

# Genetic Variation in Provenance-Progeny Trials of *Cupressus sempervirens* in Türkiye

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## ABSTRACT

In this study, the genetic and phenotypic relations among tree height, diameter at breast height and survival at 18 years of age were investigated in Mediterranean cypress (*Cupressus sempervirens* L. var. *horizontalis* (Mill.) Gordon) provenance-progeny trials established in two locations in southern Türkiye. It was found that the variation among families within one provenance was higher than among different provenances. At the joint analysis, the narrow-sense heritability ( $h^2$ ) was 0.36 for height, and 0.24 for diameter. Family mean heritability ( $h_f^2$ ) was 0.78 for height, while it was 0.53 for diameter. Diameter showed higher (13.98%) genetic diversity than height (12.71%). Genetic correlation between traits was high (0.84). According to the breeding values of the families estimated by the BLUP method, when the best 50 families by two traits are selected separately, 12.5% genetic gain in terms of height and 13.2% in terms of diameter can be achieved. In the selection of the best 30 families, the estimated genetic gain calculated was 15.2% for height and 16.3% for diameter.

**Keywords:** cypress; heritability; genetic gain; selection; genetic diversity

## INTRODUCTION

*Cupressus sempervirens* L. var. *horizontalis* (Mill.) Gordon is a variety of Mediterranean cypress (*Cupressus sempervirens* L.), which is the only cypress species naturally distributed in Türkiye (Anşın and Özkan 1997). The natural distribution of the Mediterranean cypress is fragmented and discontinuous, extending from the southwestern Mediterranean basin to the Caucasus and southwestern Iran in the east, at altitudes ranging from the sea level (Crete Island) to 2000 m (Türkiye). The Mediterranean cypress is drought-resistant and capable of thriving in areas with an annual precipitation of up to 200 mm (Caudullo and de Rigo 2016).

The natural distribution of Mediterranean cypress in Türkiye is 4,796.9 ha (OGM 2021). Despite its small-scale natural distribution, the species has an important role in forestry studies in Türkiye due to the following reasons:

- It may form mixtures with other species that can be used to provide species and product diversity in suitable habitats in potential Turkish red pine (*Pinus brutia* Ten.) afforestation areas (Sabuncu and Çalışkan 2008), especially considering its fast growth in juvenile age and useful wood (Saatçioğlu 1976).

- Its branched stem and dense coniferous top structure make it an effective barrier against wind, dust, noise, and unsightly views. (Caudullo and de Rigo 2016).
- Research in pharmacology has revealed that this aromatic plant has crucial medicinal properties that protect against bacteria, fungi, and viruses, repel parasites and insects, and increase resistance to cancer due to its chemical components (Al-Snafi 2016).
- It is a tree species with high landscape value (Farjon and Filer 2013). Not only due to its body form, but also because it functions as a solitary object in the urban landscape. On the other hand, with its vertical silhouette, it cuts and balances the static horizontal lines in the landscape. In addition, thanks to its dark green color tones, it creates a visual contrast in the form of scattered spots in the light green and brightly colored Mediterranean vegetation (Çalikoğlu et al. 2010).
- It is one of the tree species used by the General Directorate of Forestry of Türkiye within the scope of the Rehabilitation of Burned Areas and the Establishment of Forest with Fire Resistant Species Projects (OGM 2010).

Due to the reasons mentioned above, silviculture and arboriculture of Mediterranean cypress are gaining importance day by day. In this respect, it is important to determine quality seeds and saplings, best seed source, breeding potential and protection of natural populations. Additionally, it is a necessity to protect Mediterranean cypress's natural gene resources and develop appropriate policies against the risks posed by various biotic and abiotic factors. In the early studies on the Mediterranean cypress in the nursery, Sabuncu (2004) reported high genetic diversity and heritability for seedling height within the population. Uslu and Bilir (2020) stated that the species outperformed pyramidal cypress in seedling height and diameter at root collar. Regarding the knowledge and general information on the cypress, some prominent studies include: Farahmand (2020), on genetic-breeding studies; Korol et al. (1997), Capuana et al. (2000), Papageorgiou et al. (2005), Gallis et al. (2007), Al-Hawija et al. (2014), Nocetti et al. (2017), Bagnoli et al. (2020), and Ismael et al. (2021).

