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BREEDING FOR THE IDEAL TYPE OF GRAIN YIELD IN TRITICALE USING DIALLEL ANALYSIS

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ABSTRACT: *Heterosis and combining ability analysis were studied in a 7 × 7 diallel set of tritical for plant height, spike length, number of spikelets per spike, 1000- kernel weight, number of kernels per spike and seed setting. Genotype and the resultant twenty one crosses mean squares were found to be highly significant for all traits studied at the two generations F_1 and F_2 data. Parents vs. crosses mean squares as an indication to average heterosis overall crosses, were found to be highly significant for all traits studied, except 1000-kernel weight at the tow generations F_1 and F_2 as well as number of kernels per spike and seed setting at F_1. General combining ability and specific combining ability were found to be highly significant for most characters studied. Line 4 exhibited highly significant general combining ability effects in plant height, number of spikelets per spike and number of kernels per spike. Also, line 3 proved to be good combiner for spike length and number of kernels per spike.Line 3 x line 7 showed significant specific combining ability effects at the tow generations F_1 and F_2 data for plant height, number of spikelets per spike, 1000-kernel weight and number of kernels per spike. The GCA / SCA ratios were found to be greater than unity. Information generated from this study can be useful to predict hybrid for selecting parents and hybrid development to maximize the grain yield and its components.*

Key words: *Triticale, diallel cross, heterosis, combining ability, general and specific combining ability.*

INTRODUCTION

In the first-ever published report describing a fertile hybrid between wheat and rye, Carman (1884). Triticale is one of the genotypes which interested for breeders. It is able to surpass the parental species in many aspects. Triticale preferred because of its high adaptability to cold and leaf diseases, than wheat and much more productive than rye. Like rye, it can grow on salty and acid soil and give satisfactory grain yield. Its grain contains more lysine, than wheat. That is why breeders are interested in this species (Grebennikova et al,.2011). A fertile wheat x rye hybrid was produced by W. Rimpau in Germany in 1888. Wheat x rye hybrids were later developed in Russia and Sweden, and more recently in the U.S.A., Canada, Mexico, Hungary and other countries (Poehlman, 1979). Diallel analysis is one of the most effective methods to study the genetic control system of quantitative traits in plant growing. Heterosis or hybrid vigor is defined as the advantage of F_1 hybrid performance over its parents in terms of viability, growth, and productivity, and has been widely used in agriculture. However, up to date, the mechanism of heterosis is still an area to be elucidated. The inheritance of height in triticale, additive effects seemed to be more important than non-additive ones (*Reddy 1976; Rao and Joshi(1979).* The objectives of the present study were to assess the potentiality of general combining ability (GCA), specific combining ability (SCA) and heterosis expression for plant height, spike length, number of spikelets/spike, number of kernels /spike, 1000-kernel weight and grain yield/plant.

MATERIALS AND METHODS

Seven of triticale lines have been used in half diallel crossing design, The material are obtained from Department of Agriculture Genetic, University of Sydney, Australia. Table (1).

In 2009/2010 growing season, in Giza Agricultural Research Center, grain from each of the seven parental genotypes were sown at various planting dates in order to overcome the differences in time of heading during this season. All possible cross combinations (without reciprocals) were made among the seven genotypes, giving seeds of F1 21crosses.

Second season 2010/2011,the F1 plants of each cross were selfed to produce F2 seeds.

Third season 2011/2012; one experiment included the seven parents, their twenty one crosses and F2 plants were sown in a randomized complete block design (RCBD) with three replications. Each plot consisted of one row, of 1.5 meters long and 30 cm wide. Grains were individually sown in hills at 20 cm space between plants within row. The other cultural practices of growing wheat were properly practiced. Data for all morphological and yield component traits were recorded on ten guarded plants chosen at random from each plot as follows: for plant height, spike length, number of spikelets/spike, number of kernels /spike, 1000-kernel weight. The combined analysis of the experiment was carried out whenever homogeneity of error variance was detected (Gomez and Gomez, 1984). Heterosis was calculated for individual crosses as the percentage deviation of F1 mean performance from its better-parent average values. Appropriate L.S.D. values were computed according to the following formula to test the significance of these heterotic effects;

Better parent heterosis = $\frac{\overline{F}_1 - B.P.}{B.P.} x100$

Where: $\overline{F}_1$ is the mean of F1.

