Inheritance patterns of major phenological traits in pear and breeding effectiveness of parental varieties

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Abstract

This study was conducted to plan targeted breeding programs in pear cultivation and, as a result, genetic parameters of major phenological traits (full bloom time, harvest time, and the duration from full bloom to harvest) were calculated along with the breeding values of parental varieties for these traits. In this context, phenological records of 2,051 hybrid plants obtained from 37 crossing combinations were collected. It was determined that all examined traits were quantitative. The genetic effect on the inheritance of full bloom time was found to be low at 31%, whereas it was higher for harvest time (83%) and the duration from full bloom to harvest (86%). In the development of early-maturing genotypes, the 'Akça' variety stood out both as a maternal parent (204.88 days) and as a pollinator (211.32 days). For late-maturing genotypes, 'Kieffer' (236.11 days) as a maternal parent and 'Ankara' (239.09 days) as a pollinator were prominent. Among the study materials, hybrids of 'Williams×Conference,' which bloomed after the 100th day of the year and completed their physiological development in approximately 150 days, showed promise for breeding late-blooming, late-maturing genotypes. Conversely, the 'Santa Maria×Akça' combination, which bloomed in the same period and required less than 100 days from full bloom to harvest, was significant for developing late-blooming, early-maturing genotypes. The results of this study provide valuable insights for planning new breeding projects addressing the impacts of global climate change.
Keywords: Phenology, Heterosis, Inheritance, Hybrid, *Pyrus communis* L.

INTRODUCTION

With its favorable climatic conditions, Türkiye demonstrates its potential in early, mid, and late-season pear (*Pyrus communis* L.) production and ranks among the top five pear-producing countries globally (FAO, 2022). Despite this advantageous position in production, the country's export volume is still quite low with 89,302 tons (FAO, 2022). The pear market offers significant economic opportunities because the global trade volume of fresh pears exceeds 3 million tons. Achieving higher export levels in this economically promising species seems feasible by ensuring quality and standardization in production. In this context, breeding programs aimed at developing genotypes that meet the demands of both producers and consumers are essential. The traits targeted in breeding programs are predominantly quantitative, controlled by multiple genes, and exhibit a complex inheritance pattern (Evrenosoğlu et al., 2019; Karaat and Serce, 2020). Consequently, hybrid breeding remains the most widely employed method (Bilgin et al., 2020; Saridas et al., 2021; Kurnaz et al., 2024). However, in hybrid breeding programs, the emergence of desirable traits in new genotypes largely depends on chance, making the process unpredictable (Lyrene, 2018; Paranhos et al., 2022).

Wild species are often favored in breeding programs due to their superior resistance against diverse biotic and abiotic stressors. However, hybridizations involving wild species frequently lead to the expression of undesirable traits in progeny, such as grittiness (caused by stone cells), small fruit size, thorniness, and irregular fruit shapes

(Simionca Marcașan et al., 2023). To address these issues, subsequent backcrossing with high-quality cultivars is typically required. Despite this approach, the unpredictable inheritance of desirable traits in backcrossed progeny, coupled with the lengthy, labor-intensive, and resource-intensive nature of such breeding efforts, has redirected contemporary breeding strategies toward utilizing cultivars with greater commercial value (Evrenosoğlu et al., 2010). The limited number of pear varieties cultivated globally has further resulted in the reuse of parental lines from previous programs in contemporary breeding initiatives.

To enhance the effectiveness of hybrid breeding programs, researchers must undertake comprehensive genetic studies aimed at improving both the predictability and efficiency of these initiatives. A key component of such efforts is the meticulous evaluation of parental lines for their breeding values, determined based on the traits under investigation. Additionally, the prediction of genetic parameters for each trait and the detailed elucidation of their inheritance mechanisms are indispensable for shaping the direction of future breeding programs. By carefully selecting optimal parental lines during the initial stages, the probability of obtaining progeny with the desired traits can be substantially increased. This strategy not only streamlines the hybrid breeding process but also reduces the time and financial resources required to achieve targeted breeding outcomes. Recent research efforts have increasingly prioritized addressing uncertainties in breeding programs by pinpointing the genetic loci associated with specific traits (Sanchez-Perez et al., 2012; Zhen et al., 2018) and elucidating their inheritance mechanisms (Liu et al., 2024). This line of investigation has not only gained significant prominence but also exhibited a marked upward trend in recent years reflecting its critical importance in advancing the field of plant genetics and breeding (Nyadanu et al., 2017; Evrenosoğlu et al., 2019; Fallah et al., 2022).

