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Proceedings of the tenth FORUM HERBULOT 2018. Integrative taxonomy, a multidisciplinary approach to answer complicated taxonomic questions

(Stuttgart, Germany, 11–16 June 2018)

Axel Hausmann & Hossein Rajaei (eds)

Hausmann, A. & Rajaei, H. (eds) 2019. Proceedings of the tenth FORUM HERBULOT 2018. Integrative taxonomy, a multidisciplinary approach to answer complicated taxonomic questions (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2): 291–320.

The tenth International Congress of FORUM HERBULOT on “Integrative taxonomy, a multidisciplinary approach to answer complicated taxonomic questions” took place in the Staatliches Museum für Naturkunde Stuttgart (SMNS), from 11.–16.06.2018, with 77 participants and 52 scientific presentations. The proceedings provide short information on the meeting and the abstracts of the oral presentations.

Axel Hausmann (corresponding author), SNSB – ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany;
e-mail: hausmann.a@snsb.de

Short report and results

Axel Hausmann & Hossein Rajaei

Hausmann, A. & Rajaei, H. 2019. Short report and results. Pp. 291–292 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018. Integrative taxonomy, a multidisciplinary approach to answer complicated taxonomic questions (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Axel Hausmann (corresponding author), SNSB – ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany; e-mail: hausmann.a@snsb.de

The meeting was organized by an organization team of the ‘Staatliches Museum für Naturkunde Stuttgart’ (SMNS). The scientific presentations during nine sessions were chaired by Axel Hausmann (Munich, Germany), Robert Trusch (Karlsruhe, Germany), Pasi Sihvonen (Helsinki, Finland), Hossein Rajaei (Stuttgart, Germany), Gunnar Brehm (Jena, Germany), Sei-Woong Choi (Jennoam, South Korea), Feza Can (Hatay, Turkey), and Nan Jiang (Beijing, China). As an innovative in this congress, a one-hour workshop entitled “large-scale scientific projects: workshop on partner search” was organized and presented by Pasi Sihvonen (Helsinki, Finland).

The conference started with a lecture on the groundbreaking effects of “Willi Hennig and the synthesis of phylogenetics and taxonomy”. Other presentations and break-out discussions followed on integrative taxonomy of geometrid moths. The following keynote talks included contributions of Malcolm J. Scoble, Toomas Tammaru, Rodolphe Rougerie, Jeremy Holloway, Martin Krüger and Sei-Woong Choi (abstracts see below). The participants enjoyed two guided tours in the Black Forest National Park and to the city of Tübingen / Hohenzollern castle. Some participants of this congress were financially supported by the German Research Foundation (DFG).



Participants of FORUM HERBULOT 10 in Stuttgart, Germany.

Geometrid taxonomy: will past and present approaches meet future needs?

Malcolm J. Scoble

Scoble, M. J. 2019. Geometrid taxonomy: will past and present approaches meet future needs? Pp. 293 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42(2).

Malcolm J. Scoble, Natural History Museum, Cromwell Road, London SW75BD, UK; e-mail: m.scoble@nhm.ac.uk

Geometridae taxonomy has been through three main phases. At first the rate of species description was slow, following the establishment of taxonomy as a subject – notably by Linnaeus and his immediate followers. A second phase occurred that was characterised by a rapid rate of species description, an activity associated with colonization of many areas of the globe allowing extensive collection of material. Third, there was a phase of revisionary taxonomy where genera were examined more critically. While new species continued to be described, many names were synonymised as taxonomists took a more analytical approach to taxonomic structure.

The formation and development of the Internet has focused the attention of many taxonomists on the dissemination and democratisation of taxonomic results. Neither a paper-based nor an Internet solution has prevailed as both formats exist in an ‘ecosystem’ of outputs. A powerful addition to the taxonomic armoury is the barcoding initiative, which provides potentially a rapid means of identification of specimens. Barcodes, like names, are keys that can unlock and give access to information – especially when such information is accessible through computerised databases.

Yet against this benign picture of a growing synthesis of information, better data access, and

more collaboration between taxonomists, lies the depressing loss of biodiversity. A recent study of insects in protected areas in Germany shows a massive decline in insect numbers, a situation that surely includes the Geometridae. That study can be viewed against the undermining of what has been termed a ‘safe operating space for humanity’ in the form of challenges to geophysical ‘planetary boundaries’, including biodiversity loss.

This picture of decline suggests that geometrid (and other) taxonomists might contemplate a fourth phase in their evolution. Should they, and can they, start to collect and collate data in a form that is useful to the conservation community? If so, how might such a contribution be made? If taxonomy can be perceived, *inter alia*, as a form of scientific infrastructure, then its practitioners and disseminators might try to break the silos of data in the legacy taxonomic literature and make these data available on the Internet. Much progress has been made to develop taxonomic infrastructure, but impediments remain. Further progress will require the adoption of evolving e-technologies alongside a determination by the taxonomic community to collaborate more closely. After reviewing the current situation, this contribution will summarise some of these developments.

Museomics and micro-CT: non-destructive micro-CT approach for female Lepidoptera exemplified with the genus *Prasinocyma* (Lepidoptera, Geometridae)

Julia Wildfeuer & Axel Hausmann

Wildfeuer, J. & A. Hausmann 2019. Museomics and micro-CT: non-destructive micro-CT approach for female Lepidoptera exemplified with the genus *Prasinocyma* (Lepidoptera, Geometridae). Pp. 293–294 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42(2).

Julia Wildfeuer (corresponding author), SNSB – ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany; e-mail: julia.wildfeuer@aol.com

Due to the 6th mass extinction of insects in the world, there is a large consensus for the need of integrative taxonomy, which is most commonly a combination of morphological and molecular data. Recent technological progress allows to gather key data with non-destructive methods. We present a new approach to retrieve morphological data

of the reproduction organs of Lepidoptera: three-dimensional micro-CT-scanning of the abdomina. This is a time-saving and non-destructive tool for the revision of large and taxonomically difficult groups, which is shown at the example of the genus *Prasinocyma* Warren, 1897 (Lepidoptera, Geometridae) with approx. 300 Afrotropical species. The genus

Prasinocyma is particularly difficult because of the large number of species which are very similar to each other externally which entails many genitalia dissections for species identification for a revision. Approximately 1000 dissections are necessary to revise a genus like *Prasinocyma*. This would be very time consuming with 'conventional' dissections and in just a few cases, males can unequivocally be assigned to females. Moreover, it causes damage of the abdomen and therefore an inherent loss of tissue and information on structures as tufts or glands. In other words, the important parts of the vouchers are destroyed which is often the case even in the name-bearing type specimens. This problem can now be solved by the new x-ray microcomputed tomography (micro-CT) technique. In the framework of a master

thesis, it was shown, that the results of a micro-CT scan are not only comparable with the results of traditional dissection, but obtain also several other advantages like a 3-D view of the genitalia. In that work, the focus was on male Lepidoptera and a fast scan technique was developed, to describe a male specimen within one hour. But for some species, there are only female vouchers and also the male to female assignment is very important. From the 118 described Afrotropical *Prasinocyma* species 19 were based on females only. Therefore, we focus now on female micro-CT scans. Female abdomen revealed to be more challenging because of the membranous nature of the differential characters (ductus and corpus bursae) and the more internal position within the abdomen.

Updates on the German campaign for DNA barcoding of Lepidoptera and on the European and global campaigns for geometrid barcoding

Axel Hausmann

Hausmann, A. 2019. Updates on the German campaign for DNA barcoding of Lepidoptera and on the European and global campaigns for geometrid barcoding. Pp. 294 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Axel Hausmann, SNSB – ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany; e-mail: hausmann.a@snsb.de

DNA barcoding of German Lepidoptera was started in the Bavarian State Collection of Zoology (ZSM) in the year of 2006. By June 2018, coverage could be raised to more than 90 %, including DNA barcodes for 3320 of the 3682 German Lepidoptera species in a public database (BOLD data systems). The last 362 missing species are now added in a Next-Generation-Sequencing (NGS) approach of old collection material at the ZSM in the framework of the German GBOL project. The European campaign for Geometridae was similarly successful and currently covers 990 of the 999 European geometrid species. With seven other species which were subsequently

submitted to sequencing, just two species are missing, *Asthenia lactularia* and *Liodesina homochromata*. The global campaign for Geometridae currently includes some 160 000 barcodes clustering to some 22 700 BINs making it the best represented family in absolute numbers and in species coverage among all animals on BOLD. The number of BINs (barcode index numbers; a good proxy for species) closely approaches the number of described species (23 000). The value of this data for taxonomy is high as shown by forthcoming revisions of the genera *Oospila* (neotropical) and *Victoria* (afrotropical).

Striking species of Geometridae (Ennominae, Hypochrosini) from the Philippines and Sulawesi, with the first observation of “Reflex Bleeding”

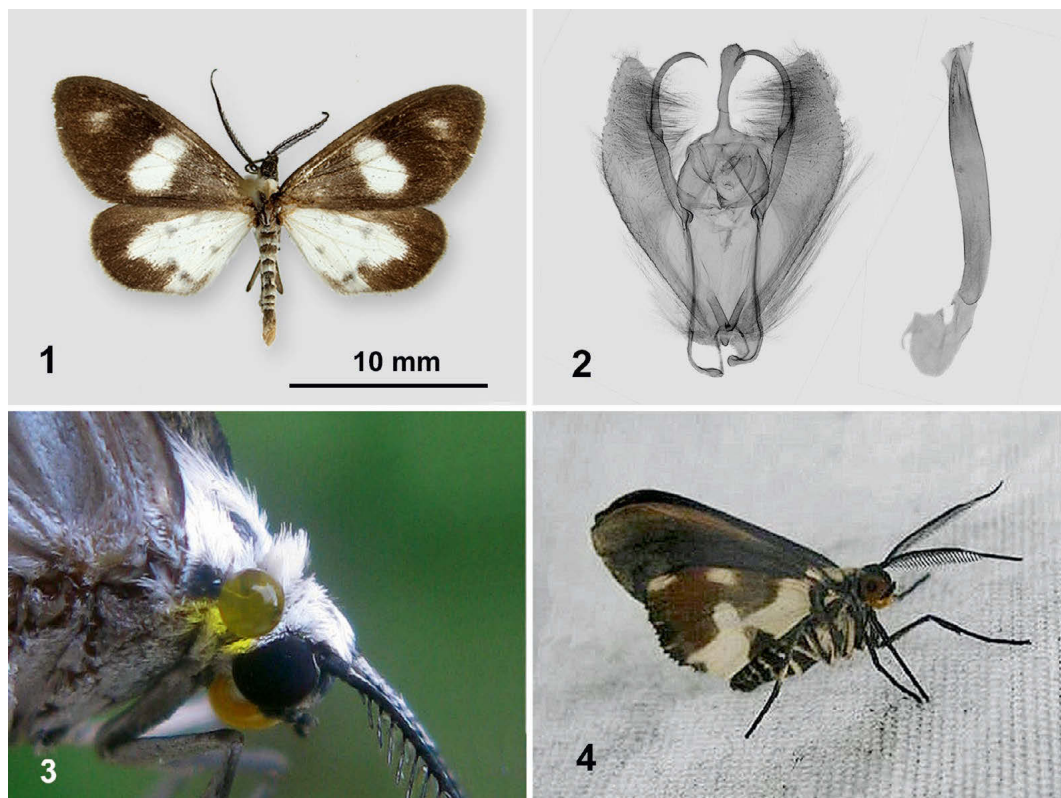
Claude Tautel & Dieter Stünig

Tautel, C. & Stünig, D. 2019. Striking species of Geometridae (Ennominae, Hypochrosini) from the Philippines and Sulawesi, with the first observation of “Reflex Bleeding”. Pp. 294–296 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Claude Tautel (corresponding author), Attaché MNHN Paris, 272 rue du Faubourg Saint-Antoine, 75012-Paris, France; e-mail: ateliertautel@gmail.com

We present a remarkable group of Hypochrosini from the Wallacea region, containing four species,

three of them being described already: “*Hypochrosis*” *hausmanni* Koçak & Kemal, 2008 (= *prouti* West, 1929;



Figs 1–4. Representatives of the new genus. 1–3. “*Hypochrosis*” *hausmanni* Koçak & Kemal, 2008; 1. adult, male from Luzon; 2. male genitalia; 3. female from Luzon, showing the defensive body fluid from a thoracic opening closely behind the head. 4. “*Hypochrosis*” *dolorosa* Yazaki, 2018, Sibuyan Island.

