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HETEROSIS AND DIALLEL ANALYSIS OF YIELD AND YIELD COMPONENTS OF BREAD WHEAT F_1 GENERATION

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Abstract: In this study, half-diallel crosses were performed using six wheat genotypes (Adana-99, Flamura-85, Masaccio, Lucilla, 1635 and 2115). This research was conducted in Kahramanmaras ecological conditions during the 2019-2020 growing season in a randomized complete block design with three replications. Heading date (HD), grain filling period (GFP), days to maturity (DM), plant height (PH), spike length (SL), grain number per spike (GNS), grain weight per spike (GWS), thousand kernel weight (TKW), grain yield per plant (GY), and chlorophyll content of flag leaf (SPAD value) traits were investigated on F_1 plants and parents. When the mean values of parents and F_1 generations were examined, F_1 mean values were higher than the mean values of parents in heading date (134.06 days), days to maturity (164.04 days), spike length (13.31 cm), grain number per spike (51.64 units), grain weight per spike (2.11 g), thousand-grain weight (36.58 g), grain yield per plant (35.99 g), and chlorophyll content of flag leaf (49.60 SPAD), while lower in grain filling period (41.77 days) and plant height (88.80 cm). According to diallel analyses, it was found that HD, DM, GFP, PH, GWS, and SPAD traits had additive and dominant gene effects, while SL, GNS, TKW, and GY traits had significant dominant gene effects. Partial dominance was observed for HD, DM, PH, GWS, GY, and SPAD traits, while superior dominance was observed for GFP, SL, GNS, and TKW traits. The effects of general combining ability (GCA) and specific combining ability (SCA) were significant for all the traits studied. Positive average heterosis and heterobeltiosis values were determined for GNS, GWS, TKW, and GY traits. In terms of grain yield per plant, the genotypes Adana-99, Lucilla, and Masaccio were identified as potential parents for breeding programs. Combinations of 1635 × 2115, Masaccio × Lucilla, Adana-99 × Lucilla, Adana-99 × Masaccio, Adana-99 × 1635, and Flamura-85 × Lucilla were identified as promising hybrids for grain yield.

Keywords: Bread wheat, Diallel analysis, Combining ability, Heterosis, Heterobeltiosis, Inheritance

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1. Introduction

Wheat plays a fundamental role in human nutrition and is strategically vital for food security; therefore, with the global population increase, improving the yield per unit area is crucial to ensure sufficient and balanced nutrition. In Türkiye, various studies are conducted to improve the quality and productivity of bread wheat, and new varieties and technologies are being developed to enhance both quantity and quality of production. However, breeding programs also need to develop commercial varieties that adapt to changing climate conditions; hence, lines derived from high-performance genotypes (Bayhan et al., 2023). Plant breeders create variations in genetic material by making crosses to develop varieties suitable for their objectives. Parents and hybrid offsprings in recently developed hybrid populations are evaluated for agronomic traits at early stages, and those with superior characteristics are selected. The average values obtained for the parents' features are essential in predicting hybrid performance and selecting superior parents (Poehlman and Sleeper, 1995). Various methods such as diallel, partial diallel, and line x tester are used for parent selection in hybrid breeding, however the diallel analysis is the most commonly preferred method. Diallel analysis is used to examine the genetic structures of hybrid populations using data obtained from the F_1 generation, determining promising hybrid combinations and parents' general and specific combining abilities (Sing and Chaudhary, 1985). The heterosis concept is utilized to determine the hybrid performance of parents. A high heterosis value is preferred in identifying high-yielding and high-quality hybrid genotypes (Knott, 1965). Heterosis (Ht) refers to the superiority of the F_1 hybrid over the average of parents when two pure lines are crossed. At the same time, heterobeltiosis (Hb) indicates the superiority of the F_1 hybrid over the superior parent (Dumlupinar et al., 2015). The performance of a genotype in the hybridization sequence is defined as a general combining ability.

In contrast, the superiority of hybrid performance between specific genotype pairs is expressed as specific combining ability (Yildirim and Cakir, 1986). General combining ability reflects additive gene effects, while specific combining ability reflects non-additive, dominant and epistatic gene effects (Falconer, 1980). While aiming to develop any trait, the most helpful information for the breeder is to detect the ability of the considered varieties to be parents and the genetic variance that the hybrid population generated from them may have in early generations (Sener et al., 2000). Knowing the inheritance degrees of the selected traits of parents according to the purpose, eliminates the unnecessary combinations and provides insight into which generation to start selection (Toklu and Yagbasanlar, 2005).

This study was aimed to investigate the inheritance of yield and yield components on F_1 combinations obtained from half-diallel crosses among six bread wheat genotypes to determine inheritance degrees and heterosis values to identify general and specific combining abilities, and to select promising hybrid combinations and suitable parents.

2. Materials and Methods

This research was conducted during the 2019-2020 growing season in the Kahramanmaraş ecological conditions. The total precipitation during the 2019-2020 growing season was recorded as 492.10 mm, with an average temperature of 13.66 °C (Table 1). The experiment was conducted in a clay-loam, slightly alkaline, high lime content, salt-free soil with low organic matter, P_2O_5, and Mn content, high K_2O_5 content, and medium Ca, Mg, and Fe content, while Cu and Zn content were at sufficient levels (Table 2).

The study utilized six bread wheat genotypes (Adana-99, Flamura-85, Masaccio, Lucilla, 1635, and 2115) and 15 F_1 combinations obtained using the half diallel analysis method. F_1 seeds and parents were sown on December 22, 2019, in a randomized complete block design with three replications. Plant rows spaced 20 cm apart, 10 cm between two plants and 1 meter long of two rows, as a total plot size of 2 m^2. At the sowing, 80 kg ha^{-1} of phosphorus (P_2O_5) and 80 kg ha^{-1} of nitrogen (N) in the form of 20-20-0, and 100 kg ha^{-1} of nitrogen from 33% ammonium nitrate (NH_4NO_3) as top dressing were applied as fertilizer. Weed control was performed chemically on March 10, 2020, during tillering, and the trial was conducted on rainfed conditions. Harvest was done manually on May 13, 2020 with sickle.

In the study, heading date, grain filling period, days to maturity, plant height, spike length, grain number per spike, grain weight per spike, thousand kernel weight, and chlorophyll content of flag leaf were calculated for the selected ten plants. The grain yield was calculated as per plant.

Table 1. Means of climate data of trial year and long years

Months	Precipitation (mm)		Temperature (°C)	
	2019-20	Long Years	2019-20	Long Years
November	39.10	72.28	13.50	12.06
December	198.50	131.88	8.40	7.31
January	88.00	112.15	6.30	5.42
February	72.70	106.58	6.10	7.62
March	173.40	97.74	12.50	12.00
April	61.80	58.56	15.90	16.25
May	18.50	39.66	21.60	20.41
Jun	4.10	6.71	25.00	25.99
Total	492.10	625.56		
Mean			13.66	13.38

Table 2. Physical and chemical properties of the trial area

Features	2019-2020	
Saturation	% 58	Clay-Loam
pH	7.75	Slightly Alkalinity
EC $dS.m^{-1}$	0.42	No salinity
$CaCO_3$ %	20.3	High Lime
Organic matter %	0.57	Slightly
P_2O_5 kg da^{-1}	3.38	Low
K_2O kg da^{-1}	47.96	High
Ca (ppm)	10671	Medium
Mg (ppm)	574	Medium
Cu (ppm)	2.16	Sufficient
Fe (ppm)	5.93	Medium
Mn (ppm)	7.52	Low
Zn (ppm)	0.92	Sufficient

Heterosis (Ht) and heterobeltiosis (Hb) were computed utilizing the formula provided in Equations 1 and 2 (Chang and Smith, 1967; Fonseca and Patterson, 1968):

$$Ht(\%) = \frac{F_1 - MP}{MP} 100 \qquad (1)$$

$$Hb(\%) = \frac{F_1 - BP}{BP} 100 \qquad (2)$$

where F_1= value of F_1; MP= mean value of parents and BP= value of better-parent.

