J. of Plant Production, Mansoura Univ., Vol. 13 (8):549 - 553, 2022

Journal of Plant Production

Journal homepage & Available online at: www.jpp.journals.ekb.eg

Genetic Parameters Estimation for Yield and its Components in Two Bread Wheat Crosses by Using Six Populations Model

Cross Mark

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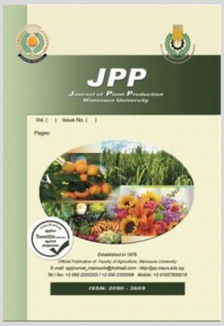

ABSTRACT

This research aims to determine the types of gene action that control yield and its components in two crosses of bread wheat so that wheat breeders can select the most appropriate breeding approaches. The six-generation model is the best model for estimating the additivity of genes and deviations from additivity, including epistasis. Therefore, this research was done at Sids Agricultural Research Station, ICARC-WIP Project, throughout the three growing seasons, 2018/2019, 2019/2020, and 2020/2021, to determine heterosis, gene action, and mean performances, as well as inbreeding depression for grain yield and yield components. In addition, six populations (for the two crosses were produced from Gemmeiza 12 × Sids 14 and Misr 3 × Misr 1. Six parameters were estimated. In both crosses, the mean effects for all investigated characteristics are extremely substantial, demonstrating that these traits are quantitatively inherited. In the 1st cross, inbreeding depression was found to be signifcant and positive for all characteristics, except for the 100-kernel weight. In the two crosses, potency ratio values were more than unity for number of grain spike^{-1}. The possibility of developing hybrid cultivars for plant breeders was examined in self-pollinated crops, such as bread wheat. Therefore, the exploitation of heterosis in various crops in the world has substantially increased human food or livestock feed production.

Keywords: Inbreeding depression, Gene action, Heterosis, Triticum aestivum L.

INTRODUCTION

Bread wheat is considered the most economically significant cereal crop globally (Hussain *et al*., 2021). Wheat trade represents an essential component of the economy's trade balance. Wheat is used and processed in many products, demonstrating its importance for the large quantities produced by humankind from diverse social groups and cultures (Faridi and Faubion 1995). It is essential to provide food to all people around the world, and wheat is known as the king grain crop of the world.

The overall cultivated area for wheat in Egypt is projected to be 1.4 million hectares, while the total production was about 8.9 million tons. In addition, Egypt is also the world's largest consumer and a wheat importer (FAO 2020). Bread wheat grain yield is a complicated trait comprised of three components: kernel weight, kernel number per spike, and spike number per square meter; hence, the direct selection is ineffective (Sharma, 1994).

Wheat breeders are interested in assessing the relative amount of genetic variation and the genetic labor required for the manifestation of traits. Therefore, they need more detailed information about genetic influences dominance mean degree, heterogeneity, and yield inbreeding depression as well as its components. Several researchers investigated the type of genetic effect in bread wheat and demonstrated that the dominance impact was relatively more significant compared to the additive impact in yield, while the additive genetic effect was dominant in terms of plant height and days to heading (Hendawy 2003 and Moussa 2010).

The wheat breeder's strategy is based on gene action, including additive, dominance, and epistasis (none-allelic interactions). Generation means analysis is a method for determining the optimal breeding strategy for developing wheat cultivars with desirable traits and is often utilized to comprehend quantitative trait inheritance. Knowledge of the level of heterosis and inbreeding depression plays a crucial role in the selection of breeding techniques (Novoselovic *et al.* 2004 and Zaazaa *et al.* 2012).

The grain yield of bread and durum wheat is a multi-component feature based on more than one component: kernels spike^{-1} number, spikes m^{-2} number, and kernels weight. Therefore, the direct selection is not efficient (Sharma, 1994). The potential of the wheat crop can be enhanced via indirect selection for yield components; the increase in one of the component characters may contain a negative or positive influence on other contributing characters (Chandra *et al.*, 2004).

Join the mean generation analysis biometric methods by phenotype performance metrics for various quantitative traits of different breeding populations: parents, F$_1$, F$_2$, and backcrosses (Gamble, 1962).

The purpose of this study is to a) study gene action, genetic advance, the average degree of dominance, inbreeding depression, and grain yield heterosis as well as its components in two bread wheat crosses via generation mean analysis of six populations.

b) estimate the types of gene effects that impact yield as well as its components in two bread wheat cross to help wheat producers to choose the most appropriate breeding strategies.

