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**Proceedings of the ninth FORUM HERBULOT 2017.
The geometrids of southern South America:
state of the art – conservation, phylogeny, taxonomy and biodiversity**

(Concepción, Chile, 9–14 January 2017)

Axel Hausmann (ed.)

Hausmann, A. (ed.) 2018. Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1): 117–131.

The ninth FORUM HERBULOT 2017 in Concepción, Chile, focused on the diversity and conservation of Geometridae from South America and other parts of the world, but included interesting aspects on genomic advances and other modern tools and techniques for addressing difficult questions in taxonomy and biodiversity research. New studies, projects and results from lepidopteran research were presented in twenty-one lectures.

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Short report and results

Luis E. Parra & Axel Hausmann

Parra, L. E. & Hausmann, A. 2018. Short report and results. Pp. 117–118 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Altogether 25 participants from 13 countries were registered for the ninth FORUM HERBULOT (see Forum Herbulot 2017, <http://www.herbulot.de/>) and were welcomed at a cultural inauguration ceremony. FORUM HERBULOT 9 was focused on the diversity and conservation of Geometridae from South America and other parts of the world and on genomic advances. Progress was shown which allows to generate DNA barcodes from old type specimens, the use of non-destructive tools for geometrid taxonomy, various aspects of the Centre for Biodiversity Genomics in Guelph, Canada, and the use and the utility of DNA barcodes.

The seven seminary sessions contained twenty presentations on the phylogeny, biogeography, conservation, systematics and taxonomy. The Forum presented new strategies for systematic studies, new taxonomic arrangements in Geometridae, aspects of the Chilean legislation on insect conservation and the use of moths as indicators of environmental changes. Two studies showed progress in the exploration of the microlepidopteran fauna of Southern Australia and Cecidosidae of South America.

Participants of FORUM HERBULOT 9 enjoyed two field trips: An afternoon excursion and nocturnal light collecting on the Peninsula of Hualpén allowed studying the coastal sclerophyllous forest of the cen-



Fig. 1. Participants of FORUM HERBULOT 9 in Concepción, Chile.

tral zone of Chile and its fauna. During a two-days visit to the impressive Cordillera de Chillán (Las Trancas) collecting was possible in the mountainous temperate forests of southern Chilean Andes.

Participants expressed their thanks to the organizers and sponsors of FORUM HERBULOT 9 (2017). The research initiative FORUM HERBULOT was, once again, generally welcomed and the need for, and the advantages of, close scientific cooperation among

geometrid experts were stressed. A proposal to have the next FORUM HERBULOT 10 in Stuttgart, Germany, June 11–16 2018 was generally appreciated. The audience suggested to organize one of the next meetings in Far East Asia.

Here, we present the abstracts of FORUM HERBULOT 9 in order to make the results public to a broader community.

Biodiversity of Geometridae from Chile

Luis E. Parra

Parra, L. E. 2018. Biodiversity of Geometridae from Chile. Pp. 118–119 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). *Spixiana* 41 (1).

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Geometridae is a diverse group of insects with about 23 000 species described. This work presents an updated view of the Chilean geometrids, based on their diversity, distribution, natural history and research needs. The first descriptions of Chilean geometrids date back to the 19th century. Most contributions were published in the second half and towards the end of the twentieth century, mostly provided by Chilean naturalists. So far, 329 species, 111 genera and 5 subfamilies of Geometridae have been described or recorded for the fauna of Chile. *Ennominae* and *Larentiinae* are, by far, the most diverse families. The highest concentration of Lepidoptera

(and Geometridae) is found in central-southern Chile, between 30° and 44° southern latitude and between 800 and 2000 meters a.s.l. on the Cordillera de la Costa and Cordillera de los Andes. 76 % of the species are present in the central zone, 56 % in the southern area and only 13 % in the northern and southernmost areas of the country. Endemic species are concentrated between 33° and 41° latitude. Compared with other regions, the geometrids of Chile constitute a species-poor group; however, it stands out for its high percentage of endemism (ca. 50 %). Regarding their biology, there is scarce data, since we do not know the life cycles, immature stages,

hosts, predators and parasites for an important part of the species diversity. In addition, little is known about their ecological relationships with other species. Future research needs to focus on studies of taxonomy and systematics based on morphology

and molecular data, on natural history, on diversity in non-prospected regions or in natural ecosystems with accelerated deterioration, as well as on the effect of habitat loss, fragmentation, and alteration on species richness, abundance, and distribution.

Biodiversity of the family Geometridae in Argentina

Adriana E. Chalup

Chalup, A. E. 2018. Biodiversity of the family Geometridae in Argentina. Pp. 119 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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The geometrids represent the second most diverse group within the Lepidoptera, with about 23 000 species belonging to eight subfamilies. The family has a worldwide distribution, showing the highest generic diversity in the Neotropical region. Classification of the subfamilies is weakly supported and requires deeper studies to define groups and relations between described taxa. Numerous contributions to the knowledge of the Geometridae of Argentina have been made by different authors in extensive work on the South American fauna and all these have been of great importance, but Louis B. Prout (1910: “On the Geometridae of Argentina”) was the first author who refers to the fauna of Geometridae of Argentina, collecting the necessary material to give rise to the first revision of the family for the country. Based on the above-mentioned work and other authors from Argentina and abroad, a review

is presented of the faunal composition of Argentinian geometrids. So far, in Argentina representatives of the five subfamilies Archiearinae, Desmobjathrinae, Larentiinae, Geometrinae, Ennominae and Sterrhinae have been recorded, Ennominae and Larentiinae being the most diverse subfamilies. The Argentinian geometrid fauna can be assigned to three important biogeographic groups: the “Yungueño”, formed entirely of genera originated from the Bolivian Yungas; “Paranaense”, shares faunistic elements with SE Brazil and Paraguay; and the “Andean-Patagonian” group (Argentine–Chilean region), with a lower species number than the previous ones but with a high percentage of endemic genera.

