

GENE ACTION OF YIELD AND ITS COMPONENTS OF F₂ GENERATIONS POPULATION IN BREAD WHEAT UNDER RAINFALL CONDITIONS

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ABSTRACT

A full diallel crosses among five bread wheat genotypes were made during the growing season 2009-2010 . Grains of 20 F₁s and their five parents was cultivated during the growing season 2010-2011. During the growing season, 2012-2013, the 5 parents and their 20 F₂ crosses was planted on 15 Nov., 2012 at the experimental farm, Agriculture Research Station/Koya, Erbil under rainfall conditions by using Randomized Complete Block Design with three replications in order to analysis genetic control of grain yield and yield components by using Griffing, Hayman and Jinks – Hayman approach's. The results basis on the performance and combining ability revealed that two parents proved as a best general combiner which can be used in hybridization program for obtaining desirable combinations and two crosses had a best specific combiner in desirable direction for most traits. Additive genetic component (*a*) were important in the inheritance of all traits except no. of grains/spike and harvest index, in opposite non-additive component (*b*) were significant of plant height, 1000-grain weight, biomass yield/plant and grain yield/plant. Additive genetic component (\bar{D}) was smaller in magnitude than both components of dominance (\bar{H}_1 and \bar{H}_2) for all traits. The average degree of dominance $(H1/D)^{1/2}$ being greater than unity indicated involvement of over-dominance for phenotypic expression of all traits. The ratio of the symmetry of the frequency of dominant and recessive alleles in all gene location controlling traits ($H_2/4H_1$) is less than 0.25 for all traits except days to flowering, plant height, no. of spikes/plant and harvest index. Five traits have shown above unity value for the proportion of dominant and recessive genes among the parents (KD/KR). The narrow sense heritability $H_{n.s.}$ was high for all traits except days to flowering, plant height and no. of spikes/plant, indicating that selection for improvement of these traits would be effective in early generation.

Keywords: bread wheat, full-diallel cross, combining ability, gene action.

الفعل الجيني للحاصل ومكوناته للجيل الثاني في حنطة الخبز تحت الظروف الديمية

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الخلاصة

أجري تهجين تبادلي كامل بين 5 تراكيب وراثية من حنطة الخبز خلال موسم النمو 2009-2010. زرعت حبوب هجن الجيل الأول العشرين مع الآباء الخمسة خلال موسم النمو 2010-2011. خلال موسم النمو 2012-2013 زرعت حبوب هجن الجيل الثاني مع الآباء الخمسة في 15 تشرين الثاني 2012 في محطة البحوث الزراعية/كويبا/أربيل تحت الظروف الديمية باستخدام تصميم القطاعات العشوائية الكاملة بثلاثة مكررات لتحليل الفعل الجيني المتحكم بالحاصل ومكوناته باستخدام تطبيقات كرفنك وهايمان وجنكز-هايمان. أظهرت النتائج تفوق اثنين من الآباء من حيث المقدرة على الانتلاف والأداء والذان يمكن الاستفادة منهما في برامج التهجين للحصول على الانتلافات المرغوبة كما أظهر هجينان مقدرة انتلافية خاصة في الاتجاه المرغوب في أكثر عدد من الصفات. أظهر المكون الوراثي الإضافي (*a*) أهمية في وراثة جميع الصفات باستثناء عدد الحبوب/سنبلة وودليل الحصاد، بالمقابل كان المكون الوراثي غير الإضافي معنوياً لارتفاع النبات ووزن 1000 حبة والحاصل البيولوجي/نبات وحاصل الحبوب/نبات. كان للمكون الوراثي السيادة (\bar{D}) قيمة أقل من كل من المكونين السيادة (\bar{H}_1 و \bar{H}_2) في جميع الصفات. كان معدل درجة السيادة ($\sqrt{H_1/D}$) أكبر من واحد لجميع الصفات. كانت نسبة التكرار الجيني للأليلات السائدة إلى المتنحية ($H_2/4H_1$) أقل من 0.25 لجميع الصفات عدا عدد الأيام للازهار وارتفاع النبات وعدد السنابل/نبات وودليل الحصاد. أظهرت خمس صفات مقداراً أكبر من واحد في نسبة مجموع عدد الجينات السائدة إلى المتنحية في جميع الآباء (KD/KR).

