

cloud forest zone from 1950-3750 m along the West and East Cordillera of Ecuador. Only one site was situated at the elevation of 1150 m in the western premontane forest.

In all sites moths were attracted to 160W UV-light and collected manually and afterwards subjected to standard preparation procedures to enable their identification. Identification to the species level was made when possible, by comparing them with specimens stored in the British national research collection at the Natural History Museum, London. Genital dissections were made for more than 490 specimens to cross-check their status. Species number,  $\alpha$ - and  $\beta$ -diversity indices (Fisher's alpha  $\alpha$ , Shannon H, and Whittaker  $\beta_w$ ), extrapolated species number (Chao1, ACE, bootstrap) were calculated. Sørensen and CNESS indices were used to describe faunal differences between particular collection sites, as well as a cluster analysis, and CCA techniques were used to group and ordinate samples. Spearman correlation coefficient was computed to evaluate altitudinal changes in examined moth assemblages.

A total of 24911 specimens representing 2468 species were analysed. Extrapolated number of species ranged from 2806-3052 species. Geometridae were represented by 15516 specimens and 1701 species, whereas Noctuidae by 9395 specimens and 767 species, respectively. At a single site (Golondrinas, 2000 m, West Cordillera) up to 550 species were observed and more than 750 were expected. Values for Fisher's alpha appeared to be the highest ever measured in the tropics, reaching 148 and 85 for Geometridae and Noctuidae respectively, at the

most species rich site. Other indices were also very high. Both, diversity and proportional contribution of families and subfamilies were changing with altitude. Diversity of Ennominae and Geometrinae appeared to decrease, while that of Larentiinae to increase with altitude. Similar tendency was observed in Noctuidae, where diversity of Amphipyrrinae, Ophiderinae and Hypeninae decreased with altitude and in Hadeninae and Noctuinae increased. The increase in diversity was also observed at generic level, in *Eupithecia* and *Eriopyga*. Canonical correspondence analysis (CCA) confirmed faunal differences between moth assemblages recorded on sites located in West and East Cordilleras at comparable latitudes as well as between the upper most section of the cloud forest and semi-opened and opened type of vegetation of the ecotone and páramo.

The results obtained indicate that the changes of species diversity related with the change of altitude may likely correspond to the decrease of vegetation diversity, the changes of larval host plants distribution and to the climatic changes. The overall pattern of species geographical distribution appeared to be strongly influenced by the presence of the dry environment of the Central Valley that separates the West and East Cordillera, although the effect of other factors, such as the isolation by the deep river valleys constituting significant geographical barriers, cannot be excluded. Further investigations may add more information and complement our data, and may help to identify areas of the highest species diversity for the purpose agricultural planning and for efficient wildlife protection.

## Diversity of Geometridae of Chile with presentation of some particular cases and examples

Luis E. Parra

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Dr. Luis E. Parra, Departamento de Zoología, Universidad de Concepción, Casilla 160-C, Concepción, Chile; e-mail: luparra@udec.cl

**Diversity of Geometridae in the sclerophyllous and temperate forests of Chile.** South America presents its biota of hybrid origin, which reflects a history that clearly separates it into a northern and southern zone (Crisci 1991a and 1991b). The fauna of the southern region shows clear relationships and shares a common history with New Zealand, Australia and Tasmania (Craw 1989, Crisci 1991a, Jerez 1996).

In the late Tertiary period, the conjugation of a series of events such as the glaciations of Western Antarctica and Patagonia, the formation of the cold Humboldt Current, and the final lifting of the Andes, caused the development of the "Arid Diagonal" of South America. In turns, the diagonal was the cause of: a) the fragmentation of Tertiary subtropical forests in the southern cone of America and its restriction to the Pacific and Atlantic margins of the

continent; b) the fragmentation and contraction of the northern part of the Pacific coastal subtropical forests as a result of an increment of the aridity of the Atacama Desert; and c) the expansion of the sclerophyllous subtropical forests in central Chile, due to the "barrier" effect of the Andes to the flow of the Amazonian moist winds. The Arid Diagonal and the Andes are the main climatic and geomorphologic barriers in southern South America. While the first barrier limits the floristic exchange between northwest and southwest, the second one prevents exchanges between east and west (Rambo 1952).

The forested region, south of the 30° S, is under the climatic influence of the westerly wind belt, a system responsible for most of the rainfall in southern South America (Villagrán & Hinojosa 1997). These forests constitute a reserve of global biodiversity, by possessing a biota extraordinarily rich in endemic species, particularly mono-specific genera and families of both plants and animals (Armesto et al. 1996). In its vascular flora there is a 34 % endemism, while in vertebrates 80 % of amphibians, 50 % of the fish, 36 % of reptiles, 30 % of birds and 33 % of mammals are endemic. This high level of endemism is also observed in Lepidoptera, particularly in Geometridae, with 60 % of endemism (Parra 1995). Here I will discuss three issues related to the diversity, evolution and biogeography of the geometrids from this region of the world.

