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*Strengthening Global Teak Resources and Markets for Sustainable Development*

## **Genetics of Growth in Teak CSO Families and Provenances in Two Contrasted Tropical Sites**

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Teak is diploid ( $2n=36$ ), has a small genome (480Mpb), and display a high level of heterozygosity (more than 70% in the less depleted forests), all favorable traits for improvement through selection and breeding. In spite of the interest of teak for the world market, R&D efforts in teak genetic improvement are still rare. As a result, forest companies still have little choice for their investment in genetically superior materials.

As a first step towards a better exploitation of teak genetic potential, we tested 16 families derived from a clonal seed orchard (CSO) and 10 common provenances (Prov) of teak in two different tropical sites, a) to compare, in a statistically sound experiment, the provenances among them and with the CSO families and, b) to estimate the heritability of growth traits and the genetic gains that can be expected via breeding.

Both sites are located in Sabah, East Malaysia. For the statistical analysis we used a mixed model accounting for spatial variation. Nine years after planting, the two genetic entries, CSO and Prov, showed highly significant differences for height, DBH and volume in both sites. The superiority of the CSO families compared with the Prov class was large for volume production, resulting in an advantage of +67.9% and +40.3% in Luasong and Taliwas, respectively. Narrow-sense heritabilities for the 16 CSO families were larger for height (0.38) and volume (0.23). These promising results will translate in even better outcomes in the field, once geneticists will be able to concomitantly deal with the improvement of stem form, wood quality and tolerance to biotic and abiotic stresses.

In combination with the deployment of new modern DNA technologies, these favourable traits should make teak genetic improvement through selection and breeding attainable and effective with a reasonable R&D investment.

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