Prout, L. B. 1910. On the Geometridae of the Argentine Republic. Transactions of the Entomological Society, London 1910: 204–345.

Preliminary remarks of the genus *Iridopsis* (Lepidoptera, Geometridae) on the western slopes of the Andes of northern Chile

Héctor A. Vargas

Vargas, H. A. 2018. Preliminary remarks of the genus *Iridopsis* (Lepidoptera, Geometridae) on the western slopes of the Andes of northern Chile. Pp. 119–120 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Only two species of the New World moth genus *Iridopsis* Warren (Lepidoptera: Geometridae: Ennominae: Boarmiini) have been described from Chile, both have narrow geographic ranges restricted to the arid landscapes of the Atacama Desert: *I. hausmanni* inhabits the coastal valleys, close to the sea level, while *I. parrai* is endemic to the Pampa del Tama-

rugal, at about 1000 m altitude. The two Chilean *Iridopsis* also have narrow host plant ranges: the larvae of *I. hausmanni* feed on leaves of two species of Anacardiaceae (*Haplorhus peruviana* and *Schinus molle*), while the larvae of *I. parrai* feed on leaves of *Prosopis tamarugo* (Fabaceae). In addition, some adults of *Iridopsis* were recently obtained from larvae collected on the western slopes of the Andes of north-

ern Chile at about 3300 m a.s.l. Although male and female genitalia of these specimens are remarkably similar to that of *I. hausmanni*, a definitive taxonomic identification remains uncertain. The main objective

of this work is to provide a preliminary assessment of the taxonomic status of the highland specimens of *Iridopsis* of the Andes of northern Chile based on morphology, host plants, and DNA barcodes.

About biogeographic patterns of Geometridae in Chile

Carlos Zamora-Manzur & Luis E. Parra

Zamora-Manzur, C. & Parra, L. E. 2018. About biogeographic patterns of Geometridae in Chile. Pp. 120 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Large climatic gradients and geographic barriers may generate and facilitate evolution in most taxonomic groups. The biogeographic history of South America includes a series of geological and climatic events that have shaped the diversity patterns of plants, and animals. In southwestern South America, Chile, events such as the rise of the Andes, the appearance of a cold sea current on the coast, the formation of valleys in low latitudes, the fragmentation of the coastal edge and glacial fluctuations along with the formation of lakes in high latitudes contributed to shape the biodiversity patterns currently exhibited by multicellular and even unicellular organisms (Fernández et al. 2016). In Chile, these events also imposed important biogeographical barriers to dispersal of organisms from and to this territory, submitting it to a condition of “insularity” that promoted the appearance of a particular flora and fauna. The moths of the family Geometridae, for instance, exhibit high levels of species richness and endemism in Chile, apparently as a consequence of the above mentioned historical processes. Biogeography can be a powerful tool to explore data on the diversity, phylogeny, and distribution of organisms, to reveal the biological and geographical history of Earth. Comparative biogeography allows establishing the evolutionary history of taxa through their current and historical geographic range and to establish relationships between areas, assessing the taxa that inhabit them and their distribution (Parenti & Ebach 2009). These relationships allow the identification of areas of endemism, which are geographical zones with a unique history, where the biota have evolved according to a set of historical and ecological processes unique of that area. Here, we present the

evaluation of the distribution of Chilean geometrids through different biogeographic methods applied to several spatial scales, including local and regional. The main results were the identification of several areas of endemism throughout Chile through optimal criterion (Szumik et al. 2002, Szumik & Goloboff 2004), associated with important land-geography landmarks such as forest relics, transverse valleys and mountain forests, among others; and an important species richness in the Biobío region and some priority sites for conservation inside this zone (Zamora-Manzur et al. 2011), where the two vegetation types sclerophyll and temperate forest meet.

Fernández, L. D., Fournier, B., Rivera, R., Lara, E., Mitchell, E. A. D., Hernández, C. E. & Xu, X. 2016. Water-energy balance, past ecological perturbations and evolutionary constraints shape the latitudinal diversity gradient of soil testate amoebae in southwestern South America. *Global Ecology and Biogeography* 25: 1216–1227.

Parenti, L. R. & Ebach, M. C. 2009. Comparative biogeography: discovering and classifying biogeographical patterns of a dynamic earth. 312 pp., London, England (University of California Press Ltd).

Szumik, C. A. & Goloboff, P. A. 2004. Areas of endemism: an improved optimality criterion. *Systematic Biology* 53: 968–977.

—, Cuezco, F., Goloboff, P. A. & Chalup, A. E. 2002. An optimality criterion to determine areas of endemism. *Systematic Biology* 51: 806–816.

Zamora-Manzur, C., Parra, L. E. & Jaque, E. 2011. Patrones de distribución de los geometridos de la Región del Biobío, Chile: una aproximación para su conservación. *Revista Chilena de Historia Natural* 84: 465–480.

The *Larentia* of Chile and Argentina: a concise revision (Geometridae, Larentiinae)

Carolina A. Rose-Garrido, Mario I. Ramos-González & Luis E. Parra

Rose-Garrido, C. A., Ramos-González, M. I. & Parra, L. E. 2018. The *Larentia* of Chile and Argentina: a concise revision (Geometridae, Larentiinae). Pp. 121 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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The genus *Larentia* Treitschke, 1825 includes 25 species worldwide (Scoble 1999), most of them occurring in the Palearctic region. Six species are present in southern South America: *L. scarata* (Felder & Rogenhofer, 1875), *L. macerata* (Felder & Rogenhofer, 1875), *L. edmondsii* (Butler, 1882) and *L. lineolaria* (Blanchard, 1852) for Chile, while for Argentina *L. irma* Prout, 1923 and *L. horismata* Fletcher, 1953 are recognized, distributed at the eastern side of the Cordillera de los Andes. This group of species shows a high morphological variation and presents incongruities with respect to the Palearctic concept of *Larentia*, especially at the level of genitalia morphology.

The Chilean and Argentinean *Larentia* species were taxonomically revised and redefined using morphological and molecular phylogenetic approaches: 1) 31 morphology characters derived from external anatomy and genitalia were analysed employing the parsimony criterion; 2) 23 COI gene sequences of *Larentia* and other larentiines were

analysed in a Bayesian framework. The results of the phylogenetic hypotheses suggest the presence of a polyphyletic group, where the Chilean-Argentinean species of the genus *Larentia* do not correspond to this genus and need to be excluded from the tribe Larentiini. Furthermore, we add two new records for the Geometridae fauna of Chile: *L. irma* and *L. horismata*, which are also distributed in the western region of the Cordillera de los Andes and Chilean Patagonia. Based on these results and on morphological structures of their genitalia three new genera and one new species will be proposed in the related, forthcoming paper, completely excluding the presence of the genus *Larentia* in southern South America.

Scoble, M. J. (ed.) 1999. Geometrid moths of the world: a catalogue (Lepidoptera, Geometridae). 1016 pp., London (CSIRO Publishing).

Diversity patterns and integrative analysis (morphology, DNA barcoding) of geometrid moths of western Himalaya

Pritha Dey, Virendra P. Uniyal, Kailash Chandra & Axel Hausmann

Dey, P., Uniyal, V. P., Chandra, K. & Hausmann, A. 2018. Diversity patterns and integrative analysis (morphology, DNA barcoding) of geometrid moths of western Himalaya. Pp. 121–123 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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In many countries, a comprehensive fauna inventory is lacking, particularly in threatened and fragmented landscapes like the Western Himalaya. This prevents effective geographical mapping, understanding their ecology and eventually their conservation in the present situation of habitat degradation reinfused by resource extraction. Integrative analysis of diversity allows the exploration to a scale that is currently not feasible using morphology alone.

Nanda Devi Biosphere Reserve, with an area of 6403 km² and elevation ranges from 1800–7817 m a.s.l., represents the typical physical attributes of the western Himalaya. Collection of moths was done along two different mountain slopes (locations: Joshimath and Lata) across 96 plots between 2000 and 3800 m at every 200 m for 3–4 hours at randomly selected sites starting from dusk. Hourly variation of temperature, relative humidity and wind

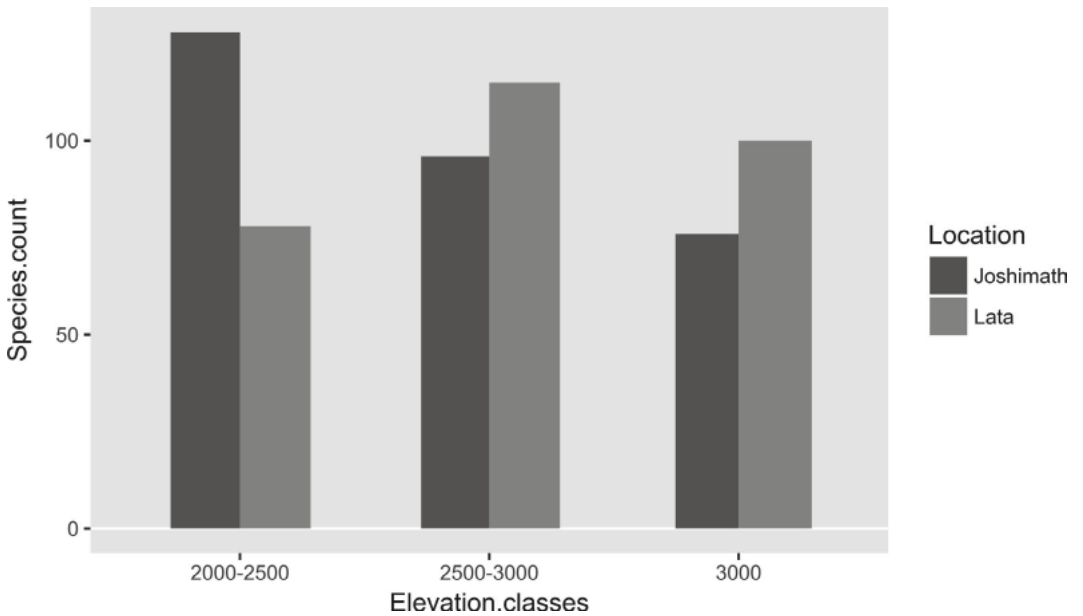


Fig. 1. The graph shows the number of morphospecies at different elevation classes in the two elevational gradients (locations: Joshimath and Lata). Lata gradient showed a higher number of species in the mid-elevational range.

