

VOL. 7, Issue 1

March 2017



A newsletter for geometrid specialists

FORUM HERBULOT NEWSLETTER

Proceedings of the IX Forum Herbulot

The IX Forum Herbulot with 27 participants 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 and different aspects of the Centre for Biodiversity Genomics in Guelph, Canada, and the use and the utility of the DNA barcodes.

The 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 IX Forum Herbulot enjoyed two field trips: An afternoon excursion and nocturnal light collecting on the Peninsula of Hualpén allowed studying the coastal sclerophyllous forest of the central 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 Chile.

For those Herbulotians who could not attend Forum Herbulot IX, this Newsletter contains the welcome letter, program, abstracts, list of participants and some photos of the meeting.

Luis Parra, Axel Hausmann



The Forum Herbulot Newsletter appears irregularly one or several times per year and will be posted on the Forum Herbulot webpage www.herbulot.de. Old issues can be accessed there. Membership in the

Forum Herbulot initiative is free.

For more information contact Axel Hausmann: Axel.Hausmann@zsm.mwn.de or,

Hossein Rajaei: hossein.rajaei@smns-bw.de

Welcome / willkommen / karşılama teretunud / dobrodošli / bienvenidos

The Organizing Committee of the 9th Forum Herbulot of the Department of Zoology and the Facultad de Ciencias Naturales y Oceanográficas of the Universidad de Concepción, is pleased to extend a warm welcome to our colleagues and entomologist friends.

This is the first time that the Herbulot Forum takes place in Latin America and in a country that is constantly being affected by natural disasters, as it has been with the last earthquakes and volcanic eruptions. But still, it is interesting to visit a country like Chile. Benjamin Subercaseaux in his book "Chile or a crazy geography" describes a country full of contrasts that is often difficult to find elsewhere in the world ... its diverse climates, vegetative floors, natural history, etc ... makes it a true natural laboratory suitable for the studies of biota.

This is because the biotic resources that inhabit the Chilean territory are the result of a joint action of a diversity of natural modeling forces that, in the past, produced strong oscillations and profound changes in the physiognomy of the landscapes. This geological dynamics has constituted a powerful evolutionary force, which has alternately received tropical and temperate influences. This explains the coexistence of species of both origins, especially in the central zone of the country. Our territory, due to its configuration, presents a great diversity of physical environments, with varied combinations of climate and soils. Despite this, the biological diversity is moderate due to the insular nature of the territory and the relative isolation given by the important natural barriers. This explains the strong endemism of the current flora and fauna. For example in Lepidoptera it is estimated that, at the species level, endemism can reach about 50 percent (including the Geometridae), with a great number of species restricted mainly to the central area of the country and oceanic islands.

All of this makes Chile of special interest for scientific study and, here we are ... I imagine that you are also very interested in our moths coming from so far to be present at the IX Forum Herbulot, here in Concepcion, Chile.

We hope to not defraud your expectations. The effort that has been made in the coordination and organization of this meeting has been truly rewarding and now is fully compensated with your presence. We will have five days to share our experiences and activities in the study of geometrid and other Lepidoptera, which will undoubtedly be extremely enriching and exciting.

We must not forget the active participation of young students, from whom we wish to listen to their experiences with this group of animals, many just starting in this exciting and broad field of science.

to be continued...



Geometrids of the temperate forests of southern Chile and Argentina, characterized by a long history of geographic isolation, resulting in the presence of taxa with high levels of endemism, relict and / or retained ancestral characters¶

This reflects that entomology, and the study of Lepidoptera, is an important area of our academic work and so we must continue to support young people in this type of activities.

Dear friends, once again welcome to the 9th Forum Herbulot, we would like the University of Concepción to be a symbol of fraternity, friendship, a center of scientific enrichment for all of you and that all the academic and professional expectations of this event should be fulfilled.

Finally, all we want to wish you is a pleasant stay in the city of Concepcion and that you all enjoy this meeting.

Luis E. Parra
President Organizing Committee
IX Forum Herbulot
Concepción, January 2017



IX Forum Herbulot

9 – 14 January, 2017

Universidad de Concepción, Concepción - CHILE



<http://www.herbulot.de/> - <http://www.geometridosdechile.cl/forum-herbulot-2017/>

Program

Monday, January 9, 2017

Arrivals, Transfers.

17:00 – 18:00 hrs. Registration in Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción

18:00 hrs. Inauguration Ceremony (Auditorium Claudio Gay)- Welcome Cocktail

Tuesday, January 10, 2017 (Auditorium Jaime Baeza-EMPREDUC)

Morning plenary session 1: "The geometrids of southern South America: State of the Art"

09:00 hrs. Luis E. Parra. BIODIVERSITY OF GEOMETRIDAE FROM CHILE

09:20 hrs. Adriana Chalup. BIODIVERSITY OF THE FAMILY GEOMETRIDAE IN ARGENTINA

09:40 hrs. Héctor A. Vargas. PRELIMINARY REMARKS OF THE GENUS *IRIDOPSIS* (LEPIDOPTERA: GEOMETRIDAE) ON THE WESTERN SLOPES OF THE ANDES OF NORTHERN CHILE