= *westi* Yazaki, 2018; Fig. 1) from Luzon and Mindanao, “*H.*” *dolorosa* Yazaki, 2018 from Negros, Panay and Sibuyan (Fig. 4) and “*H.*” *inexpecta* Yazaki, 2018 from Mindanao. Also on Mindanao a population of “*H.*” *hausmanni* occurs which deserves a subspecific separation from Luzon representatives. In addition, a species new to science occurs on the island of Sulawesi (Indonesia). All four species are, to our opinion, misplaced in their present genus *Hypochrosis* and a new genus will be formally described for their reception in a separate paper. Presumably, all four species (observed in two species so far) have the ability, well known from Arctiinae, but not yet recognized within Geometridae, to exude a probably defensive body fluid from a thoracic opening closely behind the head (Fig. 3).

All species of this group exhibit the main characters which define the majority of *Hypochrosini*: bipectinate antennae in both sexes, with shorter branches in females; fovea in forewing of male and comb of setae on sternite 3 of abdomen absent, hind-tibia not dilated; vinculum in male genitalia

(Fig. 2) slender, elongate, looping caudally, with a single corema in the loop (rarely double or absent in other genera of *Hypochrosini*). A double asymmetrical furca, which characterizes a number of *Hypochrosini* genera but may be secondarily reduced in others (Holloway [1994]), is also absent in the new genus. With *Hypochrosis* s. str. the new genus shares the presence of a process arising distally from the sclerotized valve costa in male genitalia (Fig. 2). It is digitate, flattened or lobe-like in *Hypochrosis*, but like a long, evenly curved spine in the new genus (except in the Mindanao-species where it is a short, straight spine). Size, pattern and coloration is much different and the hammer-headed apex of uncus is only found in *Hypochrosis* s. str. *Achrosis* Guenée, another possibly related genus, is distinguished by more elongate forewings with a centrally angled distal margin and the presence of a double furca in male genitalia, symmetric in most cases, sometimes asymmetric or even absent. A further related genus may be *Ctimene* Boisduval. Two of the four species mentioned above have previously been named

and placed into *Ctimene* by L. B. Prout, based on historical material housed at the NHMUK, London (photographs checked), but his manuscript names remained unpublished.

For comparison, we studied and dissected a male of the type-species of *Ctimene*, *C. xanthomelas* Boisdual, and we found it clearly distinct from our new genus, in appearance as well as in the structure of male genitalia. A more detailed description of the new genus is given in our presentation. “*H.*” *hausmanni*, the designated type-species, is compared to the described congeners and to the new taxa. It shares black and white coloration with its new subspecies from Mindanao and with “*H.*” *dolorosa* (Fig. 4) from Sibuyan, Panay and Negros, whereas the new species from Sulawesi is of a lighter grey, with partly white hindwings, and “*H.*” *inexpecta* from Mindanao shows a dark brown coloration. All four species agree in a conspicuous pattern of the

underside of the wings. This rather unusual pattern character is presumably related to an also remarkable behavioural character: wings are folded closely above the thorax in a butterfly-manner while resting or walking on the ground, displaying the striking aposematic coloration (Fig. 4). COI-DNA studies have been carried out in this group but the results are not yet really satisfying. Due to the old age of most specimens investigated, only a few could be barcoded successfully. However, available data indicate the specific distinctness of the four species which are so far recorded from Luzon, Mindoro, Sibuyan, Panay, Negros, Mindanao and Sulawesi, but may be found on other Philippine islands as well.

Holloway, J. D. [1994] (dated 1993). The moths of Borneo, part 11: Family Geometridae, subfamily Ennominae. *Malayan Nature Journal* 47: 1–309.

The enigmatic *Triphosa* genus: taxonomic revision and two new species from Middle East and Central Asia (Lepidoptera, Geometridae, Larentiinae)

Dominic Wanke, Hossein Rajaei & Axel Hausmann

Wanke, D., Rajaei, H. & Hausmann, A. 2019. The enigmatic *Triphosa* genus: taxonomic revision and three new species from Middle East and Central Asia (Lepidoptera, Geometridae, Larentiinae). Pp. 296 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42 (2).

Dominic Wanke (corresponding author), Department of Entomology, Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany; e-mail: dominic.wanke@smns-bw.de

Moths of the genus *Triphosa* Stephens, 1829 are well-known from the western Palearctic and eastern Asia regions, even though their occurrence in middle Asia remains mysterious. This is due to the fact, that most *Triphosa* species share similar wing patterns, whereby efforts for identifications can be misleading and challenging. The aim of this project is to shed light on *Triphosa* fauna of Middle East and Central Asia and to highlight the diagnostic characters, which easily help with species identification. The type series of little-known species *T. agnata*, *T. taochata* and *T. ravulata* in combination with further distribution data

of these and other *Triphosa* species (including two new species) occurring in this region were studied. Distribution data, morphological and diagnostic characters and new taxonomic changes are discussed (cf. Wanke et al. 2019).

Wanke, D., Hausmann, A. & Rajaei, H. 2019. An integrative taxonomic revision of the genus *Triphosa* Stephens, 1829 (Geometridae: Larentiinae) in the Middle East and Central Asia, with description of two new species. *Zootaxa* 4603 (1): 39–65.

Wing shape can tell us stories: the use of geometric morphometrics in Lepidoptera wings

Hugo A. Benítez

Benítez, H. A. 2019. Wing shape can tell us stories: the use of geometric morphometrics in Lepidoptera wings. Pp. 297 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Hugo A. Benítez, Departamento de Recursos Ambientales, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile; e-mail: hugobenitezd@gmail.com

The comparison of anatomical traits between organisms has been a central topic in comparative biology. Historically, taxonomic classification and understanding of biological diversity have been based on morphological descriptions. Derived from a mathematical quantitative revolution, morphological studies have experienced an important renewal due to the development of shape analysis rooted in statistical multivariate methods and novel visualisation techniques. The aim of the present talk is to provide

an updated perspective regarding the progress in geometric morphometrics (GMM) applied to the study in Lepidoptera, and focusing on examples in geometrid moths. Thus, it is expected to provide a broad point of view with respect to the application of geometric morphometrics in evolutionary biology, highlighting its usefulness as an effective, accurate, user-friendly and inexpensive method to quantify and study shape variation.

“Geometridae mundi”, a new way of summarizing the diversity of global Geometrid species

Hans Löbel & Axel Hausmann

Löbel, H. & Hausmann, A. 2019. “Geometridae mundi”, a new way of summarizing the diversity of global Geometrid species. Pp. 297 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Hans Löbel (corresponding author), Wilhelm Külz Str. 11, 99706 Sondershausen, Germany; e-mail: hans.loebel@web.de

The digital database of the project “Geometridae mundi” will be presented and its functions will be demonstrated. In this html-programmed database, a list of all worldwide described taxa of Geometrid moths have been included (following Scoble 1999, Scoble & Hausmann 2007). The overall data about these roughly 28000 taxa have been divided into three parts: overview, genus pages and species pages. These levels can be accessed either via tables of contents or via alphabetical indexes of genus and species. They are linked with each other additionally with the start page, the tables of contents and the respective ABC-Centers. All species and subspecies of the Herbulot collection in the Bavarian State Collection of Zoology (ZSM) and of the Australian National Insect Collection (ANIC) (Canberra) are illustrated, as well as numerous other species from the Ditsong Museum Pretoria, the British Museum London (NHMUK) and other museums, the collections Staude (Magaliesburg) (ex database “Lepidops”), Löbel and other private collections. With currently about 49200 digital photos, 12534 taxa are depicted (ca. 42 % of the treated species). Images of the holotypes or lectotypes are available for 1419 taxa. Additionally, 774 photos illustrate paratype specimens. The database of the “Geometridae mundi” could be

regarded as a valuable help for determination tasks and taxonomical investigations. In further expansion steps, the database will be supplemented with the pictures of the missing species, genital preparations, text information on the species pages and related literatures. A digital data collection such as the one presented here can take over the tasks of a classical reference book generally. Regarding the possibilities of imaging of butterflies, their caterpillars or genital preparations, the index functions and the possibility of involving literature, the database of the “Geometridae mundi” is superior to a conventional book. The essential advantage, however, is the lack of a deadline. This allows an unlimited extension and development of all contents as well as the correction of detected errors. In contrast to expensive books no costs for printing services arise.

Scoble, M. J. (ed.) 1999. Geometrid moths of the world, a catalogue. 1400 pp., Collingwood/Australia (CSIRO Publishing).

Scoble, M. J. & Hausmann, A. [update 2007]. Online list of valid and nomenclaturally available names of the Geometridae of the World. <http://www.herbulot.de/globalspecieslist.html>

The Geometrid Moths of Switzerland, publication announcement

Daniel Bolt

Bolt, D. 2019. The Geometrid Moths of Switzerland, publication announcement. Pp. 298 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Daniel Bolt, Via Crusch 8A, 7013 Domat/Ems, Switzerland; e-mail: Daniel.Bolt@anu.gr.ch

In the last years, the Swiss Lepidoptera group has published several books about the butterflies and moths of Switzerland: “Tagfalter und ihre Lebensräume”, “Schmetterlinge und ihre Lebensräume”, “Die Schmetterlinge der Schweiz – Eine kommentierte, systematisch-faunistische Liste” and “Die Eulenfalter der Schweiz (Noctuidae)”. The only missing group of macromoths are the geometrid moths. Therefore, in 2012 a group has been formed to publish a volume of books to complete the knowledge of

Swiss macromoths, their distribution and biology. Actually, about 460 geometrid species are known from Switzerland. The 2 or 3 volumes will present, for each species, their distribution, the specific life history for Switzerland, for every species presenting life photographs of adults and of about 80 % of the different larval stages. Also eggs, pupae and the typical habitats are shown. All the species are drawn by a scientific painter and presented on several plates.

A new efficient lamp to collect Lepidoptera and general remarks on light-trapping

Gunnar Brehm

Brehm, G. 2019. A new efficient lamp to collect Lepidoptera and general remarks on light-trapping. Pp. 298 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Gunnar Brehm, Institut für Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany; e-mail: gunnar.brehm@uni-jena.de

Most nocturnal Lepidoptera can be attracted to artificial light sources, particularly to those that emit a high proportion of ultraviolet radiation. LepiLED is a new lamp on the market, that is lightweight, handy, robust, and energy-efficient. The emitted electromagnetic spectrum corresponds to the peak sensitivity in most Lepidoptera eye receptors (ultraviolet, blue and green). Power LEDs with peaks at 368 nm (ultraviolet), 450 nm (blue), 530 nm (green), and 550 nm (cool white) are used. I also compared the irradiance (Ee) of many commonly used light-trapping lamps. The new lamp proved to be the most energy efficient, and it emitted more radiation in the range between 300 and 400 nm than other lamps tested. Cold cathodes are the second most energy-efficient

lamps. Irradiation from fluorescent actinic tubes is higher than from fluorescent blacklight-blue tubes. High-wattage incandescent lamps and self-ballasted mercury vapour lamps have highest irradiance, but they mainly emit in the long wave spectrum. The use of gauze and sheets decreases the proportion of UV radiation and increases the share of blue light, probably due to optical brighteners. Compared with sunlight, UV irradiance is low at a distance of 50 cm from the lamp. LepiLED has already successfully been used in many places around the world. UV photographs demonstrate different optical properties of materials used in light trapping. In addition, some general aspects of light-trapping are discussed.

The digitisation of Madagascan type specimens at the Natural History Museum, London, UK with special reference to the Geometridae

**Geoff Martin, Alberto Zilli, Alessandro Giusti, Louise Allan, Peter Wing,
Phaedra Kokkini, Flavia Toloni & David C. Lees**

Martin, G., Zilli, A., Giusti, A., Allan, L., Wing, P., Kokkini, P., Toloni, F. & Lees, D. C. 2019. The digitisation of Madagascan type specimens at the Natural History Museum, London, UK with special reference to the Geometridae. Pp. 298–299 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Geoff Martin (corresponding author), Natural History Museum, Cromwell Rd, Kensington, London SW75BD, UK; e-mail: G.Martin@nhm.ac.uk

The Lepidoptera collections at the NHMUK contain 125000 primary types, however very few of these are available digitally to the research community. In June 2017 we obtained funding for a two month pilot project to digitise (i. e. image both sides of specimen & labels, image genitalia, transcribe label data, verify type status) all the Lepidoptera type specimens from Madagascar in the NHMUK collections. Although much was achieved in two months, with some 2600 specimens imaged and a revised workflow,

it became clear that far more time was needed to complete the project. Further funding was sought and obtained, and to date 5778 specimens have been imaged. We are currently verifying type status and intend to publish an online type catalogue before the end of 2020. This talk will outline methods used for digitising, discuss the many issues that arose and then concentrate on the outcomes with regard to the Geometridae and issues around typification.

Unlocking genomic treasure chests – high-throughput collection genomics

Christian König

König, C. 2019. Unlocking genomic treasure chests – high-throughput collection genomics. Pp. 299 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Christian König, Universität Hohenheim, Institut für Zoologie, Fachgebiet Tierökologie, (220c), Garbenstr. 30, 70599 Stuttgart, Germany; e-mail: christian.koenig@uni-hohenheim.de

By sequencing highly fragmented DNA, the application of efficient high throughput methods, and the reduction of costs through miniaturization (microfluidics) using state-of-the-art laboratory equipment, we try to overcome the limits of current methods in molecular genomics of insect collections. We like to

open new perspectives in collection-related phylogenomics and taxonomy, which could serve as a key to genomic treasure chests – our natural science collections. This short talk will give an overview about a submitted research project in cooperation with the CSIRO in Canberra/Australia.