In this study, the genetic variation, heritability and genetic correlation, genetic gain of height and diameter at breast height, as well as the distribution of genetic variance between and within populations in provenance-progeny trials of Mediterranean cypress were studied.

## MATERIALS AND METHODS

### Materials

Material of the study consisted of 204 Mediterranean cypress families from 14 provenances (populations). Trees belonging to these provenances were grown from seeds collected from the provenances in the natural distribution

area of the Mediterranean cypress in 1999 (Table 1). To keep the kinship relations between the saplings at a minimum level, the distance among the selected trees was attentively 100 meters or less. Seeds collected from each family were planted separately in Enso-type trays in Denizli Forest Nursery Directorate in 2000 (Sabuncu 2004).

Trials were established with 1+0 seedlings produced in the 2000-2001 planting season in Antalya and Fethiye regions (Çalikoğlu et al. 2010) (Table 2). The trials were situated in the same Mediterranean bioclimate layer, and the climatic conditions were similar to each other. Trials were established with 17 provenances. In the preliminary evaluations, statistically significant difference was not observed between the two provenances selected from Fethiye region and the three origins selected from Kemer region for both height and diameter. Therefore, Fethiye and Kemer were accepted as provenances for further analysis. Completely randomized block design with 4-row plot configuration was used in all trials with 5 blocks.

### Methods

At the end of the 2018 growing season (18<sup>th</sup> year of the trials), the height (cm) and diameter at breast height (mm) of the trees in both trials were measured and the survival rate was observed. The provenances were compared by multiple analyses of variance (MANOVA). Families' genetic parameters were estimated based on the mixed model. BLUP (Best Linear Unbiased Prediction) method was used to estimate the breeding values of families. Analysis of variance in the survival rate was determined for the averages of families in a block. Provenances were grouped by Duncan's multiple range test (Duncan 1955) based on the results of analyses of variance.

**Table 1.** Details of the provenances and families.

Provenance	Code	Number of families	Latitude (N)	Longitude (E)	Altitude (m)
Marmaris	11	9	36° 45' 55"	28° 11' 05"	400
Dilek Peninsula	12	4	37° 39' 55"	27° 10' 06"	150
Datça	13	4	37° 02' 55"	27° 39' 05"	50
Fethiye	14	9	36° 30' 55"	29° 07' 05"	200
Köprülü Canyon	21	68	36° 34' 55"	29° 20' 05"	70
			37° 11' 55"	31° 08' 05"	700
Kemer	22	34	36° 36' 07"	30° 29' 05"	200
			36° 29' 55"	30° 25' 05"	900
Kumluca	23	4	36° 34' 55"	30° 32' 05"	50
			36° 26' 55"	30° 25' 05"	350
Kaş	24	3	36° 16' 55"	29° 22' 05"	60
Antalya	25	11	36° 44' 55"	30° 26' 05"	750
Bozyazı	31	3	36° 04' 55"	32° 55' 05"	20
Göksu	32	19	36° 23' 55"	33° 48' 05"	150
Gülnar	33	13	36° 12' 55"	33° 26' 05"	50
Aydıncık	34	4	36° 08' 55"	33° 20' 05"	30
Greece Samos	35	19	37° 45' 55"	26° 59' 15"	430

**Table 2.** Details of the trials.

Properties	Antalya	Fethiye
Annual precipitation (mm)	1089	933
Annual average temperature (°C)	18.4	18.1
Emberger drought index	0.3	0.2
Bioclimate layer	Temperate humid	Temperate humid
Bedrock soil	Travertine-sandy mud-medium deep	Alluvial-sandy clay-deep
Slope (%)	2	3
Altitude (m)	265	215

