

**Plant Biodiversity Science, Discovery, and Conservation:
Case Studies from Australasia and the Pacific**

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ABSTRACT

This thesis advances plant biodiversity knowledge in three separate bioregions, Micronesia, the Queensland Wet Tropics, and South Australia. A systematic treatment of the endemic flora of Micronesia is presented for the first time thus advancing alpha taxonomy for the Micronesia-Polynesia biodiversity hotspot region. The recognized species boundaries are used in combination with all known botanical collections as a basis for assessing the degree of threat for the endemic plants of the Palau archipelago located at the western most edge of Micronesia's Caroline Islands. A preliminary assessment is conducted utilizing the IUCN red list Criteria followed by a new proposed alternative methodology that enables a degree of threat to be established utilizing existing data. Historical records and archaeological evidence are reviewed to establish the minimum extent of deforestation on the islands of Palau since the arrival of humans. This enabled a quantification of population declines of the majority of plants endemic to the archipelago.

In the state of South Australia, the importance of establishing concepts of endemism is emphasized even further. A thorough scientific assessment is presented on the state's proposed biological corridor reserve network. The report highlights the exclusion from the reserve system of one of the state's most important hotspots of plant endemism that is highly threatened from habitat fragmentation and promotes the use of biodiversity indices to guide conservation priorities in setting up reserve networks.

In the Queensland Wet Tropics the thesis achieves two additional outcomes. A localized pilot study test the accuracy of plant DNA barcodes to estimate species richness. Species richness estimations were performed with high accuracy suggesting the suitability of the approach in poorly known floras where the identity of samples is known or from samples in a cryptic life stage that are difficult to identify. The methodology is promising for areas of the world, such as the tropics, that contain a high percentage of undescribed or poorly known taxa.

In addition, a large dataset from northeast Queensland was utilized to assess broad scale patterns of phylogenetic diversity. A linear relationship between phylogenetic diversity and genus richness is found to have high statistical support suggesting that taxon richness is an accurate predictor of hot spots of evolutionary history. When the affects of taxon richness are removed through linear regression however, a strong biogeographic pattern is unveiled. Sites with higher phylogenetic diversity than expected based on genus richness are best explained by having a lower percent of Gondwanan or endemic Australian elements of the flora. These sites have a higher percentage of Indomalayan or other foreign lineages that dispersed to Australia and are more frequent in the lowland rainforest areas below 200 meters. Phylogenetic diversity is shown to be effective at unraveling broad scale patterns of evolutionary history at the biome scale, which may prove useful for justifying the preservation of not just species but assemblages of species that represent different epochs of the earth's evolutionary history.

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