Following preliminary variance analysis using the JMP (Kalayci, 2005), diallel tables were created for each block for traits showing statistically significant variance between F_1 hybrids generations and parents, and analyzed (Hayman, 1954a; Aksel and Johnson, 1963).

Variance analyses of diallel tables were performed by writing necessary formulas into the EXCEL computer program based on the diallel variance analysis method suggested by Jones (1965). The estimation of genetic variance components through diallel hybrid analysis and the analysis of combining abilities were conducted using the statistical package program TARPOPGEN developed by Ozcan (1999) based on the method proposed by Jinks-Hayman (1953), Jinks (1954), and Hayman (1954b, 1958); while the analysis of combination abilities was performed according to Griffing's (1956) Method II and Model I, which include parents.

3. Results and Discussion

The average phenotypic values for the examined traits are presented in Table 3, while the heterosis (Ht) and heterobeltiosis (Hb) values (%) are shown in Table 4. The values for genetic parameters calculated for each trait are provided in Table 5, and the general and specific combining ability effects of parents and hybrids are presented in Tables 6 and 7.

Table 3. Mean values of agronomic traits from parents and F_1 crosses

Parental Genotypes / Crosses	HD	GFP	DM	PH	SL	GNS	GWS	TKW	GY	SPAD
Adana 99 (1)	121^{K}	54.66^{B}	159.66^{J}	106.4^{B}	14.76^{B}	59.33^{D}	1.95^{F}	31.13^{JK}	28.49^{FGH}	44.64^{KL}
Flamura-85 (2)	124^{J}	53.33^{C}	167^{B}	92.5^{E}	13.3^{C}	47.9^{G}	2.15^{DE}	40.23^{C}	19.24^{LM}	51.2^{CDE}
Masaccio (3)	121^{K}	53^{C}	161.66^{I}	88.46^{FG}	9.4^{G}	32.5^{J}	1.29^{IJ}	33.86^{H}	23.39^{IJK}	49.93^{EFG}
Lucilla (4)	$131^{G H}$	44.66^{FG}	163.33^{FGH}	90.63^{EF}	11.46^{E}	43.53^{HI}	1.43^{HI}	30.83^{K}	24.56^{IJ}	52.58^{BC}
1635 (5)	139^{C}	38.33^{J}	164.33^{CDEF}	121.56^{A}	13.33^{C}	31.73^{J}	1.12^{JK}	35.23^{FG}	22.49^{JKL}	40.8^{M}
2115 (6)	141^{B}	34.66^{K}	165.33^{C}	102.96^{C}	11.53^{DE}	33.56^{J}	1.04^{K}	28.93^{L}	15.75^{N}	43.15^{L}
1x2	128.66^{I}	61^{A}	177^{A}	81.16^{HI}	15.76^{A}	89.06^{A}	4.11^{A}	46.8^{A}	29.68^{FGH}	51.46^{CDE}
1x3	133.66^{F}	40.66^{I}	159.66^{J}	82.3^{H}	16.03^{A}	60.13^{D}	2.45^{BC}	41.36^{B}	45.7^{D}	49.2^{FG}
1x4	130^{H}	44.33^{G}	160^{J}	81.3^{HI}	16.26^{A}	69.76^{B}	2.58^{B}	38.73^{D}	55.98^{B}	47.37^{HI}
1x5	133.33^{F}	41^{I}	164^{DEFG}	90.23^{EF}	10.46^{F}	54.83^{E}	2.05^{EF}	35.66^{F}	37.74^{E}	46.39^{IJ}
1x6	131.66^{G}	42.66^{H}	162.66^{HI}	107.13^{B}	12^{DE}	56.16^{E}	2.2^{DE}	38.63^{D}	29.99^{F}	46.64^{IJ}
2x3	130.33^{H}	45.66^{F}	165.33^{C}	90.93^{EF}	15.76^{A}	64^{C}	2.55^{B}	41.43^{B}	30.88^{F}	50.88^{DE}
2x4	127.66^{I}	48.66^{D}	165^{CD}	89.23^{F}	13.43^{C}	53.23^{EF}	2.18^{DE}	38.66^{D}	49.53^{C}	53.88^{B}
2x5	137.66^{D}	38^{J}	166^{B}	102.73^{C}	10.43^{F}	45.3^{GH}	1.65^{G}	32.8^{I}	25.65^{HIJ}	48.38^{GH}
2x6	136.33^{E}	38.66^{J}	164.66^{CDE}	97.53^{D}	11.96^{DE}	41.96^{I}	1.42^{HI}	37^{E}	16.68^{MN}	45.56^{JK}
3x4	128^{I}	47.33^{E}	159.66^{J}	86.66^{G}	14.63^{B}	64.16^{C}	2.26^{CD}	34.63^{GH}	64.14^{A}	52.08^{CD}
3x5	127.66^{I}	44.66^{FG}	160^{J}	107.43^{B}	14.43^{B}	51.33^{F}	1.71^{G}	30.93^{K}	26.13^{HI}	48.54^{GH}
3x6	139^{C}	35.33^{K}	163.66^{EFGH}	79.7^{I}	12.26^{D}	45.83^{GH}	1.44^{HI}	31.96^{IJ}	26.4^{GHI}	51.4^{CDE}
4x5	140.66^{B}	35^{K}	164.66^{CDE}	82.03^{HI}	11.83^{DE}	51.43^{F}	1.54^{GH}	30.13^{K}	20.57^{KL}	45.45^{JK}
4x6	150^{A}	25^{L}	163^{GH}	47.43^{J}	10.16^{F}	31.6^{J}	1.21^{JK}	31^{JK}	15.3^{N}	56.47^{A}
5x6	136.33^{E}	38.66^{J}	165.33^{C}	106.23^{B}	14.2^{B}	55.83^{E}	2.25^{D}	39^{D}	65.5^{A}	50.23^{EF}
F_1 mean values	134.06	41.77	164.04	88.80	13.31	55.64	2.11	36.58	35.99	49.60
Parental mean values	129.50	46.44	163.55	100.42	12.30	41.43	1.50	33.37	22.32	47.05
General mean values	126.14	41.42	156.11	88.33	12.43	49.40	1.86	34.14	30.83	46.42

HD= heading date, GFP= grain filling period, DM= days to maturity, PH= plant height, SL= spike length, GNS= grain number per spike, GWS= grain weight per spike, TKW= thousand kernel weight, GY= grain yield per plant, and SPAD= chlorophyll content of flag leaf.