10:00 hrs. Carlos Zamora-Manzur & Luis E. Parra. MAJOR BIOGEOGRAPHIC PATTERNS OF GEOMETRIDAE IN CHILE

10:30 hrs. Coffee break

11:00 hrs. Carolina Rose, Mario Ramos-González & Luis E. Parra. THE *LARENTIA* OF CHILE AND ARGENTINA: A CONCISE REVISION (GEOMETRIDAE: LARENTIINAE)

Morning plenary session 2: "Geometrids and other Lepidoptera of the World"

11:20 hrs. Pritha Dey, V.P. Uniyal, Kailash Chandra & Axel Hausmann. DIVERSITY PATTERNS AND INTEGRATIVE ANALYSIS (MORPHOLOGY, DNA BARCODING) OF GEOMETRID MOTHS OF WESTERN HIMALAYA

11:40 hrs. Feza Can Cengiz, Başak Ulaşlı & Axel Hausmann. AN INTEGRATIVE APPROACH TO UNDERSTAND THE BIOGEOGRAPHY, TAXONOMY AND ECOLOGY OF THE MACROHETEROCERAN FAUNA OF THE AMANOS MOUNTAINS IN SOUTHERN TURKEY

13:00 hrs. Lunch break

Afternoon plenary session 1: "Geometrids and other Lepidoptera of the World"

15:00 hrs. Martin Krüger. ON THE SCLEROTIZATIONS OF THE INTRAVINCULAR MEMBRANE IN ENNOMINE GENERA ATTRIBUTED TO THE TRIBE NACOPHORINI

15:20 hrs. Andy Young. NEW FINDINGS FROM THE MICRO-MOTH FAUNA OF SOUTHERN AUSTRALIA

15:40 hrs. Silva, Gabriela T.; Parra, Luis E., Vargas, Héctor A., Mundaca, Enrique, San Blas, Germán, Goncalves, Gislene L. & Moreira, Gilson R. P. CECIDOSIDAE OF CHILE: BIOLOGY AND GEOGRAPHIC DISTRIBUTION

16:00 hrs. Coffee break

Afternoon plenary session 2: "Geometrids and other Lepidoptera of the World"

16:30 hrs. Hugo A. Benítez & Héctor A. Vargas. LEFT-RIGHT ASYMMETRY AND MORPHOLOGICAL CONSEQUENCES OF A HOST SHIFT IN THE OLIGOPHAGOUS NEOTROPICAL MOTH *MACARIA MIRTHAE* (LEPIDOPTERA: GEOMETRIDAE).

20:00 hrs. Social event / Congress dinner

Wednesday, January 11, 2017 (Auditorium Jaime Baeza-EMPREDUC)

Morning plenary session 3: "Conservation of geometrid moths"

09:30 hrs. Viviane Jerez. INSECTS CONSERVATION IN CHILE. REEC² ACTIONS AND CHALLENGES

09:50 hrs. Patricia Bocaz. NOCTURNAL LEPIDOPTERA AS ECOLOGICAL INDICATORS IN A FOREST LANDSCAPE OF CHILE

10:10 hrs. Coffee break

Morning plenary session 4: "Phylogeny and taxonomy of Geometridae"

10:30 hrs. Erki Öunap. DYSPTERIDINI: A WIDESPREAD AND ANCIENT LINEAGE OF GEOMETRID MOTHS (LEPIDOPTERA: GEOMETRIDAE)

10:50 hrs. Catherine Byrne. CURRENT RESEARCH ON AUSTRALIAN GEOMETRIDAE – BLITZING THE AUSTRALIAN OUTBACK AND THE RELATIONSHIPS OF THE AUSTRALIAN SATIN MOTHS.

11:10 hrs. Andro Truuerk & Erki Öunap. PRELIMINARY INSIGHT INTO THE PHYLOGENY OF SOUTH AMERICAN LERENTIINAE (GEOMETRIDAE) i

13:30 hrs. Lunch break

16:00 – 23:00 hrs. Trip to Parque Hualpén, Comuna Hualpén, 11 kms of Concepción (collecting near the sea in sclerophyllous forest)



From the left to the right: Axel Hausmann, Luis Parra (organizers) with wife Edilia Jaque

Thursday, January 12, 2017 (Auditorium Jaime Baeza-EMPREDUC)

Morning plenary session: "GENOMICS"

09:30 hrs. Axel Hausmann. 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)

09:50 hrs. Julia Wildfeuer & Axel Hausmann. MICRO-CT: THE USE OF NON-DESTRUCTIVE TOOLS FOR GEOMETRID TAXONOMY

10:10 hrs. Jeremy deWaard. THE CENTRE FOR BIODIVERSITY GENOMICS: ONGOING PROJECTS AND RECENT ADVANCES

10:30 hrs. Coffee break

11:00 hrs. Evgeny V. Zakharov. HIGH-THROUGHPUT METHODS FOR DNA BARCODING: FROM REFERENCE LIBRARIES TO ENVIRONMENTAL APPLICATIONS

11:20 hrs. Hossein Rajaei & Axel Hausmann. WELCOME MESSAGE FOR THE TENTH FORUM HERBULOT IN STUTTGART (GERMANY)

