Study on genetic diversity in an effort to protect the genus *Dacrydium* in Central Kalimantan, Indonesia

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The tropical coniferous genus Dacrydium is widespread in Kalimantan. Locally known as *alau*, this genus thrives in a range of habitats from heath to deep-peat forests, especially in Central Kalimantan. It is threatened by logging, fires, and forest conversion. The objectives of this study were to investigate the genetic diversity of Dacrydium in the study area, which is a large, diverse landscape. Our research was conducted in a heath forest located within PT Taiyoung Engreen, PT Dasa Intiga and a deep-peat swamp forest located in Sebangau National Park. The four species that are suspected to exist in Kalimantan, namely, Dacrydium beccarii, Dacrydium pectinatum, Dacrydium elatum, and Dacrydium xanthandrum, were found in various abundances. Isoenzyme markers were applied to analyze the genetic diversity of *D. beccarii* and *D. pectinatum* using twenty samples per species from each site. The results showed that D. beccarii and D. pectinatum have a large number of missing alleles, rare alleles, and individual alleles. This makes it necessary to develop a strategy to protect the *alau*, especially D. pectinatum, which is quite threatened. D. beccarii and D. pectinatum have similar total heterozygosity, namely 0.686 and 0.700. Most of the genetic diversity of both species was between 71.1% and 0.65%, with fixation index values close to zero (-0.021 and 0.187, respectively), which means both species have a tendency to random mating. It is necessary to implement a strategy for saving *Dacrydium*. Conservation actions will include the translocating individual seedlings between research sites where each has a unique allele with different advantages, to be planted in original habitat to increase genetic variation, establishing demonstration plots to safeguard genetic variation, and additionally carrying out genetic enrichment planting, especially for D. pectinatum.