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Full Length Research Paper

Clonal variation in growth, flowering and cone production in a seed orchard of Scots pine (*Pinus sylvestris* L.) in Turkey

Ahmet Sıvacıoğlu*, Sezgin Ayan and Durmuş Ali Çelik

Kastamonu University, Faculty of Forestry, Department of Forest Engineering, 37200 Kastamonu, Turkey.

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In this study, observations and measurements were made on five grafts for each of 30 clones in three successive years (2006, 2007 and 2008) on Scots pine (*Pinus sylvestris*) seed orchard established in 1995 by using 2 years-old grafts in Turkey. The examined characters were total height, diameter at base, number of branches, length of terminal shoot, length of lateral shoot, length of longest branch, number of male whorls, number of male flowers in a whorl, number of male flowers, length of male whorl, number of female flowers, cone number and crown diameter. Variation, broad-sense heritability and correlations between characters were estimated. Variation among clones was lower than among grafts for all studied characters. The broad sense heritability varied in a range of 0.15-0.38 for growth related characters, while it varied in a range of 0.15-0.59 for flowering related characters. The genetic variation for female and male flowering number is 36.5% and 82.8%, respectively. The number of flowers increased with the graft size. Significant correlations between the growth and flowering related characters varied in a range of 0.20-0.59 and 0.17-0.26 for male and female flowering, respectively.

Key words: Scots pine, heritability, correlation, clone, graft, variation, cone, flowering, growth.

INTRODUCTION

Scots pine (*Pinus sylvestris* L.) is one of the most common and important forest tree species in Turkey due to usefulness of its wood to many commercial uses. Also, for this great importance in Turkish forestry, this species is classified as one of the economically important tree species in the "National Tree Breeding and Seed Production Program" (Koski and Antola, 1993). Stands of this species occupy roughly 1239578 ha and also 715643 ha and 523935 ha of which are classified as productive (crown closure is 11-100%) and unproductive (crown closure is under 10%) (Anonymous, 2006).

As seen in the data, rougly 42% of Scots pine forest area of Turkey is unproductive. These unproductive areas have been evaluated as potential areas for artificial regeneration and rehabilitation practices to diminish the wood supply deficit and for supplying the other forest functions to the community in Turkey. Of course big amount of reproductive material is necessary to keep present Scots pine forest stock even to continue with increasing trend by rehabilitating the degraded areas. Presently, Turkey has 21 Scots pine seed orchards on 114 ha (Anonymous, 2001), only 9.2% of annual seed demand for plantations was covered from the orchards at the beginning of the millenium (Cengiz, 2003). But, there are some problems in seed production on these seed orchards (Sıvacıoğlu and Ayan, 2008).

In spite of the fact that most ortets originate from phenotypically selected seed stands, seed orchards are becoming gradually more important (Bilir et al., 2006). High and genetically improved seed yield from the seed orchard is an integral part in the success of a tree breeding program. Moreover, clonal seed orchards are one of the important seed sources for forest plantations. And also, these seed sources constitute an important link between tree breeding and plantation forestry. In recent years, considerable progress has been made in under-

*Corresponding author. E-mail: asivacioglu@kastamonu.edu.tr ahmets1973@gmail.com. Tel.: +90 366 2150900. Fax: +90 366 2152316.

standing the reproductive biology of conifers in seed orchards (Kang, 2001; Bilir et al., 2006). Differences in growth and other characters in seed orchards will affect the seed crop. The economy of seed orchards is dependent on a high seed production, which is convenient to collect.

Thus, it is important to get information of variation in reproductive characters. Production of seed and pollen and feasibility of cone collection, depend on the size and morphology of the tree. Thus, it is important to know how reproductive characters vary and relate to growth characters (Bilir et al., 2006).

In this study, variation in growth, flowering and cone related characters were investigated. Also, variation of broad-sense heritability and correlations were evaluated among the clones and grafts. These characters were evaluated for effective management of seed orchards of Scots pine in Turkey.

MATERIALS AND METHODS

This study was carried out in Tekçam clonal seed orchard, located at Taşköprü, Kastamonu (1160 m). The orchard was established by the Forest Tree Seeds and Tree breeding Research Directorate in 1995 and comprises 1987 grafts of 30 clones derived from intensively selected trees in Araç-Dereyayla seed stand which was pheno-typically selected from the natural stands. Grafts were 2 years-old at the time of establishment and were planted at a spacing of 6 x 6 m. Commercial cone harvesting from this orchard was started in the 2003 when the grafts were 10 years-old. So far, no artificial pruning has been conducted in the orchard. For this study, data related to 13 of characters were collected on five grafts, chosen randomly, from each of 30 clones.

The observations and measurements were made in 2006, 2007 and 2008. The characters related to male/female flowering were observed in May of each year whereas other traits were measured at the end of the growing season. The examined characters are total height (H_T, cm), diameter at base (D_B,cm), number of branches (N_B), length of terminal shoot (L_{TS}, cm), length of lateral shoot (L_{LS} ,cm), length of longest branch (L_{LB}, cm), number of male whorls (N_{MW}), number of male flowers in a whorl (N_{FW}), number of total male flowers (N_{MF}), length of male whorl (L_W, cm), total number of female flowers (N_{FF}), total cone number (N_C) and crown diameter (D_C, cm).

Data of all characters for the each year and overall mean were subjected to one-way analysis of variance. Duncan test was used for determining homogenous groups. Variables were tested for normality and homogeneity of variances and logarithmic transformation for counting values were made. Differences were considered significant at $P < 0.05$ level. Year to year Pearson and Spearman correlation coefficients were used for examining the relationships between the years for the studied characters. Moreover, Pearson correlations among characters were calculated at the levels of individual grafts and clonal means.

