The Pattern of Genetic Variation in Shoot Growth of *Pinus brutia* TEN. Populations Sampled from the Toros Mountains in Turkey

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Summary

The pattern of genetic variation in shoot growth of Turkish red pine (*Pinus brutia* TEN.) was studied in 180 open-pollinated families from a south to north transect in southern Turkey. Seedlings from 1 coastal, 1 inland and 2 centrally located populations (45 open-pollinated families each) were grown for 2 growing seasons in a forest nursery located near Antalya. The study revealed that both populations and families within populations varied significantly in all seedling traits except for free growth in the second year (SCHT92). In most seedling traits, the pattern genetic variation among populations suggests that there may be a as a clinal variation with respect to the distance from the Mediterranean Coast, but this needs to be tested further. The component of variation due to populations varied from 0% in SCHT92 to 57% in total height growth in the first growing season (FINHT91) while variance component due to families was from 0% in SCHT92 to 75.7% in seed weight (SW). Estimated family heritabilities were generally high for most traits, ranged from 0.20 in number of flushing in the first year (FLU91) to 0.96 in SW (estimated heritability for this trait is really a repeatability value). Genetic correlations between seed related traits and growth traits were moderately strong and positive, suggesting presence of maternal effect on early performances of seedlings. Generally, there were also moderate (0.22) to strong (0.93) genetic correlations between number of flushing and increment traits. Genetic correlations between phenological traits and increment as well as biomass related traits were not very strong and in most cases they were negative, indicating that those seedlings with more height growth and biomass are not necessarily the ones with longer growing seasons. In general, centrally located and coastal populations had similar shoot growth pattern-that is, families in these populations had more shoot flushes, heavier, more lateral branches and greater contribution to annual height increment by second more flushes than those families from the inland population. But, in all populations, the great portion of annual height increment in Turkish red pine was due to first flush (i.e. predetermined growth) indicating a conservative shoot growth pattern in early ages. The implications of this kind of shoot growth pattern as related to early evaluations of families in Turkish red pine breeding programs were also discussed in the paper.

Key words: Pinus brutia, shoot growth pattern genetic variation, genetic correlation, adaptation.

FDC: 165.53; 161.4; 174.7 *Pinus brutia;* (560); (235.1).

Introduction

Turkish red pine (*Pinus brutia* TEN.) is found throughout the eastern Mediterranean (PANETSOS, 1981). The Mediterranean Regions, the Aegean Regions and northwestern Turkey are the places where the species has its natural distribution in Turkey (*Figure 1a*) and it is a commercially important timber species in the country (KAYACIK, 1954; ARBEZ, 1974; KAYA *et al*., 1997). Frequent forest fires, changes in land use and grazing occurred in the past have narrowed the original distribution of the species in Turkey. These anthropogenic effects are also most likely impacted the genetic diversity of Turkish red pine populations, however, the magnitude of the impact is unknown. Today, there are large areas of degraded forest lands present in Turkey that could be reforested with Turkish red pine. For successful regeneration programs in such areas, there is a great need of information concerning the adaptive significance of genetic variation which may exist in seedling traits of the species. The previous studies indicated that there is considerable variation between populations in seed and seedling traits (IKTÜEREN, 1977; ASLAN and UĞURLU, 1986; CALAMASSI *et al*. 1988; FALUSI, 1992). It has been demonstrated that Turkish red pine populations sampled from an elevational transect in the Toros mountains in southern Turkey revealed a clinal genetic variation in seedling traits, gradual changes of genetic variation with along the elevational gradient (IŞIK, 1986). However, there is a lack of studies dealing with the adaptive significance of variation in shoot-growth-pattern of seedlings. Turkish Red pine tree improvement programs have been already established (Anonymous, 1995; IŞIK, 1986, 1993; IŞIK and KAYA, 1993, 1995). The information on pattern of genetic variation in adaptive traits and overall genecology of species will be vital for the success of tree improvement programs at the early stages, but such information is not available yet. Since Turkish red pine has ability of rapid growth (with several flushes in a year) and there is a high demand for its wood various industries, Turkish Forest Service is interested greatly in the species as a timber tree (Anonymous, 1989). Although there are isolated stands or trees grown close to the continental parts of Turkey, main body of Turkish red pine forests is distributed along the Mediterranean, Aegean and Black Sea Regions (*Figure 1a*).

There is vast of land available for afforestation/reforestation in central Turkey, but numbers of species for afforestation purposes are limited to a few species. Currently, *Pinus nigra* is the most widely used species. Large areas, especially in transition zones from the Mediterranean Coast towards to central Turkey, could be reforested or afforested with suitable Turkish red pine seed sources if the pattern of genetic variation is known in natural populations of the species. But the lack of information on the pattern of genetic variation concerning adaptive traits such as shoot-growth-pattern in Turkish red pine populations located along the south (from the Mediterranean Sea) to north (central Turkey) transect hinders the establishment of large plantations in such areas with Turkish red pine.

