



Tropentag, September 20-22, 2023, hybrid conference
“Competing pathways for equitable food systems transformation:
Trade-offs and synergies”

Revealing the genetic diversity of *Pinus merkusii* in Aceh via simple sequence repeat (SSR)

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Abstract

The genus *Pinus* is classified as one of the most widely distributed genera of conifer trees, with *P. merkusii* being the only member that grows naturally in the tropics including on the Sumatran island. Three native strains are known on Sumatra: Aceh, Kerinci, and Tapanuli, while the first one is known as the largest population among the three. Its resin is highly valued and classified as one of the most valuable Non Timber Forest Products (NTFP) worth up to US \$ 50 million/year. *Pinus* forests have played an immense role in maintaining the cool climate condition of the tropical highlands, however, their existence has been threatened due to massive planting of citron grass (*Cymbopogon* sp.) over the past two decades, due to its attractive selling price. Therefore, their genetic assessment at the DNA level is essential, before some of them may have disappeared due to massive deforestation. Simple sequence repeat (SSR) markers were applied to assess DNA variations due to its co-dominant, and effective characteristics. There were three to six SSR markers applied based on previous references, e.g. pm01, pm05, etc., whose lengths were varied from 100 to 3,000 base pair (bp). The DNA leaf samples from two distinct populations (low- & high-lands) were employed as material in this study. Thus, four accessions from Tapanuli, and three accessions from Kerinci were also applied as outgroup members. Gel electrophoreses was made in order to separate the bands, and band scoring was conducted via NTSYS programme, which calculated the bands based on similarity index. Finally, a dendrogram graph was produced in order to study further the phylogenetic among the samples. In general, there were five clades, with the majority of accessions (around 80 %) clustered in I, with an overall genetic distance calculated between 0.50 until 0.88.

Keywords: Biodiversity, conservation, DNA extraction, Gayo high lands, micro satellites