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Genetic Variation in Fruitfulness in a Hinoki (*Chamaecyparis obtusa* Endl.) Seed Orchard and Its Impact on the Maintenance of Genetic Diversity in Seedlots

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Genetic variation in seed/cone production among clones was studied in a hinoki (*Chamaecyparis obtusa* Endl.) seed orchard containing 25 plus-trees by analyzing the number of cones, the yield of cones and seeds of individual ramets for 5 successive years (1982 to 1986). There was significant variation among clones each year and parental contribution in the seed orchard. Specifically, in the years 1982, 1983, 1984, 1985, and 1986, 20% of the clones produced 37.2, 60.6, 36.0, 44.3, and 44.8% of the total cones, respectively. The size of the crop greatly influenced the parental balance in the resulting seed/cone crops. The product moment correlation coefficients and Spearman's coefficients of rank correlation were small and insignificant between consecutive years, but large and highly significant between alternate years, suggesting the presence of carry-over effects in seed/cone production. The broad-sense heritability on a clone mean basis was 0.74 ± 0.15 for the number of cones, 0.72 ± 0.14 for the yield of cones, and 0.68 ± 0.13 for the yield of seeds. The corresponding heritabilities from analyses combined over all years were 0.24, 0.558, and 0.724, respectively. These results indicate that seed/cone production in hinoki is under strong genetic control. Several managerial measures are discussed that maintain the genetic diversity in seedlots used for reforestation, by reducing the variation in seed/cone production among clones and producing seed crops with equal contributions from all parents.

Key words: *Chamaecyparis obtusa*, clones, genetic diversity, parental balance, seed orchard

Long-term breeding aims at achieving a balance between continuous genetic gains and an adequate level of genetic variation. The most common method used in the long-term breeding of forest trees is the establishment of seed orchards, which link breeding programs and reforestation by delivering consistent yields of genetically improved seeds. Ideally, several biological conditions are required to meet these objectives in seed orchards (Eriksson *et al.*, 1973). In practice, however, seed-orchard crops are collected, extracted, and stored in bulk seedlots. Therefore, seed orchard crops are usually composed of undetermined proportions of seeds from each parent. Seed orchards often deviate from their "ideal" expectations. In particular, the parental contribution to seed/cone crops varies substantially among clones in seed orchards of many coniferous species (Griffin, 1982; Byram *et al.*, 1986; El-Kassaby *et al.*, 1989; Chaisurisri *et al.*, 1992; Matziris, 1993, 1997). The unequal contribution of clones could be the major factor responsible for minimizing the genetic base of a seedlot (El-Kassaby *et al.*, 1989). For this reason, it is important to collect a considerable amount of reproductive and phenological data in order to determine the ordinal parental influences within an orchard and then use this information for successful seed-orchard management.

Hinoki (*Chamaecyparis obtusa* Endl.) is one of the most important tree species used for reforestation in Japan. Seeds from plus-tree seed orchards are generally used for reforestation. As part of an ongoing investigation of fluctuations in genetic diversity in the process of reforestation in hinoki, we investigated the actual seed/cone production of every clonal ramet for a period of 5 years. The phenotypic and genetic variation in seed/cone production were analyzed among open-pollinated clones in a seed orchard, and this information was used to manage the genetic diversity of the seedlot for hinoki reforestation.

Materials and Methods

This study was conducted in a 7.2-ha hinoki seed orchard, located in Hamakita, Shizuoka Prefecture, Japan (latitude 34°46′N, longitude 137°46′E; elevation 110 m). The orchard was established in 1966 and consists of 25 clones, derived from intensively selected plus-trees from artificial stands throughout Shizuoka Prefecture. The grafted trees were planted at 3.5-m intervals in a randomized incomplete block design, and top-pruned to maintain an accessible crown 3 m high. However, no pruning was carried out during the 5-year study period. This seed orchard is not located in the main range of hinoki and is isolated by pine belts, so contaminating fertilization by background hinoki pollen is negligible. Commercial cone harvesting started in 1974, when the trees were 9 years old.

There are seven blocks in the seed orchard. Block 4, which contains 129 trees, was selected for this investigation. The cones were harvested separately from each tree. Table 2 lists each clone and the number of ramets (replicates) of each clone. The basic data for phenotypic and genetic variation analyses were collected in 5 successive years (1982 to 1986). The cones were weighed and counted. Then the seeds were extracted from the cones to determine the 1,000-kernel weight and the rate of filled seed according to the presence of embryos (data for years 1982, 1984, and 1986 only) for each tree, according to the rules of the International Seed Testing Association (1985).

