BREEDING FOR SOME QUANTITATIVE TRAITS IN COMMON WHEAT (TRITICUM AESTIVUM L) USING DIALLEL CROSSES.

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ABSTRACT: *A diallel cross set was carried out among six parents of common wheat without reciprocal crosses to study the inheritance of heading date, maturity date, plant height, spike length, number of spikes per plant, number of kernels per spike,1000 grain weight and grain yield per plant using Hayman approach and Jones method. The parental varieties and their possible 15 crosses were sown under two different nitrogen levels i.e.,70 kg /faddan (normal) and 35 kg/faddan (stress) using randomized complete block design with three replicates per each nitrogen level . The diallel cross analysis were carried out using the approaches proposed by Hayman (1954) and Jones (1965).*

Mean squares for fertilizations were found to be significant for all traits studied except days to maturity and plant height, indicating differences between the two different nitrogen fertilization levels for most characters.

Genotypes, parents and the resultant crosses mean squares were found to be highly significant for most traits studied at the two different nitrogen levels and their combined data.

The additive genetic variance ($\widehat{D}$) was found to be highly significant for all traits studied at the two different nitrogen fertilizations except number of grains per spike and grain yield per plant at the two different nitrogen levels .

The dominance genetic variation $\widehat{H}_1$ and $\widehat{H}_2$ were found to be highly significant for all traits studied at the two different nitrogen fertilizations. Moreover, the estimated values of dominance components $\widehat{H}_1$ and $\widehat{H}_2$ were found to be greater in their magnitude than the corresponding additive genetic variations ($\widehat{D}$) for most traits under investigation.

Estimates of the ratio of dominant to recessive alleles in the parents (K_D / K_R) were found to be more than unity for all traits studied at the two different nitrogen levels, except grain yield per plant.

Moderate heritability values were detected for heading date, plant height and spike length . For the other traits, low heritability in narrow sense was detected.

The additive genetic variance (a) was found to be highly significant for all characters studied at both two nitrogen fertilizer levels. The dominance genetic variation (b) was highly significant for all-characters studied at the different two nitrogen fertilizer levels. The (a) values were found to be larger in magnitude than the corresponding (b) values for most traits studied.

Key words: Wheat - genetic components - additive - dominance.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most important cereal crop in Egypt. Increasing wheat production to narrowing the gap between production and consumption is vital in Egypt. Big variation in wheat productivity in different parts of the country should be reduced to achieve high productivity, through using wheat breeding programs and developing new set of wheat varieties with high yielding capacity.

Egypt is the most importing country of wheat worldwide producing about 8.5 million tons per year, while the annual requirements are about 13.5 million tons.

The diallel analysis provides a unique opportunity to test a number of lines in all possible combinations. The present study is aimed to evaluate of the different genetic components according to Hayman (1954) and Jones (1965).

MATERIALS AND METHODS

The experiment was carried out at Shebin El-kom Agricultural Research Station Fac. of Agric., Menoufia University during the two successive seasons 2014/2015 and 2015/2016.The Egyptian wheat genotypes (Sids12, Gemmieza-11, Line1, Line2, Line3 and Line4) representing a wide range of variability were provided by Agriculture Research Center (ARC), Egypt. These cultivars were selected to study the genetic components according to (Hayman 1954) and (Jones 1965).

A diallel cross without reciprocal set was carried out among the six parents in 2014/2015 growing season. The parental varieties and their possible 15 crosses were sown in 2015/2016 under two nitrogen fertilizer levels 30 kg. Nitrogen per fadden and 70 kg. Nitrogen per

fadden, which would be mentioned in the text as stress condition (S) and normal condition (N), respectively.

The two experiments were arranged in a randomized complete block design with three replicates per each fertilizer level. Each plot comprised single rows 3 meters long with 30 cm. between rows, plants within rows were 10 cm. apart allowing a total of 30 plants per plot. Normal agricultural practices were applied as usual for the ordinary wheat fields in the area. Ten guarded plants were randomly selected from each plot for subsequent measurements as follows:

1. Days to heading.
2. Days to maturity.
3. Plant height (cm).
4. Number of spikes /plant.
5. Spike length (cm).
6. Number of grains per spike.
7. 1000- grain weight (gm).
8. Grain yield / plant (gm).

A. Statistical procedures

Two steps are involved in the analysis of the data. The first step is the ordinary analysis of variance. Only when the significant differences among the parents and F_1's are established, there is need to proceed for second step analysis, i.e. Hayman method (1954) and Jones method (1965). The combined analysis of the two nitrogen levels was done to test the interaction of the different genetic parameters with the two different fertilizer levels and that was done whenever the homogeneity of variances was detected.