كانت قوة التوريث بالمعنى الضيق ($H_{n.s.}$) عالية لجميع الصفات عدا عدد الأيام للازهار و ارتفاع النبات و عدد السنابل/نبات مما يعني بأن الانتخاب لتحسين هذه الصفات يكون فعالاً في الأجيال المبكرة.
الكلمات الدالة: حنطة الخبز، التهجين التبادلي الكامل، المقدرة على الائتلاف، الفعل الجيني.

INTRODUCTION

Development of high yielding cultivars of bread wheat cultivars is a major task in breeding programs particularly under rainfed conditions. A diallel mating design was used in breeding programs to obtain information about genetic properties of parental and their crosses (Iqbal *et al.*, 2007). In addition to diallel cross provides early information on the genetic behavior of attributes in the early generation (Griffing, 1956). Up to now, several methods have been proposed for the genetic analysis of data from a diallel cross. The Griffing's method involves analysis of variance and estimation of general combining ability (GCA) and specific combining ability (SCA) effects, while Hayman's (1954) and Jinks (1954) method includes analyses of array variances and covariances, and estimation of a number of genetic parameters which provides the necessary genetic information on the plant characters to determine the right breeding approach. So, to construct an effective breeding program in bread wheat for improving grain yield and its components under rainfed conditions, information on the type of gene action controlling the inheritance of these traits in the available genetic material should be studied.

Researchers have reported the importance of additive, non-additive, gene action for the inheritance of various traits among wheat populations. Minhas *et al.*, (2014) reported that genetic analysis revealed to both additive and dominance genetic components were involved in the manifestation of characters under study.

MATERIALS AND METHODS

The experiment was conducted at the experimental farm, Agriculture Research Station/Koya, Erbil. Five bread wheat genotypes (Table 1) were crossed in all possible combinations in a 5×5 diallel fashion during the growing season 2009-2010. Grains of 20 F₁s and their five parents was cultivated on 15 November 2010. During the growing season, 2012-2013, the 5 parents and their 20 F₂ crosses was cultivated on

However, additive gene effects were more pronounced in the genetic control of these traits. Non significance of b_1 , b_2 and b_3 values revealed the absence of directional dominance, symmetrical distribution of genes among the parental lines and absence of specific genes action respectively in all the traits.

Navabi *et al.*, (2004) reported that transgressive segregation among all the F₂ wheat populations and F₅ single seed-decent lines. Results of Jadoon *et al.*, (2012) by using 8×8 F₂ half diallel wheat populations showed that the genetic components of variance revealed all variance components including additive (\bar{D}), dominance (\bar{H}_1 and \bar{H}_2), \bar{F} , \hat{h}^2 and environmental variance (\bar{E}) were significantly different for all traits, except days to anthesis, while additive component \bar{D} and \bar{F} were non-significant, and biomass yield where only \bar{F} component was non-significant. As well as additive component was smaller in magnitude than both components of dominance (\bar{H}_1 and \bar{H}_2) for plant height, spike length, no., of grains per spike and biomass yield indicating preponderance of non-additive gene action for these traits.

The goal of this study was to find mode of gene action that is operative for different yield contributing parameters at rainfed conditions by using a full diallel mating system.

15 November 2012 by using Randomized Complete Block Design with three replications under rainfed conditions. All the 25 genotypes were randomly assigned to experimental units. Each plot comprised one row of 3 m with space of 20 cm between rows and 10 cm between plants within rows. At maturity, a ten plants was taken randomly from each experimental unit for recording data on individual plant basis for days to

anthesis, plant height (cm), spike length (cm), number of spikes/plant, number of grains/spike, 1000-grain weight (g), biomass yield/plant (g), grain yield/plant (g) and harvest index (%).

The data was analyzed by using analysis of variance to determine the genotypic differences

were significant for the characters under consideration or not. Then estimates of combining ability were computed by using the method as described by Griffing, method I. The data also analyzed according to Hayman's and Jinks – Hayman approach (Singh and Chaudhary, 1985).