11:40 hrs. Final discussions, Date and venue of FH 2019

13:00 hrs. Lunch break

15:30. hrs Transfer to Termas de Chillán (Las Trancas, Cordillera de Los Andes)

19:30 hrs. Dinner

21:00 hrs. Collecting

Friday, January 13, 2017

08:00 hrs. Breakfast

09:00 hrs. Safari Tour "Reserva Ñuble"

19:30 hrs. Dinner

21:00 hrs. Collecting

Saturday, January 14, 2017

09:00 hrs. Transfers to Concepción



Group photo in the Parque Hualpén

List of participants – IX FH - 2017

Name	Address
1. Adriana Chalup	Instituto Miguel Lillo, Universidad Nacional de Tucumán, Argentina; adriana.chalup@yahoo.com.ar
2. Alfred Moser	Associate researcher, area of Zoology, Insects, UFRGS, (Universidade Federal do Rio Grande do Sul) Porto Alegre, Brazil; a.moser@ensinger.com.br
3. Andro Truuverk	Department of Zoology, Chair of Entomology, University of Tartu, andro.truuverk@ut.ee
4. Andy Young	Kangaroo Island, Australia del Sur; dayoung@adam.com.au
5. Axel Hausmann	Bavarian State Collection of Zoology; axel.hausmann@zsm.mwn.de
6. Carlos Zamora-Manzur	Depto. de Zoología, Universidad de Concepción, Concepción; carzamora@gmail.com
7. Catherine Byrne	Tasmanian Museum and Art Gallery, Department of State Growth; Catherine.byrne@tmag.tas.gov.au
8. Daniel Bolt	Amt für Natur und Umwelt Graubünden, Schiers – Switzerland; bolt.dani@bluewin.ch ; Daniel.Bolt@anu.gr.ch
9. Erki Öunap	Institute of Ecology and Earth Sciences, University of Tartu – ESTONIA; erki.ounap@ut.ee
10. Evgeny Zakharov	Director, Canadian Centre for DNA Barcoding, Centre for Biodiversity Genomics, Biodiversity Institute of Ontario- Canada; zakharov@uoguelph.ca
11. Feza Can Cengiz	Mustafa Kemal University , Faculty of Agriculture, Plant Protection Dept.; cezafan_onurcan@hotmail.com
12. Mario Galov	Croatian Natural History Museum, Department of Zoology
13. Gabriela Thomaz	Departamento de Zoologia, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brasil; gabi_thomaz@hotmail.com
14. Héctor A. Vargas	Facultad de Agronomía, Universidad de Tarapacá, Arica; havargas@uta.cl
15. Hermann Staude	DITSONG National Museum of Natural History, (formerly Transvaal Museum), Republic of South Africa; hermann@busmark.co.za
16. Hugo Benítez	Facultad de Agronomía, Universidad de Tarapacá, Arica; hugobenitez@gmail.com
17. Iva Mihoci	Senior curator, Croatian Natural History Museum, Department of Zoology; ivami-hoci@gmail.com
18. Jeremy Dewaard	Associate Director – Collections, Centre for Biodiversity Genomics, Biodiversity Institute of Ontario, University of Guelph, dewaardj@uoguelph.ca
19. Julia Wildfeuer	Bavarian State Collection of Zoology- Germany; juliawildfeuer@aol.com
20. Luis E. Parra	Depto. de Zoología, Universidad de Concepción, Concepción; luparra@udec.cl luiparra@gmail.com
21. Mario Ramos	Depto. de Zoología, Universidad de Concepción, Concepción; marioramos@udec.cl ; oiram.ramos@gmail.com
22. Martin Krüger	Senior Curator, Dept of Invertebrates (Lepidoptera), DITSONG National Museum of Natural History (formerly Transvaal Museum), Republic of South Africa; kruger@mitsong.org.za
23. Patricia Bocaz	Laboratorio de Diversidad Acuática, Facultad de Ciencias Naturales y Oceanográficas; pabocaz@gmail.com
24. Pritha Dey	Bavarian State Collection of Zoology – Germany; dey.pritha126@gmail.com
25. Viviane Jerez	Depto. Zoología, U. de Concepción, Chile; vijerez@udec.cl

Abstracts

Biodiversity of Geometridae from Chile

Luis E. Parra

Dept. de Zoología, Universidad de Concepción, Casilla 160-C, Concepción - CHILE e-mail: luparra@udec.cl

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 historical events, their diversity, distribution, natural history and research needs. The first descriptions of Chilean geometrids come from the 19th century. In the second half and towards the end of the twentieth century, the greatest contributions were produced, in which publications by Chilean naturalists stand out. It has been described 329 species, 111 genera and 5 subfamilies of Geometridae. The subfamilies Ennominae and Larentiinae are the most diverse. The highest concentration of Lepidoptera (and Geometridae) is found in central-southern Chile, between 30° and 44° south latitude and between 800 and 2000 meters high 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 southern areas of the country. Endemic species are concentrated between 33° and 41° latitude. Compared with other regions, the geometrids from Chile constitute a reduced group in species; 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. Research needs to focus on studies of: taxonomy and systematics based on morphology and molecular data; natural history; diversity in non-prospected regions or in natural ecosystems with accelerated deterioration; and the effect of habitat loss, fragmentation, and alteration on species richness, abundance, and distribution.



