

## Regional population differences in growth characteristics of the Dipterocarpaceae tree species *Shorea leprosula*

Excessive logging has led to the degradation and deforestation of tropical forests dominated by Dipterocarpaceae species in Southeast Asian regions. Furthermore, as the effects of climate change on tropical forests are becoming more apparent, there is an urgent need to establish sustainable afforestation techniques for Dipterocarpaceae species. One of the Dipterocarpaceae species, *Shorea leprosula*, is widely distributed in Peninsular Malaysia and is considered to be one of the most important timber species. On the other hand, there is a concern about an increasing risk of scale insect infestation due to climate change, and the collection of detailed data is becoming urgently important.

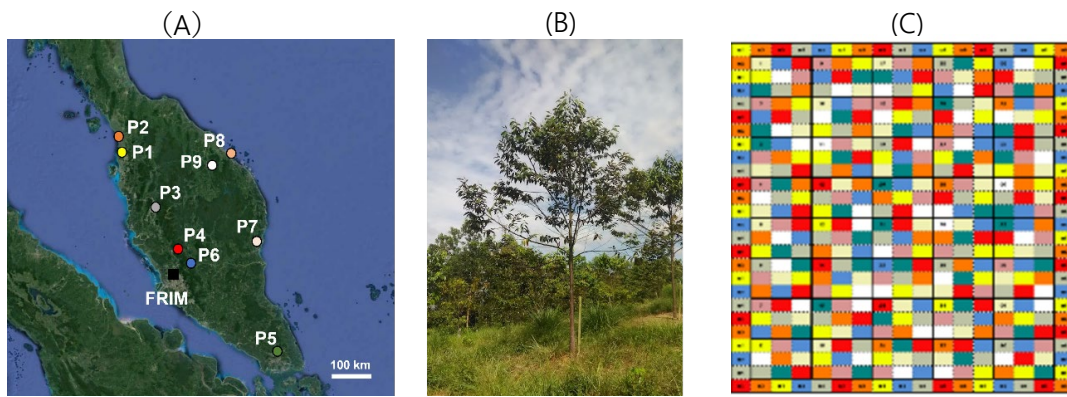
Therefore, this study aims to detect differences in growth characteristics among genetically distinct populations and to evaluate tolerance against scale insect infestation in a common garden experiment using *S. leprosula* seedlings from different forest reserves in the Malay Peninsula.

A common garden was established at the Forest Research Institute Malaysia (FRIM) to elucidate the genetic basis of the complex quantitative traits of dipterocarp through genome-wide association studies (Fig. 1A). In this common garden, *S. leprosula* seedlings (Fig. 1B) from nine populations were grown in 40 replications using the random block design (Fig. 1C). We found that the relative growth rate of tree height was highest in population P7 and significantly different from populations P2, P4, and P9 (Fig. 2,  $p < 0.05$ ) and insignificantly different from P1, P3, P5, P6, and P8 ( $p > 0.05$ ). Also, the number of scale insects (*Pedroniopsis* sp.) was the lowest in P7, with significant differences ( $p < 0.05$ ) from P3 and P9 and insignificant from P1, P2, P4, P5, P6, and P8 ( $p < 0.05$ ) (Fig. 3A). In the future, the common garden is expected to be used as a platform for genome-wide association studies, and it will be necessary to investigate the correspondence between genetic differences and phenotypes at the individual level of *S. leprosula*.

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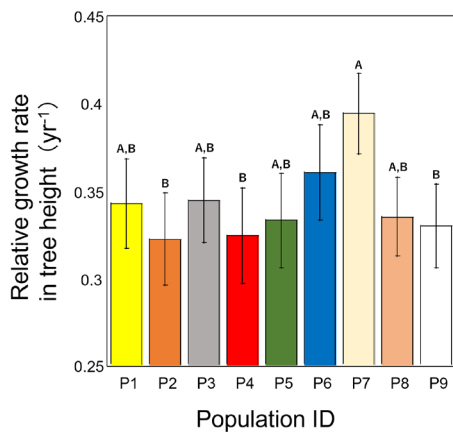
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**Fig. 1. (A) Sampling sites of seedlings in the Malay Peninsula and Forest Research Institute Malaysia (FRIM), (B) *S. leprosula* planted in the common garden, and (C) the random block design in the common garden**

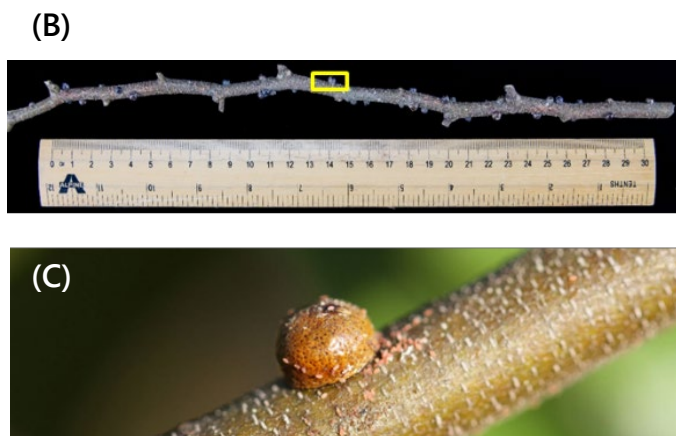
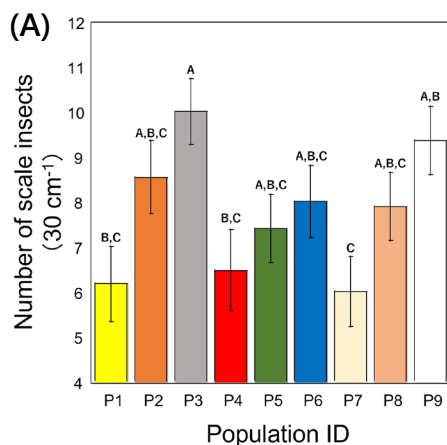
(A) The circles indicate the sampling sites, and the square indicates the location of FRIM where the common garden was established. The numbers indicate the population ID of each sampling site. (B) *S. leprosula* individuals 3 years after planting.

(C) Different colors indicate different populations of the planted seedlings.



**Fig. 2. Relative growth rate of tree height by population**

Different letters indicate significant differences ( $p < 0.05$ ).



**Fig. 3. (A) Number of scale insects on branches in each population, (B) a branch with scale insects, and (C) an enlarged view of a scale insect**

(A) Three 30-cm branches were sampled for each individual. The number of scale insects was counted, and the average value is shown. (B) A branch with scale insects, where the yellow box indicates the location of a scale insect (*Pedroniopsis* sp.).

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