Research Article

Hybrid performance and heterosis in F$_1$ offspring of triticale (× *Triticosecale* Wittm.)

Mustafa YILDIRIM[1],*, Hasan GEZGİNÇ[2], Ali Haydar PAKSOY[2]

[1]Kelkit Aydın Doğan Vocational School, Gümüşhane University, Gümüşhane, Turkey

[2]Agricultural Research Station of the Eastern Mediterranean Transition Zone, Kahramanmaraş, Turkey

Abstract: In this study, the combined ability effects and heterosis were determined for number of days to anthesis (AT), plant height (PH), fertile tillers plant^{-1} (FT), spike length (SL), spikelets spike^{-1} (SS) and grains spike^{-1} (GS), 1000-kernel weight (TW), and grain yield plant^{-1} (GY) of 4 triticale genotypes [Karma (G1), Presto (G2), Ayşehanım (G3), and Mehmetbey (G4)] and their 6 F$_1$ offspring. The mean squares of general combining ability (GCA) and specific combining ability (SCA) were statistically significant for all traits. According to the GCA/SCA, additive gene effects were found for all traits. According to the desired values for traits on the basis of GCA and SCA, parents G1 were good general combiners for 3 traits, G3 for 6, and G4 for 6. Crosses G1 × G2 were good specific combiners for 3 traits, G1 × G3 for 3, G1 × G4 for 3, G2 × G3 for 5, G2 × G4 for 6, and G3 × G4 for 4. Heterosis and heterobeltiosis were −16.78% and −25.71% for AT, −1.66% and −11.02% for PH, 34.25% and 9.87% for FT, 14.62% and 11.44% for SL, 8.09% and 3.87% for SS, 4.57% and 0.91% for GS, 9.67% and 6.13% for TW, and 30.36% and 9.11% for GY, respectively. The results revealed that G2 × G3 and G2 × G4 combinations could be recommended for improved yield of triticale.

Key words: Combining ability, heterosis, triticale, yield, yield component

1. Introduction

The world's population is growing rapidly with each passing day, creating a greater demand for food production and for cereal grains in particular. Because further increases in cereal production must occur while preserving the environment and natural resources, production increases must come mainly from enhancing the yield potential of new crops and current land space, not from expanding the global cultivated area (Pena, 2004). The greater adaptation of bread wheat has made it one of the most important global food crops (Rajaram, 2005). In addition, triticale could become a major crop after bread wheat, if it were cultivated on a large commercial scale for human consumption in the world (Pena, 2004). This is because triticale shows better adaptation to stressed environments (Süzer, 2003), particularly to water stress (Barary et al., 2002), than wheat and also resists several common wheat diseases and viruses (Varughese et al., 1996). The most concentrated triticale breeding efforts were carried out at the International Maize and Wheat Improvement Center (CIMMYT) in 1964. Only 15 years later, grain yield of triticale was increased up to 4 times by CIMMYT breeders (Zillinsky, 1985). This development has encouraged triticale breeders and there has been much work on

creating plants with the desired traits in triticale. To have good crop traits associated with the best combinations are the aims of the triticale breeding programs. High heritability, resulting in high genetic progress for yield and yield components, offers a better scope of genotype selection in early segregating populations (Memon et al., 2005).

Plant breeders produce variations through crossbreeding with genetic materials in order to develop types pursuant to their purpose. They aim to identify the parents and F$_1$ offspring in these newly developed hybrid populations in terms of agronomic characteristics and select the ones with superior features (Dağüstü and Bölük, 2002). The mean values of parents and F$_1$ combinations in terms of discussed traits are important for estimating combinative ability and the performances of hybrids as well as selecting superior parents. Hybrid performance of parents can be identified through heterosis (Mh). A genotype's ability to transfer a desirable trait to F$_1$ offspring was defined as the combination ability of that genotype (Poehlman, 1979). General combining ability (GCA) and specific combining ability (SCA) are the most important indicators showing the potential values of pure lines in hybrid combinations. Specific combinative ability depends

* Correspondence: myildirim02@yahoo.com

on the nonadditive effects of genes and general adaptation ability depends on the additive gene effects (Poehlman, 1979; Nevado and Cross, 1990).

Heterotic studies are used for getting information about the increase or decrease of F_1s over their mid-parent and better parent (Inamullah et al., 2006). The use of the best parents in crossing represents an excellent way for the next generation of elite segregating populations to be targeted by selection (Valerio et al., 2009). When enough information on the Mh and heterobeltiosis (Hh) of studied traits in breeding programs is obtained, the next steps of the breeding strategy can be accomplished more successfully. Therefore, Mh and Hh play an important role for planning the triticale breeding strategy.