It would be very valuable to know the magnitude and pattern of genetic variation in adaptive seedling traits such as component of shoot growth by studying the populations especially those located along the transect of the Toros Mountains from south to north where the Turkish Red pine makes

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its most interior distribution (north of Antalya Province). Therefore, the objectives of the present study were set as: (1) To determine the pattern and magnitude of genetic variation in shoot growth of natural populations of Turkish red pine sampled in the Toros Mountains to test if the pattern of shoot growth has and adaptive significance; (2) To estimate genetic parameters for components of shoot growth to see how these traits are related to other seedling traits. To meet the above objectives, seedlings from 45 half-sib families in each of four populations were grown in a forest nursery for two years and shoot growth-component-traits and other seedling traits were evaluated.

Materials and Methods

Sampling procedures

Four populations (2 low and 2 high elevation populations) were sampled, starting in Antalya which is a provincial center on the Mediterranean Coast, with (30 km to 40 km distances between populations in Central Toros Mountains (*Table 1*, *Figure 1b*). Sampled populations varied considerably in amount of annual rain fall, ranging from 530 mm in Bük to 1055 mm in Düzlerçamı which is a coastal population. ln each population, 45 mother trees were selected for collection of open pollinated seeds with the following restrictions: (1) maximum elevational range of mother trees were confined within 300 m, (2) within each population, minimum distance between any 2 trees had to be greater than 150 m, (3) cones had to be collected from the upper one-third of the crown of mother trees, (4) to eliminate the mixing of cone from different years, the collected cones had to be the crops of 1990 since it is common to see the cones in Turkish red pine trees from different years due to seratoniesness nature of the cones. The details of sampling procedure were given in IŞIK and KAYA (1995).

Experimental Methods

Open pollinated seeds of parent trees (families) were sown in a forest nursery bed as a 10-seedling-row plots of 180 families

