



Morphological variations among families of Manna Ash (*FRAXINUS ORNUS* L.)

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Abstract

Variations, narrow-sense heritability, and correlations for height and diameter at base were examined in a 15- years progeny trial established by 30 open pollinated families of Manna ash (*Fraxinus ornus* L. *subsp. cilicica*) to contribute genetics-breeding practices of the species. Averages of tree height and diameter at base of the family were 318.5 cm and 62.5 mm in the families, while there were large differences among trees within family for the characteristics. Averages of families ranged from 285.6 cm to 359.2 cm for tree height, and between 55.3 mm and 70.5 mm for diameter at base. They changed between 180 cm and 462 cm for tree height, and between 36.6 mm and 95.9 mm for diameter at individual trees of total families. The families showed significant ($p \leq 0.05$) difference for the tree height opposite to diameter at base according to results of analysis of variance. Variation among trees within family was higher than among families for the characters. The heritability was 0.21 for tree height and 0.06 for diameter at base. Thus, non-genetic factors seem often more important for the variation in performance of trees than their genetic structure, and forestry practices on Manna ash. Positive and significant ($p \leq 0.05$) phenotypic and genetic relations between tree height and diameter at base were found based on correlation analysis. Results of the study were discussed based on genetic-breeding and other forestry and cultivation practices of the species.

Keywords: *correlation, diameter, growth, height, heritability, variation*

Funding: this research received no external funding.

Acknowledgments: authors thanks the reviewers for their contribution to the peer review.

Conflict of interest: the authors declares no conflict of interest.

For citation: Bilir N. (2025) Morphological variations among families of manna ash (*FRAXINUS ORNUS* L.). Forest Engineering journal, Vol. 15, No. 2 (58), pp. 6-14. DOI: <https://doi.org/10.34220/issn.2222-7962/2025.2/1>.

Received 03.03.2025. **Revised** 13.04.2025. **Accepted** 05.06.2025. **Published online** 26.06.2025.

Introduction

According to the latest forestry inventory [1], Ash taxa (*Fraxinus* sp.) has about 12074 ha at 23.4 million ha of total Turkish forest area by three species (*Fraxinus excelsior*, *F. ornus* and *F. angustifolia*) [2]. However, most of them is unproductive distribution. Until recently, Common ash (*Fraxinus excelsior* L.) and Narrow-leaved ash (*Fraxinus angustifolia* Vahl.) have

been planted mainly with production objectives. Both species (but particularly common ash) have been widely planted for timber, and there has been some work on genetic improvement for common ash, based on selection for traits considered superior in a timber tree [3]. The Manna ash (*Fraxinus ornus* L.) has the most limited distribution of three Turkish and European ashes. Manna ash occurs mainly in southern Europe and its main dis-

tribution range is in Italy (mostly in the south and Mediterranean Islands), Greece, and in east regions of the Balkan Peninsula and Turkey as local population, groups or a maque element as to be a dominant or co-dominant species in most of its habitats by two subspecies (*Fraxinus ornus* subsp. *cilicica* and *F.o.* subsp. *ornus*) [3]. Silvicultural management showed *Fraxinus ornus* forest takes three different forms: high forests (of seed origin), coppices and mixed shrubs. The trees are frequently multistemmed or shrubby owing to coppicing, grazing or re-sprouting after wildfires [3]. While Common ash (*Fraxinus excelsior*) and Narrow leaved ash (*F. angustifolia*) occupy in humid area, Manna ash occupy in arid zones of Mediterranean region in Turkey [4]. Manna ash grows from sea level up to 1500 m altitude at optimum rainfall is from 500 to 650 mm, and low temperatures limit the distribution of Manna ash in central Europe [3]. It is a small deciduous tree, usually not more than 15 m tall [3]. However, wood of manna ash is an important material for such as furniture, ornamental, charcoal and equipments of music industries. Besides, oil is extracted from its bark used in medicinal purposes [2]. In addition to the species is very resistance to aridity, forest fire [5], and climate change [6]. Manna ash could be also an adaptive species to climate change. Its forests on carbonate soils possess rich species diversity. At present the main silvicultural significance of *F. ornus* in southern and central Europe is in the reforestation or afforestation of eroded and degraded soils in karst regions and other degraded ecosystems around the Mediterranean Basin. On such sites it covers the soil very quickly, and ameliorates poor soils with its annual litter-fall. It also provides good microclimatic conditions for the growth and regeneration of other tree species. It grows rapidly when young (in contrast to the oaks which grow with it), but only to a height of 8-15 m. *Fraxinus ornus* is the source of manna, an oxidised dried exudate from the bark of young trees which was formerly used as a laxative [3]. These advantages of the species are getting importance for increasing of limited distribution by plantation forestry, and also genetic-breeding studies. Estimation of morphological variation and gentic parameters are most important tools in genetic-breeding strategies and other forestry practices. It is clear that quality and quantity of forest product such as wood could be increased by intensive silviculture and