Broad sense heritability values were estimated both individual tree basis (H_1) and clone mean basis (H_2) as the ratio of total genetic variance (σ^2_C) to total phenotypic variance ($\sigma^2_{C+}\sigma^2_E$) (Matziris, 1984) for the H_1 and to ($\sigma^2_{C+}\sigma^2_{E/n}$) for H_2 (n = graft number). Cloning effect variance biases the heritability values, but the magnitude is negligible and can be ignored (Matziris, 1993). In this study, heritability components were estimated as σ^2_E = error mean square and σ^2_C = (clone mean square-error mean square/ number of grafts per clone) (Wright, 1962). Variance components, expressed as coefficient of variation among clones (CV_C) and within clone (CV_E) were estimated as the ratio of $100\,\sigma_C$ and $100\,\sigma_E$ to arithmetic means (Bilir et al., 2006).

RESULTS AND DISCUSSION

The analysis of variance showed that there were significant differences among clones at 0.001, 0.01 and 0.05 probability level in all studied characters for the studied years except for L_{TS}, N_{FF} and N_C for some years (Table 1). Moreover, as to the overall mean of the years the mentioned characters was not showed significant difference (Table 2).

As seen on Tables 1 and 2, there were large differences among the characters for broad-sense heritability (H_1 and H_2). As to the average, there was higher clonal variation (CV_C) for N_{MW} (71.4%), N_{MF} (82.8%) and N_{FF} (36.5%) (Table 5). And, parallel to this, H_1 becomes 0.53, 0.39 and 0.25 for N_{MW} in 2006, 2007 and 2008, respectively. Also, H_1 values for N_{MF} varied from 0.27 to 0.59 in studied years. Moreover, H_1 values varied in a range of 0.18-0.19 for N_{FF}. H_1 ranged 0.15 (N_B in 2006, 2007; L_{LB} in 2007; N_{FW} in 2007) to 0.59 (N_{MF} in 2006) whereas H_2 ranged 0.46 (N_{FW} in 2007) to 0.88 (N_{MF} in 2006) (Table 1). The broad-sense heritability values of H_1 exceeded 0.5 only for N_{MW} (2006), N_{FW} (2006) and N_{MF} (2006). As to the average values, the H_1 values never exceeded 0.5 (Table 2) and this reflects that the variation among grafts caused by environmental variation was always higher than that caused by the genetic variation in the studied orchard. In sight, there is uniform ecological condition in the studied orchard. But, because of micro-ecological differences, the environment was more important than genetics in the orchard.

The differences in broad-sense heritability among the characters in the orchard could be caused by differences among the plus trees selected in the establisment phase of the orchard from the seed stand. Heritability was generally low for flower production (0.27-0.59 for N_{MF} and 0.18-0.19 for N_{FF}) (Table 1). Also, heritability values vary among the years. Heritability differences among Scots pine seed orchards as to growth and number of strobili was presented by Bilir et al. (2006). Clonal repeatability (broad-sense heritability) was 0.26 for female and 0.18 for male flowers in other clonal seed orchard of Scots pine in Turkey as to 2001 data (Bilir, 2002).

Also, Nikkanen and Ruotsalainen (2000) mentioned that broad-sense heritability averaged 0.36 and 0.37 for female and male flowering in Norway spruce. For *Picea abies* broad-sense heritability values derived for cone-set varied from 0.29 to 0.57 was reported by Almqvist et al. (2001). Narrow-sense heritability of male strobilus production (0.64 and 0.39) was higher than that of female (0.42 and 0.13) in *Pinus contorta* for different years (Hannerz et al., 2001).

Growth characters appear to have limited genetic variation and low broad-sense heritability. As overall mean va-

Table 1. Analysis of variance, variance components and heritability estimates for studied characters for the studied years.

Character	Year	Mean squares		σ^2_C	σ^2_E	H_1^2	H_2
		Between clones[1]	Within clones (Error)				
H_T	2006	4576.62***	1873.93	540.54	1873.93	0.22	0.59
	2007	5313.98***	2397.98	583.20	2397.98	0.20	0.55
	2008	5578.02**	2904.05	534.79	2904.05	0.16	0.48
D_B	2006	9.91***	4.13	1.16	4.13	0.22	0.58
	2007	10.48***	4.22	1.25	4.22	0.23	0.60
	2008	11.83***	4.95	1.38	4.95	0.22	0.58
^3N_B	2006	0.0074**	0.0039	0.00070	0.0039	0.15	0.47
	2007	0.0058**	0.0031	0.00054	0.0031	0.15	0.47
	2008	0.0049**	0.0025	0.00048	0.0025	0.16	0.49
L_{TS}	2006	176.73ns	166.32				
	2007	380.32ns	468.1				
	2008	298.70**	155.78	28.58	155.78	0.16	0.48
L_{LS}	2006	81.99***	20.43	12.31	20.43	0.38	0.75
	2007	42.85***	13.96	5.78	13.96	0.29	0.67
	2008	59.39***	16.61	8.56	16.61	0.34	0.72
L_{LB}	2006	3610.56**	1883.11	345.49	1883.11	0.16	0.48
	2007	3796.11**	1995.00	360.22	1995.00	0.15	0.47
	2008	4064.23**	2066.79	399.49	2066.79	0.16	0.49
$^3N_{MW}$	2006	1.339***	0.199	0.23	0.199	0.53	0.85
	2007	0.801***	0.188	0.12	0.188	0.39	0.77
	2008	0.475***	0.179	0.06	0.179	0.25	0.62
$^3N_{FW}$	2006	0.224***	0.034	0.0380	0.034	0.53	0.85
	2007	0.041*	0.022	0.0038	0.022	0.15	0.46
	2008	0.032***	0.009	0.0046	0.009	0.34	0.72
$^3N_{MF}$	2006	2.450***	0.299	0.43	0.299	0.59	0.88
	2007	1.078***	0.290	0.16	0.290	0.35	0.73
	2008	0.686***	0.238	0.09	0.238	0.27	0.65
L_W	2006	2.83***	0.93	0.38	0.93	0.29	0.67
	2007	2.78***	0.79	0.40	0.79	0.34	0.72
	2008	1.10**	0.55	0.11	0.55	0.17	0.50
$^3N_{FF}$	2006	0.630**	0.288	0.0684	0.288	0.19	0.54
	2007	0.084ns	0.136				
	2008	0.273**	0.132	0.0282	0.132	0.18	0.52
^3N_C	2006	0.300***	0.073	0.0454	0.073	0.38	0.76
	2007	0.738**	0.348	0.0780	0.348	0.18	0.53
	2008	0.155ns	0.179				
D_C	2006	8253.10***	3163.56	1017.91	3163.56	0.24	0.62
	2007	8386.60***	3363.82	1004.56	3363.82	0.23	0.60
	2008	8779.58***	3435.25	1068.87	3435.25	0.24	0.61