Making use of geometrid phylogenies: comparative analyses in evolutionary ecology

Toomas Tammaru, Robert B. Davis, Erki Õunap, Sille Holm & Juhan Javoiš

Tammaru, T., Davis, R. B., Õunap, E., Holm, S. & Javoiš, J. 2019. Making use of geometrid phylogenies: comparative analyses in evolutionary ecology. Pp. 299 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Toomas Tammaru (corresponding author), University of Tartu, P.O. Box. 51006, Estonia; e-mail: tammarut@ut.ee

The availability of reliable phylogenies has opened the road for the application of phylogenetic comparative analyses. With appropriate analytical methods having been developed, evolutionary ecologists can now use among-species variation in trait values to explicitly test for adaptive hypotheses. However, the vast potential of insects as objects of phylogenetic comparative studies has still received surprisingly limited attention. I will present our original research which uses phylogenetic and ecological data on the family Geometridae. In particular, phylogenetically explicit analyses have confirmed the long suspected link between body size and the degree of polyphagy.

Egg size was found to strongly depend on adult size, with little evidence of the effect of ecological selective pressures. The same applies to adult longevity measured in laboratory conditions. The gradation from income to capital breeding (= the importance of adult feeding in egg production) was confirmed to serve as an axis usable for ordinating lepidopteran life histories, with anatomical proxies available to assess the position of each species in this ordination scheme. Our most recent results concern small size of day-flying geometrids, and relate cognitive capacity of adults to ecological traits of the species.

Shaking the tree: revised phylogeny and classification of the geometrid subfamily Sterrhinae

Pasi Sihvonen, Gunnar Brehm, Leidys Murillo-Ramos, Hermann Staude & Niklas Wahlberg

Sihvonen, P., Brehm, G., Murillo-Ramos, L., Staude, H. & Wahlberg, N. 2019. Shaking the tree: revised phylogeny and classification of the geometrid subfamily Sterrhinae. Pp. 300 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Pasi Sihvonen (corresponding author), Finnish Museum of Natural History, Pohjoinen Rautatiekatu 13, 00100 Helsinki, Finland; e-mail: pasi.sihvonen@helsinki.fi

Tribus-level phylogeny of the geometrid subfamily Sterrhinae has remained robust since the 1990s, but it has been based on rather limited data. The only molecular-based hypothesis covered all known tribes but it contained 12 taxa only (Sihvonen et al. 2011). The current study is part of a larger phylogeny project (Murillo-Ramos et al.), aiming to test how the current conclusions on the Sterrhinae phylogeny hold when additional material is included from new geographical areas and from morphologically different lineages. A multi-gene maximum likelihood analysis (up to 11 genes/species), which is based on >120 species (global diversity >2800 species) and 46 genera (global diversity >100 genera), was carried out. The results generally agree with earlier phylogenetic hypotheses at tribus-level, supporting the hypothesis that Sterrhinae has two major lineages, but demonstrate unexpected novelties also: in several cases current tribes need to be either re-

defined or new tribes need to be described, several genera are non-monophyletic and few taxa need to be transferred from various subfamilies into the Sterrhinae. The suitability of exemplar approach to infer phylogenies and its implications to the classification are discussed.

Murillo-Ramos, L., Brehm, G., Sihvonen, P., Hausmann, A., Holm, S., Ghanavi, H., Öunap, E., Truuvverk, A., Staude, H., Friedrich, E., Tammaru, T. & Wahlberg, N. 2019. A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies. Peer J Journal 7: e7386. doi:10.7717/peerj.7386

Sihvonen, P., Mutanen, M., Kaila, L., Brehm, G., Hausmann, A. & Staude, H. S. 2011. Comprehensive molecular sampling yields a robust phylogeny for geometrid moths (Lepidoptera: Geometridae). PLoS ONE 6(6): e20356. doi:10.1371/journal.pone.0020356.

Morphology-based phylogeny of the tribe Chesiadini (Lepidoptera, Geometridae, Larentiinae)

Chantal Holzhaue & Hossein Rajaei

Holzhaue, C. & Rajaei, H. 2019. Morphology-based phylogeny of the tribe Chesiadini (Lepidoptera, Geometridae, Larentiinae). Pp. 300 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Chantal Holzhaue (corresponding author), Natural History Museum, Cromwell Road, London SW75BD, UK; e-mail: chantal.holzhaue@smns-bw.de

Due to heterogeneity of morphological characters of several species of the genus *Docirava* (*D. undulata*, *D. undata*, *D. fulgurata*, *D. musculata*, *D. dervenaria*) the systematic position of these species was questioned. For generic assignment of these species, a cladistic analysis of the tribe Chesiadini Stephens, 1850 was run. Selected species from most genera of this tribe were morphologically examined (*Aplocera*, *Carsia*, *Docirava*, *Lithostegia*, *Odezia*, *Schistostegia*). In total 35 morphological characters of legs, antennae, abdomen, male and female genitalia of 21 selected species were examined and the data was summarized in a data matrix. *Horisme tersata* Denis & Schiffermüller

1775, from the tribe Melanthiini Duponchel, 1845 was used as an outgroup. Data matrix was prepared in NDE (ver. 0.5.0) and analysed in TNT (ver. 1.1). Implicit enumeration analyses of the data and resulting consensus tree strongly support two new lineages that we regard valid at genus-level. First new genus includes: *dervenaria*, *musculata*, *undata* and *undulata* and the second monotypic new genus includes only *fulgurata*. Genus *Docirava* contains five species (including: *D. aequilineata*, *D. affinis*, *D. distata*, *D. flavineata*, *D. pudicata*). Apomorphies and synapomorphies, which support these new genera, will be discussed.

The genus *Hypomecis*
(Lepidoptera, Geometridae, Ennominae):
advances to the phylogenetic structure and relationships in Boarmiini

Evgeny A. Beljaev & Oleg A. Velyaev

Beljaev, E. A. & Velyaev, O. A. 2019. The genus *Hypomecis* (Lepidoptera, Geometridae, Ennominae): advances to the phylogenetic structure and relationships in Boarmiini. Pp. 301–302 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42(2).

Evgeny A. Beljaev (corresponding author), Federal Scientific Centre of the East Asia Terrestrial Biodiversity, Vladivostok 690022, Russia; e-mail: beljaev@biosoil.ru

Hypomecis Hübner 1821 is the type-genus for the Boarmiini, being the senior synonym of *Boarmia* Treitschke, 1825. The latter name has been used extensively in the literature, and numerous ennomines with bark-like wing pattern were described in *Boarmia* up to 1982, when Hiroshi Inoue established this synonymy. Currently *Hypomecis* counts nearly 150 species (Scoble 1999), but many of them were combined formally with the genus name, without the checking from the genitalia. Review of publications and available specimens allowed to select 57 species undoubtedly belonging to *Hypomecis*, which are used for the discussion. The objectives of this research were as follows: to study the morphology of the Far Eastern species of *Hypomecis* with the focus on skeleton-muscular structure of the male genitalia; to perform the molecular phylogenetic research of selected Far Eastern Boarmiini; to discover the sister group of genus *Hypomecis* in the Biarmiini; to detect the monophyletic groups of the species in *Hypomecis* based on the integrative approach.

Morphological research was realised following the method by Kuznetsov & Stekolnikov (2001) with some innovations offered by Pomomarenko (2005) and Beljaev (2008). Some results were published in Velyaev & Beljaev (2015, 2016). Molecular research was conducted based on standard protocols using the partial sequence of 6 genes (COI, 16S, 28S (D1 and D2), EF-1 α , RpS5 and GAPDH), totally about 4100 bp. Six Far Eastern species of *Hypomecis* plus 19 species from different genera of Boarmiini were involved. Some additional data were adopted from literatures and GenBank (NCBI). The main results of the investigation are summarized as follows.

Relationships of the genus *Hypomecis* in Boarmiini remain uncertain based on morphology, and controversial in different molecular analyses. In molecular trees of Boarmiini basal branching forms a “phylogenetic lawn” which consists of close nodes with poor statistic support. This corresponds with highly mosaic distribution of morphological traits in the tribe that makes morphological phylogenetic analysis difficult. Probably the “phylogenetic lawn” could be a result of rapid basal branching in Boarmi-

ini. The genus *Hypomecis* is well defined genetically and morphologically. The Far Eastern species of the genus form 3 monophyletic groups, which are supported by both kind of the data: *H. punctinalis* species group (*H. punctinalis*, *H. pseudopunctinalis*, *H. crassestrigata*, *Ematurga atomaria*); *H. roboraria* species group (*H. roboraria*, *H. diffusaria*, *H. phantomaria*); and *H. akiba* species group (with the single species). *H. akiba* has unique morphology and occupies a basal position in molecular phylogeny of the genus. Most of 57 selected true species of *Hypomecis* could be attributed to *H. punctinalis* group or to *H. roboraria* group based on the diagnostic characters in the male and female genitalia. Morphologically, the American species of *Hypomecis* (including the type species of the genus, *H. umbrosaria*), form a separate group, sister to the Eurasian *H. punctinalis* species group. *Ematurga atomaria* indicate most close affinity to *H. umbrosaria* species group and name *Ematurga* should be synonymised with *Hypomecis*. The obtained results are concordant with recent publication on the phylogeny of Chinese Boarmiini which was conducted based on different set of species and genes (Jiang et al. 2017).

This work was sponsored partially by Russian Foundation for Basic Research, project 18-04-00944.

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Molecular systematics provides new insights to the taxonomy and relationships of the major lineages of the geometrid moths (Lepidoptera, Geometridae)

Leidys Murillo-Ramos, Gunnar Brehm, Pasi Sihvonen, Hamid Ghanavi & Niklas Wahlberg

Murillo-Ramos, L., Brehm, G., Sihvonen, P., Ghanavi, H. & Wahlberg, N. 2019. Molecular systematics provides new insights to the taxonomy and relationships of the major lineages of the geometrid moths (Lepidoptera, Geometridae). Pp. 302 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Leidys Murillo-Ramos (corresponding author), Department of Biology, Lund University, Sweden; Department of Biology, Universidad de Sucre, Colombia; e-mail: leidys.murillo@biol.lu.se

Morphological classifications as well as molecular phylogenies with different numbers of taxa and markers, have supported the monophyly of the Geometridae moths. However, the subfamilies and tribal compositions and the relationships of major groups are largely unresolved, which has led to taxonomic confusion. The aim of this study is try to solve the tribe compositions of the major lineages within the Geometridae and elucidate their evolutionary relationships. We analysed a molecular dataset comprising up to 12 genetic markers that

included one mitochondrial and 11 nuclear markers for > 1000 taxa. The molecular data set was analysed using IQ-TREE, which is a stochastic algorithm to infer phylogenetic trees by maximum likelihood. We found rampant polyphyly among the subfamilies Desmobathrinae and Oenochrominae, as well as among a large number of tribes in most of the remaining subfamilies. We discuss the most efficient way to deal with this polyphyly to arrive at a classification that reflects better the evolutionary relationships of the higher taxa in the Geometridae.

Phylogeny of the emerald moths (Geometridae, Geometrinae)

David Plotkin

Plotkin, D. 2019. Phylogeny of the emerald moths (Geometridae, Geometrinae). Pp. 302–303 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

David Plotkin, University of Florida, McGuire Center for Lepidoptera and Biodiversity, 32611-2710, Gainesville, Florida, USA; e-mail: dplotkin@ufl.edu

The emerald moths (Geometrinae) are a cosmopolitan subfamily with over 225 genera and 2600 species. Most of these moths are characterized by a green ground colour, with different lineages exhibiting different shades of green. The monophyly of Geometrinae has been confirmed by multiple phylogenetic analyses, including the recent phylogeny of Ban et al. (2018). However, the relative placement of many of the geometrine tribes is poorly supported.

A document compiled by the Forum Herbulot (2003) lists 21 geometrine tribes that are still accepted by at least some current geometrid specialists; some of these are believed to be paraphyletic. Anchored hybrid enrichment was used to obtain phylogenomic data from roughly 450 loci for 98 species of emerald moths, representing all 21 proposed tribes. Maximum Likelihood and coalescent-based analyses were used to generate a strongly supported phylogeny of Ge-

ometrinae. The overall topology corresponds with the analysis of Ban et al. (2018), but due to variation in taxon sampling, some new relationships within the subfamily are revealed. New taxonomic changes are proposed in order to reconcile instances of paraphyly and polyphyly, and morphological implications of these new classifications are discussed.

