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## The International Barcode of Life Project (iBOL)

### Paul D. N. Hebert

Hebert, P. D. N. (2009): The International Barcode of Life Project (iBOL). Pp. 129 in: Hausmann, A. (ed.): Proceedings of the fifth Forum Herbulot 2008. Global strategies for plotting geometrid biodiversity in web-based databases (Munich, ZSM, 24-28 June 2008). – Spixiana **32/1**: 129

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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 lessons learned through early barcode projects, many of which have examined Lepidoptera, for further information see Stoeckle & Hebert (2008) and www.DNAbarcoding.com.

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

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## 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

Rougerie, R., Haxaire, J., Kitching, I. J., Vaglia, T., Basquin, P., Brechlin, R., Darge, P., Eitschberger, U., Melichar, T., Pierre, J. & Hebert, P. D. N. (2009): Global DNA barcoding campaigns in Lepidoptera: lessons from sphingid moths. Pp. 129-130 in: Hausmann, A. (ed.): Proceedings of the fifth Forum Herbulot 2008. Global strategies for plotting geometrid biodiversity in web-based databases (Munich, ZSM, 24-28 June 2008). – Spixiana **32/1**: 129-130

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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 and traditional taxonomy represents a very powerful approach for detection and description of cryptic species, as well as addressing synonymy issues. The ability to recover DNA barcodes from very old types is presented, emphasizing its potential for solving some of the most difficult taxonomic problems.

## DNA barcodes and monitoring forest health

### Jeremy R. deWaard & Leland M. Humble

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The economic, sociological and biological value of Canada's forests makes their sustainability essential to our well-being. To ensure their sustainability, it is critical to regularly and effectively monitor forest health. Genetic approaches, in particular DNA barcoding, have the potential to revolutionize the practice of forest biomonitoring. We describe how barcoding is being utilized in several ongoing projects concerning the Geometridae and other forest Lepidoptera in Western Canada. Firstly, a barcode library for geometrids is near completion and is currently being employed in a pilot project for the detection and surveillance of invasive defoliators. Our reliance on natural history collections for construction of this reference database, as well as the resultant discovery of invasive species and regional records, are described. Secondly, genetic methods are being applied to monitoring the diversity effects of anthropogenic disturbances (e.g. silviculture) and natural modifications (e.g. native pest outbreaks) in Canada's forests. The combined application of DNA barcoding with a North American geometrid phylogeny and a rapidly evolving marker (informative at the population level) is described, allowing the measure of multiple levels of diversity across varying treatments of disturbance. Lastly, an outline of how barcoding is facilitating the generation of regional faunal inventories is given, highlighting how a provincial geometrid checklist is being refined, while a moth inventory for one of North America's largest urban parks is being defined.

## On the systematic position and molecular phylogeny of *Lythria* Hübner (Lepidoptera: Geometridae: Sterrhinae)

### Erki Õunap, Vladimir Mironov & Jaan Viidalepp

Õunap, E., Mironov, V. & Viidalepp, J. (2009): On the systematic position and molecular phylogeny of *Lythria* Hübner (Lepidoptera: Geometridae: Sterrhinae). Pp. 130-131 in: Hausmann, A. (ed.): Proceedings of the fifth Forum Herbulot 2008. Global strategies for plotting geometrid biodiversity in web-based databases (Munich, ZSM, 24-28 June 2008). – Spixiana **32/1**: 130-131

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The geometrid genus *Lythria*, comprising five Palaearctic species, was for long treated as a member of the subfamily Larentiinae. However, detailed investigation revealed that there are several morphological characters that link *Lythria* with the subfamily Sterrhinae. Therefore, molecular phylogenetic study was conducted on a basis of three nuclear and two mitochondrial gene sequences to find out whether *Lythria* is a larentiine or sterrhine genus. The phylogenetic analysis reliably demonstrated that *Lythria* belongs to the subfamily Sterrhinae. Unfortunately, the intrageneric relationships within *Lythria* appeared to be in conflict with morphological data, as *L. sanguinaria* grouped together with *L. purpuraria*, not with *L. cruentaria*. We therefore performed an additional analysis which included also the fourth European