

## **INHERITANCE NATURE OF YIELD AND ITS COMPONENTS IN TWO BREAD WHEAT CROSSES UNDER OLD AND NEW LAND IN UPPER EGYPT CONDITIONS**

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### **ABSTRACT**

*The ultimate goal for wheat breeders is to develop high yield resilient varieties to mitigate the catastrophic impacts of climate change. To achieve this goal, the inheritance of yield and its components should be fully unraveled. The current study was undergone at two locations in Qena governorate - Egypt, representing new and old lands. Two bread wheat crosses were used during three growing winter seasons from 2019/20 to 2021/22. Data on No. of spikes/plant (S/P), No. of kernels / spike (K/S), 100-kernels weight (100-KW), and grain yield/plant (GY) were recorded. Analysis of variance showed sufficient variability between the populations of the two crosses for all studied traits. The results showed that  $F_1$  override the better parent in both crosses under both locations for all studied traits. Potence ratio pointed out the presence of over dominance for all studied traits in all cases. Scaling test showed the inadequacy of three parameters model for all the studied traits in both crosses under both locations. Six parameters model was implemented to explain the nonallelic interaction; additive effects (d) mostly was significant or highly significant with positive sign for all studied traits, while dominance effects (h) was significant with positive sign in most of the cases. The additive  $\times$  additive effects (i) was significant with negative sign in all cases, except in cross 1 under old land conditions, where it was nonsignificant. The additive  $\times$  dominance effects (j) in most cases were not significant, while dominance  $\times$  dominance effects (l) was significant with positive sign in most cases. Duplicate epistasis was found in cross 1 under both conditions for S/P; it was found in cross 2 under both conditions and in cross 1 under new land for K/S. The complementary epistasis only was found in cross 1 under both conditions for 100-KW. The values of heterosis over better parent were high with positive sign in most of the cases, meaning that it tends toward the high parent. Broad sense and narrow sense heritability and genetic advance in general ranged from moderate to high, except few cases where they were low. Inbreeding depression was (0.47 to 30.70%), (2.98 to 22.31%), (4.11 to 30.70%), and (4.85 to 19.15%) for S/P, K/S, 100KW, and GY, respectively. The current study indicated that unraveling the genetic architecture of the yield and its components enables us to determine the selection strategy under new and old land conditions.*

Key words: *Triticum aestivum*, Quantitative traits, gene action, dominance, additive, epistasis

### **INTRODUCTION**

Wheat is the most important staple food crop between all cereal crops in Egypt, where it was cultivated in 3.5 million feddan (1.45 million hectare); about 28% of the total agricultural cultivated land in 2022/2023 winter season (USDA-Egypt 2023). The total national wheat production was 9.5 million metric tons represent 47.5% of the total wheat domestic consumption (USDA-Egypt 2023). The gap between production and consumption (52.5%) can be filled by imported wheat

from the international market, which cost the Egyptian government a massive amount of hard currency. In addition, the government of Egypt subsidizes Baladi bread to be available for everyone with cheap prices, which in turn put burden on the government commitment of millions Egyptian pounds. For all these aspects, improving wheat production takes high attention from the Egyptian government for securing food. The arable land in Egypt is 8.7 million feddan (3.65 million hectares). The cultivated land in Egypt is limited while the population is growing fast, where Egypt is one of most over-populated countries all over the world; Egypt's population surpassed 113 million in early 2022 according to Worldometers (2022), 60% rise from the early 2000s according to CAPMAS (2023). For the above mentioned reasons, the Egyptian government's policy trends to plant wheat in the new lands to increase the cultivated area which in turn increase the total production by which reduce the gap between production and consumption.

The massive impacts of climatic changes, especially on the agricultural sector, became more aggressive as a result of occurrence frequency and distribution. Though growing more wheat acreage with high mitigation ability to climatic changes is a demand to increase the wheat domestic production and secure food for humankind. Otherwise, growing wheat in new lands requires wide adapted varieties for harsh environments. Identifying and studying the gene action for yield and desirable traits is a prerequisite for developing high yielding mitigated varieties.

