



Genetic parameters estimation for grain yield in two bread wheat crosses (*Triticum aestivum* L.) under Upper Egypt conditions.

Mohiy, M., * I.S.M. Abdellatif and Shaimaa E. Ibrahim

Wheat Research Department, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt.

Abstract

The main objective of this investigation was to study gene effects by the analysis generation means for grain yield and its components characters in two bread wheat crosses, (Sids1 x Giza171) and (Shandaweel1 x Sakha94). Randomize complete block design with three replications was used for P₁, P₂, F₁, F₂, BC₁, and BC₂ during 2018/2019, 2019/2020 and 2020/2021 growing seasons. The measurements of gene effect and non-allelic interaction in addition to heterosis, inbreeding depression and heritability of grain yield and yield components in bread wheat were estimated. Scaling test showed significant effect for almost characters in both crosses. The additive (d) gene effect was positive and highly significant for number of kernels/spike and grain yield/plant for the first cross and positive significant with 100-kernel weight in the second cross, but negative significant with first cross. Estimates of dominance (h) effects were highly significant for number of spikes/plant and number of kernels/spike in second cross. Better parent heterobeltiosis, significant and highly significant heterobeltiotic effect positive was found between crosses for grain yield in two crosses and number of kernel/spike for the second cross. Results of inbreeding depression were highly significant positive for all the study traits. Broad sense heritability values ranged from 45.15 to 88.01% for all studied characters in both crosses.

Keywords: Bread wheat; Genetic action; Generation mean analysis; Heterosis; Heritability.

1. Introduction

Genetic improvement of wheat grain yield is one of the most important steps to overcome other problems that we cannot improve, such as climate change. The importance of availability for wheat means the availability of food security for most countries of the world, especially developing countries, as it is considered one of the most important sources of food for many citizens in the world. (Hossain *et al.*, 2021). Plant breeders are focusing to enhance wheat yield potential by releasing new cultivars with eligible genetic structure to overcome ever-increasing population globally. (Memon *et al.*, 2007).

In Egypt wheat total cultivated area is estimated at 1.4 million hectare, while the total production amounted to approximately 8.9

million tons, also Egypt is the largest importer and consumer of wheat in the world (FAO, 2020). Bread wheat grain yield is a complex trait builds on three components: number of spikes/m², number of kernels/spike and kernels weight, hence, the direct selection is not efficient (Sharma, 1994). Wheat yield potential can be improve via the indirect selection for its components, the Increasing in one of component characters might have negative or positive impact on other contributing characters (Chandra *et al.*, 2004).

The mean generation analysis accede to the biometric methods according to phenotypic performances measurements for different quantitative characters of various breeding population: Parents, F₁, backcrosses (BC) and segregation generations (Gamble, 1962).

In addition to gene effects, the breeders want to know how much of amount of genetic variation in the crop and to what degree this variance is heritable, because the selection

*Corresponding author: Mohamed Mohiy,

Email: Mohamed.mohiy@yahoo.com

Received: November 17, 2021; Accepted: December 9, 2021; Published online: December 19, 2021.

©Published by South Valley University.

This is an open access article licensed under

efficiency mainly depends on additive genetic variance effect of environment and the interaction between environment and genotype (Novoselovic *et al.*, 2004). The present study was carried out to study gene action nature, heterosis, heritability and inbreeding effect for grain yield and its components in two bread wheat crosses under heat stress.

2. Materials and methods

2.1. Site, plant material and experimental design

A field experiment was carried out at Almatana agricultural Research Station, ARC, Egypt, during the three successive growing seasons, i.e. 2018/2019, 2019/2020 and 2020/2021. Four local of bread wheat cultivars were chosen as parents in this study are showed in (Table 1).

Table 1. Pedigree, history and origin of the four parents of bread wheat cultivars.