The genetic parameters were estimated according to the procedure described by Hayman (1954) and (Jones 1965). Heritability in narrow-sense was

also estimated according to Mather and Jinks (1982).

RESULTS AND DISCUSSION

The gaining of the maximum and quick improvement of varieties is depending up on the estimation of the type and relative magnitude of the genetic variance involved in inheritance of the characters under study. Diallel cross analysis has been used to estimate the different genetic components which make decision dealing with the traits in view.

For better representation and discussion of the results obtained herein, it would be preferred to outline these results into three parts as follows:

1. Variation and interaction with two different nitrogen levels.

Mean performance of the six parent and their fifteen crosses under the two different nitrogen levels with the combined data for all traits studied i.e. Days to heading ,days to maturity , plant height, number of spikes per plant, spike length , 1000-grain weight , number of grains per spike , and grain yield per plant are given in Table (1). Mean values of normal fertilization (N) were found to be relatively better than those of stress fertilization (S) in most traits under investigation.

The analysis of variance of each nitrogen levels together with the combined data for all traits studied under normal fertilization (N) and stress fertilization (S) with the combined data are presented in Table (2).

Nitrogen fertilizer levels mean squares were found to be significant for all traits studied except days to maturity, and plant height.

Genotypes and the resultant 15 crosses mean squares were found to be highly significant for most traits studied at the two different nitrogen levels and

their combined data, indicating the wide diversity among these populations used in the present study

Parent mean squares were found to be highly significate for all traits studied at the two different nitrogen levels and their combined data, except plant height under stress condition, indicating that parental varieties and /or lines differed in their mean performance in all traits except plant height under stress condition.

Parents Vs crosses mean squares as an indication to average heterosis overall crosses, were found to be highly significant for all traits studied at the two different nitrogen levels and their combined data except 1000 grain weight . This may indicate that the average heterosis could be pronounced for these traits (Table 2).

The interaction of genotypes with the two different nitrogen levels were found to be highly significant for number of spike per plant, spike length and grain yield per plant reflecting that these entries behaved differently from nitrogen level to another.

The interactions of the two different nitrogen levels with parents were found to be significant for all traits studied except days to heading, plant height and 1000 grain weight.

The interactions of the resultant crosses with the two different nitrogen levels were found to be highly significant for no. of spikes per plant, no. of grains per spike and grain yield per plant.

The interactions of parents Vs crosses with the two different nitrogen levels were found to be significant for no. of grains per spike and grain yield per plant, indicating the influence of the two different nitrogen levels with these two traits. Consequently, it could therefore be concluded that the test of potential

Table (1). Genotypes mean performance under the two nitrogen fertilizer levels.

Genotypes	Days to heading (day)			Days to maturity (day)			Plant height (cm)			No. of spikes/plant		
	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.
Sids 12	92.333	92.667	92.5	151	151.33	151.17	101.3	109.89	105.6	4.337	5.027	4.682
Gemmeiza 11	96.667	97.667	97.167	149.67	150	149.83	100.67	105.72	103.19	5.107	5.987	5.547
x Line1	103.333	104.667	104	154.33	154.67	154.5	102.23	109.33	105.78	6.72	10.553	8.637
x Line2	91	91.667	91.333	149.33	149.67	149.5	110.4	118.36	114.38	9.403	14.14	11.772
x Line3	90.333	91.333	90.833	154.33	154.67	154.5	102.43	109.58	106.01	7.917	10.377	9.147
x Line4	95	96.333	95.667	154.67	155.33	155	95.87	98.89	97.38	9.017	11.197	10.107
Sids 12 xGem11	95.667	96	95.833	154	154.33	154.17	103.27	103.1	103.18	9.75	13.403	11.577
x Line1	101	101.333	101.167	156.33	157	156.67	107.13	117.42	112.28	8.367	11.187	9.777
x Line2	94	95	94.5	152.67	153.67	153.17	101.37	106.8	104.08	9.093	11.123	10.108
x Line3	99	99.333	99.167	155.33	156.33	155.83	101.13	109.05	105.09	8.773	10.997	9.885
x Line4	94.333	94.667	94.5	154.33	155	154.67	96.67	105.1	100.88	8.383	9.923	9.153
Gem11 x Line1	103.333	103.667	103.5	156	156.67	156.33	103.67	114.75	109.21	10.837	12.89	11.863
x Line2	97	97.667	97.333	154.33	155	154.67	109.13	112.2	110.67	8.773	10.873	9.823
x Line3	101	101.667	101.333	153.67	155	154.33	104.57	108.12	106.35	7.663	11.3	9.482
x Line4	103	103.333	103.167	153.33	153.67	153.5	102.47	109.13	105.8	10.84	11.547	11.193
Line1 xLine2	101.333	102	101.667	154.67	155.67	155.17	108.47	112.52	110.5	8.453	10.917	9.685
x Line3	104	104.667	104.333	154.33	155.67	155	110.47	114.34	112.4	7.24	9.227	8.233
x Line4	104	105	104.5	151.33	152.67	152	106.93	116.62	111.78	12.003	14.387	13.195
Line2 x Line3	99.667	101	100.333	154.67	155.33	155	104.53	115.59	110.06	11.347	12.39	11.868
x Line4	99	99.667	99.333	154	154.67	154.33	105.67	109.05	107.36	8.59	9.82	9.205
Line3 x Line4	102.333	103.333	102.833	154.33	155.67	155	96.87	108.3	102.58	8.117	9.127	8.622
Mean	98.444	99.175	98.81	153.65	154.38	154.02	103.58	110.18	106.88	8.606	10.78	9.693
L.S.D. 5 %	1.424	1.092	1.243	1.22	0.93	1.06	1.51	2.08	1.77	1.093	1.05	1.048
L.S.D. 1 %	1.905	1.44	1.642	1.63	1.23	1.4	2.02	2.75	2.35	1.463	1.384	1.385