The objective of this study was to investigate the Mh and combinative ability for number of days to anthesis (AT), plant height (PH), spike length (SL), spikelets spike^{-1} (SS), grains spike^{-1} (GS), fertile tillers plant^{-1} (FT), 1000-kernel weight (TW), and grain yield plant^{-1} (GY) in a 4 × 4 half diallel cross experiment in Turkish triticale genotypes. The formations of this study would be useful to uncover the relationship of F_1 offspring and their parents to establish an effective triticale breeding program.

2. Materials and methods

The study was carried out at the Agricultural Research Station of the Eastern Mediterranean Transition Zone in Kahramanmaraş (located at 37°36′N, 36°55′E at an altitude of 568 m above sea level) during the 2008/2009 growing season. Rainfall during the 10-month growing season (from 1 September 2008 to 30 June 2009) was 855.8 mm (Figure 1). The mean of long-term precipitation was 857

mm. The experimental field had similar rainfall compared to long-term averages. Average rainfalls of March, April, and May are very important for wheat production in Kahramanmaraş. Therefore, this growing season had very good total precipitation for triticale production. The experimental field soil was clay-loamy and alkaline and had medium organic matter.

A total of 4 Turkish triticale cultivars were used for this research: Karma (G1), Presto (G2), Ayşehanım (G3), and Mehmetbey (G4). G1 and G2 are winter-type genotypes and G3 and G4 are spring-type genotypes. They are genetically different from each other as registered varieties in Turkey. Triticale has a higher ratio of cross-pollination compared to other wheat cereals (Yağbasanlar, 1991). For this reason, elite seed materials of genotypes were used as parents in this study. The 10 spikes per combination were emasculated by hand and were crossed to be half diallel without reciprocals in the spring of 2008, consequently resulting in 6 F_1 offspring. Seeds were sown on 8 November 2008. Plants were grown in rows 1 m long, with 2 rows spaced 30 cm apart and with 10 plants row^{-1}. The edge effect on studied traits was prevented by planting durum wheat (Fırat-93 cultivar). The experimental design was a completely randomized block design with 3 replications. Each individual plant was used as an observation unit. Diammonium phosphate (150 kg DAP ha^{-1}) was applied before planting and ammonium nitrate (200 kg AN ha^{-1}) was applied at the shooting stage (Zadoks et al., 1974). Weed control was performed by herbicide application at the main shoot stage (Zadoks et al., 1974).

AT was calculated from 1 January to flowering day according to Zadoks-60 (Zadoks et al., 1974). PH, SL, SS,
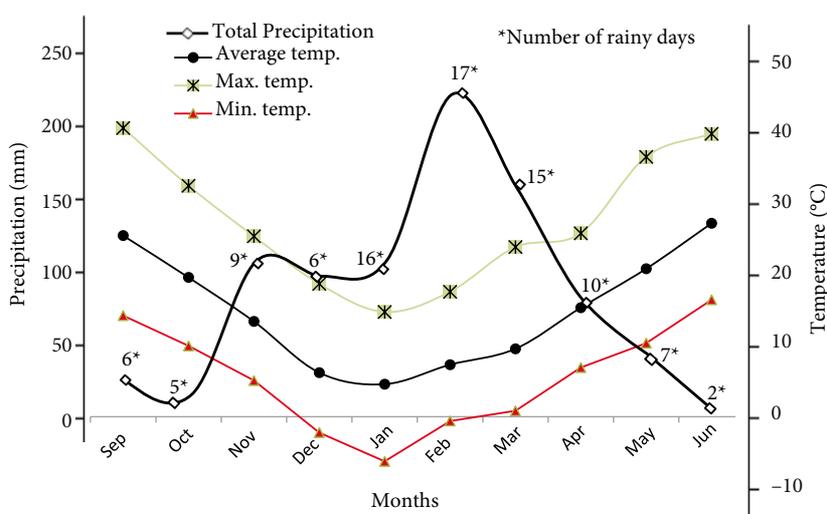
Figure. The monthly total precipitation and temperature during 2008/2009 growing season at experimental field in Kahramanmaraş (meteorological data from Kahramanmaraş Directorate of State Meteorological Service).

and GS were measured on the main stem of each plant. PH and SL were measured in centimeters. FT was counted at harvest time. At maturity, 10 plants from each replication were harvested and the mean of their weights was recorded as GY. TW was also calculated from the seeds of 10 plants.

