Conversion of a Progeny Trial of *Eucalyptus tereticornis* to a Seedling Seed Orchard Considering Gain and Fertility

R. Kamalakannan[1], Mohan Varghese[1], Nebi Bilir[2] and Dag Lindgren[3]

[1] Institute of Forest Genetics and Tree Breeding, P.B. No. 1061, Coimbatore 641002, India
[2] Forestry Faculty, Suleyman Demirel University, Isparta, 32260, Turkey
[3] Department of Forest Genetics and Plant Physiology, Swedish University of Agricultural Sciences, SE 901 83, Umeå, Sweden
Email: kamalakannanr@yahoo.com

Abstract

An open pollinated progeny trial of fifty families of *E. tereticornis* was evaluated at age four. It was thinned to 625 of initially planted 1250 trees by truncation selection for the phenotype (an index weighting the tree values for height, stem diameter and form). The remaining trees were evaluated for fertility at age seven. Only 21% of the trees were fertile. Combined index selection and phenotypic selection based on the growth data at age 4 were compared assuming an additional thinning down to 200. Gain and diversity of the predicted crop was calculated based on the fertility registrations. Combined index selection gave 5% less gain than phenotypic selection, and 25% reduction in diversity (status number). Sibling coefficient (measure of fertility variation among the retained trees) was 39% higher with index selection. Thus selection for breeding value (gain) seemed less efficient than phenotypic selection for this particular case of converting a progeny test plantation to a seedling seed orchard. Since fertility is low in first generation introductions of *E. tereticornis* in moist tropical regions, improvement in fertility is likely to reduce inbreeding in offspring and promote representation from more families.

Keywords: selection, gene diversity, status number, genetic thinning

Introduction

Seedling seed orchards are commonly used as production populations in breeding programs for short rotation tropical eucalypts (Eldridge *et al*., 1993). As land races suffer from hybrid breakdown and narrow genetic base (Davidson, 1998; Boland, 1981), open pollinated families of selected natural provenances are generally used to initiate the program. As a short term strategy for meeting the immediate seed requirement, fifty good *E. tereticornis* trees selected in existing first generation introductions from Australia were used for establishing a progeny trial and conversion to seedling seed orchard after evaluation and thinning (Varghese *et al.* 2001). Seedling orchards are expected to generate superior quality seed compared to other unimproved sources. Selection methods for increasing gain are often opposed to strategies for improving diversity of the seed crop. Different selection strategies can be employed for enhancing gain. In combined index selection weighting is given based on individual and family values (Falconer and Mackay, 1996) whereas phenotypic selection ranks the individual based on its phenotypic value without considering its family merit. An ideal strategy would be one that combines gain and diversity monitored in terms of a quantified effective population number (Lindgren *et al.*, 1996) with adequate representation from different families for production of out crossed seed. When thinning done in a half sib progeny trial, the relationship between genetic gain and diversity must be well understood. These factors must be predicted to adequately manage inbreeding in plantations and to plan seed collection. Seedling seed orchards are expected to serve as a means of packaging genes and generate improved seed at the culmination of a generation of breeding. Breeding values are normally used for culling the inferior families and individuals to maximise gain. Fertility of trees also has to be considered as it ultimately decides the transfer of the genes to the seed crop. The quality of seed output from an orchard will be judged from the possible gain and the diversity of the deployed crop. Genetic value of seed will be determined by the breeding values and the maternal and paternal gametes produced by the orchard trees. This study aims to predict the impact of a hypothetical selection thinning schedule on the genetic gain and diversity in a second generation progeny trial of *E. tereticornis.*.

Material

A progeny trial of *Eucalyptus tereticornis* was established at Tamil nadu (10° 23’N latitude, 78° 49’E longitude, 180m altitude, 650mm rainfall) in southern India. The trial comprised 50 families originating from open pollination of selections in first generation Indian plantations. The initial spacing was 2m x 1m. The trial was evaluated at age four. The progeny trial was thinned to half of initially planted by truncation selection for an index weighting the phenotype for tree height, stem diameter and tree form. The remaining trees were evaluated for fertility at age seven. Observation of the number of flowers and fruits on each tree were used as measures of female and male fertilities respectively. The trial was to be converted to a seedling seed orchard after a second thinning, as part of a breeding program for eucalypts (Doran *et al.* 1996). Predictions of breeding values of individual trees for tree height were obtained after evaluating the trial at four years of age as a combined index of maternal family and the individual phenotype = breeding value (Falconer and Mackay, 1996). A hypothetical selection of the 200 best trees was done either by combined index selection or phenotypic selection using select function of the Data Plus program (Williams *et al.* 1999).

Theory and methods

The theoretical background for seed orchards utilized in this study was developed by Lindgren and Mullin (1998). Group coancestry (Θ) is the probability that two genes taken at random from the gene pool of the expected seed orchard crop will be identical by descent. Group coancestry applied for a diploid population is the average of all coancestry values between population members (including self-coancestry), but as group coancestry depends only on the gene pool and not how it is organized into individuals, the group coancestry concept can as well be applied to successful gametes before they form diploid zygotes. Status number (N_s) is the number of non inbred non related genotypes sampled from the reference population that are expected to experience the same deviation in gene frequencies from the reference population as the population under study. These two parameters are used to monitor the diversity level in the orchard resulting from relatedness of selected trees. Sibling coefficient (ψ), which is the probability that two genes originate from the same parent, is used to quantify the extent of fertility differences between orchard genotypes. Maternal and paternal fertilities of each tree are used as the probability of contribution of each genotype in determining the group coancestry (Θ), which can be obtained by adding all possible pairings of gametes from orchard trees.