Genetic dissection and studying gene action mode of the interested traits under targeted environments is the base stone of any successful breeding program, where the mode of gene action which is controlling the inheritance of the targeted traits determines the appropriate breeding methods. The type and magnitude of gene action may vary for different characters in the same cross and for the same trait in different crosses which necessitates the handling of individual cross in segregating generations in a specific way (Kaur and Singh, 2004). The ultimate aim of any breeding program is improving yield potentiality, but yield is a complex quantitative trait with low heritability and highly affected by environment. Therefore, dissection of

yield gene action requires understanding the mode of gene action for yield components as well. Immense investigations, on biometric or quantitative traits, were carried out for studying genetic analysis and genetic architecture for qualitative traits as well as studying type of gene action and interaction either allelic or intra-allelic using different models analysis *e.g.* six parameters model, five parameters model ..... *etc* (Mather and Jinks, 1971; Mather and Jinks 1982; and Kearsey and Pooni, 1996).

Generation mean analysis as a biometrical technique was worked out by Jinks and Jones (1958). Three different models *i.e.* three, five, and six parameter model, they differ from each other in included material and procedure of analysis. Six parameters' model was deployed to estimate the presence of interallelic (Additive-dominance) and intra-allelic (Epistasis) interaction (Mather and Jinks, 1971; Mather and Jinks, 1982). Scaling test and six parameters model; six populations include the first and second filial ( $F_1$  and  $F_2$ ), backcross filial for the first and second parent ( $BC_1$  and  $BC_2$ ), the first and second parent ( $P_1$  and  $P_2$ ), it is an effective measure for gene effect and nature of inheritance. The aims of this study were 1) implementing generation mean analysis in measuring the mode of gene action of yield and its components for two bread wheat crosses under two contrasting environments *i.e.* new and old lands conditions, 2) Understanding the genetic architecture of yield and its components as polygenic traits for two crosses under two different conditions (new and old lands), consequently determine the breeding methods and selection strategy for the studied traits.

## **MATERIAL AND METHODS**

### **Experiments set-up**

The current study was conducted mainly at El Matanaa Agricultural Research Station - Field Crops Research Institute (FCRI) - Agricultural Research Center (ARC) – Egypt during 2019/20 and 2020/21 winter growing seasons. While, the evaluation experiments in 2021/22 were conducted at El Matanaa Agricultural Research Station and Tomas 3 location as well; El Matanaa Agricultural Research Station and Tomas 3 locality represent the old and new lands, respectively. The plant material consists of two crosses, which were made from four

Egyptian cultivars *i.e.* Misr 3, Gemmiza 11, Giza 168, and Giza 171. The pedigree, selection history, and origin of the four cultivars are described in Table (1).

**Table 1. Pedigree, history, and source of the four cultivars.**

Cross	Cultivar	Pedigree and selection history	Origin
Cross 1	Misr 3	Rohf 07*2/Kiriti CGSS 05 B00123T-099T-0PY-099M-099N- 6WGY-0B-0BGY-0GZ.	Egypt
	Giza 168	MIRL/BUC//SERI CGM7892-2GM-2GM-0GZ	Egypt
Cross 2	Gemmiza 11	BOW"S"/KVZ"S"//7C/SERI-82/3/GIZA 168/SAKHA61 GM7892-2GM-1GM-2GM-1GM-0GM	Egypt
	Giza 171	Gemmeiza9 / Sakha93 GZ2003-101-1GZ-4GZ-1GZ-2GZ-0GZ	Egypt

In the first season, the four parents were planted in three planting dates *i.e.* 15<sup>th</sup> November, 25<sup>th</sup> November, and 5<sup>th</sup> December 2019. The three planting dates give flexibility in crossing period. Emasculation and pollination were made between each two parents to develop hybrid seeds (F<sub>1</sub> seeds) for two different crosses *i.e.* cross 1 (Misr 3 x Giza 168) and cross 2 (Gemmiza 11 x Giza 171).