Table (1). Cont.

Genotypes	No. of grains/spike			Spike length			1000 - Grain weight			Grain yield/plant		
	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.
Sids 12	60.147	69.467	64.807	15.027	18.103	16.565	53.583	52.487	53.035	17.547	21.947	19.747
Gemmeiza 11	56.43	65.087	60.758	12.707	14.423	13.565	53.917	52.72	53.318	18.287	20.773	19.53
Line 1	57.813	65.303	61.558	9.903	11.667	10.785	43.38	42.443	42.912	14.383	18.017	16.2
Line 2	55.06	69.467	62.263	11.643	12.19	11.917	51.06	49.943	50.502	19.89	25.01	22.45
Line 3	70.5	82.78	76.64	10.527	12.787	11.657	41.347	39.053	40.2	15.15	22.55	18.85
Line 4	58.92	74.49	66.705	10.47	14.2	12.335	62.653	60.687	61.67	15.317	22.09	18.703
Sids 12 x Gem11	72.98	85.537	79.258	14.69	15.433	15.062	52.003	51.01	51.507	20.967	28.773	24.87
x Line1	62.813	72.293	67.553	11.587	13.017	12.302	61.327	60.147	60.737	19.123	26.577	22.85
x Line2	82.617	106.99	94.803	10.893	13.213	12.053	51.603	51.103	51.353	19.547	27.78	23.663
x Line3	87.18	110.37	98.775	11.393	13.14	12.267	53.25	51.333	52.292	21.273	35.613	28.443
x Line4	90.297	109.717	100.007	13.273	14.8	14.037	51.043	49.583	50.313	19.007	28.29	23.648
Gem11 x Line1	73.593	80.627	77.11	12.46	13.883	13.172	57.243	54.373	55.808	22.653	40.503	31.578
x Line2	75.59	87.977	81.783	12.403	14.107	13.255	52.18	50.757	51.468	20.953	31.377	26.165
x Line3	66.243	74.257	70.25	10.303	12.517	11.41	51.12	48.323	49.722	14.883	23.293	19.088
x Line4	72.133	84.963	78.548	13.413	14.337	13.875	51.34	47.833	49.587	15.683	28.32	22.002
Line1 x Line2	60.35	73.09	66.72	8.69	11.48	10.085	50.213	58.62	54.417	16.7	27.743	22.222
x Line3	62.183	72.273	67.228	11.01	12.153	11.582	51.51	51.157	51.333	13.31	22.7	18.005
x Line4	53.05	62.87	57.96	13.497	15.7	14.598	51.71	49.913	50.812	12.29	22.407	17.348
Line2 x Line3	71.747	86.59	79.168	10.857	13.147	12.002	49.963	46.65	48.307	15.66	30.243	22.952
x Line4	82.18	97.953	90.067	11.13	13.733	12.432	41.74	40.157	40.948	17.733	27.447	22.59
Line3 x Line4	73.43	86.753	80.092	13.263	15.337	14.3	55.173	53.16	54.167	17.923	27.87	22.897
Mean	68.822	81.85	75.336	11.864	13.779	12.822	51.779	50.545	51.162	17.537	26.634	22.086
L.S.D. 5 %	1.878	2.57	2.195	0.895	1.061	0.958	1.238	6.47	4.522	1.059	1.361	1.19
L.S.D. 1 %	2.512	3.388	2.901	1.198	1.399	1.267	1.657	8.53	5.976	1.417	1.794	1.572

Table (2). Mean square estimates of ordinary analysis and combining ability analysis for all traits studied under the two different fertilization levels.

