

## DIALLEL AND CLUSTER ANALYSIS FOR SOME QUANTITATIVE CHARACTERS IN BREAD WHEAT (*Triticum aestivum* L.)

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### ABSTRACT

The present study was carried out at Gemmeiza Agricultural Research Station during 2000/2001 and 2001/2002 seasons. Diallel cross excluding reciprocals among nine parents of wheat namely: Peg"s" // HD2206 / Hork"s" (P1), CETTIA (P2), KVZ / BJY"s" (P3), Sakha 61 (P4), Giza 168 (P5), Sids 6 (P6), CAR 422 / ANA // URES (P7), Gemmeiza 5 (P8) and Gemmeiza 3 (P9) were used to estimate hybrid vigour, general and specific combining ability, phenotypic and genotypic correlation coefficients and cluster analysis for yield and its variables viz.: plant height, spike length, number of spikelets/spike, number of spikes/plant, 1000 -kernel weight, grain weight/spike, number of grains/spike and grain yield/plant. Highly significant differences among genotypes, parents and crosses were recorded for all studied traits. GCA/SCA ratio exceeded the unity in all traits except grain weight/spike and grain yield/plant. This indicated the importance of additive and additive X additive genetic effects controlling the majority of the studied traits. While the non-additive gene effects had the highly importance for grain weight/spike and grain yield/plant. The estimates of heterosis for grain yield/plant indicated that thirty crosses out of 36 F1 hybrids significantly surpassed their better parent with percentage ranged from 6.94 % for P4 X P6 to 98.84 % for P6 X P8. These relatively high heterotic percentages along with the variability existed among all diallel set increase the chance of good recombinations that can be isolated in the following generations particularly, when selfing in the following generations gives an essentially homozygous state and enhances the role of selected plants in reducing the masking effect of dominance. Results revealed that P1, P7 and P9 were the best combiners for yielding ability and three or four of its attributes, also two crosses P1 x P5 and P1 x P9 were the best specific combining ability effects for grain yield/plant and its attributes. All correlation coefficients between grain yield/plant and its components were significant with positive expression except spike length.

Clusters were formed by sequentially dividing groups of genotypes using un-weighted pair grouped method using arithmetic average (UPGMA). Cluster analysis produced four main groups. These groups are split into many subgroups based on similarity and dissimilarity of genotypes. The results indicated that genotypes 1 (P1), 5 (P1 X P5), 7 (P1 X P7), 18 (P3), 20 (P3 X P5), 28 (P4 X P7), 30 (P4 X P9), 32 (P5 X P6), 38 (P6 X P8) and 42 (P7 X P9) have a high distance level between each other and will produce good newly genetic combination if they are used in a crossing program.

### INTRODUCTION

It is well known that wheat (*Triticum aestivum* L.) is one of the most important major cereal crops in the world. In Egypt, it represents a principal part in man's diet. The total national wheat production reached 6.3 million tons which represents more than 55 % of staff sufficient for local needs

(Gomaa, 1999). Increasing production per unit area appears to be one of the important factors for narrowing the wheat production gap. In this respect, plant breeders need important knowledge about nature of gene actions for several yield attributes controlling the inheritance of wheat yield. These information help breeders in selecting desirable parents and crosses for further exploitation. The diallel analysis is considered as a method for studying the genetics of complex traits and as a tool in plant breeding (Baker, 1978).

The exploitation of heterosis through synthetics and ultimately hybrids could pay off in improved yield potential. Superiority of the F<sub>1</sub>s over their better parent is usually interpreted to indicate some type of gene action in addition to hybrid vigor for grain yield is associated with manifestations of heterotic effects in main yield components, which might be reflected in yielding ability.

Information on the relative importance of general (GCA) and specific (SCA) combining abilities is essential for this reason. Generally, GCA is associated with additive genes. It helps the breeder to identify the best combination that may be hybridized either to exploit heterosis or to build up the favorable fixable genes. In self-fertilized crops where commercial exploitation of heterosis, if advantageous, is not feasible, the breeder will primarily be interested in higher magnitude of additive genetic variance for establishing superior genotypes. SCA is attributed primarily to non-additive (dominance and epistasis). It is very essential that the breeder should evaluate the potentialities of the available germplasm for new recombinations and eventually combining ability have proved to be of considerable use in crop plants. In this regard, several studies have been reported in wheat, ( El-Marakby *et al.* (1993); Mann and Sharma (1995); Afiah and Abdel-Sattar (1998); Afiah *et al.* (2000) and Ashoush *et al.* (2001) ).

Genotypic and phenotypic correlation for yield and its component traits are important for wheat improvement.

Cluster analysis can be used to identify genotypes with similar adaptation, which can be useful for sampling in subsequent studies and parental selection in breeding program. Genetic relationships among genotypes can be measured by similarity of any number of quantitative characters, where characters are agronomic parameters of the plant such as characters mentioned above. This assumes that the differences between characters of the genotypes reflect the genetic divergence of the genotypes. Genetic relationships among a large number of genotypes can be summarized using cluster analysis to place similar genotypes into phonetic groups. In oat (*Avena sp.*), Sidhu and Mehndiratta (1981) have measured genetic relationships among genotypes based on quantitative characters..

The present investigation was undertaken to :1- estimate the magnitude of heterosis and obtain information from a diallel cross of wheat on the type of gene action and relative magnitude of combining ability influencing yield and some important of components, and 2- calculate similarity and dissimilarity between genotypes using cluster analysis method.

## MATERIALS AND METHODS

This study was conducted during the two growing seasons 2000/2001 and 2001/2002 at Gemmeiza Agricultural Research Station to study some breeding parameters for bread wheat grain yield and its contributing characters. Nine bread wheat genotypes that represent a wide range of diversity for several traits were selected for this study. Five of them are local cultivars namely: Sakha 61, Giza 168, Sids 6, Gemmeiza 5 and Gemmeiza 3. The other four genotypes were introduced from Mexico and Syria. The pedigrees of these genotypes are given in Table 1. In 2000/2001 season, the nine parents were crossed in all possible combinations excluding reciprocals to produce 36 F1 hybrids. In 2001/2002 season, 45 genotypes, included nine parental genotypes and 36 F1 hybrids, were grown in a randomized complete block design with three replications. Each block contained 45 plots. The plot consisted of a single row with 4 m length for each genotype. Spacing between rows were 20 cm, and 10 cm within hills. Cultural practices were applied as usually recommended for the ordinary wheat fields.

