Genetic Gain and Diversity in a Clonal Seed Orchard of *Pinus koraiensis* under Various Thinning Intensities

C.Y. Oh, K.S. Kang, W.Y. Choi, S.U. Han, and C.S. Kim[1]

There are various orchard management options to increase genetic gain while conserving genetic diversity, including selective harvesting, genetic thinning and combination of both. Genetic improvement is defined as a process that enhances the genetic value while giving deliberate consideration to the genetic diversity of deployed materials (Kang et al. 2001). The calculations of genetic gain and diversity in seed orchard populations are of great theoretical and of practical importance.

The objectives of this study were to evaluate the genetic gain and diversity of seed crops from a *P. koraiensis* clonal seed orchard under different thinning intensities, and to determine appropriate selection intensity.

MATERIALS AND METHODS

The clonal seed orchard of *P. koraiensis* is located in Dukduwon, mid-northern part of Korea (lat. 37° 52'N, long. 127° 37'E, alt. 500m and area 12ha) and was established in 1981. A total of 179 clones (total 5,268 ramets) were included at the stage of establishment. Additive genetic values for each orchard-parent genotype were obtained from open-pollinated progeny tests (represented by general combining ability, *GCA*). Parental *GCA* values for volume growth were estimated by the method of best linear unbiased prediction (BLUP). Clonal fertility was estimated from assessments of strobilus production over twelve consecutive years from 1991 to 2003.

Genetic thinning was computed from 10% to 90% thinning intensities with 10% interval and compared with truncation (50%) thinning.. Since selection criteria for genetic thinning were based on clonal genetic values and flower production, clones with inferior general combining abilities (*GCA*) and poor seed production were targeted for ramet removal more than superior clones.

Genetic gain is the average of the genetic values of female and male parents. In the presence of pollen contamination, the genetic value of male parent is reduced due to the inferiority of contaminating pollen. Genetic gain (ΔG) was estimated (cf., GRIFFIN, 1982) as follows,

$$\Delta G = \sum_{i=1}^{N}\left(\frac{GCA_{female}+GCA_{male}}{2}\times q_{i}\right)$$

$$= \sum_{i=1}^{N}\left(\frac{GCA_{fi}+\{(1-2M)GCA_{mi}+(2M)GCA_{mc}\}}{2}\times q_{i}\right)$$

where GCA_{fi} and GCA_{mi} are general combing abilities of orchard female and male parents of the *i*-th clone, GCA_{mc} is the general combing ability of contaminating pollen, M is the rate of gene

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[1] Div. of Tree Breeding, Korea Forest Research Institute, Suwon 441-350, Republic of Korea

migration (i.e., half of pollen contamination), and q_i is the relative frequency of i-th clone, which considers ramet number and seed production.

Genetic diversity was measured by status number (N_s) that was defined as half the inverse of group co-ancestry by LINDGREN *et al.* (1996). For unrelated and non-inbred orchard clones, N_s can be estimated from the contribution of the clones. The status number was calculated (cf., KANG and LINDGREN, 1998) as,

$$N_s = \frac{1}{\sum_{i=1}^{N}(p_i \times r_i)^2} = \frac{1}{\sum_{i=1}^{N}\left(\frac{f_i + (1-2M)m_i}{2} \times r_i\right)^2}$$

$$= \frac{4}{\sum_{i=1}^{N} f_i^2 r_i^2 + (1-2M)^2 \sum_{i=1}^{N} m_i^2 r_i^2 + 2(1-2M)\sum_{i=1}^{N} f_i m_i r_i^2}$$

where p_i is the contribution of the i-th clone, f_i and m_i are the contributions of females and males of the i-th clone and r_i is the ramet proportion of the i-th clone. In the present study, the rate of pollen contamination was set to 30% ($M = 0.15$) and an additive variance of contaminating pollen (GCA_{mc}) was assumed to be –0.1.

RESULTS AND DISCUSSION

Genetic gain increased as thinning rates were set from 10% to 60% (Table 1). However, for the higher thinning intensities, the increase of genetic gain was not remarkable. Genetic thinning by means of truncation selection resulted in a greater genetic gain but a large decrease in status number. Status number was represented around 40 clones for 10% through 60% thinning intensities, but for the higher thinning intensities, it was a bit fluctuated.

In most first-generation seed orchard, it is difficult to establish with near-equal numbers of ramets for each clone. And the large variation of ramet numbers among clones always exists due to graft availability, graft incompatibility and etc. The average number of ramets per clone at the time of establishment was 29.4 but the range was 1 to 123. The clonal linear deployment concept applied in this study capitalizes on the differential variation of genetic gain among orchard clones. It can thus be beneficial to intentionally use an unequal number of ramet per clone, where clones with high breeding value contribute most to the seed orchard crop, thus gain is maximized without appreciable genetic diversity loss.

The present study has demonstrated the effective use of seed orchard's clonal information, such as genetic gain and fertility variation. Based on the present results, it could be concluded that thinning rate should not be stronger than 60% to optimize genetic gain while conserving genetic diversity. Consequently 50% or 60% thinning rate might be appropriate for genetic thinning in the clonal seed orchard of *P. koraiensis*.

Table 1. Census clone number (*N*), ramet number (*n*), genetic gain (*G*), status number (N_s) and relative status number (N_r) after the implementation of each genetic thinning intensities in a clonal seed orchard of *P. koraiensis*

	Initial establishment	Linear thinning									Truncation (50%)
		10%	20%	30%	40%	50%	60%	70%	80%	90%	
N	179	165	165	165	165	165	165	165	165	165	87
n	5268	4741	4214	3687	3160	2634	2107	1580	1053	526	2634
G	-0.01	0.18	0.27	0.34	0.39	0.43	0.45	0.45	0.46	0.44	0.64
N_s	41.4	40.2	40.1	38.2	40.3	40.5	39.6	43.1	48.4	55.8	23.7
N_r	0.23	0.24	0.24	0.23	0.24	0.25	0.24	0.26	0.29	0.34	0.27

Note that ramet variation was considered to calculate genetic gain and status number. Rate of genetic thinning was based on the number of ramets/clone.

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