Table 4. Heterosis (Ht) and heterobeltiosis (Hb) values (%) for all studied traits

Crosses		HD	GFP	DM	PH	SL	GNS	GWS	TKW	GY	SPAD
1x2	Hb	5.02	12.62	8.25	-18.41	12.33	66.12	100.48	31.16	24.30	7.38
	Ht	3.75	11.59	5.77	-23.72	6.77	50.10	91.16	16.33	4.17	0.50
1x3	Hb	10.16	-24.46	-0.62	-15.52	32.70	30.97	51.23	27.29	76.10	4.06
	Ht	9.86	-25.61	-1.23	-22.65	8.60	1.34	25.64	22.14	60.42	-1.46
1x4	Hb	-4.05	-10.73	-0.92	-17.47	24.02	35.66	52.66	25.01	128.30	-2.55
	Ht	-13.33	-18.89	-2.03	-23.59	10.16	17.60	32.30	24.41	96.55	-9.90
1x5	Hb	2.56	-11.82	1.23	-20.83	-25.49	20.42	33.98	7.50	48.11	8.60
	Ht	-4.07	-24.99	0.20	-25.77	-29.13	-7.58	5.12	1.25	32.51	3.92
1x6	Hb	0.50	-4.47	0.09	2.34	-8.67	20.90	47.65	28.63	35.63	6.26
	Ht	-6.62	-21.95	-1.61	0.68	-18.70	-5.34	12.82	24.09	5.30	4.48
2x3	Hb	5.83	-14.38	0.50	0.46	38.85	59.20	48.25	11.82	44.86	0.63
	Ht	5.10	-14.90	-1.19	-1.76	18.22	33.61	18.60	2.98	31.97	-0.62
2x4	Hb	-6.81	-1.01	-0.20	-2.58	8.30	16.45	21.78	8.83	148.84	3.83
	Ht	-14.89	-10.17	-1.40	-3.60	0.75	11.12	1.40	-3.87	140.85	2.47
2x5	Hb	4.68	-17.39	0.50	-4.04	-21.75	13.80	1.23	-13.06	22.96	5.17
	Ht	-0.96	-29.18	-0.40	-15.50	-21.75	-5.42	-23.25	-18.46	14.05	-5.50
2x6	Hb	2.89	-12.45	-1.00	-0.23	-3.78	3.01	-11.25	6.99	-4.68	-3.41
	Ht	-3.31	-27.95	-1.59	-5.27	-10.27	-12.40	-33.95	-8.02	-0.54	-11.01
3x4	Hb	-5.76	-3.07	-1.74	-3.2	40.26	68.8	66.17	7.04	191.89	1.61
	Ht	-14.66	-10.69	-2.24	-4.36	27.66	47.4	58.04	2.24	174.17	-0.95
3x5	Hb	-2.04	-2.19	-1.84	2.3	27.02	59.85	42.5	-10.47	14.00	7.01
	Ht	-8.15	-15.73	-2.63	-11.62	8.25	57.93	32.55	-12.2	11.71	-2.78
3x6	Hb	5.84	-19.39	0.09	-16.72	17.3	38.75	25	1.81	34.9	10.44
	Ht	-1.41	-33.33	-1.01	-22.6	6.41	36.52	12.4	-5.6	12.86	2.94
4x5	Hb	-2.65	-15.66	0.5	-22.68	-4.6	36.67	22.04	-8.78	-4.46	-2.65
	Ht	-6.22	-21.63	0.2	-32.51	-11.25	18.14	8.4	-14.47	-8.58	-13.56
4x6	Hb	3.09	-36.96	-0.8	-51	-11.65	-18.02	-1.62	3.74	-15.75	17.99
	Ht	0	-44.02	-1.4	-53.93	-11.88	-27.4	-15.38	0.55	-25.63	7.4
5x6	Hb	-2.62	5.91	0.3	-5.37	14.23	70.99	108.33	20.54	242.57	19.68
	Ht	-3.31	0.86	0	-12.61	6.52	66.3	100.9	9.76	191.24	16.4
Mean	Ht	1.11	-10.36	0.29	-11.53	9.27	34.90	40.56	9.87	65.84	5.60
	Hb	-3.88	-19.11	-0.70	-17.25	-0.64	18.79	21.78	2.74	49.40	-0.51

Ht= heterosis value (%), Hb= heterobeltiosis value (%). P(1)= Adana-99, P(2) = Flamura-85, P(3)= Masaccio, P(4)= Lucilla, P(5)= 1635, P(6)= 2115. HD= heading date, GFP= grain filling period, DM= days to maturity, PH= plant height, SL= spike length, GNS= grain number per spike, GWS= grain weight per spike, TKW= thousand kernel weight, GY= grain yield per plant and SPAD= chlorophyll content of flag leaf.

Table 5. Genetic parameters for investigated traits

Genetic Parameters	HD	GFP	DM	PH	SL	GNS	GWS	TKW	GY	SPAD
a	123.46**	167.51**	23.87**	350.43**	350.43**	350.40**	0.88**	37.11**	120.54**	29.32**
b	26.75**	33.62**	11.13**	192.16**	192.16**	147.11**	0.34**	17.03**	271.70**	9.20**
b_1	89.21**	93.30**	1.02	578.37**	578.37**	866.07**	1.59**	44.24**	801.02**	27.76**
b_2	6.05**	6.18**	9.53**	89.71**	89.71**	50.14**	0.14**	22.32**	31.54**	4.34**
b_3	31.31**	42.24**	13.14**	206.15**	206.15**	121.10**	0.32**	11.07**	346.30**	9.84**
E	0.175	0.18	0.18	0.81	0.07	1.26	0.01	0.13	1.45	0.32
D	77.837*	73.31*	7.39	159.34	3.651	121.60	0.21	16.66	19.62	23.31
F	26.552	-9.966	-0.83	38.26	5.921	-39.07	-0.21	12.53	-35.30	14.05
H_1	99.605	127.53*	48.90	748.14	20.277	519.81	1.32	74.08*	1018.37	37.12
H_2	136.54*	188.39*	52.71	817.83	17.216	627.53*	1.59	71.98*	1050.78	42.64
$(D-H_1)$	-21.77	-54.21	-41.50	-588.84	-16.626	-398.22	-1.11	-57.42	-998.74	-13.81
$(H_1/D)^{1/2}$	1.131	1.319	2.57	2.17	2.357	2.07	2.51	2.109	7.20	1.26
$(H_2/4H_1)$	0.343	0.369	0.27	0.27	0.212	0.30	0.30	0.24	0.26	0.29
KD/KR	1.355	0.902	0.96	1.12	2.049	0.86	0.66	1.43	0.78	1.63
h^2	55.047	60.40	0.54	375.19	2.801	560.73*	1.04	28.59	518.21	17.79
$K=h^2/H_2$	0.403	0.321	0.01	0.46	0.163	0.89	0.65	0.40	0.49	0.42
Hg	0.976	0.985	0.927	0.97	0.849	0.96	0.94	0.96	0.89	0.85
Hd	0.513	0.347	0.13	0.18	0.200	0.18	0.12	0.21	0.02	0.49
GCA	121.58**	167.50**	25.58**	350.46**	3.932**	350.42**	0.89**	37.12**	120.52**	29.32**
SCA	26.37**	33.64**	10.92**	192.17**	4.51**	147.15**	0.35**	17.03**	271.68**	9.20**
GCA/ SCA	4.61	4.97	2.34	1.82	0.87	2.38	2.55	2.17	0.44	3.18

*, ** significant at 5% and 1% probability levels, respectively; “D”-“a”-“GCA”= measures additive effect, “H_1”-“H_2”-“$(b-b_1-b_2-b_3)$”-“SCA”= measures dominance effect, F= determines frequencies of dominant to recessive alleles in parents, E= shows environment effect, $H_2/4H_1$= determines proportion of genes with positive and negative effects in the parents, $\sqrt{(H_1/D)}$= measures average degree of dominance, (KD/KR)= ratio of the total number of dominant against recessive alleles, GCA= general combining ability, SCA= specific combining ability.

