DIALLEL ANALYSIS FOR GRAIN YIELD AND YIELD COMPONENTS IN WHEAT USING GRIFFING'S METHOD AND BIPLOT GRAPH

Y.A EL-Gohary[1] and Wafaa W.M. Shafie[2]

1. Wheat Res. Sec., Field Crop Res. Ins., ARC.
2. Central Lab. for Design & Stat. Analysis Res., ARC.

ABSTRACT

The present investigation was carried out at the Experimental Farm of Etai El-Baroud Agricultural Research Station, El-Beheira Governorate (Agricultural Research Center) during the two successive seasons of 2016-2017 and 2017-2018. Eight bread wheat cultivars and lines representing a wide range of diversity for several agronomic characters were selected for the study in a half diallel mating design which were analyzed by using Griffing's method and GGE biplot graph. The genetic analysis (variance, combining ability, heterosis, and Biplot) of grain yield per plant and some agronomic traits were evaluated. Genotypes were randomly distributed using RCBD design with three replications. Results revealed highly significant variations within parents and F_1 genotypes indicating a wide genetic variability for the studied characters and the possibility of genetic improvement using such genetic pools of wheat. Both general (GCA) and specific (SCA) combining abilities were significant for all studied characters revealing the important role of both additive and dominant components in the inheritance of the studied characters. Gemmeiza9 was good general combiner for grain yield/plant, biological yield, spike length, number of spikes per plant, number of kernels per spike and chlorophyll content. Several crosses exhibited highly significantly positive SCA effects for studied characters especially Gemmeiza9 × Line2 for grain yield/plant and most attributes. Highly significant heterosis was detected in two crosses (Gemmeiza9 x Line2) and (Sids13 x Line2) for grain yield/plant and some agronomic traits. Biplot graph is considered quickly and effective tool for assessing the genetic interrelationship among the genotypes.

Key words: *Triticum aestivum, Combining ability, Heterobeltiosis, Diallel analysis, Biplot*.

INTRODUCTION

Wheat crop (*Triticum aestivum* L.) is considered the most important cereal crop for urban and rural societies as well as the major source of straw for animals feeding in Egypt. The efforts of wheat breeders and genetics must be continue to improve wheat varieties and increase the productivity of unit area in order to minimize the gap between production and consumption.

Diallel cross technique is a good tool for identification of hybrid combinations that have the potentiality of producing maximum improvement and identifying superior lines among the progeny in early segregation generations (Soheir, M.H. Abd Allah and EL-Gammaal 2009). During breeding programs, it is necessary to select pure lines of high general combining ability (GCA) indicating the additive gene effect (Samier 2015).

Combining ability estimates provide information useful for the selection of parents and also provides information regarding the nature and magnitude of gene action involved. The knowledge of genetic structure

and mode of inheritance of different characters helps breeders to select appropriate breeding methodology (Kiani *et al* 2007).

Diallel crossing was usually done by using Griffing's methods (1956). These methods are less interpretative, difficult to understand without the aid of some graphical display (Dehghani *et al* 2010). Yan and Hunt (2002) have developed a quick evaluation method called GGE biplot model for analyzing the diallel data. This technique enhances the capability of interpreting the phenotypic variation to obtain combining ability and interrelationships of parents based on graphical presentation using PC1 and PC2 which are derived through PC analysis of environment-centered yield data. Genotype main effects and Genotype x Environment interaction effects (GGE biplot) model is a recent method and has been widely used to determine combining ability and heterotic responses (Shang *et al* 2006 and Darvishzadeh *et al* 2009). The GGE biplot methodology was developed for multi-environments trial (MET) data (Yan and Hunt 2002), in which, genotypes are entries and environments are testers. GGE biplot is also preferred to interpret the conventional diallel approach because it gives jointly GCA and SCA effects of the population and the preferences of the crosses as well as grouping pattern of similar genotypes, (Bertoia *et al* 2006).

The possible heterosis exploitation in wheat crop continues to be a critical question. The choice of parental material used in the hybridization scheme does contribute significantly for the development of a suitable genotype. The parents which are genetically superior and diverse in the traits of interest are utilized for varietal development programme (Rasul *et al* 2002).

Knowledge of the relative importance of additive and non-additive gene action is essential to plant breeder for the development of efficient hybridization programme. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbreds. Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value, and in the selection of suitable parents for hybridization (Singh and Narayanan 1993). During breeding programs, it is necessary to select pure lines of high general combining ability (GCA) that indicates the additive gene effect (Samier 2015). Knowledge about genetic mechanism, involved in the expression of yield-related traits, is helpful in developing superior genotypes. The information about the relative contribution of components

584

of variation i.e., additive, non-additive and epistasis, is essential for effective plant-improvement exercise (Azhar and Ajmal 1999).

The objectives of the present investigation were to: 1) identify good combining parents to be use in future breeding program. 2) Determine general combining ability (GCA) as well as specific combining ability (SCA) for genotypes. 3) Estimate heterosis in the experimental hybrids for grain yield and contributing traits. 4) Analyze diallel data using GGE biplot model to gather information about genetic interrelationships among parents, general and specific combining ability for grain yield, chlorophyll content and number of kernels/spike in wheat.

MATERIALS AND METHODS

Field experiments were conducted at the experimental farm of Etai EL-Baroud Agricultural Research Station, El-Beheira Governorate, Egypt, during 2016/2017 and 2017/2018 wheat growing seasons. The experimental materials consists of eight genotypes comprised of four cultivars namely, Gemmeiza 9 (P1), Sids 13 (P2), Shandweel 1 (P3), Giza 171 (P4), and four lines of bread wheat one Line1 (P5), Line2 (P6), Line3 (P7) and Line4 (P8) as shown in Table (1). In 2015/2016 growing season, grains for each of the parental genotypes were sown and all possible cross combinations excluding reciprocals were made among all the eight parental genotypes to produce their twenty eight F1 crosses. During 2016/2017 season, the experimental materials comprising 36 genotypes (8 parents in addition to their 28 F1's) were evaluated, using a randomized complete block design (RCBD) with three replicates. One row plot was used with 3.0 m long and 0.30 m apart. The grains were sown at a spacing of 20 cm within one row. All the recommended cultural practices of wheat production were done properly at the required time. Data for heading date, physiological maturity date, plant height, flag leaf area, chlorophyll content were recorded in the field. At harvesting time, the aimed characters were recorded as follow: number of spikes per plant, spike length, number of kernels/spike, 1000-kernel weigh, biological yield and grain yield, and harvest index (%). The chlorophyll content was quickly recorded using SPAD 502 meter in the field to assess the need for N- top dressing during pre panicle initiation and panicle differentiation growth stages of wheat.

Statistical analysis

The plant material was evaluated by analyzing the data on heterosis and combining ability for the studied traits at the F_1 generation. The genotypes are then analyzed according to Griffing's (1956) model I method

585

II (half-diallel set), fixed model to estimate the effects for general and specific combining ability for studied traits.

Table 1. Names and pedigree of the studied wheat parental genotypes.

No.	Name	Pedigree
P1	Gemmeiza 9	ALD'S'/HUAC'S'//CMH74.630/5X CGM 4583-5GM-1GM-0GM
P2	Sids 13	ALMAZ.19=KAUZ''S''// TSI/ SNB''S'' ICSBW 1-0375-4AP-2AP-030AP-0APS-3AP-0APS-050AP-0AP--0SD
P3	Shandweel 1	Site//Mo/4/Nac/Th.Ac./3*Pvn/3/Mirlo/Buc CMSS93B00567S-72Y-010M-010Y-010M-0HTY
P4	Giza 171	SAKHA 93/GEMMEZA 9 Gz2003-101-1Gz-4Gz-1Gz-2Gz-0Gz
P5	Line 1	PFAU/MILAN/5/WEAVER/4/NAC/TH.AC//3*PVN/3/MIRLO/BUCS.16258-021S-012S-1S-0S
P6	Line 2	CROC-1/AE.SQUARROSA(213)/ /PGO/3/SODAT/ /4/Gemmeiza#7GM9247-5GM-5GM-1GM-1GM2GM-0GM
P7	Line 3	PF74354//LD/ALD/4/*BR12*2/3/JUP//PAR214*6/FB6631/7/BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BBGLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX. GM-9659-1GM-2GM-2GM-0GM.
P8	Line 4	SAKHA80/6/SAKHA3/5/CNO79/4/BBSYG/3/RA/2F2/OM/7/SAKHA73/5/IAS58/4/KAL/BB//CJ"S"/3/ALD"S". SD9240-7SD-1SD-0SD.

