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Archives of Applied Science Research, 2014, 6 (4):209-218
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Development and polymorphism of simple sequence repeats (SSRs) in Kelampayan (*Neolamarckia cadamba*–Rubiaceae) using ISSR suppression PCR method

Seng-Loi Phui¹, Wei-Seng Ho^{1*}, Shek-Ling Pang² and Julaihi Abdullah²

¹Forest Genomics and Informatics Laboratory (fGiL), Department of Molecular Biology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak

²Applied Forest Science and Industry Development (AFSID), Sarawak Forestry Corporation, Kuching, Sarawak

ABSTRACT

Simple sequence repeat (SSR) marker is a polymerase chain reaction (PCR)-based marker system which has become a marker of choice for understanding plant genetic diversity and a powerful tool in addressing genetic resources questions. However, the availability of SSR markers especially for forest tree species is limited thus far due to the high development cost, labour-intensive and time-consuming. The present study aimed to develop an array of SSR markers for *Neolamarckia cadamba* using inter-simple sequence repeat (ISSR) suppression PCR method and further assessed the polymorphisms and transferability of the markers to other species. In total, 15 out of 31 SSR markers specific for *N. cadamba* were successfully developed and further characterized and validated by using 30 individuals of *N. cadamba*. The markers exhibited a considerable high level of polymorphism across the tested *N. cadamba* genotypes whereby 66 alleles were detected with an average of four alleles per locus. Most of the SSR loci analyzed showed high polymorphism as indicated by their PIC value which was above 0.5. The most polymorphic loci were: NCAC11 (PIC=0.849), NCAC12 (PIC=0.722) and NCAG01 (PIC=0.712). The transferability rate was ranging from 26.7% to 73.3% among the four cross-genera species tested. The present study is the first report on the development of SSR markers in *N. cadamba*. These markers provide valuable genomic resources that could pave the way for exploiting SSR genotype data for effective selection of plus trees, provenance trials and establishment of forest seed production areas (SPAs) of *N. cadamba* in the selected forest areas dedicated to planted forest development, and molecular breeding of *N. cadamba* and other indigenous tropical tree species in future.

Keywords: SSRs, *Neolamarckia cadamba*, kelampayan, ISSR suppression PCR method, genetic diversity, molecular breeding

INTRODUCTION

Understanding the genetic variation of forest tree species is a prerequisite for the appropriate utilisation of forest genetic resources. This information will be a basis for establishing tree improvement programme and for management or conservation of natural communities. Our previous findings have shown that populations with little genetic variation are more vulnerable to the arrival of new pests or diseases, pollution, changes in climate and habitat destruction due to human activities or other catastrophic events [16, 19, 46]. Such genetic information of a forest tree species is assessable either through measurement of morphological characters in the field or through the study of molecular markers in the laboratory. However, those morphological characters can be influenced by environmental factors meanwhile molecular markers avoid many of the complications of environmental factors acting upon characters by looking directly at variation controlled by genes or by looking at the genetic material itself [14].