GENOTYPE-ENVIRONMENT INTERACTION
IN SEEDLING SEED ORCHARDS OF Eucalyptus pellita IN INDONESIA

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Introduction

Eucalyptus pellita is one of the most promising Eucalyptus species for plantation programs in tropical lowlands. It has been planted in a wide range of sites in Indonesia, especially in Sumatra and Kalimantan Islands, as part of the development of an industrial forest plantation program. In the first rotation, E. pellita is considered to be less productive than the tropical acacias (Harwood et al., 1997). Thus, the tree improvement program for E. pellita, currently under way with seedling seed orchards established at several locations in Indonesia, is expected to increase the level of productivity by supplying genetically improved seed. However, there no data are available as yet describing the change in productivity at each location resulting from the first generation tree improvement and the use of an optimum seed transfer zone to reduce the loss of genetic gains due to genotype-environment interactions (GEI). This is because the effects of GEI complicate the tree breeding programs and may reduce the rate of genetic progress by selection. Heterogeneity among forest sites, due to variations in soil and/or climatic conditions, may cause GEI (Gwaze et al., 2001). Therefore, the magnitude of the GEI will affect to decisions on testing, selection and deployment. The objective of this study was to examine the magnitude of GEI by predicting expected genetic gains for single site selection compared to multi-site selection in seedling seed orchards of E. pellita in Indonesia.

Materials and Methods

Data used in this study were obtained from seven seedling seed orchards of E. pellita established at three locations in Indonesia: one location on Kalimantan Island (South Kalimantan province) containing a single seed orchard and two locations on Sumatra Island (South Sumatra and Riau provinces) with three seed orchards at each location. The seed orchards at each location were consisted of 121 families from three geographically distinct provenances from Papua New Guinea. Height and diameter were measured, at all three locations, when the threes were six years old. The pooled sum of squares derived from an analysis of variance of growth of the three provenance populations was used to estimate genetic parameters at each location and between the locations. These parameters were then used to calculate genetic gain as a result of both direct and indirect selection.

Result and Discussion

The GEI across the three locations was very strong, while the results of pairwise site analysis show very clear differences in GEI between the pairs of locations. These findings are consistent with ratios of GEI to family variance component ($\sigma^2_{fj}/\sigma^2_f$), which, for both traits, is high between South Kalimantan and the other locations (>0.5) and lower between South Sumatra and Riau, suggesting that the interactions in these seed orchards are likely to be of practical importance in selection and testing (Shelbourne, 1972). The result of genetic correlation between pairs of locations support the ratios of GEI to family variance components for the three locations and suggest that family ranking in Riau is similar to that in South Sumatra, but that they are different from the ranking in South Kalimantan. The genetic gains resulting from direct selection were apparently greater than those resulting from indirect selection. Calculated losses in gain as a result of inter-island transfer were generally high, reductions of approximately 60%. In contrast, the loss of gains resulting from transfer on a single island, Sumatra, was only 24%. Therefore, to maximize the efficiency of selection between different locations and to minimize losses in genetic gain, the breeding population in South Kalimantan should be developed separately from those in South Sumatra and Riau.

Literature cited


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