B.P. is the better parent mean.

L.S.D. for better-parent heterosis = t 0.05- 0.01 $\sqrt{\frac{2MS_e}{r}}$

Estimates of combining abilities were obtained by employing Griffing's diallel cross analysis (1956) designated as method 2 model I.

Morphological and yield components:

Data for all morphological and yield components traits were recorded on ten guarded plants chosen at random from each plot as follows:-

1. Plant height (cm); length of the main culm measured from soil surface to the tip of spike excluding owns.
2. Spike length: measured as the length of main stem spike (cm).
3. Number of spikelets/ spike; it was determined by counting the number of fertile spikelets per spike.
4. 1000- Kernel weight (g):1000-kernel from individual guarded plants bulked and weighted.
5. Number of kernels /spike; estimated by counting number of grains of the main spike.
6. Seed setting : determined by dividing the number of kernels / spike by twice the number of spikelets per spike.

Table (1): Source and Pedigree from parented genotypes of triticale.

No. of lines	Source	Pedigree
1	Australia	I II79 – 12 – 14 A C155
2	Australia	IS 2774 B75 RT 1186 C207
3	Australia	II 81 – 575 C217
4	Australia	III79 – 12 – 15 RT 1172C82
5	Australia	80447 II 76 211025 C214
6	Australia	I 80377 (1) 406 C141
7	Australia	II 76 10 0 B4 C2O4

RESULTS AND DISCUSSION

The analysis of variance for all traits studied i.e plant height (cm), spike length(cm), number of spikelets/ spike, 1000- Kernel weight (g), number of kernels /spike and seed setting at the two generations F1 and F2 data are presented in Table (2).

Genotypes and the resultant crosses mean squares were found to be highly significant for all traits studied, except seed seting at F1 indicating wide diversity between the parental used in the present study.

Parent mean squares were found to be either significant or highly significant for all traits studied at the two generations, indicating that parental lines differed in their mean performance in most traits and presence of sufficient heterosis. These result are in harmony with those previously obtained by Moussa and Morad (2009) and Seleem and Koumber (2011).

Highly significant differences of crosses mean squares at F1 amd F2 generations were detected for all traits, except seed setting at F1 , reflecting the diversity of the parents and that these diversity could be transmitted to the progenies.

Parents vs. crosses mean squares as an indication to average heterosis overall crosses, were found to be highly significant for all traits studied except 1000-kernel weight at the two generations F1 and F2 as well as number of kernels per spike and seed setting at F1. This means that genetic constitutions of the parents as well as their crosses are widely different and the parents had a wide range of genetic variability.

Table (2): Mean square estimates of ordinary analysis and combining ability analysis for all traits studied .

S.O.V.	d.f.	Plant height (cm)		Spike length (cm)		No. of spikelets per spike	
		F1	F2	F1	F2	F1	F2
Genotypes	27	482.63**	553.98**	12.72**	20.68**	76.91**	112.84**
parent	6	382.21**	382.21**	11.75**	11.75**	96.16**	98.54**
Cross	20	432.65**	400.97**	5.77**	10.49**	58.75**	100.64**
Par.vs.cr.	1	2084.66**	4644.87**	157.62**	278.04**	324.59**	442.68**
Error	54	51.05	21.95	0.90	0.71	2.49	2.89

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (2): cont.

S.O.V.	d.f.	1000- kernel weight		Number of kernels per spike		Seed setting	
		F1	F2	F1	F2	F1	F2
Genotypes	27	215.69**	106.59**	285.61**	386.90**	0.35	0.10**
parent	6	73.78**	70.98**	247.22**	234.27**	1.36*	0.02*
Cross	20	267.88**	122.42**	304.46**	430.69**	0.06	0.11**
Par.vs.cr.	1	23.53	3.81	138.77	426.92**	0.10	0.31**
Error	54	8.77	6.06	34.40	32.76	0.43	0.01