**Table 1: Names and pedigrees of the evaluated parental varieties and or lines.**

No	Variety or lines pedigree	Origin
P1	Peg <sup>s</sup> // HD2206 / Hork <sup>s</sup> lcw 84 - 0250 - 09 AP - 300 L - 2AP - 300 L - 0 AP	Syria
P2	CETTIA CM 92313 - 31Y - OH - OSY - 6M - ORES - OSY	Mexico / Syria
P3	KVZ / BJY <sup>s</sup> SWM 11027 - 2 AP - 2AP - 2AP - 1AP - 0AP	Mexico
P4	Sakha 61 Inia / RL 4220 // 7c / 3 / Yr <sup>s</sup> CM15430 - 2S - 5S - 0S - 0S - 61S - OEGY	Egypt
P5	Giza 168 MRL / Buc // Seri cM 93046 - 8M - 0Y - 0M - 2Y - 0B - 0GZ.	Egypt
P6	Sids 6 Maya <sup>s</sup> / Mon <sup>s</sup> // cMH 74 A. 592 / 3 / Sakha 8 <sup>s2</sup> SD / 0002 - 4 sd - 3 sd - 1 sd - 0 sd.	Egypt
P7	CAR 422 / ANA // URES CM93553 - 14M - 0Y - 0M - 1Y - 0B - 0SY	Mexico
P8	Gemmeiza 5 Vee <sup>s</sup> / Swm 6525 GM 4017 - 1Gm - 7Gm - 3Gm - 0Gm.	Egypt
P9	Gemmeiza 3 Bb / 7c <sup>s2</sup> // Y50E / Kal <sup>s3</sup> / 5 / Sakha8 / 4 / Rrv / wwi 5 / 3 / Bj <sup>s</sup> // 0n CGm 4024 - 1Gm - 13Gm - 2Gm - 0Gm.	Egypt

At harvest, data were recorded from random sample of 20 guarded plants in each plot for the following traits:

- |                               |                             |
|-------------------------------|-----------------------------|
| 1- Plant height (cm).         | 2- Spike length (cm).       |
| 3- Number of spikelets/spike. | 4- Number of spikes/plant.  |
| 5- 1000-kernel weight (gm)    | 6- Grain weight/spike (gm). |

7- Number of grains/spike.

8- Grain yield/plant (gm).

The heterotic effects of F1 crosses were estimated as a percentage over the better parent including parents on F1 without reciprocal as follows:

$$\text{Heterosis} = (F1 - BP/BP) \times 100$$

Where: F1 is the first diallel generation.

Bp is the better parent.

Estimates of general (GCA) and specific (SCA) combining abilities were computed according to Griffing's (1956) diallel cross analysis approach designed model-1, method 2. Comparison among means of all studied traits for genotypes was practiced by least significant difference values (L.S.D) according to Snedecor and Cochran (1980). Phenotypic and genotypic correlation coefficients were calculated as outlined by Steel and Torrie (1980).

Cluster analysis was performed on genotypes "r" matrix using a measure of Euclidean distance. Genotypes were clustered using UPGMA calculated by MVSP STAT program (Kovach, 1995). Genotypes are the average of genotypes group sequentially clustered based on similarity of genotypes. The cluster routine was arbitrarily stopped to form three to five discrete clusters, the distance between clusters was measured using the original quantitative characters. The symbols of genotypes are:

1 = p1	10 = p2	19 = p3Xp4	28 = p4Xp7	37 = p6Xp7
2 = p1Xp2	11 = p2Xp3	20 = p3Xp5	29 = p4Xp8	38 = p6Xp8
3 = p1Xp3	12 = p2Xp4	21 = p3Xp6	30 = p4Xp9	39 = p6Xp9
4 = p1Xp4	13 = p2Xp5	22 = p3Xp7	31 = p5	40 = p7
5 = p1Xp5	14 = p2Xp6	23 = p3Xp8	32 = p5Xp6	41 = p7Xp8
6 = p1Xp6	15 = p2Xp7	24 = p3Xp9	33 = P5Xp7	42 = p7Xp9
7 = p1Xp7	16 = p2Xp8	25 = p4	34 = p5Xp8	43 = p8
8 = p1Xp8	17 = p2Xp9	26 = p4Xp5	35 = p5Xp9	44 = p8Xp9
9 = p1Xp9	18 = p3	27 = p4Xp6	36 = p6	45 = p9

## RESULTS AND DISCUSSION

Mean squares for appropriate sources of variation in the experiments are given in Table 2. Differences among genotypes (parents and crosses) were highly significant for all studied characters indicating the wide diversity between the parental materials used in the present study and increases the chance of isolating good new recombinations in the following generations.

Similar findings were reported by Afiah *et al.* (2000). The analysis of variance for combining ability for yield and yield components is presented in Table 2. Mean squares associated with general and specific combining ability were highly significant for all studied traits indicating the importance for inheritance of both additive and non-additive gene effects that involve in determining the performance of single cross progeny. Results also showed that all cases expressed high GCA/SCA ratios which exceeded the unity indicating that additive and additive by additive types of gene action were of great importance in the inheritance of all studied characters except grain weight /spike and grain yield/plant. Also, these ratios indicated that GCA effects appeared to be more important than SCA effects for the inheritance of

various studied characters. It is evident that the presence of large amount of additive effects suggests the potentiality for obtaining yield and yield components improvements. Moreover, selection procedures based on the accumulation of additive effect would be successful in improving all studied characters. These findings are in accordance with those obtained by Mohammed (1990), Eissa *et al.* (1994), Walia *et al.* (1994), El-Adl *et al.* (1996) El-Seidy and Hamada (2000).

**Table 2: Mean square estimates of ordinary analysis and combining ability analysis for all studied traits in wheat**

Source of variance	d.f	Plant height	Spike length	Number of spikelets/spike	Number of spikes/plant	1000-Kernel weight	Grain weight/spike	Number of grains/spike	Grain yield/plant
Blocks	2	6.1	0.4	0.703	0.89	16.938	0.292	39.344	4.438
Genotypes	44	217.9**	2933.8**	5.073**	28.15**	208.839**	0.837**	314.069**	138.636**
Parents (P)	8	248.2**	12.2**	8.379**	50.62**	278.242**	0.635**	331.759**	20.485**
Crosses (C)	35	127.3**	3573.2**	3.612**	17.24**	193.179**	0.809**	304.621**	123.191**
P. vs C.	1	3146.5**	3927.9**	45.743**	230.11**	201.723**	3.433**	503.242**	1264.425**
Error	88	2.9	0.4	0.628	0.38**	24.283	0.057	9.514	0.985
GCA	8	127.4**	2085.6**	2.051**	14.07**	142.839**	0.269**	124.952**	17.397**
SCA	36	60.5**	731.8**	1.611**	8.34**	53.386**	0.281**	100.187**	52.615**
Error	88	1.0	0.1	0.210	0.11	8.088	0.019	3.171	0.322
GCA/SCA		2.1	2.9	1.273	1.89	2.672	0.957	1.247	0.331

\* and \*\* denote significance at 5% and 1% levels, respectively.