In this study, some phenological characteristics of 2051 F_1 pear hybrids obtained from 37 hybridization combinations involving 12 pear varieties were analyzed, and the parental varieties' breeding values were assessed. regarding related traits. Additionally, hybridization combinations that produced heterotic individuals were determined, providing practical recommendations for future pear breeding programs regarding the selection of parental lines and combinations. Furthermore, genetic parameter estimates were calculated for all evaluated traits, providing insights into the efficiency of hybridization in trait development, the genetic malleability of these traits, and their sensitivity to environmental factors.

MATERIALS AND METHODS
Material
The study material consisted of 2051 hybrids obtained from 37 distinct hybridization combinations involving 5 maternal and 11 pollinator varieties within the scope of projects aimed at developing fire blight-resistant pear genotypes with high fruit quality parameters (TUBITAK TOVAG 106O719 and TUBITAK TOVAG 110O938) (Evrenosoğlu et al., 2010).

The study material that was located in experimental fields of Eskisehir Osmangazi University, Faculty of Agriculture in Eskişehir, where has a typical continental climate. The climatic characteristics observed during the experimental period at the trial site are presented in Table 1. Due to global climate change, air temperatures in both experimental years were generally observed to be higher than the long-term averages. This increase in air temperature, which enhances the potential for water vapor dissolution in the air, was accompanied by a similar trend in relative humidity. Regarding precipitation, an examination of long-term data reveals consistency across seasonal months; however, during the study period, irregular rainfall and drought periods were observed.

Table 1. Climate Characteristics of the Experimental area.

	Precipitation (mm)			Humidity (%)			Temperature (°C)		
	2018	2019	LTA	2018	2019	LTA	2018	2019	LTA
December	63.6	74.1	45.1	96.0	89.9	93.6	2.7	2.9	3.6
November	29.6	33.9	29.2	79.2	76.2	80.3	8.4	7.9	7.5
October	41.0	18.3	27.0	75.5	70.1	79.6	14.0	14.2	12.9
September	**2.8**	**4.0**	**17.0**	**65.4**	**62.1**	**58.4**	**18.6**	**18.3**	**17.3**
August	**18.0**	**3.2**	**12.4**	**63.5**	**61.0**	**54.7**	**22.9**	**22.3**	**21.8**
July	**39.2**	**36.4**	**14.2**	**65.5**	**62.4**	**53.0**	**22.3**	**21.3**	**21.9**
June	**46.6**	**36.6**	**29.9**	**69.5**	**67.9**	**57.2**	**19.9**	**20.9**	**18.9**
May	**62.2**	**39.8**	**41.9**	**74.8**	**65.1**	**60.8**	**16.8**	**16.5**	**14.8**
April	**12.6**	**24.8**	**40.5**	**61.6**	**69.3**	**62.8**	**13.8**	**9.5**	**9.9**
March	**53.6**	**9.2**	**30.3**	**73.5**	**64.5**	**65.1**	**9.2**	**6.3**	**5.3**
February	40.5	50.1	32.5	90.7	79.6	92.6	6.6	3.4	4.7
January	31.5	60.2	38.7	95.5	91.0	98.2	2.2	4.3	0.3
Average	36.8	32.6	29.9	75.9	71.6	71.4	13.1	12.3	11.6

LTA: Average climate data between 1929 and 2019, bold lines mean growing periods.

Phenonological observations

The full bloom stage was recorded as the period when 70–80% of flower buds had fully bloomed (Karaçalı, 2012). The determination of whether the fruits had reached harvest maturity was based on criteria such as color development, abscission layer formation, and taste (Mertoğlu and Evrenosoğlu, 2017). The total number of days between the full bloom date and the harvest date was calculated (Karaçalı, 2012).