genetic-improvement studies (i.e., progeny test, estimations of genetic parameters) togetherwith solution of environmental problems such as global warming by resistance breeding. However, limited genetic studies were carried out on Manna ash [e.g., 3, 7-11].

The present study aims to evaluate the variations in tree height and diameter at base within and among families and individual trees, to estimate their relations, and heritability in 15-years progeny test of the species to discuss on silvicultural and genetic-breeding managements, and other forestry and cultivation practices of *F. ornus*.

Material and Methods

Data Collection

Tree height and diameter at base were important characters in forestry practices because of easy measurement, and biomass estimation. Data of tree height (**H**) and diameter at base (**D₀**) was collected from a 15- years progeny trial established (latitude 37°45' N, longitude 30°35' E, altitude 1050 m) by 30 open pollinated families as three replicates 2x2 m spacing at southern of Türkiye in 2009 (Fig. 1).



Figure 1. A view from the progeny trial

Source: author's composition

Three healthy individuals were sampled from each replicate and family. However, 24 of the families had enough survival for this study. No any practice was applied to the progeny trial such as pruning, fertilization, and removing of trees etc.

Data Analysis

The families was compred for the tree height and diameter at base by following model of Analysis of Variance (ANOVA) at SAS package [12]:

$$Y_{ijk} = \mu + F_i + B(F)_{j(i)} + e_{ijk} \quad (1)$$

Where Y_{ijk} is the observation from the k^{th} tree of the j^{th} family in the i^{th} replicate, μ is overall mean, $B(F)_{j(i)}$ is effect of the j^{th} family in the i^{th} replicate, and e_{ijk} is random error.

Individual (h_i^2 ; narrow-sense heritability) heritability (h_i^2) used for different purposes in plant science was estimated as [13]:

$$h_i^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{k\sigma_F^2}{\sigma_P^2} \quad (2)$$

σ_A^2 is the additive genetic variance, σ_F^2 is the genetic variance of families or phenotypic variance, k is the covariance coefficient between half-sibs.

Variability of both the phenotype and genotype could be measured, although the genotype was more important from the point of view of breeding, conservation and utilization [3]. Variance components, expressed as coefficient of genetic (CV_g) and phenotypic (CV_p) variations were estimated as:

$$CV_g = 100\sigma_A / \bar{x}$$

$$\text{and } CV_p = 100\sigma_F / \bar{x} \quad (3\&4)$$

Where \bar{x} is overall character mean.

Phenotypic (r_p) and genetic (r_g) correlations between tree height and diameter at breast height were estimated as [14]:

$$r_p = \frac{COV_{f(x,y)}}{\sqrt{\sigma_{f(x)}^2} \sqrt{\sigma_{f(y)}^2}}$$

$$\text{and } r_g = \frac{COV_{g(x,y)}}{\sqrt{\sigma_{g(x)}^2} \sqrt{\sigma_{g(y)}^2}} \quad (5\&6)$$

Where $COV_{f(x,y)}$ is the phenotypic covariance between characters x and y , $\sigma_{f(x)}^2$ and $\sigma_{f(y)}^2$ are the phenotypic variances for characters x and y , respectively. Where $COV_{g(x,y)}$ is the genetic covariance between characters x and y , $\sigma_{g(x)}^2$ and $\sigma_{g(y)}^2$ are the additive genetic variances of characters x and y , respectively.

