

Heritability estimates and the variation of pomological traits, total phenolic compounds, and antioxidant capacity in two apricot progenies

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Abstract: Even though pomological traits are important in fruit breeding for quality, antioxidant capacity and the total content of phenolic compounds have also gained importance, together with a rising awareness of their health benefits. As a result, this study was conducted to evaluate the variation and heritability levels of antioxidant capacity and total phenolic compounds, as well as pomological traits in 'Hacıhaliloğlu' × 'Stark Early Orange' and 'Çataloğlu' × 'Stark Early Orange' apricot crosscombinations based on phenotypic assessments of fruit samples. The results indicated significant differences among F₁ progenies in the samples involved in the study. Broad-sense heritability coefficients ranged from 0.59 to 0.98 in the combinations examined. Parent-offspring regression coefficients for antioxidant capacity and total phenolic compounds were calculated to be 0.433 and 0.164, respectively. The results of the study can be useful in deciding selection strategies and choosing parents in relevant breeding programs.

Key words: Antioxidants, breeding, fruit quality, inheritance, *Prunus armeniaca* L.

1. Introduction

The commercial values of fruit crops are linked to their quality attributes, and pomological traits are a main commercial interest. In particular, fruit sizes and weights are related to yield, and consumers are concerned about fruit color and eating quality for fresh consumption. However, the firmness of the flesh and the maturity index (Total Soluble Solids/Titratable Acidity) are the main factors affecting the acceptability of the fruits by consumers (Krška et al., 2009; Suszek et al., 2017). For apricot fruits, color is another very important factor, and shiny, yellow, and orange genotypes with a high red blush ratio are desirable (Callahan, 1995; Moreau-Rio, 2006).

In the last century, health problems have increased because of a variety of reasons, and chronic diseases that directly threaten human life, especially cancer, have created global awareness about the necessity to promote a healthy life; as a result, the search for permanent solutions to health problems has become very important. Phytochemicals are plant compounds found naturally in plant foods, fruits, and vegetables (Alibabic et al., 2018; Fadda et al., 2018; Ozdemir et al., 2018) and are known to reduce the risk of chronic diseases due to their antioxidative effects (Liu, 2003). Therefore, the antioxidant capacity and phenolic

compound content that constitute the main part of the phytochemicals have recently been accepted as important quality parameters like fruit weight and attractiveness, and plant breeders consider this an important issue (Gökçen et al., 2017).

For these reasons, it is important to improve both pomological and phytochemical attributes. In this sense, plant breeding plays a key role in selecting genotypes with the desired characteristics and which are present in optimum levels from a population obtained by different plant genetic methods (Galiana-Belaguer et al., 2018; Guliyev et al., 2018). Crossing is the most widely used method to obtain a breeding population and, according to this method, a plant breeder uses crossings to combine the required genes for the desired traits by considering their genetic background (Öktem and Yücel, 2012).

In order to understand the genetic background of apricot fruit quality traits, various studies have been performed to date. Paunović (1987) investigated the inheritance of fruit weight, fruit shape, fruit flavor, flesh firmness, flesh color, and skin color in several apricot lines. Couranjou (1995) studied 11 characteristics of the apricot, including flowering date, maturity date, yield, fruit size, fruit skin background color, flesh color, skin

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over color, fruit firmness, flavor, aroma, and juiciness. Krška et al. (2009) studied fruit weight, over color, flesh color, fruit attractiveness, flesh firmness, and fruit flavor in the 'Minaret' × 'Betinka' apricot progeny. Audergon et al. (2010) investigated bloom and maturity dates, fruit and stone weight, fruit color, soluble solid content, acidity, and flesh firmness—as well as the polyphenolic profile—and the sugar and organic anion concentrations in 2 apricot progenies: 'Goldrich' × 'Moniqui' and 'Lito' × 'BO81604311'. However, there are no studies to be found on heritability estimates of apricot total phenolic compound content and antioxidant capacity.