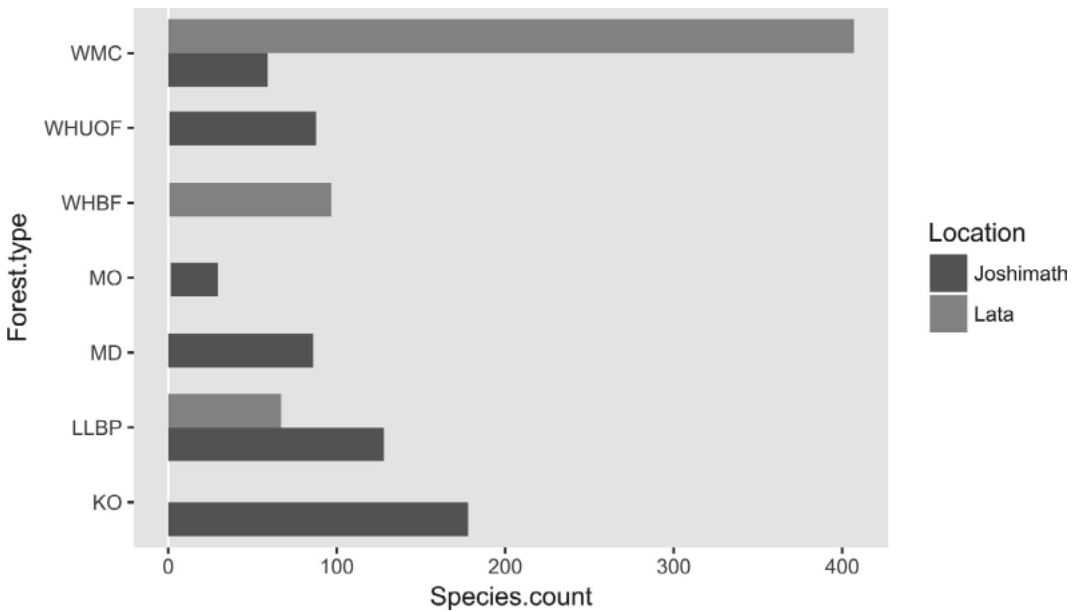


Fig. 2. The distribution of the Geometridae species in different forest types (LLBP = Low Level Blue Pine; MD = Moist Deodar; WMC = Western Mixed Coniferous; MO = Moru Oak; WHUOF = Western Himalayan Upper Oak-Fir; KO = Kharsu Oak; WHBF = Western Himalayan Birch-Fir) in both the gradients. The Western Mix Coniferous forest type held the most number of species attributable to its complex vegetation structure providing more habitats.

speed was recorded. Presence of disturbance signs was noted and vegetation sampling was done in a nested method. The subfamily Ennominae represents the maximum number of species and the subfamily Larentiinae was found to be restricted to higher elevations. Western Mixed Coniferous forest held the maximum number of species (Fig. 1). The species diversity showed differential response to vegetation structure at the two locations. There was a higher number of species in the mid-elevation class (2500–3000 m) in the gradient at Lata (Fig. 2). A negative impact of resource extraction on moth populations was observed. Interestingly, the forest types have more prominent effect in disturbed mountain gradients. The molecular analysis showed that three

species: *Photoscotosia amplicata*, *Loxaspliates obliquaria* and *Electrophaes recta* collected from different habitats and elevation showed significant intraspecific sequence divergence, giving rise to the existence of overlooked, cryptic species, which requires further taxonomic investigation. Two other species, *Perizoma micropunctum* and *Perizoma constricta* collected from different altitudes and habitats show no sequence divergence, suggesting that they are widespread in different altitudes and habitats. The study initiates to build up a DNA reference library allowing molecular identification for future referencing along with habitat-quality assessment programs for conservation management of the landscape.

An integrative approach to understand the biogeography, taxonomy and ecology of the macroheteroceran fauna of the Amanos Mountains in southern Turkey

Feza Can Cengiz, Başak Ulaşlı & Axel Hausmann

Can Cengiz, F., Ulaşlı, B. & Hausmann, A. 2018. An integrative approach to understand the biogeography, taxonomy and ecology of the macroheteroceran fauna of the Amanos Mountains in southern Turkey. Pp. 123 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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In 2014 and 2015, Macroheterocera were collected in three altitudinal transects in the Amanos mountains from 0 up to 1104 m a.s.l. Altogether, 249 specimens were registered. Tissues from 91 selected specimens (42 Noctuidae/Erebidae, 35 Geometridae, 14 others) were submitted to DNA barcoding, partly for identification purposes, partly to investigate zoogeographical questions about the relationships between Anatolian and Levantine populations.

The sequencing was very successful (97 %, only three failures) and revealed to include 81 BINs. Three species (*Eublemma* cf. *gratissima*, Erebidae, 3.4 % from *E. suppuncta*; *Dyspessa* cf. *ulula*, Cossidae, 9.1 % from *D. ulula*; *Cryphia* cf. *ravula*, Noctuidae, 4.7 % from *C. ravula*) may be new for science and require further taxonomical analysis. All of them differ by more than 3.4 % from their nearest neighbours, as currently present on BOLD database. In two other cases (genera *Mythimna* (Noctuidae) and *Zeuzera*

(Cossidae), we found smaller genetic divergences (1.3–2.0 %) from their European relatives, which require further taxonomic investigation. *Geometra papilionaria* (Linnaeus, 1758) and *Macaria notata* (Linnaeus, 1758) (Geometridae), previously only known from the Black Sea region in Turkey, now were reported in the Amanos mountains, thus considerably extending the distribution areas southwards. Moreover, *Lomasipilis marginata* (Linnaeus, 1758) (Geometridae), is possibly new for Turkey as the only previous literature record (Koçak & Kemal 2009) is doubtful as no authentic specimens have been traced. We present several cases where the DNA barcodes helped to clear up zoogeographical patterns.

Koçak, A. Ö. & Kemal, M. 2009. Revised checklist of the Lepidoptera of Turkey. Priamus, Serial Publication of the Centre for Entomological Studies Ankara 17: 117.

On the sclerotizations of the intravincular membrane in Ennomine genera attributed to the tribe Nacophorini

Martin Krüger

Krüger, M. 2018. On the sclerotizations of the intravincular membrane in Ennomine genera attributed to the tribe Nacophorini. Pp. 124 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Nacophorini have proved difficult to define as a monophyletic taxon. It has been proposed that the presence of paired processes of the anellus in the male genitalia serves to characterize the tribes Nacophorini, Lithinini, and Anagogini, as well as the Afrotropical Diptychini (cycad moths), with some morphological and molecular evidence suggesting a relationship of the latter to Old World Nacophorini.

Although a Gondwanan origin has been postulated for the tribe, suggesting present-day diversity results from original vicariance followed by long-time isolation, this scenario is difficult to reconcile with a hypothesized age of Geometroidea of not more than c. 55 Ma based on the fossil record on the one hand side, and estimates for the breakup of Gondwanaland on the other. Recent studies incorporating both molecular and morphological data suggest that Nacophorini *sensu lato* are in fact polyphyletic, and further point at a relationship between Old World (Africa and Australia) Nacophorini, but not of either to the New World forms. Furthermore, Afrotropical Nacophorini as presently defined may themselves be polyphyletic, so further studies involving molecular data in particular from the New World taxa are needed.

