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Determination of genetic parameters for yield components in bread wheat

Imren Kutlu*, **Murat Olgun**

Department of Field Crops, Faculty of Agriculture, Osmangazi University, Eskisehir, Turkey

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Abstract

This study was conducted to investigate the genetic control of yield components. A six parent diallel cross, including reciprocals, of wheat was tested for heading and maturing time, plant and peduncle height, spike length, spikelet number per spike, grain number and weight per spike, harvest index and grain yield per plant. These traits measured were analyzed employing the techniques of Jinks-Hayman type diallel analyses. Results revealed that significant variance among the genotypes to make diallel analyses for all traits and the scaling test suggested that the additive-dominance model was adequate for data analysis for all characters except for maturing date, spike length and grain weight per spike. Additive (a and D) and non-additive (b and H_1, H_2) gen effects were involved in the heritance of all traits according to diallel variance analyses and estimation of genetic parameters. The Wr/Vr graphs and $(H_1/D)^{0.5}$ value revealed that partial dominance for plant height, peduncle length, spikelet and grain number per spike, while over dominance for harvest index and grain yield per plant. Furthermore, the regression coefficient of Wr on Vr was significant from unity for heading and maturing time, spike length and grain weight per spike indicating the presence of epistatic gene effects. The effective selection was possible in early generations for plant height, peduncle length, spikelet number per spike, grain number per spike and harvest index, since these traits had high narrow sense heritability, which estimated that according to additive gene action.

* **Corresponding Author:** Imren Kutlu ✉ ikutlu@ogu.edu.tr

Introduction

Wheat is the most important cereal of Turkey as well as in the world. Although our country has a significant status on account of acreage and production, it doesn't play a remarkable role in export. Since, yield per unit area is low and almost all of the wheat production used to meet domestic demand. In addition, comparison of wheat production with the increase of population revealed that wheat production failed to meet increasing demand and, it decreased by 8,8 % in 2009 from the previous six years (Gunaydın, 2009). The rapidly increasing population demands improvement in wheat production. The production of wheat can be increased either by greater area under cultivation or by increasing per hectare yield. However, it is not feasible to increase area under wheat cultivation. Therefore, the only alternate left is to increase per hectare yield, and there is a continuous need to evolve new cultivars, which have desirable yield potential (Ozgen, 1991).

Wheat breeding for improving varieties is requires primarily understanding of the genetic mechanism governing yield and yield components. Because, grain yield is basically a complex trait being the consequence of several genes and their interaction (Agrawal, 1998; Rashid *et al.*, 2012). Diallel cross technique is extensively used in breeding program for introduce different genes which are known to be yield contributor. (Yıldırım *et al.*, 1979). Because this technique offers crossing of selected parents in all possible combinations and provides the information about the inheritance pattern and gene action in F_1 generations (Aksel *et al.*, 1982; Mather and Jinks, 1982).

A breeder who uses diallel cross technique in breeding programmes achieve the success in less time. Because diallel technique, allowed estimate different genetic parameters, helps most effective breeding method. Several researchers studied that genetic parameters and heritability of yield and its components in wheat by used to diallel technique and presented that useful information such as significant additive gene effects and partial dominance (Khan *et al.*, 2010; Hussein *et al.*, 2012; Jatoi *et al.*, 2012), high narrow sense heritability and early generetaion selection for yield components (Aydem, 1979; Ciftci and Yagdı, 2007; Dagustu, 2008;). However, these studies reported that there was sporadic information on selected local cultivars. Therefore, there is still need to work with different populations in different locations.

The objective of this study was to ascertain the mechanism of gene action responsible for the development of yield related traits in 6x6 diallel crosses and thereby suitable breeding strategies can be made.

Material and methods

Research Area

This study was carried out in experimental area of Faculty of Agriculture, Eskisehir Osmangazi University, Eskisehir, Turkey. Eskisehir lays between 30-32 degrees east latitude and 39-46 degrees northern longitudes and continental climate prevails in region. Total annual precipitation was 423,7 mm and mean temperature 9,6°C, which were more than the long year (1970-2011) average (311,5 mm and 9,0°C) of the site. The soil was loam, with pH 7,6-8,2, and organic matter and $CaCO_3$ contents of 1.7 and 4,34%, respectively.