Table 6. GCA and SCA values of HD, GFP, DM, PH and SL for crosses and their parents

Parental Genotypes / Crosses	HD		GFP		DM		PH		SL	
	GCA	SCA	GCA	SCA	GCA	SCA	GCA	SCA	GCA	SCA
Adana 99 (1)	-3.77**		4.65**		-0.63**		1.26**		1.11**	
Flamura-85 (2)	-2.61**		4.61**		3.21**		0.23		0.35**	
Masaccio (3)	-3.44**		2.24**		-2.00**		-2.62**		0.10	
Lucilla (4)	1.09**		-1.51**		-1.08**		-9.62**		-0.24	
1635 (5)	3.01**		-3.47**		0.21		10.86**		-0.39**	
2115 (6)	5.72**		-6.51**		0.29*		-0.12		-0.94**	
1x2		2.26**		8.63**		10.46**		-12.45**		1.28**
1x3		8.09**		-9.33**		-1.66**		-8.47**		1.80**
1x4		-0.11		-1.92**		-2.24**		-2.46**		2.37**
1x5		1.30**		-3.29**		0.46		-14.01**		-3.28**
1x6		-3.07**		1.42**		-0.95**		13.87**		-1.20**
2x3		3.59**		-4.29**		0.17		1.19**		2.30**
2x4		-3.6**		2.46**		-1.08**		6.50**		0.30
2x5		4.47**		-6.25**		-0.70*		-0.49		-2.55**
2x6		0.42		-2.54**		-2.79**		5.29**		-0.47
3x4		-2.4**		3.50**		-1.20**		6.77**		1.75**
3x5		-4.65**		2.79**		-2.16**		7.06**		1.70**
3x6		3.92**		-3.50**		1.42**		-9.70**		0.08
4x5		3.76**		-3.13**		1.59**		-11.34**		-0.56
4x6		10.38**		-10.08**		-0.16		-34.95**		-1.68**
5x6		-5.19**		5.54**		0.88**		3.36**		2.50**

*, ** significant at 5% and 1% probability levels, respectively; HD= heading date, GFP= grain filling period, DM= days to maturity, PH= plant height, SL= spike length.

Table 7. GCA and SCA values of GNS, GWS, TGW, GY and SPAD for crosses and their parents

Parental Genotypes / Crosses	GNS		GWS		TKW		GY		SPAD	
	GCA	SCA	GCA	SCA	GCA	SCA	GCA	SCA	GCA	SCA
Adana 99 (1)	10.94**		0.47**		1.73**		3.93**		-1.47**	
Flamura-85 (2)	3.54**		0.34**		3.44**		-4.21**		1.31**	
Masaccio (3)	-1.33**		-0.07		-0.20		1.93**		1.23**	
Lucilla (4)	-0.48**		-0.11		-1.85**		3.76**		2.29**	
1635 (5)	-4.86**		-0.26		-1.33**		-0.50**		-2.69**	
2115 (6)	-7.82**		-0.37**		-1.78**		-4.90**		-0.68**	
1x2		23.00**		1.37**		5.97**		-2.13**		2.75**
1x3		-1.07**		0.11		4.18**		7.75**		0.56
1x4		7.72**		0.30		3.20**		16.21**		-2.32**
1x5		-2.83**		-0.09		-0.39		2.23**		1.67**
1x6		1.46**		0.16		3.02**		-1.12**		-0.08
2x3		10.21**		0.35		2.53**		1.07		-0.53
2x4		-1.41**		0.03		1.42**		17.90**		1.41**
2x5		-4.95**		-0.36		-4.97**		-1.71**		0.89**
2x6		-5.33**		-0.49		-0.33		-6.29**		-3.94**
3x4		14.39**		0.51		1.02**		26.37**		-0.32
3x5		5.94**		0.11		-3.20**		-7.38**		1.12**
3x6		3.40**		-0.06		-1.73**		-2.71**		1.98**
4x5		5.19**		-0.02		-2.35**		-14.70**		-3.02**
4x6		-11.69**		-0.24		-1.04**		-15.64**		5.99**
5x6		16.93**		0.95**		6.44**		38.82**		4.73**

*, ** significant at 5% and 1% probability levels, respectively; GNS= grain number per spike, GWS= grain weight per spike, TKW= thousand kernel weight, GY= grain yield per plant, and SPAD= chlorophyll content of flag leaf.

3.1. Heading Date

In the study, the average heading date for parents was 129.50 days, while the average for F_1 hybrid combinations was 134.06 days. Among the parents, the longest heading date was observed in the genotype 2115 (141.0 days), while the shortest heading date was obtained from the genotypes Adana-99 and Masaccio (121.0 days). Among the hybrids, the longest heading date was measured in the hybrid Lucilla × 2115 (150 days), while the shortest heading date was recorded in the combinations Flamura-85 × Lucilla and Masaccio × 1635 (127.66 days) (Table 3). Heterosis values for heading date ranged from -6.81% (Flamura-85 × Lucilla) to 10.16% (Adana-99 × Masaccio), while heterobeltiosis values varied from -14.89% (Flamura-85 × Lucilla) to 9.86% (Adana-99 × Masaccio) (Table 4). In terms of heading date, an average heterosis of 1.11% and an average heterobeltiosis of -3.88% were obtained in the hybrid populations (Table 4). Diallel variance components a, b, b_1, b_2, and b_3 were significant for heading date in the study. Among the calculated genetic parameters for heading date, additive gene variance (D) and dominance variance corrected for gene distribution (H_2) were significant at 0.05. The significance of D and H_2 and the negative value of D-H_1 highlight the importance of dominant gene effects in heading date. The fact that the square root of the mean dominance degree $(H_1/D)^{1/2}$ is greater than 1 (1.131) indicates the presence of overdominance. The difference in the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.343) suggests unequal frequencies. Additionally, the ratio of dominant to recessive alleles (KD/KR) greater than 1 (1.355) supports the predominance of dominant alleles. However, as the value of K = (h^2/H_2) is below 1 (K = 0.403), the adequate number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.976 and 0.513, respectively. The ratio of general combining ability to specific combining ability greater than 1 indicates the superiority of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effects were obtained from the parents 2115 (5.72) and 1635 (3.01), while the lowest were from the parents Adana-99 (-3.77) and Masaccio (-3.44). The highest specific combining ability effect was obtained from the hybrid Lucilla × 2115 hybrids (10.38), while the hybrids showing the lowest specific combining ability effects were the combinations 1635 × 2115 (-5.19), Masaccio × 1635 (-4.69), and Flamura-85 × Masaccio (-3.61) (Table 6). For heading date, the significance of both additive and dominant gene variance, epistatic effects, and the inability to determine the adequate gene pair number suggest that selection for this trait should be deferred to later generations. Tulukcu (2004) identified dominant gene effects as dominant in the inheritance of heading date, whereas Nazeer et al.

(2004) and Akram et al. (2008) stated that additive gene effects were dominant. Sharma et al. (2002) found that dominant and additive gene effects control heading date.