Genetic Parameter Estimation and Statistical Analyses

The genetic parameters of the traits under consideration were calculated using estimates of variance components. Variance component estimates were obtained using the REML (Restricted Maximum Likelihood) method, based on the mathematical model (1) provided below, and computed through the ASReml software.

$$y = Z_1 YIL + Z_2 a + Z_3 b + Z_4 melez + E \qquad (1)$$

Here;

YIL; $\sim N\left(0, A\sigma^2_{yıl}\right)$ impacts of the chance regarding year,

a; $\sim N(0, A\sigma^2_a)$ impacts of the chance regarding maternal parents,

b; $\sim N(0, A\sigma^2_b)$ impacts of the chance regarding pollinators,

$melez$; $\sim N(0, I\sigma^2_{melez})$ impacts of the chance regarding hybrids,

E; $\sim N(0, I\sigma^2_E)$ impacts of the chance regarding error,

Z_1, Z_2, Z_3 and Z_4; the design matrices are displayed.

By using the results of the model-based estimates namely; additive genetic variance (V_A), non-additive genetic variance (dominance and epistasis), total genetic variance (V_{nona}), total phenotypic variance (V_P), total genetic variance (V_g); genetic parameter estimates such as narrow-sense heritability (h^2), broad-sense heritability (H^2), maternal effects (M^2), general combining ability (V_{GCA}), and specific combining ability (V_{SCA}) variance components were calculated using the formulas below (2) (Baker, 1978; Evrenosoğlu et al., 2019).

$$V_A = 2(\sigma^2_a + \sigma^2_b) \qquad (2)$$

$$V_D = 4(\sigma^2_{melez})$$

$$V_G = V_A + V_D$$

$$V_p = \sigma^2_{YIL} + \sigma^2_a + \sigma^2_b + \sigma^2_{melez} + \sigma^2_E$$

$$H^2 = V_G / V_p$$

$$h^2 = V_a / V_p$$

$$M^2 = \sigma^2_h / V_p$$

$$d^2 = V_D / V_p$$

RESULTS AND DISCUSSION

In the F_1 hybrids obtained from different hybridizations, measurements were taken over two consecutive years, and the results regarding the variance components and genetic parameters of the phenological traits are presented in Table 2. The variance attributed to additive genes for full bloom was proportionally lower within the total phenotypic variance compared to harvest time and the duration from full bloom to harvest. Consequently, the narrow-sense heritability derived from these ratios was estimated as 32% for full bloom time. In contrast, it was 83% and 86% for harvest time and the duration from full bloom to harvest, respectively. These results indicate that environmental factors significantly influence full bloom traits compared to harvest time and the duration from full bloom to harvest (Table 2). This phenomenon can be attributed to the requirement for specific climatic thresholds to initiate flowering. Szabo et al. (2019) and Legave et al. (2013) emphasized that meeting temperature requirements is a critical factor influencing the initiation of flowering, with a reported linear regression relationship between temperature and flowering at $R^2 = 0.55$. In contrast, fruit development is a dynamic process that continues uninterrupted from fertilization to harvest. Assimilation products generated during daytime photosynthesis are transported to the fruits day and night, making harvest time and the duration from full bloom to harvest less susceptible to year-to-year environmental variations compared to full bloom time. Similar findings have been reported in other studies, which also noted that the narrow-sense heritability for full bloom time is lower than that of other phenological traits due to the reduced influence of genotype on this trait (Piaskowski et al., 2018; Hajnajari et al., 2019). The inclusion of data spanning two vegetation periods in this study allowed for a clearer delineation of these trait differences.

The broad-sense heritability, which incorporates the effects of non-additive genes, was estimated at 52%, 92%, and 98% for full bloom time, harvest time, and the duration from full bloom to harvest, respectively. These results indicate that multiple genes are involved in the inheritance of these phenological traits, demonstrating a polygenic inheritance pattern. Similar findings have been reported in studies on other fruit species, including almond (Sanchez-Perez et al., 2007), peach (Rakonjac et al., 2011), sour cherry (Piaskowski et al., 2018), and apple (Hajnajari et al., 2019), where phenological traits were also shown to exhibit polygenic inheritance. In such cases, identifying the chromosomal loci of the genes controlling these traits becomes crucial, with an emphasis on achieving genetic progress through major-effect genes (Sanchez-Perez et al., 2007). The dominance heritability estimates from additive genes were found to be relatively low, at 5%, 2%, and 3% for full bloom time, harvest time, and the duration from full bloom to harvest, respectively. This suggests that epistatic interactions have a greater influence on inheritance compared to dominance effects. A study by Hwang et al. (2015) on Asian pears examined the inheritance of harvest time using 13 varieties and 15 hybrid combinations. Their findings, consistent with our results, reported heritability values generally exceeding 80%.

