

Assessment of Genetical Parameters of Yield and its Attributes in Bread Wheat (*Triticum aestivum*, L.)

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ABSTRACT

The experiment was performed at the Experimental Farm of Agronomy Department, Faculty of Agric. Al-Azhar Univ. Naser City, Cairo, Egypt during the two following growing seasons 2016/2017 and 2017/2018. Eight parents of bread wheat (*Triticum aestivum*, L.) illustrate a wide range of diversity for some agronomic traits were selected for the study namely; Gemmiza 11, Giza 168, Sids 14, Masr 2, Sids 12, Sakha 95, Masr 1 and Sakha 94 were crossed at 2016/2017 growing season in one direction diallel cross. The genetic analysis (variance, combining ability, heterosis, and type of gene actions) of grain yield / plant and some related traits were evaluated at 2017/2018. Results indicated that variances of genotypes, parents and crosses were highly significant for all evaluated traits. The variances connected to general and specific combining abilities were established be highly significant for all evaluated traits, except number of kernels /spike for GCA. The estimates of GCA/SCA were less than unity recommended the greater amount of non-additive gene actions in determining the performance of all traits. The crosses (P₁xP₂), (P₂xP₆); (P₃xP₅), (P₃xP₆) and (P₅xP₆) recorded greatest mean values for grain yield/plant. P₆ and P₈ were considered as the best general combiners for grain yield /plant. The best crosses for SCA and heterosis effect for grain yield / plant recorded for P₁xP₂, P₃xP₈ and P₅xP₆ where be revealed highly significant and positive SCA and high percent heterosis making them hybrid promising in breeding programs for crop improvement. Hayman and Morley – Jones testing showed that the ratio of (H₁/D)^{1/2} is larger than one for all the studied traits, so over dominance is participating in the genetic of these traits. Estimates of percentage of negative and positive genes (H₂/4H₁) in the parents ranged from 0.18 for plant height to 0.23 for number of kernels /spike and grain yield /plant hence, negative and positive alleles are consistent distributed in this traits. Heritability in broad-sense were high values detected for all the studied traits, indicated that these traits are more genetic, while narrow sense heritability were low for no. of spikes/plant, spike length and grain yield / plant, so the role of additive part is low. Significant differences were observe for additive ("a") effect for all the studied traits in Morley Jones method, Also, dominance ("b") part was significant for all the studied traits, appropriately these traits are controlled by both dominance and additive type of gene actions. As (b₂) and (b₃) were highly significant for all the studied traits, thus epistasis is participating in their genetics. As the part (b₁) was significant for all the evaluated traits, with the exception of plant height and 1000-kernel weight, so dominance genes were attributable to directional dominance. Significant (b₂) part for all traits showing imbalance of gene giving out for these traits. Significant (b₃) part for all traits showed residual dominance effect (b₃) outcome from additive × additive, additive × dominance and dominance × dominance interactions.

Keywords: Wheat, combining ability, heterosis, gene action and heritability.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is considered one of great important food crops in the greatest part of the world and in Egypt. Due to its high converting and various utilization, high nutritive value, connected with high crop production it is used as major food for further one third of the globe population. It is one of the oldest domesticated grain crops and since then it has been the basic principal food of different human development of Europe, West Asia, and North Africa. As major food crop, wheat is fulfilling the calorie demands of growing population. It is only behind the pulses for the protein satisfied, (Kandhare, 2014). Wheat breeding programs considered the major role in the grow new high yielding varieties. Increasing wheat productivity as public goal could be accomplished across increasing productivity per unit area. Combining ability researches performed by breeders to choose parents with efficient remove valuable genes to the progenies (Madic *et al.*, 2005). For improvement in wheat yield, the study of the genetic structure and trend of combining ability is of great significance for the wheat scientist, knowledge of general and specific combining ability along with the method of gene action in the obtainable breeding material is very significant to start the successful, wheat breeding programme. Half diallel mating is an effective strategy to assess genotypes used as parents for combining ability effects in order to select acceptable, parents for developing recently developed cultivars Hayman (1954a, b) and Jinks (1954). Successful breeding programs need to know the type of gene action and genetic system controlling the inheritance of the interest traits and the best breeding strategy to be used to improve them.

Diallel cross methods is acceptable, tool for recognition of crosses fusions that have the potentiality to build greatest improvement and discover higher lines among the progeny in advanced segregation generations. In this techniques, whole, genetic variation is parting into the variance effects of (GCA), as calculate of additive gene action and (SCA), as calculate of non-additive gene action. Through breeding programs, it is required to choice pure lines of high general combining ability (GCA) that demonstrate the additive gene effect. On the base of that predicting progenies and manufacture choice of cross combination and genotypes can be performed. Combining ability researches performed by breeders to select parents with structured removal valuable genes to the progenies (Madic *et al.*, 2005). Many investigators have studied the combining ability and genetic construction of bread wheat hybrid populations using half diallel mating procedure connected to yield and yield components. Several researchers like Khalifa *et al.* (1984), Hendawy (1990), El-Shal *et al.* (2014), Khaled and Abd El-dayem (2014) Samier and Ismail (2015) and Rahul and Kandalkar (2018), showed that both additive and non-additive gene actions played an equal part in the inheritance of grain yield, number of spikes /plant, number of kernels /spike and 100-kernal weight. While, El-Hennawy (1992), Darwish (1992) and Abd El-Mageed (1995) indicated that dominance and additive gene effects were significant for grain yield/plant, number of kernels/spike and 100-kernal weight. On the other hand, Mahmoud (1999) indicated that additive and non-additive gene effects were of great value rule, the genetic systems of grain yield and its components. The additive gene effect mainly influenced the inheritance

of studied characters .Similar results were obtained by El-Sayed *et al.* (2000), Hamada and Tawfeleis (2001) El-Sayed (2004), Abdel-Nour, Nadya *et al* (2009), Moussa (2010) and El-Awady,Wafaa (2011).

Significant and valuable heterotic effects were obtained for many traits by El-Beially and El-Sayed (2002), Hamada and El-Beially (2003), Eman, *et al* (2014) and Samier and Ismail(2015).

This investigation was performed to estimate the greatness of both GCA and SCA in addition to heterosis percentages and type of gene action for grain yield and some attributes in 28 wheat crosses produced from eight

bread wheat genotypes utilized half diallel crosses.