Biodiversity of the Family Geometridae in Argentina

Chalup, Adriana Elizabeth

Fundación Miguel Lillo, Fac. Cs. Naturales e IML- Tucumán, Argentina. e-mail: adriana.chalup@yahoo.com.ar

The geometrids represent the second most diverse group within the Lepidoptera, with about 21,000 species belonging to eight subfamilies. The family has worldwide distribution, showing most genera diversity in Neotropical Region. Classification of the subfamilies is weakly supported and requires deeper studies to define groups and relations between existing. 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 they have been of great importance, but Louis Prout (1910): "On the Geometridae of Argentina" was the first author that refer to the fauna of Geometridae of Argentina, here the author collects the necessary material to give rise to the first revision of the family for the country. Based on the work mentioned above and others authors of Argentina and abroad, a review of the faunal composition Geometridae family for Argentina it is presented. Of the eight cited subfamilies is concluded so far are represented in Argentina: Archierinae, Oenochrominae, Desmobathrinae, Larentiinae, Geometrinae, Ennominae and Sterrhinae. Ennominae and Larentiinae are most diverse. According to studies conducted and despite the lack of extensive sampling in certain regions, distinguish, within Argentina fauna of Geometridae a three important biogeographic groups: the "Yungueño", formed entirely of genera originated from the Bolivian Yungas; Paranaense, shares elements of wildlife with SE Brazil and Paraguay; and Andean-Patagonian group (Argentine-Chilean region), with a number lower than the previous ones but with a high percentage endemic genera.



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

Héctor A. Vargas

Dept. de Recursos Ambientales, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile

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 Tamarugal, at about 1,000 m of altitude. The two Chilean *Iridopsis* also have narrow host plant ranges: the larvae of *I. hausmanni* feeds on leaves of two species of Anacardiaceae (*Haplorhus peruviana* and *Schinus molle*), while the larvae of *I. parrai* feeds 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 northern Chile at about 3,300 m of altitude. 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.



Major biogeographic patterns of Geometridae in Chile

Carlos Zamora-Manzur^{1,2} & Luis E. Parra³

¹Depart. de Ecología, Facultad de Ciencias, Universidad Católica de la Santísima Concepción, Concepción, Chile.

²Programa de Doctorado en Sistemática y Biodiversidad, Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Concepción, Chile.

³Depart. de Zoología, Facult. de Ciencias Naturales y Oceanográficas, Uni. de Concepción, Concepción, Chile.

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. 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 they distribution. These relationships allow the identification of areas of endemism, which are geographical zones with a unique history, where the biota has evolved according to a set of historical and ecological processes unique of that area. Herein, I 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 (1) the identification of an austral biota, historically closely related to the southern cone of South America; (2) the identification of several areas of endemism throughout Chile, associated with important land-geography landmarks such as forest relics, transverse valleys and mountain forests, among others; and (3) an important species richness in the Biobío region and some priority sites for conservation inside this zone, where two vegetation types meet.



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

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

¹Depto. de Zoología, Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Casilla 160-C, Concepción, Chile. E-mail: marioramos@udec.cl

² Programa Magister en Ciencias con mención Zoología, Universidad de Concepción, Casilla 160-C, Concepción, Chile. Becario CONICYT Magister Nacional año 2016, Folio 22162333.

The genus *Larentia* Treitschke, 1825 consist of 25 species worldwide. Six species are present in Chile, while for Argentina only two species are listed, which are shared with Chile. This group of species has a high morphology variation and present incongruities respect of the Palearctic concept of *Larentia*. The Chilean and Argentinean *Larentia* are revised and redefined using morphological and molecular phylogenetic approaches. Based on morphology 31 characters derived from external anatomy and genitalia were analyzed, employing the parsimony criterion. The molecular analysis was performed using 23 COI gene sequences of *Larentia* and other larentiines employing a Bayesian framework. The results of the phylogenetic hypotheses suggest the presence of a polyphyletic group, where the Chilean-Argentine species of the *Larentia* genus does not correspond to this genus and are excluded of the tribe Larentiini. These results allow proposing three new genera and postulate a new species, completely excluding the presence of the genus *Larentia* in southern South America.



Diversity patterns and integrative analysis (morphology, DNA Barcoding) of geometrid moths of Western Himalaya

Pritha Dey^{1,3}, V.P. Uniyal¹, Kailash Chandra² & Axel Hausmann³

¹ Department of Landscape Level Planning and Management, Wildlife Institute of India, Post Box-18, Chandrabani, Dehradun-248001, Uttarakhand. E-mail id: dey.pritha126@gmail.com

² Zoological Survey of India, M Block, New Alipore, Kolkata 700053, West Bengal.