Heritability estimates are useful for the breeding of quantitative characteristics to investigate whether a particular characteristic can be improved by breeding studies, what the most effective selection strategy is for a breeding program, and how to predict the genetic gain to be obtained through selection. Heritability estimates are population specific and mainly evaluated by using 2 methods. The first method is the calculation of individual sample variance for different populations. This calculation method has 2 different definitions: a broad and a narrow sense of inheritance. In the broad sense, the inheritance level (H) is the ratio of genotypic variation (V_G) to phenotypic variance (V_p), whereas the narrow sense of inheritance is calculated by the proportion of additive genetic variance (V_A) to phenotypic variance (V_p) (Acquaah, 2009). Narrow sense calculations were not included in this study because of the necessity for results to be obtained from the F_2 generation. However, the second heritability evaluation method was included in this study, which is based on a calculation using the results of different populations with parental relationships. The top-cross combination mating design, which is included in this study, can be given as an example. The advantages of a calculation based on this method are the opportunity to determine whether additive and nonadditive (dominance and epistatic effects) genetic effects are effective on the inheritance of a given trait and a comparison of General Combining Abilities (GCA) of parents mated with an individual tester (Morishita, 1994; Ohtsuka et al., 2004; Gopal et al., 2008).

This study was conducted to evaluate the heritability of total phenolic content and antioxidant capacity, together with different pomological characteristics of apricot fruits sampled from hybrids of 2 half-diallel apricot F_1 progenies. It also analyzes the variation among the progenies for each trait and compares the GCA of 2 female parents.

2. Materials and methods

This study was conducted on the Battalgazi Campus of the Apricot Research Institute in the Malatya province of Turkey, situated 730 m above sea level. The study

was carried out in 2016 and minimum and maximum temperature and rainfall records were -0.7°C , 11.2°C , 42.7 mm for February, 0.9°C , 14.8°C , 24.3 mm for March, 5.5°C , 23.3°C , 1.7 mm for April, 9.0°C , 25.1°C , 33.9 mm for May, 14.6°C , 31.6°C , 13.3 mm for June, and 18.0°C , 35.1°C , 16.6 mm for July, respectively (<https://www.mgm.gov.tr/eng/forecast-5days.aspx>). The soil was clay textured with a pH of 7.5 and a lime content of 40%. Pest management, weed control, and soil cultivation were done as required. Drip irrigation and fertigation were utilized, and no nutrient deficiencies and water stress were observed during the season.

2.1. Plant materials and experimental design

Two apricot F_1 progenies were obtained by crossing 'Hacıhaliloğlu' ('HH'), 'Çataloğlu' ('ÇO'), and 'Stark Early Orange' ('SEO') cultivars in the following combinations: 'Hacıhaliloğlu' × 'Stark Early Orange' ('HH × SEO') and 'Çataloğlu' × 'Stark Early Orange' ('ÇO × SEO'). In addition, 25 hybrid plants from each progeny planted over an area of 2.5×1.5 m constituted the plant material for this study. The trees were 9 years old during the experiment and 3 plants of parents were included. The progenies were obtained as part of the Multipurpose Apricot Breeding Program carried out by the İnönü University Apricot Research and Application Center. Fruit samples were collected at harvest maturity—described by GTHB (2014)—from each tree and analyzed for pomological fruit quality attributes, trolox equivalent antioxidant capacity (TEAC), and total phenolic compound (TPC) content.

2.2. Pomological evaluations, antioxidant capacity and total phenolic compound analyses

In terms of pomological parameters, fruit length (FL), fruit lateral width (FLW), fruit ventral width (FVW) fruit weight (FW), stone weight (SW), flesh/stone ratio (F/S), flesh firmness (FF), fruit skin color indices (L^* , a^* , b^*), total soluble solids (TSS) content, and titratable acidity (TA) were evaluated. FL, FLW, and FVW were measured as described in International Union for the Protection of New Varieties of Plants (UPOV) (2007) in millimeters using digital hand calipers. FW and SW were measured with precision scales to an accuracy of 0.01 g, and F/S was calculated according to these measurements. FF was measured with a hand penetrometer (Akyol GY-3) in kg/cm^2 . For fruit skin color indices, L^* represented lightness from black (0) to white (100), a^* indicated the degree of redness varying from negative values for green to positive values for red, and b^* indicated the degree of yellowness varying from negative values for blue to positive values for yellow using a Color Meter (Konica Minolta, CR-400, Tokyo, Japan) according to CIELAB objective color indices (McGuire, 1992). TSS contents were detected by a digital

hand refractometer (ATAGO Pal-1, Tokyo, Japan). TA was measured according to Haffner and Vestrheim (1997) and expressed as a percentage of malic acid. The TSS/TA ratio, which indicates the maturity index, was calculated by dividing the TSS value by the TA value.

Sensory analyses were performed for fruit shape (FS) and flesh color (FC). For this, fruit samples were numbered from 1 to 8 for FS and from 1 to 6 for FC according to UPOV. The numbers for FS from 1 to 8 indicated triangular, ovate, oblong, elliptical, circular, oblate, obovate, and oblique rhombic shapes, respectively. The numbers for FC from 1 to 6 indicated whitish green, white, cream, light orange, medium orange, and dark orange color, respectively.