MATERIALS AND METHODS

The investigation was performed at the Experimental Farm of Agronomy Department , Faculty of Agric. Al-Azhar Univ. Naser City, Cairo , Egypt during the two seasons of 2016/2017 and 2017/2018 . Eight local wheat cultivars namely Gemmiza 11 (P₁), Giza 168 (P₂), Sids 14 (P₃), Masr 2 (P₄), Sids 12 (P₅), Sakha 95 (P₆), Masr 1 (P₇) and Sakha 94 (P₈) of wheat (*Triticum aestivum*, L) were chosen to establish this study .Names and pedigree of the parental materials are present in Table (1)

Table 1. Parents, pedigree and origin of the eight wheat parents used in the study

No	Parents	Pedigree	Origin
P ₁	Gemmiza 11	BOW,,s,,/KVZ/ 7C/SERI82/3/GIZA168/SAKHA61	Egypt
P ₂	Giza 168	MRL/BUC//Seri CM93046-8M-OY-OM-2Y-OB	Egypt
P ₃	Sids 14	SW8488*2/ KUKUNA CGSS01Y00081T099M-099Y-099M-099B-9Y-0B-0SD.	Egypt
P ₄	Masr 2	SKAUZ/BAV92.CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S	Egypt
P ₅	Sids 12	BUC//7C/ALD/5/MAYA74/0N//1160- Egypt/47/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.63014*SX.SD7096-4SD-1SD-1SD-0SD.	Egypt
P ₆	Sakha 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1.CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.	Egypt
P ₇	Masr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR.CMSS00YO1881T-050M-030Y-030M-030WGY-33M-0Y-0S	Egypt
P ₈	Sakha 94	Sakha 93/ Ri4220 CM15430- 2S-5S- 0S- 0S	Egypt

A half diallel cross set involving eight genotypes of bread wheat parents were made in winter of 2016/2017 season. All possible plant amalgamations excluding reciprocals were hand crossed among these parents to produce 28 F_{1,s} cross seeds. In 2017/2018 season , the eight parents and the obtained 28 crosses (36 genotypes) were grown for assessment in a randomized complete blocks design (RCBD) with three replications .Each plot include of two rows of 4 meters in length spaced at 30 cm . Distance between plants to plant was kept at 10 cm.

Data were account on a random sample of 10 guarded plants for parents and F₁ hybrids in each plot were chosen to investigate the following traits i.e., days to heading , days to maturity, plant height (cm), number of spikes /plant, spike length (cm), number of spikelets /spike, number of kernels /spike, 1000- kernel weight (g) and grain yield /plant (g). Recommended agricultural practices for wheat were applied from sowing to harvest.

Analysis of variance achieved as maintained by Steel and Torrie (1980).The obtained data were analyzed to determine general and specific combining abilities according to the technique of Griffing (1956). Diallel cross technique designated as method 2 model 1 for the experiment. The percentages of heterosis as reported by Mather and Jinks (1971) were estimated as deviation of the F₁ mean from mid-parents and better parent values and explicit in percentage as follows:

Percentage of heterosis (H) over mid parents :

$$H \text{ (Mid P), \%} = \left[\frac{F_1 - \text{Mid parent}}{\text{Mid parent}} \right] \times 100$$

Percentage of heterosis (H) over better-parent :

$$H \text{ (B. P), \%} = \left[\frac{F_1 - \text{Better parent}}{\text{Better parent}} \right] \times 100$$

Appropriate LSD values were determined to know the significance of the heterotic percentages as stated by the following formula recommend by Wynne *et al.* (1970),

$$LSD = t \times S. E$$

Where:

$$S.E \text{ for mid parent} = \sqrt{\frac{3M.S.E}{2R}}$$

$$\text{For better parent} = \sqrt{\frac{2M.S.E}{R}}$$

t = tabulated value at the degree of freedom for the error.

M.S.E=Mean squares for pooled error.

R=number of replications.

Components of genetic variance and genetic parameters:

Morley Jones modification for diallel without reciprocal

Mean squares for the whole diallel table was designated by Hayman (1954b). Presume the absence of reciprocal contrast. Morley Jones (1965) imparted some alteration of Hayman's approach. In this alteration as Hayman, estimating of the sum of squares corresponding to additive effects (a), and on the presume of no epistasis to mean dominance (b₁), to farther dominance effects that can be described for genes own one allele present in only one line (b₂) and to residual dominance effects (b₃), is in essence a straight forward application of fitting constants by least squares.

After defined the validity of hypothesis that epistasis is absent, estimation of genetic variance parts along with allied genetic parameters, which were obtained by Hayman (1954b).

RESULTS AND DISCUSSION

Analysis of variance:-

Data reported in Table (2) indicate that the mean square attributable to genotypes i.e. parents , parents vs . crosses, and crosses were highly significant for all the evaluated traits, excluding plant height and 1000-kernel weight for P.V.S.C, indicating that these genotypes were genetically different for genes controlling yield and related

traits. In this connection significant differences among wheat genotypes , for yield and related traits were also found by Sanjeev *et al* (2017) and Rahul and Kandalkar (2018).

Analysis of variance in (Table 2)for combining ability, showed highly significant variance for both general (GCA) and specific combining abilities (SCA) for all the evaluated traits excluding number of kernels /spike for GCA .This showed that both type of gene effects were attached in the inheritance of the traits. However , SCA variances were higher than GCA for all the studied traits ,

indicating the prevalence of non- additive gene action in the genetic control of these traits , resulting in GCA/SCA ratios were under unity, revealing that the largest part of the whole genetic variance associated with non- additive group of gene action . Thus, selection in the late segregating generations could be successfully applied to improve these traits.

Similar findings were reported by El-Hennawy (1996), Vanpariya *et al.*, (2006) , Ezatollah *et al* (2013). El-Shal, *et al* (2014) , Jaydev *et al* (2017) and Rahul and Kandalkar (2018).

Table 2. Mean squares from ordinary analysis of parents and F₁cross diallel for the studied traits

S.O.V	d.f	Days to heading	Days to maturity	Plant height (cm)	No of spikes/plant	Spike length (cm)	No of spikelets /spike	No of kernels/ spike	1000- kernel weight(g)	Grain yield/plant (g)
Replications	2	5.86	14.06	41.04*	4.983**	0.724	0.663	27.50	0.913**	0.419
Genotypes	35	86.61**	79.17**	233.44**	5.786**	6.320**	11.538**	244.462**	88.86**	58.29**
Parents	7	103.78**	77.30**	174.24**	0.757**	3.097**	14.151**	97.157**	66.367**	3.512**
Crosses	27	75.08**	82.18**	256.98**	5.594**	4.244**	10.018**	230.301**	97.694**	58.783**
P.VS.C	1	277.71**	10.83*	12.283	46.172**	84.944**	34.260**	1657.94**	7.901	428.694**
GCA	7	98.90**	46.74**	128.005**	1.427**	0.550**	7.254**	102.903	30.541**	4.918**
SCA		11.36**	21.30**	65.267**	2.054**	2.495**	2.993**	76.133**	29.391**	23.061**
Error	70	2.84	2.23	4.66	0.133	0.541	0.843	12.738	5.368	0.379
GCA/SCA		0.94	0.22	0.198	0.068	0.015	0.257	0.137	0.104	0.020

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level

Mean performance, GCA and SCA effects :

The mean performance of the eight parents and their F₁ crosses are shown in Table (3) and revealed that the P₁ and P₅ gave the lowest value for days to heading and P₁ for days to maturity. The most promising genotypes were P₈ for plant height .P₃ and P₄ for No. of spikes /plant , P₃ , P₇ and P₈ for spike length .P₇ and P₈ had the highest number of spikelets /spike and number of kernels /spike . P₄ and P₅ recorded heaviest 1000-kernel weight and P₈ gave the greatest grain yield /plant .

