



ON THE USE OF DNA BARCODES AS A PROXY FOR LEPIDOPTERAN SPECIES RICHNESS IN HYPERDIVERSE REGIONS

DECAËNS, T. (1), Bayendi, S. (2), Mavoungou, J. (3), Adeime Eyene, M. (2), Oslisly, R (4), Sebag, D. (1), Rougerie, R. (1)

(1) University of Rouen, France

(2) CENAREST-IRAF, Libreville, Gabon

(3) University of Masuku, Franceville, Gabon

(4) IRD, Yaoundé, Cameroon

In this study, we investigate the potential of DNA barcoding as a tool to accelerate the inventory and analysis of biodiversity for complex species assemblages of tropical Lepidoptera. The study was carried out in the National Parks of La Lopé and Ivindo in Gabon, a recognized hotspot of biodiversity. Moths were collected by light trapping during three successive nights in each site, and a selection of 2803 morphologically sorted specimens was processed through DNA barcoding. We obtained sequences for 2730 specimens belonging to 1100 distinct barcode clusters. Rarefaction curves and richness indices were further calculated using the number of clusters as a proxy for species richness, while species lists were obtained for some families by identifying the sequences against reference libraries in BOLD. Although saturation points were never reached in rarefaction curves, richness estimates suggest higher species diversity in the forests of Ivindo compared to the savanna/forest patchwork of La Lopé. This study provides evidence for the potential of DNA barcoding as a standardized tool permitting the rapid assessment of lepidopteran biodiversity in hyperdiverse ecosystems.

Keywords: Insects, Ecological Applications