TEAC was detected with a spectrophotometric method described by Rice-Evans et al. (1996) and modified by Özgen et al. (2006), expressed as $\mu\text{molTE/gFW}$. TPC was determined according to the Folin–Ciocalteu reagent method described by Slinkard and Singleton (1977) and expressed as $\mu\text{gGAE/gFW}$.

2.3. Heritability estimates

In order to estimate and express the inheritance properties through frequency of inheritance traits, the correlation dependencies between the mean values of parents and their F_1 progeny (r) and broad-sense heritability (H) coefficients were calculated for each progeny. Additionally, parent–offspring correlation (r_{PF1}) and parent–offspring regression (b_{PF1}) coefficients were calculated using the results of both progenies together in a top-cross test design.

The expression frequencies of inherited traits were examined by calculating the amount of resulting hybrids with values below, between, and above their parents. The frequency of inheritance for each trait was evaluated according to the percentage of resulting hybrids between their parents using the chart given by Krška et al. (2009). Accordingly, the frequency levels indicated by the percentages were as follows: very stable inherited trait (83%–100%), stable inherited trait (66%–82%), constantly inherited trait (50%–65%), averagely inherited trait (34%–49%), variable trait (17%–33%), very variable trait (5%–15%), and highly variable trait (0%–4%). The GCA levels of parents were evaluated according to the amount of resulting hybrids with values higher than their parents (Couranjou, 1995; Gopal et al., 2008).

H values for the evaluated traits of each progeny were calculated according to the equations described by Acquah (2009) and Krška et al. (2009) given below. Here, V_p represents the total phenotypic variance of a segregated population, V_G represents the total genetic variance, V_E represents the environmental variance, and V_{P1} and V_{P2} represent the variance of the parents:

$$H = V_G/V_p \quad V_p = V_G + V_E \quad V_E = (V_{P1} + V_{P2})/2$$

Heritability levels were considered to be low, medium, and high when the H coefficient obtained for each trait was below 0.2, between 0.2 and 0.5, and above 0.5, respectively. Dependency levels between the mean values of parents and their F_1 progeny were considered as weak, medium strong, and strong when the r value obtained for each trait in a given F_1 progeny was below 0.4, between 0.4 and 0.6, and above 0.6 (Krška et al., 2009).

Coefficients r_{PF1} and b_{PF1} of the characteristics investigated in the study were calculated according to the equations mentioned by Ohtsuka et al. (2004) given below. Here, r_{EF1} and b_{PF1} represent the correlation and regression coefficients, while VP , VF_1 , and Cov_{PF1} are the variance in midparent values, variance of the F_1 population, and the covariance in the midparent value and mean value of the F_1 population, respectively.

$$r_{PF1} = \frac{\text{Cov}_{PF1}}{\sqrt{VP \cdot VF_1}} \quad b_{EF1} = \frac{\text{Cov}_{PF1}}{VP}$$

Parent–offspring correlation coefficients were used to determine the dependency levels between the midparent value and progeny means. Parent–offspring regression coefficients were calculated to estimate heritability levels. Accordingly, the coefficients below 0.4 indicated low heritability, between 0.4 and 0.6 indicated average heritability, between 0.6 and 1 indicated high heritability, and above 1 indicated very high heritability levels (Ohtsuka et al., 2004).

3. Results and discussion

3.1. Variation among progenies

The results of parents included in the study and the differences between parents evaluated at a significance level of 0.05 are given in Table 1. The results of hybrids included in the study were compared with their parents and with each other according to ANOVA ($P \leq 0.05$); significant differences and high variations were obtained for each progeny. Cumulative variances varied between 9.69% (FVW) and 44.48% (FF) in ‘HH \times SEO’, and between 10.36% (FL) and 65.32% (TPC) in ‘ÇO \times SEO’. In both populations, seedlings with lower or higher values than their parents were seen for all traits.

Similar results obtained by Ruiz et al. (2011) who reported Gaussian trends for skin color, acidity, TSS, and normal distribution for FF in the progenies studied, confirming the quantitative inheritance and polygenic nature of the traits. The authors found a number of seedlings with lower or higher values in comparison to their parents for all of the characteristics investigated in their study. Similarly, Audergon et al. (2010) studied FW, FC, FF, TSS, and TA—as well as some specific phenolic

Table 1. Pomological traits, TEAC, and TPC results of parents.