Table 2. Variance Components and Genetic Parameter Estimates for Phenological Traits.

	Variance components					Genetic parameters		
	V_A	V_D	σ^2_{YIL}	σ^2_E	σ^2_P	h^2	H^2	d^2
NDBH	366.47	50.69	7.38	172.54	425.83	0.86	0.98	0.03
Harvest time	452.43	53.27	142.76	164.61	546.91	0.83	0.92	0.02
Full Bloom	3.72	2.54	12.08	7.42	12.08	0.31	0.52	0.05

NDBH: Number of days from full bloom to harvest, V_A: additive genetic variance, V_D: non-additive genetic variance (dominance and epistasis), σ^2_{YIL}: variance of year, σ^2_E: Error variance, σ^2_P: total phenotypic variance, h^2: narrow-sense heritability, H^2: broad-sense heritability, d^2: Heritability of dominance

Descriptive statistics and breeding values for full bloom time, harvest time, and the duration from full bloom to harvest across parent varieties and years are provided in Table 3. Significant statistical differences were observed among maternal parents, pollinators, and years for all traits examined.

The mean values of hybrids derived from maternal parents for full bloom indicated the following sequence of reaching full bloom: 'Kieffer' (93.39 days), 'Akça' (96.60 days), 'Williams' (98.06 days), 'Santa Maria' (98.13 days), and 'Maggness' (99.79 days). Similarly, the ranking of pollinators for this trait was as follows: 'Conference' (95.51 days), 'Santa Maria' (96.29 days), 'Moonglow' (96.97 days), 'Bursa' (96.97 days), 'Taş' (97.18 days), 'Kieffer' (97.23 days), 'Ankara' (97.35 days), 'Williams' (97.40 days), 'Kaiser Alexandre' (98.57 days), 'Limon' (99.30 days), and 'Akça' (101.19 days). In a study conducted under the ecological conditions of Bingöl-Türkiye, the full bloom times of five varieties ('Akça,' 'Ankara,' 'Deveci,' 'Santa Maria,' and 'Williams') ranged between the 83rd ('Williams') and 119th ('Santa Maria') days of the year across two consecutive years (Osmanoğlu et al., 2013). Similarly, in Serbia, under a harsh continental climate, hybrids reached full bloom between the 105th and 146th days of the year over three years (Gordana, 2019). Another study conducted at the Horticulture Research Institute in Erzincan observed that approximately 15% of genotypes reached full bloom early, 70% during the mid-period, and 15% late (Öz and Aslantaş, 2015). Full bloom variations for both maternal and pollinator varieties showed approximately 10% variation (Table 3), suggesting a low and uniform level of variation for this trait.

When evaluating the effects of maternal parents on ripening, the 'Akça' (204.88 days) stood out as the leading candidate for obtaining early genotypes, while 'Kieffer' (236.11 days) was prominent for late-ripening genotypes.

Other maternal parents, such as 'Santa Maria' (220.33 days), 'Williams' (229.93 days), and 'Maggness' (230.99 days) were identified within this range. The 'Akça' (211.32 days) also stood out as a pollinator for early ripening, while 'Ankara' (239.09 days) was promising for late-ripening generations. Among pollinators, 'Bursa' (219.68 days) and 'Moonglow' (220.39 days) contributed to early ripening, while 'Limon' (234.70 days) and 'Kieffer' (235.33 days) were effective for obtaining late-ripening genotypes. Studies with similar materials indicated that harvest times for the examined varieties and genotypes ranged between July 17 and September 9, reflecting the population's broad variation (Mertoğlu and Evrenosoğlu, 2017; Evrenosoğlu and Mertoğlu, 2020). A study in Bosnia and Herzegovina under ex-situ conditions also reported wide variation, ranging from extremely early ripening to late-season maturity (Zeljkovic et al., 2019).

The coefficients of variation for harvest time were generally between 6-7%, lower than those for full bloom. Similarly, hybrids derived from 15 different crossing combinations showed that the coefficient of variation for harvest time did not exceed 4% (Hwang et al., 2015). In the current study, the coefficients of variation for full bloom ranged from 9-11%, while those for harvest time ranged from 6-8%, suggesting that subsequent generations resemble the parent varieties more closely for harvest time than for full bloom.

