

BIODIVERSITY ASSESSMENT OF A HYPERDIVERSE ARTHROPOD GROUP: DNA BARCODING THE ANTS OF MADAGASCAR

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INTRODUCTION

The increasing loss of biodiversity presents a daunting challenge to taxonomists and requires the discovery and analysis of biodiversity at a greatly accelerated pace. To truly consider “zero biodiversity loss” in Madagascar and elsewhere, conservation planning needs to be based more fundamentally on biodiversity data, and this requires taxonomic knowledge. However, if nothing is done to change the slow pace of current taxonomic efforts and practice, it will take centuries to complete even a preliminary “encyclopedia of life” on Earth. It is clear that if systematics is going to play a practical role in directing the preservation and development of natural systems, changes need to occur throughout the entire taxonomic process, from collection to description, from publication to dissemination, and from public outreach to advocacy.

In this paper, we show how DNA barcoding (using cytochrome oxidase 1 (CO1) – Hebert et al 2003a; Hebert et al. 2003b), enables taxonomic data on hyperdiverse arthropods to be gathered, analyzed, and synthesized into useful products in a timeframe that meets the challenge presented by the rate of biodiversity loss. We test a model for accelerating the taxonomic process with the aims of providing the necessary data for effective taxonomy, and — most importantly — the tools for making data accessible and applicable to the conservation agenda. The model is tested on a key taxonomic group, ants, and in an especially threatened area, Madagascar. We describe how CO1 DNA barcoding enables rapid identification of Molecular Operational Taxonomic Units (MOTU – Blaxter 2004) for the assessment of richness and turnover across landscapes.

The ant fauna of Madagascar is currently estimated to include approximately 1,000 species, of which 96% are endemic (Fisher 1996a). An estimated 75% of the ant fauna in Madagascar, however, remain undescribed (Fisher 1996b). For example, of the 71 species of the genus *Strumigenys* described in a recent revision, 70 were endemic and newly described (Fisher 2000). Although ants dominate the biomass of most terrestrial communities, are critical pollinators and seed dispersers, and are critical to nutrient cycling and ecosystem function, there is a global lack of studies of ant diversity or community structure. This may be largely because of the difficulty of species-level identifications (Bolton 2003).

A DNA-based system of species identification using a single gene was proposed by Hebert et al. (2003a; 2003b) who coined the term “DNA barcoding”. Since then, the utility of DNA barcodes for species identification has been successfully demonstrated with several taxonomic groups. The potential for such a system is evident to many who study biodiversity, especially in smaller, understudied, or hyperdiverse groups or in areas where the estimates of diversity lag well behind what is actually there.

In our analysis we test whether a diversity estimate based on DNA barcode MOTU is significantly different from estimates based on traditional morphological taxonomy using an understudied taxa from a part of the world where established taxonomic frameworks are only now emerging. We demonstrate that DNA barcode functional units are an effective surrogate for traditional morphological species and discover the same relative patterns of diversity within and between collection sites.

FINDINGS

There was no significant difference between richness (number of morphospecies or MOTU) using the molecular approach or morphological taxonomy. There was a significant difference between sites using the different methodologies to assign individuals to morphospecies or MOTU. Molecular similarity thresholds tended to emphasize the uniqueness of each site while morphological taxonomy tended to find more overlap between sites. Generally, morphological taxonomy “lumped” MOTU separated using the threshold approach. The average molecular divergence of morphospecies which contained multiple MOTU was 16.27%.

RECOMMENDATIONS

DNA barcoding proved an effective surrogate for morphospecies diversity patterns across localities in northern Madagascar. We demonstrated how inventories of hyperdiverse taxa such as ants can provide rapid analyses of diversity for conservation assessment. Sequence data generated during the inventory process will also provide an alternative set of characters to assist in inferring species boundaries during future taxonomic studies. Thus, the application of DNA tools during diversity assessment will facilitate and complement taxonomic study. The combination of DNA sequencing data coupled with inventory and traditional taxonomy is a model that can be applied across disciplines and will allow analytical needs to scale to the enormity of the biodiversity crisis. It will help to identify and conserve the evolutionary processes that generate and preserve biodiversity.

Our analysis is unique in that it has compared diversity measures at four sites in Madagascar using both the morphologically defined species units and MOTU based on two different threshold values for DNA barcode sequence divergence. Patterns of richness and turnover of MOTU and morphospecies were not significantly different. The take-home message is not that the values are the same (although for the most case they are remarkably similar), but rather that the patterns of richness within sites and turnover between sites were so similar. Thus, richness and turnover assessments determined using DNA barcode variability, *accrued within less than three weeks of preparatory analysis*, provided an effective surrogate for species determined through time-consuming intensive detailed morphological analyses.

DNA barcodes allow the rapid identification of functional units of diversity that can scale to the magnitude of hyperdiverse arthropod assemblages at a timeframe needed by conservation groups responding to habitat destruction and degradation. Measuring diversity, using MOTU in collaboration with taxonomists should provide the essential fine-scale maps for assessing biodiversity at a scale at which conservation decisions are made. Little time remains for the documentation of global biodiversity. Taxonomists, equipped with modern tools and collaborations, have a chance to move systematics to the forefront of conservation and the public’s attention. With increased taxonomic output and improved public access and visibility, public support for the discovery of life on this planet should follow.

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Further Information

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