In Genotype main effects and Genotype x Environment interaction effects (GGE biplot) model, mean and stability genotypes referred to GCA and SCA parents, respectively. The mean values for hybrids and parental populations across environments are used to form a symmetrical diallel data matrix from which the first two principle components (PC1 and PC2) were extracted. Each population corresponded to one row and one column of data, after obtaining the first two principle components of the adjusted data. The model for data analysis is:

$$Y_{ij} - \beta_j = \lambda_1 \varepsilon i_1 \eta_{j1} + \lambda_{2\varepsilon i2} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is genotypic values of the combination between two entries i and j for a given trait; βj is an average value of all combinations with entry j, λ_1 and λ_2 are singular values for PC1 and PC2. εi1 and εi2 are PC1 and PC2 eigenvectors for entry i, respectively; η_{j1} and η_{j2} are PC1 and PC2 eigenvectors for entry j, respectively; εij is the residual of model for entries i and j. This statistical method has been described by Yan and Hunt (2002) and Yan and Kang (2003). This analysis is done using GGE biplot software (Yan 2001).

The polygon view of the biplot is drawn by connecting the entries. The perpendicular line to each side drawn from the origin of the plot divides the biplot into several sectors. Entries falling in a sector shares the best mating partner with another entry present at the vertex of the polygon in that sector. Entries located near the biplot origin are less responsive to change of the entries.

Percentages of heterosis as proposed by Mather and Jinks (1982) were determined as the deviation of F_1 mean performance from better parent (BP) values and expressed as percentages as follows:

Better parent heterosis (%) = ($\overline{F_1}$-$\overline{BP}$)/$\overline{BP}$ x 100.

RESULTS AND DISCUSSION

Analysis of variance

Mean squares of the analysis of variance for the studied characters of 36 wheat genotypes (8 parents and 28 F_1 hybrids) are shown in Table (2). Results illustrated that differences among genotypes as well as parents and crosses are significant, except parent's vs. crosses for heading date, maturity date, and chlorophyll content. Rasul *et al* (2002) reported that, the analysis of variance for spike length, number of grains per spike, 1000-grain weight and grain yield per plant manifested highly significant differences among genotypes. Inamullah *et al* (2006) showed that, highly significant differences among the genotypes for all the traits studied. Akinci (2009) mentioned that, the analysis of variance showed significant differences among genotypes for heading time, thousand kernel weights and grain yield/plant traits.

Mean squares of both general (GCA) and specific (SCA) combining ability were significant for all studied characters (Table 2). Thus, both additive and non-additive gene effects were important in controlling the inheritance of all characters studied. Genetic component of variances is assessed through the estimates of GCA and SCA variances. The additive genetic variance is equal to GCA variance and dominance variance is equal to SCA variance. The ratio of GCA/SCA was more than unity for all studied characters except grain yield per plant, indicating that additive gene effects were more important than non-additive for these characters. The higher importance of GCA than SCA variance for studied characters was also reported by Abdel Nour (2006) , Salem and Abdel Dayem (2006), Kumar *et al* (2011), Singh *et al* (2013) and Rahul and Kandalkar (2018).

Table 2. Mean squares from analysis of variance and general and specific combining ability analysis for all studied characters in eight parent half diallel crosses of wheat.

SOV	df	Heading date	Days to maturity	Flag leaf area	Chlorophyll content	Plant height (cm)	Spike length (cm)
Replication	2	23.51	16.67	7.15	2.10	1.99	0.01
Genotypes	35	26.42**	22.37**	105.72**	48.65**	81.36**	7.21**
Parents (P)	7	51.14**	43.69**	195.23**	76.53**	221.09**	18.87**
Crosses (C)	27	20.97**	17.66**	84.52**	43.22**	46.88**	4.28**
P vs C	1	0.32	0.28	51.46**	0.19	34.42**	4.44**
GCA	7	26.28**	53.25**	31.07**	15.30*	34.95**	82.28**
SCA	28	6.72**	10.56**	14.37**	7.01**	13.18**	14.46**
Error	70	0.357	0.44	2.91	2.73	2.11	0.09
GCA/SCA		3.91	5.04	2.16	2.18	2.65	5.69
SOV	df	No. of spikes/ plant	Number of Kernels/ spike	1000-kernel weight	Biological yield/pl	Grain yield/pl (g)	Harvest index (%)
Replication	2	1.41	45.65	0.11	156.7**	7.10	16.76
Genotypes	35	61.92**	417.07**	64.48**	2378.9*	247.35**	27.36**
Parents (P)	7	48.93**	713.91**	125.79**	2240.9*	230.13**	49.83**
Crosses (C)	27	60.13**	341.30**	50.82**	2150.2*	231.25**	19.34**
P vs C	1	201.34**	385.08**	4.42**	9520.5*	802.66**	86.52**
GCA	7	48.39**	31.32**	62.57**	1671.1*	148.87**	19.19**
SCA	28	29.02**	14.56**	18.04**	1302.6*	160.31**	15.01*
Error	70	1.47	11.36	1.271	74.66	22.97	8.44
GCA/SCA		1.28	2.15	3.47	1.28	0.93	1.28

Performance of wheat genotypes

Mean values of different studied characters of the eight wheat parental genotypes and their 28 half diallel F_1's are presented in Table (3). Days to heading for parents ranged from 89.67 for P8 to 101.00 for P5 with an average of 96.67 while the F_1 crosses ranged from 90.33 for cross P5xP8 to 102.33 for cross P1xP7 with an average of 96.54 days.

588

Table 3. Mean performance of eight Parents and their F1 crosses for all studied characters in bread wheat.

Parents and crosses		Heading date	Days to maturity	Flag leaf area	Chlorophyll content	Plant height(cm)	Spike length(cm)
P1		100.00	145.33	42.61	53.43	105.00	14.52
P2		99.00	142.33	36.56	48.20	82.45	10.69
P3		95.00	141.67	50.49	51.87	107.11	15.17
P4		95.00	143.33	51.98	54.30	104.89	13.29
P5		101.00	142.33	41.99	53.30	88.56	8.35
P6		93.00	136.33	42.07	46.63	99.17	9.47
P7		100.67	149.00	58.85	60.90	97.39	12.94
P8		89.67	139.00	57.23	58.40	99.89	14.12
Mean parent		96.67	142.42	47.72	52.75	98.06	12.32
P1	P2	98.33	143.33	46.78	41.43	98.30	13.04
	P3	97.33	143.67	39.15	49.53	100.69	14.21
	P4	98.00	145.00	52.55	53.33	99.32	14.20
	P5	97.67	141.67	47.47	47.93	97.00	12.61
	P6	101.67	145.67	47.86	52.43	102.33	12.99
	P7	102.33	146.67	49.25	56.73	97.67	13.90
	P8	98.00	142.67	49.59	53.67	101.78	13.53
P2	P3	93.00	140.67	42.64	52.10	95.00	13.46
	P4	95.67	142.67	46.44	52.37	99.53	12.99
	P5	94.00	138.67	41.35	49.47	90.67	10.51
	P6	95.00	131.67	42.91	50.17	99.77	12.86
	P7	97.00	132.00	45.81	53.97	92.42	12.03
	P8	95.67	141.00	47.29	49.67	100.22	13.74
P3	P4	95.00	142.67	54.30	53.57	105.00	14.52
	P5	95.33	147.33	42.84	51.43	94.92	11.60
	P6	96.00	141.00	46.61	54.10	101.50	11.64
	P7	99.33	144.00	48.16	57.67	102.33	13.78
	P8	94.00	142.33	47.89	55.10	106.50	15.02
P4	P5	95.33	144.67	47.25	50.77	97.67	11.30
	P6	97.67	143.33	55.03	52.30	104.55	12.75
	P7	100.67	143.67	54.52	54.80	98.00	13.08
	P8	93.67	145.00	53.13	51.83	100.67	13.83
P5	P6	96.33	141.67	49.45	48.83	97.65	10.76
	P7	95.33	145.67	58.77	62.50	92.33	11.01
	P8	90.33	146.67	57.01	52.10	104.22	12.45
P6	P7	99.33	142.67	59.08	55.70	97.89	11.08
	P8	95.33	140.67	54.25	54.00	103.48	12.65
P7	P8	95.67	142.67	55.38	56.90	102.17	13.03
Mean		96.54	143.19	49.38	52.66	99.41	12.81
L.S.D5%		0.97	1.07	2.76	2.67	2.35	0.49
L.S.D1%		1.26	1.39	3.59	3.48	3.06	0.64

Table 3. Cont.

