

Genetic Diversity and Species Distribution Modeling of Teak
(*Tectona grandis*) in Java Island to Identify the Origin of the
Plantation Materials and Potential Plantation Area

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Abstract

Tectona grandis (teak) is one of the most valuable timber species in the tropics. This species was introduced to Indonesia more than 100 years ago, and large plantations—covering 1.2 million ha—have been created in Java, the main island of the nation. Since then, demand for *T. grandis* timber has increased mainly for furniture. However, *T. grandis* habitats are considered to be susceptible to future climate change. Particularly in Java, there is little research about the impact of climate change on *T. grandis* plantations. In addition, there are few molecular studies about seeking the origins of *T. grandis* trees in Indonesia. Therefore, there is still much to be clarified in terms of the ecology and genetics of the species in Java.

The first aim of this study was to clarify the genetic diversity and to identify the origin of *T. grandis* in Java. Leaf samples were taken from three regions across Java (east, central, and west). The samples were taken from trees within three different age classes in each of the three regions. Additional samples were collected from selected clones of *T. grandis*. All the samples were investigated using multiplexed ISSR genotyping by sequencing (MIG-seq). Then, the genetic diversity and structure were compared with the provenance test populations obtained from native *T. grandis* forests in India, Myanmar, Thailand, and Laos.

Analyses using 459 single-nucleotide polymorphism (SNP) loci revealed that native populations had higher genetic diversity than the Indonesian *T. grandis* plantations. Moreover, old *T. grandis* plantations demonstrated lower genetic diversity than young plantations. Further analyses revealed that most Indonesian *T. grandis* plantations genetically originated from Laos, Thailand, or Myanmar.

Second, to know potentially suitable plantation areas for *T. grandis* under future climate, species distribution models (SDMs) were developed. Foremost, site index (SI) of *T. grandis* was calculated by using the relations between recorded age of plantation sites and measured tree heights at each site. The SI for *T. grandis* in this study was defined as potential tree height at 40 years, which is the shortest time period of long-term rotation for *T. grandis* plantations in Java. The data on stand age and tree height were surveyed from 282 *T. grandis* plantation sites around the island. The SI was calculated following the Mitscherlich equation based on Leibig's Law of the Minimum. The SI values were used as the response variable for SDMs. For predictor variables, a bioclimatic data set was obtained from WorldClim (<https://worldclim.org/data/index.html>) and a set of climatic variables was selected, using correlation coefficients to prevent multicollinearity. Three types of soil data, including soil type, pH and cation exchange capacity, were extracted from SoilGrids250m (<https://soilgrids.org/>).

Three statistical approaches—generalized linear models (GLM), general additive models (GAM) and random forest (RF)—were applied to construct the SDMs. The best model was used to project the current and future SI throughout Java. Two emission scenarios (RCP 2.6 and RCP 8.5), two global climate models (MIROC-ESM-CHEM and HadGEM2-ES), and two projected periods (the 2050s and 2070s) were used to compare the changes in suitable conditions and habitats for *T. grandis* growth in the future.

The RF model showed the best fit with observed values. This model predicted that West Java would become less suitable for *T. grandis* plantations both in both the 2050s and the 2070s. In contrast, southern Central Java Province would be suitable for *T. grandis* in the 2050s and 2070s. Precipitation of warmest quarter was a good predictor for *T. grandis* growth in Java. None of the three soil variables were the important predictors of suitability in the RF model.

I found that there was a weak genetic structure for *T. grandis* plantations among the regions in Java, which indicates that most plantations were established using plant materials from a specific part of the natural *T. grandis* distribution area. This study recommends that seed production areas (SPAs) are conserved within the management areas of Perhutani, a state forest company. Gene conservation plots should be established in SPAs before these genetic resources disappear because of natural disasters or anthropogenic activities. Areas in southern Central Java Province should be prioritized for *T. grandis* plantation in the future. Therefore, I recommend testing the various genotypes that were identified in the study in the prioritized future locations to find the best combination of genetics and site quality. Conservation of not only genetic diversity but also suitable plantation areas for future are essential aspects of sustainable forest management in Java.

Keyword: climate change, genetic structure, introduced species, plantation, prediction, seed origin, site index, SNP