3.2. Grain Filling Period

In the research, the average grain-filling period for parents was 46.44 days, whereas it was 41.77 days for F_1 hybrid combinations. Among the parents, the highest grain filling period was observed in the genotype Adana-99 (54.66 days), while the lowest was obtained from the genotype 2115 (34.66 days). Among the hybrids, the highest grain-filling period was recorded in the hybrid Adana-99 × Flamura-85 (61 days), whereas the lowest grain-filling period was found in the hybrid Lucilla × 2115 (25 days) (Table 3). Heterosis values for the grain filling period in F_1 hybrid populations ranged from -36.96% (Lucilla × 2115) to 12.62% (Adana-99 × Flamura-85), while heterobeltiosis values varied from -44.02% (Lucilla × 2115) to 11.59% (Adana-99 × Flamura-85) (Table 4). An average heterosis of -10.36% and an average heterobeltiosis of -19.11% was determined for the grain-filling period in the hybrid populations (Table 4). Significant diallel variance components a, b, b_1, b_2, b_3 were found for the grain filling period in the study. Among the calculated genetic parameters for the grain filling period, additive gene variance (D), dominance gene variance (H_1), and dominance gene variance corrected for gene distribution (H_2) were found to be significant at the 0.05 level. According to the diallel hybrid analysis, the significance of additive gene variance (D) and dominance variance (H_1 and H_2), along with the negative value of D-H_1, emphasizes the importance of dominant gene effects in the manifestation of the grain-filling period. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (1.319) indicates the presence of overdominance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.369) suggests unequal frequencies of dominant and recessive alleles in the parents. The negative F value determines the direction of dominant and recessive alleles (-9.966), and the KD/KR ratio is less than 1, which indicates the predominance of recessive alleles. Since the value of $K = (h^2/H_2)$ is below 1 ($K = 0.321$), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.985 and 0.347, respectively. The ratio of general combining ability to specific combining ability (4.97) was calculated to be greater than 1. This ratio above 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effects were obtained from the parents Adana-99 (4.653) and Flamura-85 (4.611), while the lowest were from the parents 2115 (-6.514) and 1635 (-3.472). The highest specific combining ability effect was obtained from the combination Adana-99 × Flamura-85 (8.625). The hybrid showing the lowest specific combining ability effects was the combination Lucilla × 2115 (-10.08) (Table 6). For the grain-filling period, the significance of both additive and dominance variance, the inability to determine the effective gene pair number, and the moderately low narrow-sense heritability suggest that selection for this trait should be deferred to later generations. Kutlu (2012) and Celik (2016) have also found similar results. The significance of additive and dominance gene variance, the inability to determine the adequate gene pair number, and the moderately low narrow-sense heritability suggest that selection for this trait should be deferred to later generations.

3.3. Days to Maturity

In the study, the average days to maturity were 163.55 for the parents and 164.04 for the F_1 hybrids. Among the parents, the highest DM was observed in the genotype Flamura-85 genotype (167 days), while the lowest DM was obtained from the genotype Adana-99 (159.66 days). Among the hybrids, the highest DM was recorded in the hybrid Adana-99 × Flamura-85(177 days). In contrast, the lowest DM was 159.66 days in the combinations Adana-99 × Masaccio and Masaccio × Lucilla (Table 3). Heterosis values for DM in F_1 hybrid populations ranged from -1.84% (Masaccio × 1635) to 8.25% (Adana-99 × Flamura-85), while heterobeltiosis values varied from -2.63% (Masaccio × 1635) to 5.77% (Adana-99 × Flamura-85) (Table 4). Regarding the DM, an average heterosis of 0.29% and an average heterobeltiosis of -0.7% were determined for the hybrid populations (Table 4). In the half-diallel variance analysis table for the studied population, additive variance (a), dominance variance (b), and its components (b_2, b_3) were found to be significant. In the half-diallel hybrid analysis, all genetic parameters were found to be insignificant, and it was observed that D-H_1 was negative. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.572) indicates the presence of overdominance. The negative value of the difference between additive and dominance variance (D-H_1) indicates that dominance gene variance is more significant than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.269) is consistent with the significance of the b_2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The negative F value determining the direction of dominant and recessive alleles (-0.825) and the KD/KR ratio less than 1 (0.958) suggest that recessive alleles are predominant. Since the value of $K = (h^2/H_2)$ is below 1 ($K = 0.01$), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.927 and 0.128, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (2.34) was calculated to be greater than 1. This ratio above 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effect was obtained from the parent Flamura-85 (3.208), while the lowest was from the parent Masaccio (-2.0). The highest specific combining ability effect was obtained from the combination Adana-99 × Flamura-85 (10.464), and the phenotypic value obtained from this combination was the highest (177 days). The hybrids showing the lowest specific combining ability effects were the combinations Flamura-85 × 2115 (-2.786) (Table 6). For DM, the significance of both additive and dominance variance, the inability to determine the effective gene pair number, and the fit of the inheritance of the trait to the additive-dominant model can be expressed. Hammad et al. (2013) and Celik (2016) have also found similar results. Our findings align with previous studies, and Hammad et al. (2013) reported that specific combining ability is positive.

3.4. Plant Height

In the investigation, the average plant height for parents was 100.42 cm, while it was 88.80 cm for F_1 hybrid combinations. The average plant height for F_1 hybrid combinations was lower than for parents. Among the parents, the highest plant height was observed in the genotype 1635 (121.56 cm), while the lowest plant height was obtained from the genotype Masaccio (88.46 cm). Among the hybrids, the highest plant height was recorded at 107.43 cm in the hybrid Masaccio × 1635, whereas the lowest plant height was 47.43 cm in the hybrid Lucilla × 2115 (Table 3). Heterosis values for plant height in F_1 hybrid populations ranged from -51% (Lucilla × 2115) to 2.34% (Adana-99 × 2115), while heterobeltiosis values varied from -53.93% (Lucilla × 2115) to 0.68% (Adana-99 × 2115). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Flamura-85 as the parent (Ht: -4.96%, Hb: -9.97%), while the lowest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Lucilla as the parent (Ht: -19.39%, Hb: -23.60%). Average heterosis of -11.53% and heterobeltiosis of -17.25% were determined for plant height in hybrid populations (Table 4). Components a, b, b_1, b_2, and b_3 were significant in the diallel variance analysis for plant height. Additive gene variance (D), dominant gene variance (H_1), genes' distribution corrected dominant gene variance (H_2), and environmental variance (E) were found to be insignificant for plant height. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.167) indicates the presence of overdominance. The negative difference between additive and dominance variance ($D-H_1$) suggests that dominant gene variance is more remarkable than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.273) is consistent with the significance of the b2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The positive F value determining the direction of dominant and recessive alleles (38.258) and the KD/KR ratio greater than 1 (1.117) suggest that dominant alleles are predominant. Since the value of K = (h^2/H_2) is below 1 (K = 0.459), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.969 and 0.183, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (1.82) was calculated to be greater than 1. This ratio greater than 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effect was obtained from the parent 1635 (10.864), while the lowest was from the parent Lucilla (-9.619). The highest specific combining ability effect was obtained from the combination Adana-99 × 2115 (13.866) and the combination Masaccio × 1635 (7.058), while the hybrids showing the lowest specific combining ability effects were the combination Lucilla × 2115 (-34.95) (Table 6). There is a complete similarity in the significance of the additive (a, GCA) and dominant (b, b_2, b_3, SCA) gene effect components obtained by the two evaluation methods. This contradictory situation arises from non-allelic gene interactions. For plant height in the population, both additive and dominance variance were found to be effective, indicating that the inheritance of the trait fits the additive-dominant model. Similar results have also been found by Akgun and Topal (2002). The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.167) indicates the presence of overdominance. In this study, the significance of both additive and dominance variance for plant height, epistatic effects, the inability to determine the effective gene pair number, and the low narrow-sense heritability suggest that the selection planned for this trait should be postponed to future generations.

