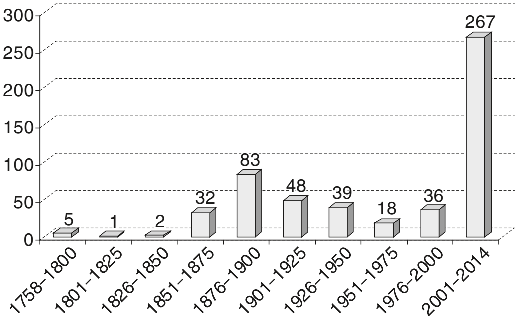

Fig. 1. Numbers of valid taxa (species and subspecies) having been described since 1758.

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. P. 251 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 37(2).

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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. & An, J.-S. 2014. Spatial and temporal pattern of species richness and abundance of macromoths including Geometridae in Mt. Jirisan National Park, South Korea. Pp. 251–252 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 37(2).

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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 1185 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 (± 68.34) and 5161 individuals (± 1349.9). Yearly change of species richness and abundance of Geometrid moths was 173 species (± 20.17) and 2328 individuals (± 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. & Throssell, A. 2014. Current research on Australian Geometridae – redefining the Tasmanian “Archiearinae” and the blitzing of Australia’s remote fauna. Pp. 252–254 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 37 (2).

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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 of the 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, Regier et al. (2009), Mutanen et al. (2010), 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, 1823, *Boudinotiana* Leraut 2002, Palaearctic *Leucobrephos* Grote, 1874 fauna and the Neotropical *Lachnocephala* Fletcher, 1953 and *Archiearides* Fletcher, 1953 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 most species. These adaptations are a recurring theme in alpine moths. It is probable, therefore, that *Acalyphes* Turner, 1926 and *Dirce* Prout, 1910 (cf. Fig. 1) 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 (2014, 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) WA 2009 – 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, 1858 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.

Fig. 1. Larva of *Dirce solaris* on *Epacris serpyllifolia* with reduced number of prolegs (photo: Peter Robinson, TMAG).

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, 1939 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, 1892), *Chrysolarentia ptochopis* (Turner, 1907) and *Epyaxa agelasta* (Turner, 1904). In addition a rare known undescribed species of the Hepialidae from the genus *Fraus* Walker, 1856 was collected. This species is known from only five specimens collected on the mainland of Tasmania from one collection event in 1986.

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

- Redescription of *Omoplatica* Turner, 1926 (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 *Lipogya* Warren, 1898 (Geometridae: Boarmiini) with the description of two new species, and redescription of three species.
- Redescription of *Nisista* Walker, 1860 (Geometridae: Nacophorini) with the description of five new species and the redescription of three species.
- Redescription of *Scioglyptis* Guest, 1887 (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. & Õunap, E. 2014. On the phylogeny and systematics of the tribe Larentiini (Lepidoptera: Geometridae). P. 254 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 37(2).

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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-1α), 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* Treitschke, 1825, 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 (Lepidoptera, Geometriformes) – discordant or concordant

Evgeny A. Beljaev

Beljaev, E. A. 2014. Molecular and morphological phylogenies in geometroid lepidopterans (Lepidoptera, Geometriformes) – discordant or concordant. Pp. 255–258 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 37 (2).

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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 & Stekolnikov (2001). This series corresponds to the drepanoid/geometroid assemblage plus superfamily Cimelioidea following Minet & 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.

Morphological data for this analysis was taken from my morphological and phylogenetic research of the geometrid moths and related families that had been partially published in a series of papers (Beljaev 1992, 1997, 1998a, 1998b, 2000, 2003a, 2003b, 2006a, 2006b, 2007, 2008b, 2009a, 2009b) and in a book (Beljaev 2008a). Most of these works are based on the combination of functional-morphological analysis (mainly following Kuznetzov & Stekolnikov 2001) and manual cladistics. The principal theoretical point of my reconstruction of the phylogeny in Geometriformes is the statement, that "apomorphy – is not a character state but a fact that this state was acquired once" (formulated in Russian by Rasnitsyn 2002: 74). This understanding of apomorphy does not permit us to take a morphological character as is, without prior analysis of possible origins and transformation; it implies deep comparative-morphological analysis focused on identification of morphological homologies and on construction of polarized rows of morphological transformations (morphoclines); it requires stringent selection of characters that carry 'phylogenic signal' at the targeted taxonomic level prior to the formulation of hypotheses about probable synapomorphies; it entails manual reconstruction of a phylogenic tree that is consistent with a priori selected characters. That is, this understanding of an apomorphy requires it to be considered not as a logical construction, but as a morphological innovation with its own history.