Table (3) show that wheat crosses P₁ x P₅ and P₁ x P₆ gave good levels of earliness for days to heading(73 and 72.66 days) and days to maturity(119 and 122.33 days) and P₂ x P₅ and P₂ x P₆ for days to maturity(118 and 119 days). In continuous the latest crosses P₄ x P₇ and P₄ x P₈ were the greatest (63.53 and 63.90) in number of kernels /spike .The cross P₄ x P₇ was the tallest in plant height and cross P₁ x P₂ was the highest in spike length(19.40 cm)and number of spikelets /spike(20.10). Whereas the maximum value of number of spikes/plant (6.80) obtained from P₃ x P₅ . Two crosses (P₁ x P₆ and P₁ x P₈) recorded heaviest 1000-kernel weight (55.93 and 54.20 g). The highest number of kernels / spike recorded for cross P₁ x P₆ and P₇ x P₈ (71.34 and 66.42). The greatest grain yield /plant (17.06 and 16.63 g) was obtained for the cross P₃ x P₅ and P₂ x P₆ .

Estimates of G.C.A effects of the parents for each evaluated traits are shown in Table (4). Data showed that genotypes exhibited highly significant values for the most studied traits in all cases with either positive or negative significant values. The results also showed that P₁ (Gemiza 11) and P₅ (Sids 12) may be evaluate as good general combiners for developing early genotypes (days to heading and days to maturity) and P₁ for 1000 -kernel weight, while, P₄ (Masr 2) gave positive GCA effects for plant tallness. On the other hand, P₁ (Gemiza 11) and P₂ (Giza 168) for plant shortness.P₅ (Sids 12) was good

general combiner for number of spikes /plant. For spike length, number of spikelets / spike, number of kernels / spike, P₇ (Masr 1)expressed positive and significant general combining ability effects for these traits .It is worth to note that P₈ (Sakha 94) was good combiners for grain yield/plant and three of its component traits . In bread wheat, parents having good general combining ability have been recorded by Ajmal *et al.*, (2011) , Ankita *et al.*, (2012), Samier and Ismail (2015) and Jaydev *et al* (2017).

Estimates of S.C.A effects in F1 crosses for each traits are shown in Table (5). Results showed highly significant SCA effects values for all the evaluated traits. For days to heading, negative and highly significant or significant SCA effects were detected in six crosses(P₁ x P₅ ,P₁ x P₆ ,P₂ x P₆ ,P₃ x P₄ ,P₃ x P₈ and P₇ x P₈).Concerning days to maturity , twelve crosses (P₁ x P₅ ,P₁ x P₆ ,P₂ x P₅ ,P₂ x P₆ ,P₃ x P₄ , P₃ x P₆,P₃ x P₇ ,P₃ x P₈ ,P₄ x P₅ ,P₅ x P₇ ,P₆ x P₇ and P₇ x P₈) exhibited negative and significant SCA effects. For plant height, eleven crosses(P₁ x P₂ ,P₁ x P₃ ,P₂ x P₄ ,P₂ x P₆ ,P₂ x P₇ , P₃ x P₄,P₃ x P₅ ,P₃ x P₆ ,P₅ x P₈ ,P₆ x P₇ and P₆ x P₈) showed positive and significant SCA effects, while , thirteen crosses(P₁ x P₄ ,P₁ x P₅ ,P₁ x P₆ ,P₁ x P₈ , P₂ x P₃ , P₂ x P₅ , P₃ x P₈,P₄ x P₅ ,P₄ x P₆ ,P₄ x P₇ ,P₅ x P₆ , P₅ x P₇ and P₇ x P₈) exhibited negative and significant effects. As for number of spikes /plant fourteen crosses (P₁ x P₂ ,P₁ x P₅ ,P₂ x P₅ ,P₂ x P₆ , P₂ x P₇ ,P₂ x P₈ , P₃ x P₄,P₃ x P₅ ,P₃ x P₆ ,P₄ x P₆ ,P₄ x P₇ , P₄ x P₈ , P₅ x P₆ and P₆ x P₈) revealed positive and highly significant SCA effects for this trait .Regarding spike length, twelve crosses (P₁ x P₂ ,P₁ x P₇ ,P₁ x P₈ ,P₂ x P₅ ,P₂ x P₆ , P₂ x P₈,P₃ x P₅ ,P₃ x P₆ ,P₄ x P₅ ,P₄ x P₆ ,P₄ x P₇ and P₅ x P₆) exhibited positive and highly significant SCA effects. With regard to number of spikelets/ spike, eleven crosses(P₁ x P₂ ,P₁ x P₆,P₁ x P₈ ,P₂ x P₅ ,P₂ x P₆ , P₂ x P₈,P₃ x P₄ ,P₃ x P₅ ,P₃ x P₆ ,P₃ x P₇ and P₄ x P₇) revealed positive and highly significant SCA effects for this trait .For number of kernels/ spike thirteen crosses crosses (P₁ x P₂ ,P₁ x P₃ ,P₁ x P₆ ,P₁ x P₇ , P₂ x P₆ , P₂ x P₈ ,

P₃ x P₅, P₃ x P₇, P₄ x P₇, P₄ x P₈, P₅ x P₆, P₆ x P₇ and P₇ x P₈ exhibited positive and significant effects. As for 1000-kernel weight, ten crosses (P₁ x P₂, P₁ x P₆, P₁ x P₈, P₂ x P₅, P₂ x P₆, P₃ x P₅, P₃ x P₇, P₄ x P₇, P₄ x P₈, P₅ x P₆, P₆ x P₇ and P₆ x P₈) were positive and significant effects. Furthermore for grain yield /plant, eleven crosses (P₁ x P₂

, P₁ x P₆, P₁ x P₇, P₂ x P₆, P₃ x P₇, P₃ x P₈, P₄ x P₇, P₄ x P₈, P₅ x P₆, P₅ x P₇ and P₆ x P₈) recorded positive and significant SCA effects for this trait. It could be concluded that generally combining ability effects of the parental lines in general variant to the SCA effects of their particular crosses.