Table (1): Pedigree of used genotypes as parents and their sources

No	Source	Pedigree
1	A.R.C. Erbil	Saberbeg × UP 114 (Adnania)
2	A.R.C. Sulaymania	PBW 450 – ONPL
3	A.R.C. Sulaymania	BHRIKUTI NL623 - ONPL
4	A.R.C. Sulaymania	PASTOR/3/KAUZX2/OPATA/KAUZCMSS93 B003085-29Y-010M-010Y-010M-7Y-OM
5	A.R.C. Sulaymania	KAUZ//ALTRA84AOS/3/MILAN/KAUZ/4/HUITES CMSS97-M03912T-040Y-020Y-030M-020Y-040M-LY-2M-OY

A. R. C. = Agriculture Research Station.

RESULTS AND DISCUSSION

The GCA effects of the parents along with the mean value of the parents indicated that there was close relationship between parental mean performance and GCA effects for all studied characters excluding grain yield/plant due to the grain yield is a complex trait which is influenced by many other traits especially yield components (Table 2). On the basis of overall performance, parent 1 was found to be desirable combiner for early flowering, spike length and grain yield/plant. The parent 2 was responsible for shorter plant height, The parent 4 was found to be desirable combiner for no. of grains/spike. The parent 5 was responsible for 1000-grain weight, biomass yield/plant and harvest index. Consequently, the perfect relationship could be established between performance and GCA effects of the parents. Similar finding was reported by other researchers (Kumar *et al.*, 2011).

The desirable SCA effects of F₂ crosses along with the mean value of each cross are presented in Table (3). Out of 10 crosses 2, 3, 2, 1, 4, 3, 2, 3, and 2 were observed to be desirable with positive significant value of SCA effects for days to flowering, plant height, spike length, no.

of spikes/plant, no. of grains/spike, 1000-grain weight, biomass yield/plant, grain yield/plant and harvest index, respectively. However, the desirable crosses on the basis of performance and SCA effects were 2 × 5 for days to flowering and spike length; 2 × 3 for shorter plant height; 1 × 4 for no. of spike/plant, no. of grains/spike, biomass yield/plant and harvest index and 4 × 5 for grain yield/plant. It can be noticed that some crosses showed desirable SCA effects for more than one characters. Other researchers also obtained crosses which showed a desirable SCA effects of for different traits using different genotypes (Adel and Ali, 2013).

Regarding to reciprocal effects; the data in Table (4) showed that the cross 4 × 1 had a desirable reciprocal effects for days to flowering and spike length; a cross 5 × 1 for no. of grains and biomass yield/plant; a cross 3 × 2 for days to flowering and no. of spikes/plant; a cross 5 × 2 for plant height and no of grains/spike; a cross 5 × 3 for 1000-grain weight, grain yield/plant and harvest index and a cross 5 × 4 for plant height, no. of spikes/plant, biomass yield/plant, grain yield/plant and harvest index. While the best

reciprocal crosses on the basis of performance and SCA effects were 5×2 for plant height; a cross 4×1 for spike length; a cross 5×3 for harvest index.

It can be concluded from the results of combining ability basis on the performance and

combining ability that the parents 1 and 5 proved as a best general combiner which can be used in hybridization program for obtaining desirable combinations, while the crosses 1×4 and 5×4 had a best specific combiner in desirable direction for three and five traits, respectively.

Table (2) Estimation of GCA effects of 5 parents along with their mean performance for studied characters in F2 generation of bread wheat.

Parents	Days to flowering		Plant height (cm)		Spike length (cm)		No. of spikes/plant	
	GCA effect	Parent mean	GCA effect	Parent mean	GCA effect	Parent mean	GCA effect	Parent mean
1	-1.02*	115.33	3.86*	81.00	0.36*	11.24	-0.32*	6.55
2	0.18*	117.33	-2.48*	62.97	-0.31*	9.28	0.08*	7.53
3	0.98*	119.33	-1.59*	72.07	0.07*	10.75	0.22*	7.37
4	0.55*	119.00	-0.79*	71.47	-0.17*	10.62	0.30*	7.73
5	-0.69*	117.00	1.00*	69.80	0.06*	10.15	-0.27*	6.45
<i>S.E.(g_i-g_j)</i>	0.12		0.40		0.06		0.07	

