

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

Carlos Lopez-Vaamonde, INRA-Orléans, UR633, Unité de Zoologie, Orléans, France,
Carlos.lopez-vaamonde@orleans.inra.fr

David C. Lees, Department of Zoology, Cambridge University, CB2 3EJ, UK

Akito Kawahara, Florida Museum of Natural History, University of Florida, Gainesville,
Florida 32611 USA

Rodolphe Rougerie, INRA, UR633 Zoologie Forestière, F-45075 Orléans, France

Issei Ohshima, Department of Life and Environmental Sciences, Kyoto Prefectural University,
Kyoto, Japan

Atsushi Kawakita, Center for Ecological Research, Kyoto University, Kyoto, Japan

Olivier Bouteleux, INRA, UR633 Zoologie Forestière, F-45075 Orléans, France

Jurate De Prins, Entomology Section, Royal Museum for Central Africa, Leuvensesteenweg
13, B-3080 Tervuren, Belgium

Abstract

Higher taxa often show increasing species richness towards tropical low latitudes, a pattern known as the latitudinal biodiversity gradient (LBG). A rare reverse LBG (with greater richness towards temperate high latitudes) is exhibited by Gracillariidae moths, in which most described species, occur in northern temperate areas. We carried out the first assessment of gracillariid species diversity in two Neotropical regions to test whether the relatively low tropical species diversity of this family is genuine or caused by insufficient sampling and a strong taxonomic impediment. Field surveys in six French Guianan and one Ecuadorian site produced 516 gracillariid specimens that were DNA barcoded to facilitate identification and to match larvae inside leaf-mines with adults. 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. Strikingly, at least 85% of the species collected as adults were found to be undescribed. The results from both our molecular and morphological analyses indicate that the current reverse LBG seen in this group is an artifact of insufficient sampling and a strong taxonomic deficit in the Neotropics.