**Mean performance:**

Mean performance values of nine wheat parental lines and/or cultivars and F<sub>1</sub>s (excluding reciprocals) are presented in Table 3. There were highly significant differences among parents and crosses for all studied characters indicating genetic variation for these traits. Results clearly showed that P6 gave the highest values for spike length, number of spikelets/plant, grain weight/spike and number of grains/spike being 17.0 cm, 23.7, 3.27 gm and 72.7, respectively. Concerning plant height, P3 ranked first where it gave the tallest plants (110.3 cm). parental cultivar, P8 recorded the highest number of spikes/plant being 16.6. With regard to weight of 1000 Kernels, P2 gave the highest value for this trait recording 67.1 gm. P5 gave the highest grain yield/plant being 21.7 gm, (Table 3).

Mean performance values of the tested thirty six crosses are also presented in Table 3. Results indicated that three crosses namely: P3 x P6, P3 x P8 and P4 x P6 had the lowest mean values for plant height. Crosses: P5 x P9 and P5 x P8 exceeded the better parent values for spike length. For number of spikelets/spike, the highest values were performed by the crosses P5 x P7, P7 x P9 and P5 x P8. Three crosses: P5 x P7, P1 x P4 and P4 x P7 had the highest values for number of spikes/plant. Crosses: P1 x P5, P1 x P9 and P2 x P9 possessed the highest values for weight of 1000 kernels. The highest values of grain weight/spike were produced by the crosses P1 x P9, P2 x P9 and P7 x P9. Five crosses: P5 x P9, P2 x P9, P6 x P8, P3 x P8 and P6 x P7 had the highest number of grains/spike. Highest grain yield/plant was

performed by three crosses, P1 x P2, P5 x P9 and P1 x P9. It is suggested that the above mentioned crosses could be useful in wheat breeding for improving grain yield and its components.

**Table 3: Mean performance values of nine parental wheat genotypes and their F<sub>1</sub> crosses for yield and its components.**

Genotypes	Plant height	Spike length	No of spikelets/spike	No. of spikes/plant	1000 - kernel weight	Grain weight/spike	No of grains/ Spike	Grain yield/ Plant
P <sub>1</sub>	105.7	12.1	20.2	7.7	45.8	2.57	56.0	19.4
P <sub>2</sub>	95.3	11.3	22.4	10.1	87.1	2.73	41.2	19.0
P <sub>3</sub>	110.3	11.3	19.7	8.7	48.4	2.54	52.3	21.1
P <sub>4</sub>	86.7	10.4	19.4	14.2	41.2	1.72	41.9	16.1
P <sub>5</sub>	105.3	11.0	21.5	8.1	35.3	2.19	62.3	21.7
P <sub>6</sub>	82.8	17.0	23.7	3.3	45.0	3.27	72.7	17.3
P <sub>7</sub>	94.9	11.7	22.6	13.6	42.8	2.41	56.5	17.0
P <sub>8</sub>	101.9	11.5	22.1	16.8	38.0	1.88	49.6	17.1
P <sub>9</sub>	95.5	10.3	20.6	12.9	55.0	2.32	42.2	13.3
P <sub>1</sub> x P <sub>2</sub>	113.7	12.1	22.3	13.7	49.7	2.79	56.4	54.5
P <sub>1</sub> x P <sub>3</sub>	109.6	11.7	22.9	14.1	37.2	1.81	48.9	36.2
P <sub>1</sub> x P <sub>4</sub>	108.3	11.5	23.0	17.3	49.2	2.53	51.4	33.1
P <sub>1</sub> x P <sub>5</sub>	109.9	12.1	23.6	15.1	62.5	3.34	53.5	31.7
P <sub>1</sub> x P <sub>6</sub>	108.9	12.8	22.9	12.8	53.0	1.78	34.2	21.0
P <sub>1</sub> x P <sub>7</sub>	114.3	11.8	22.9	14.5	46.9	2.82	60.2	27.6
P <sub>1</sub> x P <sub>8</sub>	121.2	9.8	21.3	13.5	54.5	3.42	62.8	23.4
P <sub>1</sub> x P <sub>9</sub>	110.4	11.8	23.4	14.7	65.0	3.98	61.1	36.7
P <sub>2</sub> x P <sub>3</sub>	108.8	11.8	22.7	14.8	46.4	2.65	57.2	33.8
P <sub>2</sub> x P <sub>4</sub>	113.1	11.9	23.0	10.0	52.2	3.22	61.8	35.2
P <sub>2</sub> x P <sub>5</sub>	115.5	12.3	21.0	15.9	54.8	2.67	48.8	28.7
P <sub>2</sub> x P <sub>6</sub>	106.4	12.2	21.7	10.1	53.9	3.20	59.5	14.3
P <sub>2</sub> x P <sub>7</sub>	109.1	12.3	23.2	16.4	45.8	2.36	51.5	31.3
P <sub>2</sub> x P <sub>8</sub>	110.8	11.6	23.0	10.7	46.6	2.69	56.2	18.6
P <sub>2</sub> x P <sub>9</sub>	116.5	12.3	23.8	15.7	72.3	3.62	75.8	22.8
P <sub>3</sub> x P <sub>4</sub>	100.8	11.6	23.5	13.5	48.4	2.64	57.0	23.6
P <sub>3</sub> x P <sub>5</sub>	108.9	12.2	23.1	14.9	55.3	2.59	46.7	20.8
P <sub>3</sub> x P <sub>6</sub>	94.5	12.4	22.9	11.9	37.2	1.67	44.9	26.7
P <sub>3</sub> x P <sub>7</sub>	100.3	12.1	22.9	13.8	38.1	2.54	66.8	24.9
P <sub>3</sub> x P <sub>8</sub>	98.6	9.5	19.8	12.3	45.8	3.23	70.7	27.0
P <sub>3</sub> x P <sub>9</sub>	111.0	12.2	22.5	13.5	54.1	3.20	59.1	25.4
P <sub>4</sub> x P <sub>5</sub>	101.7	11.3	21.7	15.1	58.2	2.14	36.7	15.2
P <sub>4</sub> x P <sub>6</sub>	99.8	12.0	21.7	13.1	58.5	2.98	51.1	16.5
P <sub>4</sub> x P <sub>7</sub>	105.9	11.6	23.3	16.9	43.4	2.42	56.0	24.1
P <sub>4</sub> x P <sub>8</sub>	107.1	11.2	21.5	13.1	44.9	2.66	59.3	33.3
P <sub>4</sub> x P <sub>9</sub>	107.3	10.4	21.1	16.3	58.5	2.82	48.1	23.3
P <sub>5</sub> x P <sub>6</sub>	112.4	11.5	22.7	14.9	42.6	2.43	57.2	15.7
P <sub>5</sub> x P <sub>7</sub>	117.7	12.5	25.3	19.7	46.8	2.88	59.1	27.7
P <sub>5</sub> x P <sub>8</sub>	117.8	12.8	24.2	15.2	44.8	2.61	58.3	29.1
P <sub>5</sub> x P <sub>9</sub>	119.5	13.0	23.7	16.1	38.4	3.15	66.9	39.5
P <sub>6</sub> x P <sub>7</sub>	103.8	12.5	22.6	14.1	47.9	3.38	70.5	27.4
P <sub>6</sub> x P <sub>8</sub>	107.5	12.3	22.8	10.4	48.9	3.59	73.4	34.4
P <sub>6</sub> x P <sub>9</sub>	119.0	10.7	22.7	12.3	46.1	2.86	62.5	30.7
P <sub>7</sub> x P <sub>8</sub>	104.7	11.1	23.3	9.7	38.8	2.60	66.9	25.5
P <sub>7</sub> x P <sub>9</sub>	117.1	11.5	24.9	13.8	52.6	3.63	69.3	28.8
P <sub>8</sub> x P <sub>9</sub>	116.5	11.2	23.3	8.2	47.2	2.63	56.0	27.3
L.S D 5%	788	1.009	1.268	0.933	4.589	0.388	5.012	1.596
L.S D 1%	699	1.339	1.709	1.238	6.088	0.515	6.649	2.118