Trait		HH	ÇO	SEO
FL	(mm)	40.74 b	38.93 b	46.64 a
FLW	(mm)	40.01 b	36.17 c	43.56 a
FVW	(mm)	36.29	34.63	36.32
FW	(g)	35.74 b	31.63 c	56.05 a
SW	(g)	2.40 b	2.20 c	3.92 a
F/S	-	13.93	13.42	13.37
FF	(kg/cm ²)	7.26 a	6.12 a	3.52 b
L*	-	62.89 a	58.14 a	39.00 b
a*	-	13.35 c	24.18 b	34.72 a
b*	-	43.51 a	39.96 a	9.40 b
TSS	(%)	25.08 a	22.43 b	19.24 c
TA	(%)	0.82 b	0.82 b	1.57 a
TSS/TA	-	30.59 a	27.35 a	12.25 b
TEAC	(µmol TE/g FW)	0.81 c	0.84 b	1.18 a
TPC	(µg GAE/g FW)	652.24 b	621.34 b	1208.33 a

Differences between values with different letters are significant at $P \leq 0.05$.

compounds—in 2 hybrid apricot populations and found high variations in the progenies. The authors reported normal distribution of hybrids in their populations, indicating that most of the resulting hybrids were between their parents; however, for FW and FF, transgressive hybrids were obtained both below and above the parents. Hegedus et al. (2010) suggested that the high variation found between genotypes showed that the traits could be improved by breeding studies using appropriate parents and selection strategies.

The results of a few previous studies on inheritance of fruit quality traits in apricot indicated quantitative inheritance for most of the traits and various heritability levels for fruit quality characteristics; however, most characteristics are inherited in accordance with Mendel's laws (Krška et al., 2009).

3.2. GCA and expression frequency of inherited traits

The survey of the percentages of hybrids with values below, between, and above their parents is given in Table 2. According to these results, the inheritance frequency of FW, F/S, FF, TSS, and TPC were placed in the same group in both populations. Frequency of color indices and TEAC values were higher in 'HH × SEO', while inheritance of fruit sizes, SW, TA, and TSS/TA values were more stable in 'ÇO × SEO'. When the parents 'HH' and 'ÇO' were compared, the GCA of 'HH' was higher in terms of FL, FLW, F/S, TA, and TSS/TA traits, while the GCA of 'ÇO'

was higher in color indices, TEAC, and TPC. Figures 1a and 1b demonstrate the frequency of inheritance for FS and FC sensory traits. Accordingly, inheritance of FS was more stable in 'HH × SEO', but FC was more stable in 'ÇO × SEO' and the GCA of 'HH' was found to be higher for FS but similar for FC.

Paunović (1987) found fruit shape and flesh firmness to be very stable, skin color to be stable, and fruit weight to be variable inherited characteristics. Krška et al. (2009) found fruit weight, skin color, and flesh color to be variable, and flesh firmness to be averagely well inherited traits. The results for inheritance frequency obtained by Salazar (2013) varied between the years for most of the traits examined. According to the results reported by the authors, the expression frequency varied between very variable to variable for FW and fruit skin color (H°), very variable to average for FC, average to stable for SW, and variable to average for TSS; the frequency of FF and TA did not vary between years and were found to be variable and stable, respectively.

3.3. Broad-sense heritability estimates and correlations between parents and their progenies

Broad-sense heritability values varied between 0.63 (TSS/TA) and 0.97 (TPC) in 'HH × SEO' and between 0.59 (FVW) and 0.98 (TPC) in 'ÇO × SEO' (Table 3). High heritability was assessed for all traits in both populations considering the H values, indicating a high influence of genotype on phenotypic variation. Krška et al. (2009) confirmed a high H value for fruit weight over color and flesh firmness in their study.

Correlations between hybrids and their parents were found to be weak in most of the traits, whereas negative, significant, and strong correlations were found in TEAC and TPC in both populations (Table 3). Other significant correlations were FW and SW in 'HH × SEO', and FL, FLW, and FW in 'ÇO × SEO'. All of these significant correlations were negative. Krška et al. (2009) found a strong dependency for fruit over color but a weak dependency for fruit weight and flesh firmness.