S.O.V.	d.f		Days to heading (day)			Days to maturity (day)			Plant height (cm)		
	S	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.
Fertilization		1			16.794**			16.7937**			1372.8001**
Rep x F.	2	4	1.444	0.825	1.135	0.7778	0.1429	0.4603	0.4154	2.3935	1.4045
Genotypes (G)	20	20	58.344**	58.821**	116.971**	10.4492**	11.8095**	22.0484**	54.0252**	72.7573**	111.3134**
Parents (P)	5	5	70.089**	77.522**	147.383**	18.7556**	19.7889**	38.5167**	66.3317**	120.5609**	180.4576**
Crosses (F1)	14	14	34.117**	34.889**	68.852**	4.5556**	4.1651**	8.5349**	49.7951**	56.5278**	86.5359**
P vs F1	1	1	338.800**	300.357**	638.579**	51.4286**	78.9349**	128.8960**	51.7147**	60.9529**	112.4779**
GxF.		20			0.194			0.2103			15.4691**
PxF.		5			0.228			0.0278			6.4350**
F1xF.		14			0.154			0.1857			19.7870**
p vsF1 x F.		1			0.579			1.4675			0.1897
Error	40	80	0.744	0.425	0.585	0.5444	0.3095	0.427	0.8384	1.5471	1.1927

Comb. = combined data.

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

Table (2). Cont.

S.O.V.	d.f		No. of spikes/plant			No . Of grains/spike			Spike length "cm"		
	S	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.	Stress	Normal	Comb.
Fertilization		1			148.917**			5346.795**			115.585**
Rep x F.	2	4	0.069	0.657	0.363	1.805	4.647	3.226	0.094	0.709	0.401
Genotypes (G)	20	20	10.358**	15.406**	23.941**	351.172**	627.647**	945.102**	7.802**	7.323**	14.218**
Parents (P)	5	5	12.839**	35.176**	44.182**	91.893**	133.807**	209.420**	10.920**	16.310**	25.349**
Crosses (F1)	14	14	6.038**	6.705**	11.583**	322.729**	640.789**	923.894**	7.205**	4.613**	11.258**
P vs F1	1	1	58.441**	38.362**	95.750**	2045.775**	2912.863**	4920.438**	0.575	0.337	0.016
GxF.		20			1.823**			33.717**			0.907**
PxF.		5			3.833**			16.280**			1.881**
F1xF.		14			1.160**			39.624**			0.56
p vsF1 x F.		1			1.053			38.200**			0.896
Error	40	80	0.439	0.393	0.416	1.295	2.355	1.825	0.294	0.402	0.348

Comb. = combined data.

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

Table (2). Cont.

S.O.V.	d.f		1000 - Grain weight "gm"			Grain yield/plant "gm"		
	S	Comb.	Normal	Stress	Comb.	Normal	Stress	Comb.
Fertilization		1			47.9397**			2606.968**
Rep x F.	2	4	2.8392*	1.2225	2.0308**	0.053	0.5	0.276
Genotypes (G)	20	20	82.3034**	93.9860**	167.8665**	23.887**	80.768**	83.667**
Parents (P)	5	5	181.3410**	182.1225**	363.0014**	13.842**	15.787**	24.392**
Crosses (F1)	14	14	51.6909**	67.4583**	107.3179**	28.100**	66.468**	81.795**
P vs F1	1	1	15.6894**	24.6906**	39.8720**	15.133**	605.875**	406.256**
GxF.		20			8.4229**			20.987**
PxF.		5			0.4621			5.237**
F1xF.		14			11.8314**			12.772**
p vsF1 x F.		1			0.508			214.752**
Error	40	80	0.5632	0.4875	0.5253	0.412	0.66	0.536

Comb. = combined data.

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

a number of environmental conditions. Also, genetic diversity alone would not guarantee the expression of heterosis, but the suitability of the environments would be required in case of the above mentioned two characters. The same results were previously obtained by EL-Refaey *et al.,* (2010), Al-Naggar *et al.,* (2015), Kumar *et al.,* (2015) and Ali (2018).

2. Hayman's method (1954):

Genetic components and heritability

Hayman (1954) suggested certain assumptions which need to be fulfilled for valid diallel analysis. These include homozygous parents, diploid segregation, no reciprocal differences, no genotype environmental interaction, no epistasis, no multiple alleles and uncorrelated gene distribution. Failure of any one or any combinations of the assumptions invalidates to some degree the conclusion obtained by means of analysis.