The parental balance of the seed-orchard crops was summarized using seed-/cone-yield curves (Griffin, 1982). The

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clones were arranged in decreasing order of number or yield, and cumulative percentage calculations were plotted against the percentage of clones counted. Thus, the percent contribution of any proportion of clones to the total cone crop could be easily estimated. The product moment correlation coefficients and Spearman's coefficients of rank correlation based on clonal rank by yield of cones were computed across years in order to examine the ability to predict the clonal contribution to the cone crop from year to year.

Two- and one-way analyses of variance (ANOVA) were used to analyze the seed/cone data for the clonal trees over the five years (Table 3) and for each year (Table 4), respectively. All the data were transformed to log (*count* + 1) to fulfil the homogeneity of the variance test before the analyses were done. Estimates of broad-sense heritability were obtained on an individual tree (H_1) and clone mean basis (H_2), each of which had different phenotypic variation, in the following manner (Matziris, 1993, 1997).

For each year:

$$H_1 = \frac{\sigma_c^2}{\sigma_c^2 + \sigma^2} \quad \text{(individual tree basis)}$$

$$H_2 = \frac{\sigma_c^2}{\sigma_c^2 + \sigma^2/n} \quad \text{(clone mean basis)}$$

For the combined years:

$$H_1 = \frac{\sigma_c^2}{\sigma_c^2 + \sigma_{yc}^2 + \sigma^2} \quad \text{(individual tree basis)}$$

$$H_2 = \frac{\sigma_c^2}{\sigma_c^2 + \frac{\sigma_{yc}^2}{n} + \frac{\sigma^2}{yn}} \quad \text{(clone mean basis)}$$

The symbols in the equations are described in detail in the footnotes for Tables 3 and 4.

Results and Discussion

The average yield of cones per tree showed considerable variation over the 5 years investigated. The variation in the average number of cones and the yield of seeds per tree followed the same trend (Fig. 1). The seed/cone crops produced per tree were average, lean, bumper, reduced, and average in 1982, 1983, 1984, 1985, and 1986, respectively. A similar fluctuation in seed/cone production was observed in another hinoki seed orchard in Gifu Prefecture (Katsuta, 1982), suggesting that periodicity in seed/cone production seems to be a common phenomenon for hinoki seed orchards.

To estimate each clone's contribution to the annual cone production, the percentage that each clone contributed to the total crop was estimated for each of the 5 years. Figure 2 shows each clone's contribution to the total yield of cones in 1985. The 5 best cone producers (20% of the trees) produced 44.3% of the total cones, while the 5 poorest produced only 7.6% of the total cones. For the years 1982, 1983, 1984, and 1986, the 5 best cone-producing clones produced 37.2, 60.6, 36.0, and 44.8% of the total cones, and the 20% with the lowest production produced only 5.0, 2.1, 5.7, and 5.1% of the total cones, respectively. These results indicate that some clones produced a great mass of cones, while others did not produce any cones or contributed only a very small percentage to the final cone crop. This unequal contribution of the clones to the cone crop indicates that the seed orchard departs from the ideal situation of equal cone production by all the clones.

The degree of departure from the ideal situation for the bumper, average, and lean cone-producing years is shown in Fig. 3. It is evident from this figure that the degree of distortion in the parental balance in the seed orchard was influenced by the crop size. The curve for 1984 (the bumper cone year) was closest to the ideal situation, represented by the straight line in the figure. The greatest departure from a straight line is observed in 1983, the leanest cone year. The curve for 1986, the average cone year, is intermediate. As implied by the cone-yield curves, the closer the curve approaches the straight line, the higher the possibility that each clone contributes equally to the gene pool in the seed orchard (Matziris, 1993). The results indicate that the genetic base of the seed produced from the seed orchard was much broader in bumper cone years than in mean and lean cone years.