**Heterosis:**

Parents vs crosses mean squares in Table 2, as an indication to average heterosis overall crosses, were found to be highly significant for all studied traits. It could be concluded that the test of potential parents for the expression of heterosis would be necessarily conducting over a number of

environmental conditions. Similar results were previously reported by Hamada *et al* (1997), Ashoush *et al* (2001) and Hamada and Tawfelis (2001).

Heterosis expressed as the deviation percentage of F1 mean performance from better parent for the studied characters are presented in Table 4. The direction and magnitude of heterosis was relative to characters investigated. Significant positive heterotic effects relative to better parent values would be of interest for most traits under study, however plant height of high negative values would be useful from the breeder's point of view. Results showed that six crosses expressed significant negative heterotic effect relative to the better parent values and ranged from -3.48 to -14.38 for plant height. For spike length, twenty crosses out of the studied thirty six crosses showed significant heterotic effects which ranged from 2.06 to 836.81 % relative to the respective better parent. Twenty three crosses exhibited highly significant useful heterosis for number of spikelets/spike and this increase varied from 1.33 % to 19.46 % over the better parent. Concerning number of spikes/plant, twenty three hybrids showed highly significant and positive desirable heterotic effects with a range of 1.72 % to 87.60 % relative to the better parent. Fifteen crosses exhibited highly significant heterosis for 1000-kernel weight and ranged from 6.34 % to 41.23 % over the better parent. For grain weight/spike, twenty two hybrids expressed highly significant heterotic effects with a range of 2.198 % to 55.47 % relative to the better parent. Regarding number of grains/spike, seventeen hybrids showed highly significant desirable heterotic effects which ranged from 6.55 % to 47.30 % relative to the respective better parent. Highly significant heterotic effects were shown by thirty hybrids for grain yield/plant which ranged from 6.94 % to 98.84 % relative to the respective better parent. These results are similar to those obtained by El-Rassas and Mitkees (1985), Ibrahim (1994), Hamada *et al* (1997) and Hamada and Tawfelis (2001).

From the results shown in Table 4, it could be concluded that the crosses P3 x P7, P2 x P9, P3 x P9, P4 x P9, P5 x P9 and P5 x P7 are useful for the breeder's because they are correlated in most traits.

#### **Combining ability:**

##### **General combining ability effects:**

Estimates of general combining ability effects for individual parental line are given in Table 5. General combining ability effects computed herein were found to differ significantly from zero in all cases. High positive values would be of interest under all traits in question except plant height where high negative effect would be useful from the breeder point of view. The results revealed that parental line P1 expressed significant (gi) effect for spike length, 1000-kernel weight and grain yield/plant. Parental line P2 exhibited significant (gi) effect for 1000-kernel weight and grain weight/spike. Parental line P3 showed significant negative (gi) effects for plant height and significant positive desirable effects for grain yield/plant. Parental cultivar P4 expressed significant positive (gi) effect for number of spikes/plant. However, it gave significant negative (gi) effect for plant height. Parental cultivar P5 showed significant positive (gi) effect for number of spikelets/spike and number of spikes/plant. Parental cultivar P6 expressed significant positive (gi) effect for grain weight/spike and number of grains/spike. Moreover, it gave significant

negative effect for plant height. Parental line P7 was the best donor for number of spikelets/spike, number of spikes/plant and number of grains/spike. However, it gave significant negative (gi) effects for plant height. Parental line P7 could be considered as an excellent parent in breeding programs towards releasing varieties characterized by higher grain yield and its components. The parental cultivar P8 expressed significant positive (gi) effects for number of grains/spike. Parental cultivar P9 exhibited significant (gi) effects for number of spikes/plant, 1000-kernel weight, grain weight/spike, number of grains/spike and grain yield/plant. This parent could be considered as an excellent parent in breeding programs for the last mentioned characters.