Cross	Parents	Pedigree and history	Origin
Cross I	(P ₁) Sids1	HD 2172 / Pavon "S" // 1158.57/ Maya 74 "S" Sd 46-4Sd-2Sd-1Sd-0Sd	Egypt
	(P ₂) Giza171	SAKHA 93/GEMMEIZA 9 Gz 2003-101-1Gz-4Gz-1Gz-2Gz- 0Gz.	Egypt
	(P ₃) Shandaweel1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH	Egypt
Cross II	(P ₄) Sakha94	OPATA/RAYON//KAUZ CMBW90Y3180-0TOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.	Egypt

In (2018/2019) growing season, parents were intercrossed to produce the two F₁ crosses. The crosses were assigned as follows: Cross I (Sids1 x Giza171) and Cross II (Shandaweel1 x Sakha94). In 2019/2020 growing season, a part of seed obtained from each parent and the F₁ seeds were sown. Each one (F₁-hybrid) was crossed with its two respective parents to produce backcrosses (BC₁ and BC₂). In the last growing season (2020/2021), the six populations, P₁, P₂, F₁, F₂, BC₁ and BC₂ for each cross were planted in a randomized complete blocks design (RCBD) with three replications.

2.2 Data collection

Each replication included 60 plants in two rows for parents and F₁; 120 plants in four rows for each backcross and consisted of 240 plants in eight rows for the F₂-generation. Each Row was 3 m long and 10 cm was the distance between plants and 30 cm between rows. Data were collected on 30 plants for parents and F₁; 80 plants for BC₁ and BC₂ and 160 plants for F₂. The recommended practices of wheat production were followed throughout the three

growing seasons. The studied characters were number of spikes per plant, number of kernels per spike, 100-kernel weight (g) and grain yield per plant (g).

2.3. Statistical analysis methods

The A, B, C and D scaling tests as outlined by (Mather, 1949) was applied to test presence non-allelic interactions as follows:

$$A = 2 \frac{\overline{BC_1} - \overline{P_1} - \overline{F_1}}{2}$$

$$VA = 4 V (BC_1) + V (P_1) + V (F_1)$$

$$B = 2 \frac{\overline{BC_2} - \overline{P_2} - \overline{F_1}}{2}$$

$$VB = 4 V (BC_2) + V (P_2) + V (F_1)$$

$$C = 4 \frac{\overline{F_2} - 2 \overline{F_1} - \overline{P_1} - \overline{P_2}}{2}$$

$$VC = 16 V (F_2) + 4V (F_1) + V (P_1) + V (P_2)$$

$$D = 2 \frac{\overline{F_2} - \overline{BC_1} - \overline{BC_2}}{2}$$

$$VD = 4 V (F_2) + V (BC_1) + V (BC_2)$$

In the case of non-allelic interaction, the analysis was continued to calculate the interaction types implicated using six-parameter genetic model according to (Jinks and jones, 1958) as follows:

$$m = \text{Mean of } \overline{F_2}$$

$$d = \text{Additive effect} = \overline{BC_1} - \overline{BC_2}$$

$h = \text{Dominance effect} = \overline{F_1} - 4\overline{F_2} - (1/2)\overline{P_1} - (1/2)\overline{P_2} + 2\overline{BC_1} + 2\overline{BC_2}$.

$i = \text{Additive} \times \text{Additive} = 2\overline{BC_1} + 2\overline{BC_2} - 4\overline{F_2}$

$j = \text{Additive} \times \text{Dominance} = \overline{BC_1} - 1/2\overline{P_1} - \overline{BC_2} + 1/2\overline{P_2}$.

$I = \text{Dominance} \times \text{Dominance} = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{BC_1} - 4\overline{BC_2}$

Estimation of heterosis and heterobeltiosis:

The increasing or decreasing of F_1 hybrids for mid-parents and better-parent was computed for the studied characters by (Fonseca and Patterson, 1968) as follows:

$Ht\% = (\overline{F_1} - \overline{MP}) / \overline{MP} \times 100$ and $Hbt\% = (\overline{F_1} - \overline{BP}) / \overline{BP} \times 100$ where:

Ht= Heterosis; Hbt= Heterobeltiosis; MP= mid parent and BP= better parent.

Estimation of inbreeding depression:

Inbreeding depression was calculated the procedure of (Singh and Narayanan, 1993). Inbreeding depression (ID) = $(\overline{F_1} - \overline{F_2}) / \overline{F_1} \times 100$.