Parents and crosses		No. of spikes/plant	No. of Kernels/spike	1000-kernels weight	Biological yield/plant	Grain yield/plant	Harvest index (%)
P1		17.00	98.89	47.22	145.22	52.29	36.00
P2		11.42	86.03	37.58	70.31	29.84	42.44
P3		9.78	89.45	49.27	100.00	35.62	35.61
P4		9.78	83.00	53.82	102.89	35.91	34.96
P5		13.67	84.78	38.57	86.78	38.08	43.96
P6		11.25	68.42	46.88	86.00	29.17	33.92
P7		5.44	121.72	50.50	77.22	29.38	38.02
P8		4.67	95.44	55.43	53.44	23.14	43.26
Mean parent		10.38	90.97	47.41	90.23	34.18	38.52
P1	P2	16.72	88.12	44.77	127.26	46.06	36.20
	P3	16.28	102.00	42.20	124.58	44.34	35.54
	P4	16.02	94.20	45.52	124.95	43.76	34.97
	P5	24.56	98.11	42.92	173.89	59.12	34.02
	P6	21.67	88.66	47.38	181.67	63.90	35.17
	P7	16.00	108.00	51.83	136.67	47.04	34.44
	P8	10.67	93.55	48.13	102.44	35.93	35.14
P2	P3	12.22	89.58	41.95	112.33	39.26	34.97
	P4	13.00	92.33	46.43	105.40	40.79	38.69
	P5	15.00	91.00	39.52	95.27	36.57	38.39
	P6	17.04	81.04	47.70	121.10	39.92	32.96
	P7	10.00	103.42	46.40	104.67	38.75	37.05
	P8	11.45	101.56	49.38	110.56	49.01	43.85
P3	P4	17.00	103.44	46.75	144.11	50.53	35.10
	P5	14.25	93.75	42.93	94.08	35.13	37.33
	P6	14.58	81.75	48.95	115.58	42.80	37.15
	P7	12.00	102.00	50.42	114.50	40.30	35.23
	P8	12.67	98.00	53.28	115.00	41.78	36.36
P4	P5	19.00	85.17	44.37	116.83	41.78	35.60
	P6	14.63	90.88	48.07	117.25	36.75	31.35
	P7	11.67	107.83	49.98	105.00	40.93	39.00
	P8	13.00	100.23	49.65	110.00	42.40	38.60
P5	P6	16.77	83.80	45.38	120.50	39.73	32.93
	P7	4.14	127.85	50.67	63.61	25.23	39.52
	P8	7.33	106.78	53.05	84.89	33.57	39.50
P6	P7	8.22	90.78	52.93	81.11	29.19	36.02
	P8	10.58	74.37	54.93	100.62	35.04	34.92
P7	P8	6.00	96.00	55.57	55.00	21.00	38.31
Mean		13.66	95.51	47.90	112.82	40.74	36.37
L.S.D5%		1.96	5.45	1.82	13.97	7.75	4.70
L.S.D1%		2.56	7.10	2.37	18.19	10.09	6.11

590

For maturity date, P6 was the earliest one with value of 136.33 and P5 was the latest one with value of 145.33 days, with an average of 142.42 days, also cross P2xP6 and P2xP7 were the earliest with value of 131.67 and 132.00 and P3xP5 was the latest one with value of 147.33 days, respectively, with an average of 143.19 days. Regarding flag leaf area, mean values for parents ranged from 36.56 for P2 to 58.85 cm^2 for P7 with an average of 47.72 cm^2 while the F_1 crosses ranged from 39.15 cm^2 for cross P1xP3 to 59.08 cm^2 for cross P6xP7 with an average of 49.38 cm^2. Concerning Chlorophyll content, the mean values for parents developed differences with range of 46.63 (P6) – 60.90 (P7) with an average equal to 52.75 while the mean values of F1 hybrids displayed significantly differed and varied from 41.43 (P1xP2) to 62.50 (P5xP7) with an average of 52.66.

The results revealed that, the mean values of parents showed differences with range of 82.45 (P2) to 107.11 (P3), mean while crosses ranged from 92.42 (P2×P7) to 106.52 (P3×P8) with an average of 99.41 for plant height. Regarding spike length ranged from 8.35 (P5) to 15.17 (P3) with an average equal to 12.32 while the F1 crosses ranged from 10.51 (P2×P5) to 15.02 (P3×P8), with an average equal to 12.81. Concerning number of spikes/plant ranged from 4.67 (P8) to 17.00 (P1) with an average 10.38 while the crosses ranged from 4.14 (P5×P7) to 24.56 (P1×P5) with an average 13.66. Number of kernels/spike for 68.42 (P6) to 121.72 (P7) with an average 90.97, while the F1 crosses ranged from 74.37 (P6×P8) to 127.85 (P5×P7) with an average 95.51, 1000-grain weight for, 37.58 (P2) to 55.43 (P8) with an average 47.41 while the F1 crosses ranged from 39.52 (P2×P5) to 55.57 (P7×P8) with an average 47.90. Biological yield/plant for, 53.44 (P8) to 145.22 (P1) with an average 8.10 while the F_1 crosses ranged from 10.51 (P2×P5) to 15.02 (P3×P8), with an average 112.82. Harvest index 33.92% (P6) to 43.96% (P5) with an average 38.52 while the crosses ranged from 31.55 (P4×P6) to 43.85 (P2×P8) with an average 36.37. Grain yield/plant for 23.14 (P8) to 52.29 (P1) with an average 34.18 while the crosses ranged from 21 (P7×P8) to 63.90 (P1×P6), with an average 40.74, respectively.

The parental genotype (P1) recorded the highest number of spikes per plant, biological and grain yield/plant. However, P3 recorded the highest values of plant height and spike length (cm). Parents no. 6 and 8 were the earliest heading date and maturity date, Parent no. 5 recorded the highest harvest index. Parent no. 7 had the maximum values of flag leaf area,

chlorophyll content and number of kernels per spikes. P8 recorded the highest 1000 kernels weight and was the earliest for heading date.

The crosses of (P2xP3) and (P2xP6) were the latest in heading date and maturity, respectively. The crosses registered the highest values of flag leaf area, (P6xP7), (P5xP7) chlorophyll content and number of kernels per spikes, P3xP8 plant height and spike length, respectively. The maximum values for number of spikes per plant, 1000 kernels weight, biological yield, grain yield per plant and harvest index were recorded by crosses (P1xP5, P7xP8, P1xP6 and P2xP8), respectively.

In general, there were magnitudes of increases toward the cross averages over the parent averages for the characters of number of spikes/plant (13.66 and 10.38), number of kernels/spike (95.51 and 90.97), biological yield (112.82 and 90.23 g), and (grain yield (40.74 and 34.1 g) indicating positive heterotic effect. It could be concluded that the above mentioned parents and crosses would be valuable for improving grain yield via its component characters.

General combining ability (GCA) effects.

Combining ability plays a major role in the evaluation of inbred in terms of their breeding values; and this will help to decide efficient breeding method to be applied in segregating generations. It is primarily a function of additive genetic variance; it helps in the selection of suitable good general combining parents for hybridization. The (GCA) effects are presented in Table (4).

Data presented in Table (4) revealed that two parents *viz* P5 and P8 reported significant and negative GCA effects for heading and maturity date, suggesting good general combiner for improvement of earliness in the breeding program. Results showed that the three parents P4, P7 and P8, were good combiners for flag leaf area and P1, P7 and P8 for chlorophyll content while parents, P2 and P5 had good (negative) GCA effects for short plant height and P1, P3, P4 and P8 had good (positive) GCA effects for tall plant height. However, P1 was good general combiner for grain yield, biological yield, spike length, number of spikes per plant and number of kernels per spikes. For yield attributes, the largest positive GCA effect was exhibited by P3, P4 and P8 for spike length (cm) P5 and P6 for number of spikes per plant, P8 for number of kernels per spikes, P4, P7 and P8 for 1000 kernels weight, and P2, P5 and P8 for harvest index (%). Accordingly, these parents are considered good genotypes for breeding programs to increase and develop yield and yield components in bread wheat.

Table 4. Estimates of general (GCA) and specific (SCA) combining ability effects for studied characters.