Phylogenetic considerations aside, a remarkable feature of the taxa placed in this tribe is that although the male and female genitalia display a marked overall similarity, the sclerotizations of the intravincular membrane in the male are of considerable diagnostic value at genus level, raising the possibility that they may form part of the mate recognition system of the species involved. To illustrate this, the male genitalia of the type species of the 113 genera of Ennominae placed at one time of their taxonomic history in the tribe Nacophorini were examined. Eleven of these (including the type genus *Phaeoura* Hulst (= *Nacophora* Hulst)) occur in the Nearctic Region, 39 in the Neotropical Region, 14 in Africa south of the Sahara and 58 in Australia, with nine genera inhabiting both parts of the New World. Between them these genera include a total of 638 valid species.

Despite their remarkable diversity, the various modifications of the anellus (*juxta*) observed may be grouped into a limited number of categories, an overview of which is presented. Although several of these occur in more than one zoogeographical region, there is no concomitant similarity in adult habitus, suggesting they evolved independently.

New findings from the micro-moth fauna of Southern Australia

Andy Young

Young, A. 2018. New findings from the micro-moth fauna of Southern Australia. Pp. 124–125 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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We have been researching the micro-moth fauna of southern Australia. The most significant finding was the discovery of the new monotrysian moth family, the Aenigmatineidae, in the form of the new species *Aenigmatinea glatzii*. It was discovered on Kangaroo Island, off the southern coast of South Australia. Molecular tools were used to elucidate the position of the family, in combination with detailed morphological analysis.

Our work with *Aenigmatinea* has demonstrated that transcriptome sequencing is an efficient method for generating many gene sequences, enabling us to resolve older splits, including up to superfamily level. In the *Aenigmatinea* study, we used a combination of PCR to amplify two conserved genes and transcriptome sequencing to obtain a further 14 nuclear genes. The combined data set (19512 bp in total) allowed us to place the new family Aenigmatineidae amongst the Glossata (or 'tongue moths'), as

a sister group to the Neopseustidae, and forming a clade which is sister to all Heteroneura, the vast majority of known Lepidoptera.

Our second discovery was that of the association between a newly discovered genus within the Australian Heliozelidae (Adeloidea) with the pinnate-leaved species in section *Boronia* of the genus *Boronia* (Rutaceae). Both are involved in an obligate-mutualism, with exclusive pollination of the *Boronia* species flowers on the one hand and with the moth entirely dependent on their host for their early life stage biology on the other. – Within the rest of the Lepidoptera, the only similar obligate-mutualism is found within the sister family of the Heliozelidae, the Prodoxidae (*Tegeticula* sp.), which are the sole pollinators of the North American *Yucca* (Asparagaceae) species. Pollination by these ‘*Boronia* moths’ is enacted by the use of an organ on the abdomen of the female moth during oviposition. We have found that a second genus of related ‘opportunistic’ moths has arisen from the *Boronia* pollinators. They lay their eggs into the fertilised *Boronia* flowers. The presence of both pollinator and opportunist species mirrors

the biology of the Prodoxidae genera, *Tegeticula* and *Parategeticula*. Around 50 species of these ‘*Boronia* moths’ are in the process of being described as a result of our ongoing work.

We have been constructing both higher level and genus-group specific phylogenies of the Australian Heliozelidae. Initially we produced a preliminary phylogeny of Heliozelidae using two mitochondrial (COI and COII) and two nuclear genes (28S and H3). We sequenced a number of specimens from most Heliozelidae genera, including several undescribed genera we have discovered in Australia. This phylogeny resulted in a number of strongly supported clades, with clear separation between most Australian and northern hemisphere groups. However, this phylogeny did not resolve the older, higher level relationships between the clades. To address these issues, we have comprehensively collected fresh specimens from across the Australian Heliozelidae genera. We are in the process of using these to generate full transcriptomes. Our aim is to use transcriptome data to produce a well-resolved phylogeny of the Heliozelidae.

Fluctuating asymmetry and morphological consequences of a host shift in the Neotropical moth *Macaria mirthae* (Lepidoptera, Geometridae)

Hugo A. Benítez

Benítez, H. A. 2018. Fluctuating asymmetry and morphological consequences of a host shift in the Neotropical moth *Macaria mirthae* (Lepidoptera, Geometridae). Pp. 125 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Phytophagous insects are excellent model organisms to study the genetic and ecological components of adaptation and morphological divergence, because their host plants are one of the main environmental factors influencing their early life stages. Although many lepidopterans are highly specialized in their host use, shifts to exotic plants have been reported for some species. *Macaria mirthae* is a native moth from Northern Chile that feeds preferentially on the Fabaceae species *Acacia macracantha*, however due to habitat loss a recent host shift to the introduced fabacean *Leucaena leucocephala* has been observed. We have studied the impact that different host plants have on the developmental instability levels in the moth wing morphology evaluating fluctuating asymmetry (FA) and directional asymmetry (DA). FA measures the small random deviations existing between the left and right sides of bilaterally sym-

metrical traits and it is widely used as a biomonitor of environmental quality. Our results confirmed the presence of FA in *Macaria mirthae* forewings by applying geometric morphometric techniques. Furthermore, we found that the individuals feeding on the endemic tree (*Acacia macracantha*) showed marked DA levels, while the specimens inhabiting the exotic plant (*Leucaena leucocephala*) did not. The absence of DA in the individuals occupying the exotic plant is striking, because it has been established that this asymmetry pattern is widespread among insect wings. This phenomenon could be related to the influence of *L. leucocephala* on normal wing development. Despite the reduced quality of *L. leucocephala* as host plant, its wider presence in the Azapa valley (Chile) could explain the host shift made by *M. mirthae*.