In the second season, the parents for each were planted in three planting dates *i.e.* 15<sup>th</sup> November, 25<sup>th</sup> November, and 5<sup>th</sup> December 2020 while F<sub>1</sub> seeds were planted on 25<sup>th</sup> November 2020 for each cross separately, proportion of F<sub>1</sub> seeds were planted to produce either F<sub>2</sub> seeds by selfing or backcross 1 (BC<sub>1</sub>) and backcross 2 (BC<sub>2</sub>) by backcrossing F<sub>1</sub> plants with first and second parent, respectively. For abundant F<sub>1</sub> seeds, along with F<sub>1</sub> seeds which were kept from previous season, crossing between each two parents for each cross has been repeated to produce F<sub>1</sub> seeds. By the end of this season sufficient seeds of the six populations were available *i.e.* F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub>, BC<sub>2</sub>, P<sub>1</sub>, and P<sub>2</sub>.

In the third season, the six populations were planted on 25<sup>th</sup> November 2021 in randomized complete block design "RCBD" with three replications at El Matanaa Agricultural Research Station as well as at Tomas 3. Each replication consists of 12 rows with 2 m long

separated by 40 cm between rows and 10 cm between plants. Each of P<sub>1</sub>, P<sub>2</sub>, and F<sub>1</sub> were sown in one row, while BC<sub>1</sub> and BC<sub>2</sub> were sown in two rows and F<sub>2</sub> were sown in five rows of 20 plants in each row. Data were recorded on ten guarded plants/row for each replication randomly selected from each generation for no. of spikes/plant (S/P), 100-grain weight (100-KW) in g, no. of kernels/spike (K/S), and grain yield/plant (GY) in g.

#### **Statistical and biometrical analysis:**

Statistical analysis (Analysis of variance, ANOVA) was performed using GenStat 21<sup>th</sup> Ed. statistical software. Means were compared using least significant difference (L.S.D). Biometrical analysis was performed using SAS V9.3 (2015) software package. A, B, C, and D scaling test (Mather 1949 and Hayman and Mather 1955) were used to test presence of non–allelic interaction “Epistasis”. Six parameters *i.e.* F<sub>2</sub> mean (m), Additive effects (d), Dominance effects (h), Additive × Additive (i), Additive × Dominance (j), and Dominance × Dominance (l) were estimated according to Mather and Jinks (1982). The equation of Falconer (1989) was used to estimate inbreeding depression (ID %) as the average percentage decrease of F<sub>2</sub> from F<sub>1</sub> and Potence ratio (PR) was computed by the formula suggested by Griffing (1950). The genetic components of variance were calculated according to Mather and Jinks (1971). Heritability and heterosis were estimated according to Mather and Jinks (1982) and Bhatt (1971), respectively. Heterosis was expressed as the deviation of F<sub>1</sub> generation from the mid-parent or better parent average values. Genetic advance from selection was estimated according to Allard (1960) with selection intensity (K) of 5% = (2.06) for all characters.

## **RESULTS AND DISCUSSION**

### **Analysis of variance**

Analysis of variance, the variability between populations was significant or highly significant for all studied traits under new and old land conditions in both crosses (Table 2). The significant variance among populations enabled us to go further for six parameters model.