Plant Material, Agronomic Treatments and Measured Traits

Six bread wheat varieties (Alpu-01, Altay 2000, Bezostaja-1, Harmankaya 99, Mufitbey and Sonmez-01) were crossed in a complete diallel design during 2009-2010 crop seasons. Parents and their 30 F_1 hybrids (complete diallel set) were grown in a randomized complete block design with four replications during 2010-2011 crop seasons. Each plot consisted of 20 F_1 or parent plants on two rows of 2 m length and 30 cm interrow and 20 cm intrarow spacing. Sprinkler irrigation was applied twice during stem elongation and flowering. Plants were fertilized 1,2 kg/ha N and 1,0 kg/ha P_2O_5 and harvested on with in July 2011. Ten plants for each parent and cross were tagged at random from each replication and data were recorded on heading time, maturing time, plant height, peduncle length, spike length, spikelet per spike, grain number per spike, grain weight per spike, harvest index and grain yield per plant (Genc, 1974; Yurur *et al.*, 1981).

Statistical Analysis

Firstly, the data were analyzed to ascertain the significant differences among mean values of genotypes. Then, diallel variance analysis was performed according to Hayman 1954a. In this technique, the total sum of squares is partitioned into various components, namely, a (additive gen effects), b (non-additive gen effects, which is further subdivided into b_1, b_2 and b_3), c (maternal effects) and d (reciprocal differences other than c). After ANOVA, the validity of the assumptions for diallel analysis (diploid segregation, no reciprocal effects, homozygous parents, no epistasis, no multiple allelism, independent genes of distribution among parents) was tested with the regression coefficient (b) of Wr on Vr for each character is expected to be non-significantly different from unity (1).

The genetic parameters i.e. E (environmental effects), D (additive genetic variance of the parents), H_1 (dominance genetic variance), H_2 (adjusted dominance variance according to gene distributions), F (relative frequencies of dominant and recessive alleles in parents), h^2 (overall dominance effects), $H_1/D^{1/2}$ (mean degree of dominance), $H_2/4H_1$ (the proportion of genes with positive and negative effects in the parents), KD/KR (the proportion of dominant and recessive genes in parents), K (number of gene groups, which control the character), D-H_1 (relative dominance to each other dominance and additive gene effects) and H (narrow heritability according to Crumpacker and Allard (1962) were computed according to Jinks (1954), Hayman (1954b), Mather and Jinks (1982) and Singh and Chaudhary (1985). The diallel variance analysis was performed in Microsoft Office Excel 2003 following function given in Mather and Jinks (1982). Genetic parameters and the ratios between these parameters were performed using the TarPopGen Statistical Package Program developed by Ozcan (1999).

Results and discussion

In this study, the data on examined traits were analyzed using ordinary variance analysis technique and the mean squares of the analysis presented Table 1. According to Table 1, highly significant ($P<0,01$) differences among 36 genotypes for all traits. Therefore, the data were arranged in diallel tables for formal analysis of variance. The results obtained from the scaling test (Table 1) suggested that the additive-dominance model was adequate for data analysis for all traits except for maturing date, spike length and grain weight per spike. For these traits, the regression coefficient (b) was significantly different from unity and the assumptions were invalid for these traits. Since the genetic parameter safely calculated, two methods suggested that Hayman (1954), Crumpacker and Allard (1962), Singh and Chaudhary (1976) are used. These methods;

1. The genotypes and their generations, which coming out confidence limits by showing deviation of the regression line, excluded from analysis.

2. Blocks, which not meet to the regression coefficient ($b = 1$) hypothesis, excluded from analysis.

Following these methods, “Sonmez-01 and its generations”,“Altay 2000 and Mufitbey and their generations” and “Bezostaja-1 and its generations” were excluded from analysis for maturing date, spike length and grain weight per spike , respectively. These traits re-analysed of variance and t values were non-significant.

Variance analysis of full diallel table presented in Table 3. The highly significant ($P\leq 0,01$) “a” and “b” item indicated that both additive and dominance variations in the heritance of all traits. Further separation of components of dominance (b) displayed that b_1 was significant for all traits except for grain number of spike and harvest index. This showed unidirectional dominance for these traits. The highly significant mean squares for b_2 depicted the asymmetry of gene distribution among parents for all traits except for heading time and maturing time and significant b_3 component depicted the presence of specific combining ability of the parents for all traits. Significant "c" and "d" items for all traits revealed that maternal and reciprocal effects had played role in the genetic mechanism controlling these traits.

Table 1. Variance analyses and scaling test for yield components.

