DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artifact of tropical under-sampling

Carlos Lopez-Vaamonde, David C Lees, Akito Kawahara, Rodolphe Rougerie, Issei Ohshima, Atsushi Kawakita, Olivier Bouteleux, Jurate de Prins

Neotropical species of the genera *Lophochorista*, *Oospila*, *Nemoria* and *Lissochlora*. The Natural History museums of Munich, London and Pretoria (ZSM, NHM, NFI; "Afroemeralds Project") initiated an integrated assessment of all type specimens of Geometrinae including DNA barcoding, genitalia dissection, digital photography and accurate databasing to rapidly achieve an objective, close-to-complete knowledge of the Geometrinae fauna of the whole African continent. Furthermore, representatives of all BIN-clusters on the barcode of Life Datasystems (BOLD) are submitted to genitalia dissection.

References

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Lopez-Vaamonde, C., Lees, D. C., Kawahara, A., Rougerie, R., Ohshima, I., Kawakita, A., Bouteleux O. & J. De Prins (2014): DNA barcoding reveals that the reverse latitudinal gradient of Gracillariidae leaf-miners is an artifact of tropical under-sampling. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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With thousands of undescribed tropical Lepidoptera species and alarming rates of deforestion, developing methods that allow rapid biodiversity assessment is crucial to quantify levels of endemism and identify areas of high conservation value. DNA barcoding has been shown to be an efficient tool to speed up the identification of known species and the discovery of new ones. Barcodes can be used as proxy for clustering unidentified specimens into operational units and estimate levels of diversity within and between sites. This approach can be used to carry out rapid biodiversity asessments of hyperdiverse, mostly undescribed, insect fauna in tropical areas. Here we use DNA barcode data to quantify species richness of Gracillariidae leaf-mining moths of several sites in French Guiana and Ecuador.

Field surveys in six French Guianan (Figure 1) and one Ecuadorian sites produced 516 gracillariid specimens that were DNA barcoded to facilitate identification and to match larvae inside leaf-mines with adults. We obtained 485 barcodes (372 adults and 104 larvae). Species delineation from sequence data was approximated using Automatic-Barcode-Gap-Discovery and Refined-Single-Linkage-Analysis through the Barcode Index Number system, and the proportion of described/undescribed species was estimated after comparison with types. The total number of candidate species ranged from 142 (ABGD) to 151 (BINs). For Nouragues we obtained 108 BINs. 64 BINs (59.3%) are represented by singletons. 33% of specimens were

identified down to genus level. We were able to assign 17 species names to 38 specimens. Strikingly, at least 85% of the species collected as adults were found to be undescribed. Nearly all barcodes were novel to BOLD. The results from both our molecular and morphological analyses indicate that most of the gracillariid fauna in the studied region is unknown and undescribed. The estimated lower bound of species richness of Gracillariidae for Nouragues ranged from 240 species (Chao1) to 260 species (ACE). Our results show that DNA barcoding allows researchers to overcome the taxonomic impediment and carry out rapid biodiversity assessments in poorly documented regions (Lees et al 2013).

References

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Using DNA barcoding as a tool to describe moth community patterns in Lopé and Ivindo National Parks, Gabon

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Delabye, S., Decaëns, T., Bayendi, S., Ntie, S., Le Gall, P., Lopez Vaamonde, C., Moulin, N., Sebag D., Rougerie, R. & Ecotrop team (2014): Using DNA barcoding as a tool to describe moth community patterns in Lopé and Ivindo National Parks, Gabon. Pp. ### in Hausmann, A. (ed.): Proceedings of the eighth Forum Herbulot 2014. How to accelerate the inventory of biodiversity (Schlettau, 30 June – 4 July 2014). – Spixiana ###

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The existence of a taxonomic shortfall has been stressed as an important constraint for invertebrate biodiversity studies, especially in tropical countries where natural communities are more diverse and less studied. Here, we used DNA barcoding to achieve a rapid description of moth communities in two contrasted ecosystems of central Gabon: the rainforest of Ipassa research station (November 2009), and the savannah/forest patchwork near La Lopé (November 2009, March 2011). Specimens collected at light-trap were subsequently sorted by morphospecies, of which up to four individuals were selected and processed through DNA barcoding. The diversity and composition of the communities are described using Barcode Index Numbers (BINs) as operational taxonomic units considered here as proxy for species. Family-level assignment was carried out using morphology and/or existing DNA barcode libraries in BOLD (the Barcode of Life Data System, www.boldsystems.org).

A total of 3307 DNA barcodes were obtained from the 3387 specimens collected, representing 1305 BINs and 22 families, of which the most represented are Noctuidae, Erebidae and Geometridae. We found 733 singletons (i.e. 56% of the total BINs number), suggesting a high proportion of rare species in communities and/or a significant level of under-sampling, which is