**Table 2. Analysis of variance for the six populations under new and old lands.**

SOV	df	Cross 1 under new land				Cross 1 under old land			
		S/P	K/S	100KW	GY	S/P	K/S	100KW	GY
Replication (Rep)	2	1.07	7.62	0.02	1.318	0.38	8.37	0.047	7.99
Populations (Pop)	5	2.27**	118.28**	0.96**	17.87**	3.47**	137.00**	1.001**	37.14**
Error	10	0.27	6.27	0.03	4.61	0.092	13.34	0.031	8.643
C.V	---	8.50	4.90	5.30	9.30	3.00	6.00	4.10	10.80
		Cross 2 under new land				Cross 2 under old land			
Replication (Rep)	2	0.57	15.22	0.024	4.31	0.23	22.75	0.08	10.55
Populations (Pop)	5	1.59**	69.03**	0.83**	19.60**	3.15**	109.83*	1.74**	62.00**
Error	10	0.41	1.93	0.031	1.87	0.08	11.85	0.02	6.67
C.V	---	10.40	3.30	5.40	6.40	3.30	5.70	3.50	8.60

C.V = coefficient of variation, S/P = No. of spikes/plant, K/S = No. of kernels/spike, 100-KW = 100-grain weight, and GY = Grain yield/plant. \* & \*\* = significant at 0.05 and 0.01 levels, respectively.

### Mean performance

Table 3 shows mean performance and standard error values of all populations for all studied traits in the two crosses. The results indicated that F<sub>1</sub> override better parent in both crosses under new and old lands for all studied traits. Regards to S/P trait, the highest and lowest values in cross 1 and cross 2 under new and old lands were 7.30 (F<sub>1</sub>) & 5.00 (P<sub>1</sub>), 6.82 (F<sub>1</sub>) & 5.19 (P<sub>1</sub>), 11.40 (F<sub>1</sub>) & 8.77 (P<sub>1</sub>), and 9.77 (F<sub>1</sub>) & 6.97 (P<sub>1</sub>), respectively. The same situation were found in K/S trait, the highest values for F<sub>1</sub> were 53.30, 46.88, 68.81, and 66.73 for cross 1 and cross 2 under new and old lands, respectively, while the lowest values were 38.25 (BC<sub>2</sub>), 35.05 (BC<sub>2</sub>), 49.53 (BC<sub>2</sub>), and 52.32 (BC<sub>2</sub>) for cross 1 under both conditions and cross 2, respectively.

**Table 3. Mean performance  $\pm$  standard error of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub>, and BC<sub>2</sub> populations and potence ratio (PR) of two bread wheat crosses for yield and its components under new and old lands conditions.**