[1]***, **,* Statistically significant of the 0.001, 0.01, 0.05 probability level, respectively; ns: non-significant $^2H_1 = \sigma^2_C / \sigma^2_C + \sigma^2_E$, $H_2 = \sigma^2_C / \sigma^2_C + \sigma^2_{E/n}$

[3]As to the logoritmic transformed values.

lues, the H_1 values of growth characters such as, H_T, D_B, N_B, L_{TS}, L_{LS}, L_{LB} and D_C ranged from 0.04 to 0.37. For the same characters the H_2 values varied in a range of 0.19-0.75. Also, as seen on Table 1, H_1 values varied from

Table 2. Analysis of variance, variance components and heritability estimates for studied characters for overall mean of the years.

Character	Mean squares[4]		σ^2_C	σ^2_E	H_1^2	H_2
	Between[1] clones	Within clones (Error)				
H_T	5074.73***	2249	565.15	2249	0.20	0.56
D_B	10.47***	4.22	1.25	4.22	0.23	0.60
^3N_B	0.00586**	0.003045	0.0006	0.003045	0.16	0.48
L_{TS}	124.62ns	100.89	4.75	100.89	0.04	0.19
L_{LS}	42.92***	10.88	6.41	10.88	0.37	0.75
L_{LB}	3793.36**	1972.75	364.12	1972.75	0.16	0.48
$^3N_{MW}$	0.597***	0.174	0.0846	0.174	0.33	0.71
$^3N_{FW}$	0.0548***	0.0148	0.0080	0.0148	0.35	0.73
$^3N_{MF}$	0.809***	0.242	0.1134	0.242	0.32	0.70
L_W	1.78***	0.48	0.26	0.48	0.35	0.73
$^3N_{FF}$	0.09ns	0.102				
^3N_C	0.085ns	0.082				
D_C	8352***	3285.32	1013.34	3285.32	0.24	0.61

[4] The explanations of [1],[2],[3] are as in Table 1.

0.15 to 0.59 for flowering related characters while these values varied 0.32 to 0.35 as to the overall data (Table 2). In general, higher heritability was affirmed for the flowering related characters than growth related characters in the previous studies (Bilir et al., 2006). Despite the higher heritability for flowering than growth, limited genetic variation can be affirmed for flowering characters in the orchard. Therefore, it is doubtful to use graft characters that are desirable in a seed orchard when selecting orchard clones.

In this study, large within-clone variation is attracted attention. Meanwhile, there are large variation as to the flowering related characters among the grafts. Similarly, considerable difference was reported among the grafts by Varghese et al. (2006) in a clonal seed orchard of *Tectona grandis*. For this reason, to create desirable characters in seed orchard trees, there ought to be a large potential of management, which affects ‘‘the environment’’ (Bilir et al., 2006).

All clones combined, clones had a mean of 480 cm H_T with range among the clones from 426 to 549 cm (SD_C = 5.89 cm). As a result of Duncan test, the biggest H_T values were determined for clone 17 (549 cm) and the lowest for clone 19 (426 cm). The D_B ranged from 13.45 cm (clone 25) to 18.87 cm (clone 27) while D_C ranged from 332.3 (clone 6) to 489.6 cm (clone 28). The N_B ranged 32 (clone 5) to 42 (clone 3). The L_{TS} values ranged from 28 (clone 20) to 47 cm (clone 9) while L_{LS} values ranged from 17.4 (clone 30) to 32.6 cm (clone 18). Moreover, the L_{LB} values ranged 212.2 (clone 30) to 350.9 cm (clone 26) (Table 3).

The N_{MW} values varied in 32 (clone 1)-824 (clone 27) interval among the clones and 2-1053 interval among the grafts. Also, the biggest N_{FW} values were determined for clone 28 (47 number) and the lowest for clone 14 (16 number). The L_W varied from 1.29 (clone 14) to 3.99 cm (clone 28) among the clones. This value was estimated in a range of 1.23-2.07 cm for the natural populations of Scots pine (Boydak, 1977). The N_{MF} ranged in 1163 (clone 1) –36691 (clone 27) interval while N_{FF} ranged in 223 (clone 27)-833 (clone 29) interval. In addition, N_C varied from 103 to 468 among the clones (Table 4).