The following model was used in the analysis of each trial:

$$Y_{ijkl} = \mu + B_i + P_j + F_{k(j)} + BP_{ij} + BF_{ik(j)} + e_{ijkl} \quad (1)$$

where  $Y_{ijkl}$ : observation from  $l^{\text{th}}$  tree of the  $k^{\text{th}}$  family in the  $j^{\text{th}}$  provenance in the  $i^{\text{th}}$  block,  $\mu$ : overall mean,  $B_i$ : block effect,  $P_j$ : provenance effect,  $F_{k(j)}$ : family within provenance effect,  $BP_{ij}$ : block-provenance effect,  $BF_{ik(j)}$ : block-family effect,  $e_{ijkl}$ : random error.

$$Y_{ijkmn} = \mu + S_i + B_{j(i)} + P_k + F_{m(k)} + SP_{ik} + SF_{im(k)} + BP_{j(i)k} + BF_{jk(m)} + e_{ijkmn} \quad (2)$$

where  $Y_{ijkmn}$ : observation from  $n^{\text{th}}$  tree of the  $m^{\text{th}}$  family of the  $k^{\text{th}}$  provenance in the  $j^{\text{th}}$  block in the  $i^{\text{th}}$  provenance,  $S_i$ : trial effect,  $B_{j(i)}$ : block within trial effect,  $P_k$ : provenance effect,  $F_{m(k)}$ : family within provenance effect,  $SP_{ik}$ : trial-provenance effect,  $SF_{im(k)}$ : trial-family effect,  $BP_{j(i)k}$ : block-provenance effect,  $BF_{jk(m)}$ : block-family effect. The analyses were carried out in 196 families that had common traits in both trials.

If there are significant differences between provenances in provenance-progeny trials, this is also reflected in heritability. The population or provenance effect should be freed from genetic variance (Williams et al. 2002). For this reason, while calculating the variance components and genetic parameters at joint analysis, the provenance effect was eliminated by taking the family variance.

Narrow-sense heritability ( $h^2_1$ ) was estimated as (3) (Becker 1984, Cotterill 1987):

$$h^2_1 = \frac{\sigma^2_A}{\sigma^2_p} = \frac{k\sigma^2_f}{\sigma^2_p} \quad (3)$$

where  $\sigma^2_A$  is the additive genetic variance,  $\sigma^2_f$  is the genetic variance of families,  $\sigma^2_p$  is the phenotypic variance,  $k$  is the covariance coefficient between half-sibs.

Family mean heritability ( $h^2_f$ ) was estimated as (4) (Liu et al. 2013):

$$h^2_f = \sigma^2_f / (\sigma^2_f + \sigma^2_{sf} / s + \sigma^2_{fb} / sb + \sigma^2_e / sbn) \quad (4)$$

where  $\sigma^2_f$  is the family variance,  $\sigma^2_{fb}$  is the family-block variance,  $\sigma^2_{sf}$  is the trial-family variance,  $\sigma^2_e$  is the error variance,  $s$  is the trial number,  $b$  is the block number, and  $n$  is the harmonic mean of the number of trees per family.

Genetic correlation ( $r_g$ ) between tree height and diameter at breast height were estimated as (5) (Falconer 1996):

$$r_g = \frac{COV_{f(x,y)}}{\sqrt{\sigma^2_{f(x)}} \sqrt{\sigma^2_{f(y)}}} \quad (5)$$

where  $COV_{f(x,y)}$  is the genetic covariance between traits  $x$  and  $y$ , and  $\sigma^2_{f(x)}$  and  $\sigma^2_{f(y)}$  are the additive genetic variances of traits  $x$  and  $y$ , respectively.