Analysis of variance was performed for studied traits using 1991 MSTAT-C statistical software. Significant differences between parents and hybrids were determined by the LSD test (α = 0.05). The estimates of general and specific combinative ability were calculated according to Griffing's (1956) Method-II by using the TarPopGen Statistical Package Program developed by Özcan (1999). Mh and Hh were calculated using the following formulas (Özgen, 1989; Budak and Yıldırım, 1996; Beche et al., 2013).

$$Mh_{ij} = \frac{F_{1ij} - Mp_{(F1ij)}}{Mp_{(F1ij)}} \times 100,$$

$$Hh_{ij} = \frac{F_{1ij} - Hp_{(F1ij)}}{Hp_{(F1ij)}} \times 100,$$

where Mh_{ij} is the heterosis of the *ij*th cross; Hh_{ij} is the heterobeltiosis of the *ij*th cross; F_{1ij} is the mean of the *ij*th F_1 cross; $Mp_{(F1ij)}$ is the mid-parent [(Parent1 + Parent2) / 2] for the *ij*th cross; and $HP_{(F1ij)}$ is the high parent values for the *ij*th cross.

The t-test was used to determine whether F_1 hybrid means were statistically significant for Mh and Hh means as follows (Wynne et al., 1970):

$$t_{ij(Mh)} = \frac{F_{1ij} - Mp_{(F1ij)}}{\sqrt{3 / 8 \; Ems}} \times 100,$$

$$t_{ij(Hh)} = \frac{F_{1ij} - Hp_{(F1ij)}}{\sqrt{1 / 2 \; Ems}} \times 100,$$

where $t_{ij(Mh)}$ is the t value for Mh; $t_{ij(Hh)}$ is the t value for Hh; and Ems is the error mean square.

3. Results

The analysis of variance and mean squares for the parents and hybrids are given in Table 1. Variance analysis results were significant in all traits for all genotypes (P ≤ 0.01). Similarly, the analysis of variance results of the GCA for all traits were significant (P ≤ 0.01). SCA was significant at P ≤ 0.01 in the AT, PH, SL, FT, TW, and GY traits, and at the 5% level in the SS and GS traits. This shows the presence of variances worth examining among genotypes in terms of all examined traits. GCA/SCA proportions showed that all examined traits were under additive gene effect.

The mean performances of 8 traits of 4 triticale genotypes and their 6 F_1 offspring are summarized in Table 2. According to mean values of traits, the G3 genotype had the highest values for FT (9.3 fertile tillers plant^{-1}), TW (41.4 g), and GY (20.9 g) traits; G4 for SL (12.37 cm) and

Table 1. Analysis of variance (mean square values) for 8 traits in 4 triticale genotypes and their 6 F_1 offspring in Kahramanmaraş during the 2008/2009 growing season.

Sources	df	AT (days)		PH (cm)		SL (cm)		FT (no.)		SS (no.)		GS (no.)		TW (g)		GY (g)	
		Mean squares															
GCA	3	332.3	**	282.2	**	1.9	**	2.2	**	8.2	**	21.2	**	4.3	**	13.1	**
SCA	6	72.9	**	38.8	**	0.5	**	1.0	**	1.4	*	1.2	*	2.9	**	6.0	**
Genotypes	9	478.0	**	359.4	**	3.0	**	4.1	**	10.9	**	23.6	**	10.0	**	25.1	**
Error	18	0.2		2.1		0.1		0.1		0.3		0.7		0.1		0.1	
GCA / SCA		4.6		7.3		3.8		2.3		6.0		17.5		1.5		2.2	
CV (%)		0.4		1.3		2.6		4.2		1.9		1.4		0.7		1.9	

* and **: significant at P values of 0.05 and 0.01, respectively.
AT: Number of days to anthesis, PH: plant height, SL: spike length, FT: fertile tillers plant^{-1}, SS: spikelets spike^{-1}, GS: grains spike^{-1}, TW: 1000-kernel weight, GY: grain yield plant^{-1}.

Table 2. Mean performances of 8 traits of 4 triticale genotypes and their 6 F_1 offspring in Kahramanmaraş during the 2008/2009 growing season.