Variation among the clones (CV_C) and grafts (CV_E) (within the clones) were compiled on Table 5. As seen on Table 5, there were considerable variation among the years for most characters. In general, variation among the grafts is higher than among the clones. The highest variation among the clones were observed in N_{MF} (82.8 %), N_{MW} (71.4 %) and N_{FF} (36.5 %). As to the Table 5, per-hectare values of N_{MW} are 17747, 82168, 118087 for the 2006, 2007 and 2008, respectively.

In addition, the per-hectare N_{MF} vary; 559742, 3338593, 5291351 for the studied years (2006, 2007 and 2008), respectively. This means, pollen production will be increase together with male flower number. As for N_{FF}, this character vary 33437, 234619 and 110027 number/ per hectare for the years (2006, 2007 and 2008). The variation of N_{FF} as to the years reflect the effect of seedlot interval in the base stand. For that reason, N_{FF} do not indicate a linear increase with the age as N_{MW},N_{FW} and N_{MF} . Also, the N_C vary 45661, 23289 and 160922 in the same years. Furthermore, the N_{MF} /N_{FF} ratio was calculated as 16.7, 14.2 and 48.1 for 2006, 2007 and 2008, respectively. The genetic variation, here expressed as CV_C, was always lower (Table 5) than CV_E. Genetic variation varied from 54.3 and 121.4 % for N_{MF} among the clones

Table 3. Clonal means of studied morphologic characters for average of the years.

S/N	H_T		D_B		N_B		L_{TS}		L_{LS}		L_{LB}		D_C	
1	480	abcdef	15.02	bcdef	39	abcd	31	bc	30.2	ab	305.3	abc	418.9	abcdef
2	491	abcdef	13.54	f	38	abcde	35	abc	24.1	cdefgh	282.2	abc	361.3	def
3	492	abcdef	15.99	abcdef	42	a	42	abc	24.1	cdefgh	285.8	abc	411.1	abcdef
4	467	bcdef	17.67	abc	36	abcde	33	abc	25.4	bcdefgh	280.1	bc	433.3	abcde
5	482	abcdef	15.52	bcdef	32	e	38	abc	27.1	bcdefg	304.1	abc	430.4	abcdef
6	536	ab	14.51	cdef	40	abcd	38	abc	23.9	cdefgh	298.0	abc	332.3	abcdef
7	440	def	13.49	f	34	bcde	31	bc	25.9	bcdefgh	246.8	cd	354.5	ef
8	484	abcdef	15.68	bcdef	40	abcd	38	abc	27.1	bcdefg	289.5	abc	429.3	abcdef
9	466	bcdef	15.35	bcdef	39	abcd	47	a	28.9	abc	279.5	bc	479.5	ab
10	531	abc	16.88	abcde	33	cde	40	abc	24.3	cdefgh	299.0	abc	471.8	abc
11	443	def	15.13	bcdef	39	abcd	31	bc	28.5	abcd	293.9	abc	418.8	abcdef
12	488	abcdef	14.82	cdef	37	abcde	40	abc	26.3	bcdefgh	241.4	cd	366.4	def
13	490	abcdef	14.29	def	36	abcde	34	abc	27.4	bcdef	253.1	cd	378.7	def
14	434	ef	13.92	ef	37	abcde	30	bc	27.8	bcde	282.1	abc	393.6	bcdef
15	460	cdef	13.59	f	39	abcde	32	abc	23.3	efgh	266.2	cd	403.7	abcdef
16	430	f	16.38	abcdef	36	abcde	37	abc	26.0	bcdefgh	285.3	abc	434.4	abcde
17	549	a	16.31	abcdef	40	abc	46	ab	21.7	h	279.4	bc	445.8	abcd
18	466	bcdef	16.67	abcdef	33	cde	36	abc	32.6	a	298.9	abc	423.2	abcdef
19	426	f	13.80	ef	33	cde	29	c	22.5	fgh	290.1	abc	364.3	def
20	481	abcdef	15.39	bcdef	33	cde	28	c	27.9	abcde	296.2	abc	388.4	cdef
21	464	bcdef	14.22	ef	34	cde	39	abc	24.7	cdefgh	272.6	cd	374.8	def
22	442	def	15.85	abcdef	33	de	30	bc	22.1	gh	276.9	bcd	396.9	bcdef
23	477	abcdef	15.98	abcdef	38	abcde	29	c	24.3	cdefgh	308.5	abc	376.5	def
24	475	bcdef	18.07	ab	37	abcde	38	abc	26.3	bcdefgh	299.9	abc	380.6	def
25	469	bcdef	13.45	f	36	abcde	31	bc	25.5	bcdefgh	283.6	abc	395.8	bcdef
26	521	abc	17.43	abcd	33	cde	33	abc	26.7	bcdefgh	350.9	a	482.2	ab
27	531	abc	18.87	a	40	abcd	34	abc	28.9	abc	344.9	ab	478.2	ab
28	510	abcd	16.69	abcdef	34	bcde	42	abc	23.5	defgh	248.1	cd	489.6	a
29	508	abcde	16.14	abcdef	41	ab	33	abc	23.8	cdefgh	290.7	abc	439.7	abcde
30	472	bcdef	14.32	def	36	abcde	37	abc	17.4	i	212.2	d	342.4	f

and from 84.6 to 153.8 % among the grafts.