Character		Heading date	Days to maturity	Flag leaf area	Chlorophyll content	Plant height	Spike length
P1		2.43**	1.68**	-2.33*	3.22**	1.51*	0.92**
P2		-0.24	-0.79	-5.48**	-2.85**	-5.12**	-0.43**
P3		-0.91*	-0.56	-1.86*	0.31	2.82**	1.03**
P4		-0.31	1.14*	2.61**	0.35	2.25**	0.50**
P5		-1.88**	-2.66**	-1.30	-0.45	-4.04**	-1.73**
P6		1.43**	0.01	-0.18	-1.33	1.35	-1.06**
P7		2.19**	2.71**	4.75**	4.60**	-1.44	-0.05
P8		-2.71**	-1.53**	3.79**	1.60*	2.68**	0.82**
LSD gi 5%		0.20	0.22	0.58	0.56	0.50	0.10
LSD gi 1%		0.27	0.30	0.77	0.75	0.66	0.14
LSD gi-gi 5%		0.62	0.69	1.78	1.72	1.52	0.32
LSD gi-gi 1%		0.83	0.92	2.36	2.29	2.01	0.42
P1	P2	-0.42	-0.06	5.57**	-6.17**	2.80**	-0.16
	P3	-0.75*	0.04	-5.68**	-1.24	-2.74**	-0.44*
	P4	-0.68*	-0.33	3.26*	2.53**	-3.55**	0.08
	P5	0.55	0.14	2.08*	-2.08**	0.42	0.72**
	P6	1.25**	1.47**	1.35	3.30**	0.36	0.43*
	P7	1.15**	-0.23	-2.20*	1.68	-1.51**	0.33
	P8	1.72**	0.01	-0.88	1.61	-1.52**	-0.91**
P2	P3	-2.41**	-0.49	0.96	1.96	-1.81	0.16
	P4	-0.35	-0.19	0.30	2.20**	3.29**	0.22
	P5	-0.45	-0.39	-0.88	0.09	0.72	-0.03
	P6	-2.75**	-0.06	-0.45	1.67*	4.43**	1.65**
	P7	-1.51**	-2.43**	-2.48	-0.45	-0.13	-0.19
	P8	2.05**	0.81*	-0.03	-1.75	3.55**	0.64**
P3	P4	-0.35	-0.43	4.54**	0.23	0.82	0.30
	P5	1.55**	1.37**	-3.02**	-1.11	-2.97**	-0.39*
	P6	-1.08**	-1.63**	-0.37	2.44**	-1.78	-1.02**
	P7	1.49**	1.34**	-3.76**	0.08	1.85**	0.10
	P8	1.05**	-0.76	-3.05**	0.51	1.89**	0.47*
P4	P5	0.95**	3.01**	-3.07**	-1.81	0.35	-0.16
	P6	-0.01	-0.33	3.59**	0.61	1.84**	0.61**
	P7	2.22**	0.97	-1.85*	-2.82**	-1.92	-0.06
	P8	0.12	0.21	-2.28**	-2.79**	-3.38**	-0.18
P5	P6	0.22	0.81	1.92*	-2.07	1.23	0.85**
	P7	-1.55**	-1.56**	6.31**	5.67**	-1.29	0.09
	P8	-1.65**	-1.66**	5.51**	-1.73	6.47**	0.67**
P6	P7	-0.85**	-1.23**	5.49**	-0.24	-1.13	-0.51*
	P8	0.05	1.34**	1.63	1.06	0.34	0.19
P7	P8	-0.38	0.97	-2.17**	-1.97	1.82**	-0.44*
LSD Sij 5%		0.54	0.60	1.55	1.50	1.32	0.28
LSD Sij 1%		0.72	0.80	2.06	1.99	1.75	0.37
LSD sii-sik 5%		0.92	1.02	2.63	2.55	2.25	0.47
LSD sii-sik 1%		1.23	1.35	3.50	3.39	2.98	0.63
LSD sii-skl 5%		0.87	0.96	2.48	2.41	2.12	0.44
LSD sij-skl 1%		1.16	1.28	3.30	3.19	2.81	0.59

Table 4. Cont.

Character		No. of spikes/plant	No. of Kernels/spike	1000-kernels/spike	Biological yield/plant	Grain yield/plant	Harvest index (%)
P1		3.95**	1.99**	-1.29*	29.17**	9.12**	-1.42*
P2		0.19	-3.14*	-3.88**	-5.30	-0.35	1.54*
P3		0.22	-1.11	-0.51	5.00*	1.19	-0.87
P4		0.75	-1.04	0.83*	5.91*	1.53	-0.84
P5		1.20*	0.55	-3.4**	-4.76*	-0.62	1.36*
P6		0.96*	-12.24**	0.90	3.96*	-0.78	-2.33*
P7		-3.75**	2.10**	2.87**	-15.52**	-5.23**	0.40
P8		-3.53**	12.88**	4.48**	-18.48**	-4.85**	2.16*
LSD gi 5%		0.41	1.15	0.38	2.94	1.63	0.99
LSD gi 1%		0.55	1.52	0.51	3.91	2.17	1.31
LSD gi-gj 5%		1.26	3.52	1.18	9.02	5.00	3.03
LSD gi-gj 1%		1.67	4.67	1.56	11.98	6.64	4.03
P1	P2	-0.35	-5.23**	2.15**	-4.41	-1.99	-0.77
	P3	-0.83	5.61**	-3.79**	-17.39**	-5.25*	0.98
	P4	-1.62**	-1.25	-1.81**	-17.93**	-6.16**	0.37
	P5	6.47**	1.07	-0.17	41.68**	11.34**	-2.77*
	P6	3.82**	4.41**	-0.02	40.73**	16.28**	2.06*
	P7	2.86**	-1.38	2.46**	15.22**	3.87	-1.39
	P8	-2.68**	-4.03*	-2.84**	-16.05**	-7.62**	-2.45
P2	P3	-1.12*	-1.67	-1.45	4.83	-0.86	-2.55
	P4	-0.87	2.01	1.69**	-3.01	0.33	1.14
	P5	0.68	-0.91	-0.98	-2.48	-1.74	-1.35
	P6	2.96**	1.92	2.89**	14.64**	1.77	-3.09*
	P7	0.63	-0.83	-0.38	17.69**	5.05*	-1.74
	P8	-1.48**	9.11**	0.99	26.54**	14.93**	3.31*
P3	P4	3.10**	10.09**	-1.36	25.40**	8.54**	-0.04
	P5	-0.10	-1.19	-0.94	-13.96**	-4.72*	0.00
	P6	0.47	-0.41	0.77	-1.18	3.12	3.51**
	P7	2.60**	-5.28**	0.26	17.22**	5.07*	-1.15
	P8	3.05**	2.52	1.52	20.68**	6.17**	-1.77
P4	P5	4.12**	-8.84**	-0.84	7.88**	1.60	-1.77
	P6	-0.01	9.66**	-1.46	-0.43	-3.27	-2.33
	P7	1.73**	1.49	-1.51	6.81	5.36*	2.60
	P8	2.85**	5.69**	-3.45**	14.77**	6.44**	0.43
P5	P6	1.67**	0.99	0.10	13.49**	1.86	-2.94**
	P7	-6.25**	19.92**	3.42**	-23.91**	-8.19**	0.92
	P8	-3.27**	10.64**	4.20**	0.33	-0.24	-0.87
P6	P7	-1.93**	-4.37**	1.37**	-15.13**	-4.07	1.10
	P8	0.22	-8.98**	1.76*	7.33	1.40	-1.75
P7	P8	0.35	-12.47**	0.43	-18.80**	-8.20**	-1.10
LSD Sij 5%		1.10	3.06	1.02	7.85	4.35	2.64
LSD Sij 1%		1.45	4.07	1.36	10.42	5.78	3.50
LSD sij-sik		1.86	5.21	1.74	13.35	7.40	4.49
LSD sij-sik		2.47	6.91	2.31	17.72	9.83	5.96
LSD sij-skl		1.76	4.91	1.64	12.59	6.98	4.23
LSD sij-skl		2.33	6.52	2.18	16.71	9.27	5.62

594

These genotypes can be used in the development of high yielding varieties through the pedigree selection and progeny selection or mass selection in later generations in promising segregating generations in wheat. Present findings are in confirmation with those Kapoor *et al* (2011), Kumar *et al* (2011), Singh *et al* (2013), Aslam *et al* (2014), Raj and Kandalkar (2013), Samier (2015), Kalhoro *et al* (2015), Kandil *et al* (2016) and Rahul and Kandalkar (2018).

Specific combining ability (SCA) effects

It is mainly a function of dominance variances; it helps in the identification of superior cross combination for commercial exploitation of heterosis. In self–pollinated crops like wheat, SCA effects are not much important as they are mostly related to non-additive gene effects excluding those of arising from complementary gene action or linkage effects .They cannot be fixed in pure lines. Further superiority of the hybrids might not indicate their ability to create transgressive segregates, rather SCA would provide satisfactory criteria. However, if a cross combination exhibiting high SCA as well as high per se performance having at least one parent as good general combiner for a specific trait, it is expected to throw desirable transgressive segregants in later generations.

