

Ratree Yooyuen 2013: Assessment of Genetic Diversity and Genetic Structure of *Dalbergia cochinchinensis* Pierre using DNA Data from Chloroplast Genome. Master of Science (Forest Biological Science), Major Field: Forest Biological Science, Department of Forest Biology. Thesis Advisor: Mr. Sutee Duangjai, Dr.rer.nat. 100 pages.

The Siamese rosewood (*Dalbergia cochinchinensis* Pierre) is an valuable important tree species. This species has been illegally logged since the last few decades which may become extinct. This study aimed to assess genetic diversity and genetic structure of *D. cochinchinensis* using sequencing data from chloroplast genome and test of effective DNA extraction methods from the bark, wood and leave of *D. cochinchinensis*. The results showed that the DNA extraction of Sharma *et al.* (2002) was the best successful method. Eight non-coding chloroplast DNA regions were screened for polymorphism three regions, *trnS-trnG*, *trnV-trnM* and *trnC-ycf6* revealed polymorphisms and were selected for the further genetic diversity and genetic structure studies in *D. cochinchinensis*. A total of 10 polymorphic sites, including 8 single nucleotide polymorphisms (SNPs) and 2 insertions/deletions (INDEL) were detected in the 1,841 bp from three non-coding chloroplast DNA sequences. Genetic diversity and genetic structure of 108 individuals of *D. cochinchinensis* collected from 10 populations in the Northeast and the Central part of Thailand as well as Laos were assessed. Genetic diversity was low as shown by haplotype diversity (h) and nucleotide diversity (π) of 0.608 and 0.00033, respectively. There were eleven haplotypes, of which each haplotype was presented in different proportions, ranged from 1-4 haplotypes per population. The most common haplotype was H1, presented in 9 of 10 populations which was 61% of the total samples. Seven haplotypes were unique to populations. No genetic structure was found on the basis of haplotype distribution due to the common haplotype H1 in most populations, except the Khao Yai National Park population. This result was consistent with the AMOVA analysis showing genetic variation within populations greater than the variation between populations. Neutrality tests by Tajima's D and Fu and Li's D^* and F^* statistics, were under neutral equilibrium, indicating that genetic variation of *D. cochinchinensis* populations was influenced by the balance between mutation and genetic drift.

The genetic diversity results can be used to select genetic sources for *ex situ* conservation area of *D. cochinchinensis*. The unique haplotype may be used to identify the source of illegally logged wood in the future.

Student's signature

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