The Delta Method was used to calculate the standard errors of the heritabilities and genetic correlation (Lynch and Walsh 1997). Type B genetic correlations between trials were determined by the following equation (Burdon 1977):

$$r_{Bg} = \frac{\sigma^2_f}{\sigma^2_f + \sigma^2_{sf}} \quad (6)$$

Coefficient of variation of genetic ( $CV_g$ ) was estimated based on genetic  $\sigma^2_g$  variance, and mean ( $\bar{x}$ ) of the traits according to the following equation (Sun 1980):

$$CV_g = \left[ \frac{\sqrt{4\sigma^2_f}}{\bar{x}} \right] \times 100 \quad (7)$$

Genetic gain ( $\Delta G$  (%)) was estimated as:

$$\Delta G = \frac{(\overline{ID}_s - ID_k)}{(MID_k)} \times 100 \quad (8)$$

where  $\overline{ID}_s$  is the average of breeding value of the highest 30 families,  $ID_k$  is the breeding value of the control material, and  $MID_k$  is the absolute breeding value of the control material.

## RESULTS

Some descriptive statistics of the measured traits are given in Table 3. Survivals in the Antalya and Fethiye trials were 84% and 91%, respectively. Averages of height were 748.04 cm in Antalya and 627.82 cm in Fethiye. Means of diameter were 103.54 mm in Antalya and 93.58 mm in Fethiye (Table 3).

**Table 3.** Descriptive statistics of the measured traits.

Trial	Survival rate (%)	Height (cm)			Diameter at breast height (mm)		
		$\bar{x}$	S	VK	$\bar{x}$	S	VK
Antalya	84	747.95	162.46	21.72	105.53	31.07	29.44
Fethiye	91	627.30	141.20	22.50	93.57	28.69	30.66

$\bar{x}$ : mean, S: standard deviation, VK: coefficient of variation

### Antalya Trial

The differences between provenances were not significant ( $P>0.05$ ) for both traits (Table 4).

Significant differences ( $P<0.05$ ) were found between provenances for survival rate (Table 5) and the provenances were grouped (Table 6).

**Table 4.** Results of analysis of variance for Antalya.

Source of variation	Traits	Degrees of freedom	Pr>F
Block	Height	4	0.0001
	Diameter		<.0001
Provenance	Height	13	0.0994
	Diameter		0.3913
Fam. Prov.	Height	189	<.0001
	Diameter		<.0001
Block x Prov.	Height	52	0.6073
	Diameter		0.5763
Block x Fam. (Prov.)	Height	706	<.0001
	Diameter		<.0001
Error	Height	2459	
	Diameter		

**Table 5.** Results of analysis of variance for survival rate between provenances.

Source of variation	Degrees of freedom	Pr>F
Prov.	13	<.0001
Block	4	0.5119
Error	52	

The family effect on survival rate was significant ( $P=.0011$ ) (Table 7). The lower limit of the best family group had a 65% survival rate. Families under this limit were 1324, 3401, 1102, 2148, 3312, 1405 and 3101.

### Fethiye Trial

The differences between provenances were significant ( $P<0.05$ ) for both traits (Table 8) and the provenances were grouped (Table 9).

**Table 6.** Homogeneous groups in terms of survival rate between provenances.

Prov.	Mean	
Kemer	89.60	a*
Samos	88.60	a
Kaş	88.02	a
Köprülü Canyon	87.00	a
Gülnar	86.80	a
Dilek Peninsula	86.60	a
Göksu	86.20	a
Kumluca	85.20	a
Antalya	85.00	a
Fethiye	81.60	a b
Marmaris	84.40	a b
Aydıncık	75.80	a b
Datça	71.60	b
Bozyazı	57.60	c

\*: The same letters indicate similar groups.