Results and Discussion

Characters and variations

Means of tree height and diameter at base of the family were 318.5 cm and 62.5 mm in the families, while there were large differences among trees within family for the characteristics. Averages of families ranged from 285.6 cm to 359.2 cm for tree height, and between 55.3 mm and 70.5 mm for diameter at base (Table 1, Fig. 2). The growth increment were lower than young ages of the families [9-11]. There were about 2.6 times difference in both tree height (180 cm and 462 cm) and diameter at base (36.62 mm and 95.87 mm) among individual trees of total families (Table 1). Similar variations were also reported for reproductive traits in the species [15]. Averages of seedling height and diameter at base were 149.5 cm and 24.3 mm in fifth year results of the families [10], and 161.7 cm and 2.3 cm in sixth year results of the progeny [11]. The results indicated that the families showed higher growth performance based on annual growth increments during the last decade. However, there could be many biotic and abiotic factors such as maternal or paternal effect [3], climate, biological characteristics of plants could impact on growth performance of tree species. For instance, 26% higher growth performance could be obtained for the characters by better selection.

Averages and ranges of for the tree height and diameter at base

	Tree height (cm)	Diameter at base (mm)
Average	318.5	62.5
Ranges of families	285.6-359.2	55.3-70.5
Individual ranges	180.0-462.0	36.62-95.87