Table 1, which lists the product moment correlation coef-

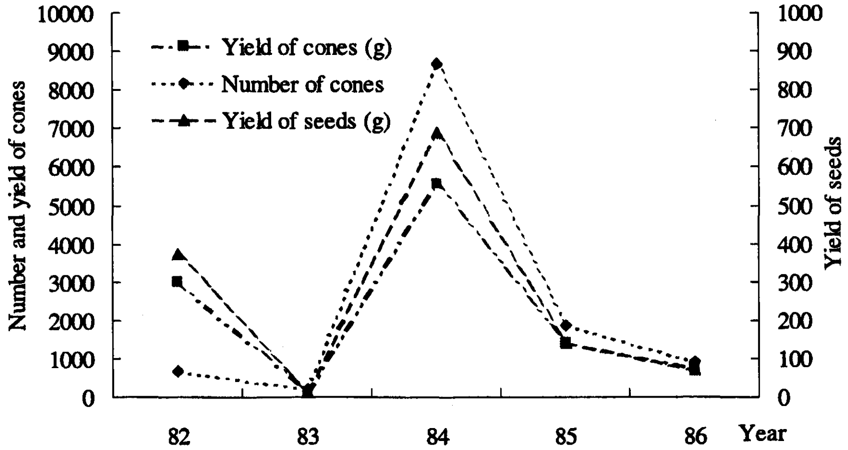

Fig. 1 Development of annual seed/cone production averages.

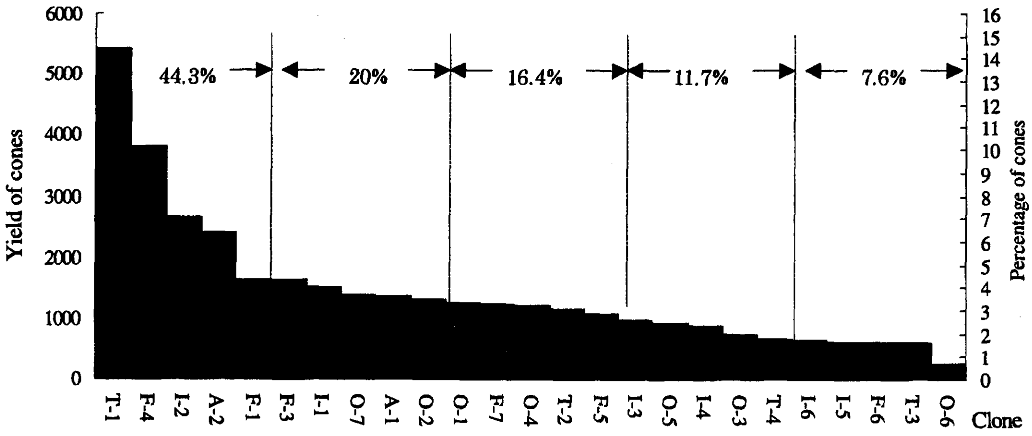

Fig. 2 Average yield of cones/clone ramet in a hinoki seed orchard (year 1985).

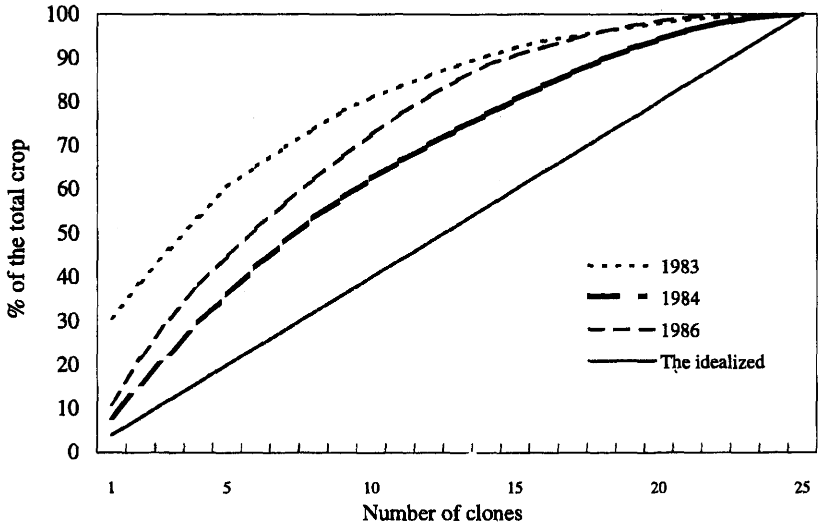

Fig. 3 Cumulative cone production curves for clones for a bumper crop year (1984), mean crop year (1986), and lean crop year (1983). Clones are arranged in order of decreasing yield of cone.