Four recent molecular-phylogenetic studies were included in the analysis. The first two were focused on Geometridae (Yamamoto & Sota 2007, Sihvonen et al. 2011). The other two covered all Lepidoptera (Regier et al. 2009, Mutanen et al. 2010), and I took from them only the portions with geometroid families. The resulting phylogenetic trees in both publication sets are generally similar in branching pattern. In the each molecular phylogeny all basal nodes (approximately up to tribal level) were separated into 3 groups. First – nodes that are congruent with my morphological notions on cladistic relationships of relevant taxa (called here for clarity as 'green' nodes; in Fig. 1 reproduced in grey); second – nodes that differ from my morphological notions ('red' nodes; in Fig. 1 in dark grey); and third – nodes that are omitted from the analysis either due to me lacking an opportunity to examine relevant taxa or because morphological data were insufficient for clarifying their phylogenetic position ('white' nodes).

Also, all selected 'colour' nodes were divided into 2 groups: with bootstrap support values 50 and more, and less than 50 (Table 1, Fig. 1.). Nodes with low bootstrap support values (usually less than 50) are ambiguous for indication of phylogenetic relationship, and they commonly referred to as area of low resolution or unresolved nodes. For short, below I shall name nodes from the first group as resolved nodes, and nodes from the second group as unresolved nodes.

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

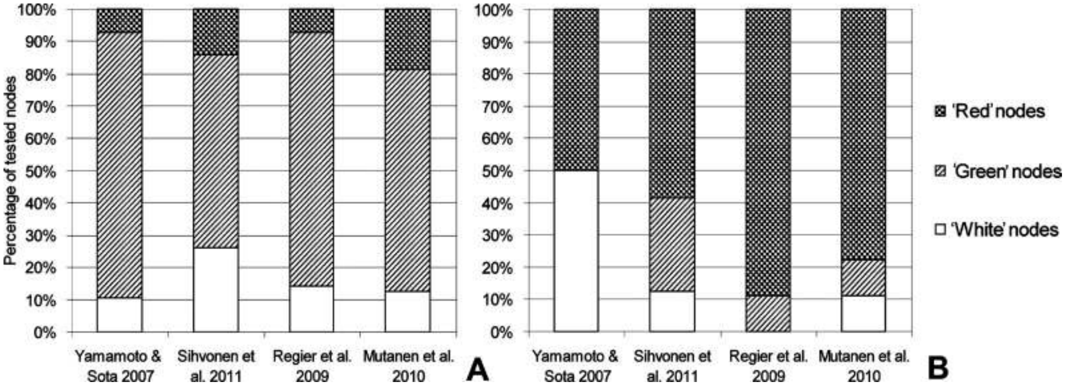

Fig. 1. Percentage of 'white', 'green' and 'red' resolved nodes (**A**) and unresolved nodes (**B**) in phylogenies by Yamamoto & Sota (2007), Sihvonen et al. (2011), Regier et al. (2009) and Mutanen et al. (2010).

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 Figure 1B. It is clear that 'red' nodes are absolutely predominant in this area.

In the phylogeny by Sihvonen et 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 cannot be used as the argument for rejection of relationships established on the basis of morphological criteria and for revision of taxonomic systems.

Noteworthily, 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

Table 1. Congruence of nodes in the molecular phylogenies with morphological phylogenetic hypothesis. Percentages are rounded to whole numbers.

		All tested nodes: number, 'colour' type and percentage				Resolved nodes: number, 'colour' type and percentage			
N	Author of molecular phylogeny	Number of all tested nodes	Number of 'white' nodes / %	Number of 'green' nodes / %	Number of 'red' nodes / %	Number of tested nodes	Number of 'white' nodes / %	Number of 'green' nodes / %	Number of 'red' nodes / %
	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 et al. 2011	67	14 / 21 %	33 / 49 %	20 / 30 %	42	11 / 26 %	25 / 60 %	6 / 14 %
3.	Regier et al. 2009	23	2 / 9 %	12 / 52 %	9 / 39 %	14	2 / 14 %	11 / 79 %	1 / 7 %
4.	Mutanen et al. 2010	25	3 / 12 %	12 / 48 %	10 / 40 %	16	2 / 12 %	11 / 69 %	3 / 19 %

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

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Rajaei, H., Greve, C., Letsch, H., Stüning, D., Wahlberg, N., Minet, J. & Misof, B. 2014. Molecular and morphological investigations suggest family level for the little known *Pseudobiston pinratanai* Inoue, 1994. P. 258 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 37 (2).

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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-1α, 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) strong 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. & Mutanen, M. 2014. Enigmatic cycad moths of Africa: a holistic approach to examine their systematic position (Lepidoptera, Geometridae). P. 258 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 37 (2).