3.4. Parent-offspring correlation and regression

Results indicated strong dependencies between parents and their progenies for FL, FLW, FF, L*, TSS, and TA; medium strong dependencies for TSS/TA and TEAC and weak dependencies for FVW, SW, F/S, a*, and TPC (Table 4). Almost all correlations for pomological traits were negative, and none of these correlations were significant. Couranjou (1995) calculated parent-offspring correlations for 2 characteristics included in the current study, and their results were similar for FF but slightly lower for FW (by approximately 0.1). The authors reported that results given by Lapins et al. (1957) were slightly

Table 2. Survey of inheritance frequency of characters in the F₁ progenies.

Trait	HH × SEO				ÇO × SEO			
	Below parents (%)	Between parents (%)	Above parents (%)	Frequency	Below parents (%)	Between parents (%)	Above parents (%)	Frequency
FL	12	56	32	constant	28	68	4	stable
FLW	24	52	24	constant	12	68	20	stable
FVW	32	-	68	highly variable	20	12	68	very variable
FW	20	76	4	stable	24	72	4	stable
SW	16	76	8	stable	4	88	8	very stable
F/S	68	4	28	highly variable	84	-	16	highly variable
FF	4	44	52	average	8	40	52	average
L*	12	80	8	stable	28	8	64	very variable
a*	16	68	16	stable	52	28	20	variable
b*	4	92	4	very stable	4	36	60	average
TSS	92	8	-	very variable	84	16	-	very variable
TA	4	20	76	variable	-	56	44	constant
TSS/TA	88	8	4	very variable	68	32	-	variable
TEAC	44	56	-	constant	60	36	4	average
TPC	88	12	-	very variable	72	16	12	very variable

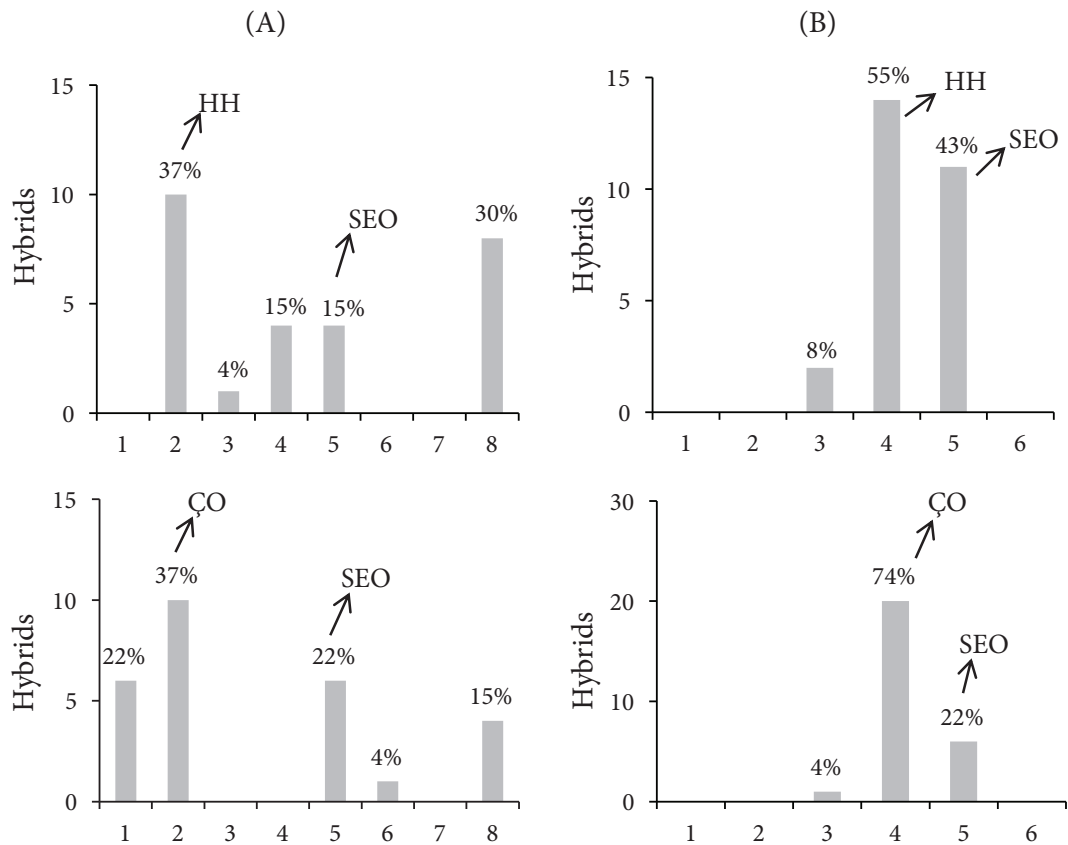
**Figure 1.** Survey of inheritance frequencies of fruit shape (a) and flesh color (b) results in the F₁ progenies.