Table 1 Product moment correlation coefficients (above the diagonal) and Spearman's coefficients of rank correlation (below the diagonal) between cone crop production for 25 open-pollinated clones.

Year	1982	1983	1984	1985	1986
1982	—	0.062	0.667**	0.074	0.624**
1983	0.156	—	0.029	0.582**	− 0.320
1984	0.732**	0.242	—	− 0.230	0.656**
1985	0.398*	0.455*	0.085	—	− 0.317
1986	0.631**	− 0.298	0.693**	− 0.167	—

*, ** Values are statistically significant at the 0.05 and 0.005 probability level respectively.

ficients and Spearman's coefficients of rank correlation, shows the relationships between the yield of cones for the years examined. The product moment correlation coefficients between the yields for any 2 consecutive years (*i.e.*, 1982 and 1983) were small (0.029–0.062, NS) or negative (− 0.23– − 0.317, NS). On the other hand, there was a highly significant positive correlation between alternate years (*i.e.*, 1982 and 1984, 1983 and 1985, and 1984 and 1986). These suggest the presence of a carry-over effect; namely, a similar cone crop was repeated after 2 years. No regular relationships were observed for the product moment correlation between seed/cone crops separated by 3 years. The 4-year separation from 1982 to 1986 was highly significant.

The relative ranking of clones changed from year to year (Table 2). The changes were less obvious when bumper crop years were compared with average crop years. The better cone producers (clones F-1, I-2, and I-6) placed in the top 5 every year with an average or bumper cone crop (1982, 1984, and 1986). A similar trend was observed in the ranking of the least productive clones (clone F-6, O-6, and O-3), which were at the bottom all three of these years. However, the ranking of intermediate cone producers changed from year to year. This was more obvious when examining the best cone-producing clones in a lean cone year. For example, clone I-6 ranked 5, 4, and 1 in 1982, 1984, and 1986, respectively, but ranked 24 and 21 in 1983 and 1985, respectively. Similarly, clone O-5

Table 2 Variation among ramets within clones and clone ranking in yield of cones for 5 successive years (1982–1986).

		1982		1983		1984		1985		1986	
Clone	Replication	No.	Mean ± SD	No.	Mean ± SD	No.	Mean ± SD	No.	Mean ± SD	No.	Mean ± SD
A-1	7	16	1630 ± 2048.7	6	155 ± 177.2	16	4676 ± 3754.0	9	1360 ± 1130.4	20	191 ± 234.7
A-2	5	6	4983 ± 3806.0	2	278 ± 268.2	15	4933 ± 2350.0	4	2408 ± 1428.9	12	683 ± 173.3
F-1	5	1	6599 ± 5459.1	10	103 ± 157.3	5	9450 ± 9152.2	5	1628 ± 1066.7	2	1833 ± 1524.3
F-3	6	14	2816 ± 2463.4	18	35 ± 33.1	21	3174 ± 1883.5	6	1623 ± 893.1	15	376 ± 114.7
F-4	5	13	3330 ± 2370.5	1	1043 ± 840.4	12	5678 ± 3848.2	2	3804 ± 3904.6	21	137 ± 155.8
F-5	4	4	5165 ± 4628.4	3	259 ± 304.9	1	12115 ± 7688.1	15	1075 ± 847.2	8	960 ± 594.0
F-6	13	24	627 ± 853.6	14	73 ± 66.7	25	532 ± 339.9	23	609 ± 493.0		-
F-7	12	11	3420 ± 1336.9	20	29 ± 45.7	19	3741 ± 2208.4	12	1230 ± 789.6		-
I-1	5	2	5616 ± 3904.1	17	35 ± 39.4	9	6770 ± 2939.0	7	1504 ± 1001.7	10	869 ± 378.4
I-2	6	3	5603 ± 1888.2	8	143 ± 128.6	3	10562 ± 5090.9	3	2666 ± 2473.0	5	1124 ± 704.0
I-3	4	10	3570 ± 4296.8	7	151 ± 137.3	14	5080 ± 4856.8	16	975 ± 812.6	16	325 ± 472.3
I-4	4	12	3390 ± 1258.7	11	87 ± 66.0	2	11456 ± 3378.5	18	870 ± 584.8	9	899 ± 732.5
I-5	5	15	2799 ± 1542.9	12	83 ± 79.1	6	9236 ± 2837.8	22	620 ± 275.7	6	1092 ± 512.4
I-6	5	5	5094 ± 3048.9	24	12 ± 9.9	4	10167 ± 3569.6	21	644 ± 468.9	1	1915 ± 1813.1
O-1	4	17	1330 ± 1011.7	9	140 ± 199.2	13	5202 ± 1944.1	11	1250 ± 1124.6	17	322 ± 289.1
O-2	4	19	1128 ± 766.5	4	245 ± 378.4	7	8781 ± 7893.7	10	1300 ± 410.9	13	662 ± 957.5
O-3	4	22	970 ± 1553.7	22	17 ± 29.6	20	3232 ± 4649.6	19	750 ± 462.0	22	124 ± 123.8
O-4	5	23	740 ± 745.8	21	29 ± 58.2	23	1703 ± 1413.6	13	1192 ± 1558.6	14	586 ± 224.5
O-5	4	7	4866 ± 2292.8	13	81 ± 114.7	8	8125 ± 1748.6	17	925 ± 824.8	4	1321 ± 763.4
O-6	2	25	382 ± 328.8	16	53 ± 75.0	22	2140 ± 2177.9	25	260 ± 84.9	19	219 ± 285.7
O-7	4	8	4040 ± 2706.8	23	13 ± 16.1	10	6668 ± 5119.9	8	1390 ± 929.6	11	828 ± 975.0
T-1	4	21	1065 ± 1030.2	5	231 ± 375.4	24	994 ± 518.4	1	5410 ± 2738.4	23	4 ± 8.5
T-2	4	9	3973 ± 2786.9	19	31 ± 43.5	11	5833 ± 3034.7	14	1155 ± 634.4	7	988 ± 1055.2
T-3	5	18	1144 ± 720.9	15	63 ± 66.0	18	4391 ± 2632.1	24	604 ± 445.5	18	291 ± 213.3
T-4	3	20	1121 ± 1159.3	25	1 ± 1.7	17	4640 ± 4007.0	20	673 ± 411.0	3	1562 ± 846.2