Also, genetic variation for N_{FF} varied from 15 to 48% among the clones and from 83.0 to 87.9% among the grafts. As for the growth characters, the less variation is noticeable such as, the CV_C ranging between 4.9 (H_T) and 11.5% (L_{LS}); CV_E between 10.2 (H_T) and 49.6% (L_{TS}) (Table 5).

Variance among clones (CV_C)) was rather low than within the clones (CV_E) (Table 5). The variation seemed higher for N_{MF} (range: 72.6-121.4%, mean: 82.8%) than for that of N_{FF} (range: 15.0-48.0%, mean: 36.5%) among the clones (CV_C); the difference seemed marginal among clones while it appeared considerable within clones. The heritability of N_{MF} seemed higher (range: 0.27-0.59) than that of N_{FF} (range: 0.18-0.19) (Table 1). Clonal seed orchard was established with plus trees phenotypically selected in a specific seed stand. That the genetic variation in the seed orchards only reflects genetic variation within a single stand could be one reason for genetic variation to be low, but genetic variation in forest trees is generally dominated by variation within stands (Bilir et al. 2006).

Similarly, only a few percent of the variation among stands was stated by El-Kassaby (1991). Turna (2003) estimated, based on isozymes studies in 11 Turkish Scots pine seed stand populations that 6% of the average gene diversity was among populations and the rest within. In the seed orchard, differences in gamete contribution to gene pool among clones could be genetic (Eriksson et al., 1973), environmental (Hedegart, 1976) and management of orchard (Zobel and Talbert, 1984). As the environmental variation seems larger for male (109% as to the mean and 84.6-153.8% among the years) than female flowering (84.7% as to the mean and 83-87.9% among the years) (Table 5), increasing of polen production can be evaluated as a method for increasing seed production. Variable male and female flowering occurs among the years and many factors may be involved (Lindgren et al., 1977).

The Pearson correlation coefficients were relatively

Table 4. Clone mean values of studied characters related to male and female flowering for overall mean of the years.

S/N	N_{MW}		N_{FW}		N_{MF}		L_W		N_{FF}		N_C	
1	32	j	22	ghi	1163	g	1.39	fg	322	bc	172	a
2	324	cdefgh	37	abcde	14684	bcdefg	2.82	bc	225	c	103	a
3	439	bcd	41	ab	21970	b	2.48	bcde	743	ab	286	a
4	374	bcdef	39	abcd	17505	bcd	3.32	ab	765	ab	450	a
5	230	defghij	29	defgh	8624	cdefg	2.64	bcde	392	abc	246	a
6	230	defghij	29	defgh	8394	cdefg	2.46	bcde	312	bc	225	a
7	251	defghij	31	bcdefgh	10157	bcdefg	1.85	cdefg	547	abc	325	a
8	225	defghij	32	bcdefgh	8709	cdefg	2.17	cdefg	352	abc	258	a
9	326	cdefgh	32	bcdefg	11967	bcdefg	3.27	ab	420	abc	302	a
10	400	bcde	38	abcde	16637	bcde	2.69	bcde	402	abc	283	a
11	212	defghij	27	efgh	7430	cdefg	2.46	bcde	405	abc	309	a
12	106	hij	29	defgh	3944	efg	1.94	cdefg	321	bc	187	a
13	166	efghij	28	efgh	6269	defg	2.07	cdefg	358	abc	193	a
14	48	ij	16	i	1265	g	1.29	g	496	abc	304	a
15	130	fghij	25	fghi	4776	defg	2.16	cdefg	374	abc	240	a
16	296	cdefghi	39	abcd	12868	bcdefg	2.83	bc	375	abc	250	a
17	513	bc	37	abcde	20116	bc	2.76	bcd	526	abc	315	a
18	222	defghij	36	bcde	10067	bcdefg	2.86	bc	404	abc	254	a
19	83	hij	24	ghi	3022	fg	1.89	cdefg	526	abc	378	a
20	142	fghij	28	defgh	5282	defg	2.56	bcde	564	abc	247	a
21	128	fghij	27	efgh	5481	defg	1.83	cdefg	566	abc	280	a
22	365	cdefg	36	bcdef	15188	bcdef	2.33	bcdef	413	abc	231	a
23	193	defghij	28	defgh	7040	cdefg	1.67	efg	337	bc	289	a
24	219	defghij	21	hi	5988	defg	1.72	defg	484	abc	415	a
25	123	ghij	27	efgh	3969	efg	1.86	cdefg	394	abc	265	a
26	186	efghij	35	bcdef	7281	cdefg	2.64	bcde	317	bc	255	a
27	824	a	40	abc	36691	a	2.74	bcd	223	c	105	a
28	594	b	47	a	32845	a	3.99	a	526	abc	356	a
29	233	defghij	29	defgh	10270	bcdefg	1.92	cdefg	833	a	328	a
30	276	cdefghij	30	cdefgh	12815	bcdefg	2.35	bcdef	750	ab	468	a

Table 5. Average; coefficients of variation among the clones (CV_C%) and within the clones (CV_E%) for the studied characters.