The duration from full bloom to harvest followed trends similar to harvest time. The 'Akça' variety contributed to the fastest completion of developmental physiology as both a maternal parent (109.29 days) and a pollinator (111.38 days). Conversely, 'Kieffer' (143.69 days) as a maternal parent and 'Ankara' (142.75 days) as a pollinator contributed to the slowest development. Other maternal parents such as 'Santa Maria' (123.22 days) supported relatively faster development, whereas 'Maggness' (132.46 days) and 'Williams' (132.91 days) contributed to later-season genotypes. Among pollinators, varieties such as 'Bursa' (123.70 days), 'Moonglow' (124.42 days), and 'Williams' (127.51 days) supported moderate fruit development speed, while 'Limon' (136.39 days), 'Santa Maria' (138.35 days), and 'Kieffer' (139.10 days) contributed to slower fruit development. A study in northern Anatolia reported that promising pear genotypes required 89 to 212 days from full bloom to harvest maturity across years (Öztürk and Demirsoy, 2013). Variation observed for harvest time was higher than for full bloom. The 'Kieffer' variety was promising for developing late-ripening genotypes, as indicated by its low coefficient of variation (4.75%).

During the first year of the study, data from all hybrids indicated that full bloom occurred around the 90th day of the year, while in the second year, it extended to the 110th day. The earlier bloom in 2018 was likely due to higher average temperatures in April of that year (Table 3). Legave et al. (2013) and Szabo et al. (2019) identified temperature requirements as the most critical factor influencing the onset of bloom. The delay in bloom during the second year also affected harvest time, which occurred on average 15 days later (238th day) than in the first year (223rd day). Additionally, the shorter duration from full bloom to harvest in 2018 (129 days) compared to 2019 (135 days) highlights the role of warmer temperatures in accelerating development, whereas cooler conditions prolonged it (El Yaacoubi et al., 2014).

The performances of hybridization combinations for the evaluated phenological traits obtained from 37 hybridizations are presented in Table 4. For full bloom, combinations ranged between the 88th day (Akça × Taş) and the 112th day (Maggness × Moonglow) of the year, while harvest dates occurred between the 194th day (Akça × Taş) and the 246th day (Williams × Conference). Regarding the duration from full bloom to harvest, the hybrid combinations exhibited a distribution between 99.86 days (Santa Maria × Akça) and 144.82 days (Williams × Conference).

In regions where early-season cultivation is emphasized, genotypes that complete their development quickly gain importance. In this context, among the hybridizations the Akça used, especially the 'Santa Maria × Akça' (99.86 days) stands out prominently. Conversely, genotypes that bloom after late spring frosts and do not require a very high accumulated temperature are needed in areas with high altitudes and a predominant continental climate. Within the study material, the 'Williams × Conference' combination, which blooms after the 100th day of the year and has a harvest time exceeding 140 days from full bloom, appears promising for such conditions.

Table 3. Descriptive Statistics and Breeding Values of Parent Varieties for Phenological Traits