Table 3. Mean performance for all the studied traits of parents and their 28 F1 wheat cross.

Genotypes	Days to heading	Days to maturity	Plant height (cm)	No of spikes /plant	Spike length (cm)	No of spikelets /spike	No of kernels/spike	1000-kernel weight (g)	Grain yield/plant (g)
P ₁ (Gemiza 11)	72.00	120.66	73.96	3.86	13.13	16.12	50.67	48.50	10.10
P ₂ (Giza 168)	73.66	123.33	69.53	3.93	11.38	17.65	45.26	39.96	10.10
P ₃ (Sids 14)	83.33	132.66	71.13	4.86	14.34	16.20	44.93	39.33	10.09
P ₄ (Masr 2)	84.66	136.00	75.20	4.63	16.93	19.30	48.12	49.26	11.65
P ₅ (Sids 12)	71.00	125.00	87.46	4.16	15.15	18.38	37.63	50.43	11.40
P ₆ (Sakha 95)	80.33	127.00	79.23	3.23	12.73	16.29	46.30	40.86	8.23
P ₇ (Masr 1)	84.66	131.00	72.85	4.00	14.26	18.13	55.21	48.93	10.86
P ₈ (Sakha 94)	83.00	127.66	90.18	4.55	14.20	17.93	54.37	47.86	11.04
P ₁ x P ₂	75.00	127.00	73.11	4.80	19.40	20.10	62.31	50.86	15.33
P ₁ x P ₃	81.33	132.00	75.19	5.12	14.06	17.69	63.33	43.33	13.46
P ₁ x P ₄	82.66	134.66	71.10	3.77	14.36	16.14	53.02	47.13	8.79
P ₁ x P ₅	73.00	119.00	62.68	4.86	13.96	16.31	34.44	49.30	9.87
P ₁ x P ₆	72.66	122.33	70.24	4.20	15.70	18.79	71.34	55.93	12.53
P ₁ x P ₇	83.33	129.00	72.77	3.77	16.73	19.57	65.17	49.20	13.20
P ₁ x P ₈	83.00	131.33	66.05	4.15	16.83	19.48	60.33	54.20	14.66
P ₂ x P ₃	78.66	132.33	59.16	4.74	15.00	14.25	48.11	45.53	10.73
P ₂ x P ₄	83.66	135.66	82.58	4.03	14.13	19.70	50.01	45.83	9.10
P ₂ x P ₅	78.33	118.00	70.65	5.78	15.43	18.44	47.01	52.40	13.30
P ₂ x P ₆	77.00	119.00	83.61	5.13	15.86	19.16	62.80	47.66	16.63
P ₂ x P ₇	88.00	129.00	78.51	5.40	14.73	18.45	51.09	43.06	12.66
P ₂ x P ₈	83.00	133.00	78.31	5.90	15.80	19.03	66.11	37.56	14.53
P ₃ x P ₄	75.00	125.00	91.47	6.47	14.11	19.68	43.79	41.33	11.53
P ₃ x P ₅	80.33	131.66	94.55	6.80	16.64	18.82	69.20	47.86	17.06
P ₃ x P ₆	84.00	124.33	82.56	5.23	16.30	19.70	58.02	45.66	16.60
P ₃ x P ₇	85.66	124.00	78.51	3.96	15.73	19.52	63.08	43.96	10.73
P ₃ x P ₈	77.00	121.66	71.53	4.44	14.08	17.53	49.99	52.26	12.86
P ₄ x P ₅	80.33	123.33	81.63	4.50	15.33	16.63	49.48	37.46	9.43
P ₄ x P ₆	85.00	132.33	85.00	5.66	16.16	14.87	53.91	42.36	13.79
P ₄ x P ₇	90.33	132.33	97.70	6.23	16.43	18.85	63.53	41.73	13.73
P ₄ x P ₈	91.33	132.33	85.13	5.55	14.70	18.11	63.90	47.44	14.58
P ₅ x P ₆	80.00	123.66	79.13	5.79	16.26	14.78	61.63	44.43	16.20
P ₅ x P ₇	87.33	121.66	74.16	5.36	15.13	16.38	48.55	50.43	13.96
P ₅ x P ₈	86.00	131.66	86.50	6.16	14.13	15.17	54.96	40.73	14.73
P ₆ x P ₇	91.66	121.66	83.30	4.83	15.93	18.89	65.06	42.06	12.76
P ₆ x P ₈	89.00	127.00	87.30	5.02	15.60	18.58	56.02	50.96	14.04
P ₇ x P ₈	84.33	125.00	68.68	4.93	16.06	19.18	66.42	34.60	10.83
L.S.D at									
5%	2.74	2.43	3.51	0.59	1.19	1.49	5.81	3.77	1.00
1%	3.64	3.23	4.67	0.79	1.59	1.98	7.71	5.00	1.33

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Table 4. Estimates of general combining ability effects for the parents used in the F1 half diallel cross in bread wheat

Genotypes	Days to heading	Days to maturity	Plant height	Spikes /plant	Spike length	Spikelets /spike	Kernels/spike	1000-kernel weight	Grain yield/plant
P ₁	-4.375**	-0.925**	-6.359**	-0.678**	0.188	0.347*	1.499*	3.86**	-0.257*
P ₂	-2.775**	-0.525*	-3.766**	0.049	-0.231	0.084	-1.831**	-0.550	-0.240*
P ₃	0.525	1.041**	-0.742*	0.135*	-0.081	0.207	-1.088	-1.673**	0.010
P ₄	2.758**	4.175**	4.232**	0.329**	-0.234	-0.539**	-2.240**	-0.96*	-0.721**
P ₅	-3.141**	-2.691**	2.156**	0.344**	-0.227	-1.786**	-5.574**	0.813*	-0.030
P ₆	0.125	-2.125**	2.692**	0.017	0.185	0.050	2.511**	-0.453	0.622**
P ₇	4.125**	-0.091	-0.333	-0.466**	0.385**	1.026**	3.705**	-1.453**	-0.744**
P ₈	2.758**	1.141**	2.119**	0.268**	0.016	0.609**	3.019**	0.206	1.361**
LSD gi	0.574	0.509	0.735	0.124	0.250	0.312	1.215	0.789	0.209
5%									
1%	0.762	0.676	0.976	0.165	0.332	0.415	1.613	1.047	0.278

Table 5. Estimates of specific combining ability effects of 28 F₁s for all the traits in bread wheat .

