

Poster Abstract

Plant DNA barcodes and assessment of phylogenetic community structure of a tropical mixed dipterocarp forest in Brunei Darussalam (Borneo)

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DNA barcoding is a fast and reliable tool to assess and monitor biodiversity and to investigate ecological and evolutionary processes that may be responsible for the community structure of forests. We used DNA barcodes (*rbcL* and *matK*) to contribute to identification of morphologically undetermined individuals and to assess phylogenetic community structure of a 25-ha forest-dynamics plot in Brunei (Borneo, Southeast Asia) via community phylogenetics. With a total number of 555 haplotypes (from ≥ 154 genera, 68 families and 25 orders *sensu* APG, Angiosperm Phylogeny Group, 2016), our dataset makes a substantial contribution to tree barcode sequences from Southeast Asia. Based on the barcode sequences, we reconstructed phylogenetic relationships and used the resulting tree to calculate community metrics [net relatedness index (NRI) and nearest taxon index (NTI)]. In order to investigate the influence of phylogenetic resolution on community metrics, the traditionally used program Phylomatic was also used for phylogenetic reconstructions. Phylomatic trims a reference tree to taxa occurring in the community, and the resulting trees are usually only resolved at family or generic level. In most cases, the community metrics detected either random community assembly or phylogenetically clustering (co-occurring species are more closely related than expected), irrespective of the phylogenetic tree used for calculations. However, the phylogenetic tree produced greater variation across plots for NRI and NTI values, presumably due to noise introduced by using an unresolved phylogenetic tree. This suggests that using a DNA barcode tree has benefits over the Phylomatic approach by increasing precision and accuracy and allowing the incorporation of taxonomically unidentified individuals into analyses. Mechanisms responsible for the observed phylogenetic clustering, which indicates the importance of habitat filtering in structuring the forest assembly, can be identified once niche-associated plant functional traits are available. This project was funded by the Austrian Science Fund (FWF; project P26548-B22, grant given to Prof. Dr. Mary Rosabelle SAMUEL).

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