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Mean performance

Mean performance of the seven parent and their twenty one crosses at the two generations F1 and F2 for all traits studied are given in Table (3). The parental Line5 and Line 1 at the two generations F1 and F2 recorded the highest plant height also, the cross Line 4 x Line7 at F1 and Line 3 x Line 5 at F2 recorded the highest values. For spike length, the Line 3 and Line 1 at the two generations F1 and F2 recorded the greatest mean value. The crosses Line 3 x Line 7 at F1 and Line 1 x Line 3 at F2 had the highest mean values. The parental Line5 and Line 4 at the two generations F1 and F2 recorded the highest number of spikelet per spike. While, the crosses Line 1 x Line 5 at F1 as well as Line 4 x Line 6 at F2 showed the highest mean values. For 1000- kernel weight, the parental Line 6 at F1 and Line 1 at F2 had the greatest mean values. The crosses Line 1 x Line 2 at F1 and Line 5 x Line 7 at F2 had the greatest mean value. The parental Line 6 at F1 and Line 4 at F2 recorded the highest number of kernels per spike Also, the cross Line1 x Line2 at F1 and F2 recorded the highest values. For seed setting, the parental Line 6 at F1 and Line 7 at F2 had the greatest mean values. The crosses Line 6 x Line 7 at F1 and Line 1 x Line 2 at F2 had the greatest mean

Table (3): The genotypes mean performance

Genotypes	Plant height (cm)		Spike length(cm)		No. of spikelets per spike	
	F_1	F_2	F_1	F_2	F_1	F_2
Line 1	118.67	118.67	16.10	16.10	28.00	28.00
Line 1x Line 2	78.20	85.63	9.87	10.57	25.00	34.33
Line 1x Line 3	96.20	86.13	10.13	13.07	27.33	31.67
Line 1x Line 4	91.60	102.73	11.53	10.87	27.67	23.00
Line 1x Line 5	94.93	78.13	11.73	10.87	32.00	23.33
Line 1x Line 6	98.87	86.73	10.00	11.07	27.00	26.00
Line 1x Line 7	79.13	83.20	8.93	7.80	20.67	19.67
Line 2	103.33	103.33	13.70	13.70	27.67	27.67
Line 2x Line 3	78.20	74.47	9.87	6.93	25.00	16.33
Line 2x Line 4	96.20	87.67	10.13	8.40	27.33	16.33
Line 2x Line 5	91.60	68.00	11.53	5.67	27.67	14.00
Line 2x Line 6	94.93	92.80	11.73	8.53	32.00	19.00
Line 2x Line 7	98.87	88.27	10.00	8.80	27.00	19.33
Line 3	104.00	104.00	17.50	17.50	30.67	30.67
Line 3x Line 4	108.00	107.67	11.20	11.40	31.67	24.00
Line 3x Line 5	103.13	108.80	11.27	10.33	23.00	22.67
Line 3x Line 6	117.00	98.00	10.83	11.93	23.33	22.67
Line 3x Line 7	116.67	99.13	14.50	11.47	26.00	25.33
Line 4	109.67	109.67	14.53	14.53	34.33	34.33
Line 4x Line5	100.27	102.20	12.80	10.67	22.67	24.00
Line 4x Line 6	100.27	102.40	12.80	11.13	22.67	35.00
Line 4x Line 7	123.67	108.47	10.33	11.60	16.33	27.33
Line 5	124.67	124.67	15.07	15.07	35.33	35.33
Line 5x Line 6	89.33	85.20	12.57	10.73	19.00	32.00
Line 5x Line 7	97.33	82.20	13.07	11.60	19.33	28.00
Line 6	111.67	111.67	11.83	11.83	31.33	32.33
Line 6x Line 7	90.00	97.53	12.53	12.13	19.00	24.67
Line 7	90.00	90.00	12.53	12.53	18.33	18.33
L.S.D 5%	11.79	7.73	1.57	1.39	2.60	2.81
L.S.D 1%	15.78	10.34	2.10	1.85	3.48	3.75

Table (3): Cont.