2.4. Estimation of heritability

Heritability (h^2) in broad and narrow sense was estimated according to (Falconer, 1989) using eq.

$h^2_{\text{broad sense}} = (1/2D + 1/2H_1 - 1/2H_2 - 1/2F) / (1/2D + 1/2H_1 - 1/2H_2 - 1/2F + E)$

$h^2_{\text{narrow sense}} = (1/2D + 1/2H_1 - 1/2H_2 - 1/2F) / (1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E)$,

where:

D= Additive effects variation.

H_1 = dominance effects variation.

H_2 = Component of variation increment of all segregating genes.

F= Relative frequencies of dominant vs recessive genes in the parents.

E= Expected environmental component of variation.

3. Results and discussions

3.1. Mean Performances

Average of the studied characters for parents, F_1 , F_2 , and back-crosses populations of the two bread wheat crosses are given in (Table 2). Means of the generations for the studied traits of the two bread wheat crosses had significant differences between all the six generations. Values mean of F_1 generation were higher than the parents for all the studied traits in the two crosses. The outperformance of F_1 generation over parents for mean was also reported by (Zaazaa *et al.*, 2012). Results of BC_1 mean values were higher than BC_2 population in the two crosses for all the studied traits except 100-kernel weight in cross I and No. of kernels/spike in cross II.

Table 2. Mean and standard error (\pm SE) of the six populations for all the studied traits in the two bread wheat crosses.

Crosses	Generations	No. spikes /plant	No. kernels /spike	100-kernel weight (g)	GY /plant (g)
Cross I	P ₁	21.37 \pm 0.63	59.58 \pm 1.58	5.05 \pm 0.12	43.67 \pm 1.26
	P ₂	25.15 \pm 0.65	66.03 \pm 1.47	5.01 \pm 0.09	45.52 \pm 1.37
	F ₁	26.93 \pm 0.68	70.13 \pm 1.97	5.06 \pm 0.11	50.05 \pm 1.02
	F ₂	22.17 \pm 0.91	62.38 \pm 1.75	4.05 \pm 0.12	30.23 \pm 2.04
	BC ₁	20.96 \pm 0.74	64.90 \pm 1.39	4.04 \pm 0.10	32.79 \pm 1.62
	BC ₂	19.96 \pm 0.72	50.32 \pm 1.61	4.07 \pm 0.09	24.62 \pm 1.51
Cross II	P ₁	17.60 \pm 0.80	62.98 \pm 1.51	4.07 \pm 0.13	43.19 \pm 1.51
	P ₂	20.73 \pm 0.73	56.48 \pm 1.56	4.07 \pm 0.10	37.89 \pm 1.87
	F ₁	22.51 \pm 0.68	68.93 \pm 1.58	4.09 \pm 0.11	52.74 \pm 2.25
	F ₂	10.49 \pm 0.57	61.77 \pm 1.60	4.06 \pm 0.11	28.28 \pm 1.94
	BC ₁	14.48 \pm 0.56	65.73 \pm 1.65	4.04 \pm 0.09	29.34 \pm 1.54
	BC ₂	13.33 \pm 0.45	66.94 \pm 1.42	4.01 \pm 0.10	28.83 \pm 1.80

3.2. Gene Effects

Improving many traits simultaneously as grain yield and its components, it is necessary to estimate the amount of the genetic variability and the nature of gene action to express about these traits (Khaled, 2013). analysis of mean generations is a useful and effective method for the estimates of gene effects, i.e. additive, dominance and binary gene interactions additive x dominance, additive x additive and dominance x dominance. Thus, it is possible to choose the most appropriate breeding methods. (Dvojković *et al.*, 2010). For example, selection is the appropriate method for improving in the case the additive gene effects are high. Conversely, evolving the hybrid varieties can enhance the traits once the dominance gene effects are high.

Joint scaling test was used to determine significant Add. (d), Dom. (h) and interactions inclusive of Add. × Add. (i), Add × Dom. (j) and Dom. × Dom. (l) effects for the studied traits (Table 3). The values of mean effects were highly significant for all recorded traits in the two crosses. Results indicated that additive (d) gene effects were positive and highly significant for No. of kernels/spike and grain yield/plant in cross II and positive significant for 100-kernel weight in cross II, but negative significant in cross I. These results indicated that using the pedigree selection method may be increases the chance of improvement of these

traits (Hendawy, 2003; Khaled, 2013; Manel *et al.*, 2019).