Conditions Trait Populations	New lands				Old lands			
	S/P	K/S	100-KW	GY	S/P	K/S	100-KW	GY
Cross 1-P <sub>1</sub>	5.00 $\pm$ 0.41	51.48 $\pm$ 1.31	2.74 $\pm$ 0.30	24.17 $\pm$ 0.90	8.77 $\pm$ 0.59	59.49 $\pm$ 1.45	4.08 $\pm$ 0.38	30.15 $\pm$ 0.97
P <sub>2</sub>	6.17 $\pm$ 0.31	51.52 $\pm$ 1.43	3.45 $\pm$ 0.09	23.76 $\pm$ 0.42	10.50 $\pm$ 0.57	62.81 $\pm$ 1.43	4.44 $\pm$ 0.38	28.24 $\pm$ 0.99
F <sub>1</sub>	7.30 $\pm$ 0.28	57.30 $\pm$ 1.18	4.05 $\pm$ 0.06	27.16 $\pm$ 0.69	11.40 $\pm$ 0.24	68.81 $\pm$ 1.21	5.11 $\pm$ 0.08	31.04 $\pm$ 0.26
F <sub>2</sub>	6.98 $\pm$ 0.13	52.45 $\pm$ 0.86	2.80 $\pm$ 0.05	21.54 $\pm$ 0.85	11.35 $\pm$ 0.14	60.64 $\pm$ 0.90	3.87 $\pm$ 0.05	26.11 $\pm$ 1.05
BC <sub>1</sub>	5.87 $\pm$ 0.23	53.51 $\pm$ 1.45	2.53 $\pm$ 0.08	22.32 $\pm$ 1.39	9.80 $\pm$ 0.24	63.87 $\pm$ 1.34	3.50 $\pm$ 0.08	25.74 $\pm$ 1.47
BC <sub>2</sub>	5.50 $\pm$ 0.26	38.25 $\pm$ 1.49	3.32 $\pm$ 0.09	21.53 $\pm$ 1.65	9.35 $\pm$ 0.23	49.53 $\pm$ 1.60	4.41 $\pm$ 0.09	21.66 $\pm$ 1.48
L.S.D <sub>0.05</sub>	1.00	4.60	0.30	3.90	0.60	6.6	0.32	5.35
PR	-2.94	3.89	-2.69	-3.79	-2.04	4.61	-4.71	1.93
Cross 2-P <sub>1</sub>	5.19 $\pm$ 0.42	36.73 $\pm$ 1.11	3.68 $\pm$ 0.35	23.58 $\pm$ 0.89	6.97 $\pm$ 0.42	54.60 $\pm$ 1.53	5.22 $\pm$ 0.07	33.87 $\pm$ 0.53
P <sub>2</sub>	6.37 $\pm$ 0.19	44.51 $\pm$ 1.00	3.04 $\pm$ 0.07	20.75 $\pm$ 0.39	9.10 $\pm$ 0.23	61.37 $\pm$ 1.76	4.23 $\pm$ 0.11	31.74 $\pm$ 0.52
F <sub>1</sub>	6.82 $\pm$ 0.23	46.88 $\pm$ 0.81	3.82 $\pm$ 0.05	24.98 $\pm$ 0.19	9.77 $\pm$ 0.18	66.73 $\pm$ 1.19	5.43 $\pm$ 0.08	34.94 $\pm$ 0.26
F <sub>2</sub>	6.45 $\pm$ 0.11	44.95 $\pm$ 0.64	3.00 $\pm$ 0.06	20.20 $\pm$ 0.60	9.09 $\pm$ 0.12	63.50 $\pm$ 0.93	4.12 $\pm$ 0.06	28.27 $\pm$ 0.91
BC <sub>1</sub>	5.74 $\pm$ 0.16	44.07 $\pm$ 0.93	2.51 $\pm$ 0.06	20.82 $\pm$ 1.11	7.93 $\pm$ 0.22	63.87 $\pm$ 1.34	3.40 $\pm$ 0.08	27.38 $\pm$ 1.55
BC <sub>2</sub>	5.93 $\pm$ 0.18	35.05 $\pm$ 1.11	3.25 $\pm$ 0.07	17.64 $\pm$ 1.12	8.33 $\pm$ 0.23	52.32 $\pm$ 1.66	4.33 $\pm$ 0.09	23.15 $\pm$ 1.56
L.S.D <sub>0.05</sub>	1.76	3.80	2.25	5.93	1.78	4.11	2.45	7.39
PR	-1.75	1.61	1.44	1.99	-1.63	2.59	1.44	2.01

Similarly, in 100-KW trait, the highest values for F<sub>1</sub> were 4.05 g, 3.82 g, 5.11g, and 5.43 g for cross 1 and cross 2 under new and old lands, respectively, and the lowest values were 2.53 (BC<sub>1</sub>), 2.51 (BC<sub>1</sub>), 3.50 (BC<sub>1</sub>), and 3.40 (BC<sub>1</sub>) for cross 1 and cross 2 under new and old lands, respectively. Grain yield per plant (GY) manner did not differ from its components; the highest and lowest values in cross 1, cross 2 under new and old lands were 27.16 g (F<sub>1</sub>) & 21.53 g (BC<sub>2</sub>), 24.98 g (F<sub>1</sub>) & 17.64 g (BC<sub>2</sub>), 31.04 g (F<sub>1</sub>) & 21.66 g (BC<sub>2</sub>), and 34.94 g (F<sub>1</sub>) &

23.15 g (BC<sub>2</sub>), respectively. The results highlight the major role of dominance gene effects in controlling the genetic variation for all studied traits in the two crosses under new and old lands. The obtained findings are in line with Feltaous (2020), who found that F<sub>1</sub> generation means was higher than better parent for 100-KW, and GY. Same results were found by Rady (2022) and Sandhu *et al* (2023). F<sub>1</sub> generation mean in both crosses were higher than F<sub>2</sub> population mean, this can be reasoned to the segregation and inbreeding depression in F<sub>2</sub> generation, this is supported in earlier findings by Mohammadi *et al* (2022).