Genotypes	1000- kernel weight		Number of kernels per spike		Seed setting	
	F_1	F_2	F_1	F_2	F_1	F_2
Line 1	42.33	42.33	52.33	52.33	0.93	0.93
Line 1x Line 2	39.00	46.67	43.00	66.33	0.93	0.94
Line 1x Line 3	26.00	45.33	49.00	50.67	0.97	0.80
Line 1x Line 4	32.67	39.00	56.67	52.00	0.98	1.13
Line 1x Line 5	39.00	41.00	48.00	44.33	0.90	0.94
Line 1x Line 6	52.67	30.33	56.67	34.67	1.19	0.66
Line 1x Line 7	52.00	35.33	45.67	23.33	1.09	0.62
Line 2	47.67	47.67	44.33	44.33	0.80	0.80
Line 2x Line 3	39.00	49.67	43.00	43.33	0.93	1.20
Line 2x Line 4	26.00	36.67	49.00	32.00	0.97	0.95
Line 2x Line 5	32.67	40.33	56.67	29.67	0.98	0.97
Line 2x Line 6	39.00	40.33	48.00	42.00	0.90	1.03
Line 2x Line 7	52.67	30.67	56.67	43.00	1.19	1.10
Line 3	38.00	38.00	55.67	55.67	0.91	0.91
Line 3x Line 4	50.67	45.33	64.00	57.67	1.20	1.23
Line 3x Line 5	41.33	37.33	55.67	49.67	1.10	1.07
Line 3x Line 6	58.33	44.67	74.67	66.00	1.20	1.40
Line 3x Line 7	55.67	51.00	63.33	60.00	1.10	1.17
Line 4	43.67	43.67	63.00	63.00	0.91	0.91
Line 4x Line5	38.00	39.00	68.00	38.00	1.23	0.79
Line 4x Line 6	38.00	51.00	68.00	62.33	1.23	0.89
Line 4x Line 7	45.33	39.00	47.00	58.67	1.20	1.07
Line 5	33.33	33.33	65.00	65.00	0.92	0.92
Line 5x Line 6	36.67	51.67	73.33	45.67	0.96	0.80
Line 5x Line 7	53.33	49.00	60.33	51.00	0.90	0.91
Line 6	38.67	40.00	46.67	49.33	2.64	0.72
Line 6x Line 7	45.67	39.00	41.67	54.33	0.75	1.07
Line 7	45.67	45.67	41.67	41.67	0.75	0.75
L.S.D 5%	4.89	4.06	9.68	9.44	1.08	0.14
L.S.D 1%	6.54	5.44	12.95	12.64	1.45	0.19

Heterosis

Useful heterosis expressed as the percentage deviation of F1 mean performance from the better parent for all traits studied are presented in Table (4).

Table (4): Percentage of heterosis over better parent for all traits studied

Crosses	Plant height (cm)	Spike length (cm)	No. of spikelets per spike
Line 1x Line 2	-34.10**	-38.72**	-10.71*
Line 1x Line 3	-18.93**	-42.10**	-10.87*
Line 1x Line 4	-22.81**	-28.36**	-19.42**
Line 1x Line 5	-23.85**	-27.12**	-9.43*
Line 1x Line 6	-16.69**	-37.89**	-13.83**
Line 1x Line 7	-33.31**	-44.51**	-26.19**
Line 2x Line 3	-34.10**	-38.72**	-10.71*
Line 2x Line 4	-7.50	-42.10**	-10.87*
Line 2x Line 5	-16.47**	-20.64**	-19.42**
Line 2x Line 6	-23.85**	-22.12**	-9.43*
Line 2x Line 7	-11.46*	-27.01**	-13.83**
Line 3x Line 4	4.52	-18.25**	14.46**
Line 3x Line 5	-0.19	-17.76**	-16.87**
Line 3x Line 6	6.69	-38.10**	-32.04**
Line 3x Line 7	-6.42	-17.14**	-26.42**
Line 4x Line5	-10.21	-26.86**	-27.66**
Line 4x Line 6	-3.59	-26.86**	-26.09**
Line 4x Line 7	18.91**	-40.95**	-46.74**
Line 5x Line 6	-28.34**	-16.59**	-46.23**
Line 5x Line 7	-12.84*	-10.09	-43.69**
Line 6x Line 7	-17.93**	-13.76**	-44.66**
L.S.D 5%	11.79	1.57	2.60
L.S.D 1%	15.78	2.10	3.48

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Table (4): cont.