#### Diversity of Geometridae in the transitional zone.

The Chilean transition zone lies between the rivers Maule (34° S) and Biobío (36° S). In this area sclerophyllous and temperate forests are mixed. The "Península Hualpén" has a relict coastal forest (absence of *Nothofagus*), which corresponds to a transition between sclerophyllous forest and Mediterranean scrubs and temperate evergreen broadleaved forests. Thirty-six species of 29 genera, belonging to the subfamilies Ennominae, Larentiinae and Sterrhinae, are found in this relictual forest where species of the sclerophyllous and temperate forests geographically overlap. These species have univoltine life cycles and are closely associated to the vegetation.

#### Diversity and evolution of Geometridae in the temperate forest relict of Fray Jorge.

The Fray Jorge National Park contains the northernmost temperate relict forest of Chile (30°40' S); it is located more than 1000 kilometers north of the remnant of coastal *Aextoxicum punctatum* R. et P. ('Olivillo') communities of southern Chile. In this contribution we present two undescribed species of moths from the Fray Jorge relict forest belonging to the genera *Hasodima* Butler 1882 and *Euclidiodes* Warren, 1895. The sister species of these new taxa are distributed in the central-southern zone of Chile, in plant associations where

*Aextoxicum punctatum* is present. We hypothesize that the common ancestor of each of these species was widely distributed in association with coastal "Olivillo" forests, which became fragmented during interglacial periods, resulting in the isolation of insect populations and their subsequent speciation. Other genera and species in this forest are: *Proteopharmacis* sp. (probably close to *P. valdiviata*); *Perusia praecisaria*; *Eupithecia mallecoensis*; *E. oenone*; *Ennada flavaria*; *Mallomus chilienaria*; *Syncirsodes primata*; *Maeandrogonaria undilineata* and six non-described species.

**Systematics and biogeography of *Hoplosauris*.** The genus *Hoplosauris* includes 8 species distributed in Chile from the 33° to 52° S. Its distribution also includes the province of Neuquen, Argentina. The main synapomorphies supporting the monophyly of *Hoplosauris* are: males with small bladder in the anal margin of the hindwings; microspinules in the inner surface of the corpus bursae; and androconia in the subapical region of the valves. *Hoplosauris* is endemic to the following provinces, *sensu* Morrone (2001): Magellan; Santiago; Valdivian Forest; Central Patagonia, and Maule. The biogeographic analysis shows that *Hoplosauris* has a southern origin and that its distribution reflects vicariant events that occurred during the split of Gondwana in the Cretaceous-Tertiary, the Quaternary fragmentation of southern forests, and dispersion events during the Pleistocene period.

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## The International Barcode of Life Project (iBOL)

Paul D. N. Hebert

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Dr. Paul D. N. Hebert, Biodiversity Institute of Ontario, University of Guelph; e-mail: phebert@uoguelph.ca

Over the past 5 years, many barriers to large-scale DNA barcode analysis have been overcome, but reference sequences are only available for 40K? species. The International Barcode of Life (iBOL) Project will increase coverage to 500K? species by 2014. My presentation summarizes the key research goals of iBOL, progress towards its activation and some les-

sons learned through early barcode projects, many of which have examined Lepidoptera, for further information see Stoeckle & Hebert (2008) and [www.DNAbarcoding.com](http://www.DNAbarcoding.com).

Stoeckle, M. Y & P. D. N. Hebert (2008): *Barcode of Life*. *Scientific American* October, 2008: 82-88.

## Global DNA barcoding campaigns in Lepidoptera: lessons from sphingid moths

Rodolphe Rougerie, Jean Haxaire, Ian J. Kitching, Thierry Vaglia, Pierre Basquin, Ronald Brechlin, Philippe Darge, Ulf Eitschberger, Tomas Melichar, Jacques Pierre & Paul D. N. Hebert

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Corresponding author: Dr. Rodolphe Rougerie, Biodiversity Institute of Ontario, Canadian Centre for DNA Barcoding, University of Guelph, Guelph, Ontario, Canada; e-mail: rrougeri@uoguelph.ca

Lepidoptera is the most sampled insect order in DNA barcoding studies. From regional, continental and global campaigns, more than 180000 barcodes have been obtained in 123 families and for ca. 20000 species. Global campaigns, seeking planetary coverage, have been initiated recently for the families Geometridae, Saturniidae and Sphingidae. The latter campaign, benefiting from the involvement of an international network of expert taxonomists and collectors, has progressed rapidly. Eighteen months after its start, it is now close to completion with almost 12000 sequences obtained for more than 1400 species and subspecies. This campaign represents a pilot project for similar efforts in other families. We present its development with emphasis on: (1) its

organization and management, based on the use of the Barcode of Life Datasystems (BOLD); (2) the material used and the success of high-throughput protocols for collection specimens; (3) the overall results in terms of observed genetic divergences at the species level, and estimated impact on the recognized diversity of the family. For each of these three points, we address potential challenges and pitfalls such as (1) facilitating collaborative work and respecting data privacy, (2) detecting and avoiding misidentifications or cross contaminations, (3) optimizing success for collection specimens, and (4) properly interpreting levels of variations in interspecific and intraspecific divergences. From practical examples, we show how the combination of DNA barcoding

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