**Table 4: Heterosis as percentage of better parent for the eight studied characters in wheat.**

Genotypes	Plant height	Spike Length	No. of spikelets/spike	No. of spikes/plant	1000 - Kernel weight	Grain weight/spike	No. of grains/spike	Grain yield/Plant
P <sub>1</sub> X P <sub>2</sub>	7.57	836.81**	-0.15	35.53**	-25.88	2.198	0.71	-6.36
P <sub>1</sub> X P <sub>3</sub>	-0.67	803.30**	13.53**	81.07**	-23.14	-29.46	-12.62	71.41**
P <sub>1</sub> X P <sub>4</sub>	2.52	792.86**	13.86**	22.35**	7.47**	-1.40	-8.21	70.79**
P <sub>1</sub> X P <sub>5</sub>	4.04	806.04**	10.09**	87.60**	36.34**	17.30**	-14.12	45.86**
P <sub>1</sub> X P <sub>6</sub>	3.03	540.39**	-3.52	63.91**	15.71**	-45.57	-52.98	8.25**
P <sub>1</sub> X P <sub>7</sub>	8.14	-2.47	1.33*	6.63**	2.27	10.03**	8.55*	42.10**
P <sub>1</sub> X P <sub>8</sub>	14.70	-18.96	-3.83	-18.47	18.91**	33.59**	12.20**	20.45**
P <sub>1</sub> X P <sub>9</sub>	4.51	-2.47	13.75**	13.92**	18.23*	55.47**	9.17**	89.18**
P <sub>2</sub> X P <sub>3</sub>	-1.39	0.00	1.64*	46.05**	-30.86	-2.81	9.30**	60.03**
P <sub>2</sub> X P <sub>4</sub>	18.84	0.57	2.83**	-29.18	-22.08	18.07**	47.30**	85.76**
P <sub>2</sub> X P <sub>5</sub>	9.88	4.52**	-8.11	58.58**	-18.32	-2.20	-21.71	22.70**
P <sub>2</sub> X P <sub>6</sub>	11.87	-28.24	-8.44	-0.68	-19.80	-12.23	-18.07	-24.78
P <sub>2</sub> X P <sub>7</sub>	14.48	4.52**	2.50**	21.13**	-31.71	-13.55	-8.74	85.20**
P <sub>2</sub> X P <sub>8</sub>	8.73	-1.98	2.83**	-35.34	-30.53	-1.34	17.34**	-2.11
P <sub>2</sub> X P <sub>9</sub>	22.09	3.96**	8.41**	21.13**	7.78**	32.48**	19.75**	20.21**
P <sub>3</sub> X P <sub>4</sub>	-8.82**	2.06**	19.46**	-4.47	-4.10	4.23**	8.92**	11.85**
P <sub>3</sub> X P <sub>5</sub>	-1.33**	7.35**	7.45**	70.23**	14.24**	2.13**	-25.13	-4.45
P <sub>3</sub> X P <sub>6</sub>	-14.38**	-27.26	-3.52	36.64**	-23.12	-49.03	-38.28	28.54**
P <sub>3</sub> X P <sub>7</sub>	-8.12**	2.84**	1.33*	1.72**	-21.32	0.16	18.30**	17.85**
P <sub>3</sub> X P <sub>8</sub>	-10.83**	-17.15	-10.27	-25.70	-5.45	27.50**	35.03**	27.96**
P <sub>3</sub> X P <sub>9</sub>	0.63	7.35**	9.22**	4.64**	-1.75	26.18**	12.99**	25.28**
P <sub>4</sub> X P <sub>5</sub>	-3.48*	3.343**	1.24	8.82**	41.23**	-2.44	-41.18	-30.22
P <sub>4</sub> X P <sub>6</sub>	15.15	-29.41	-8.30	-7.29	29.90**	-8.77	-29.63	6.94**
P <sub>4</sub> X P <sub>7</sub>	11.58	-1.42	2.80**	19.06**	1.64	0.97**	-0.83	41.29**
P <sub>4</sub> X P <sub>8</sub>	5.04	-2.04	-2.72	-20.88	8.97**	42.73**	19.62**	95.12**
P <sub>4</sub> X P <sub>9</sub>	12.35	2.27**	2.27**	14.82**	6.39**	21.41**	14.06**	44.22**
P <sub>5</sub> X P <sub>6</sub>	8.68	-4.38	-4.38	64.30**	-5.33	-25.59	-21.24	-27.78
P <sub>5</sub> X P <sub>7</sub>	11.77	11.64**	11.64**	45.48**	14.18**	20.14**	-5.13	27.45**
P <sub>5</sub> X P <sub>8</sub>	11.87	9.67**	9.67**	-8.23	18.09**	19.03**	-6.42	34.05**
P <sub>5</sub> X P <sub>9</sub>	13.48	10.25**	10.25**	24.74**	-33.91	35.83**	39.36**	81.59**
P <sub>6</sub> X P <sub>7</sub>	9.34	-5.20	-5.20	3.93**	6.34**	3.36**	-2.94	58.38**
P <sub>6</sub> X P <sub>8</sub>	5.49	-3.66	-3.66	-37.15	8.62**	9.79**	1.01	98.84**
P <sub>6</sub> X P <sub>9</sub>	24.56	-4.08	-4.08**	-5.16	-18.13	-12.44	-14.04	77.46**
P <sub>7</sub> X P <sub>8</sub>	2.75	2.80**	2.80**	-41.77	-9.16	8.19**	18.54**	49.22**
P <sub>7</sub> X P <sub>9</sub>	22.61	10.02**	10.02**	1.72**	-4.32	51.39**	22.67**	69.08**
P <sub>8</sub> X P <sub>9</sub>	14.32	9.97**	9.97**	-50.4	-14.16	13.51**	12.84**	60.16**
L.S.D 5%	2.788	1.009	1.288	0.933	4.589	0.388	5.012	1.596
L.S.D 1%	3.699	1.339	1.708	1.238	6.068	0.515	6.649	2.118

\* and \*\* significant at 5% and 1% levels of probability, respectively.



**Table 5: Estimates of general combining ability effects (gi) from nine Wheat parents.**

Parents	Plant height	Spike length	No. of spikelets /spike	No. of spikes/ Plant	1000 - Kernel weight	Grain weight/ Spike	No. of grains/ Spike	Grain yield/ plant
P <sub>1</sub>	3.178	34.660**	-0.215	-0.087	1.831*	0.003	-2.320	1.566**
P <sub>2</sub>	1.098	-0.477	0.031	-0.387	6.019**	0.1002*	-3.611	-0.988
P <sub>3</sub>	-1.798**	-1.180	-0.491	-0.502	-2.945	-0.166	-0.923	1.102**
P <sub>4</sub>	-5.046**	-1.613	-0.682	1.083**	0.395	-0.213	-5.528	-0.986
P <sub>5</sub>	3.769	-0.853	0.273*	1.023**	-1.436	-0.124	0.528	0.035
P <sub>6</sub>	-4.995**	-0.035	0.191	-2.353	-1.030	0.08*	2.962**	-2.374
P <sub>7</sub>	-0.892**	-9.823	0.758**	1.286**	-3.803	0.021	4.292**	0.172
P <sub>8</sub>	1.411	-10.392	-0.085	-0.487	-3.832	-0.001	3.525**	0.302
P <sub>9</sub>	3.275	-10.289	0.219	0.423**	4.801**	0.300**	1.074*	1.151**
L.S.D gi 5%	0.561	0.202	0.258	0.187	1.607	0.077	1.006	0.320
L.S.D gi 1%	0.742	0.268	0.342	0.247	2.125	0.103	1.331	0.423
L.S.Dgi-gj 5%	0.839	0.304	0.388	0.280	2.411	0.117	1.510	0.481
L.S.Dgi-gj 1%	1.109	0.402	0.513	0.371	3.188	0.155	1.996	0.636

\* and \*\* denotes significance at 5% and 1%, respectively.