The data obtained here were subjected to the genetical analysis of half diallel table as described by Hayman (1954). The mean values of each cross were used to estimate the different genetic components of variation $\hat{D}$, $\hat{F},\hat{H}_1,\hat{H}_2$, h² and F as defined by Hayman (1954).The different genetic components of variation and their portions for all traits studied at the two different fertilizer level , are given in Table (3).

The additive genetic variance ($\hat{D}$) was found to be exceeded its standard error for all traits studied at the two different nitrogen fertilizations except number of grains per spike and grain yield per plant at the two different nitrogen levels , confirming the importance of additive effects in the inheritance of these traits . These results are in harmony with those previously obtained by Al-Naggar (2015) and Ali (2018).

The presence of dominance genetic variation $\hat{H}_1$ and $\hat{H}_2$ were found to be exceeded its standard error for all traits studied at the two different nitrogen fertilizations. Moreover, the estimated values of dominance components $\hat{H}_1$ and $\hat{H}_2$ were found to be greater in their magnitude than the corresponding additive genetic variations ($\hat{D}$) for all traits under investigation. These results indicated that the dominance genetic variations had greater role in the inheritance of all traits under study. Similar results were previously obtained by Okan (2009), EL-Refaey *et al.,* (2010), Ullah *et al.,* (2010) and Ahmad *et al.,* (2016), Al-Naggar (2015) and Ali (2018).

A positive F value indicates an excess of dominant genes while a negative value indicates an excess of recessive genes. In the present investigation, the positive values of (F) showed that there were more dominant genes present in the parental varieties than recessive alleles, irrespective of whether these dominant alleles are increasing or decreasing in their effects for all traits studied under the two different levels of fertilizations except grain yield per plant under normal fertilizations. Consequently, the excess of genes either dominant or recessive controlling these three traits were consistent at the two different environments.

The overall dominance effects, as the algebric sum over all loci in heterozygotes in all crosses symbolized as (h²) were found to be exceeded its standard errors for heading date maturity date, no. of grains /spike., plant height, no. of spikes /plant under the two nitrogen levels and grain yield /plant at the stress condition only, indicating the prevalence of dominant effect over all loci in all crosses.

Insignificant estimates of (h²) were detected for, spike length and 1000grain weight at both nitrogen fertilizations and

Table (3). Components of variation and other statistics for traits studied under the two nitrogen fertilizer levels. (Hayman 1954)

Parameters	Heading date		Maturity date		Plant hight "cm"		No. of spikes/plant	
	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal
$\hat{D}$	23.10 ± 2.35	25.69 ± 2.45	6.07 ± 1.66	6.50 ± 1.43	21.84 ± 3.77	39.66 ± 7	4.14 ± 1.1	11.59 ± 1.59
$\hat{F}$	8.94 ±5.74	11.05 ± 5.98	8.57 ± 4.05	8.71± 3.48	8.82 ± 9.22	39.84 ± 17.11	5.20 ± 2.68	18.52 ± 3.89
$\hat{H}_1$	38.38 ±5.97	37.70 ± 6.21	13.57 ± 4.21	13.58 ± 3.62	42.90 ± 9.58	74.63 ± 17.77	13.12 ± 2.78	23.74 ± 4.04
$\hat{H}_2$	30.17 ± 5.33	28.86 ± 5.55	10.12 ± 3.76	10.42 ± 3.23	33.18 ± 8.55	50.02 ± 15.88	11.11 ± 2.49	15.83 ± 3.61
$\hat{h}_2$	73.05 ± 3.59	64.81 ± 3.74	11.01 ± 2.53	17.00 ± 2.18	11.02 ± 5.76	12.87 ± 10.69	12.55 ± 1.67	8.21 ± 2.43
$\hat{E}$	0.26 ± 0.89	0.15 ± 0.92	0.19 ± 0.63	0.10 ± 0.54	0.72 ± 1.43	0.53 ± 2.65	0.14 ± 0.41	0.14 ± 0.6
$(\hat{H}_1/\hat{D})^{0.5}$	1.29	1.21	1.5	1.45	1.4	1.37	1.78	1.43
$(H_2/4H_1)$	0.2	0.19	0.19	0.19	0.19	0.17	0.21	0.17
KD/KR	1.35	1.43	2.79	2.54	1.34	2.16	2.09	3.53
h(n.s)	0.59	0.61	0.15	0.22	0.57	0.48	0.14	0.11
YD	78.8	81	148.21	147.8	91.53	87.02	5.83	6.55
Yr	116.55	116.87	163.35	164.81	116.45	155.27	9.72	20.05
R	-0.87	-0.82	-0.97	-0.96	-0.53	-0.33	-0.97	-0.76
t^2	9.6	17.79	1.46	0.68	2.39	0.07	0.5	1.29
B	0.62	0.57	0.81	0.89	0.4	0.62	0.26	0.4

Table (3). Cont.

