

Evaluation of an Open-Nucleus Model for Forest Tree Breeding

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Poster Abstract

Open-nucleus breeding was evaluated by stochastic simulation. Methodology was developed for unrestricted migration rate between two tiers (main and elite). Genetic progress in the breeding population was iteratively maximized for a wide range of restrictions on diversity varying from strong family selection to balanced within-family selection. The model assumed genetic parameters typical for growth traits in conifers and accounted for inbreeding depression. Comparison was made with a single population without hierarchical structure assuming constant testing effort. A seed orchard was established in each breeding cycle as a selected subset of the breeding population. The extra gain achieved by assigning better mates into the elite population was counteracted by increased group coancestry (relatedness) among seed orchard selections. The size of elite tier was found to have little importance in this study. When more effort was concentrated into elite crosses, potential for inbreeding in the seed orchard crop increased.

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Note: Also presented as a contributed paper.