Ban, X. S., Jiang, N., Cheng, R., Xue, D. Y. & Han, H. X. 2018. Tribal classification and phylogeny of Geometrinae (Lepidoptera: Geometridae) inferred from seven gene regions. *Zoological Journal of the Linnean Society* 184: 653–672.

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Molecular phylogeny of New World geometrid moths (Lepidoptera, Geometridae)

**Gunnar Brehm, Leidys Murillo-Ramos, Pasi Sihvonen, Florian Bodner, Daniel Bolt,
Christian B. Schmidt, Alfred Moser, Axel Hausmann, Erki Õunap, Jaan Viidalepp,
Aare Lindt, Luis Parra, Toomas Tammaru & Niklas Wahlberg**

Brehm, G., Murillo-Ramos, L., Sihvonen, P., Bodner, F., Bolt, D., Schmidt, C. B., Moser, A., Hausmann, A., Õunap, E., Viidalepp, J., Lindt, A., Parra, L., Tammaru T. & Wahlberg, N. 2019. Molecular phylogeny of New World geometrid moths (Lepidoptera, Geometridae). Pp. 303 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42(2).

Gunnar Brehm (corresponding author), Institut für Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany; e-mail: gunnar.brehm@uni-jena.de

Our molecular phylogeny comprises more than 450 samples of Geometridae from the New World, by far most of them representing different genera not analysed before. Photographs of all sampled specimens are provided together with relevant type material in order to make identification and taxonomic changes fully transparent. While many previously suggested phylogenetic relationships can be confirmed, several new lineages are discovered, including tribes, and those are formally described. We assign around 100 genera for the first time to a tribe. In an attempt

towards a system of monophyletic taxa, we also propose many new tribal and generic combinations, we synonymise several tribes and genera, and provisionally exclude a large number of species from non-monophyletic genera, which often have been defined by Palaearctic species. While the Nearctic species are often nested within the predominantly Neotropical clades, the southern South American fauna usually forms larger and distinct clades, hinting to a long isolation from the other New World fauna.

A phylogenetic comparison of Afrotropical Geometridae and their host-plants

Hermann S. Staude, Pasi Sihvonen & Axel Hausmann

Staude, H. S., Sihvonen, P. & Hausmann, A. 2019. A phylogenetic comparison of Afrotropical Geometridae and their host-plants. Pp. 303–304 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42(2).

Hermann Staude (corresponding author), Caterpillar Rearing Group (CRG), LepsoAfrica, 33 Golden Valley, Magaliesburg, South Africa; e-mail: hermann@busmark.co.za

Ever since Ehrlich & Raven's classical 1964 paper on the co-evolution of plants and their insect herbivores, scientists have been searching for the elusive evolutionary mechanisms underlying the extraordinary extant species diversity in both these groups. Various hypotheses have been proposed but no generally accepted universal theory has been found to date. These hypotheses have not been tested with data from the Afrotropical region.

To test potential speciation mechanisms, the authors are in the process of developing a robust molecular phylogeny for the African Geometridae and a database for Afrotropical Lepidoptera and their hosts, from the Caterpillar Rearing Group (CRG) data as well as from host associations extracted from published literature. The caterpillar database consists of some 9500 host associations. 1135 of these are of Geometridae established in the wild

(578 historic records, 557 CRG records), comprising 375 geometrid species (97 % southern Africa, 3 % rest of Afrotropical region). The database was expanded to 30 fields representing among others collecting, biogeographical, ecological, temporal and respective phylogenetic data for each association. Fields representing geometrid deep phylogeny were placed in the preliminary molecular phylogeny context (Murillo-Ramos et al. 2019). At the species and population level the “Geometridae of Africa” barcoding project (Hausmann et al., unpublished) was used. For fields representing plant phylogeny the SANBI (South African National Biodiversity Institute) family-genus classification database (R. Kloppe, unpublished) was used. The data were analysed using pivot tables and charts in Excel 2016. Preliminary results are presented.

The family Geometridae and its subfamilies were found to be polyphagous with members feeding on 82 plant families, 217 plant genera and 363 plant species. 50 % of caterpillar associations were in four plant families (Fabaceae 300, Celastraceae 125, Anacardiaceae 63, Rubiaceae 60). No associations were found for Poaceae, a dominant plant family in most southern African biomes. All analysed tribes were also found to be polyphagous except for Caberini, which was found only on Rhamnaceae.

At the species level, four types of feeding strategies were detected: generalist occurring in more than one biome; generalist restricted to a single biome; specialist occurring in more than one biome; specialist restricted to a single biome. Of the 70 species, for which five or more associations were recorded, 69 % were found to be specialists and 31 % generalists. Forty-one (59 %) were of a geometrid species occurring in a single biome feeding on a single plant genus. When generalists and specialists occurring in more than one biome (17 spp.) were excluded, only specialists were found in the savanna and fynbos biomes, 66 % in grasslands were found to

be specialists, but, by contrast, 63 % in forests were found to be generalists.

In most tribes, clustering around specific plant families were detected and frequently genus groups, genera or species groups were found specifically associated with a plant family, subfamily or genus, but on several occasions a species within the group was found to have shifted host from one plant taxon to an unrelated other one. The data suggests that such specialisation resulted in an increase in the effectiveness of survival strategies such as crypsis and aposematism. No shift of a species to a generalised feeding strategy from a group of specialists was detected, but a shift of a species from a group of generalists to a specialist feeding strategy was detected on several occasions. No regional differentiation in host specialisation could be detected.

We present an example of apparent recent speciation in the *Argyrophora trofonis* species group, based on barcoding and the biogeography of the group and their host plants (*Erica* spp.). It is suggested that the narrow moisture and temperature tolerance of *Erica* spp., resulting in the frequent retraction of *Erica* populations into refugia in response to natural climatic fluctuations (taking their *Argyrophora* herbivores with them), resulted in a number of vicariance events in *Argyrophora*. Our data highlighted several similar cases and it seems likely that this form of speciation could have been a major contributor towards the extraordinary extant species diversity in plants and their insect herbivores.

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The research status of phylogeography and biodiversity of Lepidoptera in China; case studies of Geometridae

Rui Cheng, Nan Jiang, Dayong Xue & Hongxiang Han

Cheng, R., Jiang, N., Xue, D. Y. & Han, H. X. 2019. The research status of phylogeography and biodiversity of Lepidoptera in China; case studies of Geometridae. Pp. 304–305 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT* 2018 (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42 (2).

Hongxiang Han (corresponding author), Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, No. 1 Beichen West Road, Chaoyang District, Beijing 100101, China; e-mail: hanhx@ioz.ac.cn

China, lying in the East of Asia, holds special and diverse topography and fauna with several mountainous regions, of which the Himalaya and Heng-

duan Mountains (HHM) are considered as the most important mountain system. The HHM locates at the border of the Qinghai-Tibet Plateau (QTP) and is the

consequence of the uplift of the QTP. The complex topography and glacial oscillations may have contributed to shaping the high genetic diversity and endemism of China. Allopatric speciation is one of the most important and simplest types of speciation in animals. Mountain barriers may play a particularly important role in shaping animal communities in East Asia. The geographical isolation induced by the HHM produces multiple speciation or population differentiation in plants, birds and insects. For moths living in different altitudes, the response of mountainous isolation is different. The Gaoligong Mountain, Daxue Mountain, Yunling Mountain, and the low land between two mountains are famous barriers within the HHM. However, in our study, the Qinling Mountain is only the boundary of spe-

cies distribution, not the isolation barrier. Climatic oscillation is another factor influencing species differentiation. Within the HHM, glaciations were restricted to high altitudes (>2000 m). So, mountain areas at such low latitudes as the Qinling mountains can provide relatively stable environmental conditions and act as refuges, which is congruent with the ecological stability hypothesis. Despite changes in global climate, species living at low altitudes can stay in situ to avoid glaciations, whereas species living at high altitudes can make short altitudinal movements to remain in the same climate zone. According to previous studies, during the Last Glacial Maximum (LGM), southern China did not experience strong climatic oscillation, which promoted the dispersal mode of species in this area not focusing on LGM.

Recent progress on taxonomy and phylogeny of the family Geometridae from China

Nan Jiang, Rui Cheng, Dayong Xue & Hongxiang Han

Jiang, N., Cheng, R., Xue, D. Y. & Han, H. X. 2019. Recent progress on taxonomy and phylogeny of the family Geometridae from China. Pp. 305–306 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Hongxiang Han (corresponding author), Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, No. 1 Beichen West Road, Chaoyang District, Beijing 100101, China; e-mail: hanhx@ioz.ac.cn

China bestrides both the Palaearctic and the Oriental Regions, and has high species diversity of geometrid moths. Recent progress (2008 to 2018) on the taxonomy and phylogeny of Chinese Geometridae is summarized. Within Geometrinae, the monograph of Han & Xue (2011), which was the first to summarise the studies of the systematics and fauna of the Geometrinae in China, was published. The tribe Comibaenini of China was reviewed by Han et al. (2012), including eight genera with one new genus and 11 new species. A molecular phylogenetic analysis of Geometrinae based on 116 species representing 17 of the 18 recognized tribes was constructed (Ban et al. 2018), and a new classification composed of 13 tribes was proposed, two of which were proposed as new: Ornithospilini Ban & Han, 2018 and Agathiini Ban & Han, 2018. Within Ennominae, a monograph “Fauna Sinica Volume Ennominae” is under preparation. In this work, about 700 species have been recognized; 56 new species have been described; 24 new synonyms and 18 new combinations or status revisions have been established; three genera and 50 species and subspecies have been newly recorded to the fauna of China. Part of these achievements were published in 16 related papers. A molecular phylogeny of the Palaearctic and Oriental members of Boarmiini was reconstructed, and the relationships among tribes within the ‘boarmiine’ lineage were

discussed (Jiang et al. 2017). A monograph “Fauna Sinica Volume Sterrhinae” is also under preparation. Two papers about the tribe Scopulini were published (Cui et al. 2018b, Xue et al. 2018). A new genus *Aquilargilla* Cui, Xue & Jiang, 2018 of the tribe Scopulini, and two new species are described from China (Cui et al. 2018b). The Chinese species of the genus *Problepsis* Lederer, 1853 were reviewed, 18 species were reported, two new species were described, and one new combination and two new synonyms were established (Xue et al. 2018). The genus *Synegiodes* Swinhoe, 1892 of the tribe Timandrinini was reviewed (Cui et al. 2018a), and two new species from China and Vietnam were described.

Ban, X. S., Jiang, N., Cheng, R., Xue, D. Y. & Han, H. X. 2018. Tribal classification and phylogeny of Geometrinae (Lepidoptera: Geometridae) inferred from seven gene regions. Zoological Journal of the Linnean Society 184: 653–672.

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Saturniid and sphingid moths as novel models for the study of insect diversity and macroecology

Rodolphe Rougerie, Liliana Ballesteros-Mejia & ACTIAS/SPHINX consortia

Rougerie, R., Ballesteros-Mejia, L. & ACTIAS/SPHINX consortia 2019. Saturniid and sphingid moths as novel models for the study of insect diversity and macroecology. Pp. 306 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42(2).

Rodolphe Rougerie (corresponding author), Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, 45 rue Buffon CP50, 75005 Paris, France; e-mail: rrougerie@mnhn.fr

Insects are the most speciose group of terrestrial organisms and are strongly affected by global environmental and climatic changes. They exhibit a remarkable variety of forms and life history trait combinations not represented among vertebrates and are responsible for many ecosystem services and disservices. Yet, our knowledge of their diversity and distributions, as well as our understanding of their evolution and diversification dynamics through space and time, remains fragmentary. We have identified a group of herbivorous insects – the Saturniidae and Sphingidae, two sister families of moths – that represent an unparalleled insect model. This group comprises about 5000 species and has been thoroughly documented worldwide, through comprehensive DNA barcode libraries, hundreds of thousands of occurrence records in databases, and a broad documentation of their life histories.

Thus, they offer for the first time an opportunity to study patterns of diversity and distribution at a global scale in insects, together with their underlying macroevolutionary processes. Here we present the comprehensive database built by our research group and the different approaches – such as integrative taxonomy, biogeographical analyses, phylogenomics, analysis of traits and community ecology – that we combine to address key questions about the macroecological patterns and the evolutionary history of these moths. This is the first time that such a holistic approach will have been applied to insects on a global scale. We expect that it will shed light on the processes governing the extant diversity of insects and help us understand how global changes will affect them, how they may or may not adapt to these changes, and how best we can act to conserve the species and preserve their roles in our ecosystems.

The hostplant profile of the Geometridae in comparison with other Obtectomera families in the Indo-Australian tropics

Jeremy D. Holloway

Holloway, J. D. 2019. The hostplant profile of the Geometridae in comparison with other Obtectomera families in the Indo-Australian tropics. Pp. 306–307 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42(2).