Character	2006			2007			2008			Average		
	Mean	CV_C	CV_E	*Mean*	CV_C	CV_E	*Mean*	CV_C	CV_E	*Mean*	CV_C	CV_E
H_T	446.60	5.2	9.7	472.56	5.1	10.4	519.87	4.4	10.4	479.68	4.9	10.2
D_B	14.18	7.6	14.3	15.46	7.2	13.3	16.88	6.9	13.2	15.51	7.2	13.6
N_B	32.01	6.2	13.8	36.54	5.4	12.5	41.21	5.0	11.3	36.59	5.5	12.5
L_{TS}	32.91	4.4	39.2	25.97	16.1	83.3	47.31	11.3	26.4	35.40	10.6	49.6
L_{LS}	27.96	12.6	16.2	22.76	10.6	16.4	26.1	11.2	15.6	25.61	11.5	16.1
L_{LB}	260.88	7.1	16.6	283.64	6.7	15.7	309.75	6.5	14.7	284.76	6.8	15.7
N_{MW}	64.30	101.3	112.6	297.71	50.3	71.3	427.85	62.5	65.1	263.29	71.4	83.0
N_{FW}	20.55	38.2	32.6	34.17	14.1	37.8	39.28	15.8	21.0	31.33	22.7	30.5
N_{MF}	2028.05	121.4	153.8	12096.35	54.3	88.7	19171.56	72.6	84.6	11098.65	82.8	109.0
L_W	1.80	34.2	53.4	2.43	26.0	36.7	2.86	11.6	26.0	2.36	23.9	38.7
N_{FF}	121.15	46.6	87.9	850.07	15.0	83.1	398.65	48.0	83.0	456.62	36.5	84.7
N_C	165.44	33.3	51.6	84.38	46.5	96.1	583.05	7.4	90.0	277.62	29.1	79.2
D_C	364.87	8.7	15.4	410.4	7.7	14.1	462.61	7.1	12.7	412.63	7.8	14.1

Table 6. Pearson correlation coefficients among the grafts (below diagonal) and clones (above diagonal) as to the overall mean of the studied years.

	H_T	D_B	L_{TS}	L_{LS}	N_B	L_{LB}	D_C	N_{MW}	N_{FW}	L_W	N_{MF}	N_{FF}	N_C
H_T	-	0.57[a]	0.47[a]	0.12[c]	0.39[a]	0.47[a]	0.62[a]	0.49[a]	0.43[a]	0.41[a]	0.45[a]	0.19[b]	0.13[c]
D_B	0.42[b]	-	0.22[a]	0.26[a]	0.29[a]	0.59[a]	0.72[a]	0.62[a]	0.51[a]	0.51[a]	0.56[a]	0.26[a]	0.25[a]
L_{TS}	0.45[b]	0.23[c]	-	0.12[c]	0.11[c]	0.06[c]	0.25[a]	0.23[a]	0.19[b]	0.28[a]	0.20[b]	-0.03[c]	-0.02[c]
L_{LS}	-0.10[c]	0.22[c]	-0.09[c]	-	0.04[c]	0.41[a]	0.30[a]	-0.001[c]	0.003[c]	0.13[c]	0.011[c]	-0.06[c]	-0.11[c]
N_B	0.29[c]	0.05[c]	0.23[c]	-0.003[c]	-	0.13[c]	0.23[a]	0.26[a]	0.09[c]	0.09[c]	0.21[b]	0.09[c]	-0.02[c]
L_{LB}	0.29[c]	0.53[a]	-0.20[c]	0.48[a]	0.07[c]	-	0.63[a]	0.31[a]	0.30[a]	0.30[a]	0.31[a]	0.02[c]	0.04[c]
D_C	0.35[c]	0.66[a]	0.35[c]	0.31[c]	0.03[c]	0.44[b]	-	0.61[a]	0.55[a]	0.60[a]	0.59[a]	0.17[b]	0.18[b]
N_{MW}	0.50[a]	0.61[a]	0.42[b]	-0.15[c]	0.19[c]	0.13[c]	0.53[a]	-	0.73[a]	0.66[a]	0.96[a]	0.14[c]	0.10[c]
N_{FW}	0.40[b]	0.51[a]	0.43[b]	-0.12[c]	-0.03[c]	0.04[c]	0.54[a]	0.81[a]	-	0.80[a]	0.78[a]	0.17[b]	0.11[c]
L_W	0.32[c]	0.44[b]	0.49[a]	-0.03c	-0.12[c]	0.00[c]	0.57[a]	0.67[a]	0.83[a]	-	0.70[a]	0.08[c]	0.09[c]
N_{MF}	0.47[a]	0.57[a]	0.40[b]	-0.17[c]	0.15[c]	0.06[c]	0.53[a]	0.98[a]	0.84[a]	0.70[a]	-	0.12[c]	0.07[c]
N_{FF}	-0.13[c]	0.03[c]	0.05[c]	-0.41[b]	0.01[c]	-0.39[b]	-0.06[c]	0.03[c]	0.04[c]	0.04[c]	0.09[c]	-	0.17[b]
N_C	-0.25[c]	0.10[c]	0.06[c]	-0.42[b]	-0.15[c]	-0.36[c]	-0.05[c]	-0.06[c]	-0.09[c]	0.07[c]	-0.04[c]	0.75[a]	-

[a], [b] Statistically significant at 0.01, 0.05 probability level, respectively. [c] Non-significant.