Crosses	Days to heading	Days to maturity	Plant height	Spikes/ plant	Spike length	Spikelets /spike	Kernels /spike	1000-kernel weight	Grain yield/plant
P ₁ x P ₂	0.066	1.125	5.162**	2.077**	4.393**	2.241**	7.496**	8.404**	8.545**
P ₁ x P ₃	3.10**	4.559**	4.221**	0.314	-1.09**	-0.288	7.773**	-5.005**	0.260
P ₁ x P ₄	2.20**	4.092**	-4.850**	-1.270**	-0.637	-1.098*	-1.384	-1.918	-3.676**
P ₁ x P ₅	-1.566**	-4.707**	-11.186**	0.848**	-1.044**	0.321	-16.627**	-1.525	-3.295**
P ₁ x P ₆	-5.166**	-1.940**	-4.166**	-0.491**	0.276	0.968*	12.187**	6.374**	2.981**
P ₁ x P ₇	1.500	2.692**	1.389	-0.437*	1.11**	0.766	4.819**	0.431	0.749**
P ₁ x P ₈	2.533**	3.792**	-7.786**	-0.785**	1.578**	1.099*	0.672	3.981**	0.109
P ₂ x P ₃	-1.166	4.492**	-14.400**	-0.790**	0.263	-3.465**	-4.114*	1.604	-2.490**
P ₂ x P ₄	1.60*	4.692**	4.040**	-1.698**	-0.451	-2.715**	-1.062	1.191	-3.390**
P ₂ x P ₅	2.166**	-6.107**	-5.816**	1.034**	0.842*	1.411**	-0.722	5.984**	0.117
P ₂ x P ₆	-2.433**	-5.674**	6.607**	0.713**	0.863*	1.598**	6.978**	2.518*	2.797**
P ₂ x P ₇	4.566**	2.292**	4.539**	0.468**	-0.47	-0.083	-5.921**	-1.291	0.198
P ₂ x P ₈	0.933	5.059**	1.887	1.229**	0.965**	0.909*	9.777**	-8.241**	-0.040
P ₃ x P ₄	-1.70*	-7.540**	9.902**	1.652**	-0.624	0.914*	-8.019**	-2.185*	-1.104**
P ₃ x P ₅	0.866	5.992**	15.059**	1.974**	1.906**	3.974**	20.724**	2.574*	-1.104**
P ₃ x P ₆	1.266	-1.907**	2.539*	0.727**	1.146**	2.011**	1.458	1.641	-1.208**
P ₃ x P ₇	-1.066	-4.274**	1.515	-1.054**	0.38	0.859*	5.324**	0.731	-11.632**
P ₃ x P ₈	-1.70*	-7.840**	-7.920**	-1.310**	-0.901**	-0.714	-7.082**	7.581**	2.513**
P ₄ x P ₅	-1.366	-5.474**	-7.065**	-1.526**	0.745*	1.524**	2.149	-8.538**	-3.267**
P ₄ x P ₆	0.033	2.959**	-7.065**	0.966**	1.165**	-2.071**	-1.499	-2.371*	0.439
P ₄ x P ₇	1.366	0.925	-2.832**	2.017**	1.232**	0.939*	6.926**	-2.215*	5.746**
P ₄ x P ₈	3.733**	-0.307	0.704	2.615**	-0.132	0.609	7.979**	5.968**	12.843**
P ₅ x P ₆	0.933	1.159	-3.792**	1.078**	1.259**	-0.908*	9.547**	-2.078	2.160**
P ₅ x P ₇	4.266**	-2.874**	-5.733**	0.136	-0.074	-0.290	-4.719**	4.711**	1.288**
P ₅ x P ₈	4.30**	5.892**	4.047**	0.201	-0.705*	-1.084*	2.376	-6.438**	-0.051
P ₆ x P ₇	5.333**	-3.107**	2.863**	-0.070	0.313	0.386	3.705*	-2.388	-0.571*
P ₆ x P ₈	4.033**	0.659	4.410**	1.384**	0.348	0.492	-4.655**	5.061**	2.609**
P ₇ x P ₈	-4.633**	-3.374**	-11.176**	-0.221	0.615	0.120	4.556**	-10.515**	-3.233
L.S.D									
SiJ at 5%	1.531	1.358	1.961	0.332	0.668	0.833	3.241	2.104	0.559
1%	2.032	1.803	2.604	0.441	0.887	1.107	4.303	2.794	0.742

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Heterosis percentage:

Heterosis percentages calculated for each cross as shown in (Table 6), parents vs. crosses variances as an evidence for average heterosis of overall crosses, were establish to be significant for all the evaluated traits, with the exception of plant height and 1000-kernel weight. The high positive and significant percentages of heterosis would be useful in most traits under investigation, however for days to heading , days to maturity and plant height , high negative percentage values would be interest from the breeders point of view. The negative values of days to maturity indicate that the hybrid is earlier than the earliest or mid parents.

However, three out of the 28 crosses were significant earlier than their corresponding mid parents (P₁ x P₆ , P₃ x P₄ and P₃ x P₈) and two earlier than earliest parent(P₃ x P₄ and P₃ x P₈) . With respect to days to maturity, eleven crosses and for plant height, twelve crosses exhibited negative and significant heterotic effects relative to mid parents .

Regarding days to maturity and plant height nine and six crosses showed significant negative heterotic effects, comparative to better parents respectively. In this respect, negative and significant heterotic effects comparative to mid parent and or the better parent values were described by El-Beially and El-Sayed (2002), Hamada and El-Beially (2003), Aida Rizkalla *et al.* (2012)

Moreover positive and significant heterotic effects comparative to mid parents were recorded for spikes /plant

(22 crosses) ,spike length (20 crosses), spikelets /spike (20 crosses), kernels /spike (24 crosses),1000-kernel weight (11 crosses)and grain yield /plant (23 crosses). Furthermore positive and significant heterotic effects comparative to better parent were recorded for spikes /plant (20 crosses) ,spike length (16crosses), spikelets /spike (16 crosses), kernels /spike (17 crosses),1000-kernel weight (9 crosses)and grain yield /plant (21 crosses). These results are in agreement with those found by Krishna and Ahmad, (1992), Abdel-Majeed *et al.* (2004), Nagwa Salem (2007), Aida Rizkalla *et al.* (2012) and Samier and Ismail (2015)

Morley-Jones analysis of variance

Morley-Jones mean squares for the studied traits in the eight parents diallel crosses (Table 7). The model suggest by Morley-Jones (1965) believes the homozygous varieties taken as random from some base population about which the conclusion are to be drained. Therefore, his model is interested in variances and not the determinations of genetic components (Singh *et al.*, 1990; Farshadfar *et al.*, 2011b). In this method the sum of squares corresponding to a, b₁, b₂ and b₃ can be measured .