Jeremy D. Holloway, Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, UK; e-mail: j.holloway@nhm.ac.uk

The publication of Robinson et al. (2001) on hostplants of the Lepidoptera of the Oriental region was used as a metasample to provide an overview of the range of plants utilised by the families of Macrolethocera and Rhopalocera, and of the differences

between them and the degree of specialism within this. The datum points (records) obtained were all of the unique insect species/plant genus combinations. These were summed for plant families and higher categories within insect genera and higher categories.

The sampling was limited to Lepidoptera genera recorded from Borneo so as to provide an essentially tropical picture, given that the data included many records from montane areas on the Asian mainland. Records for Geometridae were from just below half of the genera present, relatively low compared to other groups, and for 96 plant families, though 37 of these were single records. Amongst the Macroheterocera, the geometrids had the highest level of records from the magnoliids, primarily from the Laurales, with only the more polyphagous saturniids approaching this level. Exploitation of gymnosperms was amongst the highest in the Macroheterocera, but only low exploitation of monocots and campanulids was revealed.

The top ten families exploited by Geometridae as a whole were Fabaceae, Lauraceae, Euphorbiaceae, Sapindaceae, Anacardiaceae, Rubiaceae, Apocynaceae, Myrtaceae, Verbenaceae and Rosaceae. There were almost twice as many records for Fabaceae as for Lauraceae. Subfamily preferences differed, with the top five families for the larger ones as follows: Larentiinae on Euphorbiaceae, Lauraceae, Sapindaceae, Myrsinaceae and Rosaceae; Sterrhinae on Fabaceae, Rubiaceae, Myrtaceae, Oleaceae and Lauraceae; Geometrinae on Fabaceae, Sapindaceae, Anacardiaceae, Apocynaceae and Fagaceae; the Ennomini clade of Ennominae on Lauraceae, Euphorbiaceae, Rhamnaceae, Rubiaceae, Flacourtiaceae and Vitaceae; the Boarmiini clade on Fabaceae, Euphorbiaceae, Lauraceae, Sapindaceae and Myrtaceae. Records for Desmobathrinae were only from Verbenaceae, for Oenochrominae (*Sarcinodes*) only from Proteaceae, and for Eumeleini only from Euphorbiaceae. Almost all feeding was on woody plants, primarily young foliage but also reproductive parts in some groups.

The increasingly greater resolution provided by DNA sequencing in the higher classification of both Lepidoptera and higher plants has enabled analyses to be made of the interpredictability between their phylogenies that might be indicative of the degree of coevolution. A test of this on hostplant data from the Holarctic Macroheterocera (with a high proportion of Geometridae) was made by Holloway & Hebert (1979), treating hostplant taxa as 'islands' that might be classified in terms of their herbivore faunas, as originally suggested by Janzen (1968). This revealed a strong primary signal on taxonomic lines. A more sophisticated two-way test of phylogenetic interpredictability in the Geometridae and

Pyraloidea of New Guinea was undertaken by Segar et al. (2017), sampling from trees in lowland forest plots. Interpredictability was significantly higher for Pyraloidea using phylogenies alone, but increased for Geometridae when a component for polyphenol oxidative activity was factored in. This suggested that geometrids had an evolutionary history with more polyphagy and host-shifts between plant groups than was the case for pyraloids.

Across all of Indo-Australian tropical ecosystems, the highest geometrid diversity is found in natural forests and their successional cycles, but falls considerably following disturbance by humans such as logging and conversion to agricultural systems, unlike in groups such as Pyraloidea and Noctuoidea where such degraded systems can retain moderate diversity from a different suite of species to those found in forests. Thus, there are very few serious pest species noted for geometrids in the economic literature, a fact that can be gleaned from the data in Zhang (1994) by extracting the number of years in which a species is mentioned in an 80-year compilation of abstracts. Geometridae species mentioned in 10 years or more only total 35, and most of these are Holarctic pests of orchards and forestry, mostly polyphagous but also including many conifer specialists. Only five of these species are tropical, all Boarmiini, the four from the Palaetropics being polyphagous and geographically widespread: *Ascotis selenaria*, *Biston suppressaria*, *Ectopis bhurmitra* and *Hyposidra talaca*.

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Population changes of geometrid moths across southern mountains of South Korea

Sei-Woong Choi, Jeong-Seop An, Nang-Hee Kim, Bo-Ra Shin,
Jae-Young Lee & Beom-Jun Jang

Choi, S-W., An, J.-S., Kim, N.-H., Shin, B.-R., Lee, J.-Y. & Jang, B.-J. 2019. Population changes of geometrid moths across southern mountains of South Korea. Pp. 308–309 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Sei-Woong Choi (corresponding author), Department of Environmental Education, Mokpo National University, Muan 58554, Jeonnam, South Korea; e-mail: choisw@mokpo.ac.kr

Geometrid moths were collected from 2003 to 2017 at 38 sites on three mountains of southern South Korea: Mt. Hallasan (HL, maximum height 1950 m), Mt. Jirisan (JR, maximum height 1915 m) and Mt. Seungdalsan (SD, maximum height 333 m) (Fig. 1).

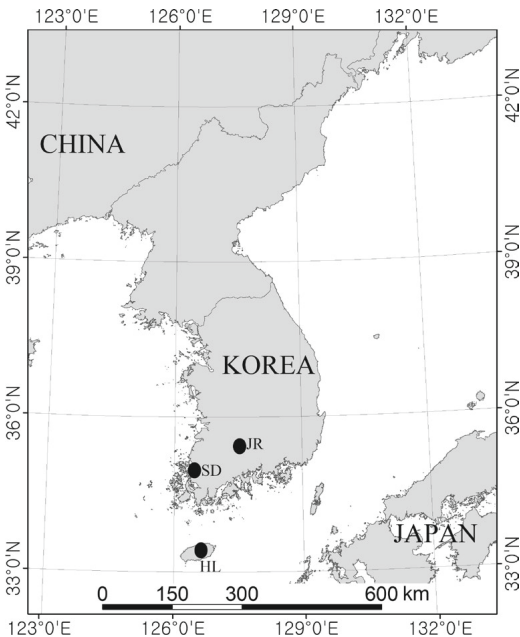


Fig. 1. Map showing the study sites in Korea: JR, Mountain Jirisan; HL, Mountain Hallasan; SD, Mountain Seungdalsan.

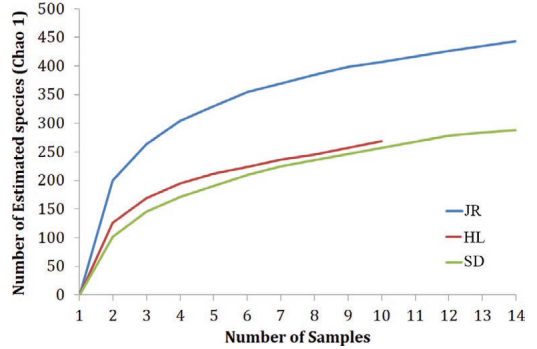


Fig. 2. Cumulative numbers of geometrids of each mountain of South Korea using estimated number of species (Chao 1). JR, Mountain Jirisan; HL, Mountain Hallasan; SD, Mountain Seungdalsan.

The purpose of the study was to track the change of moth communities from recent climate change at mixed deciduous and coniferous forests, as one of the projects of long-term ecological research by the Korean Ministry of Environment. Ultraviolet light traps (22 Watt and 12 volt) were employed to collect moths from May to October and the collected samples were identified to the species level, if possible.

A total of ca 45000 specimens belonging to 476 species (about 70 % of the Korean Geometrid species (Kim et al. 2016)) were identified (Table 1, Fig. 2). Geometrid diversity in JR was the highest among three mountains. While the total numbers of geometrids in SD (229 species) and HL (228 species)

Table 1. Summary of numbers of individuals (and species) in each subfamily of the Geometridae collected from three mountains in South Korea.

Subfamily	Coastal (SD)	Island (HL)	Inland (JR)	Total
Alsophilinae	0	0	9 (1)	9 (1)
Ennominae	4069 (103)	7397 (100)	20751 (165)	32217 (195)
Geometrinae	292 (36)	172 (25)	888 (40)	1352 (55)
Sterrhinae	1833 (38)	536 (30)	2456 (48)	4852 (62)
Larentiinae	531 (52)	935 (73)	5170 (132)	6636 (163)
Total individuals (species)	6725 (229)	9040 (228)	29274 (386)	45039 (476)

were similar, but the proportions of subfamilies were quite different according to mountain's elevational range: high proportion of Larentiinae (32 %) in high mountain (HL) and high proportions of Sterrhinae (17 %) and Geometrinae (16 %) in low mountain (SD). Highest peak of total numbers of species and individuals occurred at the middle elevation zone of three mountains. However, there were differences of seasonal diversity patterns depending on the subfamily level. This temporal and spatial pat-

tern of diversity at southern South Korea could be a baseline data to track population changes from climate change.

This work was sponsored partially by the grant from Mokpo National University, South Korea.

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No indication of high host-plant specificity in tropical geometrid moths

**Sille Holm, Juhan Javoiš, Freerk Molleman, Robert B. Davis,
Erki Õunap, Heikki Roininen & Toomas Tammaru**

Holm, S., Javoiš, J., Molleman, F., Davis, R. B., Õunap, E., Roininen, H. & Tammaru, T. 2019. No indication of high host-plant specificity in tropical geometrid moths. Pp. 309 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Sille Holm (corresponding author), Institute of Ecology and Earth Sciences, University of Tartu, Vanemuise 46, 51014 Tartu, Estonia; e-mail: sille.holm@ut.ee

Ecological specialization is one of the fundamental parameters applied to quantify ecological interactions of a species. Specificity varies dramatically across species, with both causes and consequences of this variation being at the very heart of ecological research. Specificity of phytophagous insects has been of particular interest. The debate over whether higher levels of specificity in host plant use prevail in tropical insects than in temperate ones is hindered by the lack of data, and has not yet received a clear conclusion. For temperate region Lepidoptera comprehensive lists of host plant genera are already available, whereas in the tropics, the host relations have remained largely unknown. In the present study, we used host acceptability trials to estimate host plant specialisation of forest geometrid moth species (Lepidoptera: Geometridae) in equatorial

Africa, Uganda. We tested the feeding performance of the larvae on 15 tree/shrub species, which represent a wide array of plant families, and make up a relatively high proportion of woody plants in the local assemblage. We compare our experimental data to the well-known host use patterns among closely related hemiboreal species. To provide a selection of host plant species comparable to that used in the tropics, we also chose the 15 most widely distributed and common forest tree species in the hemiboreal region, using Estonia as a reference location. Phylogenetic comparative analysis found no profound differences in specificity between the two regions. Our results are thus inconsistent with the idea that tropical insects are more specialised than temperate ones.

Investigating hostplant relationships of Peruvian Lepidoptera through DNA barcoding of fogged caterpillars and their gut contents

Axel Hausmann, Jérôme Morinière, Andreas Floren, Amelie Höcherl & Juliane Diller

Hausmann, A., Morinière, J., Floren, A., Höcherl, A. & Diller, J. 2019. Investigating hostplant relationships of Peruvian Lepidoptera through DNA barcoding of fogged caterpillars and their gut contents. Pp. 310–311 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Axel Hausmann (corresponding author), SNSB – ZSM, Bavarian State Collection of Zoology, Münchhausenstr. 21, 81247 Munich, Germany; e-mail: hausmann.a@snsb.de

In the framework of a project, financed by the Bavarian State Ministry of Science, canopy fogging samples were taken from 47 trees near the Panguana station in Peru (www.panguana.de). The insect material

is preserved in 96 % alcohol in small bottles, from which a total of 130 Lepidoptera larvae were selected, subsequently dried, photographed and databased. Tissue samples (one vertically cut central segment)

were submitted to Sanger sequencing (DNA barcoding, COI 5' gene) with Lepidoptera standard primers for identification of the larvae. All data and photographs are deposited on BOLD database. For 119 larvae (92 %) sequencing of the COI barcode gene was successful. Blasting on BOLD database resulted in 60 identifications to species level (50 %), 33 to genus level (28 %) and 23 to family level (19 %). For just three sequences no family match could be suggested. Altogether, the 119 sequences belong to 92 different lepidopteran species-clusters (BINs). The identity of the pre-identified target trees was verified by DNA barcoding (rbcL, psbA and trnL-F

markers). For ten larvae from six target trees tissue samples of the gut contents were analysed with two plant specific primers (psbA, rbcL) in a High Throughput Sequencing (HTS) approach. In some cases the feeding record on the fogged and pre-identified target tree was confirmed, in others we found indication on alternative feeding on lianas, epiphytes, and neighboring trees. Much attention must be given to potential contamination by plant material releasing their DNA into the alcohol of the fogging sample. The results are presented as a pilot model for stimulating more comprehensive studies in the future.