-Continued-

Parents	No. of grains/spike		1000-grain weight (g)		Biomass yield/plant (g)		Grain yield/plant (g)		Harvest index (%)	
	GCA effect	Parent mean	GCA effect	Parent mean	GCA effect	Parent mean	GCA effect	Parent mean	GCA effect	Parent mean
1	-	46.07	1.04*	32.67	0.35*	-	0.80*	-	-	-
2	0.98*	49.47	-	26.67	-	24.07	0.57*	10.16	0.012*	0.42
3	-	50.77	1.83*	33.33	0.57*	25.27	-	10.35	-	0.41
4	0.48*	50.70	-	32.33	-	27.07	0.78*	11.57	0.007*	0.43
5	0.29*	54.63	0.36*	35.33	0.64*	27.20	-	11.32	0.006*	0.42
	0.29*		-		-0.12	30.02	0.59*	13.29	0.004*	0.44
	0.88*		0.56*		0.99*		-		0.008*	
<i>S.E.(g_i-g_j)</i>	0.21		0.17		0.20		0.10		0.003	

Table (3) Estimation of SCA effects and corresponding mean performance for studied characters in F₂ generation of 5 × 5 diallel cross.

Crosses	Days to flowering		Plant height (cm)		Spike length (cm)		No. of spikes/plant	
	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean
1 × 2	0.49*	116.33	0.86	73.65	-0.06	10.32	-0.12	6.24
1 × 3	-0.15	116.67	-0.69	75.80	-0.21*	11.07	-0.01	6.98
1 × 4	-0.05	116.33	-0.91	79.77	0.01	11.37	0.24*	7.36
1 × 5	-0.15	115.67	-2.01*	74.35	0.14	11.05	-0.35*	6.27
2 × 3	0.65*	118.00	-2.73*	63.63	0.28*	10.18	0.04	7.70
2 × 4	-0.25	117.67	0.34	67.17	-0.10	9.75	-0.43*	6.97
2 × 5	-0.35*	116.33	4.14*	69.60	0.39*	9.50	0.09	6.55
3 × 4	-0.05	119.33	-1.91*	70.73	-0.29*	10.28	-0.10	7.29
3 × 5	-0.31*	118.00	0.62	72.93	0.02	9.93	0.10	6.73
4 × 5	-0.05	118.00	-0.02	69.11	-0.17*	9.78	0.13	7.56
<i>S.E.(g_i-g_j)</i>	0.29		0.97		0.14		0.18	

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Crosses	No. of grains/spike		1000-grain weight (g)		Biomass yield/plant (g)		Grain yield/plant (g)		Harvest index (%)	
	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean
	0.30		0.46		0.29		5.43*		-0.01*	
	-0.48		1.83*		1.20*		-		-0.008	
	2.06*		0.03		1.51*		0.71*		0.013*	
1 × 2	-0.24	44.867	-	31.667	-	24.333	-0.04	8.993	-0.03*	0.370
1 × 3	0.56*	48.633	0.74*	37.667	0.64*	28.977	-	10.800	0.007	0.373
1 × 4	0.55*	49.367	-	33.667	-0.20	29.057	1.92*	11.880	-0.002	0.412
1 × 5	-	53.000	0.97*	34.000	-	27.807	-	10.993	-0.001	0.394
2 × 3	2.16*	49.600	1.73*	28.667	0.72*	26.033	0.87*	10.833	-0.01*	0.416
2 × 4	-	49.533	0.63*	32.000	-0.04	25.250	-	10.017	0.010*	0.397
2 × 5	1.27*	49.100	-	30.667	-	24.767	1.34*	10.653	0.006	0.431
3 × 4	0.99*	48.500	3.07*	28.000	2.23*	22.087	-	9.113		0.413
3 × 5	-	51.267	0.33	36.333	-	26.633	1.10*	12.217		0.462
4 × 5	1.79*	49.100	0.03	34.667	1.38*	29.487	-	13.390		0.454
					-0.25		0.53*			
							0.31*			
							0.74*			
<i>S.E.(g_i-g_j)</i>	0.52		0.49		0.48		0.24		0.008	

Table (4) Estimation of reciprocal effects and corresponding mean performance for studied characters in F₂ generation of 5 × 5 diallel cross.