#### **Potence ratio**

Based on the majority of dominant gene effects obtained for the studied traits, the degree of dominance should be determined by calculating potence ratio (Griffing, 1950), relative potence of gene. The potence ratio categorize the degree of dominance into four categories as follows; over-dominance ( $PR > \pm 1$ ), complete dominance ( $PR = +1$ ), partial dominance ( $-1 \leq PR \leq +1$ ), and absence of dominance ( $PR = \text{zero}$ ). As shown in Table 3, the potence ratio values was  $> \pm 1$ , therefore the major dominance effect is over dominance for all the studied traits in the two crosses under new and old lands.

Over-dominance ( $P > +1$ ) tending to better parent was detected for K/S in both crosses and under both conditions, also was detected for GY in cross 1 under old lands and cross 2 under both conditions. As well as it was found for 100-KW in cross 2 under both conditions. In case of over-dominance relative to the lower parent ( $PR > -1$ ) was found for S/P in both crosses and for both conditions while, similarly it was found for 100-KW under both conditions but only in cross 1. Finally it was found for GY in cross 1 under new land conditions. These findings are in accordance with those obtained by Rady (2022).

Interallelic interaction occurs between two alleles at the same locus while the interallelic interaction occurs between alleles at different loci. For testing the dominance-additive model, scaling test *i.e.* A, B, C, and D were calculated. Joint scaling test; significance of A, B, C, and D, were applied using t test. To test the efficacy of dominance-additive model, the four scales should be non-significant *i.e.* the simple digenic model is fit. At least one scale should be significant for inadequacy of



the model. The significance of each scale of the four scales can be interpreted as follow; (1) the significance of A and B scales refer to presence of all types of non-allelic interaction *i.e.* additive  $\times$  additive, additive  $\times$  dominance, and dominance  $\times$  dominance gene interaction, (2) the significance of C scale refer to presence dominance  $\times$  dominance, (3) the significance of D scale suggest presence of additive  $\times$  additive (Mather, 1949 and Hayman and Mather 1955). Results in Table 4 showed that for S/P, three scales *i.e.* B, C, and D were significant in cross1 under both conditions, while B and D scales were significant in cross 2 under both conditions. In case of K/S, three scales *i.e.* A, B, and D were significant in cross 2 under both conditions, while B & C& D and B & D in cross 1 under old and new lands, respectively. A, B, and C scales for 100-KW were significant in cross 1 under both conditions, while A, B, C, and D were significant in cross 2 under both conditions. For grain yield, B & C and A & B & C in cross 1 under both conditions. In cross 2, A & B & C and A & B & C & D scales were significant under new and old lands, respectively. The above results suggest presence all types of non-allelic gene interaction (Epistasis) and inadequacy of dominance-additive model in both crosses under both conditions for all the studied traits. The findings lead for applying six parameters model to explain the type of gene interaction for the studied traits. Abdallah *et al* (2019), Feltaous (2020), Kandil *et al* (2023), and Sandhu *et al* (2023) found similar results.

#### **Adequacy of digenic model**

##### **Genetic architecture**

Non-allelic gene interaction was well termed and defined by Darlington and Mather (1961) but so far the most comprehensive definitions, terms and symbols were presented by Fasoulas (1971); who explained that non-allelic genes act and interact near similarly as allelic genes. He clarify that to differentiate between allelic and non-allelic gene interaction, the term epistasis is used instead of dominance. In analogous manner as dominance, epistasis realized as positive and negative epistasis (Fasoulas, 1981), semi and Co-epistasis (Fasoulas, 1971).