ranked 7, 8, and 4 in 1982, 1984, and 1986, but ranked 13 and 17 in 1983 and 1985, respectively. These results were confirmed by the Spearman's coefficients of rank correlation (Table 1). The correlations were highly significant between bumper (1984) and average years (1982 and 1986), indicating that there were no significant changes in the cone yield of clones in these three years. The rank correlations between bumper (1984) and lean (1983 and 1985) years were very low or insignificant, indicating that the changes in the ranking of clones in these years are significant. The fluctuation of the Spearman's coefficients of rank correlation, as well as the relative ranking of clones from year to year, can be explained by the build-up of nutrients in individual trees. This increases vegetative growth during lean crop years and subsequently increases the potential crop the following year, when more cone-bearing branches are produced (El-Kassaby *et al.*, 1989). This interprets the carry-over effect of seed/cone production at the individual level. Another factor may be the gnawing of cone pests, *Glaucias subpunctatus* and *Plautia stali*, in the hinoki seed orchard (Sano *et al.*, 1989). A lean crop year may interrupt the growth of the populations of these insects by reducing the intensity of predation, so that it is much safer to produce seeds the following year.

Tables 3 and 4 present the analyses of variance, variance components, and broad-sense heritability estimates for all 5 years combined and for each year separately, respectively. The variation in the annual seed/cone production among clones was very large and statistically highly significant for all the years examined (Table 4). Significant interactions ($p < 0.005$) were also observed between clones and years (Table 3). The results confirm the presence of differences among clones, and an interaction between clones and year for seed/cone production.

In single year analyses, broad-sense heritability estimates on an individual tree basis (H_1) for all characteristics of reproduction and seeds were much lower than the estimates on a clone mean basis (H_2) (Table 4). A similar trend was observed in the combined year analyses (Table 3). On the other hand, higher averaged values of broad-sense heritability (H_1 as well as H_2) were observed for seed/cone production in the single year analyses (Table 4) than in the combined years (Table 3). The main reason for this is that the interaction component clone × year confounds the genetic component of variance in the single-year analyses. Like several other coniferous species (Byram *et al.*, 1986; Chaisurisri *et al.*, 1992; Matziris, 1993, 1997), the heritability of seed/cone production traits and the seed characteristics in hinoki is high, indicating that these traits are under strong genetic control.