**Table 7.** Results of analysis of variance for survival rate between families.

Source of variation	Degrees of freedom	Pr>F
Family	202	0.0011
Block	4	0.5119
Error	765	

**Table 8.** Results of analysis of variance for Fethiye.

Source of variation	Trait	Degrees of freedom	Pr>F
Block	Height	4	<.0001
	Diameter		
Provenance	Height	13	<.0001
	Diameter		
Fam. Prov.	Height	190	<.0001
	Diameter		
Block x Prov.	Height	52	0.4054
	Diameter		0.2091
Block x Fam. (Prov.)	Height	743	<.0001
	Diameter		
Error	Height	2796	
	Diameter		

**Table 9.** Homogeneous groups in terms of height and diameter between provenances.

Prov.	Mean (height)		Prov.	Mean (diameter)	
Dilek Peninsula	670.47	a	Kumluca	105.65	a
Kemer	662.03	a b	Kemer	102.33	a b
Gülnar	656.81	a b	Greece Samos	97.87	a b c
Greece Samos	653.86	a b	Dilek Peninsula	97.25	b c d
Kumluca	642.58	a b c	Aydıncık	95.55	b c d
Göksu	637.30	a b c d	Gülnar	94.70	b c d
Aydıncık	634.12	a b c d	Kaş	94.34	b c d
Antalya	625.64	b c d	Göksu	93.01	c d
Kaş	609.64	c d e	Marmaris	91.27	c d
Köprülü Canyon	606.02	c d e	Köprülü Canyon	90.24	c d e
Datça	605.63	c d e	Antalya	88.96	d e
Marmaris	597.01	d e	Fethiye	83.09	e
Fethiye	572.61	e	Datça	82.95	e
Bozyazı	452.95	f	Bozyazı	68.00	f

Significant differences ( $P < 0.05$ ) were found between provenances for survival rate (Table 10) and the provenances were grouped (Table 11).

**Table 10.** Results of analysis of variance for survival rate between provenances.

Source of variation	Degrees of freedom	Pr>F
Family	13	<.0001
Block	4	0.0097
Error	52	

**Table 11.** Homogeneous groups in terms of survival rate between provenances.

Prov.	Mean	
Göksu	96.60	a
Köprülü Canyon	95.80	a
Antalya	95.60	a
Greece Samos	95.20	a
Kemer	94.00	a
Gülnar	92.80	a
Dilek Peninsula	92.60	a
Kaş	91.80	a
Marmaris	90.00	a
Datça	89.00	a
Fethiye	87.20	a
Kumluca	87.00	a
Aydıncık	85.20	a
Bozyazı	55.20	b

Family effect on the survival rate in the Fethiye trial area was also significant (Table 12). The lower limit of the best family group in this trial area had an 80% survival rate. Families under this limit were 3301, 2402, 3102, 1203, 1324, 2303, 1408, 1102, 3101 and 3111.

**Table 12.** Results of analysis of variance for survival rate between families.

Source of variation	Degrees of freedom	Pr>F
Family	203	<.0001
Block	4	<.0001
Error	797	

### Joint Analysis

In joint analysis of variance for trials, while provenance effect for height was significant, provenance effect for diameter was not significant (Table 13). Provenances were grouped according to height (Table 14).

The variance components of the joint analysis of the trials for both traits are given in Table 15. The ratio of the variance component for provenances was estimated as 0.92% for diameter and 2.38% for height.

### Genetic Parameters

Some genetic and phenotypic parameters of traits were calculated in joint analysis (Table 16). Narrow-sense ( $h^2$ ) and family mean heritability ( $h^2_f$ ) for height were bigger than for the diameter. Coefficient of genetic variation ( $CV_g$ ) was estimated as 13.98 for diameter and 12.71 for height. The correlation between trials (Corr bG) was estimated as 0.83 for height and 0.68 for diameter. High genetic and phenotypic correlations were observed between height and diameter.

In the joint analysis, it was estimated that a 12.5% genetic gain in height and a 13.2% genetic gain in diameter could be achieved by selecting the best 50 families from 196 families. With the selection of the best 30 families, these

rates increased to 15.2% and 16.3%, respectively. 37 of the best 50 families in terms of diameter were also included in the best 50 families in terms of height. The participation rate of provenances in the top 50 families for height ranged from 2% (Datça and Kaş) to 28% (Kemer).