**Specific combining ability effects:**

Specific combining ability effects (SCA) for all F1 crosses with respect to the studied traits are given in Table 6. Results indicated that seven hybrids showed significant negative specific combining ability effects for plant height. For spike length and number of spikelets/spike, eleven crosses gave significant positive SCA effects. Concerning number of spikes/plant twenty-three hybrids showed significant SCA effect. The results showed also that seven, fourteen, fourteen and seventeen crosses had significant positive SCA effects for 1000-kernel weight, grain weight/spike, number of grains/ spike and grain yield/plant, respectively. From breeding stand point, parents characterized by good general combining ability for yield and its components along with heterosis and high estimates of SCA effects are obviously essential. A great deal of interest has been given to select crosses that contain both good general combining parents and crosses. Table 6 involving one good and one poor combining parent with SCA effects as well as high heterosis. These results partially in harmony with those previously obtained in F1 diallel (El-Sidy and Hamada, 2000) and F1 and F2 (Ashoush *et al.*, 2001)

**Correlation analysis:**

Results in Table 7 indicated that phenotypic and genotypic correlation coefficients of grain yield/plant with its components were significant with positive expression except spike length and 1000-kernal weight. The results cleared also that most studied traits showed positive genotypic and phenotypic correlation between each other. There was highly significant positive phenotypic and genotypic correlation between plant height and each of number of spikelets and spikes/plant, grain weight/spike and number of grains/spike. On the other hand, highly significant negative phenotypic and genotypic association was found between spike length and each of grain

weight/spike and number of grains/spike. Number of spikelets/spike highly significantly correlated with each of number of spikes/plant, grain weight/spike and number of grains/spike. Significant correlation was found between number of spikes/plant and number of grains/spike. The results also showed phenotypic and genotypic correlation coefficients between 1000-kernel weight and each of grain weight/spike and number of grains/spike. Grain weight/spike was found to be highly significant and positively correlated with number of grains/spike. These results indicate that these characters might be linked to each other. A linkage of this sort would make it easier to the wheat breeder to improve these traits through selection programs. These results were similar to those reported by Yegbasanlar et al. (1995) and El-Adl et al. (1996).

**Table 6: Estimates of specific combining ability effects for thirty-six crosses for yield and its components.**

Crosses	Plant height	Spike length	No. of spikelets/spike	No. of spikes/plant	1000 - Kernel weight	Grain weight/spike	No. of grains/spike	Grain yield / plant
P <sub>1</sub> X P <sub>2</sub>	2.125	56.793**	0.001	1.021**	-7.101	-0.037	5.722**	-7.369
P <sub>1</sub> X P <sub>3</sub>	0.952	53.430**	1.122**	1.470**	-10.646	-0.751	-4.432	8.561**
P <sub>1</sub> X P <sub>4</sub>	2.934	52.596**	1.380**	3.152**	-1.934	0.017	2.838	7.616**
P <sub>1</sub> X P <sub>5</sub>	-4.281**	53.436**	1.059**	1.012**	13.124**	0.407**	-1.284	5.161**
P <sub>1</sub> X P <sub>6</sub>	3.418	51.551**	0.374	1.821**	3.283	-1.027	-23.084	-3.130
P <sub>1</sub> X P <sub>7</sub>	4.713	-35.695	-0.126	0.082	-0.121	0.069	1.586	0.592
P <sub>1</sub> X P <sub>8</sub>	9.343	-37.125	-0.950	0.921**	7.532**	0.894**	5.019**	-3.439
P <sub>1</sub> X P <sub>9</sub>	-3.287**	-35.228	0.913*	1.212**	9.465**	0.953**	5.771**	9.046**
P <sub>2</sub> X P <sub>3</sub>	2.234	-9.231	0.877	2.503**	-5.668	-0.004	5.125**	8.695**
P <sub>2</sub> X P <sub>4</sub>	9.782	-8.731	1.135**	-3.848	-3.123	0.613**	14.295**	12.249**
P <sub>2</sub> X P <sub>5</sub>	3.401	-9.025	-1.820	2.045**	1.232	-0.030	-4.726	2.861**
P <sub>2</sub> X P <sub>6</sub>	2.998	-9.978	-1.038	-0.379	-0.034	-0.034	3.574*	-7.330
P <sub>2</sub> X P <sub>7</sub>	1.661	-0.055	-0.105	2.349**	-5.378	-0.484	-5.756	7.192**
P <sub>2</sub> X P <sub>8</sub>	1.058	-0.252	0.538	-1.579	-4.561	-0.129	1.877	-5.705
P <sub>2</sub> X P <sub>9</sub>	4.995	0.345	1.035*	2.445**	12.494**	0.493**	-3.538	-2.321
P <sub>3</sub> X P <sub>4</sub>	0.176	-8.328	2.189**	-0.233	0.006	0.299*	6.841**	-1.454
P <sub>3</sub> X P <sub>5</sub>	-0.372	-8.468	0.788	1.181**	10.712**	0.156	-9.547	-5.308
P <sub>3</sub> X P <sub>6</sub>	-6.008**	-9.107	0.850	1.603**	-7.774	-0.971	-13.781	3.034**
P <sub>3</sub> X P <sub>7</sub>	-4.312**	0.381	0.150	-0.170	-4.133	-0.038	6.822**	-1.345
P <sub>3</sub> X P <sub>8</sub>	-8.281**	-1.818	-2.141	0.136	3.580	0.877**	11.456**	0.658
P <sub>3</sub> X P <sub>9</sub>	2.268	0.946**	0.258	0.427	3.252	0.342**	2.374	-0.757
P <sub>4</sub> X P <sub>5</sub>	-4.324**	-8.888	-0.375	-0.156	10.277**	-0.249	-14.844	-6.821
P <sub>4</sub> X P <sub>6</sub>	2.573	-9.040	-0.293	1.218**	10.183**	0.393**	-2.911	-3.076
P <sub>4</sub> X P <sub>7</sub>	4.804	0.315	0.674	1.312**	-2.145	-0.107	0.825	-0.057
P <sub>4</sub> X P <sub>8</sub>	3.434	0.551	-0.284	-0.648	-0.820	0.174	4.725**	9.048**
P <sub>4</sub> X P <sub>9</sub>	1.837	-0.352	-0.987	1.578**	4.388	0.006	-4.023	-1.636
P <sub>5</sub> X P <sub>6</sub>	8.325	-10.287	-0.314	3.012**	-3.669	-0.246	-2.665	-6.899
P <sub>5</sub> X P <sub>7</sub>	7.588	0.454	1.719**	4.239**	5.043	0.283*	-2.296	2.555**
P <sub>5</sub> X P <sub>8</sub>	5.385	1.390**	1.495**	1.512**	1.074	0.008	-2.329	3.858**
P <sub>5</sub> X P <sub>9</sub>	5.222	1.421**	0.659	1.503**	-15.956	0.254*	28.656**	13.343**
P <sub>6</sub> X P <sub>7</sub>	2.419	-0.364	-0.999	1.982**	3.755	0.558**	6.871**	4.864**
P <sub>6</sub> X P <sub>8</sub>	3.649	0.072	0.210	0.088	4.810	0.786**	10.304**	11.534**
P <sub>6</sub> X P <sub>9</sub>	13.452	-1.831	-0.193	1.012**	-6.579	-0.240	1.822	8.985**
P <sub>7</sub> X P <sub>8</sub>	-3.054**	8.627**	0.077	-4.316	-2.529	-0.146	2.507	0.055
P <sub>7</sub> X P <sub>9</sub>	7.482	8.957**	1.407**	-1.094	2.639	0.589**	7.292**	2.340**
P <sub>8</sub> X P <sub>9</sub>	4.579	9.227**	1.616**	-4.888**	-2.693	-0.389	-5.241	0.943
L.S.D. Sij 5%	1.802	0.652	0.831	0.602	5.174	0.250	3.239	1.030
L.S.D. Sij 1%	2.382	0.862	1.099	0.796	6.838	0.331	4.281	1.362
L.S.D. Sij-Sik 5%	2.222	0.803	1.026	0.744	6.383	0.308	3.997	1.271
L.S.D. Sij-Sik 1%	1.802	1.062	1.357	0.983	8.437	0.407	5.283	1.680

\* and \*\* denotes significance at 5% and 1%, respectively.