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DOI: 10.21608/jpp.2022.149334.1140

MATERIALS AND METHODS

This research was performed at Sids Agricultural Research Station, ICARC-WIP Project, Agricultural Research Center (ARC) during the three growing seasons of 2018/2019, 2019/2020, and 2020/2021. Four bread wheat genotypes were used as parental lines. Parents' commercial names and pedigree are displayed in Table 1.

Table 1. The commercial names and pedigree of the four parents of bread wheat cultivars.

Cross	parent	Pedigree
Cross I	P_1 Gemmeiza 12	OTUS/3/SARA/THB//VEE
	P_2 Sids 14	SW8488*2/KUKUNA.
Cross II	P_3 Misr 3	Rohf 07*2/Kiriti
	P_4 Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR.

Two crossings between the parents were performed in the first growing season of 2018/2019 to obtain F_1 hybrid grains. The two crosses were P_1xP_2 (cross 1) and P_3 x P_4 (Cross 2). Some F_1 plants from each cross were backcrossed during the 2019/2020 season to generate the backcrosses (BC_1 and BC_2). Some F_1 plants were selfed for the production of F_2 grains, and crosses between parents were again made for obtaining sufficient F_1 seeds. In 2020/2021, the six population seeds, i.e., P_1, P_2, BC_1, BC_2 F_1, and F_2 of the two crosses, were seeded with three replications following a randomized block design. Each plot consisted of 30 rows, i.e., two for each of F_1, P_1, and P_2, and eight for BC_1, BC_2 and F_2. The rows were 1.5m long, 30cm apart, and seeds were spaced 10 cm within rows.

For the examined traits, grain yield plant^{-1}(g) and yield components, data were collected from 20 individual guarded plants for F_1, P_1, and P_2 and 60 plants for each of BC_2 or BC_1 and 60 plants for F_2 in each replication. In each growing season, all suggested field techniques for bread wheat production were implemented.

Recommended fertilization was applied as 65 kg P_2O_5 ha^{-1} during preparation and 170 kg Nitrogen ha^{-1} as Ammonia injection in the soil after final land preparation and before sowing. Six irrigations were applied for normal watering at 20 days intervals.

Broadleaf weeds were controlled by spraying the herbicide Derby 175% SC after 30 days of planting.

Statistical and genetic analysis

Scaling tests (A, B, and C), according to Mather (1949) and Hayman and Mather (1955) were used to test for the existence of nonallelic interactions:

$$A = 2\,BC_1 - P_1 - F_1 \quad VA = 4V(BC_1) + V(P_1) + V(F_1)$$

$$B = 2\,BC_2 - P_2 - F_1 \quad VB = 4V(BC_2) + V(P_2) + V(F_1)$$

$$C = 4F_2 - 2F_1 - P_1 - P_2 \quad VC = 16V(F_2) + 4V(F_1) + V(P_1) + V(P_2)$$

Using Gamble's (1962) method, Jinks and Jones (1958) and Hayman (1958) presented a six-parameter model for calculating different genetic components:

$$m = \bar{F}_2$$

$$a = \bar{Bc}_1 - \bar{Bc}_2$$

$$d = \bar{F}_1 - 4\,\bar{F}_2 + 2\,\bar{Bc}_1 + 2\,\bar{Bc}_2 - \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2$$

$$aa = -4\,\bar{F}_2 + 2\,\bar{Bc}_1 + 2\,\bar{Bc}_2$$

$$ad = -\frac{1}{2}\bar{P}_1 + \frac{1}{2}\bar{P}_2 + \bar{Bc}_1\,1 - \bar{Bc}_2$$

$$dd = \bar{p}_1 + \bar{p}_2 + 2\,\bar{F}_1 + 4\,\bar{F}_2 - 4\,\bar{Bc}_1 - 4\,\bar{Bc}_2$$

Where:

m= mean effect
a = additive gene effect
d= dominance gene effect.
aa= additive × additive type of gene interaction.
ad= additive × dominance type of gene interaction.
dd= dominance × dominance type of gene interaction.

P_1 and P_2 were considered in this research as the larger and smaller parent, respectively. Also, BC_1 and BC_2 were considered P_1× F_1 and P_2× F_1, respectively.