As mentioned above, the most important objective of a seed orchard is providing a stable supply of seeds with genetic gain and a broad genetic base. However, there are few studies on the maintenance of genetic variation in the seed crop of hinoki seed orchards. It is worth discussing practical measures to maintain the genetic diversity of the seed crop in the seed orchard studied, considering the characteristics of seed/cone production. In general, the genetic diversity of the seed crop is maximized when all the clones contribute equally to the crop (Matziris, 1993). The disproportionate contributions of clones (Table 2 and Fig. 2) and significant clone × year interactions (Table 3) imply that the clones contributed to

Table 3 Analyses of variance, variance components and broad-sense heritability estimates for seed-cone production over the 5-year (1982–1986) period.

Source of variation	d.f.[1]	Expected mean Squares[2]	Number of cones		Yield of cones		Yield of seeds		1000-kernel weight		Rate of filled seeds	
			d.f.	M.S.[3]	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.	d.f.	M.S.
Years	$y-1$		3	91.60***	4	75.96***	4	54.18***	3	0.0864***	2	12.22***
Clones	$C-1$	$\sigma^2+n\sigma_{yc}^2+yn\sigma_c^2$	24	1.57***	24	1.92***	22	1.43***	22	0.0584***	22	0.17***
Clones × Years	$(C-1)(y-1)$	$\sigma^2+n\sigma_{yc}^2$	72	1.30***	96	0.97***	88	0.50***	66	0.0013*	44	0.063*
Residual	$CY(n_i\text{-}1)$	σ^2	416	0.33	520	0.279	405	0.19	324	0.0009	243	0.040
σ_c^2				0.0133		0.0379		0.0371		0.0029		0.0071
σ_{yc}^2				0.1946		0.1388		0.0622		0.0001		0.0046
σ^2				0.328		0.279		0.1917		0.0009		0.040
H_1[4]				0.025		0.083		0.127		0.753		0.137
H_2				0.243		0.558		0.724		0.991		0.848

[1] C, number of clones = 25; y, number of years; n_i, the harmonic mean of the number of ramets within clones. [2] σ^2, variance due to differences among ramets within clone; σ_c^2, variance due to differences among clones; σ_{yc}^2, variance due to interaction between clone and year effects. [3] *, **, *** Statistically significant at the 0.05, 0.01, and 0.005 probability level respectively. [4] H_1, H_2 broad sense heritability on individual tree and clone mean basis respectively.

Table 4 Analyses of variance, variance components and broad-sense heritability estimates for seed-cone production for each of 5 years, 1982 to 1986.

Source of variation	d.f.[1]	E.M.S[2]	Mean square[3]					Mean ± SD
			1982	1983	1984	1985	1986	(1982–1986)
Number of cones								
Among clones	$C-1$	$\sigma^2+n\sigma_c^2$	-	1.730***	1.100***	0.428***	2.210***	
Residual	$C\,(n_i-1)$	σ^2	-	0.702	0.154	0.159	0.295	
σ_c^2			-	0.206	0.189	0.054	0.383	
σ^2			-	0.702	0.154	0.159	0.295	
H_1[4]			-	0.23	0.55	0.25	0.56	0.40 ± 0.184
H_2			-	0.59	0.86	0.63	0.87	0.74 ± 0.146
Weight of cones								
Among clones	$C-1$	$\sigma^2+n\sigma_c^2$	0.909***	1.619***	0.878***	0.331*	2.075***	
Residual	$C\,(n_i-1)$	σ^2	0.217	0.588	0.144	0.155	0.291	
σ_c^2			0.138	0.206	0.135	0.035	0.366	
σ^2			0.217	0.588	0.144	0.155	0.291	
H_1			0.39	0.26	0.48	0.18	0.56	0.37 ± 0.154
H_2			0.76	0.64	0.82	0.53	0.86	0.72 ± 0.138
Weight of seeds								
Among clones	$C-1$	$\sigma^2+n\sigma_c^2$	0.694***	0.725***	0.486***	0.291*	1.243***	
Residual	$C\,(n_i-1)$	σ^2	0.251	0.226	0.133	0.149	0.199	
σ_c^2			0.089	0.100	0.071	0.028	0.209	
σ^2			0.251	0.226	0.133	0.149	0.199	
H_1			0.26	0.31	0.35	0.16	0.51	0.32 ± 0.130
H_2			0.64	0.69	0.73	0.48	0.84	0.68 ± 0.130
1000-grain weight								
Among clones	$C-1$	$\sigma^2+n\sigma_c^2$	0.0145***	-	0.0169***	0.0161***	0.0148***	
Residual	$C\,(n_i-1)$	σ^2	0.0007	-	0.0014	0.0007	0.0007	
σ_c^2			0.0028	-	0.0031	0.0031	0.0029	
σ^2			0.0007	-	0.0014	0.0007	0.0007	
H_1			0.80	-	0.69	0.82	0.81	0.78 ± 0.059
H_2			0.95	-	0.92	0.96	0.95	0.95 ± 0.019
Rate of embryonic seeds								
Among clones	$C-1$	$\sigma^2+n\sigma_c^2$	0.0746***	-	0.0863***	-	0.0868***	
Residual	$C\,(n_i-1)$	σ^2	0.0299	-	0.0320	-	0.0321	
σ_c^2			0.0089		0.0109		0.0109	
σ^2			0.0299	-	0.0320	-	0.0321	
H_1			0.23	-	0.25	-	0.25	0.25 ± 0.014
H_2			0.60	-	0.63	-	0.63	0.62 ± 0.018