³ SNSB –Zoologische Staatssammlung München, Münchenhausenstraße 21, 81247 Munich, Germany

Rationale: In many countries, a comprehensive inventory, particularly in threatened and fragmented landscapes like the Western Himalaya is lacking. This scanty information 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 not currently feasible using morphology alone. **Location:** Nanda Devi Biosphere Reserve, with an area of 6403 sq.km and elevation ranges from 1800-7817m asl. It represents the typical physical attributes of the Western Himalayas. **Methods:** Collection was done along two different mountain slopes across 96 plots between 2000 and 3800m at every 200m. Moths were collected for 3-4 hours at randomly selected sites starting from dusk. Hourly variation of temperature, relative humidity and wind speed was recorded. Presence of disturbance signs were noted along 50m transects around the site of collection. Vegetation sampling was done in a nested method in circular plots within 50m radius of the site. DNA Barcoding of the Geometridae moth specimens collected during fieldwork has been started at the Zoologische Staatssammlung München. **Results:** 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 maximum number of species. The species diversity showed differential response to vegetation structure at the two locations. There was a mid-elevation peak (2300-3000m) at both the locations. A negative impact of resource extraction on moth populations was observed. Interestingly, the forest types have more prominent effects in disturbed mountain slopes. **Expected Outcome/Conclusion:** 1) Molecular identification will be achieved for future referencing complementing the traditional morphological methods of taxonomy. 2) Diversity patterns and identification of indicator species in rapid habitat-quality assessment program 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 Cengiz¹, Başak Ulaşlı¹ & Axel Hausmann²

¹ Mustafa Kemal University, Hatay, Turkey (* = presenter; fezacan@mku.edu.tr)

² SNSB - Zoologische Staatssammlung, Lepidoptera, München, Germany

In 2014 and 2015, Macroheterocera were collected in three altitudinal transects in the Amanos mountains from 0 m up to 1104 m above sea-level. 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 neighbors, 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, *Lomaspilis 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.



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

M. Krüger

Department of Invertebrates (Lepidoptera), DITSONG National Museum of Natural History (formerly Transvaal Museum), P. O. Box 413, Pretoria 0001, South Africa

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 Mya 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

D'Estrees Entomology, PO Box 17, KINGSCOTE, South Australia 5223. E-mail: dayoung@adam.com.au

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 Anigmatineidae 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), involved in an obligate pollination/early-biology mutualism, with the pinnate-leaved species in section *Boronia* of the genus *Boronia* (Rutaceae). Within the rest of the Lepidoptera, the only similar group obligate-mutualism is found within the sister family of the Heliozelidae, the Prodoxidae (*Tetetigulata* 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.



Cecidosidae of Chile: biology and geographic distribution

Silva, Gabriela T.^{1*}; Parra, Luis E.²; Vargas, Héctor A.³; Mundaca, Enrique⁴; San Blas, Germán⁵,
Goncalves, Gislene L.⁶ & Moreira, Gilson R. P.¹

¹Depart. de Zoologia, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brasil

²Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Concepción, Chile

³Depart. de Recursos Ambientales, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile

⁴Facul. de Ciencias Agrarias y Forestales, Universidad Católica del Maule Escuela de Agronomía, Curicó, Chile

⁵Facultad de Ciencias Exactas y Naturales, Universidad Nacional de La Pampa, La Pampa, Argentina

⁶Depart. de Genética, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brasil ,

*gabi_thomaz@hotmail.com

Cecidosidae is a small group of micromoths that originated about 95 Mya, restricted to the Gondwana and currently represented by six genera, four distributed in South America (*Cecidoses* Curtis, 1835, *Eucecidoses* Brèthes, 1916, *Oliera* Brèthes, 1916 and *Dicranoses* Kieffer & Jörgensen, 1910), one in Africa (*Scyrotis* Meyrick, 1909) and one in New Zealand (*Xanadoses* Hoare & Dugdale, 2003). With the exception of the latter, which is a bark miner, they are all gall inducers on Anacardiaceae shrubs. The main characteristics of this monotrysian family are, adults of small size (max. 14 mm wingspan), piercing ovipositor, and atrophied mouth appendages, which leads to a very short period of life restricting their locomotion to around their host plants. Larvae have reduced thoracic legs, and no abdominal prolegs. Despite their interesting life cycle, the family is still poorly known. Recent evidence on genetic and morphological studies revealed through a MSC (Multispecies coalescent Model) a high, hidden diversity for the South American genus *Eucecidoses*. Considering that Andean uplift acted as major biogeographical event in this case, supporting a vicariant speciation in *Eucecidoses*, it may be as well found for the Cecidosidae of Chile. Although Cecidosidae have been studied in Chile before, their identity and biology are still uncertain. The main goal of this work is to provide new records of distribution and biology, and corresponding variation based on molecular and morphological data.



Left-Right Asymmetry and morphological consequences of a host shift in the oligophagous Neotropical moth *Macaria mirthae* (Lepidoptera: Geometridae).

Hugo A. Benítez¹ & Héctor A. Vargas¹

¹Depart. de Recursos Ambientales, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile.

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 Fabacea species *Acacia macracantha*, however due to habitat loss it has recently been observed a host shift to the introduced fabacean *Leucaena leucocephala*. 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 symmetrical traits and it 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, it was 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*.



Insects Conservation in Chile. RECEC₂, Actions and Challenges

Viviane Jerez¹

¹Departamento de Zoología. Facultad de Ciencias Naturales y Oceanográficas. Universidad de Concepción. E mail: vijerez@udec.cl.