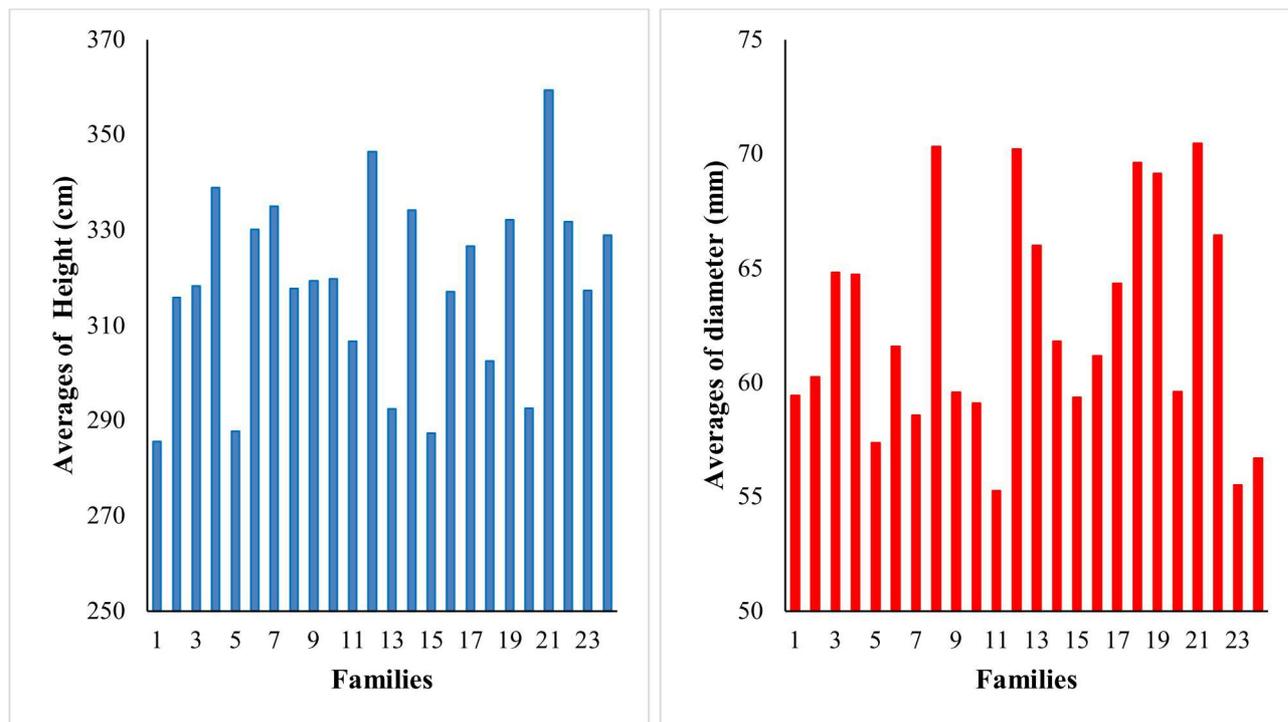


Figure 2. Averages of the characters for the families

Source: author's composition

The individual trees showed also large differences within family. For instance, tree height ranged from 225.0 cm to 336.0 cm, and also diameter at base varied between 43.8 mm and 70.8 mm in first family. They were between 250 cm and 372 cm for tree height, and between 36.7 mm and 70.2 mm for diameter at base in the last family (Table 2). They were getting larger for the characters in pooled families (Tables 1 and 2). Tree height was more variable than tree height in all families based on standard deviation (Table 2). But, standard deviation was the highest in family 15 (77.1) for tree

height, while it was the highest in family 23 (17.0) for diameter at base (Table 2). It was the lowest in family 10 (24.0) for tree height, and in family 16 (5.6) for diameter at base (Table 2). These results showed importance of control pollination and vegetative propagation for higher wood product in plantation forestry of the species. Besides, tree height had higher variation than that of diameter according to calculated standard deviations (45.9 and 12.3) of among families. It indicated that tree height was better selection character for genetic-breeding and other forestry and cultivation purposes.

Table 2

Average, range and standard deviations (SD) for the characters in the families.

Characters						
	H (m)			D ₀ (cm)		
Family	Average	Range	SD	Average	Range	SD
1	285.6	225.0-336.0	34.0	59.4	43.8-70.8	9.5
2	315.9	220.0-370.0	50.7	60.2	41.8-91.5	18.6
3	318.3	280.0-400.0	35.6	64.8	47.5-74.3	8.5
4	338.9	296.0-415.0	33.9	64.7	53.5-77.8	10.2
5	287.7	205.0-380.0	65.3	57.3	44.3-81.8	12.8
6	330.2	300.0-380.0	26.0	61.6	43.6-87.8	12.7
7	334.9	265.0-400.0	45.9	58.5	44.3-81.5	11.6
8	317.8	260.0-366.0	34.0	70.3	60.3-95.9	10.9
9	319.3	220.0-410.0	52.9	59.6	36.6-83.8	15.4
10	319.8	276.0-350.0	24.0	59.1	46.2-69.3	7.7
11	306.8	255.0-366.0	42.3	55.3	42.8-74.8	11.9
12	346.3	264.0-462.0	61.7	70.2	54.2-87.2	12.9
13	292.4	190.0-390.0	66.9	66.0	52.3-81.2	10.4
14	334.1	310.0-410.0	30.9	61.8	43.8-91.5	13.5
15	287.2	180.0-425.0	77.1	59.3	42.6-79.7	11.4
16	317.1	265.0-375.0	35.7	61.2	54.3-67.6	5.6
17	326.7	275.0-360.0	32.1	64.3	46.9-78.7	9.8
18	302.4	242.0-373.0	41.7	69.6	45.0-89.5	15.8
19	332.2	280.0-37.0	31.0	69.1	53.6-80.7	9.3
20	292.6	198.0-355.0	43.3	59.6	50.4-84.6	10.4
21	359.2	290.0-418.0	38.5	70.5	48.6-83.7	13.5
22	331.8	265.0-387.0	38.3	66.5	53.4-77.9	9.1
23	317.3	280.0-362.0	26.3	55.5	40.4-95.5	17.0
24	328.9	250.0-372.0	38.7	56.7	36.7-70.2	9.5

Higher growth variations were reported for the years based on results of early studies on families of the species for different characters [i.e., 8-11,16], and also seed characters in field stage of Manna ash [16,17]. Higher morphological variations among populations and within population for different characters were also reported at nursery stage in Manna ash [8,18], and in Narrow leaved ash [19]. It was reported that like other ash species, Manna ash showed higher variation in vegetative characters (leaves, shoots, bark etc.), and several subspecies and varieties, as well as cultivars, have been describe]. According to results of genetic variation studies had a different geographical focus, although populations were sampled across a much wider geographic area, including Hungary, Italy, Bosnia-Herzegovina, Bulgaria, Croatia,

Greece, Romania, Slovakia, Slovenia, Spain, and Türkiye [3]. The results emphasized importance of individual selection and characters for higher wood product in the species in genetic-breeding practices of Manna ash.