Estimates of dominance (h) effects were highly significant for No. of spikes/plant and No. of kernels/spike in cross II. dominance (h) effects were higher than additive (d) effects for all recorded characters in the two crosses referring predominant role of dominant gene action in controlling for these traits inheritance, therefore, these traits selection ought belated to later generations when dominance effect is reduced. Similar results obtained by Feltaous (2020) and Ataei *et al.* (2017).

The two crosses were detected. Add. x Add. (i) gene effects and was highly significant and positive for No. of spike/plant in cross II, also positive and significant for No. of kernels/spike in cross II. Meanwhile, it was negative and significant in case of No. of kernels/spike in cross I and 100-kernels weight in cross II.

Also, the dominance x dominance (l) gene effect differed according to crosses and characters, positive and highly significant estimates for all recorded characters in both crosses under study except No. of spikes/plant for cross II was negative and highly significant. The results found that epistatic gene effects were as essential as Add. (d) and Dom. (h) gene effects for most of the traits. Thus, the system of inbreeding employed in exploiting any trait relies on the gene action implicated in its expression for predicted gain in selection progress (Manel *et al.*, 2019).

Table 3. Genetic parameter estimation for the all studied characters in the two bread wheat crosses.

characters	Crosses	Main effect	Add.	Dom.	Add. x Add.	Add. x Dom.	Dom. x Dom.
		(m)	(d)	(h)	(i)	(j)	(l)
No. spikes	I	22.17**	1.00	-3.14	-6.82	2.89	25.35**
/plant	II	10.49**	1.15	17.00**	13.66**	2.72	14.06**
No. kernels	I	62.38**	14.59**	-11.77	-19.09*	17.81	54.53**
/spike	II	61.77**	-1.21	28.69**	18.29*	-4.46	-23.91**
100-kernel	I	4.48**	-0.30*	0.60	0.27	-0.48	3.36**
weight (g)	II	4.57**	0.31*	-0.93	-1.17*	0.28	3.30**
GY	I	30.23**	8.17**	-0.63	-6.09	9.10	80.56**
/plant (g)	II	28.28**	0.51	15.43	3.22	-2.15	67.00**

3.3. Heterosis and heterobeltiosis

Heterosis can be exploited to increase yield in cross-pollinated crops than in self-pollinated crops, but now there are some evidences that confirm the existence of heterosis in self-pollinated crops such as wheat (Sohan *et al.*, 2020).

High or low productivity and hybrids vigor as opposed to their parents is owing to heterotic effects in F_1 and the following generations. Regarding to the hybrids which have high heterotic effects can give best opportunities for detection of desirable pure lines in the advanced generations as compared to hybrids with low heterotic (Farshadfar *et al.*, 2001). Thus, it is possible to benefit from this phenomenon (heterosis) commercially to obtain the highest yield from this crop per unit area.

Heterotic effects calculated as percentage over mid parents for all the studied traits in both crosses (Fig 1 and 2). Significant and highly significant heterotic effect positive was found between crosses for all studied characters except 100-kernels weight in cross II. These results are in line with those by (Sohan *et al.*, 2020).

For better parent heterobeltiosis, significant and highly significant heterobeltiotic effect positive was found between crosses for grain yield in two crosses and No. of kernels/spike in cross II. (Sharshar and Genedy, 2020), found that significant positive heterosis and heterobeltiosis were obtained for No. of spikes/plant, 100-kernel weight and grain yield/plant.

3.4. Inbreeding depression

Estimation of inbreeding depression in wheat is an essential instrument in interpreting genetic effects, it has an important role for plant breeders in choosing the proper breeding

method. The inbreeding depression calculated as decrease in performance of the F_2 generation compared to the F_1 generation (Ashwani *et al.*, 2018). The results of inbreeding depression estimation for all the studied traits in cross I and cross II are presented in Fig 1 and Fig 2, respectively. Inbreeding depression values ranged from low to high for the studied traits in both crosses and were 11.1% for No. of kernels/spike to 39.6% for grain yield/plant in cross I and from 7.4% for 100-kernels weight to 53.4% for No. of spikes/plant in cross II. The low values of inbreeding depression indicating that the presence of dominance gene effect in the expression for these traits.