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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 in the knowledge of Geometrid moths of Ethiopia

Andrea Sciarretta, Axel Hausmann & Francesco Parisi

Sciarretta, A., Hausmann, A. & Parisi, F. 2014. Recent advances in the knowledge of Geometrid moths of Ethiopia. P. 259 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 37 (2).

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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 600 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 95 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* Warren, 1897, with 44 species currently identified for the fauna of Ethiopia, of which at least 22 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. P. 259 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 37 (2).

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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* (Hampson, 1891) (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 sympatricly 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. & Hausmann, A. 2014. Advances in the knowledge of the larentiine fauna of southern Italy by DNA barcoding (Lepidoptera, Geometridae). P. 260 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 37 (2).

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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 leave 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 tophaceata* (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* Millière, 1864, previously identified as *E. lentiscata* Mabille, 1869, 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

Glaucia Marconato

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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 on the upper side of wings. 115 valid species are distributed in the Neotropics from Argentina to the southern United States. In the current concept, six genera are included in Palyadini: *Palyas* Guenée, 1858, *Phrygionis* Hübner, 1825, *Pityeja* Walker, 1861, *Argyrotome* Warren, 1894, *Opisthoxia* Hübner, 1825 and *Ophthalmoblysis* Scoble, 1995. This group was proposed by Guenée (1858) (as "Palyade"), including *Eumelea* Duncan, 1841, *Palyas*, *Ophthalmophora* Guenée, 1858 and *Byssodes* Guenée, 1858. Hulst (1896), has noticed that all the species of *Palyas* and *Phrygionis*, which occur in the USA, did not have frenulum and retinaculum. Later, Warren included it in the tribe Baptini.

Warren described four species in *Argyrotome*, seven species in *Ophthalmophora* and seven in *Opisthoxia*. Oberthür (1916) reviewed the genera *Palyas*, *Ophthalmophora* and *Byssodes*. He followed Guenée and cited *Eumelea* as a part of the group "Palyade". Dognin described one *Argyrotome* and five *Ophthalmophora* species. Schaus described two more new species of *Argyrotome*. Prout (1933) revised the genus *Phrygionis* and Debauche (1937) splitted *Argyrotome* into two subgenera: *Argyrotome* and *Parargyrotome*. Holloway (1993, 1996) recognized Palyadini as a separate tribe from Baptini and definitively excluded the south-east Asian Eumeleini from Ennominae (with genus *Eumelea* which earlier had been regarded to be related to Palyadini).

In 1994, Scoble reviewed two genera *Phrygionis* and *Pityeja*; one year later, the same author revised the tribe, without, however, performing a phylogenetic analysis. He synonymized *Ratiaria* Walker, 1861 with *Phrygionis*, and the two genera *Aplorama* Warren, 1904 and *Callurapteryx* Warren, 1894 with *Pityeja*, describing several new species e transferring many others to these two genera. A new genus was proposed, *Ophthalmoblysis*. Moreover, *Ophthalmophora* and *Argyroplutodes* Warren, 1894 were synonymized with *Opisthoxia* and *Parargyrotome* with *Argyrotome*. Scoble (1994) discusses also the wing patterns of *Opisthoxia* species and suggests species groups based on these patterns.

The alpha-taxonomy and phylogeny of the largest genus *Opisthoxia* with almost 90 species largely 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 harbour 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.

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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. 261–263 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 37 (2).

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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, un-

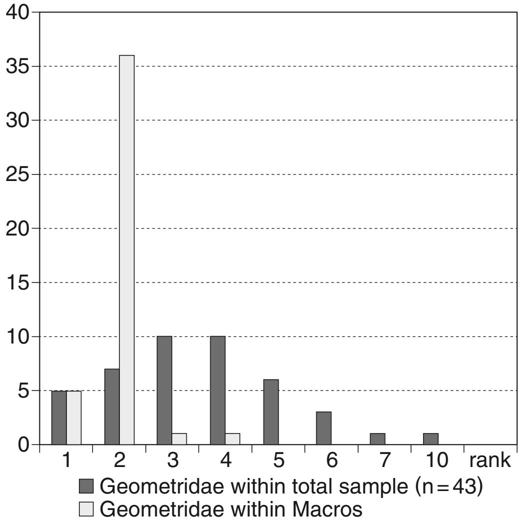

Fig. 1. Rank-abundance plot of Geometridae in light trap samples.

fortunately, 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.