Specific combining ability (SCA) effects of the F_1 crosses for studied characters are presented in Table (4). The results showed that the best SCA effects for days to heading were obtained from crosses (P1xP3), (P1xP4), (P2xP3), (P2xP6), (P2xP7), (P3xP6), (P5xP7), (P5xP8) and (P6xP7). On the other hand, crosses (P2xP7), (P3xP6), (P5xP7), (P5xP8), and (P6xP7) had good SCA effects for maturity date. So these crosses could be used for earliness breeding program for wheat.

For short plant, crosses (P1xP3), (P1xP4), (P1xP7), (P1xP8), (P3xP5) and (P4xP8), and for tall plants crosses (P1xP2),P2xP4), (P2xP6), (P2xP8), (P3xP7),(P3xP8), (P4xP6) and (P5xP8) had significant SCA effects for short or tall plant height, respectively. Maximum positive SCA effects were recorded by (P1xP4), (P1xP6), (P2xP4), (P3xP6) and (P5xP7) for Chlorophyll content. Crosses (P1xP5), (P1xP6), (P2xP6), (P3xP8) , (P4xP6) , (P5x6) and(P5xP8) for spike length (cm), (P1xP5), (P1xP6), (P1xP7), (P2xP8), (P3xP4), (P3xP8), (P4xP5), and (P4xP8) number of spikes per plant, crosses (P1xP3), (P1xP6), (P2xP8), (P3xP4), (P4xP6), (P4xP8), (P5xP7) and (P5xP8) for number of kernels per spike, crosses (P1xP2), (P1xP7), (P2xP4) , (P2xP6), (P5xP7), (P5xP8) and (P6xP8) for 1000 kernel weight and crosses (P1xP5), (P1xP6), (P2xP7) , (P2xP8),

(P3xP4), (P3xP7), (P4xP7) and (P4xP8) for grain yield per plant, and crosses (P3xP6) and (P2xP8). These crosses had significant SCA effects for grain yield and yield components. Present findings are in confirmation with those Kumar *et al* (2011), Kapoor *et al* (2011), Singh *et al* (2013), Raj and Kandalkar (2013), Aslam *et al* (2014), Desale *et al* (2014), Kalhoro *et al* (2015) and Kandil *et al* (2016) .

Heterosis effects

The heterosis plays an important role for increasing the productivity of crop without much increase in the cost of production. Grain yield is a complex character rely on many traits. Yield potential accompanied with desirable combination of traits has always been the major objective of wheat breeding program (Kumar, 2013). Thus, the phenomenon of heterosis has revolutions the production in many crops including wheat in commercial basis. Percentages of heterosis relative to better (BP) parent for studied wheat crosses are presented in Table (5). Values of heterosis percentage relative to (BP) were significant and negative in (4) and (2) for better parents in heading and maturity date, respectively. Meanuelile, only (3) crosses exhibited significant positive hetrosis relative to better parent for plant height trait. Value of hetrosis percentage relative to better parent were significant and positive in 6,2,8, 17, 6, 3,12 and 14 with a range of (4.46 to 17.54),(4.09 to 4.30), (13.62 to 32.83), (4.24 to 73.82), (5.78 to 15.64), (1. 75 to 4.81) , (12.33 to 40.81) and (10.22 to 64.24) for flag leaf area, Chlorophyll content, spike length, number of spikes, number of kernels, 1000 kernel weight, biological yield and grain yields, respectively, (Table 5). The best heterobeltiosis was recorded by (P2xP6) (-4.04%), (-7.85) and (P2xP7 (-2.02%) and (-7.25) for days to heading and day to maturity. P5xP6 (17.54%), P3xP6 (4.30%), P5xP8 (4.33%), P1xP4 (32.83%), P3xP4 (73.82%), P3xP4 (15.64%), P6xP7 (4.81%) ,P2xP6 (40.81%) and P2xP8 (64.24%) for flag leaf area, chlorophyll content, plant height, spike length, number of spikes, number of kernels, 1000 kernel weight ,biological yield and grain yield. Pronounced and favorable heterosis has been obtained by several researchers for wheat characters among them are Munir *et al* (1999), Rasul *et al* (2002) and Motawea (2006).

Biplot analysis

Biplot graph is considered quickly and effective tool for assessing the genetic interrelationship among the genotypes.

596

Table 5. Heterosis over better parent (BP) for studied characters.

Character		Heading date	Days to maturity	Flag leaf area (FLA)	Chlorophyll content	Plant height	Spike length
P₁	P₂	-0.68	0.70	9.79**	-22.46**	-6.38**	21.98**
	P₃	2.45**	1.41*	-22.46**	-7.30**	-5.99**	-6.33**
	P₄	3.16**	1.17*	1.10	-1.79**	-5.41**	32.83**
	P₅	5.02**	3.92**	11.41**	-10.29**	-7.62**	17.96**
	P₆	1.67**	2.35**	12.32**	-1.87	-2.54**	21.52**
	P₇	2.33**	0.92	-16.31**	-6.85**	-6.98**	30.03**
	P₈	9.29**	2.64**	-13.35**	-8.10**	-3.07*	26.57**
P₂	P₃	-2.11**	-0.71	-15.55**	0.44	-11.31**	-11.27**
	P₄	0.71	0.24	-10.66**	-3.55*	-5.11**	-2.26
	P₅	1.08*	1.72**	-1.52	-7.19**	2.38*	-1.68
	P₆	-4.04**	-7.85**	2.00	4.09**	0.61	20.30**
	P₇	-2.02**	-7.25**	-22.16**	-11.38**	-5.10**	-7.03**
	P₈	6.69**	1.44**	-17.37**	-14.95**	0.33	-2.69*
P₃	P₄	0.00	0.71	4.46**	-1.34	-1.97	-4.28**
	P₅	2.51**	8.07**	-15.15**	-3.51**	-11.38**	-23.53**
	P₆	1.05*	-0.47	-7.68**	4.30**	-5.24**	-23.27**
	P₇	4.56**	1.64**	-18.16**	-5.30**	-4.46**	-9.16**
	P₈	4.83**	2.40**	-16.32**	-5.65**	-0.57	-0.99
P₄	P₅	2.51**	6.12**	-9.10**	-6.50**	-6.88**	-14.97**
	P₆	2.81**	0.70	5.87**	-3.68**	-0.32**	-4.06**
	P₇	5.97**	0.24	-7.36**	-10.02**	-6.57**	-1.58
	P₈	4.46**	4.32**	-7.16**	-11.25**	-4.02**	-2.05
P₅	P₆	3.58**	3.92**	17.54**	-8.39**	-1.53	13.62**
	P₇	2.51**	6.85**	-0.14	2.63	-5.20**	-14.91**
	P₈	0.74	7.58**	-0.38	-10.79**	4.33**	-11.83**
P₆	P₇	-1.33**	0.24	0.39	-8.54**	-1.29	-14.37**
	P₈	6.31**	1.20*	-5.21**	-7.53**	3.59**	-10.41**
P₇	P₈	6.69**	2.64**	-3.23*	-2.57	2.28	-7.72**
L.S.D5%		0.97	1.08	2.78	2.69	2.37	2.50
L.S.D1%		1.29	1.43	3.69	3.57	3.14	3.66

Table 5. Cont.

