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## USING DNA BARCODES TO ASSESS PHYLODIVERSITY AND CONSERVATION OF SE QUEENSLAND'S RAIN FORESTS.

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Australian rain forests have been fragmented due to past climatic changes and more recently landscape change due to clearing. The subtropical rain forests of South Eastern Queensland are significantly more fragmented than the tropical World Heritage listed northern rain forests and are subject to greater population pressures. The Australian rainforest flora is relatively diverse at the family-level, but less so at the species-level. Current methods to assess biodiversity based on species numbers fail to adequately capture this richness at higher taxonomic levels. We developed a DNA barcode library for the SE Qld rain forest flora to support a methodology for biodiversity assessment that incorporates both taxonomic diversity and phylogenetic relationships. We calibrated our SE QLD phylogeny based on a three-marker DNA barcode within a larger international rain forest barcode library and used this to calculate phylogenetic diversity (PD). We compared phylogenetic diversity measures, species composition and richness, and ecosystem diversity of the SE Qld rain forest estate to identify which bio-subregions contain the greatest rain forest biodiversity, subregion relationships, and their level of protection. Diversity was not correlated with rain forest area in SE Qld subregions, but PD was correlated with both the percent of the subregion occupied by rain forest and the diversity of regional ecosystems (RE) present. The patterns of species diversity and phylogenetic diversity suggest a strong influence of historical biogeography. Some subregions contain significantly more PD than expected by chance, consistent with the concept of refugia, while others were significantly phylogenetically-clustered, consistent with recent range expansions.