



## **Genetic diversity of *Neolamarckia cadamba* using dominant DNA markers based on inter-simple sequence repeats (ISSRs) in Sarawak**

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### **ABSTRACT**

*Neolamarckia cadamba* or commonly known as kelampayan has been selected as one of the important plantation tree species in Malaysia. Thus, the molecular characterization of this indigenous tropical tree species is needed to maintain its high quality. Inter simple sequence repeats (ISSR) markers were used in this study to determine the genetic diversity and relatedness of *N. cadamba* in two planted forests and six natural forests in Sarawak. Three ISSR primers had generated a total of 239 loci, of which 32.6% - 59.4% of the loci were polymorphic among 236 *N. cadamba* trees in eight populations. The mean Shannon's diversity index (*H'*) ranged from 0.1399 to 0.2354. The coefficient of population differentiation was low for planted forests ( $G_{st} = 0.0871$ ) and natural forests ( $G_{st} = 0.2013$ ). Both UPGMA dendrogram and NJ-tree generated by ISSR markers had divided natural forests and planted forests into two distinct clusters. Natural forests were grouped in one cluster while planted forests were grouped in another cluster. This study shows that *N. cadamba* trees are closely related within its own population and its designated forest type. In future, several specific loci can be sequenced and developed into SCAR (sequence characterized amplification region) markers for tree improvement and conservation programme of *N. cadamba*.

**Keywords:** Genetic Diversity, *Neolamarckia cadamba*, Kelampayan, Inter simple sequence repeats (ISSR), Planted Forest, Tree Improvement.

### **INTRODUCTION**

Forest plantations have become increasingly important nowadays as a result of extensive deforestation activities. Human beings have been utilizing forest trees for decades as a source of materials for providing shelter, fuel, food, fiber, medicinal plants and others. The price of industrial wood has thus increased due to the declining availability of harvesting native forests. This phenomenon has brought to the initiation of industrial forest tree planting. In the past, reforestation involved replanting of existing wild trees regardless of the genotypic trait. To date, biotechnology approaches have been used to select tree species with targeted characteristics, such as short rotation period and higher yields at the molecular level.

DNA markers are used in molecular characterization because DNA markers can act rapidly and economically to characterize cultivars, provenances or genotypes precisely and enable the measurement of genetic relationships [1]. Some DNA marker systems that are commonly used and involved PCR amplification are random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP) and more recently, simple sequence repeat (SSR) and inter simple sequence repeats (ISSR) [2]. They have been widely used in genetic analysis, gene mapping and genotype identification of forest tree species. ISSR-PCR has an advantage over other DNA fingerprinting methods such as it is fast, requires no radioactive handling facilities and involves minimal cost.

Polymorphism may be occurring within a species due to mutation or crossover of the chromosome [3]. Although there are no significant differences in morphology characteristics, polymorphism will still cause a species to have