Crosses	1000- kernel weight	Number of kernels per spike	Seed setting
Line 1x Line 2	-18.18**	-17.83	-0.71
Line 1x Line 3	-38.58**	-11.98	4.29
Line 1x Line 4	-25.19**	-10.05	5.00
Line 1x Line 5	-7.87	-26.15**	-3.93
Line 1x Line 6	24.41**	8.28	-54.80**
Line 1x Line 7	13.87*	-12.74	16.79
Line 2x Line 3	-7.87	-17.83	-0.71
Line 2x Line 4	-45.45**	-11.98	7.35
Line 2x Line 5	-31.47**	-10.05	7.30
Line 2x Line 6	-18.18**	-26.15**	-2.18
Line 2x Line 7	10.49*	21.43*	-54.80**
Line 3x Line 4	6.29	44.36**	50.63
Line 3x Line 5	-13.29*	25.56*	38.08
Line 3x Line 6	33.59**	18.52*	31.39
Line 3x Line 7	46.49**	-2.56	20.00
Line 4x Line5	-1.72	22.16*	-53.28*
Line 4x Line 6	-16.79	22.16*	36.03
Line 4x Line 7	19.30**	-15.57	32.35
Line 5x Line 6	-16.03**	12.82	5.09
Line 5x Line 7	22.14**	-4.23	-65.91**
Line 6x Line 7	0.01	-33.86**	-18.25
L.S.D 5%	3.10	9.68	1.08
L.S.D 1%	4.15	12.95	1.45

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

Plant height, fourteen crosses exhibited significant negative values of heterosis relative to better parent and would be useful from the triticale breeders point of view. It was detected in all hybrids studied at F1 generation, except Line 4 x Line 7 gave appositive value. Notes that there was no positive values for spike length and seed setting characters and most of values were negative. With regard to number of spikelets/spike, the hybrid (Line 3 x Line 4) exhibited significant positive heterotic effects relative to better parent. As for 1000-kernel weight four crosses showed significant useful heterotic at F1 generation in hybrid (line1 x line6, line1 x line7, line2 x line 7 and line 5 x line 7). Similar results were previously reported by Sharief et al. (2006) and Kumar et al. (2011). For number of kernels/spike, six hybrids (line 3 x line 4, line 3 x line 5, line 4 x line 5, line 4 x line 6, line 2 x line 7 and line 3 x line 6) exhibited significant positive heterotic effects relative to better parent in the same order.

Significant heterosis was also found by Dawwam et al. (2007) and Kumar et al. (2011).

Combining ability

The analysis of variance combining ability for all traits studied are presented in Table (5). General combining ability and specific combining ability were found to be highly significant for most characters studied. This would indicate the importance of both additive and non-additive genetic variance in determining the performance of all traits studied.

The question remains would be about the relative importance of both general and specific combining abilities. Therefore, GCA / SCA ratio was used to clarify the nature of the genetic variance involved. The GCA / SCA ratios were found to be greater than unity, indicating that additive and additive × additive types of gene action were of greater importance in the inheritance of all traits studied. It is therefore could be concluded that the presence of large amount of additive effects, suggests the potentiality for obtaining further yield and yield components improvements. Also, selection procedures based on the accumulation of additive effect would be successful in improving all character studied. However, to maximize selection advance, procedures which are known to be effective in shifting gene frequency when both additive and non-additive variances are involved, would be preferred.

Table (5): Combining ability analysis for all traits studied

S.O.V.	d.f.	Plant height (cm)		Spike length (cm)		No. of spikelets per spike	
		F_1	F_2	F_1	F_2	F_1	F_2
GCA	6	128.80**	176.67**	2.49**	6.35**	41.78**	40.88**
SCA	21	170.04**	186.94**	4.74**	7.05**	21.03**	36.68**
Error	54	17.02	7.32	0.30	0.24	0.83	0.96
GCA /SCA		0.76	0.95	0.53	0.90	1.99	1.11

Table (5): Cont.