ANOVA in one direction-diallel cross will take the structure given in Table (7). An important value of Morley-Jones ANOVA components is that it is free of the hypothesis whether maternal or reciprocal effects are ready or not and whether the parental lines are a fixed sample or a random sample of a population of inbred lines (Miranda-Filho and Geraldi, 1984 and Farshadfar *et al.*, 2011a).

Table 6. Heterosis percentages over mid (M.D) and better(B.P) parents for all the studied traits

Crosses	Days to heading		Days to maturity		Plant height		Spikes/plant		Spike length	
	M.D	B.P	M.D	B.P	M.D	B.P	M.D	B.P	M.D	B.P
P ₁ x P ₂	2.97*	4.16**	4.09**	5.24**	1.90	5.14**	23.23**	22.13**	58.25**	17.28**
P ₁ x P ₃	4.72**	12.96**	4.21**	9.39**	3.64*	5.71**	17.43**	5.34**	2.37**	-1.95**
P ₁ x P ₄	5.53**	14.81**	4.93**	11.60**	-4.67*	-3.87*	-11.18**	-18.57**	-4.45**	-15.18**
P ₁ x P ₅	2.09	2.81*	-3.12*	-1.38	-22.33**	-15.25**	21.19**	16.82**	-1.27*	-7.85**
P ₁ x P ₆	-4.59**	0.92	-1.21	1.38	-8.29**	-5.03**	18.47**	8.80**	21.39**	19.57**
P ₁ x P ₇	6.38**	15.74**	2.51	6.90**	-0.86	-0.10	-4.07**	-5.75**	22.14**	17.32**
P ₁ x P ₈	7.09**	15.27**	5.77**	8.83**	-19.52**	-10.70**	-130**	-8.79**	23.17**	18.52**
P ₂ x P ₃	0.21	6.78**	3.38 *	7.29**	-15.87**	-14.90**	7.84**	-2.46**	16.59**	4.60**
P ₂ x P ₄	5.68**	13.57**	4.62**	10.00**	14.11**	18.76**	-5.84**	-12.95**	-0.17	-16.53**
P ₂ x P ₅	8.29**	10.32**	-4.96**	-4.32**	-10.00**	1.60	42.89**	38.34**	16.32**	1.84**
P ₂ x P ₆	0.00	4.52**	-4.92**	-3.51**	12.40**	20.24**	43.29**	30.53**	31.58**	24.58**
P ₂ x P ₇	11.15**	19.45**	1.44	4.59**	10.28**	12.91**	36.19**	35.00**	14.87**	3.29**
P ₂ x P ₈	5.95**	12.66**	5.97**	7.83**	-1.93	12.63**	39.15**	29.67**	23.51**	11.26**
P ₃ x P ₄	-10.70**	-9.99**	-6.94**	-5.77**	25.01**	28.58**	36.35**	33.12**	-9.75**	-16.65**
P ₃ x P ₅	4.10**	13.14**	2.19	5.33**	19.23**	32.91**	50.77**	39.91**	12.85**	9.85**
P ₃ x P ₆	2.64	4.56**	-4.23**	-2.09*	9.82**	16.07**	29.29**	7.61**	20.38**	13.66**
P ₃ x P ₇	1.98	2.80*	-5.94**	-5.34**	9.06**	10.37**	-10.60**	-18.51**	9.97**	9.69**
P ₃ x P ₈	-7.41**	-7.22**	-6.53**	-4.69**	-11.31**	0.56	-5.63**	-8.64**	-1.33*	-1.81**
P ₄ x P ₅	3.21	13.14**	-5.49**	-1.33	0.36	8.55**	2.38**	-2.80**	-4.42**	-9.45**
P ₄ x P ₆	3.03*	5.80**	0.63	4.19**	10.07**	13.03**	44.02**	22.24**	8.96**	-4.54**
P ₄ x P ₇	6.69**	6.69**	-0.87	1.01	31.98**	34.11**	44.38**	34.55**	5.35**	-2.95**
P ₄ x P ₈	8.94**	10.04**	0.37	3.65**	2.95	13.20**	20.91**	19.87**	-5.55**	-13.17**
P ₅ x P ₆	5.72**	12.67**	-1.85	-1.06	-5.05*	-0.12	56.69**	39.18**	16.64**	7.32**
P ₅ x P ₇	12.20**	23.00**	-4.94**	-2.66**	-7.47**	1.80	31.37**	28.38**	2.89**	-0.13
P ₅ x P ₈	11.6**8	21.12**	4.22**	5.33**	-2.61	-1.10	41.44**	35.38**	-3.71**	-6.73**
P ₆ x P ₇	11.11**	14.10**	-5.42**	-3.93**	9.54**	14.34**	33.60**	20.75**	18.02**	11.71**
P ₆ x P ₈	8.97**	10.78**	-0.26	0.00	3.05	10.18**	29.04**	10.32**	15.84**	9.85**
P ₇ x P ₈	0.59	1.60	-3.35*	-2.08*	-15.73**	-5.71**	15.32**	8.35**	12.88**	12.62**
L.S.D at										
5%	2.79	2.28	2.47	2.01	3.58	2.92	0.605	0.469	1.21	0.996
1%	3.99	3.25+	3.53	2.88	5.11	4.17	0.864	0.670	1.74	1.42