Survey efficiency of sex pheromone and light traps for decreasing damages of invasive box tree moth in Iran

Farzaneh Kazerani, Mohammad Ebrahim Farashiani, Mohammad Alazmani,
Seyed Naghi Khaleghi & Samira Farahani

Kazerani, F., Farashiani, M. E., Alazmani, M., Naghi Khaleghi, S. & Farahani, S. 2019. Survey efficiency of sex pheromone and light traps for decreasing damages of invasive box tree moth in Iran. Pp. 310 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Farzaneh Kazerani (corresponding author), Research Institute of Forests and Rangelands, Agricultural Research Education and Extension Organization (AREEO), Tehran, Iran; e-mail: farzane.kazerani@gmail.com

The box tree, *Buxus sempervirens* subsp. *hyrcana* (Pojark.), is one of the major and endemic evergreen trees in northern forests of Iran (Caspian hyrcanian forests). This valuable tree was infested by twig blight disease of boxwood that caused severe defoliation of boxwood trees. The next huge shock to *Buxus* trees was created by serious damage of the box tree moth (BTM), *Cydalima perspectalis* (Walker, 1859) (Lepidoptera, Crambidae), in Iran. Various methods have been used for controlling this moth in Iran. In some parts of northern Iran *Bacillus thuringiensis* (Bt) and some other narrow-spectrum pesticides were used against *C. perspectalis*. Although insecticides may show some quick effect of population decrease, they have a lot of disadvantages for environment and other insects,

especially useful ones. In large scale, pheromone traps have been used for detection as well as control of *C. perspectalis* and show acceptable results. Sticky Delta traps baited with pheromone capsule seems to be more effective among the other types of pheromone traps. As 8137 males of BTM were captured during its life cycle in Cheshmeh-Bolbol *Buxus* reservoir (Golestan province) in 2017. Two kinds of light traps (along with pheromone capsule) were also used in *B. sempervirens* ssp. *hyrcana* habitats. The results show that plate Sticky light traps are more effective than Ferolite traps in capturing of *C. perspectalis*. The results show that non-chemical control methods can be more effective if they are used methodologically and at the right time.

Following due process(es): remarks on the occurrence of Lithinini in southern Africa (Geometridae, Ennominae)

Martin Krüger

Krüger, M. 2019. Following due process(es): remarks on the occurrence of Lithinini in southern Africa (Geometridae, Ennominae). Pp. 310–311 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Martin Krüger, Department of Invertebrates (Lepidoptera), DITSONG National Museum of Natural History (formerly Transvaal Museum), P.O. Box 413, Pretoria 0001, South Africa; e-mail: kruger@ditsong.org.za

Attempts to delineate the ennomine tribes Lithinini and Nacophorini (s.l.) have thus far largely centered

on the structure of the anellar processes of the male genitalia but, despite identifying certain areas of

resolution, none of the concepts proposed has proved satisfactory on a global scale. Although recent evidence suggests that Lithinini should be included in Nacophorini, such action, if correct, would only partly solve the problem of reconstructing the tribal classification of Ennominae as anellar processes similar to those seen in these two (putative) clades are known from at least another ten (equally putative) tribes, suggesting that these phallus-supporting structures evolved numerous times within the subfamily. The (for ditrysians) unusual habit of feeding

on Pteridophyta (ferns) has repeatedly been cited as a character defining Lithinini; unfortunately, no host plant records appear to be available for any of the members of the comparatively depauperate southern African fauna.

As no published reference exists regarding the tribal composition of southern African Ennominae, an overview and discussion of the taxa provisionally classified as Lithinini in the collection of the former Transvaal Museum is presented, including a number of new genera and species to be described shortly.

Exploring the taxonomy of drepanoid-like Geometridae from tropical Africa

Michael Ochse

Ochse, M. 2019. Exploring the taxonomy of drepanoid-like Geometridae from tropical Africa. Pp. 311–312 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Michael Ochse, Waldstr. 51, 67273 Weisenheim am Berg, Germany; e-mail: diehl.ochse@t-online.de

There is a large variety of Geometridae moths in Africa with 4057 described species, maybe about two third of the real diversity. The majority of genera lack modern taxonomic revisions and so unambiguous species identification is often difficult. Usually the assignment of collected specimens to the family Geometridae is straightforward. However, some

species groups show mimicry patterns or mimetic morphologies. A group of genera from the subfamily Ennominae (tribe Hypochrosini) was placed by early taxonomists in the hooktip family (Drepanidae). A complex of these 11 African genera (e.g. *Sphingomima*, *Gangropteryx*, *Plegapteryx*, *Euexia*) with currently recognised 43 species (e.g. *Vaena eacleoides*



Fig. 1. *Vaena eacleoides* Walker, 1869 (Geometridae, Ennominae).

Walker, 1869, Fig. 1) is under revision and it revealed a few new species and some synonymies. Comprehensive collecting over 15 years by the author and other Lepidopterologists, supplemented by museum

visits mainly in the tropical forest zone, resulted in clear picture of the taxonomic situation and the distribution pattern of the species.

A brief overview of Lepidopteran diversity in Madagascar highlighting the massive completion gap

David C. Lees

Lees, D. C. 2019. A brief overview of Lepidopteran diversity in Madagascar highlighting the massive completion gap. Pp. 312 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

David C. Lees, Department of Life Science, Natural History Museum, Cromwell Road, South Kensington, SW75BD, UK; e-mail: davidl@nhm.ac.uk

Currently approximately 4900 valid described species of Lepidoptera in Madagascar have been listed, arranged in about 70 families and 30 superfamilies. One of the first synonymically catalogued major families was the Geometridae. 696 species (756 taxa including subspecies) are listed by AfroMoths, about 14 % of the total fauna. Although the Malagasy fauna is otherwise far less well known than the fauna of Europe, this is only a slightly higher percentage than for European Geometridae (9 %). Given that relatively few described Madagascar micromoths (about 1600 species) relative to macroheterocerans and butterflies are known, it seems reasonable to suppose that for the Lepidoptera as a whole, the actual number of lepidopteran species is probably considerably in excess of twice the Malagasy total of described species. So far, DNA barcoding has yielded about 2900 approximately species-level clusters

(BINs) for the entire lepidopteran fauna, most of which are probably undescribed. Progress even on Geometridae is in early stages. Only 105 BINs are publically available for Malagasy geometrids, 26 of which were from a malaise trap, and only 18 of which have been identified to species on the publicly available interface of BOLD. At least 376 BINs (93 among which identified to species) have been barcoded on BOLD across several projects. This is still quite few considering the impressive Herbulot collection from the island but also suggestive of a large number of undescribed species. An intense effort is now needed both to identify and DNA barcode local faunas from Madagascar and to apply newly available sequencing technologies on such collections as Herbulot's, to test whether such a large completion gap is applicable to Malagasy looper moths or whether most species are already described.

Current knowledge of the Geometridae in South Korea: are we still waiting for more species?

Sei-Woong Choi & Sung-Soo Kim

Choi, S.-W. & Kim, S.-S. 2019. Current knowledge of the Geometridae in South Korea: are we still waiting for more species? Pp. 312–313 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Sei-Woong Choi (corresponding author), Department of Environmental Education, Mokpo National University, Muan 58554, Jeonnam, South Korea; e-mail: choisw@mokpo.ac.kr

South Korea has relatively rich flora and fauna diversity, with ca. 49000 species in its small territory (ca. 100000 km²). This high number is because of the country's latitudinal spread from 33° to 39°, the long north-to-south parallel mountain chain and more than 3000 islands, producing a unique topography and diverse ecological environment. The knowledge of the Geometridae has steadily increased. The first report of geometrid moths from Korea was made

by Arthur G. Butler (1883): *Scopula hanna* (Butler), *Arichanna melanaria* (Linnaeus) and *Abraxas miranda* Butler. After Butler, several researchers added geometrid species into the Korean fauna: 574 species (Shin 1996) and 647 species (Choi 2006). Kim et al. (2016) listed 684 species in eight subfamilies: Archearinae (1 species), Ennominae (285 species), Alsophilinae (8 species), Oenochrominae (1 species), Orthostixinae (1 species), Geometrinae (69 species), Sterrhinae

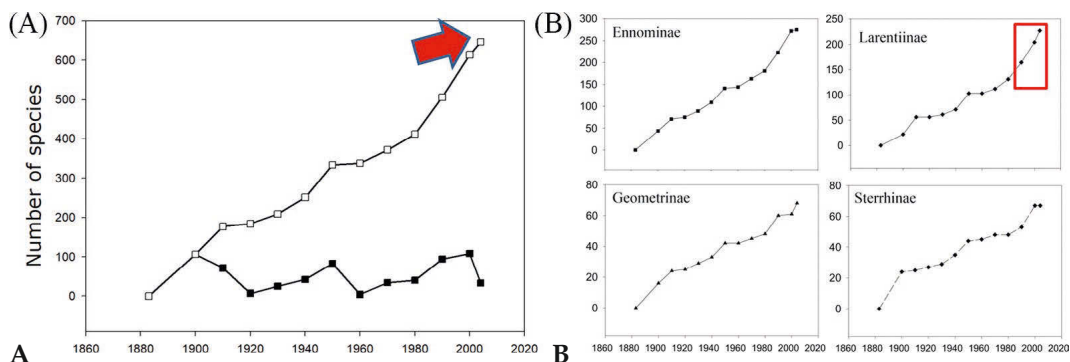


Fig. 1. Change of knowledge of the Geometridae fauna in South Korea. **A.** Total number of geometrid species (□, cumulative number of described species; ■, number of species described); **B.** Cumulative number of species of four subfamilies of Geometridae in Korea.

(74 species) and Larentiinae (245 species) (Fig. 1). Here, I will show the trend of the species discovery depending on the subfamily and few taxonomic problems in Korea.

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Recent advances in the knowledge of the tribe Cassymini in Ethiopia (Geometridae, Ennominae)

Andrea Sciarretta & Axel Hausmann

Sciarretta, A. & Hausmann, A. 2019. Recent advances in the knowledge of the tribe Cassymini in Ethiopia (Geometridae, Ennominae). Pp. 313–314 in: Hausmann, A. & Rajaei, H. (eds). *Proceedings of the tenth FORUM HERBULOT 2018* (Stuttgart, Germany, 11–16 June 2018). *Spixiana* 42(2).

Andrea Sciarretta (corresponding author), Department of Agriculture, Environmental and Food Sciences, University of Molise, Campobasso, Italy; e-mail: sciarretta@unimol.it

The geometrid tribe Cassymini (Ennominae), as currently conceived, includes 22 genera and 692 species distributed mainly in the Palaearctic, Nearctic and Afrotropical regions. In the Afrotropical region, Cassymini are represented by the genera *Orbamia* (five species), *Heterostegane* (27 species), *Pycnostega* (15 species), *Xenostega* (11 species), and *Zamarada* (276 species). Ethiopia, with a broad diversity of climatic and environmental conditions, represents one of the ‘hottest’ biodiversity hotspots on Earth, but the actual knowledge of its geometrid fauna is very limited. In this paper, we present the preliminary results of the research carried out in the country, focusing on the tribe Cassymini. So far, 493 specimens, collected in various localities of Ethiopia, were analysed by external and/or genitalia morphology and by DNA

barcoding. A total of 32 species has been identified, belonging to the genera *Orbamia* (2 species), *Heterostegane/Xenostega* (8 species), *Pycnostega* (1 species) and *Zamarada* (21 species), 20 of which not having been reported for Ethiopia previously. Among them, eight are under evaluation as potential new species for science (one *Orbamia*, five *Heterostegane* and two *Zamarada*). Additional findings are expected by the study of other material, currently underway. The genus *Heterostegane* revealed to be very interesting, rich in species, mostly endemic or limited to neighbouring countries, whereas the status of *Xenostega* may need to be reconsidered. With the addition of our data, the total number of species belonging to genus *Zamarada* known for Ethiopia is raised to 21, 14 % of which are endemics, 38 % distributed

to East and/or North Africa, whilst 48 % are more widespread in Africa. Our preliminary results confirm the strong need to continue the investigation of the lepidopteran fauna in Ethiopia and other still

poorly known countries around the Horn of Africa, even in genera for which extensive monographs are available, such as for *Zamarada*.