S.O.V.	d.f.	1000- kernel weight		Number of kernels per spike		Seed setting	
		F_1	F_2	F_1	F_2	F_1	F_2
GCA	6	96.44**	9.21**	203.51**	117.06**	0.21	0.03
SCA	21	64.88**	43.05**	64.26**	132.37**	0.09	0.03
Error	54	2.92	2.02	11.47	10.92	0.14	0.01
GCA /SCA		1.49	0.21	3.17	0.88	2.36	1.09

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

1. General combining ability effects:

Estimation of the general combining ability effects (ĝi) of the individual parents for each trait at the two generations F_1 and F_2 data are given in Table (6). Concerning plant height, line 2 exhibited negative significant general combining ability effects at the two generations F_1 and F_2 data proving to be excellent combiners in this concern. As for spike length, line 3 showed highly significant of general combining ability effects at the two generations F_1 and F_2 data proving to be good general combiners for spike length. For number of spikelets per spike the three triticale genotypes line1, line 4 and line 5 showed significant general combining ability effects at the two generations data proving to be combiners for this trait. Concerning to 1000- kernel weight both of line 6 and line 7 at F_1 had positive significant general combining ability effects. As for number of kernel per spike, the two lines; line 3 and line 4 exhibited significant general combining ability effects at the two generations F_1 and F_2 data proving to be excellent combiners in this concern. As for seed setting line 6 at F_1 exhibited significant general combining ability effect.

Table (6): Estimates of general combining effects for parents

Parents		Plant height (cm)		Spike length (cm)		No. of spikelets per spike	
		F_1	F_2	F_1	F_2	F_1	F_2
Line 1		-2.84*	-0.88	-0.26	0.66*	0.87**	1.07*
Line 2		-6.35**	-7.15**	-0.69**	-1.58**	1.28**	-3.30**
Line3		2.82*	1.60	0.67**	1.07**	1.10**	-0.04
Line 4		4.17**	6.96**	0.12	0.29	1.02**	1.55**
Line 5		2.68*	0.67	0.71**	-0.06	0.72*	1.14**
Line 6		1.32	2.02	-0.29	-0.15	-0.24	2.18**
Line 7		-1.80	-3.22	-0.26	-0.23	-4.76**	-2.60**
L.S.D ĝi	0.05	2.55	3.89	0.34	0.52	0.56	0.86
	0.01	3.39	5.17	0.45	0.69	0.75	1.14
L.S.D ĝi – ĝj	0.05	1.67	2.55	0.30	0.46	0.61	0.93
	0.01	2.22	3.39	0.40	0.61	0.81	1.23

Table (6): Cont.

Parents		1000- kernel weight		Number of kernels per spike		Seed setting	
		F_1	F_2	F_1	F_2	F_1	F_2
Line 1		-1.33*	-1.42	-3.94**	-1.90	-0.06	-0.07
Line 2		-1.59**	0.50	-6.02**	-5.35**	-0.11	0.02
Line3		1.00	1.58	2.43*	5.06**	-0.02	0.12
Line 4		-2.22**	0.24	4.39**	3.72*	0.02	0.03
Line 5		-3.37**	-1.13	5.87	-0.53	-0.07	-0.03
Line 6		1.07*	0.21	1.84	1.17	0.33**	-0.04
Line 7		6.44**	0.02	-4.57**	-2.16	-0.09	-0.02
L.S.D ĝi	0.05	1.06	1.61	2.09	3.19	0.23	0.36
	0.01	1.40	2.14	2.78	4.25	0.31	0.48
L.S.D ĝi - ĝj	0.05	0.88	1.34	2.04	3.12	0.03	0.05
	0.01	1.17	1.78	2.71	4.14	0.04	0.06

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

2. specific combining ability effects:

Estimates of specific combining ability effects (Ŝi) for the twenty one hybrid combinations at the two generations F1 and F2 data are presented in Table (7).

For plant height, the three crosses, line 2 x line 3 and line 5 x line 6 showed negative significant specific combining ability effects at F1 and F2 generations. As for spike length two crosses; line 1 x line 7 for F1 and line 6 x line 7 for F2 had a positive significant specific combining ability effects. For number of spikelets per spike the hybrid combinations line 3 x line 7 showed highly significant desirable specific combining ability effects at the two generations F1 and F2. Concerning 1000-kernel weight, the two crosses line 5 x line 7 and line 3 x line 7 showed significant specific combining ability effects at two generations F1 and F2. These results are in agreement with those obtained by Kumar et al. (2011) and Kamaluddin et al. (2011). For number of kernels per spike the three crosses line 3 x line 6, line 3 x line 7 and line 4 x line 6 showed highly significant desirable specific combining ability effects at F1 and F2 generations. As for seed setting there was no significant at F1 while ten crosses gave a significant.

