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## The International Barcode of Life Project (iBOL)

Paul D. N. Hebert

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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 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

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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

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