Parameters	No . of grains/spike		Spike length		1000 - Grain weight		Grain yield/plant	
	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal
$\hat{D}$	30.19 ± 42.21	43.78 ± 71.99	3.55 ± 0.63	5.30 ± 0.58	60.22 ± 11.38	60.53 ± 16.65	4.48 ± 2.83	5.04 ± 17.34
$\hat{F}$	34.21 ± 103.12	2.78 ± 175.88	3.02 ± 1.54	4.46 ± 1.44	103.20 ± 27.8	112.45 ± 40.68	- 1.14 ± 6.92	6.35 ± 42.37
$\hat{H}_1$	440.24 ±107.15	718.70±182.76	7.74 ±1.6	5.61 ± 1.5	137.04 ± 28.89	164.88 ± 42.27	24.25 ± 7.19	113.28 ± 44.03
$\hat{H}_2$	345.50 ± 95.72	543.40±163.27	5.37 ± 1.43	3.88 ±1.34	83.30 ± 25.81	100.69 ± 37.77	21.27 ± 6.42	106.90 ± 39.33
$\hat{h}_2$	441.74 ±64.43	628.87±109.89	0.07 ± 0.96	0.00 ± 0.9	3.27 ± 17.37	5.24 ± 25.42	3.20 ± 4.32	130.78 ± 26.47
$\hat{E}$	0.44 ± 15.95	0.82 ± 27.21	0.09 ± 0.24	0.14 ± 0.22	0.22 ± 4.3	0.17 ± 6.29	0.13 ± 1.07	0.22 ± 6.56
$(\hat{H}_1/\hat{D})^{0.5}$	3.82	4.05	1.48	1.03	1.51	1.65	2.33	4.74
$(H_2/4H_1)$	0.2	0.19	0.17	0.17	0.15	0.15	0.22	0.24
KD/Kr	1.35	1.02	1.81	2.38	3.63	3.57	0.9	1.31
h(n.s)	0.34	0.44	0.5	0.54	0.2	0.19	0.44	0.09
YD	48.75	29.25	8.8	10.14	13.82	30.22	13.56	22.15
Yr	74.77	113.86	17.02	22.81	185.64	118.59	19.68	21.19
r	-0.11	0.31	0.78	0.66	-0.17	-0.27	-0.49	-0.92
t^2	73.51	46.17	0.43	1.3	0.95	0.57	9.38	29.76
b	0.11	0.24	0.76	1.11	0.94	0.44	0.29	-0.02

grain yield /plant at normal fertilization and that would indicate the absence of the dominance effect over all loci in the heterozygotes in all crosses and that could be due to presence of a considerable amount of canceling dominance effects in the parental varieties. Similar results were previously obtained by Okan (2009), Kumar *et al.,* (2015) and Ali (2018).

The average degree of dominance $(\hat{H}1/\hat{D})^{1/2}$ was found be greater than unity at the two different nitrogen levels for all traits under investigations, indicating the presence of over dominance for these traits.

When positive and negative genes are equally distributed in the parental varieties, the proportion $(\hat{H}2/4\hat{H}1)$ is expected to be 0.25. The estimated values of $(\hat{H}2/4\hat{H}1)$ were found to be close to this value (0.25) for grain yield /plant; indicating that positive and negative alleles were equally distributed among the parents for this trait. However, the estimated values of $(\hat{H}2/4\hat{H}1)$ were fund to be below (0.25) for the remainder of the character studied, indicating that positive and negative alleles were not equally distributed among the parents in these traits.

Estimates of the ratio of dominant to recessive alleles in the parents (K_D / K_R) were found to be more than unity for all traits studied at the two different nitrogen levels, except grain yield per plant at the normal nitrogen level only. This further confirming the existence of more dominant than recessive genes in the parental varieties as previously discussed concerning the positive values of (F) parameter. It is of interest to mention that , $K_D\backslash K_R$ ratio was found to be more than unity for grain yield per plant at the stress condition but it was less than unity at the normal nitrogen fertilizer level (Table 3) this indicate an excess of dominant genes at nitrogen

level and excess of recessive genes at the other nitrogen level , suggesting that the excess of dominant or recessive genes controlling this trait was not consistent at the two different levels, therefor the degree of dominance or recessiveness may be determined by growing conditions. Similar results were previously obtained by Abd El Rahman *et al.,* (2008), Kumar *et al.,* (2015), Fellahi *et al.,* (2016) and Ali (2018).

