



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

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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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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



a classical limit in most tropical arthropod surveys. Observed richness was of 807 and 713 BINs in Ipassa and La Lopé, respectively, but richness estimators indicate that up to 1700 and 1440 species could occur in both sites. Accordingly, sampling coverage ranged from 65 to 75% (in Ipassa and La Lopé, respectively). When comparing composition among sites (2009 dataset), we found a 66% BINs turnover, suggesting a strong spatial structuring due to geographical distance and/or contrasted environmental conditions. Likewise, turnover was of 68% between two sampling periods in La Lopé, indicating that communities could also be strongly structured according to seasonal cycle.

This study represents a first step in the description of moth diversity in ecosystems of Gabon. In 2012, 2013 and 2014, sampling was intensified by involving students of the ECOTROP field school and by diversifying collecting methods. A total of 3000 additional individuals were sampled and their DNA barcodes will be sequenced in the next few months, which hopefully will strengthen and refine the description of community patterns in Lopé National Park.

The importance of the traditional taxonomy in the exploration of the real biodiversity of Lepidoptera. A study case: the Nolini (Lepidoptera, Nolinae, Noctuoidea) fauna of Eurasia

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After more than 200 years of the birth of the descriptive science taxonomy, the exploration of the real biodiversity of Lepidoptera is still far not complete. The ratio of the undiscovered taxa strongly depends on the popularity of the given Lepidoptera group: usually the larger, spectacular groups are better explored than the small, less conspicuous ones, there are, however, several new discoveries even in the most popular groups.

Our research team started the taxonomic work on the rather neglected Noctuoidea tribe Nolini (Nolidae) in 2002, in collaboration with Mr. T.J. Witt and the Museum Witt, Munich, based on recently collected material from the Himalayas, Indochina, the Philippines and the Indonesian Archipelago. After the detailed examination of all historical Nolini types preserved in large European museums, we could continue the work on the vast material harboured in these institutions that has resulted in the discovery of an unexpectedly large number of new taxa.

The history of the descriptions of Nolini species is demonstrated on the following diagram: