

**GBIF-D: Geometridae:**

<http://www.biologie.uni-ulm.de/cgi-bin/system/zoosys.pl?pr=gbif-e1&id=1029&stufe=5&typ=ZOO&sid=T&only=no&syno=n&valid=n&lang=d>

**FORUM HERBULOT:**

<http://www.herbulot.de>

### The Lepiafrica Living Books Project

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**Objective:** The objective of this project is to accumulate and to ultimately offer known baseline information and images of as many as possible Afrotropical Lepidoptera in an easy to use structured electronic format to interested parties.

**The project team:** Members of the project team consist of editors and compilers. Each compiler carries the responsibility of a taxonomically defined part of the project, while editors have specific functions covering the whole project.

**Contributors:** Contributors are individuals and/or institutions who contribute information or images to the project. There are two categories of contributors. Primary contributors contribute bulk information or images. Secondary contributors contribute bits of information or images on an ad hoc basis. Contributors grant permission to the project to use their data but ownership of data remains with the contributor.

**Distribution medium:** The LepiAfrica Living Books Project is structured to work in conjunction with the Lepidops® database program already in use by members of The Lepidopterists' Society of Africa. Lepidops® is economical, effective and easy to use.

**Duration of the project & publication units:** The project team is aware that it is unlikely that the above objective will be met within the foreseeable future and therefore treats this as an ongoing project. Copies of various sections of the project are offered separately and are made available from time to time, when the project team considers a section to be ready for release. Updates will thereafter be made available periodically.

**Structure & funding:** The LepiAfrica Living Books Project is a Section 21 Company not for gain. The project is currently privately funded by its members. Income derived from the sale of LepiAfrica units will go towards funding the project in the future.

### Molecular barcoding and larval gut content analysis in insects (Geometridae, Lepidoptera)

**Axel Hausmann, Michael A. Miller & Günter C. Müller**

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On the background of the enormous species numbers in insects, the innovative technique of molecular barcoding will more and more play a major role in entomological research by facilitating identification of all stages, and thus for assessment of biodiver-

sity. It may, however, also gain a certain importance for ecosystem research, and systematics.

In the year of 2005 the ZSM has got offered access to several thousands of neotropical Geometridae larvae collected in 1800 fogging samples of Terry

Erwin (Lucky et al. 2002; Erwin et al. 2006), who monitored the fauna of 200 trees in 9 replicates from 1994-1996 in north-eastern Ecuador. Identity of all the fogged trees, and their neighbours is known. In two pilot studies we could prove, that larvae can be identified to species by their 'barcode sequences' (mtDNA), and that sequencing of gut content is possible too, in order identify the larval plant meal and to prove feeding on the fogged host-tree, rather than on epiphytes or on the neighbouring tree (Miller et al. 2006; Matheson et al. 2006). Identification of the larvae was performed by analysis of the complete sequence of the mitochondrial gene cytochrome c oxidase I (COI) and comparison with sequences of collection specimens. The effectiveness of the 'barcoding' tool for species identification had already been shown in many other studies (cf e.g. Hebert & Mitchell 2006). Gut contents were successfully identified by comparing sequence of a 157 bp long fragment of the chloroplast gene *rbcL* with that of the pre-identified host-plant and a wide set of other plants of the study area. Plant meals could be detected, when the insects were killed and preserved in Ethanol up to 12 hours after the last feeding (Matheson et al. submitted). For large sets of possible host-plants and for discrimination of closely related plant species, e.g. in tropical countries, additional markers (fragments/genes) may be necessary.

Results from the planned research project will provide, for the first time, comprehensive informa-

tion on host-plant relationships and host specificity for a large group of phytophagous insects in the neotropical rain forest canopy. With these data the estimations of total species numbers in Geometridae and insects may be extrapolated and refined. Similar projects are planned for geometrid moth larvae in Israel.

## References

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- Hebert, P. & A. Mitchell 2006. DNA barcoding of Australian Lepidoptera. – *Spixiana* 29(3): 211-212
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## DNA barcoding of Australian Lepidoptera

Paul Hebert & Andrew Mitchell

Hebert, P. & A. Mitchell (2006): DNA barcoding of Australian Lepidoptera. – *Spixiana* 29/3: 211-212

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DNA barcodes are short (658bp) sequences from a standardized region of the mitochondrial gene cytochrome c oxidase I (COI or *cox1*). Past work has revealed that sequence diversity in this gene region is an effective tool for species identification and discovery. As a result, large-scale DNA barcoding programs are now underway, including efforts to assemble barcodes for all fish and all bird species. We intend to develop a comprehensive barcode library for Australian lepidopterans as a complement to a similar project underway in North America.

We now present results of a pilot study that has barcoded 3500 specimens representing over 800 species collected from sites in north-eastern Queens-

land and the Central West of New South Wales. All specimens were databased and photographed before DNA was extracted from a single leg. DNA barcodes were subsequently gathered from the specimens and analysed using the Barcode of Life Data System ([www.barcodinglife.org](http://www.barcodinglife.org)).

Levels of intra-specific variation at COI averaged just 0.2 %, while congeneric species showed sequence divergences that were, on average, 20 times higher. As with studies in other geographic regions, more than 95 % of the species that we examined possessed unique DNA barcodes, allowing their easy identification. Although there was little overlap in species coverage between our two sampling regions, our