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Genetic Gain and Diversity under Different Selection Methods in a Breeding Seed Orchard of *Quercus serrata*

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Abstract

Genetic gain and diversity were estimated in a 13year old Quercus serrata breeding seed orchard under three selection (rouging) methods. The selections were based on individual selection, family selection, and family plus within family selection. Genetic gain was for stem volume and gene diversity was estimated by status number concept. Both estimated genetic gain and gene diversity were compared to those before selection and among selection scenarios. Estimated genetic gain for tree volume ranged from 4.0% to 9.1% for three selection methods under 50% selection intensity. Individual selection was better than family selection for retaining higher genetic gain and status number. Family plus within family selection was the best selection method, while individual selection was more efficient at the strong selection intensity. An optimal point, which maximized gain and diversity, was occurred at 50% selection intensity that would be applied for genetic thinning in the breeding seed orchard of Quercus serrata. The effect of genetic relatedness among families and possible pollen contamination on both genetic gain and gene diversity, although were not studied but their impact, are discussed. The selection method and intensity level applied should be chosen after careful consideration of the impacts on both genetic gain and diversity for seeds produced from the seed orchard.

Key words: seedling seed orchards, coancestry, thinning, selection intensity, rouging.

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Introduction

Quercus serrata Thunb. is one of the most important oak species as well as among other broadleaves growing in South Korea. Acorns have long been employed as a source of hog feed, tannin, oil and especially food. Edible acorns of Q. serrata are frequently used to make acorn flour and acorn jelly because of high tannin contents (KFRI, 1990).

The breeding program of Q. serrata started with the selection of 110 plus-trees from natural stands of South Korea. Seedlings were originated from the selected plus-trees and used to establish seedling seed orchards. Due to the limited graft availability caused by high root stock-scion incompatibility, the establishment of clonal seed orchards for Q. serrata was limited. At present, most of the Q. serrata seed orchard was established using the concept of breeding seed orchard (BSO) (BARNES, 1995; DAVID et al., 2003). In the BSO concept, open-pollinated progeny provided the seedlings for progeny test trials that coupled with seed production, as required by the BSO design.

Breeding intensity within the BSO can be individual selection, family selection or pedigree (half- or full-sibs) control. In determining the genetic construction of BSO, the crucial issues are to select parents effectively, avoiding inbreeding and to evaluate precisely the performance of the progeny. Genetic gain depends on the effectiveness of selection that is also dependent on intensity, precision and criteria.

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Seed orchard managers typically rely on one of the below selection methods to remove undesirable trees in a seed orchard. Individual selection (mass selection) ranks each individual tree and rogues those below a minimum threshold level. Family selection ranks families based on family means and retains all the individuals on the selected families regardless of their individual performance (ADAMS and MORGENSTERN, 1991; MORRIS et al., 1992). Family plus within family selection retains a specific member of individuals in the best families (CANAVERA, 1975). Each of these selection methods will increase the expected genetic gain of a particular trait in family representation after genetic thinning, but have varying effects on the genetic diversity due to differences in family representation after selection (BONDES-SON and LINDGREN, 1993; KANG et al., 2005).

The objectives of this study were (1) to calculate the variance components and heritabilities for stem volume growth measured in a breeding seed orchard of Q. serrata and (2) by the aid of compute simulation, to compare genetic gain and diversity (status number) obtainable from the following three seed orchard thinning methods: individual selection, family selection, family and within family selection aiming at development of efficient selection options in the breeding seed orchards.

Materials and Methods

Seed orchard and data collection

The studied seedling seed orchard/progeny test of Q. serrata is located in Hwasung, Kyonggi (at 37°16'N, 126°55'E and 100 m altitude) and established in 1992. Open-pollinated families were represented by 27 blocks with one seedling from each of 17 families arranged in

single-tree plots. Seedlings were planted with 5 x 5 m spacing. At the beginning, the breeding seed orchard (BSO) consisted of 400 trees, indicating that not all families were fully represented by 27 trees. In 2004, a total of 367 individual trees remained in the BSO.

In 2004, tree height (H) and diameter at breast height (DBH) were measured in the BSO. For statistical analysis of individual stem volume, a volume index was calculated as tree height x squared DBH (H^*D^2) and used to calculate variance components and heritability.

Variance components and heritability

Variance components for stem volume (H^*D^2) were estimated using the SAS program, PROC GLM and VARCOMP (SAS INSTITUTE, 1999) and the following model,

$$Y_{ijkl} = \mu + F_j + R_k + \varepsilon_l$$

where *Y* is the stem volume, μ is the grand mean, F_j is the random effect of *j*-th family and R_k is the fixed effect of *k*-th replication, and ε_j is the random error.