Reci.	Days to flowering		Plant height (cm)		Spike length (cm)		No. of spikes/plant	
	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean
2 × 1	-0.83*	116.67	0.87	72.35	-0.08	10.47	-0.36*	6.70
3 × 1	-0.67*	117.00	3.69*	68.20	0.45*	11.17	0.12	7.30
4 × 1	-0.67*	117.00	7.07*	76.80	0.77*	11.58	0.17*	7.19
5 × 1	0.00	115.67	0.96*	72.43	0.09	10.87	0.24*	5.79
3 × 2	-1.33*	118.67	-0.10	61.77	-0.26*	9.75	0.40*	7.50
4 × 2	-0.33*	118.33	-0.45	68.07	-0.08	9.90	0.05	6.87
5 × 2	-0.33*	117.67	-3.60*	65.64	-1.04*	9.83	-0.32*	7.01
4 × 3	0.33*	120.67	4.48*	63.83	0.27*	10.70	-0.11	6.90
5 × 3	0.50*	118.00	2.37*	68.43	-0.62*	10.17	-0.29*	6.73
5 × 4	0.67*	118.00	-1.62*	71.90	-0.34*	10.47	0.43*	6.97
<i>S.E.(r_{ij}-r_{ij}')</i>	0.29		0.88		0.13		0.17	

-Continued-

Crosses	No. of grains/spike		1000-grain weight (g)		Biomass yield/plant (g)		Grain yield/plant (g)		Harvest index (%)	
	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean	SCA effect	mean
						23.21			-	0.015
						7			*	
						22.76			-	
						3			0.029	
						27.45			*	
2 × 1	-3.65*	49.00	-0.17	32.00	-1.47*	0	-0.14	9.57	-	0.412
3 × 1	0.13	52.40	3.00*	31.33	2.34*	25.05	0.16	9.51	0.008	0.418
4 × 1	-1.67*	46.73	1.00*	34.67	1.58*	7	0.38*	10.95	*	0.401
5 × 1	3.67*	45.67	-0.17	34.33	1.38*	23.40	0.79*	9.41	0.008	0.377
3 × 2	-0.45	49.47	-0.33	28.33	1.72*	0	0.57*	9.75	*	0.417
4 × 2	-0.50*	50.53	0.50*	31.00	0.93*	23.40	0.04	9.94	-0.006	0.424
5 × 2	1.18*	52.70	-2.00*	31.67	-1.34*	0	-0.15	11.11	-	0.429
4 × 3	-0.48*	50.50	-0.17	29.33	-0.66*	25.89	-0.32*	9.69	0.014	0.427
5 × 3	-0.57*	48.37	2.50*	31.67	1.94*	7	1.36*	10.48	*	0.431
5 × 4	0.05	52.17	1.33*	32.00	3.14*	22.60	1.91*	10.90	0.015	0.400
						0			*	
						24.30			-0.002	
						0			0.022	
						27.26			*	
						7			0.021	
									*	
<i>S.E.(r_{ij}-r_{ij}')</i>	0.47		0.37		0.44		0.22		0.007	

Analysis of variance according to Hayman approach are presented in Table (5). The results indicates that additive genetic component (a) were important in the inheritance of all traits except no. of grains/spike and harvest index, in opposite non-

additive component (b) were significant of plant height, 1000-grain weight, biomass yield/plant and grain yield/plant. Significance of *b*₁ component depicted dominance deviation predominantly in one direction, while significance

of b_2 value suggested asymmetric distribution of dominant and recessive alleles. This unequal distribution of genes clearly indicates that some parents have considerably more dominant alleles than others for plant height, 1000-grain weight, biomass yield/plant and grain yield/plant. Moreover, significance of b_3 values for these traits confirm an important role of specific dominant deviation of genes while non-significant b_3 value confirm the absence of residual dominance which are found from days to flowering, spike length, no. of spikes/plant, no. of grains/spike and harvest index, while non-significant 'b3' value confirm the absence of residual dominance for remaining traits. Significant c and d items indicated the presence of maternal and reciprocal effects, respectively. Component c has been significant for plant height, 1000-grain weight, biomass yield/plant and grain yield/plant while component d was significant for 1000-grain weight only. Similar results found by Kutlu and Olgun (2015).