According to results of analysis of variance, the families showed significant ($p \leq 0.05$) difference for tree height, while families were similar ($p > 0.05$) for diameter at base. However, the variations changed for the years and characters according to results of early studies on the families of the species [i.e., 8-11]. The results indicated importance of future studies.

Familyxreplicate interactions, were not significant ($p > 0.05$) for both tree height and diameter at base, indicated homogeneity of trial area (Table 3). It showed importance of future studies in different areas including arid sides.

Results of analysis of variance.

Characters	Source of variation	Degrees of freedom	Mean of square	P value
Tree height	Family (F)	23	3448.227	$p < 0.05$
	Replicate (R)	2	142.699	$p > 0.05$
	FxR	46	1927.868	$p > 0.05$
	Error	144	1977.690	
	Total	215		
Diameter at base	Family (F)	23	216.524	$p > 0.05$
	Replicate (R)	2	180.921	$p > 0.05$
	FxR	46	135.921	$p > 0.05$
	Error	144	144.578	
	Total	215		

Heritability and correlations

Heritability is used for different purposes such as increasing of quality and quantity of products, or selection target in plant science. The heritability in narrow-sense reflects the share of the variation that depends on the genotypes was very low for the tree height and diameter at base (Table 4) opposite to some seed characters of the families [17]. The heritability did not change dramatically for the years based on results of early studies [i.e., 8-11] in the same objects of the species. They well accordance with results of the present study. For instance, narrow-sense heritability (h_i^2) reflected the share of the variation that depends on the genotypes was very low. It was 0.382 for seedling height, 0.051 for root-collar diameter in sixth year of the progeny [11], and close to zero in fourth and fifth years [9,10]. Low genetic variations were reported in populations of Manna ash [3] opposite to low heritability estimated in the present study. However, it could change for the future years according to rotation age of the species. Besides, it was known that there could be many biotic and abiotic factors could be effective on genetic parameters estimated in Manna ash and different forest tree species [i.e., 20-24]. Manna ash has been defined as an ornamental plant for urban planting sites due to its aesthetic characteristics. It was frequently grown as an ornamental tree in Europe north of

its native range for its decorative flowers-the species was also sometimes called "flowering ash" [25]. *Fraxinus ornus* was also a very valuable tree species in urban forestry, because it does not reach large dimensions, and in spring is very decorative because of its large white inflorescences [3]. It showed importance flowering of the species and estimation of heritability for flowering characters togetherwith woody products in future studies.

The genetic variation, here expressed as the coefficient of variation among families (CV_g), was always lower than the variation among individual seedlings within families (CV_p) (Table 4). The environment seemed to be more important for the performance of genotypes than their genetic constitution. This emphasized importance of forestry practices such as selection of individual seed source, tending and others.

Tree height was both genetic ($r=0.414$) and phenotypic ($r=0.423$) correlated significantly ($p \leq 0.05$) with diameter at base (Fig. 3). Similar correlations were found at nursery stage and different years of the trial [8-11], and phenotypic in outplanting performances of Narrow leaved ash [24], and Common ash [26,27]. The correlation results of this study indicated that the correlations were steadily for the years. These results could be used future studies in the species.