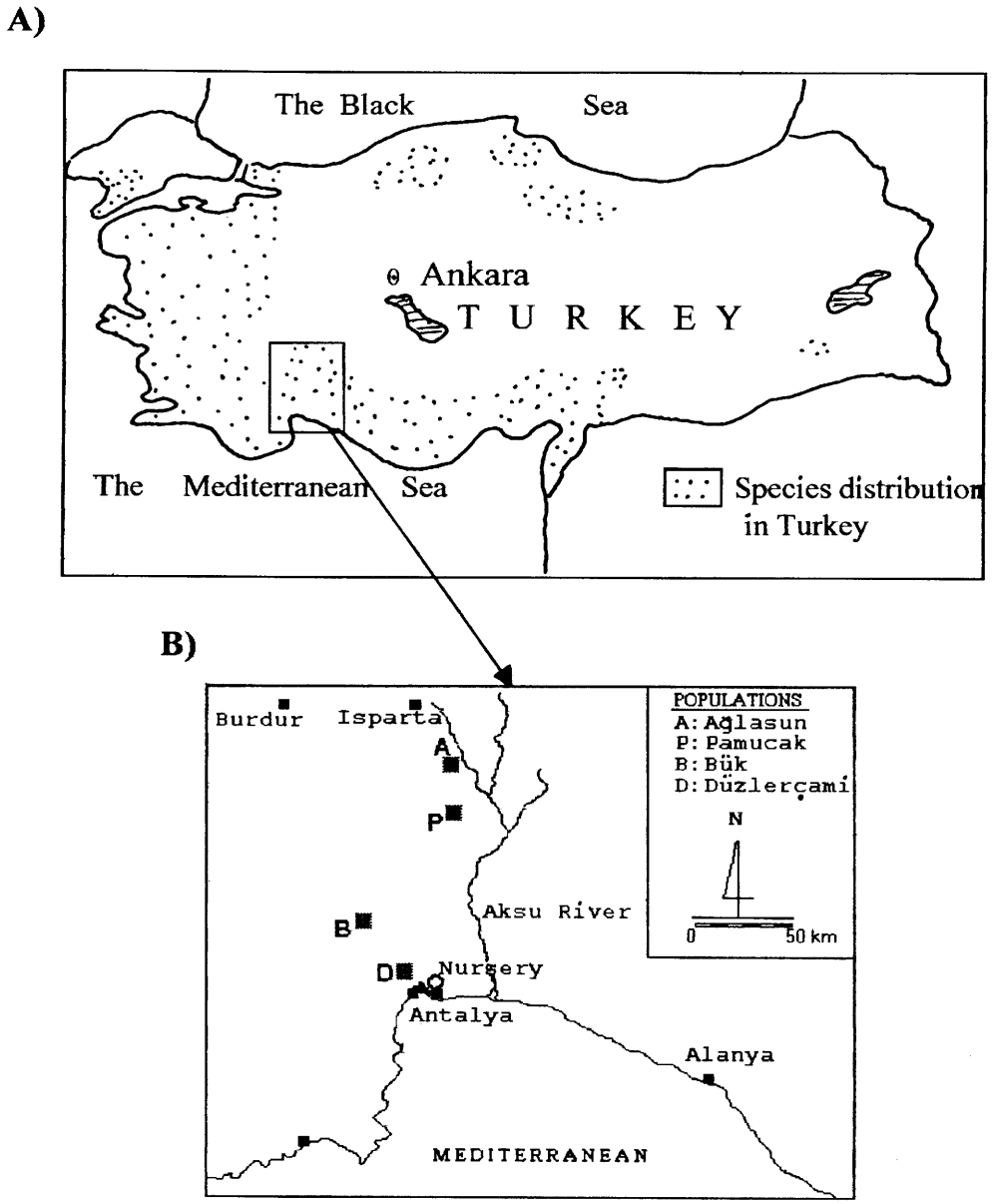

Figure 1. – A) The Map showing the natural distribution of *Pinus brutia* in Turkey. B) Map showing the locations of studied populations and the nursery where the study was carried out.

Table 1. – Description of the populations.

Populations	Altitude	Distance from the Mediterranean Sea	Latitude	Longitude	Annual rain fall
Düzlerçamı (Coastal population)	250 m	30 km	37° 50'	30° 29'	1055 mm
Bük (Centrally located)	450 m	55 km	36° 59'	30° 25'	530 mm
Pamucak (Centrally located)	750 m	90 km	37° 23'	30° 33'	700 mm
Ağlasun (Inland population)	950 m	130 km	37° 23'	30° 25'	600 mm

Table 2. – Description of studied traits.

Codes for traits	Definitions of traits	Units of traits
SW	100 seed weights	grams
CW	3 cones weight	grams
COT	Number of cotyledons	number
FRHT91	Predetermined growth in 1991	cm
SCHT91	Free growth in 1991	cm
FINHT91	Total height growth	cm
BS91	Date of bud set 1991	days from January 1991
FLU91	Number of shoot flushes in 1991	number
BB92	Bud burst date	days from January 1992
FRHT92	Predetermined growth in 1992	cm
SCHT92	Free growth in 1992	cm
FINHT92	Total height growth in 1992	cm
FLU92	Number of shoot flushes in 1992	number
WW12	Total fresh weight of seedlings (this is the total fresh weight of shoot above cotyledon scar after two years of growth).	gr
BR91	Number of lateral branches of seedlings in 1991	number
BR92	Number of lateral branches of seedlings in 1992	number
BR12	Total number of lateral branches of seedlings in 1991 and 1992	number
FINHT12	Total height growth of seedlings after two years	cm

(4 populations x 45 families per population) in Spring of 1991 and families were randomly allocated to plot location in a complete block design with 3 replicates (30 seedlings per family in total). The nursery, Zeytinköy Forest Nursery (altitude 40 m), is located near Antalya where the climate is a typical Mediterranean climate that is dry and hot summer followed by a mild and rainy winter (*Figure 1b*). There was no major climatic fluctuations in the growing seasons of 1991 and 1992. Seedlings in the nursery were irrigated once a week (until saturation) in May through September of both in 1991 and 1992. Seventeen traits expressing timing of vegetative cycle, total height increment, components of shoot growth (e. g. increment due to predetermined growth (growth by first flushing), free growth (growth by second and more flushings)), number of flushings (including the first flushing), number of lateral branches and wet weight (only above the cotyledon scars were considered) of seedlings after 2 years were measured (*Table 2*). The timing of bud set was determined as the number of days from the first day of the year (January 1st, 1991). Bud set was defined as the date when brown bud scales were first visible on the overwintering terminal bud. Observations were made weekly and began on September, 1991 in the first year and were not scored in the second year since most seedlings did not set permanent winter bud at all in the second year. Bud set observations were carried out weekly until 90% of seedlings set overwintering buds in 1991. The timing of bud-burst was determined as the number of days from the first day of the year (January 1st, 1992) and defined when the green needles from overwintering buds were appeared. Observations were made twice in a week starting on March 1st, 1992 and continued until 90% of seedlings burst bud. Height growth in 1991 (FINHT91) and 1992 (FINHT92) were measured in November 1991 and 1992, respectively. Also, in each year height increment due to first flush (FRHT91, FRHT92- i.e., predetermined growth) as well as increment due to the flushes other than the first flush (SCHT91, SCHT92- i.e., free growth) were recorded as it is described in KAYA *et al.* (1989). Additionally, number of flushings for each seedling was determined in year 1991 (FLU91) and 1992 (FLU92). The definition of other traits such as biomass traits (number of lateral branches, wet top weight of seedlings) were given in *table 2*.