3.5. Heritability

Heritability is considered one of the most parameters for determination of the phenotypic variance, which is owing to inherited reason. Heritability conception is linked with the proportional impact of inheritance and environment. The awareness of heritability assist plant breeders to predictive the behavior of the following advanced generations and making useful selections. The higher heritability, the selection method will be easier and the response to selection will be larger (Abdus *et al.*, 2003).

Concerning to the heritability, results are presented in (Table 4). The heritability values in broad sense were high and ranged from 45.15 for No. of spikes/plant in cross II to 88.01% for grain yield/plant in cross I. These results indicated that most of the phenotypic variability was due to genetic effects.

Heritability values in narrow sense ranged from 14.66 for No. of kernels/spike in cross II to 82.08% for grain yield/plant in cross I. The results of heritability in narrow-sense were similar to these obtained by (Shehab-Eldeen *et al.*, 2020; Mohamed *et al.*, 2021).

Table 4. Estimates Heritability in broad sense ($h_{b.s}$) and narrow sense ($h_{n.s}$) for all the studied traits in the two bread wheat crosses.

Traits	Crosses	Heritability	
		$h_{b.s}$ %	$h_{n.s}$ %
No. spikes/plant	I	82.56	69.00
	II	45.15	40.15
No. kernels/spike	I	69.18	52.61
	II	68.54	14.66
100-kernel weight (g)	I	73.27	63.45
	II	62.91	49.94
GY/plant (g)	I	88.01	82.08
	II	68.07	52.00

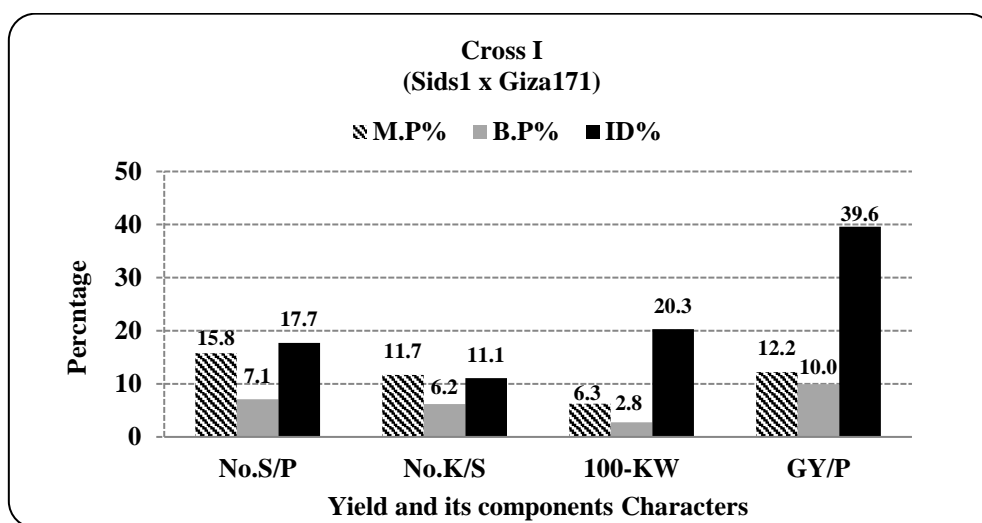


Fig 1. Percentage of heterosis, heterobeltiosis and inbreeding depression for the studied traits in cross I.