**Table 7: Phenotypic (upper), genotypic (middle) and environmental (lower) correlation coefficients among studied characters of wheat.**

Characters	1	2	3	4	5	6	7
1- Plant height							
2- Spike length	0.113 0.114 0.287**						
3- Number of spikelets / spike	0.363** 0.389** 0.030	0.135 0.143 0.314**					
4- Number of spikes / plant	0.349** 0.354** -0.002	0.151 0.152 -0.085	0.212* 0.230** -0.069				
5- 1000 – Kernel weight	0.160 0.170 0.023	0.057 0.060 0.171	0.026 0.043 -0.097	0.127 0.132 0.099			
6- Grain weight / spike	0.348** 0.364** -0.044	-0.221* -0.229** 0.095	0.265** 0.312** -0.185*	-0.061 -0.062 -0.072	0.495** 0.479** 0.679**		
7- Number of grains / spike	0.228** 0.233** 0.012	-0.258** -0.262** 0.024	0.274** 0.301** -0.064	-0.195* -0.195* -0.201*	-0.340** -0.334** -0.521**	0.627** 0.657** 0.037	
8- Grain yield / plant	0.478** 0.482** 0.110	0.161 0.161 0.012	0.404** 0.434** -0.001	0.245** 0.247** 0.111	-0.100 -0.107 0.030	0.347** 0.361** 0.014	0.441** 0.451** -0.145

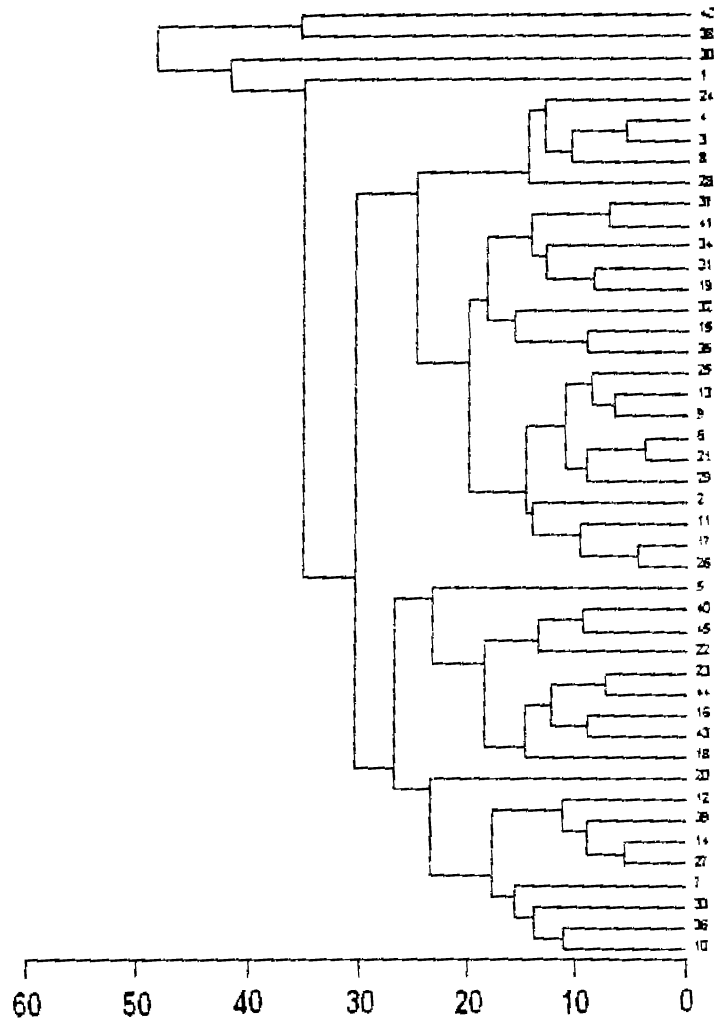
**Cluster analysis:**

Many algorithms have been proposed for cluster analysis, the hierarchical analysis was used in this study. It produces a dendrogram such as the ones shown in Fig. 1. These methods start with the calculation of the distance of each genotype to all other genotypes. A process of agglomeration division then forms groups. With agglomeration, all genotypes start by being alone in groups of one. Closed groups are then gradually merged until finally all genotypes are in a single group. This is then split into two groups, the two groups are then split, and so on until all genotypes become in groups of their own. For quantitative characters, number of clusters was chosen from the hierarchical analysis. Such genotypes were separated into meaningful genetic divisions based on knowledge of pedigree and type (Table 1). It is important when interpreting dendrograms to know that genotypes can pivot at each branching node, that each cluster may fall is arbitrary and different runs of the same data, set can give different pivots.

Genotypes started at a distance of 0.0 to 3.9 and ending with groups at distance of 48.5. In a distance of 0.0, the 45 genotypes under this study are in their own. The distance matrix in Fig. 1 and Table 8 shows that the smallest distance between two genotypes (21, 6) is 3.875. Hence, at a distance level of 3.875 there are four groups, 25, (13, 9), (6, 21) and 29. The similarity between this group is 96.125 The next smallest distance between genotypes is 4.493, between genotypes (17, 26). Hence, at a distance of 4.493 there are three groups, 2, 11 and (17, 26). This means that the similarity between this group is 95.507. The next smallest distance is 5.531 between genotypes (14, 27).