**Table 13.** Joint analysis of variance for trials.

Source of variation	Trait	Degrees of freedom	Pr>F
Site	Height	1	<.0001
	Diameter		0.0082
Block (Site)	Height	8	<.0001
	Diameter		
Prov.	Height	13	0.0068
	Diameter		0.0928
Fam. (Prov.)	Height	182	<.0001
	Diameter		
Site x Prov.	Height	13	0.0074
	Diameter		0.0002
Block x Prov. (Site)	Height	104	0.6591
	Diameter		0.5315
Block x Fam. (Site x Prov.)	Height	1598	<.0001
	Diameter		
Error	Height	5084	
	Diameter		

**Table 14.** Homogeneous groups in terms of height between provenances.

Prov.	Mean (height)			
Dilek Peninsula	733.84	a		
Gülnar	721.71	a	b	
Kemer	712.03	a	b	c
Greece Samos	696.12	b	c	d
Göksu	695.85	b	c	d
Kumluca	686.01	c	d	e
Aydıncık	684.85	c	d	e
Antalya	677.71	d	e	
Kaş	672.98	d	e	
Datça	669.11	d	e	
Köprülü Canyon	668.12	d	e	
Fethiye	662.92		e	
Marmaris	623.84			f
Bozyazı	550.58			g

**Table 15.** Variance components for height and diameter in joint analysis, ratios of components to total variance.

Variance component	Estimate	
	Height	Diameter
Site	6932.30	59.16
%	22.93	6.19
Block (Site)	893.53	31.34
%	2.96	3.28
Prov.	718.13	8.75
%	2.38	0.92
Fam. (Prov.)	1792.30	53.22
%	5.93	5.56
Site x Prov.	162.41	10.36
%	0.54	1.08
Block x Prov. (Site)	0.00	0.49
%	0.00	0.05
Block x Fam. (Site x Prov.)	3382.90	81.85
%	11.19	8.56
Error	16347.00	711.12
%	54.08	74.36

**Table 16.** Some genetic and phenotypic parameters in joint analysis.

	Height	Diameter
$\bar{x}$	684.82	99.41
$h_n^2$	0.36 ± 0.08	0.24 ± 0.07
$h_f^2$	0.78 ± 0.08	0.53 ± 0.06
$CV_G$	12.71	13.98
$Corr_{bG}$	0.83 ± 0.007	0.68 ± 0.008
$Corr_G$	0.84 ± 0.08	
$Corr_p$	0.79	

$n$ : number of trees analyzed,  $h_n^2$ : narrow-sense heritability,  $h_f^2$ : family mean heritability,  $CV_G$ : coefficient of genetic variation,  $Corr_{bG}$ : correlation between trials,  $Corr_G$ : genetic correlation,  $Corr_p$ : phenotypic correlations

## DISCUSSION

According to the 18<sup>th</sup> year assessment on field evaluations of Mediterranean cypress provenance-progeny trials, Antalya has shown better performance for both height and diameter growth. In the 8<sup>th</sup> year assessment of the trials, it was determined that the Fethiye trial showed better growth and higher survival rate. It was stated that this situation may have arisen from the deep field soil in the trial (Çalkoğlu et al. 2010). However, in the 18<sup>th</sup> year assessment, Antalya trial showed 16% improvement in height. Lower growth in the Fethiye trial was attributed to a solid gravel layer located approximately 70 cm below the surface.

It was observed that the variation between families within the provenances was higher than the variation between the provenances for height and diameter in Mediterranean cypress (Table 15). This result illustrates that selections within the provenances will be more important than the selection of provenance in a breeding program to be applied for growth of Mediterranean cypress.