Taxonomic and faunistic research program on African Lepidoptera at the African Natural History Research Trust (ANHRT)

Gyula László

László, Gy. 2019. Taxonomic and faunistic research program on African Lepidoptera at the African Natural History Research Trust (ANHRT). Pp. 314 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Gyula László, The African Natural History Research Trust, Street Court, Leominster, Kingsland, HR69QA, UK;
e-mail: gyula@anhrt.org.uk

The African Natural History Research Trust (ANHRT) was established in 2010. It aims to launch an extensive biodiversity research program focused on the Lepidoptera of poorly explored regions of Sub-Saharan Africa. Due to an extensive series of sampling expeditions, ANHRT has gathered a significant amount of specimens. This has urged the Trustees to create a purpose-built research centre and museum, with the intention of becoming a strong-hold of African entomology. The building of the research museum in Leominster-Kingsland (Herefordshire, UK) started in 2016 and became fully operational by the end of 2017. At present, one of the primary aims of ANHRT is to make the enormous amount of material available to researchers worldwide. This, in part, has been made possible by the preparation of specimens by a team of full-time mounters. Currently, ANHRT is undertaking sampling programs in the following countries: Ivory Coast, Sierra Leone, Liberia, Sao Tome, Zambia, and Mozambique. Furthermore, expeditions are under preparation to Togo, Uganda and Tanzania. Thus, freshly collected material, with appropriate collecting and export permits, is continuously arriving. Scientific processing of the collected material has begun and is primarily focused on Geometridae, Nolinae, Arctiinae and Notodontidae. As for Geometridae, two generic revisions are currently in progress: revision of the African taxa of *Racotis* Moore, 1887 in collaboration with A. Hausmann and T. Karisch; and revision of *Rhodophthitus* Butler, 1880 in collaboration with A. Hausmann. Both revisional studies will result in the description of numerous

new species (more than 10 in case of *Racotis*). The scientific processing of Arctiinae material is in progress by Anton Volynkin who is focusing on the Cisthenina and Nudariina subtribes of Lithosiini. Despite the fact that several specialists have published numerous papers on these groups, there are still many novelties to discover, especially from understudied regions (e.g. Zambia, Mozambique, West Africa). The taxonomic studies in Nolinae (focusing only on the Nolini tribe) are similarly fruitful thanks to fresh material from the above mentioned, less explored countries. At the moment, there are at least 15 new species of Nolini being described from the collection of ANHRT. Similarly, the family Notodontidae has proved to be very fruitful. Practically all genera require full revision which has started in co-operation with A. Schintlmeister. Work has begun with the *Antheua-Rigema-Phalera-Elaphrodes* generic complex with promising preliminary results. Besides taxonomic studies, ANHRT also aims to provide faunistic information to local nature conservation bodies and authorities. This not only increases the knowledge of the local fauna of a given region or protected area, but also allows local authorities to prioritise conservation effort and funding.

ANHRT is interested in co-operating with more specialists of any other Lepidoptera groups, providing a unique opportunity to study freshly collected material that has also been preserved in a way ideal for DNA studies besides the traditional morphotaxonomic ones.

Patterns along the elevation and DNA barcoding of Geometridae moths from the Western Himalaya, India

Pritha Dey, Virendra Prasad Uniyal, Kailash Chandra & Axel Hausmann

Dey, P., Uniyal, V. P., Chandra, K. & Hausmann, A. 2019. Patterns along the elevation and DNA barcoding of Geometridae moths from the Western Himalaya, India. Pp. 315 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Pritha Dey (corresponding author), Wildlife Institute of India, Chandrabani, P.O. Box 248001, Dehradun, India; e-mail: dey.pritha126@gmail

Moths are the “poor cousins” of butterflies in Lepidoptera conservation in India. Tropical regions need large-scale inventorying and taxonomic revisions of the family Geometridae, Indian Himalayan region is one such lacunae. I studied Geometrid moths from Nanda Devi Biosphere reserve, a western Himalayan Protected area, which faces degradation and loss of biodiversity but is a refuge to unique diversity. The study area was stratified on the basis of elevation and vegetation, and sampled at every 200 m along the elevation between 2000–3800 m. Two mountain gradients (1) Joshimath and (2) Lata were chosen for a comparative study. DNA extraction and sequencing were performed at the CCDB, University of Guelph. 185 species were recorded. Differential patterns of species richness exist in the two elevational gradients studied. In both cases, vegetation composition and structure define the species composition and

richness. Anthropogenic disturbances like habitat fragmentation (human habitation), resource extraction for fuelwood and timber (lopping and felling) as well grazing (pellet signs) impact the assemblage structure and their patterns across the elevation. 113 species were subjected to DNA barcoding. Distinct Barcode Gaps exist between most of the species, thus confirming their discrimination. Our results revealed one new species (*Prometopidia* sp. nov.), one new distribution record for India (*Alcis paghmana*) and distribution extensions of 15 other species within India. Four species from Sikkim show deep genetic divergences (K2P distance) from conspecifics from w. Himalaya, indicating potential cryptic species. It is the first step towards providing effective geographical distribution data, ecological understanding and foundation for conservation in the face of habitat degradation and climate change.

Additional data for the genus *Lithostege* Hübner, [1825] 1816 (Lepidoptera, Geometridae) in Turkey with DNA-based identifications

Feza Can, Zühal Okyar & Axel Hausmann

Can, F., Okyar, Z. & Hausmann, A. 2019. Additional data for the genus *Lithostege* Hübner, [1825] 1816 (Lepidoptera, Geometridae) in Turkey with DNA-based identifications. Pp. 315 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Feza Can (corresponding author), Mustafa Kemal University, Agriculture Faculty, Department of Plant Protection, 31034 Antakya, Hatay, Turkey; e-mail: cezafan_onurcan@hotmail.com

The recently published revision of the Middle East representatives of the taxonomically difficult genus *Lithostege* (Rajaei et al. 2011) presents data for eight *Lithostege* species in Turkey: *L. buxtoni**, *L. bosporaria*, *L. witzzenmanni*, *L. farinata**, *L. ancyrana*, *L. griseata*, *L. palaestinensis*, *L. flavicornata* (*occurrence in Turkey based just on literature data). In Hausmann & Viidalepp (2012) the occurrence of *L. coassata* is added for Turkey, whilst Turkish data for *L. farinata* are questioned. Genetic data were not analysed by Rajaei et al. (2011), but briefly mentioned in Hausmann & Viidalepp (2012). In recent investigations, we could analyse 14 DNA barcodes (five species) and 17 genitalia for the Turkish *Lithostege*, resulting in the genetic confirmation of the difficult morphological

discrimination between the closely related species *L. griseata*, *L. palaestinensis* and *L. ancyrana* in Turkey. Female genitalia of *L. ancyrana* are presented for the first time highlighting some differential features from *L. palaestinensis* and *L. farinata*. Further data on distribution and bionomics are added.

Rajaei, H. S., Stüning, D. & Viidalepp, J. 2011. A review of the species of *Lithostege* Hübner, [1825] 1816 (Lepidoptera: Geometridae, Larentiinae), occurring in Iran and adjacent countries, with description of two new species from Iran and Pakistan. Zootaxa 3105: 1–46.

Hausmann, A. & Viidalepp, J. 2012. Larentiinae I. In: Hausmann, A. (ed.). The geometrid moths of Europe 3. 743 pp., Vester Skerninge (Apollo Books).

A new species of the genus *Biston* from the Balkan peninsula (Lepidoptera, Geometridae, Ennominae)

Bernd Müller

Müller, B. 2019. A new species of the genus *Biston* from the Balkan peninsula (Lepidoptera, Geometridae, Ennominae). Pp. 316 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Bernd Müller, Weissdornallee 13, 13158 Berlin, Germany; e-mail: geobernd@gmx.de

Up to now, 57 species in the genus *Biston* are known in the Holarctic and Oriental regions as well as in Africa. Two similar species, *Biston strataria* (Hufnagel, 1767) and *B. achyra* Wehrli, 1936 occur in the West Palaearctic. New studies show the existence of a third, previously overlooked species on the Balkan peninsula. The third species, *Biston rosenbaueri* Müller, 2018 is classified between the two above-mentioned and was found at altitudes between 200 and

300 m a.s.l., and only male specimens are known. The new species is presented with diagnostic characters and comparative barcoding data.

Müller, B. 2018. *Biston rosenbaueri* sp. n. (Lepidoptera, Geometridae, Ennominae) from the Balkan peninsula. Nota Lepidopterologica 41 (2): 207–213. doi: 10.3897/nl.41.25099

Confusing syntypes – appearing issues during the investigation of *Triphosa taochata* Lederer, 1870 (Geometridae, Larentiinae)

Dominic Wanke & Hossein Rajaei

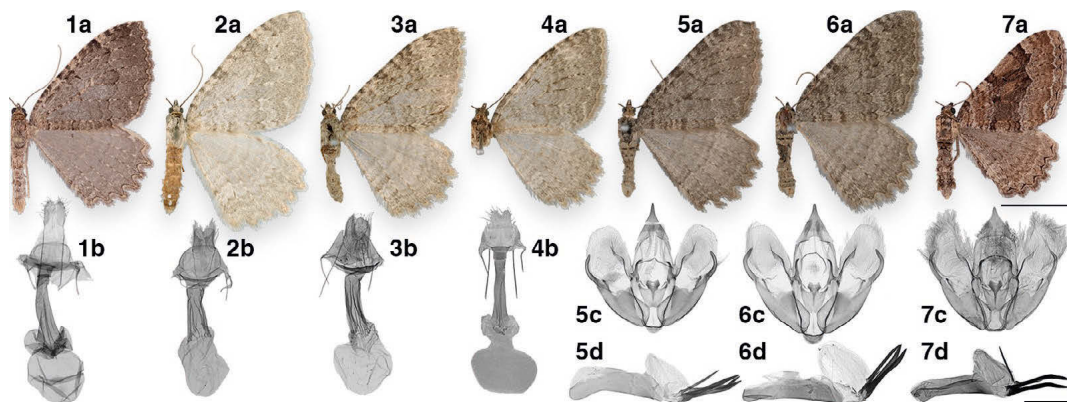
Wanke, D. & Rajaei, H. 2019. Confusing syntypes – appearing issues during the investigation of *Triphosa taochata* Lederer, 1870 (Geometridae, Larentiinae). Pp. 316–317 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Dominic Wanke (corresponding author), University of Hohenheim – Department of Entomology, Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany; e-mail: dominic.wanke@smns-bw.de

A main approach during the description of new species is the investigation of type material and the verification of their status to clear all nomenclatural doubts. Designated holotypes therefore are essential to proof the validity of species, their status and comparison with potentially new species. However, in former times, holotype designation was not a common taxonomic act and instead a series of specimens (often) from different localities were regarded as syntypes. Different cases of complication and confusion in interpretation of syntype series may happen (e.g. when more than one species present in the syntype series). A case of difficulty was observed during the recent taxonomic revision of the genus *Triphosa* Stephens, 1829 in the syntype series of *T. taochata* Lederer, 1870. This series (Figs 3–6) containing two male and two female specimens belongs to Staudinger's collection, which is now deposited in the Natural History Museum of Berlin. All these specimens, which externally are *Triphosa*, were dissected. Surprisingly, the males showed no *Triphosa* genitalia structure (Figs 5, 6), but that of *Hydria cervinalis* Scopoli, 1763 (Fig. 7). More close observation revealed that both of these specimens

were secondarily glued and repaired, and it seems that the abdomen belong to other specimens. Thereby it is also not clear if the other types remained untouched, although they show no sign of reparation. Furthermore, the genitalia structure of the females clearly not belong to the same *Triphosa* species (Figs 1–4). This issue questioned the validity of *T. taochata*, which has been a bona species for many years. For this reason, we are faced with two main problems: 1. as in original description no holotype is designated, defining the type locality is not possible; and 2. in the genus *Triphosa* the male genitalia show the best diagnostic characters in species level and an identification only based on the female genitalia is dubious. To solve this dilemma, we are going to barcode these syntype specimens and compare their COI patterns with already known species in western Palearctic.

Wanke, D., Hausmann, A. & Rajaei, H. 2019. An integrative taxonomic revision of the genus *Triphosa* Stephens, 1829 (Geometridae: Larentiinae) in the Middle East and Central Asia, with description of two new species. Zootaxa 4603 (1): 39–65. doi:10.11646/zootaxa.4603.1.2



Figs 1–7. Wing pattern and genitalia structure. 1. *Triphosa dubitata*; 2. *T. sabaudiata*; 3–6. syntype series of *T. taocha-ta*; 7. *Hydria cervinalis*. a. Wing pattern; b. female genitalia ventral view; c. genitalia capsule; d. aedeagus (cf. Wanke et al. 2019).