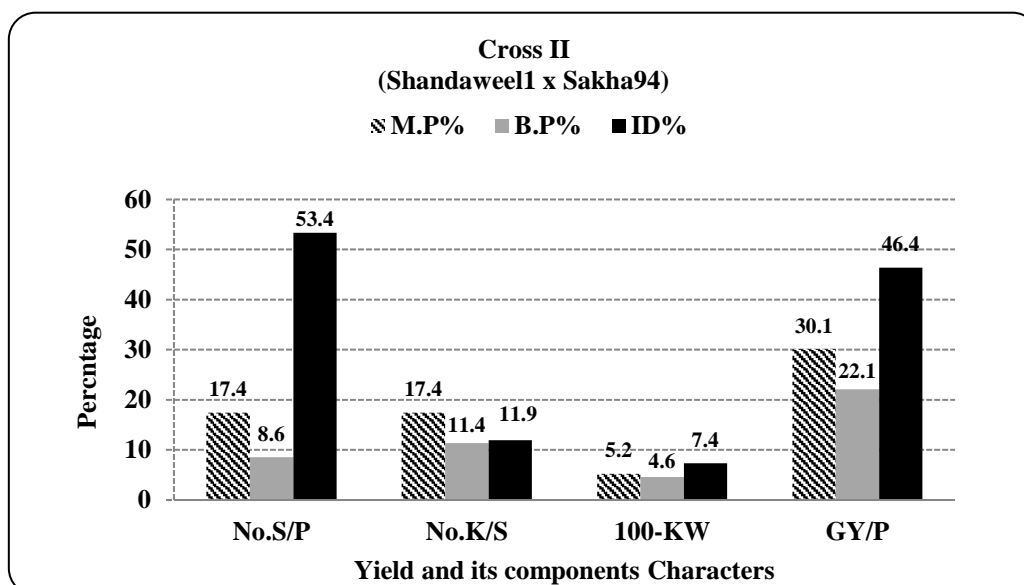


Fig 2. Percentage of heterosis, heterobeltiosis and inbreeding depression for the studied traits in cross II.

4. Conclusion

Additive, dominance and epistatic effects seemed to have played roles in the inheritance of all the studied traits for both crosses. It is recommended that selection be delayed due to the presence of epistatic gene interactions for many traits. The epistasis has been expressed through influencing yield and its components characters and it is suggested that breeders should be aware of this as a source of variation that might impact predicted gain in a selection programme.

5. References

- Abdus, S.K., Ishtiaq, S., Ali, Z. (2003). 'Heritability of Various Morphological Traits in Wheat', *Int. J. Agri. Biol.*, 5 (2), pp. 138-140.
- Amin, I. (2013). 'Genetics behavior of some agronomic traits in two durum wheat crosses under heat stress', *Alex. J. Agric. Res.*, 58 (1), pp. 53-66.
- Ashwani, K., Razdan, A.K., Sharma, V., Kumar, N., Kumar, D. (2018). 'Study of heterosis and inbreeding depression for economic and biochemical traits in bread wheat (*Triticum aestivum* L.)', *J. P. P. 2018*; 7 (4), pp. 558-564
- Ataei, R., Gholamhoseini, M., Kamalizadeh, M. (2017). 'Genetic analysis for quantitative traits in bread wheat exposed to irrigated and drought stress conditions', *Phyton-International Journal of Experimental Botany* 86, pp. 228-235.
- Chandra, D., Islam, M.A., Barma, N.C.D. (2004). 'Variability and interrelationship of nine quantitative characters in F5 bulks of five wheat crosses', *Pak. J. Bio. Sci.*, 7 (6), pp. 1040-1045.
- Dvojković, K., Drezner, G., Novoselović, D., Lalić, A., Kovačević, J., Babić, D., Barić, M. (2010). 'Estimation of some genetic parameters through generation means analysis in two winter wheat crosses', *Periodicum Biologorum.*, 112 (3), pp. 247-251.
- Falconer, D.S. (1989). 'Introduction to Quantitative Genetics', (3rd Ed). Logman Scientific and Technical, Logman House, Burnt Mill, Harlow, Essex, England.
- FAO (2020). 'Food and Agriculture Organization of United Nations', <http://www.fao.org/statistics>.
- Farshadfar, E., Aghaie, M., Sharifi, M., Yaghotipoor, A. (2008). 'Assessment of Salt Tolerance Inheritance in Barley via Generation Mean Analysis', *Journal of Biological Sciences.*, 8, pp. 461- 465.
- Feltaous, Y.M. (2020). 'Inheritance of yield and its components in two bread wheat crosses under normal and water stress conditions', *Assiut J. Agric. Sci.*, 51 (2), pp. 74-90.
- Fonseca, S., Patterson, F.L. (1968). 'Hybrid vigour in seven parent diallel crosses in common wheat (*Triticum aestivum* L.)', *Crop Science.*, 8, pp. 85-89.
- Gamble, E. E. (1962). 'Gene effects in corn (*Zea mays* L.) Separation and relative importance of gene effects for yield', *Canadian J. of Plant Sci.*, 42, pp. 339 – 348.
- Hendawy, H.I. (2003). 'Genetic architecture of yield and its components and some other agronomic traits in bread wheat', *Minufiya J. Agric. Res.* 28, pp. 71.
- Hossain, M.d.M., Azad, M.A.K., Alam, M.d.S., Eaton, T.E. (2021). 'Estimation of Variability, Heritability and Genetic Advance for Phenological, Physiological and Yield Contributing Attributes in Wheat Genotypes under Heat Stress Condition', *American Journal of Plant Sciences*, 12, pp. 586-602.
- Jinks, J.L., Jones, R.M. (1958). 'Estimation of the components of heterosis', *Genet.*, 43 (2), pp. 223- 224.
- Khaled, M.A. (2013). 'Genetic system controlling the yield and its