Genotypes and F_1s	AT (days)	PH (cm)	SL (cm)	FT (no.)	SS (no.)	GS (no.)	TW (g)	GY (g)
G1	141.33	121.00	11.70	7.43	31.00	59.53	38.63	16.10
G2	136.00	116.50	9.63	6.23	26.97	56.07	36.13	13.47
G3	115.35	94.33	10.20	9.30	26.70	57.77	41.40	20.90
G4	111.00	104.67	12.37	8.37	29.90	63.13	39.60	20.60
Average	125.92	109.13	10.98	7.83	28.64	59.13	38.94	17.77
G1 × G2	140.66	123.33	11.13	8.17	28.37	57.43	41.00	17.56
G1 × G3	120.67	117.33	11.83	9.36	30.03	57.80	42.63	18.60
G1 × G4	105.00	123.33	12.38	8.53	32.20	64.13	39.57	16.20
G2 × G3	119.34	103.67	11.37	8.27	27.34	55.93	41.60	22.40
G2 × G4	117.00	123.66	12.43	9.80	30.72	59.47	40.53	21.57
G3 × G4	116.64	100.67	12.53	10.20	30.53	61.00	40.60	20.50
Average	119.88	115.33	11.95	9.05	29.87	59.29	40.99	19.47
LSD$_{(0.05)}$	0.79	2.50	0.52	0.62	0.98	1.42	0.48	0.60

AT: Number of days to anthesis, PH: plant height, SL: spike length, FT: fertile tillers plant^{-1}, SS: spikelets spike^{-1}, GS: grains spike^{-1}, TW: 1000-kernel weight, GY: grain yield plant^{-1}.

GS (63.3 grains spike^{-1}) traits; and G1 genotype for SS (31 spikelets spike^{-1}). The G3 genotype also had the lowest value for PH (94.33 cm) compared to others. The earliest genotype was G4 (111 days) among parent genotypes. Generally, the F_1 offspring of superior genotypes for each trait also performed better, as shown in Table 2.

In this study, there was no correlation between SS and GY (Table 3). SS showed the highest positive correlations with SL and GS (r = 0.854 and 0.788, respectively). There was positive and significant correlation (r = 0.719) between the mean values of GY and TW. GY also showed positive and significant correlation (r = 0.728) with FT.

Table 3. Correlation coefficients (r) among 8 traits of 4 triticale genotypes and their 6 F_1 offspring.

r[†]	PH	SL	FT	SS	GS	TW	GY
AT	0.377 [ns]	−0.490 [ns]	−0.596 [ns]	−0.303 [ns]	−0.591 [ns]	−0.355 [ns]	−0.523 [ns]
PH		0.177 [ns]	−0.299 [ns]	0.484 [ns]	0.085 [ns]	−0.258 [ns]	−0.562 [ns]
SL			0.596 [ns]	0.854 [**]	0.726 [*]	0.350 [ns]	0.394 [ns]
FT				0.334 [ns]	0.296 [ns]	0.755 [**]	0.728 [*]
SS					0.788 [**]	0.025 [ns]	−0.082 [ns]
GS						−0.077 [ns]	0.022 [ns]
TW							0.719 [*]

**, *, and ns: Significant at the 0.01 and 0.05 probability levels and nonsignificant, respectively.
[†]df: 9.
AT: Number of days to anthesis, PH: plant height, SL: spike length, FT: fertile tillers plant^{-1}, SS: spikelets spike^{-1}, GS: grains spike^{-1}, TW: 1000-kernel weight, GY: grain yield plant^{-1}.

3.1. Number of days to anthesis

Highly significant positive differences were found in the GCA values of G1 and G2 genotypes for AT (Table 4). Contrary to this, the GCA values of G3 and G4 genotypes were found to be negatively significant. Highly significant positive differences were found in the G1 × G2 and G3 × G4 combinations (5.87 and 6.87, respectively) from SCA values of F_1 combinations. All of the other combinations were calculated to be highly negatively significant.

The highly negatively significant values were observed in 4 out of 6 crosses for Mh and 4 out of 6 crosses for Hh (Table 5). Maximum negative Mh and Hh values were observed in the cross G1 × G4 (–16.78% and –25.71%, respectively), followed by G1 × G3 (–5.97% and –14.62%, respectively). Positive significances in Mh and Hh were observed in the G3 × G4 cross (3.09% and 1.16%, respectively).