Statistical Analysis

The pattern of genetic variation in seedling traits and genetic correlations between traits in a given species are essential information to have successful reforestation and tree improvement program in that particular species. Genetic correlations are estimated from components of variance and

covariance (FALCONER, 1981) substituted into standard equation for the product-moment correlation coefficient. Heritabilities were estimated from components of variance. Analyses of traits were based on plot means. In each replication, there were some plots with no seedlings in family plots, thus, analysis of variance for all traits were carried out by using a generalized least square procedure (SAS Inst., 1988). A GLM-SAS procedure was used which gives unbiased estimates of all mean squares when a data set has missing plots. The following statistical model has been used during the data analysis.

$$Z_{ijk} = \mu + B_k + P_j + F(p)_i + e_{ijk} \quad \text{(EQ.1)}$$

where μ is the experimental mean, Z_{ijk} is the mean performance of the *i* th family in the *j* th population in the *k* th replication; B_k = the effects of replication; P_j = the effects of populations; $F(p)_i$ = the effects of families within populations; e_{ijk} = the experimental error.

Table 3. – Form of analysis of variance for the traits.

Source of variations	df	Expected Mean Squares
Replications	2	
Populations	3	$\sigma^2 + 2.97\sigma^2_{F(P)} + 131.7K^2_P$
Families/Populations	176	$\sigma^2 + 2.97\ \sigma^2_{F(P)}$
Error	345	σ^2

Components of variance and covariance of populations and families within populations were estimated according to the expectations from the analysis of variances (*Table 3*). Heritabilities were estimated from the components of variance as in NAMKOONG (1979). Family heritabilities (h^2_{fx}) were estimated by using the following equation:

$$h^2_{(fx)} = \frac{\sigma^2_{(fx)}}{\sigma^2_e/r + \sigma^2_{(fx)}} \quad \text{(EQ.2)}$$

where $\sigma^2_{f(x)}$ = family component of total variance for trait *x*, r = 2.9, σ^2_e = error variance. Genetic correlations were estimated from the component of variance and covariance (FALCONER, 1981) substituted into the standard equation for the product-moment correlation coefficient.

$$\text{Genetic correlation } (Rg_{(x,y)}) = \frac{COV_{f(x,y)}}{\sqrt{\sigma^2_{f(x)}}\sqrt{\sigma^2_{f(y)}}} \quad \text{(EQ.3)}$$

where $Rg_{(x,y)}$ = estimated genetic correlation between trait *x* and *y*, $\sigma^2_{f(x)}$ = estimated components of variance of families within populations for trait *x*, $\sigma^2_{f(y)}$ and = estimated components of variance of families within populations for trait *y* and $COV_{f(x,y)}$ = estimated component of covariance of families within populations between traits *x* and *y*, estimated from covariance analysis.

The phenotypic correlation between traits x and y were calculated from family mean squares and mean cross products for the traits according to KAYA *et al.* (1989). The standard errors of genetic and phenotypic correlations were calculated according to BECKER (1984).

Results

Pattern and Magnitude of Genetic Variation

Seed Related Traits

Seed related traits such as seed weight (SW), cone weight (CW) and number of cotyledon (COT) varied significantly among populations as well as among families within popula-

Table 4. – Mean squares, component of variance as a % of total variance (VC), and family heritabilities for the seedling traits.

Traits[1]	Replications df=2	VC %	Populations df=3	VC %	Families/ Populations df=176	VC %	Error df=345	VC %	Family heritability (h^2_f)
SW	0.01	0.0	2,97**	19.4	0.24**	75.7	0.01	4.9	0.96±0,10[2]
CW	136.68	0.0	113351,42**	48.4	2287.87**	41.5	175.08	10.1	0.92±0.10[2]
COT	1.78	2.4	10.75**	19.9	0.61 **	40.5	0.15	37.6	0.75±0.10
FRHT91	266.75	16.8	421.38**	35.4	6.56 **	13.4	3.06	34.4	0.53±0.11
SCHT91	262.34	31.2	102.45ns	15.9	2.99ns	5.3	2.26	47.6	0.24±0.12
FINHT91	6.25	0.2	935.34**	57.1	10.07 **	20.4	2.75	22.3	0.73±0.11
BS91	2277.61	3.6	8286.74**	17.6	481.00 **	33.5	152.02	45.5	0.68±0.11
FLU91	5.59	39.2	1.26**	10.2	0.05 *	4.5	0.04	45.1	0.20±0.12
BB92	0.77	3.8	1.54**	10.2	0.13 **	21.8	0.07	64.1	0.46±0.11
FRHT92	13.45	0.0	2834.07**	6.0	420.75**	12.6	308.62	81.4	0.27±0.13
SCHT92	1578.01	2.5	222.84ns	0.0	276.02ns	0.0	280.91	97.5	–
FINHT92	1283.84	14.0	2350.60**	34.0	48.41 **	22.2	15.38	30.0	0.68±0.10
FLU92	11.20	34.0	0.99**	3.3	0.18 **	16.6	0.09	46.1	0.50±0.11
WW12	1136.82	5.5	6102.98**	40.3	111.26 **	22.9	35.44	31.3	0.68±0.11
BR91	6.31	0.3	424.98**	40.8	7.97 **	22.8	2.80	36.1	0.65±0.11
BR92	168.32	25.5	21.16**	3.4	4.66 **	28.2	1.60	42.9	0.66±0.11
BR12	1195.22	0.0	6133.12**	25.8	94.37 **	33.2	27.18	41.0	0.71±0.10
FINHT12	146.59	6.5	504.23**	44.7	19.61**	22.4	5.82	26.4	0.70±0.10