- components in three bread wheat (*Triticum aestivum* L.) crosses', *Egyptian Journal of Agricultural Research*, 91, pp. 641-653.
- Manel, S., Benmahammed, A., Benderradji, L., El Abidine Fellahi, Z., Bouzerzour, H., Oulmi, A., Benbelkacem, A. (2019). 'Generation means analysis of physiological and agronomical targeted traits in durum wheat (*Triticum durum* Desf.) cross', *Rev. Fac. Nac. Agron. Medellín*, 72 (3), pp. 8971-8981.
- Mather, K. (1949). '*Biometrical Genetics*', 1st Ed. Methuen, London.
- Memon, S.M., Qureshi, M.U., Ansari, B.A., Sial, M.A. (2007). 'Genetic heritability for grain yield and its related characters in spring wheat', *Pak. J. Bot.*, 39(5), pp. 1503-1509.
- Mohamed, M.M., Eid, M.A.M., El-Areed, S.R.M. (2021). 'Genetic studies on yield and some related characters in two bread wheat crosses using five population model', *Scientific Journal of Agricultural Sciences*, 3 (1), pp. 101-110.
- Novoselovic, D., Baric, M., Drezner, G., Gunjaca, J., Lalic, A. (2004). 'Quantitative inheritance of some wheat plant traits', *Genetics and Molecular Biol.*, 27(1), pp. 92-98.
- Sharma, R.C. (1994) 'Early generation selection for grain filling period in wheat', *Crop Sci.*, 34, pp. 945-948.
- Sharshar, A.M., Genedy, M.S. (2020). 'Generation mean analysis for three bread wheat crosses under normal and water stress treatments', *J. of Plant Production, Mansoura Univ.*, 11 (7), pp. 617-626.
- Shehab-Eldeen, M.T., Darwish, M.A.H., Ghareeb, Z.E. (2020). 'Gene effect estimation for yield-characters and inheritance of yellow rust resistance among generations in three bread wheat crosses', *IJISET - International Journal of Innovative Science, Engineering & Technology*, 7 (12), pp. 113-135.
- Singh, P., Narayanan, S.S. (1993). '*Biometrical Techniques in Plant Breeding*', Kalyani Publishers.
- Sohan, L.K., Sharma, A.K., Singh, H. (2020). 'Heterosis Analysis in F1 Hybrids of Bread Wheat (*Triticum aestivum* L. em. Thell.) Over Environments', *Int. J. Curr. Microbiol. App. Sci.*, 9 (5), pp. 2052-2057.
- Zaazaa, E.I., Hager, M.A., El-Hashash, E.F. (2012). 'Genetical analysis of some quantitative traits in wheat using six parameters genetic model', *American-Eurasian J. Agric. & Environ. Sci.*, 12 (4), pp. 456-462.