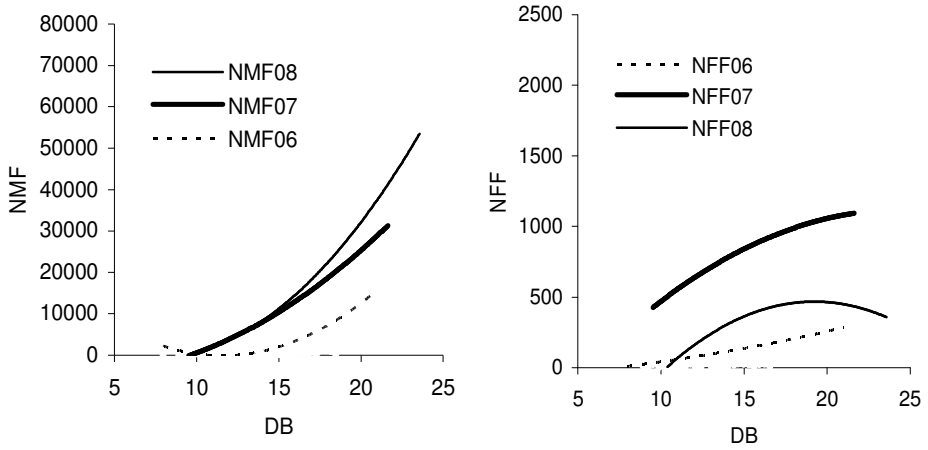


Figure 1. The relation between number of male flower (N_{MF}), female flower (N_{FF}) and diameter at base (D_B, cm) for the studied years.

high (0.22-0.72 among the clones and 0.03-0.66 among the grafts) for diameter at base (D_B). D_B proves a positive and significant correlation with generative characters as N_{MW}, N_{FW}, N_{MF} (Table 6). Also, coefficients for H_T ranged from 0.12 to 0.62 among the clones. N_{MF} has higher correlation with N_{MW}, N_{FW} and L_W as expected. Also, N_{MF} has higher correlation with D_B (0.56) and D_C (0.59) and H_T (0.45). N_{FF} has significant correlation with H_T (0.19), D_B (0.26), D_C (0.17) and N_{FW} (0.17). D_B is easy to measure, it is the most established measure of tree size and it is not much affected by pruning. And thus D_B seems a logical choice for measurement of graft size together with diameter at breast height (Bilir et al., 2006).

The N_{FF} and N_{MF} had a correlation that was positive but not significant, both for individual grafts and for clonal averages (Table 6). Correlations between growth characters and N_{FF}, N_{MF} varied. For clonal averages most correlations were positive, but few of them were significant. For grafts, almost all growth characters were significantly positive correlated to N_{FF} and N_{MF} (Table 6). The number of branches was positively correlated with the N_{MF} and N_{MW} (Table 6). The N_{FF} and N_{MF} increased with the size (D_B and D_C) of the grafts (Figure 1). Clonal means are the average of five grafts and this is subject to sampling error; we did not adjust for that when discussing relationships among characters, thus genetic correlations would be expected to be higher than reported in Table 6.

Year to year (2006, 2007, 2008) correlation coefficients on studied characters were presented in Table 7. Generally, there is conformity between Pearson and Spearman coefficients for the characters. There are statistically significant correlations in all characters between the years examined, except for L_{TS} (2006-2007 and 2007-2008), and N_C (2006-2008). The correlations

Table 7. Year to year Pearson and Spearman correlation coefficients in studied characters.

Character	2006-2007		2007-2008		2006-2008	
	Pearson	Spearman	Pearson	Spearman	Pearson	Spearman
H_T	0.92[a]	0.93[a]	0.97[a]	0.97[a]	0.90[a]	0.90[a]
D_B	0.97[a]	0.98[a]	0.97[a]	0.97[a]	0.89[a]	0.90[a]
N_B	0.99[a]	0.99[a]	0.99[a]	0.99[a]	0.98[a]	0.97[a]
L_{TS}	0.05[ns]	-0.002[ns]	0.05[ns]	-0.08[ns]	0.26[a]	0.26[a]
L_{LS}	0.56[a]	0.55[a]	0.64[a]	0.64[a]	0.36[a]	0.31[a]
L_{LB}	0.99[a]	0.99[a]	0.99[a]	0.99[a]	0.98[a]	0.97[a]
N_{MW}	0.64[a]	0.72[a]	0.69[a]	0.80[a]	0.61[a]	0.69[a]
N_{FW}	0.44[a]	0.48[a]	0.46[a]	0.49[a]	0.52[a]	0.46[a]
N_{MF}	0.63[a]	0.69[a]	0.66[a]	0.78[a]	0.67[a]	0.67[a]
L_W	0.55[a]	0.58[a]	0.69[a]	0.67[a]	0.47[a]	0.45[a]
N_{FF}	0.25[a]	0.24[a]	0.33[a]	0.47[a]	0.38[a]	0.36[a]
N_C	0.33[a]	0.39[a]	0.16[b]	0.20[a]	0.04[ns]	0.05[ns]
D_C	0.99[a]	0.99[a]	0.99[a]	0.98[a]	0.97[a]	0.95[a]

[a, b] Correlation is significant at the 0.01 and 0.05 level (2-tailed), respectively; ns: non significant.

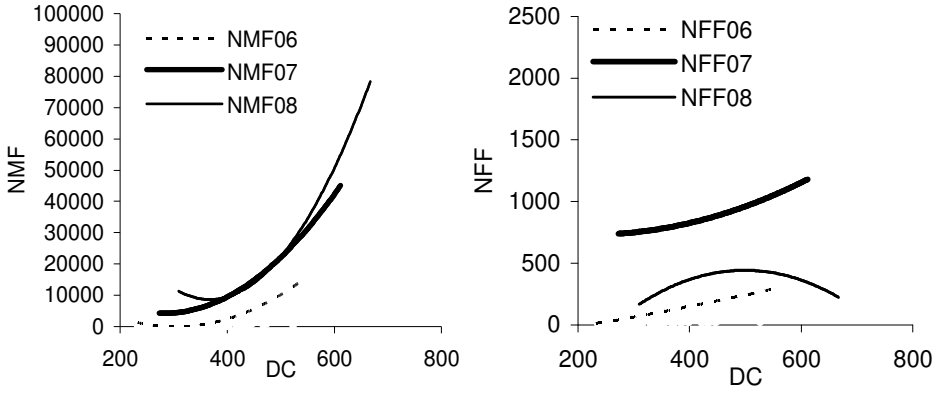


Figure 2. The relation between number of male flower (N_{MF}), female flower (N_{FF}) and crown diameter (Dc, cm) for the studied years.