Maternal	N	Full Bloom				Harvest				NDBH			
		Mean±S.D	Min	Max	C.V (%)	Mean±S.D	Min	Max	C.V (%)	Mean±S.D	Min	Max	C.V (%)
Williams	932	(0.25)98.06^B±10.45	79.00	118.00	10.66	(5.66)229.93^B±20.61	187.00	271.00	8.96	(5.30)132.91^B±19.33	84.00	184.00	14.55
Maggness	482	(1.64)99.79^A±11.01	82.00	118.00	11.04	(7.73)230.99^B±15.61	182.00	273.00	6.76	(6.23)132.46^B±16.41	74.00	221.00	12.39
Akça	42	(-0.09)96.60^C±11.26	84.00	118.00	11.65	(-22.02)204.88^D±15.85	179.00	245.00	7.74	(-21.94)109.29^D±13.57	83.00	137.00	12.42
SantaMaria	348	(-0.12)98.13^B±10.63	82.00	118.00	10.84	(-5.55)220.33^C±18.95	179.00	266.00	8.60	(-5.52)123.22^C±17.83	75.00	157.00	14.47
Kieffer	247	(-1.69)93.39^D±9.79	82.00	118.00	10.48	(14.18)236.11^A±11.21	184.00	258.00	4.75	(15.93)143.69^A±12.02	97.00	169.00	8.36
Pollinator	**N**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**
Akça	399	(0.22)101.19^A±10.86	79.00	118.00	10.74	(-21.07)211.32^F±16.64	179.00	259.00	7.88	(-21.07)111.38^E±15.68	74.00	221.00	14.08
Williams	113	(1.51)97.40^C±10.40	86.00	116.00	10.67	(6.52)223.91^{DCE}±13.76	190.00	253.00	6.14	(5.02)127.51^{DC}±12.58	100.00	157.00	9.86
Kieffer	154	(-0.93)97.23^C±10.90	82.00	117.00	11.21	(7.08)235.33^B±19.28	187.00	271.00	8.19	(7.98)139.10^B±17.86	90.00	184.00	12.84
SantaMaria	429	(0.77)96.29^{DE}±10.96	82.00	118.00	11.38	(-0.57)233.64^B±14.43	179.00	262.00	6.18	(-1.47)138.35^{BA}±14.52	91.00	169.00	10.50
Conference	70	(-0.78)95.51^E±10.24	82.00	115.00	10.72	(2.96)224.54^{DC}±18.97	187.00	269.00	8.45	(3.71)130.03^C±17.20	83.00	162.00	13.23
Kaiser	91	(2.09)98.57^B±9.50	85.00	118.00	9.64	(2.83)227.53^C±19.61	187.00	266.00	8.62	(0.74)129.96^C±17.19	91.00	156.00	13.23
Ankara	553	(-2.32)97.35^C±10.25	82.00	117.00	10.53	(7.21)239.09^A±15.18	184.00	271.00	6.35	(9.54)142.75^A±12.72	91.00	175.00	8.91
Moonglow	36	(0.58)96.97^{DC}±9.62	84.00	113.00	9.92	(-3.82)220.39^{DE}±12.61	191.00	262.00	5.72	(-4.37)124.42^D±10.25	100.00	155.00	8.24
Bursa	40	(0.35)96.97^{DC}±9.37	86.00	113.00	9.67	(-2.51)219.68^E±18.43	187.00	252.00	8.39	(-2.83)123.70^D±20.17	83.00	158.00	16.31
Taş	143	(-1.30)97.18^{DC}±10.88	83.00	118.00	11.20	(-2.44)226.43^C±18.92	191.00	273.00	8.36	(-1.16)130.26^C±15.38	97.00	164.00	11.80
Limon	23	(-0.19)99.30^B±11.41	87.00	116.00	11.49	(3.82)234.70^B±9.43	215.00	245.00	4.02	(3.91)136.39^B±10.90	117.00	154.00	7.99
Years	**N**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**	**Mean±S.D**	**Min**	**Max**	**C.V (%)**
2019		110.00^A	96.00	118.00	3.11	237.39^A	182.00	273.00	7.91	134.35^A	74.00	164.00	15.45
2018		89.23^B	79.00	99.00	3.32	222.59^B	179.00	271.00	7.52	128.39^B	86.00	221.00	12.90

N: Number of plants, NDBH: Number of days from full bloom to harvest, C.V: Coefficient of variation