Table (7): Estimates of specific combining ability effects for the twenty one crosses studied for all traits studied

Crosses	Plant height (cm)		Spike length(cm)		No. of spikelets per spike	
	F_1	F_2	F_1	F_2	F_1	F_2
Line 1x Line 2	-12.84**	-2.32	-1.28*	0.18	-3.13**	11.02**
Line 1x Line 3	-4.01	-10.56**	-2.37**	0.03	-0.61	5.09**
Line 1x Line 4	-9.96*	0.67	-0.42	-1.40**	-0.20	-5.17**
Line 1x Line 5	-5.13	-17.64**	-0.80	-1.05*	4.43**	-4.43**
Line 1x Line 6	0.16	-10.38**	-1.54**	-0.76	0.39	-2.80**
Line 1x Line 7	-16.46**	-8.67**	-2.64**	-3.94**	-1.43	-4.35**
Line 2x Line 3	-18.50**	-15.96**	-2.21**	-3.87**	-3.35**	-5.87**
Line 2x Line 4	-1.84	-8.13**	-1.39**	-1.63**	-0.94	-7.46**
Line 2x Line 5	-4.96	-21.50**	-0.57	-4.01**	-0.31	-9.39**
Line 2x Line 6	-0.27	1.95	0.62	-1.05*	4.98**	-5.43**
Line 2x Line 7	6.79	2.66	-1.15*	-0.71	4.50**	-0.31
Line 3x Line 4	0.79	3.13	-1.69**	-1.27**	3.57**	-3.06**
Line 3x Line 5	-2.59	10.55**	-2.20**	-1.99**	-4.80**	-3.98**
Line 3x Line 6	12.63**	-1.60	-1.64**	-0.30	-3.50**	-5.02**
Line 3x Line 7	15.41**	4.78*	1.99**	-0.69	3.69**	2.43**
Line 4x Line5	-6.81	-1.41	-0.12	-0.88	-5.06**	-4.24**
Line 4x Line 6	-5.45	-2.56	0.87	-0.32	-4.09**	5.72**
Line 4x Line 7	21.07**	8.75**	-1.63*	0.22	-5.91**	2.83**
Line 5x Line 6	-14.90**	-13.47**	0.06	-0.38	-7.46**	3.13**
Line 5x Line 7	-3.78	-11.23**	0.53	0.57	-2.61**	3.91**
Line 6x Line 7	-9.76*	2.76	0.99	1.19**	-1.98*	-0.46
LSD (sij) 5%	7.48	4.91	1.00	0.88	1.65	1.78
1%	10.01	6.56	1.33	1.18	2.21	2.38

Table (7): cont.