²Red Chilena Entomológica de la Conservación. RECEC. E-mail: recec.chile@gmail.com

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, 2,036 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 *Gyrinosomus 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 (1sp), Plecoptera (2 sp), Orthoptera (2 sp), Hymenoptera (3 sp), Mecoptera (1), Lepidoptera (2) and Coleoptera (28 sp) and 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* (Rotschild, 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 insects threatened and to generate scientific knowledge on the subject.



Nocturnal Lepidoptera as ecological indicators in a forest landscape of Chile.

Patricia A. Bocaz

Laboratorio de Diversidad Acuática, Facultad de Ciencias Naturales y Oceanográficas. pabocaz@gmail.com, pabocaz@udec.cl

A study of 3 consecutive years was held in the Nonguén National Reserve and surrounding areas, with the aim of analyzing the community lepidopteran present in the forest landscape, which is constituted by a single large continuous forest fragment (Nonguen National Reserve - NNR) fragments of forest and plantations of *Pinus radiata* and *Eucaliptys globulus*. Through multivariate analysis, community parameters between different habitats and annual seasons (months) were evaluated. The richness and abundance of species showed significant differences in all habitats and months of the year. The highest values are observed in the habitats of forest, that in the plantations. Together, these factors showed an interaction between habitat type and month, revealing that the diversity of nocturnal Macro-lepidoptera in each habitat type, is dependent on the observed month. Taxonomically the family Geometridae had the highest percentage of richness and abundance of species in the NNR and fragments, while in plantations the largest share was for the Noctuidae family. These results provide statistical and taxonomic basis for proposing some species or assemblages as ecological indicators.



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

Erki Õunap^{1,2}

¹Department of Zoology, Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia

²Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu, Estonia
erki.ounap@ut.ee

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 outback and the relationships of the Australian satin moths.

Dr. Catherine Byrne

Tasmanian Museum and Art Gallery, Hobart, Tasmania, Australia

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 Truuverk¹ & Erki Õunap^{1,2}

¹) Institute of Ecology and Earth Sciences, University of Tartu, Vanemuise 46, 51014 Tartu, Estonia;
andro.truuverk@ut.ee

²) Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Fr. R. Kreutzwaldi 1,
51014, Tartu, Estonia

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 have 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 and eight nuclear genes were used. Data were analysed by Bayesian phylogenetic method using program MrBayes and by maximum likelihood using RAXML. According to earlier expectations, many of the analyzed South American larentiines clustered into tribes considered valid in most recent treatments of Larentiinae. Nevertheless, phylogenetic placement of several 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 Hausmann¹

¹ SNSB - Zoologische Staatssammlung, Lepidoptera, Münchhausenstr. 21, 81247 München, Germany; ax-el.hausmann@zsm.mwn.de

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 *Prasinocyma* species, which we aim to describe in the near future. 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 taxa. 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. 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 NHM (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 Wildfeuer¹ & Axel Hausmann¹

¹ SNSB - Zoologische Staatssammlung, Lepidoptera, Münchhausenstr. 21, 81247 München, Germany (* = presenter; juliawildfeuer@aol.com)

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 '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 minimal 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.



The Centre for Biodiversity Genomics: ongoing projects and recent advances

Jeremy deWaard, PhD

Associate Director – Collections, Centre for Biodiversity Genomics, University of Guelph, Guelph, ON, Canada N1G 2W1.
dewaardj@uoguelph.ca; www.biodiversitygenomics.net

Fully comprehending the systematics of large faunas – such as the Geometridae of South America – will undoubtedly require an integrative approach to allow its timely and accurate completion. For over a decade, the Centre for Biodiversity Genomics in Guelph, Canada has been developing the tools and workflows to facilitate this integrative framework. Three ongoing projects will be discussed to illustrate the resources being created, as well as some recent advances that have transformed their efficiency, sensitivity, or universality. Firstly, the DNA barcode references 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. 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. And lastly, the retrieval of barcodes from degraded sources of DNA has dramatically improved due to the increased sensitivity offered by next generation sequencing, allowing the analysis of primary types over a century old.



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

Evgeny V. Zakharov

Canadian Centre for DNA Barcoding and Centre for Biodiversity Genomics, University of Guelph

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. The effectiveness of DNA barcoding and its applications depends on the availability of comprehensive reference libraries that meet prescribed standards. Assembling barcode libraries on a large scale requires deployment of analytical methods that perform equally well across diverse groups of organisms. 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 artifacts 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. Here we demonstrate 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 labeling 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.





Group photo in front of the clock tower in the University Campus



Lunch in the Bamboo Restaurant



Conference Dinner, from the left to the right: Stephanie deWaard, Jeremy deWaard, Evgeny Zakharov

Conference Dinner, from the left to the right: Mario Ramos-González, Gabriela Thomaz, Julia Wildfeuer, Hugo Benítez, Pritha Dey, Carlos Zamora-Manzur, Patricia Bocaz



Conference Dinner, from the left to the right: Feza Can Cengiz, Axel Hausmann, Daniel Bolt



Conference Dinner, from the left to the right: Edilia Jaque, Julia Wildfeuer, Adriana Chalup



Conference Dinner, from the left to the right: Iva Mihoci, Alfred Moser



Conference Dinner, from the left to the right: Hermann Staude, Axel Hausmann, Luis Parra



Conference Dinner, from the left to the right: Catherine Byrne, Ben Young, Martin Krüger



Conference Dinner, from the left to the right: Hugo Benítez, Axel Hausmann





Conference dinner in the Hacienda Patagonia
Restaurant close to Bio-Bio river





The organizer distributing gifts (books) to all participants during the conference dinner



Visit to Parque Hualpén: Impressive nature , Laguna Verde



Fuchsia magellanica Lam. (Onagraceae) in Parque Hualpén.