*) Significant at P<*0.05*.
**) Significant at P<*0.01*.
ns: not statistically significant at P<*0.05*.
[1]) See *table 2* for definition of codes for traits.
[2]) These family heritability estimates are really repeatability values for SW and CW.

Table 5. – Population means for the seedling traits.

Traits[1]	Populations			
	Düzlerçamı	Bük	Pamucak	Ağlasun
SW	1.74	1.51	1.51	1.38
CW	154.55	88.87	111.78	97.81
COT	8.80	8.34	8.39	8.14
FRHT91	17.70	15.29	14.82	13.48
SCHT91	3.01	2.06	1.58	0.92
FINHT91	20.71	17.35	16.40	14.40
BS91	312.12	311.48	321.07	327.96
FLU91	1.35	1.28	1.22	1.14
BB92	71.32	71.53	72.44	72.93
FRHT92	38.14	31.26	29.81	26.79
SCHT92	3.43	6.13	6.13	4.71
FINHT92	41.57	37.39	35.94	31.50
FLU92	1.98	2.00	2.02	1.84
BR91	10.91	9.01	7.85	6.76
BR92	7.23	7.40	7.71	6.76
WW12	38.01	29.66	27.57	21.81
BR12	18.15	16.41	15.56	13.52
FINHT12	62.28	54.79	52.34	45.90

[1]) See *table 2* for definition of codes for traits.

tions (*Table 4*). The component of variance (VC) due to families was significantly higher for SW (75.7% of total variance) and COT (40.5%) than the component due to populations (19.4%, and 19.9%, respectively) while this trend was not observed for CW (*Table 4*). On the average, inland population (Ağlasun) had lower SW, CW and number of cotyledons than those coastal (Düzlercamı) and more centrally located populations (Bük and Pamucak) (*Table 5*).

Phenological Traits

The timing of budset in 1991 (BS91) and timing of bud burst in 1992 (BB92) showed significant variation among both populations and families. The component of total variation attributable to families in both traits (33.5% in BS91 and 21.8% in BB92) were significantly higher than the component due to populations (17.6% in BS91 and 10.2% in BB92) (*Table 4*). Both timing of budset in 1991 and bud burst in 1992 were later in the inland population than in the other populations. For example, seedlings from coastal population completed the budset about 2 weeks earlier than those from the inland population (*Table 5*).

Flushing Traits

The number of shoot flushes in 1991 (FLU91) and 1992 (FLU92) varied significantly in both among populations as well as among families within populations. The component of total variation due to populations was higher (10.2%) in the first year than those of families (4.5%). In the second year, the pattern was the opposite of that in 1991 (FLU92, 3.3% of VC due to populations vs. 16.6% due to families) (*Table 4*). On the average, number of shoot flushes in 1991 were highest in the coastal population (1.35) while it was lowest in the inland population (1.14). In the second year, the same pattern was observed with higher number of families in each population with more than one flush. In fact, great majority of families in each population had second flushing. The mean number of flushing ranged from 1.84 (Ağlasun, inland population) to 2.02 (Pamucak, centrally located population) (*Table 5*).