3.5. Spike Length

In the study, the average spike length for parents was 12.30 cm, while it was 13.31 cm for F_1 hybrid combinations. Among the parents, the highest spike length was observed in the genotype Adana-99 (14.76 cm), while the lowest spike length was obtained from the genotype Masaccio (9.4 cm). Among the hybrids, the highest spike length was recorded at 16.26 cm in the hybrid Adana-99 × Lucilla, whereas the lowest spike length was 10.16 cm in the combination Lucilla × 2115 (Table 3). Heterosis values for spike length in F_1 hybrid populations ranged from -25.49% (Adana-99 × 1635) to 40.26% (Masaccio × Lucilla), while heterobeltiosis values varied from -29.13% (Adana-99 × 1635) to 27.66% (Masaccio × Lucilla). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Masaccio as the parent (Ht: 31.23%, Hb: 13.83%), while the lowest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype 1635 as the parent (Ht: -2.12%, Hb: -9.47%). Average heterosis of 9.27% and heterobeltiosis of 0.64% were determined for spike length in hybrid populations (Table 4). Components a, b, b_1, b_2, and b_3 were significant in the diallel variance analysis for spike length. Additive gene variance (D), dominant gene variance (H_1), genes' distribution corrected dominant gene variance (H_2), and environmental variance (E) were found to be insignificant for spike length. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.357) indicates the presence of overdominance. The negative difference between additive and dominance variance (D-H_1) suggests that dominant gene variance is more significant than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.212) is consistent with the significance of the b_2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The positive F value determining the direction of dominant and recessive alleles (5.921) and the KD/KR ratio greater than 1 (2.049) suggest that dominant alleles are predominant. Since the value of K = (h^2/H_2) is below 1 (K = 0.163), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.849 and 0.2, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (0.87) was calculated to be less than 1. This ratio of less than 1 indicates the superiority and importance of specific combining ability and, consequently, non-additive gene variance (Table 5). The highest general combining ability effect was obtained from the parent Adana-99 (1.114), while the lowest was from the parent 2115 (-0.936). The highest specific combining ability effect was obtained from the combination 1635 × 2115 (2.504) and the combination Adana-99 × Lucilla (2.367), while the hybrids showing the lowest specific combining ability effects were the hybrid Adana-99 × 1635 (-3.279) (Table 6). According to the results of three evaluation methods, the negative value of D-H_1, the low value of narrow-sense heritability (0.2), and the GCA/SCA ratio less than 1 (0.87) indicate the dominance of dominant variance for this trait. For this trait, Balci and Turgut (2002), Sharma et al. (2002), Bao et al. (2009) reported the dominance of additive gene variance; Yagdi and Ekingen (1995) reported the dominance effect; Khan et al. (2010), Nazeer et al. (2011) reported the superiority and importance of both additive and non-additive gene variance. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.357) indicates the presence of overdominance. In this study, the significance of dominant gene variance for spike length, epistatic effects, the inability to determine the effective gene pair number, and the low narrow-sense heritability suggest that the selection planned for this trait should be postponed to future generations.

3.6. Grain Number per Spike

In the research, the average grain number per spike for parents was 41.43, while 55.64 for F_1 hybrid combinations. Among the parents, the highest grain number per spike was observed in the genotype Adana-99 (59.33), while the lowest grain number per spike was obtained from the genotype 1635 (31.73). Among the hybrids, the highest grain number per spike was recorded at 89.06 in the hybrid Adana-99 × Flamura-85, whereas the lowest grain number per spike was 31.6 in the hybrid Lucilla × 2115 (Table 3). Heterosis values for grain number per spike in F_1 hybrid populations ranged from -18.02% (Lucilla × 2115) to 70.99% (1635 × 2115), while heterobeltiosis values varied from -27.4% (Lucilla × 2115) to 66.3% (1635 × 2115). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Masaccio as the parent (Ht: 51.51%, Hb: 35.36%), while the lowest average heterosis value was obtained from the hybrid series with the genotype 1635 as the parent (Ht: 23.13%), and the heterobeltiosis value was obtained from the hybrid series with the genotype Adana-99 as the parent (Hb: 11.22%). Average heterosis of 34.9% and heterobeltiosis of 18.79% were determined for grain number per spike in hybrid populations (Table 4). In the diallel variance analysis for grain number per spike, components a, b, b_1, b_2, and and b_3 were significant. Genes' distribution corrected dominant gene variance (H_2) and heterozygote locus dominance effect (h^2) were significant at the 0.05 level. In contrast, additive gene variance (D), dominant gene variance (H_1), and environmental variance (E) were found to be insignificant. The insignificance of environmental variance (E) suggests that genetic factors play a more significant role than environmental factors for this trait. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.068) indicates the presence of overdominance. The negative difference between additive and dominance variance (D-H_1) suggests that dominant gene variance is more incredible than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.302) is consistent with the significance of the b_2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The negative F value determining the direction of dominant and recessive alleles (-39.074) and the KD/KR ratio less than 1 (0.856) indicate that recessive alleles are predominant. Since the value of K = (h^2/H_2) is below 1 (K = 0.894), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were 0.955 and 0.177, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (2.38) was calculated to be greater than 1. This ratio greater than 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effect was obtained from the parent Adana-99 (10.944), while the lowest was from the parent 2115 (-7.818). The highest specific combining ability effect was obtained from the Adana-99 × Flamura-85 hybrids (23.004), and the phenotypic values obtained from this combination were also the highest (89.06). The hybrids showing the lowest specific combining ability effects were the Lucilla × 2115 combinations (-11.688), and the phenotypic values for these combinations were phenotypically low (31.6) (Table 7). According to the variance analysis method Hayman (1954) used, both the GCA variance corresponding to additive variance and the SCA variance corresponding to dominance variance were significant. Thus, we can infer that dominance gene variance is dominant for grain number per spike. For this trait, Balci and Turgut (2002), Akram et al. (2011), Yildirim et al. (2014) reported the dominance of additive gene variance; Yagdi and Ekingen (1995) reported the dominance effect; Akgun and Topal (2002) reported the superiority and importance of both additive and non-additive gene variance. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.068) indicates the presence of overdominance for the grain number per spike. In this study, the significance of dominant gene variance for grain number per spike, epistatic effects, the inability to determine the effective gene pair number, and the low narrow-sense heritability suggest that the selection planned for this trait should be postponed to future generations.