[1] C, number of clones = 25; n_i, the harmonic mean of the number of ramets within clones. [2] σ^2, variance due to differences among ramets within clone; σ_c^2, variance due to differences among clones. [3] *, **, *** Statistically significant at the 0.05, 0.01, and 0.005 probability level respectively. [4] H_1, H_2 broad sense heritability on individual tree and clone mean basis respectively.

the cone crop disproportionately and that the contribution varied as clones entered or dropped out of the breeding pool each year. Thus, the genetic diversity of the seed crops is less than that expected under panmixia, and unpredictable gene frequencies occur in the seedlots used for reforestation. Mixing seed crops from several bumper and average cone years would increase the chances of having a representative sample of most clones in the final seed crop (El-Kassaby *et al.*, 1989). The strong genetic control of seed/cone production (Tables 3, 4) and the less obvious change in clone ranking of the seed/cone production between bumper and average crop years (Table 2) make the mixing measure more practical in the seed orchard for years in which seeds are in great demand. In a lean cone year, a number of factors may ruin the goals of a seed orchard and reduce genetic quality through unbalanced clonal contribution. These include high rates of contamination and inbreeding (El-Kassaby and Ritland, 1986; Seido, 1990) and low rates of filled seeds in the resultant seed/cone crops, due to the lack of pollen and to predation (Danieis, 1978; Miller, 1983; Sano *et al.*, 1989). Aborting the seed crops from lean crop years is therefore recommended. Miller (1982) reported a practical method for aborting cone crops in Douglas-fir seed orchards.

When a bumper or average cone crop is expected, differences in the reproductive phenology and output of the clones should be eliminated to produce a seed crop with acceptable quality and parental balance. There are several practical measures for adjusting differences in reproductive phenology in seed orchards. First, hormonal treatment could be used to increase the seed/cone production of low-producing clones. In another block of the seed orchard, embedding 5 mg of gibberellin at the base of a branch enhanced the number and yield of cones 230 and 250% in 1984 and 310 and 300% in 1985, respectively (Ide and Yamamoto, 1989). Second, departure from panmictic equilibrium can be the major cause of unequal contributions of the clones in a seed orchard (Matziris, 1993). The problem could be alleviated by supplemental mass pollination (SMP) of high seed/cone producing clones using pollen mixes from low seed/cone producing clones, or using overhead spray cooling to eliminate pollen contamination, inbreeding, and consanguineous mating (Danieis, 1978; El-Kassaby and Ritland, 1986). Considering the pollen contribution, SMP seems be the preferred method.

In another study in the same seed orchard, we simulated the genetic diversity (average expected heterozygosity) of the seedlots using allozyme genotypes and the seed proportion of each clone under idealized situations. The result concurred with the actual analysis (data unpublished). Based on the characteristics of seed/cone production and their high genetic control, the genetic diversity of seedlots in bumper and average cone years could be estimated. This may have practical application in raising genetically diverse seedlings for hinoki reforestation.

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