Traits	Replication	Hybrid	Mean Squares	F	$t_{(b=1)}$
Heading time	4	6x6	3,77	2,23**	1,85
Maturing time	4	6x6	2,85	1,67*	4,45*
	4	5x5	2,91	2,22**	3,09
Plant height	4	6x6	330,471	851,88**	0,44
Peduncle height	4	6x6	32,46	415,42**	-0,87
Spike length	4	6x6	1,22	65,07**	2,70*
	2	4x4	0,41	59,14**	3,05
Spikelet number per spike	4	6x6	4,02	147,13**	0,21
Grain number per spike	4	6x6	281,91	1035,24**	0,75
Grain weight per spike	4	6x6	1,25	649,92**	3,45*
	4	5x5	1,24	713,87**	2,91
Harvest index	4	6x6	69,61	280,21**	-0,44
Grain yield per plant	4	6x6	143,30	353,54**	2,41

$^{*}P<0.05$, $^{**}P < 0.01$.

Genetic components of variation, ratios between genetic parameters and estimates of heritability for yield components are presented in Table 4. Expected environmental component of variation (E) was found non significant for all traits except heading and maturing time. The additive genetic component (D) was significant for all traits except maturing date and spike length. On the other hand dominance genetic component (H_1 and H_2) was significant for all traits. This means both additive and non additive gene effects were involved in the heritance of these traits. Dominance genetic effects however, were found the play an important role in the expression of heading and maturing date, spike length, grain weight per spike, harvest index and grain yield per plant due to higher magnitude of components H_1 and H_2 and negative D-H_1 value. This indicated that the selection in segregating generations can be difficult for the improvement these traits. However, D component was higher than H_1 and H_2 and positive D-H_1 value for plant height, peduncle height, spikelet number per spike and grain number per spike which revealed that genetics of these traits was primarily handled by additive effects. Many researchers (Mahmood and Chawdhry, 2000; Akram *et al.*, 2008; Khan *et al.*, 2010; Farooq *et al.*, 2011; Rabbani *et al.*, 2011) reported additive and dominance gene effects for yield and yield components.

Table 2. Mean squares of diallel variance analyses for yield components.

	a	b	b_1	b_2	b_3	c	d
Heading time	34,73**	4,59**	17,48**	1,34ns	4,97**	7,46**	3,21**
Maturing time	23,24**	4,49**	11,36**	1,95ns	5,14**	3,98**	3,09**
Plant height	16934,99**	2062,08**	21074,89**	630,55**	744,85**	278,25**	226,55**
Peduncle height	8804,30**	768,10**	6771,33**	439,46**	283,65**	196,20**	163,42**
Spike length	477,49**	280,31**	924,56**	214,57**	245,26**	193,07**	156,49**
Spikelet number per spike	2950,85**	259,51**	633,27**	171,56**	266,85**	117,50**	136,39**
Grain number per spike	23172,36**	1151,48**	0,23ns	1034,92**	1344,16**	804,46**	778,77**
Grain weight per spike	12927,11**	1170,09**	1499,09**	844,41**	1314,46**	250,09**	809,80**
Harvest index	5546,98**	479,87**	0,06ns	707,67**	406,62**	533,78**	162,82**
Grain yield per plant	6160,63**	824,29**	816,96**	911,15**	776,84**	884,18**	187,93**