3.7. Grain Weight per Spike

In the investigation, the average grain weight per spike for parents was 1.50 g, while it was 2.11 g for F_1 hybrid combinations. The average grain weight per spike of F_1 hybrid combinations was higher than that of the parents. Among the parents, the highest grain weight per spike was observed in the genotype Flamura-85 (2.15 g), while the lowest grain weight per spike was obtained from the genotype 2115 (1.04 g). Among the hybrids, the highest grain weight per spike was recorded at 4.11 g in the hybrid Adana-99 × Flamura-85, whereas the lowest grain weight per spike was 1.21 g in the hybrid Lucilla × 2115 (Table 3). Heterosis values for grain weight per spike in F_1 hybrid populations ranged from -11.25% (Flamura-85 × 2115) to 108.33% (1635 × 2115), while heterobeltiosis values varied from -33.95% (Flamura-85 × 2115) to 100.9% (1635 × 2115). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Adana-99 as the parent (Ht: 57.2%, Hb: 33.41%), while the lowest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Flamura-85 as the parent (Ht: 32.10%, Hb: 10.79%). Average heterosis of 40.56% and heterobeltiosis of 21.78% were determined for grain weight per spike in F_1 hybrid populations (Table 4). Components a, b, b_1, b_2, and b_3 were significant in the diallel variance analysis for grain weight per spike. Additive gene variance (D), dominant gene variance (H_1), genes' distribution corrected dominant gene variance (H_2), heterozygote locus dominance effect (h^2), and environmental variance (E) were found to be insignificant. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.51) indicates the presence of overdominance. The negative difference between additive and dominance variance ($D-H_1$) suggests that dominant gene variance is more significant than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.303) is consistent with the significance of the b_2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The negative F value determining the direction of dominant and recessive alleles (-0.213) and the KD/KR ratio less than 1 (0.662) indicate that recessive alleles are predominant. Since the value of $K = (h^2/H_2)$ is below 1 ($K = 0.651$), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were found to be 0.936 and 0.119, respectively. Both general combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (2.55) was calculated to be greater than 1. This ratio greater than 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effect was obtained from the parents Adana-99 (0.473) and Flamura-85 (0.336), while the lowest GCA effect was from the parent 2115 (-0.367). The highest SCA effect was 1.369 from the hybrid Adana-99 × Flamura-85, while the lowest SCA effect was -0.485 from the combination Flamura-85 × 2115 (Table 7). Considering the three evaluation methods, both additive and dominant variances were found to be effective for grain weight per spike in the population, indicating that the inheritance of the trait conforms to the additive-dominant model. For this trait, Borghi and Perenzin (1994), Balci and Turgut (2002), Hassan et al. (2007) reported the significance of additive gene variance, Mann and Sharma (1995), Akgun et al. (2002) reported the significance of non-additive gene effects, Nazeer et al. (2011) reported the significance of epistatic gene effects, and Sener (1997) reported the presence of non-allelic interactions. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.51) indicates the presence of overdominance for grain weight per spike. In this study, the significance of both additive and dominant gene variance for grain weight per spike, the inability to determine the effective gene pair number, and the low narrow-sense heritability suggest that the selection planned for this trait should be postponed to future generations.

3.8. Thousand Kernel Weight

In the study, the average thousand kernel weight for parents and F_1 hybrids was recorded as 34.14 g. While the average thousand kernel weight for parents was 33.37 g, it was 36.58 g for F_1 hybrid combinations. The average thousand kernel weight of F_1 hybrid combinations was higher than that of the parents. Among the parents, the highest thousand kernel weight was observed in the genotype Flamura-85 (40.23 g), while the lowest thousand kernel weight was obtained from the genotype 2115 (28.93 g). Among the hybrids, the highest thousand kernel weight was recorded at 46.8 g in the hybrid Adana-99 × Flamura-85, whereas the lowest thousand kernel weight was 30.13 g in the hybrid Lucilla × 1635 (Table 3). Heterosis values for thousand kernel weight in F_1 hybrid populations ranged from -13.06% (Flamura-85 × 1635) to 31.16% (Adana-99 × Flamura-85), while heterobeltiosis values varied from -18.46% (Flamura-85 × 1635) to 24.41% (Adana-99 × Lucilla). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype Adana-99 as the parent (Ht: 23.92%, Hb: 17.64%), while the lowest average heterosis and heterobeltiosis values were obtained from the hybrid series with the genotype 1635 as the parent (Ht: -0.85%, Hb: -6.82%). Average heterosis of 9.87% and average heterobeltiosis of 2.74% were determined for thousand kernel weight in F_1 hybrid populations (Table 4). Components a, b, b_1, b_2, and b_3 were found to be significant in the diallel variance analysis for thousand kernel weight. Dominant gene variance (H_1) and genes' distribution corrected dominant gene variance (H_2) were found to be significant at the 0.05 level. In contrast, additive gene variance (D), heterozygote locus dominance effect (h^2), and environmental variance (E) were found to be insignificant. Since environmental variance (E) was insignificant, genetic factors contribute more to this trait than environmental factors. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.109) indicates the presence of overdominance. The negative difference between additive and dominance variance ($D-H_1$) suggests that dominant gene variance is more significant than additive gene variance. The deviation of the frequency of dominant and recessive alleles ($H_2/4H_1$) from 0.25 (0.243) is consistent with the significance of the b_2 sub-parameter, indicating unequal frequencies of dominant and recessive alleles in the parents. The positive F value determining the direction of dominant and recessive alleles (12.532) and the KD/KR ratio greater than 1 (1.434) indicate that dominant alleles are predominant. Since the value of $K = (h^2/H_2)$ is below 1 (K = 0.397), the effective number of genes could not be determined for the trait. The trait's broad-sense heritability (Hg) and narrow-sense heritability (Hd) were found to be 0.960 and 0.212, respectively. Both general combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level, and the ratio of general combining ability to specific combining ability (2.17) was calculated to be greater than 1. This ratio greater than 1 indicates the superiority and importance of general combining ability and, consequently, additive gene variance (Table 5). The highest general combining ability effect was obtained from the parent Flamura-85 (3.438), while the lowest GCA effect was from the parent Lucilla (-1.854). The highest SCA effect was obtained from the combinations 1635 × 2115 (6.442) and Adana-99 × Flamura-85 (5.971), while the lowest SCA effect was from the hybrids Flamura-85 × 1635 (-4.971) (Table 7). Based on the analysis by Hayman (1954), it can be said that dominant gene variance is predominant for a thousand kernel weight. For this trait, Mann and Sharma (1995) reported the significance of overdominance, Tosun et al. (1995) reported the significance of non-additive effects, Kutlu et al. (2015) reported the significance of both additive and non-additive effects, Ronga et al. (1995) reported the significance of additive gene effects, and Sener et al. (2000) reported the significance of epistatic gene effects. The square root of the mean dominance degree $(H_1/D)^{1/2}$ greater than 1 (2.109) indicates the presence of overdominance for thousand kernel weight. In this study, the significance of dominant gene variance for thousand kernel weight, the inability to determine the effective gene pair number, epistatic effects, and the low narrow-sense heritability suggest that the selection planned for this trait should be postponed to future generations.

3.9. Grain Yield

In the research determined the average grain yield per plant for both parents and F_1 hybrids as 30.83 g. While the average grain yield per plant for parents was 22.32 g, the average for F_1 hybrid combinations was 35.99 g. The average value of grain yield per plant for F_1 hybrid combinations was higher than that of the parents. Among the parents, the highest grain yield per plant was obtained from the genotype Adana-99 (28.49 g), while the lowest was from the genotype 2115 (15.75 g). Among the hybrids, the highest grain yield per plant was recorded at 65.5 g in the 1635 × 2115 combination, while the lowest was 15.30 g in the hybrid Lucilla × 2115. Heterosis values for grain yield per plant in F_1 hybrid populations ranged from -15.75% (Lucilla × 2115) to 242.57% (1635 × 2115), while heterobeltiosis values ranged from -25.63% (Lucilla × 2115) to 191.24% (1635 × 2115). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series where genotype Lucilla was the parent (Ht: 89.76% and Hb: 75.47% respectively), while the lowest average heterosis value was from the genotype Flamura-85 (Ht: 47.26%). Heterobeltiosis value was from the 2115 genotype (Hb: 36.65%). The hybrid populations obtained an average of 65.84% heterosis and 49.40% heterobeltiosis values for grain yield per plant. In the study, diallel variance components a, b, b_1, b_2, and b_3 were significant for grain yield per plant. From the calculated genetic parameters for grain yield per plant, additive genetic variance (D), dominant genetic variance (H_1), and additive x additive interaction variance (b_2) were found to be significant at the 0.05 level. In contrast, the others were found to be insignificant. The average degree of dominance $(H_1/D)^{1/2}$ being more significant than 1 (7.204) indicates the presence of overdominance.

