

GENETIC DIVERSITY OF *Duabanga moluccana* USING DOMINANT DNA MARKERS BASED ON INTER-SIMPLE SEQUENCE REPEATS IN SARAWAK

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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 investigation of this species can provide baseline information for indirect selection in tree improvement programme. This study has employed Inter Simple Sequence Repeat (ISSR) technique to assess the genetic diversity and relatedness within and between three populations of *D. moluccana* located in Sarawak, namely, Mukah, Tatau (Bintulu) and Niah. A total of 151 loci from 90 individuals were successfully amplified with 6 selected ISSR primers and the percentage of polymorphic loci was 90.1%. The Shannon's diversity index showed that *D. moluccana* in Mukah natural forest (0.429) was the most diverse compared to Tatau (Bintulu) (0.362) and Niah natural forest (0.387). Neighbour joining tree were constructed to show relationship among the selected populations. The overall populations were completely clustered into three main groups, according to their corresponding population. Based on these results, it implies that *D. moluccana* trees are genetically diverse among populations.

Keywords: Inter simple sequence repeat, *Duabanga moluccana*, genetic diversity, genetic structure

1. INTRODUCTION

Establishment of forest tree plantations is becoming more crucial as forest resource reduction increases exponentially due to human activities. Most losses are measured in square kilometers, but a more precise loss of forest tree resources cannot be measured. As forests disappear, so do their genetic resources (Arnold, 1991; Sedjo and Lyon, 1990). For this reason, forest tree plantation development is a necessity rather than a choice to alleviate the problem arisen from forest degradation, to reinstate forest system function and productivity (Kidd and Pimentel, 1992). Forest tree such as timber has a lot of benefits and has been long used by human for many purposes. It has been used as sawn timber, construction materials, fodder, fuel wood, shelter and medicine. Conventionally, forest tree plantations use planting material from wild-type tree. Today, biotechnology allows selection of genetically good traits tree that gives better quality and higher number of yields. Obviously, forest tree plantation has a major role to play in the long term timber production strategy.

Inter simple sequence repeats (ISSR) are DNA fragments with length of about 100 to 3,000 bp located between adjacent, oppositely oriented microsatellite regions (Zietkiewicz *et al.*, 1994). ISSR marker is chosen in the present study due to its main property that no sequence information is required, thus give a strong advantage to this markers. Furthermore, ISSRs are randomly distributed throughout the genome. It permits detection of polymorphism in microsatellites and inter microsatellites loci without previous knowledge of the DNA sequence (Gupta *et al.*, 1994). ISSR produces informative loci which is suitable to discriminate closely related genotype variants (Roose *et al.*, 1997). The ISSR technique uses primers that are complimentary to a single SSR (Zietkiewicz *et al.*, 1994). The amplicons generated consist of regions