$^{*}P<0.05$, $^{**}P < 0.01$

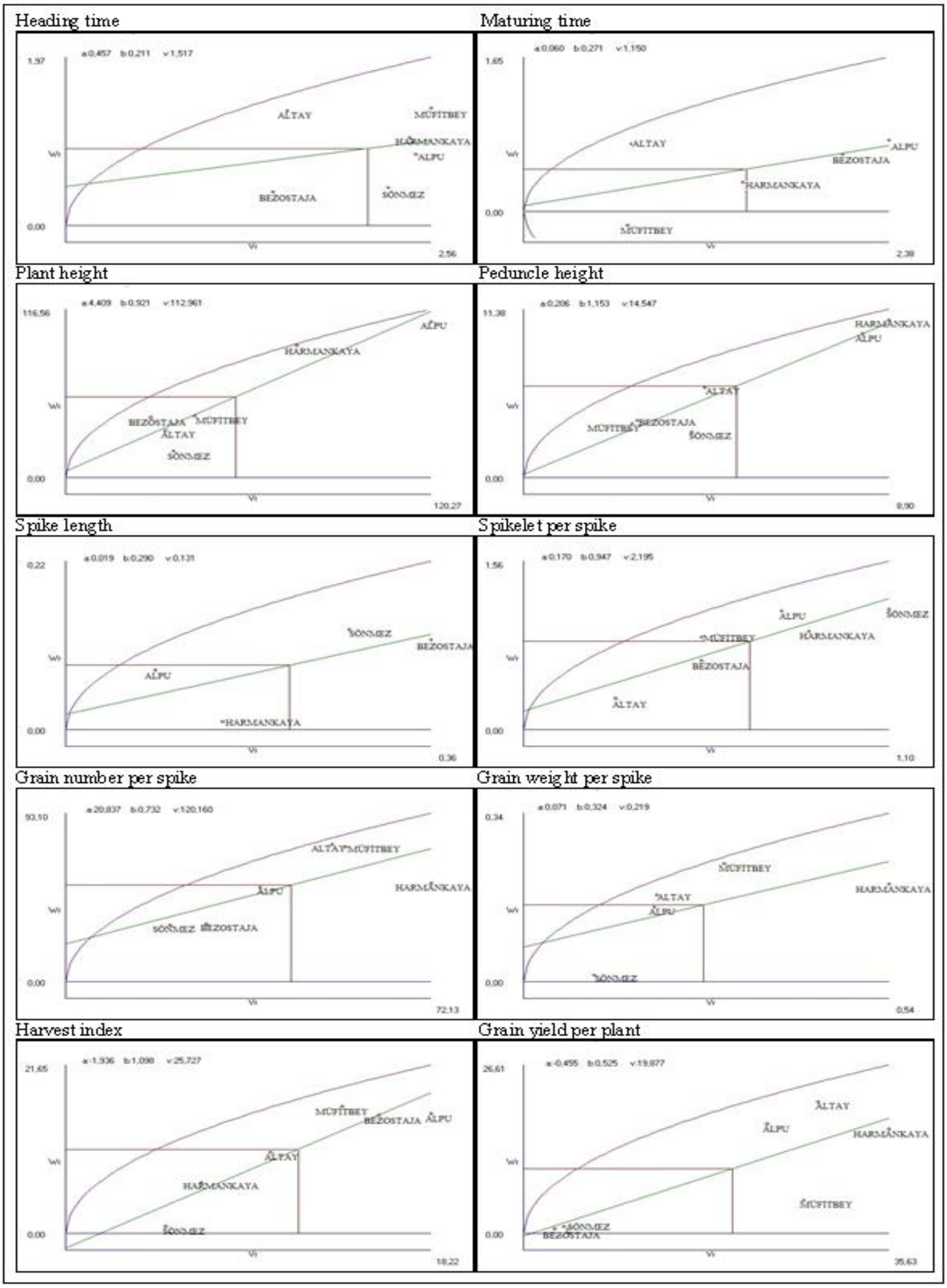
The value of F, which is the measure of relative frequency of dominant to recessive alleles in the parents, was significant ($P \leq 0,05$ and $P \leq 0,01$ respectively) and positive for peduncle length, harvest index and spikelet number per spike, implying that excess of dominant alleles was present in the parents. Maturing date, plant height, grain number per spike were positive and non significant F value while negative F value indicated that recessive alleles were more frequent in heading time, spike length, grain weight per spike and grain weight per plant. The significant effect obtained for h^2 revealed an important contribution of dominant genes toward determining plant height, peduncle length, and spike length and spikelet number per spike.

Table 3. Genetic parameters and ratios of genetic parameters.