The following variance formulae were used.

$$Vm = V\,\bar{F}_2$$

$$Va = V\,\bar{Bc}_1 + V\,\bar{Bc}_2$$

$$Vd = V\,\bar{F}_1 + 16V\,\bar{F}_2 +$$

$$4V\,\bar{Bc}_1\,1 + 4V\,\bar{Bc}_2 + \frac{1}{4}V\,\bar{P}_1 + \frac{1}{4}V\,\bar{P}_2$$

$$Vaa = 16V\,\bar{F}_2 + 4V\,\bar{Bc}_1 + 4V\,\bar{Bc}_2$$

$$Vad = \frac{1}{4}V\,\bar{P}_1 + \frac{1}{4}V\,\bar{P}_2 + V\,\bar{Bc}_1 + V\,\bar{Bc}_2$$

$$Vdd = V\,\bar{p}_1 + V\,\bar{p}_2 + 4V\,\bar{F}_1 + 16V$$

$$\bar{F}_2 + 16V\,\bar{Bc}_1 + 16\,\bar{Bc}_2$$

Fonseca and Patterson (1968) defined heterosis as the divergence of the first generation from a better parent or the mid-parents. According to Falconer's equation, inbreeding depression (ID percent) was calculated as the mean percentage decline in F_2 from the F_1. The predicted genetic advance under selection (Δg) was estimated based on Johnson *et al*. (1955). The potence ratio (PR%) was estimated by the formula obtained by Griffing (1950). The expected gain represented as a percentage of F_2 mean (Δg %) was determined according to Miller *et al.* (1958).

RESULTS AND DISCUSSION

Mean Performance

Means of the six populations of the two bread wheat crosses for yield, and its component are presented in Table 2. The results revealed substantial variations among all six populations, indicating the presence of genetic variability for these characters in the studied materials. In the first cross, the F_1 mean value surpassed the mean values of the two parental means for grain yield per plant and yield components compared with the two parents except for 100-kernels weight. The BC1 mean values were higher than the BC_2 population in the two crosses for all the studied traits except 100-kernel weight.

In the second cross, the mean F1 values overtopped the parental mean values of plant-1 grain yield and its components compared to the two parents, except BC1, resulting in the most significant number of grain spike-1 (70.88). The BC1 mean values were higher than the BC2 population in the two crosses for all the investigated traits.

These findings are compatible with those of Abd El-Hamid and Ghareeb. (2018), Abdallah *et al.* (2019), Shehab-Eldeen *et al.* (2020), Mohamed *et al.* (2021), and Mohamed *et al.* (2022).

Table 2. Mean performance of the six generations for all the studied characters in the two studied crosses.

Crosses	Traits generation	Number of spike Plant^{-1}	Number of grain Spiket^{-1}	100-Kernel weight (g)	Grain yield plant^{-1} (g)
Cross 1	P1	24.10	61.35	4.50	46.42
	P2	23.43	62.75	3.57	44.05
	F1	27.85	74.55	4.42	47.16
	F2	22.57	57.38	4.11	32.70
	BC1	20.73	62.47	4.09	32.45
	BC2	17.70	56.40	4.28	31.03
	LSD$_{0.05}$	3.57	6.80	0.79	8.04
	LSD$_{0.01}$	5.60	10.63	1.53	12.61
Cross II	P1	19.80	61.85	4.17	42.35
	P2	21.63	60.98	4.21	35.26
	F1	24.22	67.58	4.68	54.08
	F2	17.24	58.27	3.69	27.40
	BC1	16.38	70.88	4.36	27.76
	BC2	13.99	64.41	4.36	23.17
	LSD$_{0.05}$	3.92	4.85	0.34	12.13
	LSD$_{0.01}$	6.14	7.61	0.54	19.03

Gene Effects and scaling test

Utilizing the six-parameter model, the type of gene activity was estimated. The six calculated parameters are depicted in Table 3. All crossings' mean effects for all investigated features were highly significant, demonstrating that these traits are quantitatively inherited. In comparison to the dominant gene effects, the additive gene impact was relatively weak.

The results indicated that these additive gene effects were positive and substantial for No. of tillers plant^{-1} and the number of grains spike^{-1} for the two crosses, while grain yield plant^{-1} was significantly positive in the 2nd cross. These results indicated that pedigree selection might improve these traits (Hendawy 2003, Khaled 2013, Al-Bakry *et al.* 2017, Abd El-Hamid and Ghareeb. 2018, Shehab-Eldeen *et al.* 2020 and Mohamed. M. Mohamed *et al.* 2021).

In self-pollinating crops, including bread wheat, the wheat breeder usually aims to isolate parental combinations that are likely to produce desirable homozygous segregates. The interest in attempts to identify such pure lines is facilitated by prevails of additive genetic effects in autogamous crops (Joshi and Dhawan 1966).

The estimates of dominance effects were significantly negative for No. of spikes plant^{-1} in the first cross. In addition, the estimates of dominance were highly significant as well as positive for grains number spike^{-1} and the weight of 100-kernel in the 2nd cross, demonstrating that dominant genetic effects play a role in the transmission of these characteristics and that selection may be applied to late segregating generations, aligning with the findings of Novoselovic *et al.* (2004), Zaazaa *et al.* (2012), El-Areed *et al.* (2018), Abd El-Kreem (2019), and Feltaous (2020).