Flower and fruit production in the trees were recorded during the period October 2005 to January 2006. The number of primary, secondary and tertiary branches was counted in each tree and the flowers per tertiary branch recorded for all the trees during two visits in the peak flowering period of October - November. The number of developed fruits per secondary branch was recorded in two visits during the period of seed collection (December - January). Estimates of number of fruits and stamens per tree were obtained by extrapolating the counts made on stamens and fruits (Bila *et al*. 1999; Kang and Lindgren 1998).

Genetic gain - was worked out as the deviation of the average breeding value of the selected tree from the mean breeding value of all trees measured at year 4 (Lindgren *et al*., 1989) and the fertility contribution using the formula

$$G = \sum_{i=1}^{N} p_i (g_i - g_a)$$

where g_i is the breeding value of the i^{th} selected tree and g_a the mean breeding value of all (N) trees and p_i the proportion of fertility of the i^{th} tree .

Group coancestry can be divided in two (additive) terms, self-coancesty (Θ_s) and paircoancestry (Θ_p).Group coancestry of the gametes in the orchards indicates the coancestry that the seeds originate from the same parents as eucalyptus has a mixed mating system. Pair group coancestry indicates the group coancestry of the seeds originating from related trees. This causes inbreeding in seeds during the mating. Summation over other trees from the same family was done to consider the contribution from half sibs to the expected group coancestry of the expected crop, $p_i p_j$ when i and j belongs to the same family.

$$\Theta_p = 0.125 \sum_{i=1}^{N} \sum_{j=1 if j and i}^{N} p_i p_j \quad {}_{belongtosamefamily}$$

Status number (N_S): The diversity of the expected seed crop can expressed in terms of group coancestry as a type of effective number, the status number

$$N_s = \frac{0.5}{\Theta}$$

Relative status number: The relative status number ($N_r = N_s / N$, where N is the census number of selected trees) was worked out to compare the effective number of trees with the respective census number

Sibling coefficient (Ψ) : It is calculated from the number of trees in the orchard (N) and individual fertility (p_i) of each tree and used to describe fertility variation among the trees.

$$\psi = N\sum_{i=1}^{N} p_i^2$$

Gene diversity

Expected gene diversity (GD) is a function of the group coancestry and can be calculated in the orchard relative to a reference population. Since the reference population (which is the natural forest the plus trees were selected from) has zero group coancestry, gene diversity is calculated based on the increase in Θ since breeding operations started.

$$GD = 1 - \Theta$$

Results and Discussion

The results are presented in Table 1 below.

The major considerations in a selection program are selection intensity, genetic gain, inbreeding and gene diversity. For a given intensity of selection, there has to be a compromise between gain and diversity as the two effects operate in conflict with each other. Generally the prime objective of any improvement program would be to increase gain in the next generation. Genetic diversity in the orchard is however necessary for production of vigorous progeny in species with mixed mating system and number of represented families can have a great impact on the structure of the seed crop. The inbreeding that sets in is a function of the coancestry of the orchard parents, which could restrict the future improvement possible. Gene diversity can also have a value for the productivity of a stand, it can be a safe guard against calamities, and it is expected that a diverse crop utilize the site better. The impact of all these factors has to be considered when thinning is planned in the orchard.

Combined index selection, which gives emphasis to family performance, had trees from fewer families represented compared to the other two methods. Phenotypic selection which is essentially a truncation of outstanding phenotypes resulted in greater number of families being represented at the same selection intensity.

Genetic gain

Genetic gain (computed as the product of the index value and the fertility contribution) was 5% lower in index selection since the selections were from superior families where many trees were not fertile (Table 1). In phenotypic selection, phenotypically outstanding individuals from inferior families were also represented giving lower breeding values but since many trees were fertile the average gain was high. Index selection had 21% less number of families represented than phenotypic selection.

Fertility status

Only 21% of the trees were fertile in the stand at seven years. The situation appears slightly improved in this second generation orchard compared to an earlier study in a first generation orchard of *Eucalyptus tereticornis* (Varghese *et al*. 2002) where only 17.5% of the 200 selected trees were fertile resulting in high fertility variation ($\Psi = 17.4$). Sibling coefficient value in this study is considerably lower than that in the first generation orchard. It is however 28% lower for phenotypic selection than for index selection. It is still considerably higher than the predicted value ($\Psi = 2.62$) for seedling seed orchards of hardwood species (Kang *et al*. 2003). Thus fertility variation in *E. tereticornis* may be regarded as unusually high in tropical regions (Pinyopusarerk and Harwood, 2003) and due consideration should be given to this factor when planning orchards for seed production.

Diversity

Loss of diversity and increase in relatedness are expected in the advanced stages of improvement in a species. Improvement in gain is at the cost of diversity with each advance in generation. It is however important to monitor the consequences of selection and thinning done to enhance gain. As relatedness increase beyond a certain point, depending on the deviation from random mating, much of the desired benefits may not be achieved. Kang *et al*. (2001) recommended an effective clone number of at least 10 in an advanced generation clonal seed orchard with an equal number of ramets per clone. It is desirable to keep the levels of coancestry low when fertility variation is high and a strategy of retaining fertile phenotypically superior trees can enhance the effective population size by 33% than with index selection.

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Table1. Estimate of gain and diversity with different selection strategies

Parameter	Combined Index selection	Phenotypic selection
Number of trees (N)	200	200
Number of families	37	47
Group coancestry (Θ)	0.0410	0.0307
Status number (N_s)	12.2	16.29
Sibling coefficient (Ψ)	13.96	10.06
Relative status number (N_r)	0.061	0.081
Gene diversity (GD)	0.9590	0.9693
Gain (G)	92.12	96.67