Table 4. Performance of Hybrid Combinations for Phenological Traits

	Full Bloom				Harvest				NDBH			
	N	Mean±S.D	Min	Max	C.V (%)	Mean±S.D	Min	Max	C.V (%)	Mean±S.D	Min	Max	C.V (%)
Akça×Williams	7	95.14^{JO}±11.02	88.00	114.00	11.58	208.57^{JN}±4.34	194.00	224.00	11.47	114.43^{GJ}±4.51	104.00	137.00	11.93
Akça×Kieffer	5	93.60^{LO}±10.29	84.00	111.00	10.99	203.40^{LN}±2.87	199.00	214.00	6.43	110.80^{HJ}±5.49	90.00	122.00	12.28
Akça×Santa Maria	13	95.77^{FK}±11.15	85.00	115.00	11.64	201.08^{KN}±5.76	179.00	245.00	20.76	106.31^{IJ}±3.65	91.00	131.00	13.17
Akça×Conference	11	96.73^{GL}±11.73	86.00	115.00	12.13	205.09^{KN}±3.71	187.00	232.00	12.29	109.36^{IJ}±4.98	83.00	130.00	16.53
Akça×Kaiser	5	105.20^{B}±12.87	90.00	118.00	12.24	212.80^{HM}±9.84	188.00	245.00	22.00	108.60^{IJ}±6.93	99.00	136.00	15.50
Akça ×Taş	1	88.00^{P}±*	88.00	88.00	*	194.00^{N}±*	194.00	194.00	*	107.00^{IJ}±×	107.00	107.00	*
Williams×Akça	245	101.29^{DC}±11.04	79.00	117.00	10.90	210.38^{IM}±0.99	187.00	259.00	15.54	110.09^{IJ}±0.84	84.00	146.00	13.14
Williams×Kieffer	74	94.92^{JO}±10.05	84.00	113.00	10.59	236.82^{AF}±2.32	187.00	271.00	19.92	142.91^{BA}±2.00	98.00	184.00	17.17
Williams×Santa Maria	31	99.03^{CI}±10.37	84.00	113.00	10.47	229.23^{BG}±2.87	200.00	262.00	15.99	131.19^{AF}±2.51	110.00	155.00	13.95
Williams×Conference	17	101.88^{C}±10.64	88.00	115.00	10.44	245.71^{A}±4.00	217.00	269.00	16.49	144.82^{A}±3.14	108.00	162.00	12.96
Williams×Kaiser	46	99.02^{CI}±9.51	89.00	116.00	9.60	232.02^{AG}±2.41	199.00	266.00	16.33	134.00^{AE}±1.99	102.00	155.00	13.46
Williams×Ankara	46	97.02^{FK}±9.89	83.00	113.00	10.20	240.27^{BA}±0.77	192.00	271.00	15.72	144.24^{A}±0.58	91.00	175.00	11.75
Williams×Moonglow	17	93.82^{KO}±7.73	84.00	112.00	8.24	220.88^{EJ}±3.06	199.00	266.00	12.62	128.06^{AG}±2.15	116.00	155.00	8.87
Williams×Bursa	12	95.83^{IO}±9.20	89.00	113.00	9.60	237.92^{AD}±3.53	215.00	252.00	12.22	143.08^{BA}±4.08	112.00	158.00	14.13
Williams×Taş	70	95.26^{JO}±10.45	85.00	118.00	10.45	225.49^{BL}±2.34	191.00	257.00	19.61	131.23^{AF}±1.70	106.00	158.00	14.20
Williams×Limon	4	96.00^{HN}±5.20	87.00	105.00	10.39	231.75^{BG}±7.78	215.00	245.00	15.56	136.75^{AD}±2.84	129.00	141.00	5.68
Kieffer×Santa Maria	24	93.41^{LO}±9.79	82.00	118.00	10.48	236.11^{AE}±0.71	184.00	258.00	11.21	143.69^{A}±0.77	97.00	169.00	12.02
Santa Maria×Akça	44	100.52^{CE}±11.03	84.00	118.00	10.97	199.39^{MN}±2.14	179.00	228.00	14.22	99.86^{J}±2.03	75.00	134.00	13.44
Santa Maria×Williams	105	97.59^{FJ}±10.43	86.00	116.00	10.69	224.83^{BI}±1.30	190.00	253.00	13.36	128.24^{AG}±1.19	100.00	157.00	12.16
Santa Maria×Kieffer	31	101.58^{DC}±10.98	85.00	113.00	10.81	229.52^{AG}±3.99	187.00	262.00	22.24	128.94^{AG}±3.53	94.00	155.00	19.66
SantaMaria×Conference	25	92.56^{O}±9.77	82.00	110.00	10.55	219.84^{EK}±3.11	194.00	262.00	15.54	128.28^{AG}±3.03	97.00	153.00	15.16
Santa Maria×Kaiser	30	97.60^{FJ}±9.47	85.00	116.00	9.71	223.03^{CJ}±4.33	187.00	263.00	23.74	126.43^{BH}±3.70	91.00	156.00	20.26
Santa Maria × Ankara	30	95.07^{JO}±10.99	82.00	112.00	11.56	227.73^{BH}±3.40	195.00	266.00	18.62	133.67^{AE}±2.87	102.00	157.00	15.74
Santa Maria×Moonglow	18	99.11^{CI}±10.30	87.00	113.00	10.39	219.28^{FK}±3.05	191.00	237.00	12.96	121.17^{DI}±2.55	100.00	145.00	10.82
Santa Maria×Bursa	28	97.46^{FJ}±1.81	86.00	112.00	9.57	211.86^{HM}±2.79	187.00	231.00	14.78	115.39^{FJ}±3.09	83.00	141.00	16.37
Santa Maria×Taş	33	100.21^{CF}±1.94	83.00	115.00	11.15	222.00^{DL}±3.39	191.00	253.00	19.49	122.79^{CI}±2.50	97.00	149.00	14.35
Santa Maria×Limon	4	101.75^{C}±6.22	89.00	116.00	12.45	238.75^{AC}±2.93	232.00	245.00	5.85	138.00^{AC}±6.75	121.00	154.00	13.49
Maggness×Akça	110	101.22^{DC}±10.48	87.00	117.00	10.36	218.18^{GL}±1.61	182.00	248.00	16.86	118.88^{EI}±1.72	74.00	221.00	18.05