On the other hand, in Mediterranean cypress, in-provenance selections may result in higher genetic gain as well as in a breeding population with higher genetic variation. For instance, if only 30 families with the best breeding value were selected in Köprülü Canyon (21), the genetic gain for height growth would be 7%. However, regardless of provenance, the genetic gain in height with the selection of the top 30 families in the trials was estimated as 15.2%. Moreover, these 30 families belong to 9 different provenances.

A comparison can be made for narrow-sense heritability of 18-year-old trees' height and diameter traits in Mediterranean cypress with estimations from a recent Turkish red pine progeny trial.

In the 16<sup>th</sup> year assessment of low elevation breeding zone (0-400 m) of the Aegean Region Turkish red pine progeny trials, narrow-sense heritability of height and diameter was estimated as 0.27 and 0.28, respectively (Özyalçın et al. 2016). These values were found to be 0.36 and 0.24 in Mediterranean cypress, respectively. Family mean heritability of height and diameter in Turkish red pine was estimated as 0.49 and 0.59, respectively. In Mediterranean cypress these values were estimated as 0.78 and 0.53, respectively. In Turkish red pine,  $CV_g$  varied between 8% and 13% in height and 10% and 18% in diameter, depending on the trial areas. In the Mediterranean cypress, it was estimated as 12.71% for height and 13.98% for diameter.

According to the 18<sup>th</sup> year assessment of the Mediterranean cypress trials, the genetic gains to be obtained by selecting 50 or 30 families with the best breeding value in terms of height and diameter were also estimated. A population of 50 families that will form the production population (seed plantation) will form a wide-ranging basis for future thinning. A production population (seed plantation) of 50 families will provide a wide-ranging basis for future thinning. A population of 30 families will yield a higher genetic gain. As a matter of fact, this number is accepted as a number that will not significantly reduce genetic variation (Namkoong et al. 1988, Varela and Eriksson 1995).

The genetic gains to be achieved at the age of 18 in terms of height in Mediterranean cypress were estimated as follows: 12.5% in the selection of 50 families, 15.2% in the selection of 30 families with the best breeding value in terms of height. In terms of diameter, these values were: 13.2% in the selection of the best 50 families and 16.3% in the selection of the best 30 families.

High genetic correlation ( $r=0.84$ ) was estimated between height and diameter in Mediterranean cypress. This means that the selection to be made for any trait in Mediterranean cypress will not significantly change the genetic gain (Zobel and Talbert 1984).

Diameter is a parameter that affects volume more than height, and its measurement is easier and more practical. If the genetic relationship between the two traits persists at this level in the mature age, it would be more beneficial to make the selection according to the diameter.

Type B genetic correlation ( $r=0.83$ ) between trials in terms of height was high. In terms of diameter, this value was estimated at the accepted limit value (0.68) for sub-zoning. In the 8<sup>th</sup> year assessment, it was calculated for diameter as 0.85 and for height as 0.81 (Çalkoğlu et al. 2010).

The survival rate was significantly affected by family in both trials. During the selection of breeding plantations, it would be useful to pay attention to families that are not in the best group in terms of survival rate.

## CONCLUSIONS

The current family set of Mediterranean cypress selected within the scope of this study should be considered as the main breeding population of this species. The basic genetic parameters of the species have been revealed in this study. However, the increasing demand for Mediterranean cypress saplings (border tree, mixture type in Turkish red pine plantations) reveals the necessity of establishing a seed garden or a seed plantation. By deciding on a selection intensity that they deem appropriate, tree breeders will be able to benefit from the superior families determined by this study. During the establishment phase, it is recommended to begin with 40-50 families that have the best breeding value in terms of diameter. In the following years, it is advised to reduce the number of families to 20-30, as revealed in this study.

### Author Contributions

RS and ZGA established the trials, AAÖ and ZGA collect the data, AAÖ and MÇ performed statistical analyses. AAÖ and MÇ drafted the manuscript, RS and ZGA improved the manuscript draft. All authors discussed the results and contributed to the final manuscript.

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### Conflicts of Interest

The authors declare no conflict of interest.

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