3.2. Plant height

GCA values of the genotypes for PH ranged between –8.97 (G3) and 6.97 (G1) (Table 4). For PH, GCA values were found to be positively significant ($P \leq 0.01$) in G1 and G2 genotypes; however, they were negatively significant ($P \leq 0.01$) in G3 and G4 genotypes. Among SCA values of F_1 combinations, G1 × G2 was found to be insignificant (0.33); 3 combinations (G1 × G3, G1 × G4, and G2 × G4) were positively significant ($P \leq 0.01$) and 2 combinations (G2 × G3 and G3 × G4) were negatively significant ($P \leq 0.01$). G2 × G3 and G3 × G4 hybrid combinations seemed to be possible candidates for obtaining crossbreeds with short plant heights.

Highly positively significant values were observed in 4 crosses for Mh (Table 5). The highest positive significance for PH was obtained with the cross G2 × G4 and (11.83%) and it was followed by G1 × G4 and G1 × G3 (9.31% and 8.98%, respectively). Only G2 × G3 among the combinations had a negative value (–1.66%) for Mh and it was insignificant. The Hh values of G1 × G3, G2 × G3, and G3 × G4 crosses were negatively significant for PH (–3.03%, –11.02%, and –3.82%, respectively). The negative Hh values indicate that crosses between G3 and other genotypes had reduced PH.

3.3. Spike length

The GCA values of genotypes for SL ranged between –0.59 and 0.71 (G1 and G2, respectively). While the G4 genotype showed positive significant GCA value ($P \leq 0.01$), the G1 genotype was found to be positively significant ($P \leq 0.05$) (Table 4). SCA effects of SL in F_1 combinations were found to be insignificant in G1 × G2 and G1 × G4 combinations, while they were positively significant at a 1% level in all other combinations.

The results of Mh for SL values ranged from 2.77% to 14.62%, while Hh for SL ranged from –4.84% to 11.44% (G1 × G2 and G2 × G3, respectively) (Table 5). G2 × G3 had the highest positive values in both Mh and Hh for SL.

3.4. Fertile tillers plant^{-1}

While the GCA effects of FT were positively significant in G3 and G4 genotypes (0.6 and 0.41, respectively), which have spring characters, they were negatively significant in G1 and G2 genotypes (–0.32 and –0.69, respectively), which have winter characters (Table 4). SCA effects of

Table 4. Estimates of GCA and SCA for 8 traits in a 4 × 4 diallel cross of triticale.

GCA & SCA	AT (days)	PH (cm)	SL (cm)	FT (no.)	SS (no.)	GS (no.)	TW (g)	GY (g)
G1	6.25 **	6.97 **	0.16 *	–0.32 **	0.95 **	0.38 *	–0.06 ns	–1.56 **
G2	6.25 **	3.19 **	–0.59 **	–0.69 **	–1.09 **	–1.86 **	–0.91 **	–0.91 **
G3	–4.03 **	–8.97 **	–0.28 **	0.60 **	–0.93 **	–0.98 **	1.13 **	1.57 **
G4	–8.47 **	–1.19 **	0.71 **	0.41 **	1.06 **	2.46 **	–0.16 **	0.92 **
G1 × G2	5.87 **	0.33 ns	0.02 ns	0.61 **	–0.88 **	–0.32 ns	1.80 **	1.25 **
G1 × G3	–3.86 **	6.50 **	0.39 **	0.52 **	0.63 *	–0.83 *	1.40 **	–0.18 **
G1 × G4	–15.08 **	4.72 **	–0.06 ns	–0.12 ns	0.81 **	2.07 **	–0.38 **	–1.95 **
G2 × G3	–5.19 **	–3.39 **	0.68 **	–0.21 ns	–0.03 ns	–0.45 ns	1.21 **	2.97 **
G2 × G4	–3.08 **	8.83 **	0.76 **	1.52 **	1.38 **	–0.35 ns	1.43 **	2.77 **
G3 × G4	6.87 **	–2.00 **	0.54 **	0.63 **	1.02 **	0.29 ns	–0.54 **	–0.77 **

**, *, and ns: Significant at the 0.01 and 0.05 probability levels and nonsignificant, respectively.

AT: Number of days to anthesis, PH: plant height, SL: spike length, FT: fertile tillers plant^{-1}, SS: spikelets spike^{-1}, GS: grains spike^{-1}, TW: 1000-kernel weight, GY: grain yield plant^{-1}.

Table 5. Estimation of percentage heterosis (Mh %) and heterobeltiosis (Hh %) for 8 traits.

