Krongthong Jaikaewdang 2014: Genetic Variation Analysis of Wax Tree (*Rhus succedanea* L.) in Thailand by Start Codon Targeted (SCoT) Markers. Master of Science (Forest Biological Science), Major Field: Forest Biological Science, Department of Forest Biology. Thesis Advisor: Assistant Professor Wichan Eiadthong, Dr.Agr. 78 pages.

Genetic variation analysis of 96 samples of wax tree (*Rhus succedanea* L.) was studied using five suitable primers of Start Codon Targeted (SCoT) markers. In total 36 bands were revealed and 34 of them (94.44%) were polymorphic. The dendrogram was constructed using unweighted pair group method with arithmetic average (UPGMA) by NTSYS-pc version 2.10m program based on Jaccard's similarity coefficient that ranged from 0.130 to 0.923 and classified into 8 groups at the similarity of 0.43. Furthermore, the genetic variation of five populations of wax tree was investigated. The average percentage of polymorphism was 68.89. The average heterozygosity (H) and Shannon's gene diversity index (H') were 0.213 and 0.326 respectively. The dendrogram was constructed using UPGMA by POPGENE version 1.31 program in which the populations were divided into 2 groups. The coefficient of genetic differentiation (*G*st) was high (0.191). The result demonstrated that SCoT markers could be used for clone identification and used as a genetic database for wax tree improvement, domestication and genetic resources conservation in the future.

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