A case of gynandromorphism in *Aplocera annexata* (Freyer, 1830) (Geometridae, Larentiinae)

Chantal Holzhaue & Hossein Rajaei

Holzhaue, C. & Rajaei, H. 2019. A case of gynandromorphism in *Aplocera annexata* (Freyer, 1830) (Geometridae, Larentiinae). Pp. 317–318 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Chantal Holzhaue (corresponding author), Staatliches Museum für Naturkunde Stuttgart (SMNS), Rosenstein 1, 70191 Stuttgart, Germany; e-mail: chantal.holzhaue@smns-bw.de

Gynandromorphism is a phenomenon in which one individual shows characteristics of both – male and female – sexes. Generally gynandromorphism

is categorized in two different kinds: bilateral gynandromorphism and mosaic gynandromorphism. Whether an individual is a bilateral or mosaic gy-

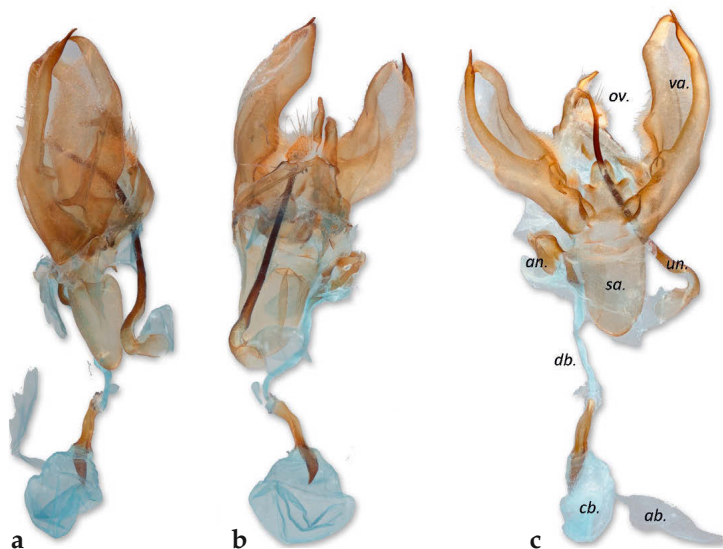


Fig. 1. Gynandromorph genitalia from different angles; a. Lateral side; b. dorsal side; c. ventral side.

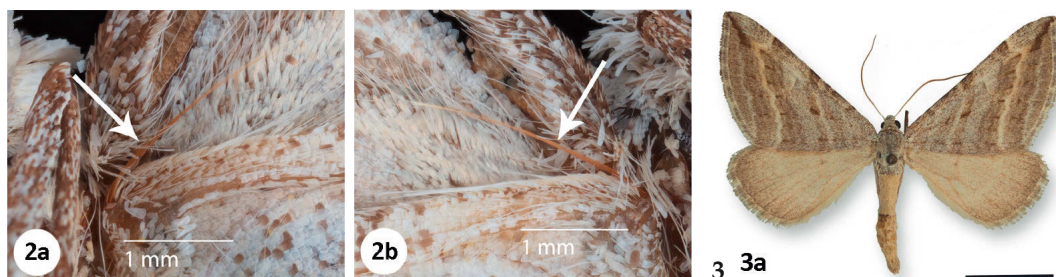


Fig. 2. Wing coupling of gynandromorph specimen; **a.** Left wing, mixture of male and female coupling; **b.** right wing, male coupling.

Fig. 3. Wing pattern *Aplocera annexata* gynandromorph specimen. *va*, valva; *un*, uncus; *sa*, saccus; *ad*, aedeagus; *ov*, ovipositor; *an*, antrum; *db*, ductus bursae; *cb*, corpus bursae; *ab*, appendix bursae.

nandromorph depends on in which state of zygote cell division a non-disjunction appears. The very first divisions of the zygote determine the bilateral body, an occurrence of a non-disjunction in this phase would lead to a half male and half female individual. A non-disjunction in later cell division phases lead to a mosaic gynandromorph. An exact rate of gynandromorphism is unknown. Many insects don't develop a sexual dimorphism, so it is difficult to see whether an individual contains both sexes. In the course of a phylogenetic study of

the tribe Chesiadini, a gynandromorph specimen of the species *Aplocera annexata* in the collection of the Staatliches Museum für Naturkunde Stuttgart (SMNS), was discovered. The outer characteristics (antennae, wings and legs) appear at first glance like a normal male (Fig. 3a), while its genitalia structure revealed a mix of the characters of male and female (Fig. 1a–c). At a closer look, the wing coupling of this specimen shows an extraordinary mixture of a male and female phenotype as well (Fig. 2a–b).

Genus *Cleora* (Geometridae, Ennominae) in tropical Uganda

Sille Holm, Tõnis Tasane, Erki Õunap & Toomas Tammaru

Holm, S., Tasane, T., Õunap, E. & Tammaru, T. 2019. Genus *Cleora* (Geometridae, Ennominae) in tropical Uganda. Pp. 318 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Sille Holm (corresponding author), Institute of Ecology and Earth Sciences, University of Tartu, Vanemuise 46, 51014 Tartu, Estonia; e-mail: sille.holm@ut.ee

Aim of this contribution was to give an overview on the species from genus *Cleora* (Curtis, 1825) that were collected from Kibale National Park and Mburo Park in Uganda during field work from 2011–2013. In this study, species were identified using combined methods: DNA results were compared with wing patterns and genitalia morphology. We found that identifying *Cleora* species based merely on wing pat-

terns is nearly impossible. In total 13 species of *Cleora* were identified. Four species were recorded as new for fauna of Uganda: *C. anacantha* (Fletcher, 1967), *C. thyris* (Fletcher, 1967), *C. nigrisparsalis* (Janse, 1932) and *C. tulbaghata* (Felder & Rogenhofer, 1875). We have compiled a poster for identifying these species together with available information on phenology, host plant use, and body size.

Notes on the distribution, biology and habitats of *Scopula separata* on St Helena Island (Lepidoptera, Geometridae)

Timm Karisch

Karisch, T. 2019. Notes on the distribution, biology and habitats of *Scopula separata* on St Helena Island (Lepidoptera, Geometridae). Pp. 319–320 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Timm Karisch, Museum für Naturkunde und Vorgeschichte Dessau, Askanische Str. 32, 06842 Dessau-Roßlau, Germany; e-mail: timm.karisch@naturkunde.dessau-rosslau.de

Scopula separata is the only endemic geometrid moth on St Helena Island. First found by Melliss in the 1870's at the Hermitage in the Central Highlands, it was rediscovered in 1965 by the Belgian expeditions. In the collection of the Musée Royal de l'Afrique Centrale there are specimens from Fisher's Valley (1965), Teutonic Hall (1966) and Rupert's Valley (1967). Karisch (2001) reported *S. separata* from Sandy Bay Valley (1995). Further observations have been made in the 21st century: Prosperous Bay Plain (Ashmole & Ashmole 2004; recorded 2012 by Cairns-Wicks and Lambdon), Sandy Bay Valley (2011 by Beard), Manati Bay (2011 by Key), Millennium Forest (2017 by Pryce and Fowler; 2018 by Dutton, Fowler, Isaac, Karisch and Stevens), Fisher's Valley (2017 by Pryce and Fowler), Baptist's church in Sandy Bay Valley (2017 by Karisch) and Knotty Ridge (2018 by Dutton).

Although Melliss (1875) writes that *S. separata* "... appears to inhabit the high land" the recent records show that this species is mainly distributed in lower and middle altitudes of the central and eastern parts

of the island. Preferred habitats are the Creeper waste (with *Carpobrotus edulis*) and semi-desert with Samphire (*Suaeda fruticosa*). The reason for *S. separata* currently inhabiting lower altitudes could be land use changes. At the beginning of the 19th century the island was largely denuded of trees due to the grazing of thousands of goats and sheep during the previous centuries. Therefore during Melliss' time, the higher habitats may have resembled the waste land of lower altitudes of today.

A caterpillar of *S. separata* was photographed on and reared from *Suaeda fruticosa* (Ashmole & Ashmole 2004), but taking into consideration all localities with records of *S. separata* the larva should be more or less polyphagous.

Special thanks go to L. Fowler, S. Isaac, N. Stevens, D. Pryce, P. Ashmole and A.-J. Dutton for their contributions to this note. The work received support by the Darwin Plus project DPLUS040 "Securing the future for St Helena's endemic invertebrates".

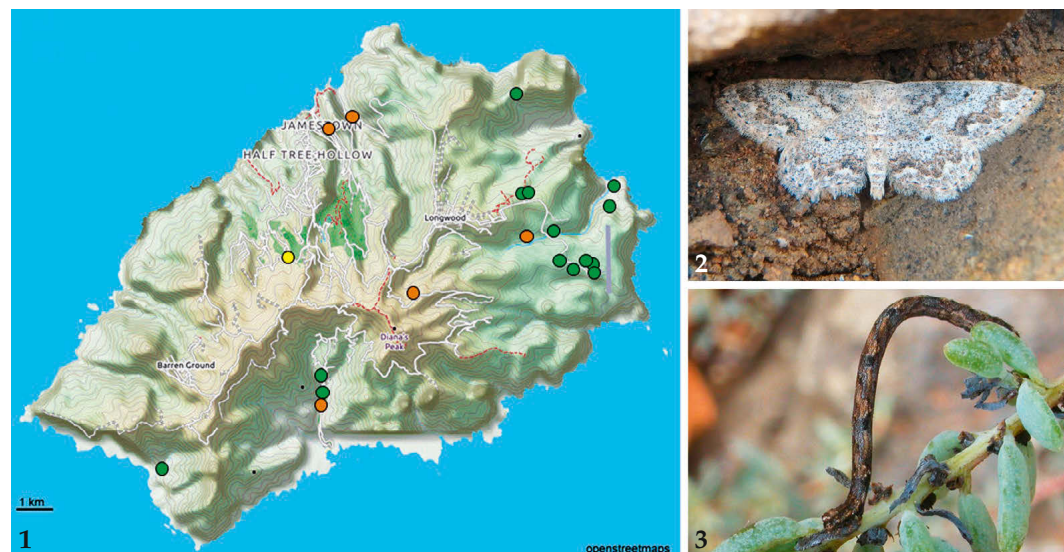


Fig. 1. Records of *Scopula separata* on St Helena Island (●, 19th century; ●, 20th century; ●, 21st century). 2. *Scopula separata*, imago, Knotty Ridge, 08.IV.2018. 3. *Scopula separata*, caterpillar, on *Suaeda fruticosa*, Prosperous Bay Plain, 2003 (photo: Ashmole).

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An integration of DNA-barcoding, morphological traits and geographic distribution data to species delimitation of *Peribatodes perversaria* (Boisduval, 1840) (Lepidoptera, Geometridae)

Donata Kamm, Chris Schäuuffele, Noa Schwabe, Michael Haas, Christian König & Hossein Rajaei

Kamm, D., Schäuuffele, C., Schwabe, N., Haas, M., König C. & Rajaei, H. 2019. An integration of DNA-barcoding, morphological traits and geographic distribution data to species delimitation of *Peribatodes perversaria* (Boisduval, 1840) (Lepidoptera, Geometridae). Pp. 320 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Donata Kamm (corresponding author), Universität Hohenheim, Institut für Zoologie, Garbenstr. 30, 70599 Stuttgart, Germany; e-mail: donatakamm@hotmail.de

The geometrid moth species *Peribatodes perversaria* (Boisduval, 1840) traditionally is split up into multiple subspecies in western Europe. The validity of most of these subspecies was controversial between lepidopterologists who rely only on morphological study. To infer species/subspecies boundaries, we critically examined the taxonomy of the three taxa

perversaria, *subflavaria* and *abstersaria* using morphological characters (wing pattern and genitalia structures), DNA barcodes, and distribution data. Integration of all studied characters confirm the synonymy of the other two taxa with *Peribatodes perversaria*.

Emerald moths of Iran (Geometrinae, Geometridae)

Shamsi Feizpour, Lida Fekrat, Axel Hausmann & Hossein Rajaei

Feizpour, S., Fekrat, L., Hausmann A. & Rajaei, H. 2019. Emerald moths of Iran (Geometrinae, Geometridae). Pp. 320 in: Hausmann, A. & Rajaei, H. (eds). Proceedings of the tenth FORUM HERBULOT 2018 (Stuttgart, Germany, 11–16 June 2018). Spixiana 42 (2).

Shamsi Feizpour (corresponding author), Department of Plant Protection, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Iran; e-mail: shamsifeizpour@gmail.com

The geographical situation of Iran, in contact with the Oriental (or Indo-Malayan) region in the southeast, with the Afrotropical region via Hormuz Strait, the Arabian Peninsula in the southwest and with the Mediterranean in the northern part makes it as one of the most complex Palaearctic faunal regions. Climate change (air warming and drought) along habitat degradation, chemical overpollution and overgrazing are the most critical threats of biodiversity in general and insect fauna in particular. Despite early researches on Iranian fauna of geometrid moths, the fauna of emerald moths is not yet fully known. An integrative taxonomic review of the subfamily Geometrinae was performed based on already collected materials in different collections and freshly collected specimens. Comprehensive morphological examination (includ-

ing type specimens) was analysed along with results of genetic data and zoogeographical considerations.

For the study of morphology the characters of wings, genitalia of male and female were used. For the molecular analysis we used DNA barcodes gathered from legs of available, fresh Iranian specimens. In addition, we compared our molecular data from Iran with DNA barcodes from the rest of the distribution areas. As a result, 36 Geometrinae species are listed for the fauna of Iran (including four new records). Undoubtedly, the lack of data on species distribution data of Lepidoptera of Iran in general makes it difficult to discuss the consequences for habitat conservation. Therefore, we need more samplings in future to fill the gaps.