Heritability (h^2), coefficient of variation among (CV_g %) and within family (CV_p %)

	Tree height	Diameter at base
h^2	0.21	0.06
CV_g	4.03	2.96
CV_p	7.74	12.27

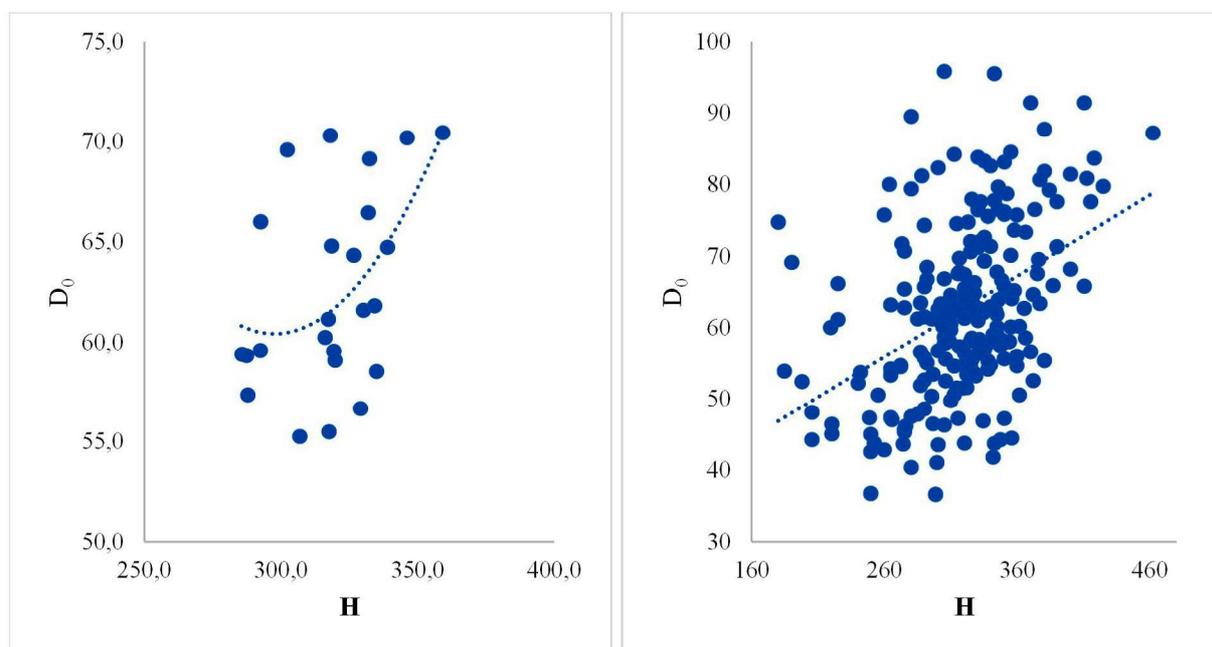


Figure 3. Correlations between tree height (H) and diameter at base (D_0) for family (left side) and individual tree levels (right side).

Source: author's composition

Diameter at base (D_0) could be formulated by tree height (H) as: $D_0 = 0.0027H^2 - 1.5782H + 295.33$ ($R^2 = 0.23$) or $D_0 = 0.113H + 26.54$ ($R^2 = 0.18$) based on the regression analysis (Fig. 3). However, they were not stable based on results of early studies [9-11]. The first equation seemed better estimator than that of second based on higher R^2 value. It could be early to give an accurate equation for future estimations.

Conclusions

Averages of tree height and diameter at base of the family were 318.5 cm and 62.5 mm in the families at 15-years progeny trial, while there were large differences among trees within family for the characteristics. The

narrow-sense heritability was very low for the tree height (0.21) and diameter at base (0.06). There were significant ($p \leq 0.05$) and positive relations between tree height and diameter at base. However, the present study was carried out by limited number of characters, families and area. Results of the study could not be well discussed because of limited number of genetic-breeding studies on the Manna ash. They emphasized importance of future studies. The families and individual trees within family showed variation practically for both tree height and diameter at base. However, the present study could be accepted as early results based on rotation age of the species. So, future studies in different trials, families, and characters including physiological, survival,

stem straight, flowering should be carried to give accurate conclusions by various genetic parameters. However, results of the study could be used in forestry practices of the species. It is clear that Manna ash could be considered as a key species in climate change due to its

biological characteristics. Future trials should be established at different habitats such as arid or semi-arid areas based on biological characteristics of the species and future directions.

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