Family (h_{f}^{2}) and individual (h_{i}^{2}) heritabilities for stem volume were calculated using the variance components and the following formulae,

$$h_f^2 = \frac{\sigma_F^2}{\sigma_F^2 + \sigma_E^2 / k} \quad \text{and} \quad h_i^2 = \frac{4\sigma_F^2}{\sigma_F^2 + \sigma_E^2}$$

where σ_F^2 is the family variance, σ_E^2 is the residual variance and *k* is the coefficient of variance component $[k=1/(f-1)(n-\Sigma n_i^2/n)]$ where *f* is the number of family, *n* is the total number of tree and n_i is the number of tree in *i*-th family.



Figure 1. – Genetic gain (%) from the three different selection methods at variable selection intensities. Family plus within family selection (FWFS) gave higher gain than individual selection (IS) under moderate and week selection intensity because IS retained more poor individuals than FWFS. Under high intensity, the expected genetic gain by FWFS was fluctuated due to the variation in the harmonic mean of trees for within family selection.

Simulation of selection scenarios

Selection intensities (ranged from 10% to 90%) that represent the likely range of selection intensities for the BSO were used to estimate the genetic gain (ΔG). To compare among the three selection scenarios, the selection intensities (interval of 5%) were kept constant for all selection methods (see *Fig. 1*). The three selection scenarios studied were theoretically simulated as (see also DAVID *et al.*, 2003),

1. *Individual selection:* superior individuals were selected for stem volume

 $\Delta G = i_a \sigma_{\mu} h_i^2$

2. *Family selection:* superior families were selected, regardless of individual performance

$$\Delta G = i_a \sigma_p h_i^2 \left(\frac{1 + (m-1)r}{\sqrt{m(1 + (m-1)t)}} \right)$$

3. Family + within family selection: family selection first and then individual selection from the selected family (cf. linear selection; LINDGREN and MATHESON, 1986); the number of seedlings selected from each family was linearly proportional to the breeding value of the family.

$$\Delta G = i_b \sigma_p h_i^2 \left(\frac{1 + (m-1)r}{\sqrt{m(1 + (m-1)t)}} \right) + i_c \sigma_p h_i^2 \left((1-r) \sqrt{\frac{(m-1)}{(1-t)m}} \right)$$

where i_a , i_b , and i_c are the selection intensities due to the individual, family and within family selections (BECKER, 1984), σ_p is the phenotypic standard deviation, m is the harmonic mean of trees for the selected families, r is the genetic correlation (0.25) among half-sib families and t is the intraclass phenotypic correlation for half-sibs (0.25 x h_i^2) (FALCONER and MACKAY, 1996).

Diversity estimated by status number

Genetic diversity was estimated by status number (i.e., accumulation of group co-ancestry). Accumulation of group coancestry means inbreeding in the next generation if successful gametes unite at random (COCKERHAM, 1967; LINDGREN and MULLIN, 1998). The group co-ancestry (Θ) of the BSO, which describes the probability that two genes are identical by descent, was calculated based on the family representation (KANG *et al.*, 2001a; DAVID *et al.*, 2003).

$$\Theta = \frac{0.5\sum_{i=1}^{N} n_i + 0.125\sum_{i=1}^{N} (n_i^2 - n)}{n^2}$$

where N is the number of family selected, n_i is the family size of *i*-th family, and n is the total number of trees selected in the seed orchard. In this case, 0.5 is the self-coancestry of tree itself where trees are not inbred and 0.125 is the coancestry between half-sibs.

Status number (N_s) is defined as half the inverse of group coancestry, N_s = 0.5/ Θ (Lindgren $et\ al.,\ 1996),$ and obtained as follows,

$$N_{s} = \frac{0.5}{\Theta} = \frac{n^{2}}{\sum_{i=1}^{N} n_{i} + 0.25 \sum_{i=1}^{N} (n_{i}^{2} - n_{i})}$$

Relative status number (N_r) was calculated as $N_r = N_s/n$ (*n* is the total number of trees selected) for comparison among different selection scenarios (KANG *et al.*, 2005).

Loss of gene diversity (GD) was calculated relatively to the reference population that has the gene diversity of 1 and where families were derived from (KANG and LINDGREN, 1999; KANG *et al.*, 2001a) as follows,

$$GD = 1 - \Theta = 1 - \frac{0.5}{N_s} = 1 - \sum_{i=1}^{N} \left(\frac{n_i}{n}\right) \left(\frac{0.5 + 0.125(n_i - 1)}{n}\right)$$

where Θ is the group coancestry, N is the number of family retained, n_i is the family size of *i*-th family and n is the total number of trees retained in the seed orchard (LINDGREN *et al.*, 1996; KANG *et al.*, 2005).

Results

There were significant differences in volume index among families and among the replications (*Table 1*). The average tree height was 710.1 cm, the average tree diameter at breast height was 16.8 cm and the average volume index was 0.22. Estimates of variance components for individual tree volume were made, and individual (h_i^2) and family (h_f^2) heritabilities were calculated as 0.62 and 0.80 respectively.

Table 1. – ANOVA for volume index in the breeding seed orchard of $Quercus \ serrata.$

Source	df	Pr > F
Family ^a	16	<.0.001
Replication ^b	26	<.0.001
Error	324	

^a: random effect, ^b: fixed effect.