Character		No. of spikes/ plant	No. of Kernels/ spike	1000-kernels/ spike	Biological yield/plant	Grain yield/ plant	Harvest index
P_1	P_2	-1.65	-10.89**	-5.19**	-12.37	-11.91**	-14.70**
	P_3	-4.24**	3.14	-14.35**	-14.21*	-15.20**	-1.28
	P_4	-5.76**	-4.74	-15.42**	-13.96	-16.31**	-2.86
	P_5	44.47**	-0.79	-9.11**	19.74**	13.06**	-22.61**
	P_6	27.47**	-10.34**	0.34	25.10**	22.20**	-2.31
	P_7	-5.88**	-11.27**	2.63*	-5.89	-10.04*	-9.42**
	P_8	-37.24**	-1.98	-13.17**	-29.46**	-31.29**	-18.77**
P_2	P_3	7.01**	0.15	-14.86**	12.33**	10.22*	-17.60**
	P_4	13.84**	7.32**	-13.73**	2.44	13.59*	-8.84**
	P_5	31.35**	5.78*	2.46*	9.78	-3.97	-12.67**
	P_6	49.21**	-5.80*	1.75*	40.81**	33.78**	-22.34**
	P_7	-12.43**	-15.03**	-8.12**	35.55**	29.86**	-12.70**
	P_8	0.26	6.41*	-10.91**	36.89**	64.24**	1.36
P_3	P_4	73.82**	15.64**	-13.14**	40.06**	40.71**	-1.43
	P_5	4.24**	4.81	-12.87**	-5.92	-7.75	-15.08**
	P_6	29.60**	-8.61**	-0.65	15.58*	20.16**	4.30
	P_7	22.70**	-16.20**	-0.16	14.50*	13.14**	-7.34
	P_8	29.55**	2.68	-3.88**	15.00*	17.29**	-15.95**
P_4	P_5	38.99**	0.46	-17.56**	13.55	9.72	-19.02**
	P_6	30.04**	9.49**	-10.68**	13.96	2.34	-10.33**
	P_7	19.33**	-11.41**	-7.13**	2.05	13.98**	2.58
	P_8	32.92**	5.02	-10.43**	6.91	18.07**	-10.77**
P_5	P_6	22.68**	-1.16	-3.20**	38.86**	4.33	-25.09**
	P_7	-69.71**	5.04	0.34	-26.70**	-33.74**	-10.10**
	P_8	-46.38**	11.88**	-4.29**	-2.18	-11.84**	-10.15**
P_6	P_7	-26.93**	-25.42**	4.81**	-5.69	-0.65	-5.26
	P_8	-5.96*	-22.08**	-0.90	17.00*	19.26**	-19.28**
P_7	P_8	10.29**	-21.13**	0.25	-28.77	-28.52	-11.44
L.S.D5%		1.98	5.49	1.84	14.07	7.80	4.73
L.S.D1%		2.62	7.29	2.44	18.68	10.36	6.28

Grain yield

The principal component explained 73.23% (41.00 and 32.23 % by PC1 and PC2, respectively) of the variation for grain yield. The average tester coordinate biplot indicates that genotypes G1, G5, G6,(G2,G3 and G4) had positive GCA effects. Where- as genotypes G7 and G8 had negative GCA effects (Fig.1) biplot the best way to demonstrate the interaction patterns between entries and testers as mentioned by Yan *et al*., (2000) and Yan and Hunt (2002). Five entries are on the vertex on which they have the largest distances from the origin. The polygon view provides a way to group testers based on their best mating partners. Testers falling in the same sector share the same best mating partner and those falling in different sectors have different best mating partners.Subsequently, the entry G1 is the best mating partner for g7, g5, and g6. G1 had the highest GCA, because three of the other eight testers were located in this sector. Therefore, heterosis between G1 and any of the other parents is not possible. Two well differentiated and opposite groups can be observed, G7 and G8. The entry G8 is the best mating partner for g2, g4, and g3. Genotypes G7 and G8 produced the worst combinations with themselves, since testers' g7 and g8 fell into opposite sectors. Testers g1 and g8 fell into sector G2, indicating that their crosses with G2, generated good hybrid combinations. The combination (G2) x (g8) would be the best among all crosses involved and therefore heterosis between G1 and any of the other parents is not possible. Moreover, the parent G1 as a tester was found in this sector. In the same manner, G2 was in the second arranging for GCA, because one tester (g 8) was located in this sector. The parent G2 as a tester was not found in sector g 2 as entry, so heterosis was suggested in the hybrids of G2 with the tester (g 8). On the other hand, G7 and G 8 was in the third arrange for GCA, because 3 testers (g2, g 3 and g 4) were located in this sector. The parents g7 and g 8 as tester were not found in sector (G7 and G 8) as entry, so heterosis was suggested in the hybrids of (G7 and G 8) with the testers (g7 and g 8). Rastogi, *et a*l (2011) reported that all the heterotic crosses obtained through biplot analysis showed similar heterotic effects for same crosses analyzed manually.

Heterosis occurred between G1 and G 8 and between G5, G6 and G 7, suggesting different dominant genes in G1 and G8 as one group and G5, G6 and G7 as another. Entry G4 and G3, located near the plot origin, was intermediate between these two heterotic groups. Therefore, Entry G4 and G3 might carry two genes, one being the same as that in G7 and G 8,

which caused heterosis when crossed with G1 and the other being the same as that in G5, G6 and G1. This explains the fact that G4 and G3 had better GCA effects than G5, G6 and G7 and showed no large heterosis with any of the testers except G1.

Chlorophyll content

The biplot in figure 2 provided the best way to demonstrate the interaction patterns between entries and testers as mentioned by Yan *et al* (2000) and (Yan and Hunt, 2002). The first two principal components explained 75.63% (44.27 and 31.36 % by PC1 and PC2, respectively) of the variation for Chlorophyll. A polygon view is shown in the biplot such that five entries are on the vertices while three are inside the polygon. Since the vertex entries have the largest distances from the origin, they are most responsive to the change of testers relative to other entries within respective groups. The biplot was divided into three sectors.

The testers g4, g8, g5, g3 and g7 fell in the sectors that have the partner G7 and G8 which represents the best mating partner. Moreover, the parents g8 and g7 as a tester was found in this sector, so heterosis was suggested rids G8 and G7 with the testers (g4, g2 and g3).The biplot clearly shows why G7 had the highest GCA, since it was the vertex entry in a sector in which five of the other eight testers. Entries and testers in the same sector represent good hybrid combinations and potential heterotic groups (Krishnamoorthy 2005). In sector G7, g8 was predicted to be the best mating partner for G7, while in sector g7, is the best partner for G8. Both G7 and G 8 were therefore, identified to be the best partners for each other. Meanwhile, the only tester G1 is located in the sector that has the vertex g 6 which represents the best mating partner. For the other sectors including G2, G3, G5 and G4 there is no testers fell in, indicating that these parents were not the best partner with any of the other parents. The distance between the x axis and a genotype in the biplot is an estimation of its SCA effect (analogous to stability in GGE biplots). Some genotype clustered near the x axis, indicating that SCA effects were not important for Chlorophyll. Two heterotic groups are suggested by Fig. 1A: Geno- types G7 and G1 ≈ G2 as one group, and Genotypes G5, G4 and G6 as the other. Therefore, eight crosses, that is, [G7, G1, G2] [G5, G4, G6] are expected to show heterosis defined as better than both parents. Entry G3 and G8 located near the origin abscissa, and did not seem to belong to any of the groups.

Number of kernels per spike

Both principal components 1 and 2 explained 76.34% (42.29 and

34.05 % by PC1 and PC2, respectively) of the variation for number of kernels per spike. Polygon view in biplot as shown in Fig. 3 provided the best way to demonstrate the interaction patterns between entries and testers as mentioned by Yan *et al* (2000) and Yan and hunt (2002). Five entries are on the vertices while three are inside the polygon. Since the vertex entries have the largest distance from the origin; they are the most responsive to the change of testers relative to other entries within respective groups. The sector that has the vertex G8 contains three testers, i.e. g4, g2 and g1 .The biplot clearly shows why entry G8 had the highest GCA effect because it was the vertex entry in a sector in which three testers from eight fell. Also, G4 contains three testers sectors (g8, g3 and g6). Only a single tester that is, G7 and G5 can be seen. These represent the one best mating partners including g5 and g7 respectively. Genotypes G2, G3 did not fit in a well-defined sector, since it could be assigned to sector G8 and G4. In sector G8, g4 was predicted to be the best mating partner for G8, while in sector G5, a is the best partner for G7. Both (G8 and G4) and (G5 and G7) were, therefore, identified to be the best partners for each other. This combination significantly out yielded all commercial hybrids.

Advantages of the Biplot Approach for Diallel Data Analysis:

Compared with conventional methods of diallel analysis, the biplot approach has two advantages. The first advantage of the biplot is its graphical presentation of the data, which greatly enhances our ability to understand the patterns of the data. The second advantage of the biplot approach is that it is more interpretative. While the conventional method of diallel analysis was designed to describe the phenotypic performance of the crosses, the biplot approach tries to interpret the phenotypic variation of the crosses by understanding the parents.

A potential constraint of the biplot method is that it may fail to explain most of the variation and therefore fail to display all patterns of the data. Another constraint of the biplot approach is lack of a measure of uncertainty. However, we suggest that the significance of the difference between two entries can be visually assessed from their plot distance relative. Biplot graph is considered quickly and effective tool for assessing the genetic interrelationship among the genotypes.