F_1s	AT	PH	SL	FT	SS	GS	TW	GY
G1 × G2								
Mh	1.44 **	3.86 **	4.37 *	19.51 **	−2.13 ns	−0.63 ns	9.67 **	18.83 **
Hh	−0.47 ns	1.93 *	−4.84 *	9.87 *	−8.49 **	−3.53 **	6.13 **	9.11 **
G1 × G3								
Mh	−5.97 **	8.98 **	8.07 **	11.95 **	4.10 **	−1.45 ns	6.54 **	0.54 ns
Hh	−14.62 **	−3.03 **	1.14 ns	0.72 ns	−3.12 *	−2.91 **	2.98 **	−11.00 **
G1 × G4								
Mh	−16.78 **	9.31 **	2.77 ns	8.02 *	5.75 **	4.57 **	1.15 *	−11.72 **
Hh	−25.71 **	1.93 *	0.00 ns	1.99 ns	3.87 **	1.58 ns	−0.08 ns	−21.36 **
G2 × G3								
Mh	−5.04 **	−1.66 ns	14.62 **	6.44 *	1.86 ns	−1.73 ns	7.31 **	30.36 **
Hh	−12.25 **	−11.02 **	11.44 **	−11.11 **	1.36 ns	−3.17 **	0.48 ns	7.18 **
G2 × G4								
Mh	−5.26 **	11.83 **	13.03 **	34.25 **	8.09 **	−0.22 ns	7.04 **	26.61 **
Hh	−13.97 **	6.15 **	0.54 ns	5.38 ns	2.79 ns	−5.81 **	2.36 **	4.69 **
G3 × G4								
Mh	3.09 **	1.17 ns	11.08 **	15.47 **	7.89 **	0.91 ns	0.25 ns	−1.20 ns
Hh	1.16 **	−3.82 **	1.35 ns	9.68 **	2.12 ns	−3.38 **	−1.93 **	−1.91 ns

**, *, and ns: Significant at the 0.01 and 0.05 probability levels and nonsignificant by the t-test, respectively.

AT: Number of days to anthesis, PH: plant height, SL: spike length, FT: fertile tillers plant^{-1}, SS: spikelets spike^{-1}, GS: grains spike^{-1}, TW: thousand kernel weight, GY: grain yield plant^{-1}.

examined traits ranged between −0.21 and 1.52 (G2 × G3 and G2 × G4, respectively). While G1 × G2, G1 × G3, G2 × G4, and G3 × G4 combinations were positively significant, G1 × G4 and G2 × G3 combinations were not significant.

Positive Mh values for FT were observed in all of the crosses (Table 5). However, positive Hh values for FT were observed in the majority of crosses, with the exception of the G2 × G3 cross (−11.11%). Maximum positive Mh values of 34.25%, 19.51%, and 15.47% for FT were displayed by G2 × G4, G1 × G2, and G3 × G4, respectively.

3.5. Spikelets spike^{-1}

GCA values of the G1 and G4 genotypes (0.95 and 1.06, respectively) were positively significant, while the G2 and G3 genotypes (−1.93 and −0.93, respectively) were negatively significant (Table 4). SCA effects of the examined trait ranged between −0.88 and 1.38. SCA values were positively significant for G1 × G4, G2 × G4, and G3 × G4 combinations, but at a 5% level for G1 × G3. SCA in the G2 × G3 combination was insignificant.

The range of Mh for SS varied from −2.13% to 8.09% (G1 × G2 and G2 × G4, respectively) (Table 5). There was only 1 positive significant Hh value in the G1 × G4 cross (3.87%) for SS. The Mh values of G1 × G3, G1 × G4, G2 × G4, and G3 × G4 crosses were highly positively significant for SS; the G1 × G2 cross was negative.

3.6. Grains spike^{-1}

The G4 genotype had a GCA value of 2.46 and the G1 genotype had a GCA value of 0.38 for GS (1% and 5%, respectively) (Table 4). G2 and G3 genotypes were negatively significant for GS (−1.86 and −0.98, respectively). The SCA value of the G1 × G4 combination (2.07) was found to be highly positively significant, while the G1 × G3 combination was negatively significant at a 5% level (−0.83). Other combinations were found to be insignificant.

In this study, the values of Mh for GS indicated that only the G1 × G4 cross (4.57%) showed positive significance (4.57%) (Table 5). The highly negatively significant Hh

values were observed in 5 crosses for GS. There was no positively significant value for Hh. The result values of Hh for GS ranged from –5.81% to 1.58% (G2 × G4 and G1 × G4, respectively).