The genetic components of variance according to Jinks-Hayman approach including additive (\widehat{D}), dominance (\widehat{H}_1 and \widehat{H}_2), \widehat{F} , \widehat{h}^2 and environmental variance (\widehat{E}) were shown in Table (6). The results revealed significant role of additive genetic component (\widehat{D}) for the inheritance of all traits. Ivanovska (2000) reported non-additive gene action for some quantitative traits in F_2 wheat populations while Khan and Ali (1998) reported additive genetic effects for most traits. Positive value of \widehat{F} suggests that dominant alleles were more frequent than recessive ones for all traits and were also in increasing order as reflected by the high positive value of \widehat{h}^2 . The results revealed that this component were positive for no. of grains/spike, 1000-grain weight, biomass yield/plant, grain yield/plant and harvest index while negative for remaining traits. Additive genetic component (\widehat{D}) was smaller in magnitude than both components

of dominance (\widehat{H}_1 and \widehat{H}_2) for all studied traits indicating preponderance of non-additive gene action for these traits. Moreover, dominance components (\widehat{H}_1 and \widehat{H}_2) showed unequal distribution of dominant and recessive genes among the parent due to difference in values of those two components.

Environmental variance (\widehat{E}) was positive and significant for all traits except biomass yield/plant, indicating the important role of environmental conditions in the phenotypic expression of these traits. The average degree of dominance ($\sqrt{\widehat{H}_1/\widehat{D}}$) has been >1 for all traits indicates that these traits were controlled by the over-dominance of genes and ample scope for heterosis breeding. The ratio of ($H_2/4H_1$) indicates the symmetry of the frequency of dominant and recessive alleles in all gene location controlling traits. This ratio is less than 0.25 for all traits except days to flowering, plant height, no. of spikes/plant and harvest index. This amount of ratio indicates the unequal frequencies of dominant and recessive allele for these traits. The component KD/KR measures the proportion of dominant and recessive genes among the parents. Five traits including no. of grains/spike, 1000-grain weight, biomass yield/plant, grain yield/plant and harvest index have shown the values for this component above unity, indicating the role of dominant genes in the expression of these traits compared with the other traits which have shown values less than unity, indicating the role of recessive genes in the expression of these traits. The value of genetic ratio (\widehat{h}^2/H_2) estimated for studied traits indicate that there has been at least one genetic group involved in the control of heredity. Similar findings have been reported by Kashif *et al.* (2003) and Fellahi *et al.* (2016). The narrow sense heritability $H_{n.s.}$ was high for all traits except days to flowering, plant height, no. of spikes/plant, indicating that selection for improvement of these traits would be effective in early generation.

Table (5): Analysis of variance for studied characters according to (Hayman, 1954) method.

SOV	df	Mean Squares			
		Days to flowering	Plant height (cm)	Spike length (cm)	No. of spikes/plant
<i>a</i>	4	26.410*	314.091*	5.976*	2.366*
<i>b</i>	10	0.675 ^{ns}	24.766*	0.218 ^{ns}	0.613 ^{ns}
<i>b</i> ₁	1	0.120 ^{ns}	15.934*	0.000 ^{ns}	0.464 ^{ns}
<i>b</i> ₂	4	0.351 ^{ns}	22.976 *	0.322 ^{ns}	0.114 ^{ns}
<i>b</i> ₃	5	1.044 ^{ns}	27.965 *	0.178 ^{ns}	1.042 ^{ns}
<i>c</i>	4	1.217 ^{ns}	30.231 *	0.165 ^{ns}	0.056 ^{ns}
<i>d</i>	6	0.467 ^{ns}	21.758 ^{ns}	0.173 ^{ns}	0.297 ^{ns}
<i>Total</i>	24				
<i>Ea</i>	8	1.890	14.547	0.190	0.500
<i>Eb</i>	20	0.909	9.754	0.194	0.454
<i>Eb</i> ₁	2	0.630	1.317	0.112	1.642
<i>Eb</i> ₂	8	1.288	5.625	0.142	0.128
<i>Eb</i> ₃	10	0.661	3.944	0.252	0.477
<i>Ec</i>	8	1.367	8.462	0.055	0.293
<i>Ed</i>	12	0.617	13.885	0.482	0.370

(Continued)