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Table 6.Continued

Crosses	Spikelets /spike		Kernels/ spike		1000-kernel weight		Grain yield/plant	
	M.D	B.P	M.D	B.P	M.D	B.P	M.D	B.P
P ₁ x P ₂	19.06**	13.88**	29.88**	22.97**	14.98**	4.86**	51.78**	51.78**
P ₁ x P ₃	9.50**	9.19**	32.47**	24.39**	-1.32	-10.65**	33.33**	33.26**
P ₁ x P ₄	-8.86**	-16.37**	7.33**	4.63	-3.57	-4.32*	-19.172**	-24.54**
P ₁ x P ₅	-5.44**	-11.26**	-21.99**	-32.03**	-0.33	-2.24	-8.18**	-13.42**
P ₁ x P ₆	15.98**	15.34**	47.12**	40.79**	25.17**	15.13**	36.71**	24.05**
P ₁ x P ₇	14.26**	7.94**	23.09**	18.04**	0.99	0.55	25.95**	21.54**
P ₁ x P ₈	14.44**	8.64**	14.87**	10.96**	12.48**	11.75**	38.69**	32.87**
P ₂ x P ₃	-15.76**	-19.26**	6.67**	6.29*	14.83**	13.93**	6.29**	6.23**
P ₂ x P ₄	6.63**	2.07**	7.10**	3.92	2.72	-6.96**	-16.32**	-21.88**
P ₂ x P ₅	2.35**	0.326	13.42**	3.86	15.92**	3.90*	23.72**	16.66**
P ₂ x P ₆	12.91**	8.55**	37.16**	35.63**	17.93**	16.64**	81.45**	64.65**
P ₂ x P ₇	3.15**	1.76**	1.70	-7.46**	-3.11	-11.99**	20.80**	16.57**
P ₂ x P ₈	6.97**	6.13**	32.69**	21.59**	-14.45**	-21.52**	37.46**	31.61**
P ₃ x P ₄	10.87**	1.96**	-5.87**	-8.99**	-6.69**	-16.09**	6.07**	-1.03*
P ₃ x P ₅	8.84**	2.39**	67.63**	54.01**	6.64**	-5.09**	77.80**	69.07**
P ₃ x P ₆	21.25**	20.93**	27.19**	25.31**	13.88**	11.747**	81.22**	64.51**
P ₃ x P ₇	13.72**	7.66**	25.98**	14.25**	-0.37	-10.15**	2.24**	-1.19**
P ₃ x P ₈	2.73**	-2.23**	0.68	-8.05**	19.87**	9.19**	58.77**	49.64**
P ₄ x P ₅	-11.73**	-13.83**	15.40**	2.82	-24.84*	-25.71**	-18.17**	-19.05**
P ₄ x P ₆	-16.43**	-22.95**	14.19**	12.03**	-5.99**	-14.00**	38.73**	18.36**
P ₄ x P ₇	0.72	-2.33**	22.97**	15.06**	-15.00**	-15.28**	21.99**	14.85**
P ₄ x P ₈	-2.71**	-6.16**	24.69**	17.52**	5.76**	-3.69*	28.51**	25.15**
P ₅ x P ₆	-14.73**	-19.58**	46.84**	33.11**	-2.66	-11.89**	65.05**	42.10**
P ₅ x P ₇	-10.27**	-10.88**	4.59*	-12.06**	1.50	0.00	25.42**	22.45**
P ₅ x P ₈	-16.44**	-17.46**	19.48**	1.08	-17.12**	-19.23**	31.28**	29.21**
P ₆ x P ₇	9.75**	4.19**	28.18**	17.84**	-6.31**	-14.04**	33.68**	17.49**
P ₆ x P ₈	8.58**	3.62**	11.28**	3.03	14.87**	6.47**	45.71**	27.17**
P ₇ x P ₈	6.39**	5.79**	21.23**	20.30**	-28.51**	-29.28**	-1.09*	-1.90**
L.S.D at								
5%	1.52	1.24	4.59	4.83	3.84	3.13	1.00	0.81
1%	2.17	1.77	5.49	6.90	5.48	4.47	1.44	1.16

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Table 7. Morly-Jones analysis of variance for the studied traits in the eight –parent diallel crosses of bread wheat

source	d.f	Days to heading	Days To maturity	Plant height	Spikes /plant	Spike length	Spikelets /spike	Kernels/ spike	1000-kernel weight	Grain yield/ plant
a	7	98.9**	46.74**	128.00**	1.42**	0.55**	7.25**	102.9**	30.54**	4.91**
b	28	28.11**	21.30**	65.26**	2.054**	2.49**	2.99**	76.13**	29.39**	23.06**
b 1	1	92.57**	3.61*	4.09 ^{n.s}	15.39**	28.31**	11.42**	552.64**	2.633 ^{n.s}	142.89**
b 2	7	6.41**	19.78**	84.94**	0.851**	1.61**	2.08**	16.31**	34.69**	4.374**
b 3	20	9.03**	22.71**	61.43**	1.80**	1.51**	2.89**	73.24**	28.87**	23.60**
Error	107	0.94	0.74	1.55	0.044	0.18	0.281	4.246	1.789	0.126

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Component "a" signifies additive genetic variance in the obscurity of the b_2 part. If b_2 is significant, the "a" part will not measure additive but it will also be mixed with non-additive variance. The b_1 part measures the mean deviations of the F_1 's from the mid-parental values and considered significant when the dominance effects at various loci are predominantly in one direction. Moreover, there is a directional dominance effect.

The significance of the b_2 part exhibited that the mean dominance deviation of the F_1 's from their mid-parental values varied significantly over the F_1 arrays and these arrays vary if some parents include further dominant alleles than others, implying asymmetry of gene distribution (Hayman, 1954b; Farshadfar *et al.*, 2011b). That is, some parents include greatly dominant alleles than others.

The " b_3 " part tests residual dominance interaction consisted additive \times additive, additive \times dominance and dominance \times dominance interactions that are not due to b_1 and b_2 and is distinct to each F_1 . The b_3 is similar to SCA variance (Singh and Narayanan, 1993). Significant differences were detected for additive ("a") effect for all the evaluated traits in Morley Jones method, Also, dominance ("b") part was significant for all traits (Table 7) accordingly these traits are due to both dominance and additive type of gene actions. As (b_2) and (b_3) were significant for all evaluated traits, thus interallelic interaction (epistasis) is associated with in their genetics. As the part (b_1) was significant for all traits (Table 7), so

dominance effects were due to directional dominance. Significant (b_2) part for all traits showing variance of gene distribution for the traits.

Significant (b_3) part for all traits showed residual dominance effect (b_3) produced from additive \times additive, additive \times dominance and dominance \times dominance interactions (Table 7).

Hayman analysis

Components of variations H_1 and H_2 were significant for the traits which emphasize the being of dominance in the inheritance of all the traits (Table 8), whereas part D was also significant for days to heading, days to maturity, plant height and spikelets /spike, thus simultaneous effect of dominant and additive gene actions associated for these traits. All (H_2) values were less than (H_1) values for all the studied traits, which observe with the theoretical assumption of Hyman (1954a) and could be a further proof for the different proportion of negative and positive alleles in the parents at all loci for the traits, exhibiting different allele frequency.

The part, F was not significant in spite of that, positive for all traits indicating that the distribution of alleles in the parents is unbeknown. The ratio of $(H_1/D)^{1/2}$ is considerable than one for all the studied traits, so, over dominance is associated in the genetic of these traits. The amount of genes with negative and positive effects in the parents were determined as $(H_2/4H_1)$. If negative and positive alleles are the same distributed this ratio equals 0.25.