Insect conservation in Chile. RECEC, actions and challenges

Viviane Jerez

Jerez, V. 2018. Insect conservation in Chile. RECEC, actions and challenges. Pp. 126 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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The Fifth Informe Nacional de Biodiversidad (2014) of the Ministerio del Medio Ambiente (MMA) recognizes for Chile a total of 30 600 species. Of these, 2036 spp. are vertebrates and 17 502 spp. invertebrates, of which 10 254 spp. are insects and represent 33 % of the total biodiversity described for the country. From the biological point of view, it is relevant to conserve the insects of our country, since this biota in general presents a high degree of endemism, restricted geographical distribution ranges and a large number of monotypic genera. Chilean legislation has now developed the “Reglamento de Clasificación de Especies Silvestres” according to its State of Conservation (CER), which establishes the risk of extinction of species or populations according to the criteria proposed by the International Union for the Conservation of Nature (IUCN, 2004). This led to the creation of the “Red Chilena Entomológica de la Conservación” (RECEC), with the objective of proposing a work methodology to incorporate insect species in accordance with the CER and Decree Supreme No.

29/2011 of the MMA. The first landmark for the conservation of insects in Chile is the incorporation of *Gyriosomus granulipennis*, “vaquita of the Choros Island” declared Vulnerable (VU). From this event to date, RECEC has categorized 39 species of insects of the orders Odonata (1 species), Plecoptera (2 species), Orthoptera (2 species), Hymenoptera (3 species), Mecoptera (1 species), Lepidoptera (2 species) and Coleoptera (28 species) that are under some degree of threat (<http://www.mma.gob.cl/clasificacionespecies/>). In the case of Lepidoptera, only two species were classified in 2015 according to the CER: *Castnia eudesmia* Gray, 1838 (Castniidae) and *Microdulia mirabilis* (Rothschild, 1895) (Saturniidae) both in the Near Threatened (NT) category. The future challenge is to continue incorporating species of Lepidoptera to the list of threatened species, to make known the threatened insects and to generate scientific knowledge on the subject.

IUCN 2004. The IUCN red list of threatened species. Version 2004, <http://www.iucnredlist.org>

Nocturnal Lepidoptera as ecological indicators in a forest landscape of Chile

Patricia A. Bocaz

Bocaz, P. A. 2018. Nocturnal Lepidoptera as ecological indicators in a forest landscape of Chile. Pp. 126–127 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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In their different stages, the Lepidoptera present close relationships with their host plants. This gives them great importance at an ecological and environmental level. Several studies carried out in tropical forests recognize them as ecological indicators. However, in southern temperate forests, attention has been lower, even more so in the forests of southern South America. In Chile there is a high degradation of the natural forests, restricting them to isolated and fragmented areas that subsist only because they are under the protection of the National Service of Protected Areas of the State (SNASPE), surrounded by large plantations of exotic forest species for commercial purposes.

For this reason, my study was focused on investigating the distribution of nocturnal moth diversity in a forest landscape, where the habitats frequented by this group of insects present a gradient of disturbance. The aim of my study was to select species or assemblages as ecological indicators, that allow monitoring changes in the forest landscape over time.

In a 16 000 ha large forest landscape including single large continuous natural forest habitats (Nonguen National Reserve), we investigated ten forest fragments, and ten plantations of *Eucalyptus globulus*. Richness (number of species) and abundance (number of individuals per species) of nocturnal moths were assessed using light traps in 21 sites. Traps were

active at night during one week in November 2006, January and March 2007, and in the same way and the same months from November 2007 to March 2009.

Through Bray Curtis and Jaccard matrix, we performed the univariate and multivariate analysis and community parameters using Permanova analysis (Primer-E program) of different habitats, months and years of collecting, to determine if there are differences in richness and abundance of moths in various habitats. Richness and abundance showed significant differences ($p < 0.0001$), as also the different months ($p < 0.0001$), but there was no difference between years of sampling ($p < 0.1540$) for species richness and ($p < 0.1460$) for abundance. Both parameters (richness and abundance) were higher in the natural forest compared to plantations.

In addition, using presence and absence matrices, nesting analysis was performed using the NODF program to determine the identity and occurrence of the species in the study sites, according to the landscape variables (distance and area of the sites

with relation to the position and area of the Nonguén National Reserve, as original habitat).

Based on the observed differences in moth diversity and the identity of the species in the different sites along the disturbance gradient, the selection of species can be monitored over time. Most informative are species which are present in most places, in my study these were 18 species for the family Geometridae, 4 species for Saturniidae, and one species each for Lasiocampidae and Noctuidae, all these being native species. These species were present in all the three years of my study.

These results provide a taxonomic and statistical framework for monitoring the forest landscape of the Biobio region, Chile, represented by the Nonguén National Reserve, where the last fraction of the Coastal Deciduous Forest is protected. These results can be transformed into a useful tool for the management of both native and managed forests, for the benefit of conservation and ecological restoration.

Dyspteridini: a widespread and ancient lineage of geometrid moths (Lepidoptera, Geometridae)

Erki Õunap

Õunap, E. 2018. Dyspteridini: a widespread and ancient lineage of geometrid moths (Lepidoptera, Geometridae). Pp. 127 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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The tribe Dyspteridini is a lineage of geometrid moths, which is sister to all other members of the subfamily Larentiinae. According to the current knowledge, the American genus *Dyspteris* comprising more than 20 species is the most species-rich group of Dyspteridini. Monotypic genera *Paradetis* from New Zealand and *Celonoptera* from southern Europe have been associated with *Dyspteris* on the basis of molecular and morphological evidence, respectively. A phylogenetic analysis based on

7000 bp of molecular data from mitochondrial and nuclear loci revealed that Dyspteridini are much more widespread than previously thought, as they comprise few additional genera of geometrid moths from eastern Asia and Africa. Divergence time analysis indicates that Dyspteridini have diverged from other larentiines more than 45 million years ago, i.e. approximately at the same time as subfamily Archiearinae branched off from the lineage comprising subfamilies Ennominae and Geometrinae.