The correlation coefficient (r) between the parental values (Y_r) and the parental order of dominance (Wr + Vr) for all characters studied at the two different fertilizer levels are presented in Table (3). If the correlation is negative, it means that the parents containing most increasing genes have the lowest values of (Wr + Vr) and thus contain most dominant genes, and the correlation would be positive if the case is reverse. Thus, on this basis, it could be concluded whether or not the increasing or decreasing genes are the dominant ones. Also, when the correlation between parental mean values and (Wr + Vr) is small, it suggests that the dominant genes with positive and negative effects in the parental line could be in equal proportions. If the correlation coefficient is high, the most dominant alleles will act in one direction and most recessive alleles will act in the opposite one (Hayman, 1954). In the present study, the correlation coefficients were found to be negative for all traits studied except number of grains\spike at stress condition and spike length at the two different fertilizer levels, however days to heading, days to maturity and number of spikes per plant at the two different fertilizers and spike length at normal condition and grain yield per plant at stress condition were found to be highly significant, and that would indicate the prevalence of dominant genes.

It is of interest to mention that the sign of the correlation coefficient values for number of grains per spike were found to be different at the two different fertilizer levels which would ascertain that dominant genes could be increases or decreases according to the growing environmental conditions. The estimated values of correlation coefficient were found to be low for plant height, number of grains per spike and 1000 grain weight at both nitrogen levels which would indicate that the dominant genes of positive and negative effects in the parental lines could be in equal proportion.

Heritability in narrow sense was estimated for all the studied characters at the two different fertilizer levels are presented in Table (3). Moderate heritability values were detected for heading date, plant height and spike length Therefore, the genetic system controlling these traits might be attributed to additive effects of genes. Consequently, pedigree selection program for these characters would be preferred for other traits; low heritability in narrow sense was detected. Therefore, breeding programs towards pure line selections seemed to be meaningless. Therefore, the bulk method program for these traits might be quite promising. These results are in harmony with Al-Naggar *et al.,* (2015), Ahmed *et al.,* (2016), Salehi *et al.,* (2014), Ali (2018) and Farshadfar *et al.,* (2013).

3- Jones Method (1965)

The data obtain here in were subjected further to the analysis of wariance of the diallel table as suggested by Jones (1965) to test the existence of both additive variation and dominance variation which controlled the inheritance of the characters under study (Table 4).

In Jones model, the (a) component which test the existence of additive effects control the inheritance of the characters under study were found to be higly significant for all characters studied in both n and s , these results are ascertained by the significant values of additive variation which obtained from the methods studied i.e. Hayman (1954) for most characcters under study (Table 3). Jones method also, exhibited that the (b) items were highly significant for all characters studied under both nitrogen fertilizer levels which indicating the existence of dominance variation of some loci. The (b) item, main effects, has been spilt into three components, b1, b2, and b3. In general item (b1) is considered as ameasure of the mean deviation of the F_1's from their mid parental values were found to be highly significant for all characters studied under the two nitrogen fertilizer levels except for spike length under both N and S . These results are in harmony with those previously obtained for the corresponding parent vs. crosses mean squares (Table 2) . Item (b2) which is taken as a further dominance deviation due to asymmetrical gene distribution were detected to be highly significant for all traits studied under both nitrogen levels , reflecting the asymmetry of the gene frequency in the parental lines.

The item (b3) which is considered a test of the part of dominance deviation that is unique for each F1 (Hayman 1954) were found to be highly significant for all traits under study at both nitrogen levels

It is worth to mention that, the (a) values were found to be lager in magnitude than the corresponding (b) values for most traits studied (Table 4).

Similar results in wheat were previously obtained by Farshadfar *et al.,* (2012) and Rania A.R. El-Said (2018).

Table (4). The analysis of variance of the dialle table (Jones method 1965)

Source of variance	D.F	Heading date		Maturity date	
		Stress	Normal	Stress	Normal
		M.S	M.S	M.S	M.S
a	5	42.220**	44.865**	3.298**	4.378**
b	15	11.857**	11.188**	3.545**	3.789**
b1	1	112.933**	100.119**	17.143**	26.312**
b2	5	8.865**	9.063**	1.493**	1.349**
b3	9	2.289**	2.486**	3.174**	2.643**
Error	40	0.248	0.142	0.181	0.103

Table (4). Cont.

Source of variance	D.F	Plant height (cm)		No. of spikes/plant	
		Stress	Normal	Stress	Normal
		M.S	M.S	M.S	M.S
a	5	41.591**	47.646**	2.855**	4.400**
b	15	10.148**	16.455**	3.652**	5.380**
b1	1	17.238**	20.318**	19.480**	12.787**
b2	5	10.466**	17.909**	0.886**	3.451**
b3	9	9.183**	15.218**	3.430**	5.629**
Error	40	0.279	0.516	0.146	0.131

Table (4). Cont.