Table 3. H values and dependences between the mean values of parents and their progenies.

Trait	HH × SEO			ÇO × SEO		
	H	r	Dependence	H	r	Dependence
FL	0.84	-0.13	weak	0.73	-0.50**	medium strong
FLW	0.82	-0.09	weak	0.79	-0.40**	medium strong
FVW	0.77	-0.11	weak	0.59	-0.17	weak
FW	0.88	-0.32*	weak	0.84	-0.65**	strong
SW	0.94	-0.57**	medium strong	0.92	0.20	weak
F/S	0.89	-0.12	weak	0.86	0.07	weak
FF	0.88	0.05	weak	0.82	0.23	weak
L*	0.96	0.10	weak	0.95	-0.19	weak
a*	0.86	0.03	weak	0.86	0.22	weak
b*	0.84	0.12	weak	0.96	-0.31	weak
TSS	0.95	0.01	weak	0.94	0.01	weak
TA	0.94	-0.80	strong	0.93	-0.96**	strong
TSS/TA	0.63	-0.37	weak	0.84	0.19	weak
TEAC	0.81	-99**	strong	0.95	-83*	strong
TPC	0.97	-99**	strong	0.98	-95**	strong

*: Correlations significant at $P \leq 0.05$; **: Correlations significant at $P \leq 0.01$.

Table 4. Parent-offspring correlation and regression coefficients.

Trait	r_{PFI}	Dependence	b_{PFI}	Heritability level
FL	-0.904	strong	1.129	very high
FLW	-0.736	strong	0.851	high
FVW	-0.335	weak	1.181	very high
FW	-0.863	strong	0.746	high
SW	-0.290	weak	0.198	low
F/S	0.279	weak	1.299	very high
FF	-0.859	strong	1.143	very high
L*	-0.982	strong	1.127	very high
a*	0.085	weak	0.081	low
b*	-0.931	strong	0.905	high
TSS	0.774	strong	0.714	high
TA	0.610	strong	0.663	high
TSS/TA	0.535	medium strong	0.660	high
TEAC	0.414	medium strong	0.433	medium
TPC	0.122	weak	0.164	low

*: Correlations significant at $P \leq 0.05$; **: Correlations significant at $P \leq 0.01$.

higher (by approximately 0.05–0.1) than their results and noted that the differences could be caused because

of the genetic distance between the cultivars used in the crossings.

Parent-offspring regression calculations were performed to estimate heritability levels for each characteristic (Table 4). Very high levels of heritability (higher than 1.0) were calculated for FL, FVW, F/S, FF, and L* (varying between 1.127 and 1.299), indicating a nonadditive effect (dominance and epistatic effect) on the inheritance of those traits caused by genetic interaction (Morishita, 1994; Ohtsuka et al., 2004). Heritability levels were at a high level for FLW, FW, TSS, b*, TA, and TSS/TA (between 0.660 and 0.905), medium for TEAC (0.433), and low for SW, a*, and TPC (0.198, 0.081, and 0.164, respectively). The values calculated by Couranjou (1995) varied between 0.294 ± 0.134 for over color and 0.936 ± 0.135 for flowering date. The values of common characteristics also included in this study were 0.615 ± 0.149 and 0.564 ± 0.099 for FW and FF, respectively.

3.5. Conclusions

Significant differences in the progenies and in the Gaussian or normal trends of distribution confirmed the quantitative inheritance of the characteristics evaluated in this study, along with their polygenic nature. These results indicated the significant influence of genotypic factors on the expression of fruit quality attributes in a given progeny.

Consequently, the genetic influence of the whole genetic background of the parents on the transmission of fruit quality traits in apricot was proven, which should be taken into consideration in intercultivar, crossbreeding studies.

When the results of GCA were considered, 'HH' was seen as a better parent for transmitting the traits of fruit size, F/S, TA, and TSS/TA. On the other hand, 'ÇO' was better with regard to color parameters, TEAC, and TPC.

Heritability estimates indicated a high level of inheritance for almost all pomological traits, whereas medium and low levels were seen for TEAC and TPC, respectively. However, the high level of variation observed

in the progenies, together with the evidence of hybrids obtained with results above their parents, suggested that the traits could be improved by breeding studies organized with appropriate parents and selection strategies.

The results of this study were obtained from a single-year experiment. Therefore, additional findings could be possible if the study is continued for a few more years.

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