Table 8. Hayman analysis of variance for the studied traits in the eight –parent diallel crosses of bread wheat

Components of variance	Days to heading	Days to maturity	Plant height	Spikes /plant	Spike length	Spikelets /spike	Kernels/ spike	1000-kernel weight	Grain yield /plant
E	1.175 ^{n.s}	2.35	7.32	0.182	0.42	0.535	10.18	3.76	2.71
D	3.52**	7.07**	21.96**	0.548	1.27	1.606**	30.56	11.30	8.14
F	8.33 ^{n.s}	16.72	51.90	1.296	3.01	3.795	72.22	26.71	19.24
H_1	8.10**	16.27**	50.50**	1.261**	2.93**	3.69**	70.26**	25.99**	18.72**
H_2	7.05**	14.15**	43.93**	1.097**	2.55**	3.212**	61.13**	22.61**	16.28**
$(H_1/D)^{0.5}$	1.09	1.93	2.32	6.77	3.18	1.62	3.088	2.546	9.044
$H_2/4H_1$	0.21	0.20	0.185	0.225	0.21	0.212	0.238	0.190	0.238
r	-0.71	-0.76	0.339	0.315	-0.903	-0.768	-0.419	-0.22	-0.508
R^2	0.50	0.579	0.115	0.099	0.817	0.590	0.175	0.05	0.258
H^2_n	0.68	0.34	0.358	0.181	0.06	0.334	0.249	0.226	0.067
H^2_b	0.96	0.97	0.979	0.958	0.914	0.932	0.951	0.949	0.994

*Significant at the 0.05 probability level and **Significant at the 0.01 probability level.

Determine of the proportion of negative and positive genes ($H_2/4H_1$) in the parents ranged from 0.18 for plant height to 0.23 for kernels /spike and grain yield /plant (Table 6) thus, negative and positive alleles are equal distributed in these traits.

This definite that H_2 was not varied from H_1 in the traits. The variation detected between the genotypes for the

studied traits discover that selection may be successful for the improvement of the traits, however selection effectual is connected the value of heritability (Table 8). High estimate of heritability (greater than 0.5; Stansfield, 2005) for all the studied traits may be clearly for the involvement of little major genes in the government of inheritance of the traits.

Broad-sense heritability were high for all the studied traits, defined that these traits are more genetic, but narrow sense heritability were low for no. of spikes/plant, spike length and grain yield / plant , so the role of additive part is low. These results are in harmony with those recorded by Awaad (2001) , Morad (2001) , Hamada and El-Beailly (2003) and Ezatollah *et al* (2013).

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تقدير بعض المقاييس الوراثية للمحصول ومساهماته في قمح الخبز

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أجريت هذه الدراسة في المزرعة التجريبية لقسم المحاصيل، كلية الزراعة، جامعة الأزهر-مدينة نصر بالقاهرة خلال موسمي ٢٠١٧/٢٠١٦ و٢٠١٧/٢٠١٨ وذلك لدراسة القدرة علي الإنتلاف، قوة الهجين، نوع الفعل الجيني ودرجة التوريث لمجموعة من الهجينة التبادلية بين ثمانية آباء لقمح الخبز وأخذت البيانات علي صفات عدد الأيام حتي طرد السنابل، موعد النضج، طول النبات، عدد السنابل /النبات، طول السنبل، عدد السنبلات/ السنبل، عدد حبوب السنبل، وزن الألف حبة ومحصول حبوب النبات. وقد تم تحليل النتائج وراثياً تبعاً للموديل الأول للطريقة الثانية لجرينج ١٩٥٦ وهامين ١٩٥٤ ومورلي ١٩٦٥. وتتلخص أهم النتائج فيما يلي: أوضح تحليل التباين وجود فروق معنوية عالية في كل الصفات المدروسة بين كل من الآباء والهجن. كان التباين الذي يعود إلي القدرة العامة و القدرة الخاصة علي الإنتلاف معنوياً لجميع الصفات المدروسة ما عدا عدد الحبوب بالسنبل للقدرة العامة علي التآلف، وكانت النسبة بين تباين القدرة العامة وتباين القدرة الخاصة علي الإنتلاف أقل من الواحد لكل الصفات المدروسة وهذه دلالة علي أن الجزء الأكبر من التباين الوراثية المرتبطة بهذه الصفات ترجع إلي الفعل الجيني من النوع غير المضيف أوضحت النتائج أن الأب الرابع والأب الخامس أفضل الآباء المختبرة في محصول حبوب النبات، وكانت أفضل الهجن بين الأب الأول xالأب الثاني، الأب الثاني xالأب الخامس، والأب الثالث xالأب الخامس، الأب الثالث xالأب السادس والأب السادس والأب الخامس xالأب السادس سجلت أعلى القيم لمحصول حبوب النبات. أظهرت كلاً من الأب السادس والأب الثامن قدرة عامة علي الإنتلاف موجبة ومعنوية لصفة محصول حبوب النبات، الأب الأول و الخامس للتبكير ووزن حبة، فيما أظهرت الهجن الأب الأول xالأب السادس، والأب الثاني xالأب السادس، الأب الثالث xالأب السابع، والأب الثالث xالأب الثامن، والأب الرابع xالأب السابع، الرابع xالأب الثامن، الخامس xالأب السادس، الأب الخامس xالأب السابع، والأب السادس xالأب الثامن قدرة خاصة علي الإنتلاف موجبة ومعنوية لصفة محصول حبوب النبات. كان أفضل الهجن علي مستوي القدرة الخاصة علي التآلف وقوة الهجين هي الأب الأول xالأب الثاني، الأب الثالث xالأب الثامن والأب الخامس xالأب السادس حيث أظهرت معنوية عالية للقدرة الخاصة علي الإنتلاف وقوة هجين عالية لمحصول الحبوب / النبات مما يجعلها هجن واعدة في برامج التربية لصفة المحصول. كانت أغلب الصفات المدروسة متأثرة بفعل الجينات المضيفة وغير المضيفة مع تفوق الفعل الجيني السيادة والتفوق وكان التأثير المتنقي للسيادة يعود إلي تفاعل المضيف x المضيف، والمضيف xالسادس والسائد xالسادس. أظهرت كفاءة التوريث بمعناها العريض قيمة مرتفعة لكل الصفات المدروسة ربما يعزى من احتمالية استخدام عدد قليل من الجينات الرئيسية التي تتحكم في توارث هذه الصفات، بينما أظهرت كفاءة التوريث بمعناها الضيق قيمة عالية إلي متوسطة فيما كانت منخفضة لصفات عدد السنابل / النبات، طول السنبل و محصول حبوب النبات مما يؤكد محدودية الفعل الجيني من النوع المضيف في توارث هذه الصفات.