Cross	N												
Maggness×Williams	1	93.00^{M-O}±*	93.00	93.00	*	235.00^{A-F}±*	235.00	235.00	*	143.00^{B-A}±×	143.00	143.00	*
Maggness×Kieffer	44	98.45^{C-I}±11.45	82.00	117.00	11.63	240.55^{B-A}±1.69	220.00	258.00	11.21	143.09^{B-A}±1.79	105.00	170.00	11.90
Maggness×Santa Maria	138	100.88^{C-E}±11.43	86.00	118.00	11.33	233.29^{A-G}±1.25	196.00	261.00	14.66	133.41^{A-E}±1.07	99.00	168.00	12.52
Maggness×Conference	17	92.71^{NO}±6.60	87.00	110.00	7.12	222.88^{C-J}±1.72	210.00	241.00	7.08	131.18^{A-F}±1.87	118.00	149.00	7.72
Maggness×Kaiser	10	96.10^{HM}±7.20	89.00	115.00	7.49	227.70^{B-H}±4.36	195.00	241.00	13.78	132.60^{A-E}±4.84	103.00	153.00	15.31
Maggness×Ankara	107	99.24^{C-H}±11.19	85.00	117.00	11.27	237.72^{A-D}±0.93	184.00	262.00	9.64	139.48^{A-C}±1.34	93.00	174.00	13.85
Maggness×Moonglow	1	112.00^{A}±*	112.00	112.00	*	232.00^{A-G}±*	232.00	232.00	*	121.00^{D-I}±×	121.00	121.00	*
Maggness×Taş	39	98.28^{D-J}±1.76	86.00	113.00	11.02	232.72^{A-G}±2.44	202.00	273.00	15.26	135.44^{A-D}±2.54	101.00	164.00	15.88
Maggness×Limon	15	99.53^{C-G}±3.09	88.00	116.00	11.98	234.40^{A-G}±2.21	218.00	245.00	8.56	135.87^{A-D}±3.05	117.00	152.00	11.82

N: Number of plants, NDBH: Number of days from full bloom to harvest, C.V: Coefficient of variation

CONCLUSIONS AND RECOMMENDATIONS

All examined traits exhibited polygenic inheritance. High heritability levels were observed for phenological traits, moderate for morphological traits, and low for pomological and chemical traits. The heritability of full bloom time (31%) was found to be significantly lower than that of harvest time (83%) and the duration from full bloom to harvest (86%). With global climate change, the duration and severity of late spring frosts have increased in recent years, making the selection of genotypes suited to specific regions more critical. Therefore, late-blooming genotypes, as well as early or late-maturing genotypes, will undoubtedly gain importance. For late blooming, the parent variety 'Maggness' and the pollinator variety 'Akça' are recommended for breeding programs.

One of the most striking results of the study is the demonstrated importance of gene interactions between parents due to their specific combining abilities. Among the study material, the 'Williams×Conference' hybrids, which bloom after the 100th day of the year and complete their development in approximately 150 days, showed promise for breeding late-blooming, late-maturing genotypes. Similarly, the 'Santa Maria×Akça' combination, which blooms late but requires less than 100 days from full bloom to harvest, was found highly promising for the development of late-blooming, early-maturing genotypes.

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