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Development, Polymorphism and Cross-Species Transferability of Genomic SSR Markers in *Duabanga Moluccana*, an Indigenous Tree Species from Sarawak

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Abstract: In this study, we used ISSR-suppression methods to develop a set of SSR markers for *Duabanga moluccana*. It is an indigenous fast growing tropical tree species. A total of 44 SSR regions were identified and specific primer pairs were designed. The SSR motifs contained perfect compound with 24 (54.5%) occurrences, followed by the imperfect compounds with 8 (18.2%), simple perfect with 8 (18.2%) and the simple imperfect repeats with 4 (9.1%). The newly identified SSR markers were characterized by screening 20 individuals of *D. moluccana* seedlings. Among 43 primer pairs tested, 25 (58.1%) SSR markers amplified the desired PCR products and 115 alleles were detected. The number of alleles per locus ranged from 2 to 8, with a mean value of 4.60. Polymorphism Information Content (PIC) values ranged from 0.225 to 0.792, with an average of 0.604. A success rate of transferability of *D. moluccana* SSR markers varied, ranging from 84% in *Duabanga grandiflora*, 36% in *Neolamarckia cadamba*, 24% in *Canarium odontophyllum* and 28% in *Shorea parvifolia*. These SSR markers herein could be used to generate useful baseline genetic information for effective selection of plus trees, provenance trials and establishment of forest Seed Production Areas (SPAs) of *D. moluccana* in the selected forest reserves for tree plantation and improvement activities. Besides, the transferability of the newly developed SSR markers across a range of species and genera suggests their potential usefulness for a variety of population genetic studies.

Keywords: *Duabanga moluccana*, Simple Sequences Repeats (SSRs), Microsatellites, ISSR-Suppression Method, Forest Plantation and Population Genetics

Introduction

The demand for quality wood is projected to increase dramatically in line with global consumption requirements. This increasing demand is mainly forced by global population growth and rise in socio-economic levels (FAO, 2010). The global consumption of industrial round wood is estimated to increase from 1,707 million m^3 in 1990 to 2,436 million m^3 in 2030 (FAO, 2009). However, the slow-growing of natural forests are unable to meet current global demand for wood, resulting in the loss and degradation of natural forests (Fenning and Gershenzon, 2002). The development of high-yielding with short rotation plantation forests is vital to supply the bulk of humanity's wood needs on a long-term basis. It is also important to ensure a sustainable supply of high genetic quality seedlings for planted forest development worldwide to maximize adaptability and yield potentials under stress-site condition (Goel and Behl, 2001).

With advances in genomics research, there has been a remarkable progress in the development of an array of potential molecular markers, including RAPD, RFLP, AFLP, SSRs and other markers for monitoring forest tree improvement activities, such as measuring genetic variation in breeding populations, germplasm