SOV	df	Mean Squares				
		No. of grains/spike	1000-grain weight (g)	Biological yield/plant (g)	Grain yield/plant (g)	Harvest index (%)
<i>a</i>	4	2.366 ^{ns}	66.707*	26.926*	9.822*	0.0030 ^{ns}
<i>b</i>	10	0.613 ^{ns}	13.142*	16.274*	3.350*	0.0011 ^{ns}
<i>b</i> ₁	1	0.464 ^{ns}	2.163*	18.362*	8.240*	0.0016 ^{ns}
<i>b</i> ₂	4	0.114 ^{ns}	11.738*	12.325*	1.611*	0.0013 ^{ns}
<i>b</i> ₃	5	1.042 ^{ns}	16.861*	19.015*	4.563*	0.0008 ^{ns}
<i>c</i>	4	0.056 ^{ns}	6.400 *	17.219*	3.467*	0.0019 ^{ns}
<i>d</i>	6	0.297 ^{ns}	14.261*	6.587 ^{ns}	1.750 ^{ns}	0.0010 ^{ns}
<i>Total</i>	24					
<i>Ea</i>	8	17.458	1.822	2.035	0.381	0.0011
<i>Eb</i>	20	7.002	1.284	1.776	0.687	0.0008
<i>Eb</i> ₁	2	7.746	0.443	1.159	0.041	0.0013
<i>Eb</i> ₂	8	6.809	0.731	1.638	0.242	0.0007
<i>Eb</i> ₃	10	7.008	1.094	1.609	1.172	0.0009
<i>Ec</i>	8	3.209	2.425	2.941	0.585	0.0008
<i>Ed</i>	12	0.085	3.261	1.234	0.643	0.0007

Table (6): Genetic parameters and their standard errors for some quantitative traits of studied characters of F_2 full diallel wheat populations according to Jinks -Hayman analysis.

	Days to flowering	Plant height (cm)	Spike length (cm)	No. of spikes/plant
\widehat{D}	2.620* \pm 0.393	33.55* \pm 5.476	0.417* \pm 0.075	0.300* \pm 0.071
\widehat{F}	-0.96 \pm 0.981	-8.085 \pm 13.68	-0.100 \pm 0.187	-0.06 \pm 0.178
\widehat{H}_1	2.811* \pm 1.061	55.88* \pm 14.79	0.755* \pm 0.202	1.122* \pm 0.192
\widehat{H}_2	3.560* \pm 0.962	64.43* \pm 13.41	0.497* \pm 0.183	1.166* \pm 0.174
\widehat{h}^2	0.147 \pm 0.650	1.981 \pm 9.056	0.024 \pm 0.124	0.400* \pm 0.118
\widehat{E}	0.359* \pm 0.160	3.901* \pm 2.236	0.081* \pm 0.031	0.138* \pm 0.029
$\sqrt{H_1/D}$	1.535	1.372	1.269	1.994
$\overline{pq} = H_2/4H_1$	0.317	0.288	0.165	0.260
KD/KR	0.699	0.829	0.836	0.898
h^2/H_2	0.162	0.048	-0.67	0.353
$H_{n.s.}$	0.267	0.297	0.584	0.184

(Continued)

	No. of grains/spike	1000-grain weight (g)	Biomass yield/plant (g)	Grain yield/plant (g)	Harvest index (%)
\widehat{D}	9.458* \pm 2.451	8.641* \pm 2.907	4.354* \pm 3.037	1.267* \pm 0.370	0.0004* \pm 0.0002
\widehat{F}	8.933* \pm 6.122	5.217 \pm 7.263	8.033* \pm 7.587	1.365* \pm 0.923	0.0006 \pm 0.0006
\widehat{H}_1	25.59* \pm 6.618	22.421* \pm 7.85	24.87* \pm 8.203	3.851* \pm 0.998	0.0031* \pm 0.0006
\widehat{H}_2	20.76* \pm 6.003	16.533* \pm 7.12	14.52* \pm 7.440	1.285* \pm 0.905	0.0019* \pm 0.0006
\widehat{h}^2	1.702 \pm 4.53	0.112 \pm 4.808	2.633 \pm 5.023	0.888* \pm 0.611	0.0004 \pm 0.0004
\widehat{E}	1.114* \pm 1.000	0.699* \pm 1.187	0.953 \pm 1.240	0.219* \pm 0.151	0.0003* \pm 0.0001
$\sqrt{H_1/D}$	1.684	1.677	2.554	1.937	3.147
$\overline{pq} = H_2/4H_1$	0.203	0.184	0.146	0.080	1.158
KD/KR	1.805	1.461	2.257	1.894	1.779
h^2/H_2	0.057	0.008	0.240	0.092	0.438
$H_{n.s.}$	0.648	0.671	0.713	0.833	0.584

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