**Table 4. Scaling test parameters for yield and its components under new and old lands conditions.**

Scaling test	Cross 1		Cross 2	
	New lands	Old lands	New lands	Old lands
<b>No. of spikes/plant (S/P)</b>				
A	-0.57 <sup>NS</sup> ±0.68	-0.57 <sup>NS</sup> ±0.80	-0.52 <sup>NS</sup> ±0.57	-0.87 <sup>NS</sup> ±0.55
B	-2.47 <sup>**</sup> ±0.67	-3.20 <sup>**</sup> ±0.77	-1.34 <sup>**</sup> ±0.47	-2.20 <sup>**</sup> ±0.55
C	2.16 <sup>**</sup> ±0.92	3.32 <sup>**</sup> ±1.10	0.62 <sup>NS</sup> ±0.78	0.76 <sup>NS</sup> ±0.70
D	2.60 <sup>**</sup> ±0.44	3.54 <sup>**</sup> ±0.44	1.24 <sup>**</sup> ±0.33	1.91 <sup>**</sup> ±0.39
<b>No. of kernels/spike (K/S)</b>				
A	1.94 <sup>NS</sup> ±3.53	-0.56 <sup>NS</sup> ±3.28	4.54 <sup>*</sup> ±2.30	6.41 <sup>**</sup> ±3.31
B	-29.82 <sup>**</sup> ±3.63	-32.56 <sup>**</sup> ±3.70	-21.29 <sup>**</sup> ±2.57	-23.47 <sup>**</sup> ±3.93
C	-1.58 <sup>NS</sup> ±4.99	-16.97 <sup>**</sup> ±4.81	4.80 <sup>NS</sup> ±3.39	4.55 <sup>NS</sup> ±5.00
D	13.15 <sup>**</sup> ±2.70	8.07 <sup>**</sup> ±2.76	10.77 <sup>**</sup> ±1.93	10.80 <sup>**</sup> ±2.83
<b>100-kernel weight (100-KW)</b>				
A	-1.73 <sup>**</sup> ±0.35	-2.19 <sup>**</sup> ±0.43	-2.48 <sup>**</sup> ±0.38	-3.85 <sup>**</sup> ±0.20
B	-0.86 <sup>**</sup> ±0.21	-0.73 <sup>*</sup> ±0.43	-0.37 <sup>*</sup> ±0.17	-1.00 <sup>**</sup> ±0.23
C	-3.06 <sup>**</sup> ±0.39	-3.27 <sup>**</sup> ±0.60	-2.36 <sup>**</sup> ±0.40	-3.84 <sup>**</sup> ±0.33
D	-0.23 <sup>NS</sup> ±0.15	-0.17 <sup>NS</sup> ±0.17	0.24 <sup>*</sup> ±0.12	0.51 <sup>**</sup> ±0.18
<b>Grain yield/plant (GY)</b>				
A	-3.85 <sup>NS</sup> ±2.99	-9.71 <sup>**</sup> ±3.11	-6.93 <sup>**</sup> ±2.39	-14.06 <sup>**</sup> ±3.15
B	-9.09 <sup>**</sup> ±2.57	-15.97 <sup>**</sup> ±3.12	-10.45 <sup>**</sup> ±2.29	-20.38 <sup>**</sup> ±3.17
C	-11.68 <sup>**</sup> ±3.81	-16.03 <sup>**</sup> ±4.47	-13.51 <sup>**</sup> ±2.62	-22.41 <sup>**</sup> ±3.75
D	0.63 <sup>NS</sup> ±2.51	4.83 <sup>NS</sup> ±2.97	1.93 <sup>NS</sup> ±1.98	6.02 <sup>*</sup> ±2.85

\* & \*\* = Significant at 0.05 & 0.01 levels of probability, respectively. NS = non-significant.