Axel Hausmann is more than happy during the IX FH in Chile



Studying the sclerophyllous forest in Parque Hualpén

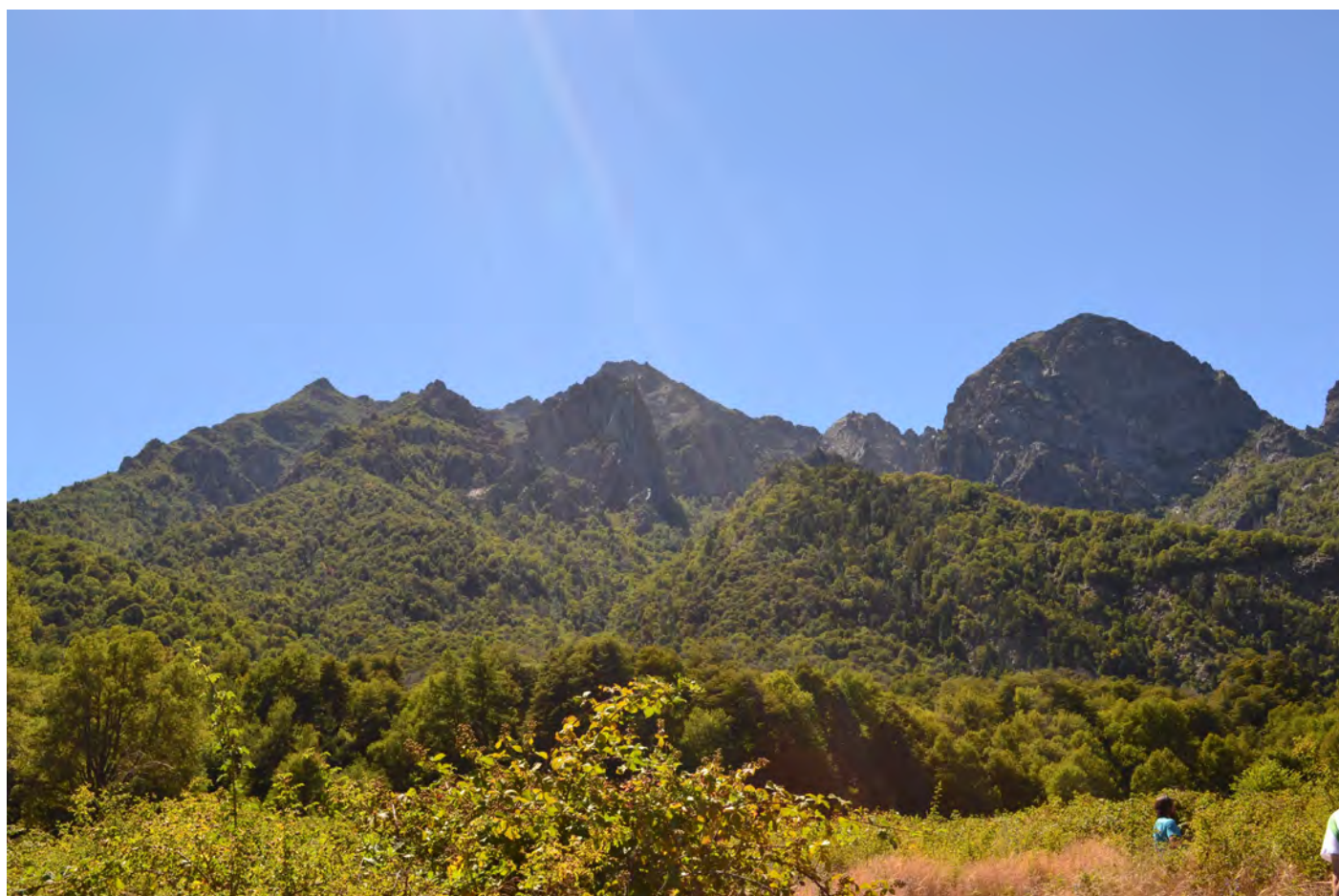


Collecting at light in Parque Hualpén; from the left to the right: Pritha Dey, Patricia Bocaz and Feza Can Cengiz.