Crosses	1000- kernel weight		Number of kernels per spike		Seed setting	
	F_1	F_2	F_1	F_2	F_1	F_2
Line 1x Line 2	-0.32	5.69**	-1.94	24.44**	0.04	0.04
Line 1x Line 3	-15.92**	3.29*	-4.38	-1.63	0.01	-0.20**
Line 1x Line 4	-6.03**	-1.71	1.32	1.04	-0.03	0.22**
Line 1x Line 5	1.45	1.66	-8.82**	-2.37	-0.04	0.10*
Line 1x Line 6	10.68**	-10.34**	3.88	-13.74**	-0.14	-0.18**
Line 1x Line 7	4.64**	-5.16**	-0.71	-21.74**	0.18	-0.24**
Line 2x Line 3	-2.66	5.69**	-8.31**	-5.52	0.01	0.11**
Line 2x Line 4	-12.44**	-5.97**	-4.27	-15.52**	0.01	-0.05
Line 2x Line 5	-4.62**	-0.94	1.92	-13.59**	0.10	0.03
Line 2x Line 6	-2.73	-2.27	-2.71	-2.96	-0.39	0.10*
Line 2x Line 7	5.56**	-11.75**	12.36**	1.37	0.33	0.15**
Line 3x Line 4	9.64**	1.62	2.29	-0.26	0.14	0.13**
Line 3x Line 5	1.45	-5.01**	-7.53*	-4.00	0.12	0.03
Line 3x Line 6	14.01**	0.99	15.51**	10.63**	-0.18	0.37**
Line 3x Line 7	5.97**	7.51**	10.58**	7.96*	0.14	0.12**
Line 4x Line5	1.34	-2.01	2.84	-14.33**	0.22	-0.16
Line 4x Line 6	-3.10*	8.66**	6.88*	8.30**	-0.18	-0.06
Line 4x Line 7	-1.14	-3.16*	-7.71*	7.96**	0.21	0.11*
Line 5x Line 6	-3.29*	10.69**	10.73**	-4.11	-0.37	-0.08
Line 5x Line 7	8.01**	8.21**	4.14	4.56	-0.01	0.01
Line 6x Line 7	-4.10*	-3.12*	-10.49**	6.19*	-0.56	0.17**
LSD (sij) 5%	3.10	2.58	6.14	5.99	0.69	0.09
1%	4.15	3.45	8.22	8.02	0.92	0.12

* and ** significant at 0.05 and 0.01 levels of probability, respectively.

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التربية لطراز النبات النموذجى للمحصول فى الترتيكال بإستخدام تحليل الدايالليل

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الملخص العربى

أجريت هذه الدراسة خلال ثلاثة مواسم زراعية متتالية 2010/2009 و 2011/2010 و 2012/2011 حيث استخدم لهذه الدراسة سبع تراكيب وراثية من الترتيكال متباعدة المصدر, في موسم 2010/2009 تم التهجين بين هذه التراكيب الوراثية باستخدام طريقة التهجين التبادلي في اتجاه واحد في موسم 2010 /2011 تم زراعة نباتات الجيل الأول للحصول على نباتات الجيل الثانى وفى موسم 2011/ 2012 تم تقييم الآباء والهجن الناتجة منها في تجربة ذات قطاعات كاملة العشوائية في ثلاث مكررات, وقد تم تحليل البيانات باستخدام طريقة الهجن التبادلية (جرفنج 1956) الطريقة الثانية الموديل الأول ولقد أجري هذا البحث بهدف:-

1- تقدير قوة الهجين.
2- القدرة العامة و الخاصة على الائتلاف.

وكانت الصفات المدروسة إرتفاع النبات، طول السنبلة ، عدد السنيبلات فى السنبلة ، وزن 1000 حبة، عدد الحبوب فى السنبلة و خصوبة الحبوب . وفيما يلي ملخص لأهم النتائج المتحصل عليها :

1. كانت قيم التباين الراجعة إلي التراكيب الوراثية عالية المعنوية لكل الصفات المدروسة في كل من الجيلين الاول و الثاني.
2. كانت قيم التباين الراجع إلى متوسط قوة الهجين عالية المعنوية وذلك لكل الصفات المدروسة فيما عدا وزن الالف حبة في الجيلين الاول و الثاني وعدد الحبوب في السنبلة وخصوبة الحبوب في الجيل الاول .
3. أظهر الهجين الناتج من السلالة 2 × السلالة 7 أهميته العملية في برامج تربية القمح وذلك بسبب تفوقه فى كل من صفتي وزن الألف حبة وعدد الحبوب في السنبلة.
4. أظهرت النسبة بين تباين القدرتين العامة والخاصة على التآلف أن التباين الوراثي المُضيف وأيضاً التفاعل بين الفعل الجيني المضيف × المضيف هما الأكثر أهمية فى وراثة جميع الصفات المدروسة .
5. أظهرت سلالة 6 وسلالة 7 قدرة تآلفية عالية لصفة وزن الالف حبة في الجيل الاول وكذلك أثبتت السلالة 3 وسلالة 4 قدرة تآلفية عالية لكل لصفة عدد الحبوب في السنبلة.
6. أظهر الهجين الناتج من السلالة 3 × السدس 7 قدرة خاصة على التآلف عالية المعنوية وذلك لصفتي وزن الالف حبة وصفة عدد الحبوب في السنبلة