The negative difference between additive and dominant variances (D-H_1) indicates that the dominant genetic variance is greater than the additive genetic variance. The F value determining the direction of dominant and recessive alleles being negative (-35.300) and the KD/KR ratio being less than 1 (0.778) indicate that recessive alleles are predominant. Since the value of K = (h^2/H_2) for the number of effective genes is less than 1 (K = 0.493), the number of effective genes could not be determined for the examined trait. The broad sense heritability (Hg) and narrow sense heritability (Hd) for the examined trait were 0.886 and 0.018, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level statistically, and the ratio of GCA to SCA was calculated to be less than 1 (0.44), indicating that SCA and hence non-additive genetic variance are superior and essential. The highest GCA effect was obtained from the female parents Adana-99 (3.933) and Lucilla (3.755), while the lowest GCA effects were obtained from the female parents 2115 (-4.903) and Flamura-85 (-4.212). The highest SCA effect was obtained from the hybrid 1635 × 2115 (38.821), while the lowest SCA effects were obtained from the hybrid Lucilla × 2115 (-15.64), which also had the lowest average grain yield per plant phenotypically (15.3 g). In the examined population, in the half-diallel variance analysis table, additive variance (a), dominance variance (b), and all components (b_1, b_2, b_3) were found to be significant. In the half-diallel hybrid analysis, genetic parameters were found to be statistically insignificant, but D-H_1 was determined to be negative. The adverse determination of D-H_1 indicates that dominant genetic variance is more important and superior for this trait. Evaluation of the compatibility abilities according to the variance analysis method found both GCA variance corresponding to additive variance and SCA variance corresponding to dominance variance to be significant. However, since the ratio of GCA to SCA (0.44) was calculated to be less than 1, it indicates that dominance genetic variance is more important and superior. Similarly, many researchers such as Sener (1997), Tulukcu (2004), and Kutlu (2012) have expressed the difficulty of selection due to the effectiveness of many genes and the low, narrow sense heritability in the inheritance of yield. Our findings are consistent with previous studies. In this study, the importance of dominant variance for grain yield per plant, epistatic genetic effects, and the low, narrow sense heritability suggest that selection planned for this trait should be postponed to subsequent generations.

3.10. Chlorophyll Content of Flag Leaf (SPAD)

Regarding chlorophyll content of flag leaf, the average for parents was 47.05 SPAD, while the average for F_1 hybrid combinations was 49.60 SPAD. Among the parents, the highest chlorophyll content of flag leaf was obtained from the genotype Lucilla (52.58 SPAD), while the lowest was from the genotype 1635 (40.8 SPAD). Among the hybrids, the highest chlorophyll content of flag leaf was recorded as 56.47 SPAD for the hybrid Lucilla × 2115, while the lowest was 45.45 SPADin the hybrid Lucilla × 1635. Heterosis values for chlorophyll content of flag leaf in F_1 hybrid populations ranged from -3.41% (Flamura-85 × 2115) to 19.68% (1635 × 2115), while heterobeltiosis values ranged from -13.56% (Lucilla × 1635) to 16.4% (1635 × 2115). The highest average heterosis and heterobeltiosis values were obtained from the hybrid series where the genotype 2115 was the female parent (Ht: 10.19%, Hb: 4.04%), while the lowest average heterosis value was from the genotype Flamura-85 (Ht: 2.72%), and the heterobeltiosis value was from the hybrid series where the genotype Lucilla was the female parent (Hb: -2.91%). In the hybrid populations, an average of 5.60% heterosis and -0.51% heterobeltiosis values were obtained for chlorophyll content of flag leaf. From the calculated genetic parameters for chlorophyll content of flag leaf, additive genetic variance (D), dominant genetic variance (H_1), and additive x additive interaction variance (b_2) were found to be statistically insignificant. The average degree of dominance $(H_1/D)^{1/2}$ is greater than 1 (1.262), indicating the presence of overdominance. The negative difference between additive and dominant variances (D-H_1) indicates that the dominant genetic variance is greater than the additive genetic variance. The F value determining the direction of dominant and recessive alleles is negative (14.054), and the KD/KR ratio is greater than 1 (1.628), indicating that dominant alleles are predominant. Since the value of K = (h^2/H_2) for the number of effective genes is less than 1 (K = 0.417), the number of effective genes could not be determined for the examined trait. The broad sense heritability (Hg) and narrow sense heritability (Hd) for the examined trait were 0.853 and 0.489, respectively. General combining ability (GCA) and specific combining ability (SCA) were found to be significant at the 0.01 level statistically, and the ratio of GCA to SCA was calculated to be greater than 1 (3.18), indicating that SCA and hence non-additive genetic variance are superior and essential. The highest GCA effect was obtained from the female parent Lucilla (2.293), while the lowest GCA effect was from 1635 (-2.685). The highest SCA effect was obtained from the hybrid Lucilla × 2115 (5.993), while the lowest SCA effects were obtained from the hybrid Flamura-85 × 2115 hybrid (-3.936). In the examined population, in the half-diallel variance analysis table, additive variance (a), dominance variance (b), and all components (b_1, b_2, b_3) were found to be significant. In the half-diallel hybrid analysis, genetic parameters were found to be statistically insignificant, but D-H_1 was determined to be negative. Evaluation of the compatibility abilities according to the variance analysis method found both GCA variance corresponding to additive variance and SCA variance corresponding to dominance variance to be significant. Additionally, the ratio of GCA to SCA being more significant than 1 (3.18) indicates that general combining ability and, hence, additive genetic variance are superior and vital despite the significance of additive x additive interactions. Furthermore, despite the significance of additive genetic variance, non-additive and epistatic genetic effects and low, narrow sense heritability suggest that selection planned for this trait should be postponed to subsequent generations.

4. Conclusion

In conclusion, six bread wheat genotypes (Adana-99, Flamura-85, Masaccio, Lucilla, 1635 and 2115) used as parents and 15 F_1 generations obtained from their half-diallel crosses were investigated using biometric-genetic diallel methods to develop high-yielding and superior-quality new domestic bread wheat genotypes. Heterosis and heterobeltiosis values were calculated. When the heritability degrees of the examined traits were considered, narrow sense heritability values were relatively small for all traits, suggesting that selection should be carried out in subsequent generations. Adequate variation was observed in the traits examined in the study, and the determination of suitable hybrids and parents for the investigated traits suggests that the population under study could be utilized to develop desired varieties. Regarding grain yield per plant, the genotypes Adana-99, Lucilla, and Masaccio exhibited high values, indicating their potential as parental genotypes for breeding programs. Additionally, hybrids such as 1635 × 2115, Masaccio × Lucilla, Adana-99 × Lucilla, Adana-99 × Masaccio, Adana-99 × 1635, and Flamura-85 × Lucilla emerged as promising hybrids.

Author Contributions

The percentage of the author(s) contributions is presented below. All authors reviewed and approved the final version of the manuscript.

	H.O.	H.G.	Z.D.
C	30	35	35
D	40	30	30
S		50	50
DCP	70	15	15
DAI	40	40	20
L	80	10	10
W	20	50	30
CR	10	60	30
SR	10	60	30
PM	40	20	40
FA	20		80

C=Concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management, FA= funding acquisition.

Conflict of Interest

The authors declared that there is no conflict of interest.

Ethical Consideration

Ethics committee approval was not required for this study because of there was no study on animals or humans.

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