3.7. Thousand-kernel weight

The GCA effects of the genotypes for TW ranged between –0.91 and 1.13 (G2 and G3, respectively) (Table 4). The G3 genotype showed positive significant GCA values among other genotypes, while the G2 and G4 genotypes gave high negative results. The G1 genotype (–0.06) was not significant. All combinations had statistically significant SCA values for TW. Among those, the G1 × G2, G1 × G3, G2 × G3, and G2 × G4 combinations were positively significant and the G1 × G4 and G3 × G4 combinations were negatively significant.

There were significant differences in most of Mh values of crosses for TW. The values of Mh for TW indicated that 5 crosses showed positive significance (Table 5). The range of Mh for TW was from 0.25% (G3 × G4) to 9.67% (G1 × G2). The highest positive value of 6.13% for Hh was exhibited by the G1 × G2 cross. It was followed by 2.98% and 2.36% (G1 × G3 and G2 × G4, respectively). Only the Hh value of the G3 × G4 cross for TW had highly negative significance (–1.93%).

3.8. Grain yield plant⁻¹

The highest GCA value for GY was observed in the G3 and G4 genotypes (1.57 and 0.92, respectively) (Table 4). While these 2 genotypes had high positive GCA values, the G1 and G2 genotypes (–1.56 and –0.91, respectively) were found to be negatively significant. SCA values in terms of examined traits ranged from –1.95 to 2.97 (G1 × G4 and G2 × G3, respectively). It is remarkable that the GCA values of G3 and G4 triticale genotypes, which have winter characters, were positively higher than G1 and G2 triticale genotypes, which have spring characters. SCA values of all combinations were significant at the 1% level for all combinations. Among those, the G1 × G2, G2 × G3, and G2 × G4 combinations were positive and the G1 × G3, G1 × G4, and G3 × G4 combinations were negative.

The highest positive significant Mh values for GY were obtained for the crosses G2 × G3, G2 × G4, and G1 × G2 (30.36%, 26.61%, and 18.83%, respectively); only the G1 × G4 cross had a negative significant Mh value (–11.72%) (Table 5). The highest positive Hh value was obtained with the cross G1 × G2 (9.11%) and it was followed by G2 × G3 and G2 × G4 (7.18% and 4.69%, respectively). The highest negative Hh values for GY were obtained with the G1 × G4 and G1 × G3 crosses (–21.36% and –11%, respectively).

4. Discussion

According to correlations among the mean values of studied traits, the highest positive correlations were between SL and GS, GY and TW, and GY and FT. These results indicate that the TW and FT can be used for indirect selection to increase grain yield potential.

GCA/SCA ratios showed that all of the traits were under additive gene effect. This result for GY was in agreement with the findings of Seitkhozhaev et al. (1990) and Yıldırım (2005) in bread wheat. Additive gene effects were found for PH in wheat by Borghi and Perenzin (1994) and Balcı and Turgut (2002). Balcı and Turgut (2002) and Yıldırım (2005) also reported additive gene effects for SL, GS, SS, and TW in wheat.

GCA and SCA mean squares were highly significant for GY. Our results were in agreement with Mann et al. (1995) and Borghi and Perenzin (1994), who reported similar results in durum wheat. The G3 and G4 genotypes had the highest GCA values for GY and the crosses G1 × G2, G2 × G3, and G2 × G4 had promising SCA values among all combinations. The highest positively significant values for GY were obtained in the G1 × G2, G2 × G3, and G2 × G4 crosses in both Mh and Hh. These results were in agreement with Sadeque et al. (1991) and Kashif and Khaliq (2004), who reported similar results in bread wheat, which reveals the importance of heterosis studies for inducing grain yield.

TW is one of the most important grain yield components for GY. GCA and SCA were highly significant for TW. Similar results have been reported by Taleei and Beigi (1996) and Hassan et al. (2007) in bread wheat. The G3 genotypes were good combiners and the G1 × G2, G1 × G3, G2 × G3, and G2 × G4 combinations had strong potential for TW. The Mh values for TW were positively significant, with the exception of the G2 × G3 cross. Pfeiffer et al. (1998), Oettler et al. (2001), and Aydogan Cifci and Yagdi (2007) determined Mh for TW in triticale. The Hh values of G1 × G2, G1 × G3, and G2 × G4 crosses had high potential for the TW trait.

SL has an important effect in increasing grain yield, along with many other parameters. The G4 genotype had positive, highly significant GCA values; the G1 genotype was positively significant for SL; and the crosses G1 × G3, G2 × G3, G2 × G4, and G3 × G4 displayed highly positively significant SL values. The negative and positive Mh and Hh values were similar to reported results by Aydogan Cifci and Yagdi (2007). Positive Mh results were found for SL in wheat by Jaiswal et al. (2010), while Akhter et al. (2003) found a negative Mh.