**Table 8: Euclidean method for 45 genotypes including two groups for genotypes and dissimilarity for each other.**

Node	Group 1	Group 2	Dissimilarity	No. of objects in group
1	21	6	3.875	2
2	26	17	4.493	2
3	14	27	5.531	2
4	3	4	5.653	2
5	9	13	6.628	2
6	37	41	7.158	2
7	44	23	7.262	2
8	31	19	8.609	2
9	Node 5	25	8.731	3
10	Node 3	39	9.056	3
11	43	16	9.057	2
12	29	Node 1	9.091	3
13	15	35	9.177	2
14	45	40	9.470	2
15	Node 2	11	9.731	3
16	Node 4	8	10.568	3
17	36	10	11.076	2
18	Node 12	Node 9	11.116	6
19	12	Node 10	11.344	4
20	Node 11	Node 7	12.372	4
21	34	Node 8	12.899	3
22	Node 16	24	13.146	4
23	Node 14	22	13.570	3
24	33	Node 17	13.841	3
25	2	Node 15	14.199	4
26	Node 6	Node 21	14.325	5
27	Node 22	28	14.550	5
28	Node 20	18	14.760	5
29	Node 18	Node 25	14.830	10
30	Node 24	7	15.676	4
31	Node 13	32	15.799	3
32	Node 30	Node 19	17.739	8
33	Node 31	Node 26	18.290	8
34	Node 28	Node 23	18.421	8
35	Node 29	Node 33	19.962	18
36	Node 34	5	23.302	9
37	Node 32	20	23.570	9
38	Node 27	Node 35	24.908	23
39	Node 37	Node 36	26.795	18
40	Node 38	Node 39	30.398	41
41	Node 40	1	35.090	42
42	42	38	35.484	2
43	Node 41	30	41.773	43
44	Node 43	Node 42	48.472	45



**Fig. 1: Similarity coefficients of the wheat genotypes calculated by cluster analysis.**

Hence, at this level of distance there are three groups, 12, 39 and (14, 27). This means a similarity of 94.469. The next smallest distance is 5.653 between (4, 3). At this level of distance there are four groups, 24, (4, 3), 8 and 28. In This group similarity was equal to 94.347. The next smallest distance is 7.158 between (37, 41). Hence at a distance of 7.158 there are three groups, (37, 41), 34 and (31, 19). This means similarity of 92.842. The next smallest distance is 7.262 between genotypes (23, 44). At this level of distance there are five groups, (40, 45), 22, (23, 44), (16, 43) and 18. The similarity between this group is 92.738. The dendrogram shown in Fig. (1) illustrates how agglomeration takes place. With Fareast neighbor linkage two groups merge only if the most distant members of the two groups are close enough together. The first cluster group includes (38, 42). In this cluster group genotype 38 did not join with genotype 42 until 35.484 distance level. The second cluster group was splitted into two sub cluster groups, the first included genotype 30. The second cluster group was splitted into two groups, the first included genotypes 24, (4, 3), 8, 28, (37, 41), 34, (31, 19), 32, (15, 35), 25, (13, 9), (6, 21), 29, 2, 11 and (17, 26). In this sub group 28, 32 and 2 did not join with genotypes 24, (15, 35) and 11 until distance level of 14.55, 15.799 and 14.199, respectively. The second sub group contained genotypes 5, (40, 45), 22, (23, 44), (16, 43), 18, 20, 12, 39, (14, 27), 7, 33 and (10, 36). In this group genotypes 5, 18, 20 and 7 did not join with genotypes (40, 45), (16, 43), 12 and 33 until 23.302, 14.76, 23.57 and 15.676 distance level, respectively. This means that there is high level of dissimilarity between genotypes.

From dendrogram, it appears that genotypes (3, 4), (37, 41), (19, 31), (15, 35), (9,13), (6, 21), (17, 26), (40, 45), (23, 44), (16, 43), (14, 27) and (10, 36) are closely related to each other. It seems fair to say, according to the results obtained, that the cluster analysis has produced a sensible description of the relationships between the different groups.

From the previous results, it could be concluded, as a result of dissimilarity, that genotypes 1, 5, 7, 18, 20, 28, 30, 32, 38 and 42 have a high distance level between each other and produce good results if they are crossed because there is dissimilarity between them. The results of the present study showed that cluster analysis is a valuable tool for subdividing genotypes into groups including similarity and dissimilarity genotypes to help the breeder working in crop species.

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### دراسة بعض الصفات الكمية باستخدام الهجن التبادلية والتحليل العنقودي على محصول القمح

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تم تقييم كافة هجن الجيل الأول التبادلية دون العكسية بين تسعة آباء وذلك لمحصول النباتات من حبوب القمح وأهم الصفات المساهمة فيه (طول النبات، طول السنبل، عدد سنبلات السنبل، عدد سنابل النبات، وزن النبات، وزن حبوب السنبل وعدد حبوب السنبل). وقد نفذت هذه الدراسة خلال موسم ٢٠٠١/٢٠٠٢ و ٢٠٠٠/٢٠٠١ بمحطة البحوث الزراعية بالجميزة - مركز البحوث الزراعية. كما قدرت قوة الهجين وقوة التآلف العامة والخاصة والارتباط الوراثي والمظهري بالإضافة للتحليل العنقودي للصفات تحت الدراسة.

وقد أوضحت النتائج وجود اختلافات جوهرية بين كافة التراكيب الوراثية في كل الصفات تحسنت الدراسة في حين كانت اختلافات الآباء ضد الهجن (كمؤشر عام لتباين قوة الهجين) عالية المعنوية في كل الصفات. وبتقدير القيم النسبية لتباين كل من القدرة العامة والخاصة على التآلف وجد إنها تزيد عن الوحدة لكافة الصفات تحت الدراسة ما عدا وزن حبوب السنبل ومحصول الحبوب للنبات. كما أوضحت النتائج تفوق ٢٩ هجينا على الأب الأفضل بنسب تراوحت بين ٨,٢٥% للهجين P6 X P4 الى ٩٨,٨٤% للهجين P6 X P8 في محصول النبات من الحبوب. هذه التأثيرات غير الإضافية لقوة الهجين مع التباين الواضح بين كافة التراكيب الوراثية قد تعطي الفرصة لعزل توليفات جديدة في الأجيال الإنمائية التالية خاصة وأن التأسيس الناتج عن التلقيح الذاتي ينشط دور النباتات المنتخبة في تقليل آثار السيادة على الفعل الجيني المضيف.

كما أوضحت نتائج دراسة القدرة العامة على التآلف أن السلالة P1 والسلالة P9 والسلالة P7 أفضل الآباء تالفا للمحصول مع ثلاث أو أربع من الصفات المساهمة في محصول الحبوب للنبات. كذلك وجد أن أفضل الهجن هما P1 X P9 , P1 X P5 للقدرة الخاصة على التآلف لمحصول الحبوب للنبات ومكوناته. كما لوحظ ارتباط وراثي معنوي وموجب لصفة محصول النبات من الحبوب مع كل الصفات تحت الدراسة ما عدا طول السنبل.

أما بالنسبة للتحليل العنقودي فقد تم تقسيم التراكيب الوراثية في هذه الدراسة إلى ثلاثة مجموعات باستخدام طريقة المتوسطات الحسابية، قسمت هذه المجموعات إلى تحت مجموعات بناء على درجة التشابه أو القواعد بين التراكيب الوراثية وقد أوضحت النتائج أن التراكيب الوراثية P1 X P5 ، P1 X P7 ، P3 ، P7 ، P3 X P5 ، P4 X P7 ، P4 X P9 ، P6 X P5 ، P6 X P8 ، P7 X P9 بينها وبين التراكيب الأخرى عدم تشابه ويمكن من خلال التهجين بينها الحصول على توافق هجينية جيدة في برامج التربية.