	E	D	F	H_1	H_2	h^2	D-H_1
Heading time	0,44**	1,08**	-1,16	5,18**	6,46**	0,78	-4,11**
Maturing time (5*5)	0,37*	0,78	0,05	4,18**	3,96**	0,47	-3,40**
Plant height	0,1	112,86**	2,72	112,80**	181,89**	283,82**	0,07
Peduncle height	0,02	14,53**	4,38*	10,51**	16,27**	18,36**	4,02*
Spike length (4*4)	0,003	0,13	-0,07	0,67*	0,82**	0,28*	-0,54*
Spikelet number per spike	0,01	2,19**	1,11**	1,64**	2,19**	0,60**	0,55*
Grain number per spike	0,08	120,08**	26,86	84,25**	139,34**	-0,04	35,83*
Grain weight per spike (5*5)	0	0,22*	-0,19	0,66*	0,96**	0,18	-0,44*
Harvest index	0,07	25,66**	8,21*	28,74**	37,19**	-0,04	-3,08
Grain yield per plant	0,1	19,78**	-1,37	60,16**	59,44**	11,45	-40,39**
Ratios of Genetic Parameters							
	$H_1/D^{0,5}$	$H_2/4H_1$	KD/KR	K	NSH	r for Yr,Wr+Vr	
Heading time	2,2	0,31	0,61	0,12	0,12	0,18	
Maturing time (5*5)	2,31	0,24	1,03	0,12	0,12	-0,41	
Plant height	1	0,4	1,02	1,56	0,51	-0,88	
Peduncle height	0,85	0,39	1,43	1,13	0,7	-0,98	
Spike length (4*4)	2,28	0,31	0,78	0,35	0,15	-0,69	
Spikelet number per spike	0,87	0,33	1,83	0,27	0,8	-0,5	
Grain number per spike	0,84	0,41	1,31	0	0,68	0,76	
Grain weight per spike (5*5)	1,73	0,36	0,6	0,19	0,21	0,89	
Harvest index	1,06	0,32	1,36	-0,001	0,55	-0,04	
Grain yield per plant	1,744	0,247	0,961	0,19	0,24	0,9	

*$P<0.05$, ** $P < 0.01$.

Mean degree of dominance $(H_1/D)^{0,5}$ for peduncle length, spikelet number per spike and grain number per spike were less than one indicating partial dominance, while the other traits were under over dominance type gene action with mean degree of dominance value greater than one. Value of $H_2/4H_1$ ratio deviated from 0,25 for all traits which confirmed asymmetrical distribution of positive and negative alleles among the parents. The dominance-recessive ratio (KD/KR) in accordance with the negative F value was less than one, indicating that recessive alleles were more frequent for heading time, spike length, grain weight per spike and grain weight per plant. Plant height and peduncle length were controlled, possibly by polygenic control of genes (K=1, 56 and 1, 13 respectively). But this value was not determined for other traits. If the value and direction of dominance effects of genes is equal, gene distribution is independent and h^2 value is positive and high, this value can be determined accurately. But if gene distribution isn't independent, H_1, H_2 and h^2 show a value less than the expected value (Jinks, 1954). In this research, h^2 value is small and number of effective gene pairs was not determined. Similar results found by (Aydem, 1979; Kılınc, 1993; Sener, 1997; Yıldırım, 2005).



Heading time

Maturing time

Plant height

Peduncle height

Spike length

Spikelet per spike

Grain number per spike

Grain weight per spike

Harvest index

Grain yield per plant

Fig. 1. Wr/Vr graph for yield components.

Narrow sense heritability (NSH) measures the magnitude of genotypic variation in the breeding material, which is mainly responsible for chancing the genetic composition of the population via selection (Falconer, 1989). Moreover, narrow sense heritability is directly proportional to additive genetic variance and is maximum in additively controlled characters, and lower in non additive genetic components

(Nazeer *et al.*, 2011). So, plant height, peduncle length, grain number per spike and harvest index coupled with significant additive variance showed relatively high heritability value and prove the importance of additive gene action in the expression of these traits and could be useful in selection of elite genotypes from segregating materials. Khan *et al.* (2010) and Rabbani *et al.* (2011) determined that high narrow sense heritability for these traits. Negative correlation coefficient between orders of theoretical dominance and means of parents indicated that the parents containing dominant genes were responsible for increased maturing time, plant height, peduncle length, spike length, spikelet number of spike and harvest index. Some researchers (Yıldırım, 1974; Sener, 1997; Yıldırım, 2005) found negative correlation these characters, while Aydem (1979) found positive correlation and reported that the parents containing recessive genes were responsible increased related traits and parents, which is suitable for aim of breeding, should be selected according to their graphic location for related traits. (Dere, 2004).
The Wr/Vr graphs (Figure 1) revealed that the regression line intercepted Wr axis above the point of origin indicating additive type gene action with partial dominance for all traits except for harvest index and grain yield per plant. The same kind of results, as reflected in Table 4, was also supported by $(H_1/D)^{0.5}$ value less than one for peduncle length, spikelet number per spike and grain number per spike. As shown by (Akgun, 2001; Yıldırım, 2005; Khan *et al.*, 2010; Hussein *et al.*, 2012; Jatoi *et al.*, 2012), these results are in agreement with our findings for these traits. However, graphical analysis was contrast with $(H_1/D)^{0.5}$ value in heading time, maturing time, spike length and grain weight per spike. The regression coefficient of Wr on Vr was significant from unity for these traits indicating the presence of epistatic gene effects. Hayman (1957) reported that multiple allelism and dependent distribution of genes effects of Wr/Vr graphs and Nassar (1965) reported that dependent distribution of genes changed point of intercept Wr axis of regression line. Epistatic gene action for these traits was also reported by (Iqbal *et al.*, 1991; Dagustu, 2002; Nazeer *et al.*, 2011); however additive gene action with partial dominance was Hussein *et al.* (2012), Rashid *et al.* (2012) and overdominant gene action was Mahmood and Chawdhry (2000), Dagustu (2002), Akram *et al.* (2008). For harvest index and grain yield per plant, the graphs show a overdominance in accordance with $(H_1/D)^{0.5}$ value. Hence selection for these traits in the early segregating generation would be difficult. Similar findings were founded that (Khan *et al.*, 2010; Ahmad *et al.*, 2012; Jatoi *et al.*, 2012).