Height Increment Related Traits

Both predetermined growth (FRHT91) and total height growth (FINHT91) in 1991 as well as in 1992 (FRHT92 and FINHT92) showed significant variation in both among populations and among families within populations. The observed variation among populations was clinal with respect to the distance from the Mediterranean Coast. But the component of variation due to populations were considerably higher in both FRHT91 (35.4%) and FlNHT91 (57.1%) in 1991 than the variance component due to families (13.4% in FRHT91, 20.4% in FlNHT91) (*Table 4*). In the second year (in 1992), the components of total variance due to families were higher than those due to populations in FRHT92 (6% due to populations vs. 12.6% due to families) while the pattern was the same like in 1991 in FINHT92 (34% due to populations vs. 22.2.% due to families). Both in the first year (1991) and second year (1992), the most of the height increment was due to the predetermined growth. For example, the amount of predetermined growth ranged from as 85.5% of the total height increment in 1991 in the coastal population (Düzlerçamı) to 93.6% of in the inland population (Ağlasun). In the second year, predetermined growth, again, made up the most of height increment, ranging from 82.95% in Pamucak (centrally located) to 91.7% in Düzlerçamı (coastal population) (*Table 5*). Height increment due to multiple flushing did not vary significantly among populations or among families in 1991 (SCHT91) as well as 1992 (SCHT92). Both components of total variance due to populations and families made up very small portions. The amount of increment due to multiple flushing as a percent of total height growth ranged from 6.4% (inland population) to 14.5% (coastal population) in the first year while it varied from 8.25% (coastal population) to 16.4% in Bük (centrally located population) in the second year (*Table 5*).

The total height increment in 2 years (FINHT12) were significantly different among populations and among families within populations. The component of total variance due to populations (VC = 44.7%) were higher than it was due to families (VC = 22.4%) (*Table 4*).

Biomass Traits

All 3 traits (number of lateral branches in 1991 (BR91) and 1992 (BR92), total fresh weight of seedlings after 2 growing seasons (WW12)) significantly varied in both among populations as well as among families. The component of total variation due to populations made up great portion of total variation in WW12 and BR91, but variance component due to families in BR92 was higher than that is of population caused ones (*Table 4*). Families from the Coastal population had more lateral branches and were heavier than from the families of the inland population (*Table 5*).

Family Heritabilities and Genetic Correlations

Family heritabilities ranged from 0.20 in FLU91 to 0.96 in SW. Generally seed-related traits were with the high family heritability estimates while flushing traits had low family heritabilities. This should be expected since estimated heritabilities for SW and CW are really the repeatability values which set up the upper limits of genetic component in the total variation in SW and CW (FALCONER, 1981). Increment and biomass traits had moderate family heritability estimates in except for the height increment traits by second flushing (*Table 4*). Generally, estimated genetic correlations and phenotypic correlations were in the same direction in sign and close in magnitude. Here only the genetic correlations between the traits will be reported. Thus, for the phenotypic correlations, the related tables could be consulted. Genetic correlations between SW and height increment, flushing as well as biomass related traits were ranged from low (Rg = 0.20 between FLU92 and SW) to high (Rg = 0.52 , between SW and WW12) (*Table 6*). Similarly, genetic correlations between CW and increment, flushing and biomass related traits were positive and ranged from 0.17 (between CW and FLU91) to 0.42 (between CW and BR91) (*Table 6*). The genetic correlations between COT and other traits (increment, flushing and biomass related traits) followed similar pattern as observed between SW and other growth traits as well as between CW and other growth traits (*Table 6*). Indicating that those families with heavy seed, cone or increased number of cotyledons tend to have seedlings with more height increment, lateral branches, second flushing and fresh total weight.

Table 6. – Genetic and phenotypic correlations between seedling traits and seed related traits.

Genetic Correlations

Seedling traits[1]	SW	CW	COT
FLU91	0.21±0.18	0.17±0.19	0.25±0.19
SCHT91	0.34±0.11	0.31±0.20	0.40±0.18
FINHT91	0.42±0.08	0.19±0.08	0.31±0.09
BR91	0.42±0.10	0.42±0.10	0.37±0.09
FLU92	0.20±0.11	0.22±0.11	-0.18±0.14
SCHT92	_[2]	_[2]	_[2]
FINHT92	0.43±0.08	0.30±0.09	0.40±0.09
BR92	0.23±0.09	0.27±0.09	0.22±0.10
FINHT12	0.50±0.08	0.39±0.09	0.38±0.09
BR12	0.30±0.08	0.38±0.09	0.33±0.09
WW12	0.52±0.08	0.41±0.09	0.44±0.09

Phenotypic correlations

FLU91	0.09±0.08	0.05±0.08	0.12±0.08
SCHT91	0.15±0.08	0.09±0.08	0.18±0.08
FINHT91	0.34±0.07	0.16±0.07	0.21±0.08
BR91	0.42±0.10	0.26±0.08	0.28±0.07
FLU92	0.11±0.08	0.13±0.08	0.14±0.08
SCHT92	0.11±0.08	0.12±0.08	0.12±0.09
FINHT92	0.32±0.07	0.21±0.07	0.27±0.07
BR92	0.05±0.07	0.18±0.08	0.16±0.08
FINHT12	0.38±0.07	0.26±0.08	0.27±0.07
BR12	0.24±0.07	0.27±0.08	0.25±0.07
WW12	0.38±0.07	0.27±0.08	0.32±0.07

[1]) See *table 2* for definition of codes for traits.
[2]) Genetic correlation could not be estimated due to the lack of genetic variation in SCHT92.