Conversely, the relevance of additive and dominance components indicated that both dominance and additive gene effects contribute to the heritability of these characters. Furthermore, choosing desired traits can be anticipated in early generations but will be more efficient in later generations, which is compatible with Hendawy (2003), Moussa (2010), Khaled (2013), El-Areed *et al.* (2018), Abdallah *et al.* (2019), and Salmi *et al.* (2019).

Estimates of epistatic gene effects are presented in Table 3. Substantial estimation of epistatic gene effects for one or more of these three kinds of epistatic gene effects was detected in the two crosses for all studied characters. Additive x additive (aa) gene effects were positive and highly substantial in grains number spike^{-1} and the weight of 100-kernel for the 2nd cross. Early generation selection for these traits can be efficient for the breeding program. Meanwhile, aa was negative and highly significant in spikes number plant^{-1} in the 1st cross and significant in the 2nd cross, which aligns with Elmassry *et al.* (2020), Waleed (2020), and Mohamed *et al.* (2022).

The data of epistatic gene effects, additive x dominance (ad), revealed an insignificant effect in the two crosses. Furthermore, the dominance x dominance (dd) gene effects differed among crosses and characters. Positive and highly significant dd estimates existed in the two crosses for grain yield plant^{-1} and spike plant^{-1} in the two crosses and the number of grain spike-1 in the first cross. However, the number of grains spike-1 number and 100-kernel weight was negative and highly significant in the second cross. This study further revealed that these characters' epistatic gene effects were as crucial as dominance and additive gene effects. Consequently, the system of inbreeding employed in the utilization of any character relies on the gene action involved in its expression for predicted gain in selection progress (Khaled 2013 and Yasser 2019).

Table 3. Scaling test and gene effects for all the studied characters in the two crosses.

Traits	Cross	Scaling test			Gene action six parameters (Gamble procedure)					
					Main effect	Additive	Dominance	Add. X Add.	Add. X Dom.	Dom.x Dom.
		A	B	C	(m)	(a)	(d)	(aa)	(ad)	(dd)
No. Of spikes plant^{-1}	I	-10.49**	-15.88**	-12.94**	22.57**	3.03**	-9.35*	-13.43**	2.7	39.81**
	II	-11.25**	-17.87**	-20.93**	17.24**	2.40*	-4.7	-8.20*	3.31	37.33**
No. Of grains spike^{-1}	I	-10.96*	-24.50**	-43.66**	57.38**	6.07*	20.7	8.2	6.77	27.26**
	II	12.33**	0.240	-24.93**	58.27**	6.48**	43.68**	37.51**	6.04	-50.09**
100-kernel weight	I	-0.75*	0.57	-0.48	4.11**	-0.2	0.69	0.3	-0.66	-0.13
	II	-0.120	-0.16	-2.98**	3.69**	0	3.19**	2.70**	0.02	-2.42**
Grain yield plant^{-1}	I	-28.68**	-29.16**	-54.01**	32.70**	1.43	-1.9	-3.82	0.24	61.66**
	II	-40.91**	-43.00**	-76.17**	27.40**	4.59*	7.53	-7.75	1.04	91.66**

Heterosis estimates:

The possibility of developing hybrid cultivars for plant breeders was examined in self-pollinated crops, such as bread wheat. Therefore, the exploitation of heterosis in various crops in the world has substantially increased human food or livestock feed production. Heterosis can be exploited to increase yields in cross-pollinated crops compared to self-pollinated crops, but there is now some evidence confirming the existence of heterosis in self-pollinating crops such as wheat (Sohan *et al*., 2020).

Tables 4 and 5 presented the heterotic effects, which were calculated as a percentage related to better parents and mid-parent for investigated traits in the two crosses. In the first cross, a highly significant and positive heterotic effect was found for grains number per spike, and substantial positive heterotic effects were found for spike number plant^{-1}.

In the second cross for mid-parent heterosis, significant as well as highly significant positive heterotic effects were detected for all characters in the study. Also, for better parent heterosis, significant, highly significant, as well as a positive heterotic effect was detected for all the examined traits. Sharshar and Genedy (2020) reported that significant positive heterosis relative to better and mid-parent was obtained for yield components as well as grain yield.