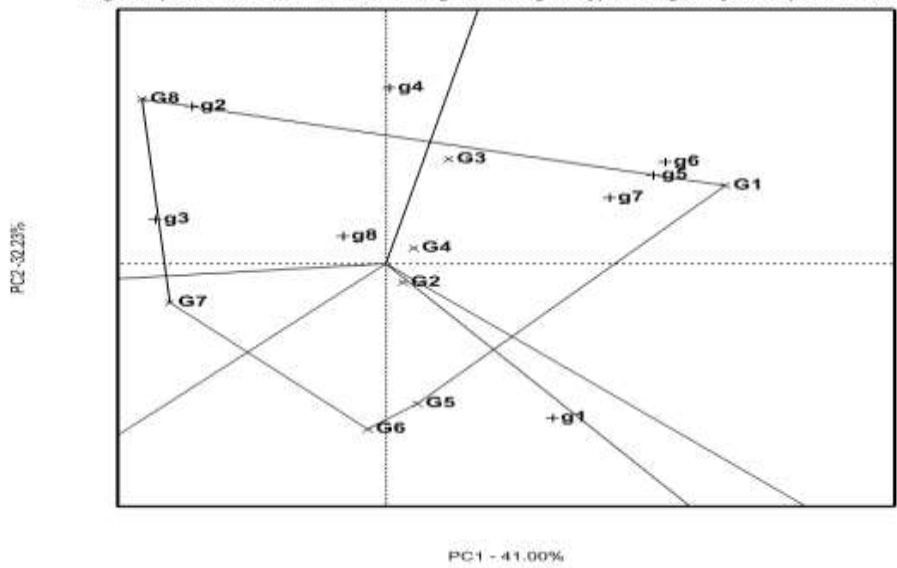Fig.1. Biplot based on diallel data of eight wheat genotypes for grain yield. (Total - 73.23%)

Fig. 2. Biplot based on diallel data of eight wheat genotypes for Chlorophyll content (75.63%)
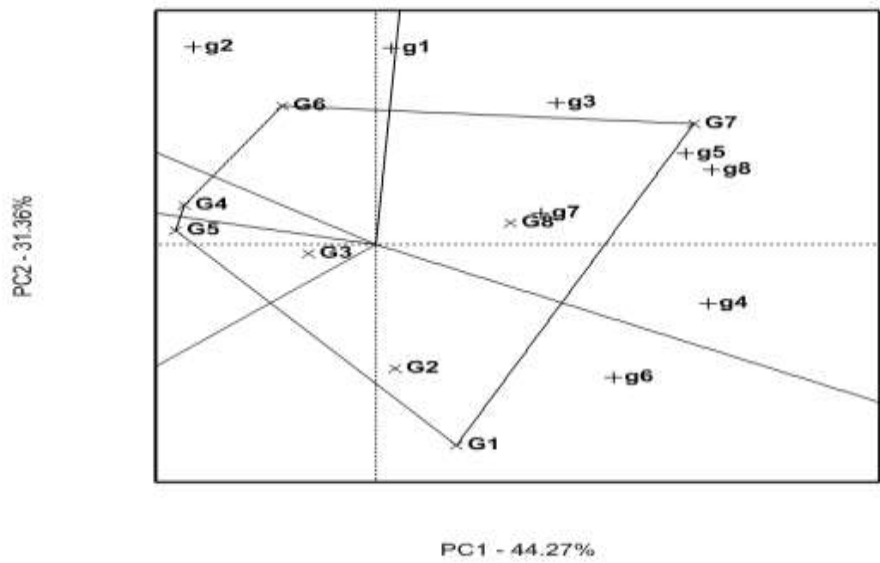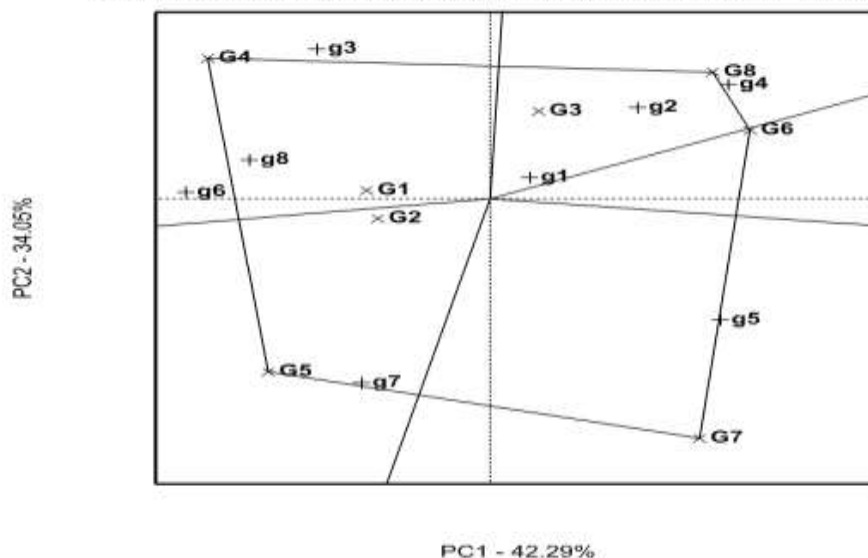

602

Fig. 3. Biplot based on diallel data of eight wheat genotypes for Number of Kernels per spik (76.43%)

REFERENCES

Abdel-Nour, Nadia A.R.(2006). Genetic studies on heading, maturity and yield and its components for late sowing conditions in wheat (*Triticum aestivum* L.). Egypt.J. Agric. 84(2):445-462.

Akinci, C. (2009). Heterosis and combining ability estimates in 6×6 half-diallel crosses of durum wheat (*Triticum durum desf*.). Bulgarian, J. of Agric. Sci., 15 (3): 214 – 221.

Aslam, R., M. Munawar and A.Salam (2014). Genetic architecture of yield components accessed through line × tester analysis in wheat (*Triticum aestivum* L.).Universal J. PL. Sci.; 2(5):93-96.

Azhar, F.M., and S.U. Ajmal. (1999). Diallel analysis of oil content in seed of *Gossypium hirsutum* L. Journal of Genetics and Breeding 53:19-23. B.

Bertoia, L.,C. Lopez., and R. Burak, (2006). Biplot analysis of forage combining ability in maize landraces. Crop Sci., vol. 46, no. 3, pp. 1346-1353.

Darvishzadeh R., I.Bernousi, P.S. Kiani, D.G. Guillaume and A. Sarrafi (2009). Use of GGE biplot methodology and Griffings diallel method for genetic analysis of partial resistance to phoma black stem disease in sunflower. Acta Agric. Scand. Plant Soil Sci. 59: 485-490.

Dehghani, H., S. E. Fayzian, M. Jalali, A.Rezai and F.Dane (2010). Use of GE biplot methodology for genetic analysis of yield-related traits in melon (*Cucumismelo* L.). Can. J. Plant Sci. 92: 77-85.

Desale C.S., D.R. Mehta and A.P. Singh (2014). Combining ability analysis in bread wheat. J. of Wheat Res. 6(1): 25-28.

603

Griffing , B.(1956). Concept of general and specific combining ability in relation to diallel crossing system . Aust.J.Biol .Sci.9:463-493.

Inamullah, H. A., F. Mohammadi, S. U. Dın, G. Hassan and R. Gul (2006). Evaluation of the heterotic and heterobeltiotic potential of wheat genotypes for improved yield. Pakistan J. Bot. 38 (4): 1159-1167.

Ismail, S. K. A. (2015). Heterosis and combining ability analysis for yield and its Components in Bread Wheat (*Triticum aestivum* L.). Int. J. Curr. Microbiol. App. Sci. ; 4(8):1-9.

Kalhoro, FA., A.A. Rajpar, S.A. Kalhoro, A. Mahar and A. Ali (2015) Heterosis and combing ability in F_1 population of hexaploid wheat (*Triticum Aestivum* L.). American J. PL. Sci.; 6:1011-1026.

Kandil A.A., A.E. Sharief, S.M. Hasnaa and M.A.Gomaa (2016) Estimation of general and specific combining ability in bread wheat (*Triticum aestivum* L.). Int. J. Agri.R.; 8(2):37-44.

Kapoor E., S. Mondal and T. **Dey (2011)** Combining ability analysis for yield and yield contributing traits in winter and spring wheat combinations. J Wheat Res. 3(1):52-58.

Kiani, G., G.A. Nematzadeh, S.K. Kazemitabarand and O.Alishah, (2007). Combining ability in cotton cultivars for agronomic traits. Int'l. J. Agric. Biol. 9: 521–532.

Krishnamoorthy,G. (2005).A study of heterotic relationships in sorghum. Ph.D. thesis,Texas A& M USA.

Kumar A, V.K. Mishra, R.P. Vyas and V.Singh (2011). Heterosis and combining ability analysis in bread wheat (*Triticum aestivum* L.). J PL. Breeding and Crop Sci.

