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Determination of genetic diversity and genetic relatedness using ISSR markers in *Duabanga moluccana*

Diyanah Musfirah Jamal^a, Wei-Seng Ho^{a*}, Kit-Siong Liew^a, Shek-Ling Pang^b

^aForest Genomics and Informatics Laboratory (fGiL), Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, 94300, Kota Samarahan, Sarawak

^bApplied Forest Science and Industry Development (AFSID), Sarawak Forestry Corporation, 93250 Kuching, Sarawak

*Corresponding Authors: e-mail: wsho@unimas.my

Abstract

Duabanga moluccana or locally known as Sawih is a widely known forest tree species for its multi-purpose timber and other natural products such as fibers. Genetic diversity is important for the maintenance of the viability and the adaptive potential of populations and species. This information will be a basis for establishing tree improvement programme and for management or conservation of natural communities. The present study was aimed to assess the genetic diversity and genetic relatedness of *D. moluccana* trees collected from three natural forests in Sarawak, namely, Mukah, Tatau and Niah using inter simple sequence repeat (ISSR) markers. A total of 73 loci from 90 individuals were successfully amplified using three selected ISSR primers, namely, (AC)₁₀, (ACC)₆G and ACG(GT)₇. The Shannon's diversity index showed that *D. moluccana* trees in Mukah (0.499) was the most diverse population compared to Tatau (0.380) and Niah (0.330). Neighbor joining tree was also constructed to determine the genetic relationship among the three *D. moluccana* populations. The populations were completely clustered into three main groups, in accordance to their corresponding population and origin. Based on the results, it implies that *D. moluccana* trees are genetically diverse and related both within and among populations.

Keywords: Inter Simple Sequence Repeat (ISSR), *Duabanga moluccana*, genetic diversity, genetic relatedness