Source of variance	D.F	No . of grains/spike		Spike length	
		Stress	Normal	Stress	Normal
		M.S	M.S	M.S	M.S
a	5	115.980**	281.224**	5.305**	5.957**
b	15	117.417**	185.213**	1.699**	1.269**
b1	1	681.925**	970.954**	0.192	0.112
b2	5	97.697**	201.956**	2.018**	0.988**
b3	9	65.649**	88.606**	1.690**	1.554**
Error	40	0.432	0.785	0.098	0.134

Table (4). Cont.

Source of variance	D.F	1000 - Grain weight		Grain yield/plant	
		Stress	Normal	Stress	Normal
		M.S	M.S	M.S	M.S
a	5	26.284**	24.736**	14.128**	7.912**
b	15	27.818**	33.526**	5.907**	33.260**
b1	1	5.230**	8.230**	5.044**	201.958**
b2	5	29.377**	37.672**	4.387**	5.516**
b3	9	29.461**	34.033**	6.847**	29.928**
Error	40	0.188	0.162	0.137	0.22

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تربية القمح الدارج لبعض الصفات الكمية بإستخدام الهجن التبادلية

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الملخص العربي

أجريت هذه الدراسة خلال موسمين متتاليين حيث استخدم لهذه الدراسة ستة تراكيب وراثية من قمح الخبز متباعدة وراثيا وهى سدس ١٢ وجميزة ١١ وسلاله ١ وسلاله ٢ وسلاله ٣ وسلاله ٤ تم التهجين بين هذه التراكيب الوراثية في موسم ٢٠١٤/٢٠١٥ باستخدام طريقة التهجين التبادلي في اتجاه واحد في محطة البحوث بكلية الزراعة جامعة المنوفية وفي موسم ٢٠١٥/ ٢٠١٦ تم تقييم الآباء والهجن الناتجة في تجربتين مستقلتين في تصميم قطاعات كاملة العشوائية ذات ثلاث مكررات تحت ظروف التسميد العادي (٧٠ كجم نتروجين/ف) والتسميد المنخفض (٣٠ كجم نيتروجين/ف).

وتهدف هذه الدراسه الي تقييم التراكيب الوراثية والهجن الناتجة منها تحت مستويين من التسميد النتروجيني وتقدير مكونات التباين الوراثي بإتباع طريقتي هايمن ١٩٥٤ ، جونز ١٩٦٥ .

- الصفات المدروسة هى: ميعاد طرد السنابل، ميعاد النضج، طول النبات، عدد السنابل في النبات، طول السنبلة، وزن الألف حبة، عدد الحبوب في السنبلة، محصول النبات الفردي من الحبوب.

وتتلخص أهم نتائج الدراسة فيما يلي :

١- التباين الراجع لمستويات التسميد الأزوتى معنويا لكل الصفات المدروسه ما عدا صفة ميعاد النضج وطول النبات.

٢- كانت قيم التباين الراجع إلى التراكيب الوراثيه والاباء والهجن عالى المعنويه لمعظم الصفات المدروسه تحت مستويي التسميد الأزوتى والتحليل المشترك لهما.

٣- كما أظهر تحليل البيانات بطريقه هايمن النتائج التاليه :

- كان التباين الوراثي المضيف (D) عالى المعنويه لكل الصفات المدروسه ما عدا عدد الحبوب في السنبله ومحصول النبات الفردى تحت مستويي التسميد الأزوتى والتباين الوراثي السيادى H_1,H_2 عالى المعنويه ومرتفعا في قيمته عن الجزء المضيف من التباين وذلك لجميع الصفات المدروسه في كل من مستويي التسميد الأزوتى العالى والمنخفض.

- أوضحت تقديرات نسبه الأليلات السائدة إلى المتنحية في الأباء $(K_D\backslash K_R)$ انها كانت تزيد عن الوحده في كل الصفات تحت الدراسه تحت مستويي التسميد الأزوتى ما عدا صفات محصول النبات الفردى .

- كانت قيم درجة التوريث بمعناها الدقيق متوسطه لصفات ميعاد طرد السنابل ، طول النبات ، وطول السنبله بينما كانت منخفضه لبقيه الصفات المدروسه .

- أظهر تحليل البيانات بطريقه جونز (1965) أن التباين الوراثي المضيف عالى المعنويه لجميع الصفات المدروسه تحت مستويي التسميد الأزوتى والتباين السيادى أيضا عالى المعنويه لكل الصفات المدروسه تحت مستويي التسميد الأزوتى وقد وجد أن التباين الوراثي المضيف أكبر في قيمته من التباين السيادى لمعظم الصفات تحت الدراسه.