Evaluation of an Open-Nucleus Model for Forest Tree Breeding

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INTRODUCTION

"Nucleus breeding" refers to hierarchical structuring of a breeding population. The top level in the hierarchy is designated as the nucleus (elite) tier. The nucleus can be "closed" (no gene flow into nucleus) or "open" in which case there is gene flow into the nucleus from tiers of lower hierarchy (Roden 1994). The open-nucleus breeding concept was first used by sheep breeders in Australia and New Zealand in the mid 60's (del-Bosque González 1989). The genetic advantage of an open nucleus comes from the assortment of mates in a group sense (Shepherd and Kinghorn 1992). The concept was adopted into forest tree breeding (Cotterill *et al.* 1989) and has been continuously considered in tree breeding programs throughout the world.

The objective of this study was to investigate if there is any genetic advantage of the open-nucleus system compared to the individual assortment of mates (positive assortative mating) across the entire breeding population. The evaluation focus of our study was the gain and diversity in a seed orchard production population (the breeder's target).

METHODS

A stochastic simulation model was developed to represent open-nucleus breeding in a multi-generation forest tree breeding program. A breeding population of 48 founders was managed in three different ways through five cycles of breeding and selection. In the first alternative there was no hierarchical structure and the population was randomly mated (**RM**) to produce the recruitment population, serving as the source of candidates for "forward selection" of breeding parents in the next cycle breeding population. Individual positive assortment of mates (**PAM**) across the entire breeding population was conducted in the second alternative. In the third approach, the top-ranking parents in each cycle were allocated into a nucleus tier and the remaining parents to the main tier (**NB**). In this latter alternative, random mating took place within both tiers.

The recruitment population was composed of 24 families, each having 100 seedlings that were each clonally replicated by 10 ramets. Group-merit selection (Lindgren and Mullin 1997) was employed to select the next cycle's breeding population considering both gain and diversity. A production population (seed orchard) was a selected subset of the 6 top-ranking parents in the breeding population in each cycle. The alternatives were compared over 5 cycles considering seed orchard gain and diversity (group coancestry).

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It is often suggested to allocate more effort to better parents. Such an approach was evaluated by performing double-pair mating in the nucleus and single-pair mating in the main tier at a fixed level of total testing resources. The mating was either random within both tiers (**NB-RM**) or positive assortative in the nucleus and random in the main tier (**NB-PAM**). These open-nucleus strategies were compared with the individual assortment of mates in the whole breeding population with the top ranking third of parents each involved in 3 crosses, the lower thirds in 2 crosses and the poorest third in only one cross (**PAM 3-2-1**).

RESULTS

Positive assortative mating enhanced the additive genetic variance in the breeding population when the restriction on diversity was moderate to high (situations closer to balanced selection within families). Though the assortative mating did not significantly alter the additive variance in the breeding population when the diversity was not considered (strong family selection), the average population additive effect increased, as there was potential for more extreme genotypes in crosses among parents with top breeding values. Average inbreeding in the breeding population was higher with positive assortative mating than with random mating. This is because trees with similar breeding values are on average expected to be more related with each other than with other trees in the breeding population. All of these impacts of parental assortment on the breeding population structure were more pronounced in magnitude at the individual level of assortment (**PAM**) compared to assortment in a group sense (**NB**).

Individual assortment of mates (**PAM**) across the whole breeding population delivered more genetic gain in the seed orchard compared to the open-nucleus alternative (**NB**) at any target level of diversity (Figure 1). Optimum nucleus sizes varied depending on what was considered the target population, what was the desired level of diversity in that population and upon other factors. Generally, larger nucleus sizes resulted in more seed orchard gain when diversity was considered as important.

Open-nucleus breeding with more effort allocated to better parents (**NB-RM**) was also inferior to the individual assortment of mates (**PAM 3-2-1**) (Figure 2). Nucleus breeding with positive assortative mating in the nucleus and random mating in the main tier (**NB-PAM**) resulted in lower seed orchard diversity in later cycles under balanced within-family selection and was still inferior to the PAM 3-2-1 alternative.

The conclusion of this study is that when seed orchard gain and diversity are considered simultaneously, individual parental assortment across the whole breeding population can result in more gain than open-nucleus breeding. This conclusion holds for balanced distribution of testing effort and also for cases when more effort is allocated to better parents.
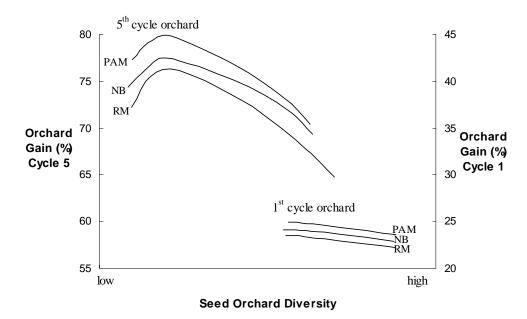
Figure 1. Genetic gain and diversity in the 1ˢᵗ and 5ᵗʰ cycle seed orchards under balanced distribution of testing effort. Alternatives are: random mating **RM**, nucleus breeding **NB**, and positive assortative mating **PAM**.
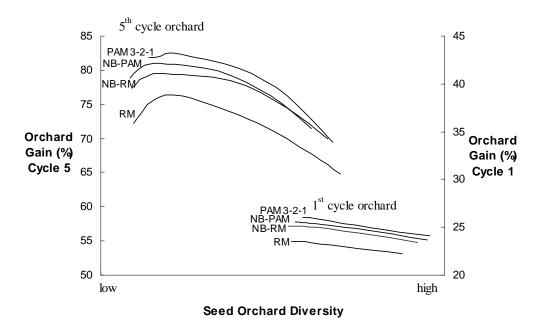

Figure 2. Genetic gain and diversity in the 1ˢᵗ and 5ᵗʰ cycle seed orchards when more resources were allocated to higher-ranking parents. Alternatives are: random mating **RM**, nucleus breeding with random mating in nucleus **NB-RM**, nucleus breeding with positive assortative mating in nucleus **NB-PAM**, and positive assortative mating **PAM 3-2-1**.

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