INSTITUTIONEN FÖR BIOLOGI OCH MILJÖVETENSKAP

Assessing biodiversity:
Beyond the taxonomic impediment

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Akademisk avhandling för filosofie doktorsexamen i naturvetenskap, inriktning biologi
som med tillstånd från Naturvetenskapliga fakulteten kommer att offentligt försvaras
fredagen den 07 september 2018 kl. 10.00 i Hörsalen, institutionen för biologi och
miljövetenskap, Carl Skottsbergs gata 22B, Göteborg.

Abstract

Precise and accurate quantification of biological diversity is crucial for many fields of biological research and for understanding ecosystem services, biological interactions, biogeography and designing management strategies for conservation. The majority of current taxonomic knowledge is concentrated on a few groups of macro-organisms, mostly vertebrates and flowering plants, which represent only c. 0.7% and 3%, respectively, of the ~11 million estimated species of eukaryotes. The overwhelming majority of the extant biodiversity is challenging to sample and/or identify, which hinders biodiversity studies. While the world's poorly known, inconspicuous organisms (e.g. fungi, insects, nematodes, and bacteria) are essential to understand the evolution, maintenance, and functioning of biodiversity, this taxonomic impediment is the strongest barrier to quantify the diversity of such groups. Recent molecular (DNA-based) tools, such as DNA metabarcoding, promise to speed up biodiversity quantification by several orders of magnitude at moderate costs. These methodological advances allow researchers to circumvent difficult, time-consuming specimen examination and identification, thereby accelerating biodiversity research in poorly studied groups and diverse ecosystems. In addition, these molecular methods make it possible to detect and identify rare and taxonomically challenging species as well as to quantify the biodiversity in virtually any location, which in turn could aid in conservation design and environmental impact assessment (EIA) studies. This thesis examines the potential and challenges of biodiversity assessments and to recommend methods to identify inconspicuous organisms. It also evaluates the use of such methods to assess the variation of biodiversity across space and ecosystems, and to identify the factors underlying the uneven distribution of biological diversity in Amazonia. The results show that the major diversity patterns observed for macro-organisms in Amazonia do not hold true for all organisms. The results also highlight the complementarity of molecular and traditional taxonomic studies to better assess the biotic-abiotic factors that underpin the community composition and turnover of biological diversity.

Keywords: Amazonia; conservation; genetic diversity; metabarcoding; molecular sequences.