Individual selection (IS) provided higher genetic gain than family selection (FS) at all selection intensities (*Fig. 1*). Also, IS retained the highest number of families and the lowest average number of individual per family at all selection intensities (data not shown).

Family plus within family selection (FWFS) was the best selection method under low and intermediate selection intensity, while IS was better than FWFS for higher selection intensity (*Fig. 1*). The variation in the harmonic mean of trees for the families selected by FWFS gave strong impact on the lower genetic gain under the high intensity, meaning that genetic contribution is not equal among families due to the variation in family sizes after genetic thinning.

The optimal selection intensity that maximizes genetic gain and diversity was determined as 50% thinning in the breeding seed orchard of Q. serrata. Genetic gain, status number and relative gene diversity under three selection methods with 50% selection intensity are presented in Table 2. Under the 50% selection intensity, the family sizes for the initial stage and after individual,

Table 2. – Number of tree retained (NT), number of family selected (NF), genetic gain (ΔG), status number (N_s) and gene diversity loss (GD) under three selection methods with 50% selection intensity in the breeding seed orchard of Quercus serrata.

Selection method	NT	NF	ΔG	N_s	GD (%)
Individual	185	17	6.2	47.4(26%) ^a	1.05
Family	185 ⁶	9	4.0	29.1 (16%)	1.72
Family+within family	185	15	9.1	38.7 (21%)	1.29

 $^{\rm a:}$ relative status number in parenthesis, $^{\rm b:}$ the number of tree retained for the family selected just above the threshold was rounded down to make 50% selection intensity.

family and family plus within family selection are shown in *Figure 2*.

Under 50% selection intensity, FS had the lowest number of families selected and the poorest genetic gain, while FWFS showed the highest genetic gain and moderate status number (*Table 2*). All selection methods showed higher relative status number than the initial relative status number (i.e., before thinning) (*Table 2*). Loss of *GD* was not remarkable for all selection methods, which ranged from 1.05% to 1.72% compared relatively to the reference population (*Table 2*).

Discussion

The initial establishment phase of the seed orchard aimed at including 16 families with equal representation (i.e., 16 families presented with equal number of 25 trees). Due to replacement after the establishment, the seed orchard consists of 17 open-pollinated families selected from the natural distribution areas through the South Korea. Also, there was a large variation in the number of seedlings among families due to unintentional variation (*Fig. 2*), such as seedling availability at the time of establishment, replacement, mortality, and biotic and abiotic injuries (KANG *et al.*, 2001b).

The variation in family sizes (number of tree per family) affected the harmonic means of trees for the families selected by family plus within family selection (FWFS) and caused the fluctuation of genetic gain, especially under strong intensity (*Fig. 1*), meaning that genetic contribution would not be equal among families due to the variation in family sizes after genetic thinning. The FWFS gave higher gain than individual selection (IS) because IS retained more poor individuals than FWFS under moderate and week selection intensity.

Linear deployment, which deploys the number of seedlings proportionally on the breeding value of the family, proposed by LINDGREN and MATHESON (1986), can



Figure 2. – Family size (number of tree per family) before selection (initial) and after individual (IS), family (FS) and family+within family selection (FWFS) in the breeding seed orchard of Q. serrata. Selection intensity applied was 50%.

be seen as the optimization of the FWFS. In their study, they didn't consider the family size and assumed the equal representation of genotypes. Seed orchard managers generally reply on one of the three methods to remove unfavorable trees in breeding seed orchards. However, as shown by the present study, the selection method should be determined after consideration of family size and heritability of the traits (c.f., BONDESSON and LINDGREN, 1993), especially when a seed orchard shows a large difference in family representation.

In the initial seed orchard, the status number was 15% of the census number. All selection methods showed higher relative status number than the initial seed orchard. From the orchard management point of view, it could be seen that contribution among families to seed production would become more equal after genetic thinning.

Loss in gene diversity is inversely proportional to the status number and relatively estimated to the reference population (KANG et al., 2005). Gene diversity is a measure of the probability that genes are not identical by descent in the gene pool (LINDGREN et al., 1996). This estimate implicates that the genetic diversity of seed produced in the seedling seed orchard is reflective of the level of gene diversity in the seed orchard after genetic thinning (ASKEW and BURROWS, 1983). This assumes that all seeds produced are half-sibs; i.e., pollination in the seed orchard is completely random. But, the actual level of sib mating is unknown due to differences in flowering phenology, the amount of male and female flowers and the level of pollen contamination (GRIFFIN, 1982; ROBERDS et al., 1991; EL-KASSABY and COOK, 1994).

Genetic gain from seedling seed orchards can be manipulated by selection method and intensity that are applied for thinning the orchard after crown closure (ZOBEL and TALBERT, 1984). But strong genetic thinning would result in a decrease of genetic diversity in the seed produced by the seed orchard.

In conclusion, our study showed that selection method and intensity level used should be chosen after careful consideration of the impacts on both genetic gain and diversity for seeds produced from the seed orchard.

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