FT is an effective yield component under optimum sowing density and a greater number would result in more grains per plant. Therefore, positive combining abilities are a desirable trait (Inamullah et al., 2006). The G3 and G4 genotypes and G1 × G2, G1 × G3, G2 × G4, and G3 × G4 combinations displayed highly positively significant combining ability effects for FT. Zubair et al. (1987) and Chowdhry et al. (1992) have also reported similar results

for FT. There were positive and negative values of Mh and Hh for FT in this study. Subhani et al. (2000) and Kashif and Khaliq (2004) reported similar results for FT in wheat.

SS is an effective yield component and a greater number would result in an increase in GS. Kashif and Khaliq (2004) and Bilgin et al. (2011) reported an increase in GY and GS by SS, which supports our results. GCA and SCA effects of SS must be positive. In this study, the GCA values of G1 and G4 genotypes were found to be highly positively significant for SS; the others were negatives. The SCA effects of G1 × G4, G2 × G4, and G3 × G4 combinations for SS were positively significant at 1%, while the G1 × G3 combination showed positive significance at 5%. There were positive and negative results of Mh and Hh for SS. Mujahid et al. (2000) and Dağüstü and Bölük (2002) observed similar results to these findings in wheat. The G1 × G4 cross had the only positively significant Hh value for SS. The Mh values of G1 × G3, G1 × G4, G2 × G4, and G3 × G4 crosses were highly positively significant and the G1 × G2 cross was negative for SS.

GS directly determines the yield potential of a genotype (Saleem and Hussain, 1988; Inamullah et al., 2006; Sinclair and Jamieson, 2006; Bilgin et al., 2011). Only the G4 and G1 genotypes had positive significant GCA values (1% and 5%, respectively). The G1 × G4 cross was the best combination among F$_1$s for GS. Similar results were reported by Borghi and Perenzin (1994) and Zubair et al. (1987). The Mh values for GS indicated that only the G1 × G4 cross showed highly positive significance, and the Hh values also exhibited highly positive significance in 5 crosses for GS. Similar results for this trait were also reported by Pfeiffer et al. (1998) and Aydogan Cifci and Yagdi (2007) in triticale and by Munir et al. (1999) in wheat.

Early AT is desirable due to the fact that an earlier start to pollination provides sufficient time for grain formation and grain filling stages (Inamullah et al., 2006). There is a deep interest in crossing studies for early AT among breeders because early AT results in greater grain filling. GCA values of G3 and G4 genotypes were highly negatively significant, while G1 × G2 and G3 × G4 F$_1$s from SCA values of F$_1$ combinations exhibited highly significant positive differences. The lowest Mh and Hh values were recorded from the G1 × G3, G1 × G4, G2 × G3, and G2 × G4 crosses. These results further confirm the findings of Sadeque et al. (1991).

PH is an important trait in bread wheat. In Turkey, shorter triticale plants (shorter than 140 cm) are selected by breeders, because taller-stemmed bread wheat genotypes are more likely to lodge under favorable conditions than shorter genotypes. For this reason, negative values of GCA and SCA are expected by breeders to decrease PH (Yıldırım, 2005; Beche et al., 2013). With regards to PH, it is important to choose combinations with negative values (Özgen, 1989). According to our results, only the GCA values of G3 and G4 genotypes (–8.97 and –1.19, respectively) and the SCA values of G2 × G3 and G3 × G4 combinations (–3.39 and –2, respectively) were found to be negatively significant for PH. The G2 × G3 cross of Mh and G1 × G3, G2 × G3, and G3 × G4 crosses of Hh were negatively significant for PH. These results were in agreement with earlier findings (Cui et al. 2002; Yao, 2011). The negative Hh values indicate that crosses between G3 and other genotypes had reduced PH.

In conclusion, the G4 genotype was the better general combiner for most traits, except TW. The G3 genotype was the better general combiner for AT, PH, FT, TW, and GY traits, and genotype G1 was the better combiner for SL, SS, and GS traits. G2 × G3 and G2 × G4 combinations were excellent specific combiners for GY. The G2 × G3 combination was also good for PH and AT, while G2 × G4 was not good for PH. G2 × G4 and G2 × G3 combinations could be useful for selecting for a higher grain yield and most agronomic traits. The G1 × G4 combination had the earliest AT, but it was not good for other traits. According to the results, there were promising triticale parents and combinations for higher grain yield and other agronomic traits in our study.

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