Mather, K. and J. L. Jinks (1982). Biometrical Genetics (3rd ed.). Chapman and Hall, Ltd., London.

Motawea, M.H. (2006). Inheritance of erarliness, yield and yield components in wheat (T.aestivum L.em. Thell). Assuit.J.of Agric.Sci.31 (2):35-52**.**

Munir, I.,M.S. Swati, F. Muhammad, R. Ahmad and M. Imtiaz (1999). Heterosis in different crosses of wheat (*Triticum aestivum* L.). Sarhad J.Agric . 15(4):299-303.

Rahul, S. R. and V.S. Kandalkar (2018). Combining ability and heterosis for grain yield and its attributing traits in bread wheat (*Triticum aestivum* L.). J.of Pharmacognosy and Phytochemistry 7(2): 113-119.

Raj, P. and V. S. Kandalkar. (2013). Combining ability and heterosis analysis of grain yield and its components in wheat. J. Wheat Res. 5(1): 45-49.

Rastogi, A., B. K.Mishra, M. Srivastava, A. siddiqui and S. Shukla (2011). Biplot approach for identification of heterosis crosses in linseed(*Linum usitatissimum* L.). J. of Botany: 1 – 7**.**

Rasul l., A.S. Khan and Z.Ali (2002). Estimation of heterosis for yield and some yield components in bread wheat .Intern. J.Agric. Biol.(4(2):214-216.

Salem, R.A.Nagwa and S.M. Abdel Dayem (2006). Genetical study on some bread wheat crosses .J. Agric Sci. Mansoura Univ.31(8):4873-4883.

Shang Y. I., L. I. Shao-Qin, L.I. Dian-Rong, T.Jian-Hual (2006). GGE biplot analysis of diallel cross of Brassica napus L. Acta. Agron. Sin. 32: 243-248.

Singh, P. and S.S. Narayanan (1993). Biometrical Techniques in Plant Breeding. Kalyani Publishers, New Delhi, 36(1): 10-15.

Singh, K., U.B. Singh, and S.N. Sharma, (2013). Combining ability analysis for yield and

its components in bread wheat (*Triticum aestivum* L. em.Thell). J. Wheat Res., 5 (1): 63-67.

Soheir, M.H. Abd Allah and A.A. EL-Gammaal (2009) Estimate of Heterosis and Combining Ability in Diallel Bread Wheat Crosses (*Triticum aestivum* L.) ALE. SCI.EX. J. 30(1):76-85.

Yan, W. (2001). GGE biplot a Windows application for graphical analysis of multi-environments trial data and other types of two way data. Agron. J.93: 1111-1118.

Yan, W. and L.A. Hunt (2002). Biplot analysis of diallel data. Crop Science 42:21-30.

Yan, W. and M. S Kang (2003). GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists. CRC Press, New York, NY.

Yan, W., L.A. Hunt, Q. Sheng and Z. Szlavnics (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., 40: 597-605.

تحليل الهجن الدائريه للمحصول ومكوناته في القمح باستخدم طريقتى جريفنج والمحاور الثنائية

ياسر أحمد الجوهرى¹ و وفاء وهبه محمد شافعى²

١. قسم بحوث القمح–معهد بحوث المحاصيل الحقلية– مركز البحوث الزراعية.

٢. المعمل المركزى لبحوث التصميم والتحليل الأحصائى– مركز البحوث الزراعية.

أجريت هذه الدراسة فى محطة البحوث الزراعية – إيتاى البارود – محافظة البحيرة –مصر. وكان الهدف من هذا البحث هو دراسة النظام الوراثى المتحكم فى بعض صفات المحصول ومكوناته فى القمح وهى عدد الأيام حتى تاريخ التزهير ، عدد الأيام حتى تاريخ النضج   ،مساحة ورقة العلم، محتوى الكلوروفيل، طول النبات، طول السنبلة، عدد السنابل فى النبات، عدد حبوب السنبلة، وزن ١٠٠٠ حبة، المحصول البيولوجى للنبات ،محصول النبات الفردى، دليل الحصاد خلال الموسمين الزراعيين ٢٠١٦/٢٠١٧ و٢٠١٧/٢٠١٨. وقد تم فى الموسم الأول التهجين بين الاباء بدون الهجن العكسيه للحصول على حبوب الجيل الاول وفى الموسم الثانى تم تقييم هذه التراكيب الوراثيه (الثمانيه وعشرون هجينا بالإضافة الى ثمانية آباء) فى تصميم القطاعات الكاملة العشوائية فى ثلاث مكررات لدراسة القدرة العامة والخاصة على الإئتلاف بطريقة (1956) Griffing وتحليل المحاور الثنائية biplot (GGE) .وقوة الهجين على مستوى الأب الأفضل. وتتلخص أهم نتائج الدراسة فيما يلى: ١. كان التباين الراجع للتراكيب الوراثية المختلفه معنويا لجميع الصفات المدروسة مما يدل على وجود إختلافات وراثية لكل الصفات المدروسة و يعطى إمكانية التحسين الوراثى. ٢. أظهر تحليل التباين معنوية لكل من القدرة العامة والخاصة على الإئتلاف بالنسبة لجميع الصفات المدروسة وكانت متوسطات المربعات للقدرة العامة على الإئتلاف أكبر من متوسطات المربعات للقدرة الخاصة على الإئتلاف ماعدا صفة محصول الحبوب للنبات ممايدل على أن تاثيرات الجين المضيف كانت أكثر أهمية عن تأثيرات الجين غير المضيف فى توريث هذه الصفات. ٣. كان ألاب الأول (Gemmeiza 9) هو أحسن الأباء فى القدرة العامة على الإئتلاف بالنسبة لمعظم الصفات ماعدا صفتى التبكير

ووزن ١٠٠٠ حبة وكان الأب *Line 1* أفضل بالنسبة لتاريخ التزهير والنضج والأب *Line 4* لعدد حبوب السنبلة ولطول النبات ومساحة الورقه والكلورفيل وعدد حبوب السنبلة وزن ١٠٠٠ حبة ودليل الحصاد. كما تميز الأب *Line 3* بالنسبه للكلورفيل. ٤. أظهرت الهجن *(P2xP7)*،*(P5xP7)* ، *(P5xP8)* أعلى قيمة سالبه للقدرة الخاصة على الإئتلاف بالنسبة لتاريخ التزهير والنضج والهجن *(P3xP8)* ,*(P4xP8)*، *(P2xP8)*، *(P1xP6)* ، *(P1xP5)*اعطت أعلى قيمة موجبة للقدرة الخاصة على الإئتلاف بالنسبة لطول النبات ، محتوى الكلورفيل، عدد السنابل فى النبات، عدد حبوب السنبلة، وزن ١٠٠٠ حبة والمحصول البيولوجى والحبوب للنبات. ٥. سجلت أفضل قيم لقوة الهجين بالنسبة للأب الأحسن بواسطة الهجين *(P2xP6)* ، *(P2xP7)* لصفات تاريخ التزهير والنضج وايضا *(P5xP8)* لصفة طول النبات,*(P2xP7)* لصفة عدد السنابل فى النبات ،*(P3xP4)* عدد حبوب السنبلة، *(P6xP7)* لوزن ١٠٠٠ حبة و*(P3xP4)*، *(P2xP8)* للمحصول البيولوجى ومحصول الحبوب للنبات. ٦. أظهرت نتائج تقنية الأشكال البيانية باستخدام طريقة المحاور الثنائية ان الأب *Gemmeiza 9* هو أحسن الأباء فى القدرة العامة على الإئتلاف والهجن *(P1xP6)*، *(P1xP5)*) بالنسبة لمحصول الحبوب للنبات و الأب *Line 3* بالنسبه للكلورفيل والهجين *(P7xP8)* و الأب *Line 4* والهجين *(P4xP8)* لعدد حبوب السنبلة.وهذه النتيجة تتفق بشكل كبير مع نتائج طريقة جريفنج. يعتبر الرسم البياني *Biplot* أداة سريعة وفعالة لتقييم العلاقة الوراثية بين التراكيب الوراثية. و يوفرشكل المضلع طريقة لتجميع الاباء المختبرة استنادا إلى أفضل شركاء التزاوج. وهكذا فإن الاباء التى تقع في نفس القطاع يشتركون في نفس أفضل شريك للتزاوج، ومع الأب الموجود عند رأس المضلع في ذلك القطاع. تمتلك الأباء التى تقع في قطاعات مختلفة شركاء مختلفين للتزاوج. تقل فرصة الحصول على هجن مبشرة من الأباء الموجودة بالقرب من نقطة الأصل فى شكل المحاور الثنائيه *(biplot)*.