

Tanat Wattanakulpakin 2014: Population Genetic Analysis of *Xylia xylocarpa* (Roxb.) W. Theob. var. *kerrii* I. C. Nielsen in Thailand. Master of Science (Economic Botany), Major Field: Economic Botany, Division of Science. Thesis Advisor: Associate Professor Siriluck Iamtham, Ph.D. 130 pages.

A study of the genetic diversity in populations of *Xylia xylocarpa* (Roxb.) W. Theob. var. *kerrii* I. C. Nielsen in Thailand was performed using molecular markers to reveal differentiation within and between populations and the geographical distribution of alleles. Samples were collected from individual trees in 14 National Parks and 2 community forests. DNA was isolated from leaves and 8 single locus gene markers were used to identify different alleles using PCR – SSCP combined with sequencing. For easier detection and differentiation of some alleles, 15 SNPs were converted into CAPS assays and 5 SNPs were converted to AS-PCR assays. From 8 to 34 alleles were identified for the different loci though the effective number of alleles ranged between 1.1 and 7.6. Several loci showed deviation from Hardy-Weinberg equilibrium with the CAT2 locus having the most significant deviations. Genetic distances calculated according to Nei (G_{st}) and Jost (D_{est}) indicated the largest genetic distances between Pang Sida National Park and Mae Ngao National Park. Direct sequencing of PCR amplified fragments revealed several alleles in addition to those distinguished by SSCP. The alleles found among *Xylia xylocarpa* differed from one another due to one or just a few substitution polymorphisms. Unexpectedly, more non-synonymous than synonymous substitutions were found in the exons of the genes. STRUCTURE revealed very weak support for population differentiation in two or maybe three subgroups. Only the most western populations (LamKhlungNgu, Erawan, MaeNgao, ThaTaFang) seemed to be slightly separated from the others in STRUCTURE and in principal component analysis. Different pollination syndromes and seed dispersal mechanisms may explain this difference in population structure between *Xylia* and teak, where clear geographically-linked population genetic structure can be observed.

Student's signature

Thesis Advisor's signature