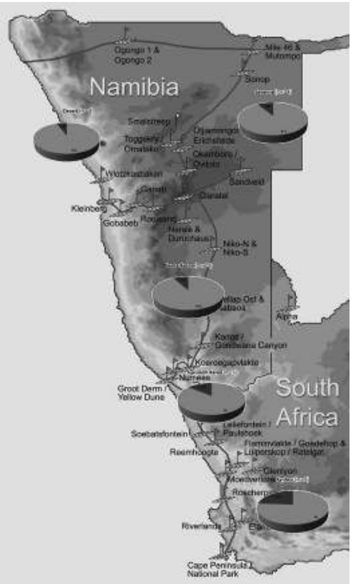

Fig. 2. Map of southwestern Africa (BIOTA project area) depicting the proportion (%) of Geometridae species in light trap samples taken in five different biomes.

The Geometridae 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

Table 1. Portions of Geometridae in light trap samples taken in five biomes in southwestern Africa.

		total species number			Geometridae species number		
Biome	localities	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

8.5 % of the total Lepidoptera fauna. The percentage rises to 14 % in Succulent Karoo and 24 % in Fynbos localities.

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The Geometridae of the Amanos mountains in southern Turkey – with a review of the historical exploration

Feza Can Cengiz & Axel Hausmann

Can Cengiz, F. & Hausmann, A. 2014. The Geometridae of the Amanos mountains in southern Turkey – with a review of the historical exploration. P. 263 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 37 (2).

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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, mammalians, 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. 263–264 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 37 (2).

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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* (Linnaeus, 1767) (Skule 1980) 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) (Ebert & Steiner 2001). 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 (Singh 1951) when the Lythriini Herbulot, 1962 were still considered larentiines (Õunap et al. 2008).

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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. 264–266 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 37 (2).

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Unexpected feature of arealogical 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 are 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 km^2), on the Bolshoi Pelis Island (area 3.1 km^2) and on the Furugelm Island (area 1.9 km^2); also literature data was infolded for the Askold Island (area 14.6 km^2). For comparison three neighbouring 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%

Territories:
Ask., Askold Islands; **Rick.**, Ricord Islands; **B.P.**, Bolshoi Pelis Islands; **Fur.**, Furugelm Islands; **Laz.**, Lazovsky Nature Reserve; **Lit.**, Litovka Mountain; **Razd.**, Razdolnaya river; **Prim.**, Primorskii region.
Arealogical groups:
Widespread: species with broad Palaearctic or Holarctic ranges;
Central Palaearctic–Far Eastern: species with ranges covering east of Central Asia, South Siberia, Mongolia, North-East China and countries around the Sea of Japan;
Far Eastern: 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;
East Asian–Indo-Malayan: species with ranges covering subtropical and tropical zones of East, South and Southeast Asia.

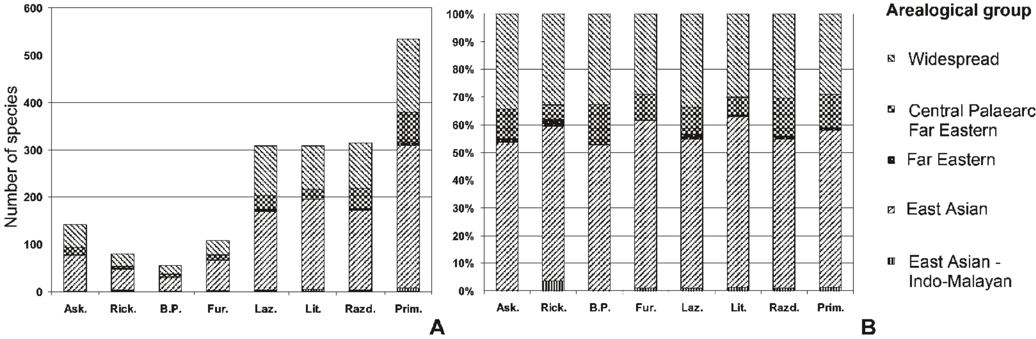

Fig. 1. Major arealogical groups of geometrid moths on the islands and in the continental local faunas in Primorskii region. **A.** Number of species; **B**. proportions (%) of species. Notations see Table 1.

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 neighbouring continental localities. Nevertheless, a high similarity of arealogical 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 & 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.

Taking into account results obtained by Nieminen & 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 alignment of arealogical 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 arealogical structure to neighbouring continental localities. However, this hypothesis assumes an equivalence of distribution of migratory ability of moths in large arealogical 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. & Erlacher, S. 2014. *Charissa*, subgenus *Pterygnophos*: little-known geometrid moths from Central Asia. P. 266 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 37(2).

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Charissa Curtis, 1826 is a species-rich genus within the Ennominae. Most of them occur in the Palaearctic 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 analyse 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. P. 266 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 37(2).

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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* Warren, 1888, *Chlorerythra* Warren, 1895 and *Traminda* Saalmüller, 1891 form a separate lineage that does not fit within any of the currently recognized tribes.