Current research on Australian Geometridae – blitzing the Australian outbreak and the relationships of the Australian satin moths

Catherine Byrne

Byrne, C. 2018. Current research on Australian Geometridae – blitzing the Australian outbreak and the relationships of the Australian satin moths. Pp. 127–128 in: Hausmann, A. (ed.). Proceedings of the ninth FORUM HERBULOT 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Research on the Australian Geometridae over the last five years has been dominated by the Bush Blitz project, which organises field work and surveys of plants and animals in remote, under-surveyed areas of Australia. The two main aims of this project are to document the biodiversity of Australia and species discovery. Here I will discuss the findings of the last three ‘blitzes’ in Tasmania and the impact these have on our knowledge of the Australian Geometridae.

In the second part of my presentation I will discuss my current research on the systematics of the Australian Geometridae. The satin moths (*Thalaina*) are an iconic and widespread genus of geometrids in Australia. My latest revision will name a new species, confirmed by DNA barcoding, provide information on immature stages, and discuss evolutionary trends in wing pattern in this group. Finally, I will provide an update on the Tasmanian Archiearinae.

Preliminary insight into the phylogeny of South American Larentiinae (Geometridae)

Andro Truuverk & Erki Õunap

Truuverk, A. & Õunap, E. 2018. Preliminary insight into the phylogeny of South American Larentiinae (Geometridae). Pp. 128 in: Hausmann, A. (ed.). Proceedings of the ninth Forum Herbulot 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Modern advances in molecular phylogenetics have significantly improved the understanding of the tribe-level classification of the subfamily Larentiinae. Despite the few relatively comprehensive studies been published during recent years, the immense diversity of South American larentiines has unfortunately been largely overlooked. Specifically, only very few species from this large continent have been included in earlier studies. Hereby we demonstrate preliminary results of possible tribal-group placements of 31 South American larentiine species. Altogether, DNA sequences of more than 100 species were included into the analysis, covering all known tribes. Sequence data from one mitochondrial (CO1)

and eight nuclear genes (EF-1 α , RpS5, CAD, MDH, GAPDH, IDH, WGL, D1-D2 (28S)) were used. Length of the data matrix was 7113 bp. Data were analysed by Bayesian phylogenetic method using program MrBayes and by maximum likelihood using RAxML. According to earlier expectations, many of the analysed South American larentiines clustered into tribes (Euphyiini, Xanthorhoini, Larentiini sensu lato and Stamnodini) considered valid in most recent treatments of Larentiinae. Nevertheless, phylogenetic placement of most of the South American species does not allow them to associate with known tribes comfortably.

Recent progress in museomics allows to generate DNA barcodes from old type specimens and helps to realize the ‘mega-revision’ of African *Prasinocyma* (Lepidoptera, Geometridae)

Axel Hausmann

Hausmann, A. 2018. Recent progress in museomics allows to generate DNA barcodes from old type specimens and helps to realize the ‘mega-revision’ of African *Prasinocyma* (Lepidoptera, Geometridae). Pp. 128–129 in: Hausmann, A. (ed.). Proceedings of the ninth Forum Herbulot 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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For a secure identification of the known biodiversity (described species and synonyms) we essentially need to base on the type specimens. We studied and photographed the type material (with the related genitalia slides) of almost all described taxa (134 species, subspecies, synonyms) of the Afrotropical

representatives of the genus *Prasinocyma*. Nevertheless, certain problems persist to attribute recent collection material to the types because of (1) the great external similarity of most taxa, (2) similar structures in the internal reproductive organs (esp. in females) in several supposed species-complexes (3) the types

exclusively belonging to the opposite sex or (4) unclear situations which females and males belong to the same species (even within the type series).

DNA barcoding of old type material helps to overcome these problems (Hausmann et al. 2016a). With the development of new, NGS-based sequencing techniques and new lab protocols in the CCDB (Guelph), we were able to get DNA sequences for the vast majority of *Prasinocyma* type specimens from NHMUK (London) and ZSM (Munich). Combination with the currently available 716 DNA barcodes from recently collected African *Prasinocyma* specimens reveals the existence of 227 genetic clusters (hypothesized species) in this section of our study material. Our vision for the future is to put taxonomy on a solid basis by fostering programs for DNA barcoding of all type specimens in Natural History museums.

Micro-CT: the use of non-destructive tools for geometrid taxonomy

Julia Wildfeuer & Axel Hausmann

Wildfeuer, J. & Hausmann, A. 2018. Micro-CT: the use of non-destructive tools for geometrid taxonomy. Pp. 129 in: Hausmann, A. (ed.). Proceedings of the ninth Forum Herbulot 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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The world catalogue of Scoble (1999) listed 94 described species for the taxonomically difficult genus *Prasinocyma* Warren, 1897 (Lepidoptera, Geometridae) in the Afrotropical region. In a few recent studies, we could raise the species number to 118. However, genitalia dissections and DNA barcodes of the comprehensive African material at the Bavarian State Collection of Zoology, Munich (ZSM) suggested the existence of at least 100 additional species, which we aim to describe in the near future. The identification of the known biodiversity (described species and synonyms) was based on type photographs and genitalia dissection of type specimens as well as on DNA barcodes from type specimens.

The goal of the present study was to test how new approaches and modern techniques can foster integrative revisions in particularly large and difficult cases. For the study of morphology, we combined

Hausmann, A., Miller, S. E., Holloway, J. D., deWaard, J., Pollock, D., Prosser, S. W. J. & Hebert, P. D. N. 2016a. Calibrating the taxonomy of a megadiverse insect family: 3000 DNA barcodes from geometrid type specimens (Lepidoptera, Geometridae). Genome 59 (9): 671–684. doi:1139/gen-2015-0197

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Scoble, M. J. 1999. Geometrid moths of the world: a catalogue (Lepidoptera: Geometridae). 2 vols: i–xxv, 1–482, 483–1016, index 1–129.

‘conventional’ morphological approaches with the three-dimensional Micro-CT-scanning. We show that Micro-CT scans (1) can provide similar information as ‘conventional’ genitalia dissections, (2) thus can render integrative taxonomic revisions minimally invasive and (3) allow three-dimensional analyses. Since Micro-CT-scanning is still time-consuming, we recommend “in situ” screen-diagnosis of the genitalia, and limitation of further digital processing to holotypes including the comparison with a dissected paratype. The Micro-CT image data should be deposited in appropriate databases for potentially being used for identification purposes and/or further digital processing.