Inbreeding depression

Inbreeding depression (ID) could be defined as the reduction of values of characters from F_1 to F_2 generations. This reduction may be due to the change of genetic constitution and decrease of heterozygosity due to inbreeding. The results of inbreeding depression are depicted in Tables 4 and 5. Positive and highly substantial ID existed for all studied characters except 100-kernel weight in the first cross, which is consistent with El-Areed *et al*. (2018) and Mohamed *et al*. (2022).

Table 4. Heterosis, inbreeding depression (ID), genetic advance, and PR% of the mean for all the studied traits in the first cross.

Parameters	Grain yield plant^{-1}	100-Kernel weight	Number of spike Plant	Number of grain spike
heterosis MP%	4.25	9.60	17.18*	20.15**
heterosis BP%	1.59	-1.80	15.56*	18.81**
Inbreeding depression	30.67**	7.10	18.95**	23.03**
P. Ratio	-1.62	-0.83	-12.24	17.86
Δg	10.25	3.17	6.87	10.89
Δg%	31.35	77.13	30.42	18.97

Table 5. Heterosis, inbreeding depression (ID), genetic advance, and PR% of the mean for all the studied traits in the second cross.

Parameters	Grain yield plant^{-1}	100-Kernel weight	Number of spike Plant	Number of grain spike
heterosis MP%	39.36**	11.69*	16.89*	10.04*
heterosis BP%	27.69**	11.19**	11.94*	9.27*
Inbreeding depression	49.33**	21.18**	28.82**	13.78**
P. Ratio	-4.31	-25.86	-3.82	14.21
Δg	13.04	0.69	4.44	11.54
Δg%	47.57	18.70	25.76	19.81

Genetic advance:

The results of the current research indicated that the predicted genetic gain(Δ g) varied between 10.89 to 11.54 for the number of spikes plant^{-1}, 4.44 to 6.87 for the number of kernels spike^{-1}, 0.69 to 3.17 for 100-kernel weight, and from 10.25 to 13.25 for grain yield plant^{-1} (Tables 4 and 5). Therefore, it might be emphasized that such crossings are vital to the wheat breeding program for genetic yield progression.

Potence ratio:

In two crosses, PR% values were more than unity for grain number spike^{-1} in the two crosses. When the PR% values were more than unity, this indicated that dominance was influential in inheriting these traits. Nevertheless, the PR% value was less than unity, indicating that partial dominance controls this character. The results are consistent with those obtained by Mann and Sharma (1995), Al-Kaddoussi (1996), Hagras (1999), Awaad (2002), and Sharshar and Genedy (2020).

CONCLUSION

We can conclude that the selection for yield and yield components should be delayed to the subsequent (late) segregating generation when the dominant influence wanes. In self-pollinating crops, such as bread wheat, the wheat breeder usually aims to isolate parental combinations that are likely to produce desirable homozygous segregates. The interest in attempts to identify such pure lines is facilitated by the prevailing additive genetic effects in autogamous crops.

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تقدير المعالم الوراثية للمحصول ومكوناته في هجينين من قمح الخبز باستخدام نموذج العشائر الستة عشائر

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الملخص

أجريت الدراسة في محطة البحوث الزراعية بسدس ، مشروع تحسين القمح ايكاردا , مركز البحوث الزراعية خلال الثلاثة مواسم زراعية ٢٠١٩/٢٠١٨ و٢٠٢٠/٢٠١٩ و ٢٠٢١/٢٠٢٠. وذلك لدراسة الأداء والفعل الجيني بالإضافة إلى قوة الهجين والنقص الناتج عن التربية الداخلية ومتوسط درجة السيادة لصفات المحصول ومكوناته لهجينين من قمح الخبز. بهدف تقدير نوع التأثيرات الجينية التي تتحكم في المحصول ومكوناته في هجينين من القمح الخبز لتمكين مربي القمح من اختيار طرق التربية المناسبة. تم استخدام ستة عشائر (الأب الأول و الأب الثانى والجيل الأول و جيل التهجين الرجعى للأب الأول و جيل التهجين الرجعى للأب الثانى والجيل الثانى) من الهجينين. وقد تم تقدير التأثير المضيف ، والسيادي ، و المضيف × المضيف ، و المضيف × السيادي ، والسيادي × السيادي. بالنسبة للنقص الناتج عن التربية الداخلية كان عالي المعنوية لجميع الصفات وأعطت قيم موجبة. أظهرت قوة الهجين لصفه محصول الحبوب للنبات و مكوناته بالنسبه لمتوسط الأبوين قيم موجبه وعاليه المعنويه للهجين الثاني, بالنسبة للتدهور الناتج عن التربية الداخلية كانت النتائج عالية المعنوية ماعدا صفة وزن ١٠٠ حبة في الهجين الاول.