Post-conference tour to Termas de Chillán (Las Trancas, Cordillera de Los Andes): Safari Tour to “Reserva Ñuble”





Getting information on nature during the Safari Tour to “Reserva Ñuble”

Refreshment after 15km walking
(Axel Hausmann)



On the way to “Reserva Ñuble” (from the left to the right: Julia Wildfeuer, Hugo Benítez, Gabriela Thomaz)

On the way to “Reserva Ñuble” (Mario Ramos-González)





On the way to “Reserva Nuble”



On the way to “Reserva Ñuble”

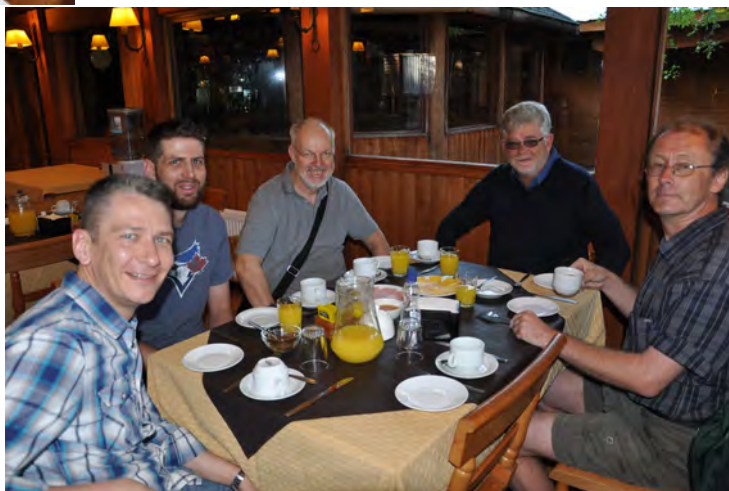


Group photo at the entrance of “Reserva Ñuble”



Breakfast in the Lodge "Bordenieve" (Termas de Chillán, Las Trancas): from the left to the right: Patricia Bocaz, Luis Parra, Gabriela Thomaz

Breakfast in the Lodge "Bordenieve": from the left to the right: Evgeny Zakharov, Jeremy deWaard, Axel Hausmann, Hermann Staude, Martin Krüger



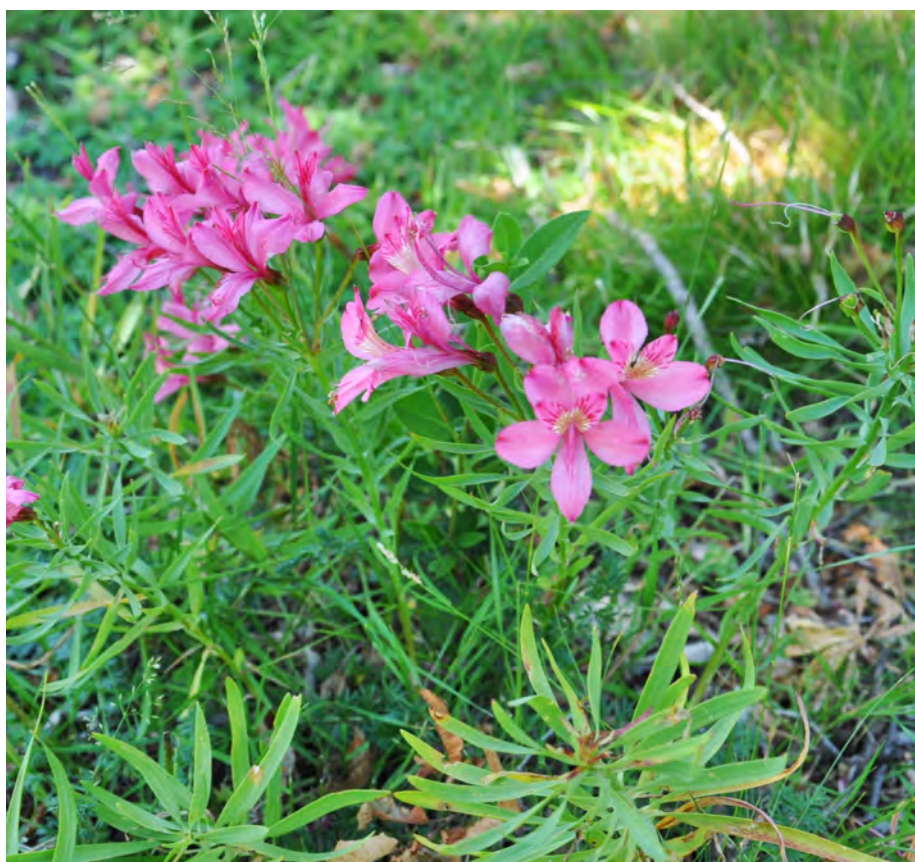
Breakfast in the Lodge "Bordenieve": from the left to the right: Andro Truuverk, Alfred Moser, Ben Young, Catherine Byrne

Breakfast in the Lodge "Bordenieve": from the left to the right: Mario Galov, Daniel Bolt, Iva Mihoci





Lodge "Bordenieve": Happy Birthday to Gabriela Thomaz



Alstroemeria sp. (Alstroemeriaceae) of the "Reserva Ñuble"



Welcome message for the tenth Forum Herbulot in Stuttgart (Germany)

11-16 June 2018, State Museum of Natural History, Stuttgart

Hossein Rajaei (Stuttgart, Germany) and Axel Hausmann (Munich, Germany) would like to welcome you for the tenth Forum Herbulot in the State Museum of Natural History Stuttgart. The meeting will be started with an ice-breaking German barbecue, we will have the possibility to present new results from our research on Geometrids and other Lepidoptera, there will be much time for discussions and for 'social networking' and we will choose one of two attractive sightseeing/collecting programs (City Tübingen and Hohenzollern Castle and collecting trip in Black Forest).