Scoble, M. J. 1999. Geometrid moths of the world: a catalogue (Lepidoptera: Geometridae). 2 vols: i–xxv, 1–482, 483–1016, index: 1–129.

The Centre for Biodiversity Genomics: ongoing projects and recent advances

Jeremy R. deWaard

deWaard, J. R. 2018. The Centre for Biodiversity Genomics: ongoing projects and recent advances. Pp. 130 in: Hausmann, A. (ed.). Proceedings of the ninth Forum Herbulot 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Fully comprehending the systematics of large faunas – such as the Geometridae of the Neotropical region – will undoubtedly require an ‘integrative taxonomic’ approach to allow its timely and accurate completion. For over a decade, the Centre for Biodiversity Genomics (CBG; www.biodiversitygenomics.net) in Guelph, Canada has been developing the tools and workflows to facilitate this integrative framework. Three ongoing projects illustrate the resources being created, as well as some recent advances that have transformed their efficiency, sensitivity, or universality.

Firstly, the DNA barcode reference libraries being constructed through the All-Leps and related campaigns (www.ibol.org) have been successful through a combination of targeted sampling at museums and field collections of fresh material. Nearly 170 000 specimens have been processed from collaborating natural history collections, and over three million specimens have been amassed in the field and subsequently barcoded and vouchered at CBG. As a result, significant progress has been made in completing DNA reference libraries: for global Lepidoptera, 96 % of the 131 families and 76 % of the 11 669 genera have been successfully barcoded; for the Lepidoptera of North America, 77 % of the 12 763 species are barcoded; and for the Noctuoidea of North America, 97.5 % of the 3671 species have now been barcoded (Zahiri et al. 2017).

Secondly, the Global Malaise Trap Program (www.globalmalaise.org) is uniting mass trapping with barcode-based identifications to begin acquiring detailed temporal and spatial information on terrestrial arthropod communities across the globe. As of January 2017, a total of 1262 week-long Malaise trap samples from 44 sites in 27 countries have been processed in their entirety. These have resulted in 1.03 M arthropod specimens analysed, of which 860 000 have generated barcode sequences that permitted Barcode Index Number (BIN) assignment. The composition and distribution of the 107 000 BINs detected have revealed interesting insights into current estimates of global insect species (Hebert et al. 2016) and temporal succession (Geiger et al. 2016).

And lastly, the retrieval of barcodes from degraded sources of DNA has dramatically improved

at CBG due to the integration of high-throughput sequencing (HTS) platforms. The massive output and increased sensitivity offered by HTS is permitting successful analysis of primary types over a century old (e.g. Hausmann et al. 2016), as well as from formalin-fixed and ethanol-preserved specimens. Experiments comparing these new approaches to Sanger-based methods show a 5–20 fold increase in the number of recovered barcode sequences with HTS (Prosser et al. 2016). Furthermore, while increased sample age has a strong negative affect on barcode recovery via Sanger analysis, the HTS-based approach recovers long barcodes regardless of age. These methods show significant promise for unlocking the three billion authoritatively identified specimens in the world’s natural history museums; these will be essential for constructing comprehensive DNA barcode reference libraries for the global fauna and an integrative framework for diagnosing and discovering species.

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High-throughput methods for DNA barcoding: from reference libraries to environmental applications

Evgeny V. Zakharov

Zakharov, E. V. 2018. High-throughput methods for DNA barcoding: from reference libraries to environmental applications. Pp. 131 in: Hausmann, A. (ed.). Proceedings of the ninth Forum Herbulot 2017. The geometrids of southern South America: state of the art – conservation, phylogeny, taxonomy and biodiversity (Concepción, Chile, 9–14 January 2017). Spixiana 41 (1).

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Once criticized for its overly simplistic view of molecular evolution, DNA barcoding has become a universally-accepted approach for species identification and discovery and is now part of the United Nations strategic plan for enhancing and protecting biodiversity (UNEP/CBD/COP 2016). The effectiveness of DNA barcoding and its applications depends on the availability of comprehensive reference libraries that meet prescribed standards (Ratnasingham & Hebert 2007). Assembling barcode libraries on a large scale requires deployment of analytical methods that perform equally well across diverse groups of organisms (Hajibabaei et al. 2005). These analytical protocols and standards for conventional, specimen-centric and Sanger-based, DNA barcoding were developed for the International Barcode of Life Project – the largest initiative ever undertaken in biodiversity genomics, and its greatest accomplishment to date – a DNA barcode library that now exceeds 5 million records representing more than 500 000 species of animals, plants, and fungi. However, the strength of conventional DNA barcoding is also its weakness and it stems from the oversimplification of the definition of a specimen. Besides their own DNA, organisms often carry a genetic fingerprint of their environment such as traces from their diet, symbionts, or even the substrate they inhabit. Because of the technological limitations of the conventional workflows, secondary sources of DNA in a sample are considered unwanted artefacts or contaminants, occasionally casting doubts on the authenticity of the barcode sequence. The use of next-generation

sequencing for metabarcoding transforms these limitations into value-added data by permitting simultaneous detection of multiple genetic targets, thus allowing a more holistic understanding of an ecosystem by including other domains of life. We demonstrated the capacity of NGS-based barcode analysis of mixed arthropod samples to expose non-arthropod diversity of the sampled habitat. Furthermore, combining this approach with multiplex DNA labelling allows the untangling of species interactions with unprecedented accuracy and scale. Finally, by pairing these capabilities with single molecule third-generation sequencing we are removing barriers that limited the adoption of high-throughput sequencing for large-scale DNA barcoding (Hebert et al. 2018).

13th Conference of the Parties to the Convention on Biological Diversity 2016. UNEP/CBD/COP/Decision XIII/31.

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