Based on the position of parental forms along regression line found that for ten traits as follows: For heading time, the parents Mufitbey, Harmankaya 99, Alpu-01 and Sonmez 01 appear to have recessive genes and Altay 2000 and Bezostaja-1 seem to have dominant and recessive genes in more or less equal proportions. The parent Alpu-01 had the maximum concentration of recessive genes, and the parent Mufitbey had relatively higher concentration of the dominant genes. For plant height and peduncle length, the parents Harmankaya 99 and Alpu-01 had recessive genes and the other parents had relatively more concentration of dominance genes. The parent Alpu-01 had dominance genes and the parent Bezostaja-1 had the maximum of recessive genes for spike length. For spikelet per spike, the parent Altay 2000 had dominant genes, while Sonmez 01 had recessive genes. The parent Altay 2000, Harmankaya 99 and Mufitbey had predominantly recessive genes, whereas Sonmez 01 and Bezostaja-1 had slightly dominant genes for grain number per spike. Harmankaya 99 appeared to have higher concentration of recessive genes for grain weight per spike, while Sonmez 01, as it located in the closest site from origin point had maximum concentration of the dominance genes. According to the distance from origin, the parent Sonmez 01 located near origin point, and then had maximum concentration of dominant genes, while the parent Alpu-01 located at farthest site from origin point indicating it is containing higher concentration of recessive genes for harvest index. For grain yield per plant, the parents Sonmez 01 and Bezostaja-1 had dominant genes, parent Harmankaya 99 had recessive genes and parents Altay 2000, Alpu-01 and Mufitbey seemed to have relatively more concentration of the recessive genes.

Conclusions

The variance analysis revealed that all genotypes had adequate genotypic variation to make genetic analysis for all traits. According to diallel variance analysis and estimates of genetic components, additive genetic variance components (a and D) and dominance genetic variance (b, H_1 and H_2) were found significant for all traits. This indicates that all traits controlled both additive and non additive gene action. On the other hand, additive gene action predominated for plant height, peduncle length, spikelet number per spike and grain number per spike, since D-H_1 values were greater than one. $H_1/D^{0.5}$ values indicated that peduncle length, spikelet number per spike and grain number per spike were shown partial dominance, while the other traits were shown over dominance. Although graphical analysis supported that plant height, peduncle length, spikelet number per spike, grain number per spike, harvest index and grain yield per plant, it was contrast to heading time, maturing time, spike length and grain weight per spike. The reason of this inconsistency is non allelic gene interactions. Additionally, the presence of genotypes away from the regression line indicated that epistatic effects.

Additive gene effects are very important in plant breeding. Because, dominance effects might be lost in further generations. The effective selection was possible in early generations for plant height, peduncle length, spikelet number per spike, grain number per spike and harvest index, since these traits had high narrow sense heritability, which estimated that according to additive gene action. Although the additive gene action founded significant in other traits, significant non-additive and epistatic gene effects and low narrow sense heritability reduced the success of early generation selection. Thus situated, selection to further generation allows that transfer of superior genotypes in further generations. Considering to (Yr, for Wr+Vr, r) value and graphical situation of genotypes might be advised Sonmez-01 was suitable parent for earliness and harvest index, Mufitbey was suitable parent for maturing time and peduncle length, Altay 2000 was suitable parent for plant height and spikelet per spike, Alpu-01 was suitable parent for spike length, Harmankaya 99 was suitable parent grain number and weight per spike and grain yield per plant.

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