

## The Centre for Biodiversity Genomics: ongoing projects and recent advances

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Fully comprehending the systematics of large faunas – such as the Geometridae of the Neotropical region – will undoubtedly require an ‘integrative taxonomic’ approach to allow its timely and accurate completion. For over a decade, the Centre for Biodiversity Genomics (CBG; [www.biodiversitygenomics.net](http://www.biodiversitygenomics.net)) in Guelph, Canada has been developing the tools and workflows to facilitate this integrative framework. Three ongoing projects 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](http://www.ibol.org)) have been successful through a combination of targeted sampling at museums and field collections of fresh material. Nearly 170 000 specimens have been processed from collaborating natural history collections, and over three million specimens have been amassed in the field and subsequently barcoded and vouchered at CBG. As a result, significant progress has been made in completing DNA reference libraries: for global Lepidoptera, 96 % of the 131 families and 76 % of the 11 669 genera have been successfully barcoded; for the Lepidoptera of North America, 77 % of the 12 763 species are barcoded; and for the Noctuoidea of North America, 97.5 % of the 3671 species have now been barcoded (Zahiri et al. 2017).

Secondly, the Global Malaise Trap Program ([www.globalmalaise.org](http://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. As of January 2017, a total of 1262 week-long Malaise trap samples from 44 sites in 27 countries have been processed in their entirety. These have resulted in 1.03 M arthropod specimens analysed, of which 860 000 have generated barcode sequences that permitted Barcode Index Number (BIN) assignment. The composition and distribution of the 107 000 BINs detected have revealed interesting insights into current estimates of global insect species (Hebert et al. 2016) and temporal succession (Geiger et al. 2016).

And lastly, the retrieval of barcodes from degraded sources of DNA has dramatically improved

at CBG due to the integration of high-throughput sequencing (HTS) platforms. The massive output and increased sensitivity offered by HTS is permitting successful analysis of primary types over a century old (e.g. Hausmann et al. 2016), as well as from formalin-fixed and ethanol-preserved specimens. Experiments comparing these new approaches to Sanger-based methods show a 5–20 fold increase in the number of recovered barcode sequences with HTS (Prosser et al. 2016). Furthermore, while increased sample age has a strong negative affect on barcode recovery via Sanger analysis, the HTS-based approach recovers long barcodes regardless of age. These methods show significant promise for unlocking the three billion authoritatively identified specimens in the world’s natural history museums; these will be essential for constructing comprehensive DNA barcode reference libraries for the global fauna and an integrative framework for diagnosing and discovering species.

Geiger, M., Moriniere, J., Hausmann, A., Haszprunar, G., Wägele, W., Hebert, P. D. N. & Rulik, B. 2016. Testing the Global Malaise Trap Program – How well does the current barcode reference library identify flying insects in Germany? *Biodiversity Data Journal* 4: e10671. doi:10.3897/BDJ.4.e10671

Hausmann, A., Miller, S. E., Holloway, J. D., deWaard, J. R., Pollock, D., Prosser, S. W. J. & Hebert, P. D. N. 2016. Calibrating the taxonomy of a megadiverse insect family: 3000 DNA barcodes from geometrid type specimens (Lepidoptera, Geometridae). *Genome* 59: 671–684. doi:10.1139/gen-2015-0197

Hebert, P. D. N., Ratnasingham, S., Zakharov, E. V., Levesque-Beaudin, V., Telfer, A. C., Milton, M. A., Pedersen, S., Jannetta, P. & deWaard, J. R. 2016. Counting species with DNA barcodes: Canadian insects. *Philosophical Transactions of the Royal Society B* 371: 20150333. doi:10.1098/rstb.2015.0333

Prosser, S. W. J., deWaard, J. R., Miller, S. E. & Hebert, P. D. N. 2016. DNA barcodes from century-old type specimens using next generation sequencing. *Molecular Ecology Resources* 16: 487–497. doi:10.1111/1755-0998.12474

Zahiri, R., Lafontaine, J. D., Schmidt, B. C., deWaard, J. R., Zakharov, E. V. & Hebert, P. D. N. 2017. Probing planetary biodiversity with DNA barcodes: the Noctuoidea of North America. *PLoS ONE* 12 (6): e0178548.