Table 7. – Genetic and phenotypic correlations between flushing and height increment traits.

Genetic correlations

Flushing traits[1]	*Increment and biomass traits*						
	FRHT91	**FINHT91**	**FRHT92**	**FINHT92**	**FINHT12**	**BR12**	**WW12**
FLU91	0.60±0.34	0.76±0.18	0.22±0.35	0.80±0.18	0.81±0.18	0.91±0.20	0.93±0.20
SCHT91	0.97±0.36	0.99±0.17	0.25±0.33	1.01±0.18	1.03±0.18	1.01±0.19	0.55±0.09
FLU92	0.32±0.14	0.54±0.10	0.002±0.22	0.75±0.07	0.71±0.08	0.81±0.07	0.69±0.09
SCHT92	_[2]	_[2]	_[2]	_[2]	_[2]	_[2]	_[2]
Phenotypic correlations							
FLU91	-0.07±0.10	0.46±0.07	0.05±0.11	0.47±0.07	0.49±0.07	0.47±0.07	0.50±0.07
SCHT91	0.06±0.10	0.59±0.06	0.06±0.11	0.56±0.07	0.60±0.06	0.53±0.07	0.45±0.06
FLU92	0.19±0.09	0.37±0.07	0.02±0.10	0.66±0.05	0.59±0.06	0.65±0.05	0.55±0.06
SCHT92	-0.04±0.10	0.05±0.09	-0.75±0.06	0.17±0.09	0.14±0.09	0.15±0.09	0.13±0.09

[1]) See *table 2* for definition of codes for traits.
[2]) Genetic correlation could not be estimated due to the lack of genetic variation in SCHT92.

In the first year (1991), there were strong and positive genetic correlations between FLU91 and total height increment (FINHT91) (Rg = 0.76) as well as FLU91 and total fresh weight (Rg = O.93). The pattern of genetic correlation between the amount of height increment due to second flushing (SCHT91) and total height increment as well as SCHT91 and WW12 were similar to above (*Table 7*). Although due to lack of genetic variation in SCHT92, genetic correlation between SCHT92 and other biomass and increment traits could not be calculated, the genetic correlations between number of shoot flushes in 1992 and increment traits as well as biomass traits were positive and strong (*Table 7*).

Genetic correlation between FLU91 and BS91 were weak and negative (Rg = –0.01) as well as between FLU91 and BB92 (Rg = –0.10). Although the magnitude and sign of genetic correlation between FLU92 and BS91 were similar to the first year, genetic correlation between FLU92 and BB92 were improved, but it was still negative (Rg = –0.44) – indicating that families with late budburst tend to have less shoot flushes. Genetic correlations between the timing of bud set and other increment and biomass related traits were ranging from low to moderate with negative sign. But genetic correlations between the timing of bud burst and increment and biomass related traits were negative and moderately strong – that is, those families with later budburst dates were the ones with less height increment and less total fresh weight (*Table 8*). Although due to the lack of genetic variation in SCHT92, genetic correlation between this trait and flushing traits could not be estimated, the genetic correlations between FLU91 and height increment due to second flushing were positive and strong (Rg = 0.96). Also, those families with more shoot flushes in l99l had also more shoot flushes in the year of l992 (Rg = 0.95) (*Table 9*).

Discussion

The results of present study revealed that there is a considerable amount of genetic variation among populations as well as families within population in Turkish red pine. In most seedling traits, pattern of genetic variation among populations suggest that there may be a clinal variation among the populations with respect to the distance the Mediterranean Coast. However, this needs to tested further by sampling more populations along the Mediterranean Coast to inland transect and studying populations in older plantations. Similarly, clinal variation among populations with respect to elevation has been also reported by IŞIK (1986). Centrally located and coastal populations had similar shoot growth pattern – that is, families in these populations had more shoot flushes, heavier, more lateral branches and greater contribution to annual height increment by second more flushes than those families from the inland population did. Nevertheless, in all populations, the great portion of annual height increment was due to the first flushes. In older trees, this trend was not observed. Although a few families involved in the study by YILDIRIM (1992), it was reported that at the age of 13, about 50% of annual height increment was due to second or more flushes in Turkish red pine. This difference is not unexpected since the dependence of young Turkish red pine trees heavily on predetermined growth for height increment increases the adaptiveness of the species to wide-range of environments. In fact, families from the inland population were more conservative while families from centrally located populations were more opportunistic in terms of utilizing the favorable environment. Also, it appears that shoot growth pattern is different in young seedlings than older trees, that is, young seedlings adopted a conservative shoot growth pattern by relying mainly on predetermined growth for annual height increment while in older trees, annual height increment can be benefited from both predetermined and free growth equally, an opportunistic shoot growth pattern. It is likely that different sets of genes are responsible for annual height increment in young seedlings than those for annual height increment of older trees. Recent work on mapping quantitative trait loci (QTL) carried out in loblolly pine revealed supporting results for this hypothesis (KAYA *et al.*, 1996).