varied from 0.05 to 0.99 for growth related characters whereas they varied 0.24 to 0.99 for flowering related characters. It is interesting that the year to year correlation coefficients for the N_{MF} were quite strong (r = 0.63-0.78) indicating that there are clones which consistently produce male whorls with high number of male flowers (Table 7). On the contrary, the correlation coefficients for the N_{FF} were quite low between the years.

Figures 1 and 2 illustrate relationships of male-female flower number and diameter at base and crown diameter. The graphs were obtained by fitting second-degree polynomials for individual graft values. As seen on Figure 1, the number of male and female flowers increases with increasing base (above the grafting point) stem diameter. But this increase more and more remarkable for male flower (N_{MF}) than female ones (N_{FF}). The N_{FF} approaches a maximum, beyond which an increase in base diameter does not produce more female flowers (Figure 1).

When considering crown diameter (D_C); as seen on Figure 2, the number of male flowers notably increases with increasing D_C. The N_{FF} approaches a maximum, beyond which an increase in crown diameter does not produce more female flowers (Figure 2).

Flower production increases with size of grafts (Figures 1 and 2), thus thinning out grafts with slow growth would probably, in the same time as improving the growth of the seed orchard trees, also increase seed production and internal pollination (Bilir et al., 2006). On the clonal base, positive significant correlation was determined between N_{MF} and most of the growth characters as H_T (r = 0.45), D_B (r = 0.56), L_{TS} (r = 0.20) , N_B (r = 0.21), L_{LB} (r = 0.31), D_C (r = 0.59) except for L_{LS} (Table 6). In addition, for N_{FF}, positive significant correlation was determined only between H_T (r = 0.19), D_B (r = 0.26) and D_C (r = 0.17). Fries (1994) found for *P. contorta* a positive correlation between number of flowers and size of the graft, which

was higher for male than female flowers.

In addition, in Scots pine seed orchard positive correlation among the flower numbers and length, diameter and volume of graft crowns was signified by Bhumibhamon (1978). Also, similar findings were reported in *P. abies* by Nikkanen and Ruotsalainen (2000). A tree can allocate its resources for vegetative growth or reproduction. A selection (intentional or unintentional) favoring reproduction could have a negative effect on growth in the forest. Negative genetic correlations between flowering and growth were reported in a natural forest of *P. taeda* by Schmidtling (1981) and in *P. sylvestris* by Nikkanen and Velling (1987), while low genetic correlations between height and flowering were reported in *P. contorta* by Hannerz et al. (2001) and in *P. abies* by Almqvist et al. (2001).

The number of strobili rises over time and the number of male strobili rises faster than the female. This was also reported by Bhumibhamon (1978). There are no significant correlations between N_{MF} and N_{FF} (Table 6). This is not in good accordance with other Scots pine studies (Jonsson et al., 1976; Bhumibhamon 1978; Burczyk and Chalupka, 1997; Bilir et al., 2002). The N_{MF} and N_{FF} values on Table 5 indicate that number of male flowers increases more than female ones. More male flowers will result in a higher genetic impact (e.g., father effect) of the seed orchard clones as polen parents and reduced impact of pollen parents outside the seed orchard, and thus increased genetic quality of the seeds. It may also raise the production of improved seeds if pollen is scarce for full pollination (Bilir et al., 2006).

The N_B has only low positive correlation with N_{MF} (r = 0.21) at the clonal base (Table 6). There are no significant correlation between N_B and N_{FF}. In accordance with this findings, Bilir et al. (2006) stated the number of branches has only a low positive or even negative correlation with the number of strobili in Scots pine seed orchards. Flowers are physically attached to branches and branch tips and therefore the amount of potential places should play an important role and that increases with the branch number. When top pruning a seed orchard, the apical dominance is broken. Cutting of tops and branches result in a decrease in strobili production for a couple of years, but the production of vegetative shoots increase, thus also the potential places for new strobili. Some years after the pruning, the number of strobili can exceed the number before pruning, and this despite the tree is smaller (Bilir et al., 2006). Also, for management reasons, it is economically advantageous to collect cones and seeds from small trees. Low cones which can be picked from the ground are cheaper to collect than if a lifting device has to be used (Lindgren et al., 2005). This is one reason pruning is an important tool for the seed orchard manager.

The high variation among / within the clones and heritability values estimated in this study, indicates opportunities of high selection intensity in the breeding programs for Scots pine. Also, the bigger variation within the clones than among the clones confirms that the genotypes have responses against to heterogeneity of growing area in seed orchard. Therefore, attention must be paid to these traits when management of existed orchards or establishment of new seed orchards. Meanwhile, the periodical and comparative experiments in the same orchard, will support to the breeding perspectives of this species and this results will evaluate as a sample for the other species.

Meanwhile, heritability values of N_{MW},N_{FW} and N_{MF} were bigger than N_{FF} in this study. This result show the possibility of increase of seed production and genetic gain by appending new genes to the breeding population from convenient main and sub breeding zones. Thus, the establisment of the seed orchards by using various origins should be discussed in the tree breeding strategies of Turkey.

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