Although the magnitude of genetic variation within and between populations varied depending on the seedling traits, the results suggest that selection practiced at population as

Table 8. – Genetic and phenotypic correlations between flushing traits and phenological traits.

Genetic correlations

Increment and biomass related traits[1]	*Phenological traits* BS91	BB92
FLU91	-0.01±0.20	-0.10±0.25
SCHT91	-0.02±0.20	-0.21±0.24
FINHT91	0.07±0.11	-0.13±0.12
FLU92	0.03±0.13	-0.44±0.12
FRHT92	-0.04±0.18	0.19±0.23
SCHT92	_[2]	_[2]
FINHT92	-0.22±0.10	-0.48±0.12
FINHT12	-0.13±0.10	-0.37±0.12
BR91	-0.31±0.10	-0.44±0.12
BR92	-0.01±0.11	-0.26±0.13
WW12	-0.29±0.10	-0.41±0.12
BR12	-0.20±0.10	-0.39±0.12

Phenotypic correlations

FLU91	0.02±0.09	-0.01±0.10
SCHT91	0.01±0.09	-0.04±0.10
FINHT91	0.01±0.08	-0.07±0.08
FLU92	0.05±0.08	-0.13±0.09
FRHT92	-0.04±0.09	0.01±0.10
SCHT92	-0.03±0.10	-0.13±0.10
FINHT12	-0.13±0.08	-0.24±0.08
BR91	0.29±0.07	-0.29±0.08
BR92	0.01±0.08	-0.15±0.08
BR12	-0.18±0.08	-0.26±0.08
WW12	-0.23±0.08	-0.28±0.08

[1]) See *table 2* for definition of codes for traits.
[2]) Genetic correlation could not be estimated due to the lack of genetic variation in SCHT92.

Table 9. – Genetic correlations (below diagonal) and phenotypic correlations (above diagonal) between flushing traits.

Traits[1]	**FLU91**	**SCHT91**	**FLU92**	**SCHT92**
FLU91	–	0.94±0.01	0.39 ±0.09	0.14±0.12
SCHT91	0.96±0.04	–	0.40±0.09	0.15±0.12
FLU92	0.95±0.25	1.01±0.25	–	0.25±0.10
SCHT92	_[2]	_[2]	_[2]	–

[1]) See *table 2* for definition of codes for traits.
[2]) Genetic correlation could not be estimated due to the lack of genetic variation in SCHT92.

well as family level will increase the genetic gain which may be captured during breeding programs. Unlike some other pine species such as *Pinus nigra* subsp. *pallasiana* (KAYA and TEMERIT, 1993), the magnitude of genetic variation between populations were considerably high for most seedling traits in Turkish red pine. Thus, selection schemes involved in both populations and families within populations will be more efficient in Turkish red pine breeding programs than selection practiced at the family level alone. For most seedling traits, moderate to high family heritabilities were estimated. But if selection of families is based on annual height increment, at least in early evaluations of families, predetermined growth should be given high priority since the contribution to annual height increment by second and more flushes are not significantly different among families as well as among populations. Furthermore, there were moderately strong genetic correlations between seed related traits and growth traits, suggesting that there is considerable amount of maternal effects on growth traits. If early evaluation of families is practiced and selection is based on only height growth, such selection scheme surely results in changes in family ranking in later ages since it is reported that seed effects diminish in later ages (SMITH *et al*., 1993). However, those families with high number of multiple flushings can be selected for favorable sites since multiple flushings in conifers occurs in higher frequencies in favorable environments (HALGREN and HELMS, 1992). It seems that families with multiple shoot flushes in a given year are most likely to flush in the following years since there is moderately strong genetic correlations between number shoot flushes in consecutive years.

Changes in management practices in Turkish red pine stands by the Turkish Forest Service and pressures from agricultural practices threaten the continuation of genetic resources of the species in Turkey. If the preventive measures are not taken, genetic variation observed among populations can be lost irreparably. This will create problems for finding proper seed sources for future afforestation programs concerning the species. Fortunately, in recently prepared *the National Plan for in situ Gene Conservation of Plant Genetic Diversity in Turkey (*KAYA et al., 1997), Turkish red pine has been determined as one of the priority species in which *in situ* gene conservation areas needed to be set aside soon in addition to the existing ones. The pattern and magnitude of genetic variation revealed in this study will be very useful in determining necessary number of *in situ* gene conservation areas and strategies for long terms conservation and management of genetic resources of the species.

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