Different genetic parameters were estimated to unravel the genetic architecture of the studied traits *i.e.* additive component of variance (D), dominance component of variance (H), heritability in broad ( $h^2_b$ ) as well as narrow ( $h^2_n$ ) sense, heterosis, inbreeding depression (ID), genetic advance from selection (GS).

The results which were extracted from Table 4 (previously well addressed) lead us to go for performing six parameters model. Therefore, the six parameters model were applied to explain the type of non-allelic gene interactions which are controlling the studied traits. The six parameters model include the following notation m, d, h, i, j, and l to represent mean, additive, dominance, additive  $\times$  additive, additive  $\times$  dominance, and dominance  $\times$  dominance effects, respectively. The results in Table (2) show that  $F_2$  mean (m) was significant or highly significant in all studied traits in both crosses under both conditions expressing the quantitative inheritance of all studied traits, it was interpreted in details earlier in analysis of variance interpretation.

#### **Number of spikes/plant (S/P)**

Additive effect (d) was highly significant with positive values and non-significant in cross 1 under new land and old land, respectively (Table 5). These results suggest reliance on mass selection for S/P in cross 1 under new land and suggest that selection in early segregating generations is ineffective in cross 1 under old land as well as in cross 2 under both conditions. Dominance effect (h) was significant with negative values which refer to inhibitory genes for S/P which reduce heterosis. These findings are in accordance with Boeven *et al* (2020). Additive  $\times$  additive effects (i) was highly significant with negative values in both crosses under both conditions refers to possibility of obtaining transgressive segregation in late generations. On the contrary additive  $\times$  dominance (j) was nonsignificant in both crosses under both conditions indicating the flexibility of improvement by selection. Dominance  $\times$  dominance (l) was highly significant with positive values. The similar sign of additive (d) and dominance (h) indicate the prevailed of additive and dominance and possibility of using bi-parental crosses. In concern to type of epistasis “duplicate and complementary”, it is applicable only in case of dominance (h) and dominance  $\times$  dominance

(l) are significant (Kearsey and Pooni, 1996). For S/P, type of epistasis was duplicate epistasis in cross 1 under both conditions but it was not applicable in cross 2 under both conditions. It is not suitable to use them in breeding programs because the presence of duplicate epistasis demonstrated that diversity in segregating generations had decreased, and hinders the process of selection (Kumar *et al* 2010). These results are in accordance of those obtained by Attri *et al* (2021) and Al-Mfarji *et al* (2023).

The genetic components of variance are presented in Table 5. The results revealed that the additive component (D) was found to be controlling S/P trait in cross 2 under both conditions, while dominance component (H) was found to be controlling the trait in cross 1 under new land. In contrast in cross 1 under old lands, both components were equally controlling the trait. Similar results were obtained by Koubis (2019), Feltaous (2020) and Kandil *et al* (2023). Average degree of dominance ( $H/D^{1/2}$ ) was more than unity (over-dominance) *i.e.* 1.81 and 3.01 in cross 1 under new land and cross 2 under old land, respectively; these findings shows exist of more dominant alleles than recessive alleles for S/P in these cases (Omrani *et al* 2022). On the other hand, it was less than unity (partial dominance) in cross 1 under old land and cross 2 under new land, respectively. These findings are consistent with those obtained by Kandil *et al* (2023).

The heritability either in broad ( $h^2b$ ) or in narrow ( $h^2n$ ) sense can be categorized into three categories *i.e.* high (> 60%), moderate (30 – 60%), and low (< 30%) according to Robinson *et al* (1949). Broad sense heritability ( $h^2b$ ) was moderate in both crosses under both conditions, where it was 36.78, 50.42, 40.76, and 47.74% in cross 1 under new lands, cross 1 under old land, cross 2 under new land, and cross 1 under new land, respectively. The present results revealed that high portion of the phenotypic variation can be attributed to the genetic variation. While,  $h^2n$  was low in cross 1 under new land ((13.99%) and cross 2 under old land (8.57%), while it was moderate in cross 1 under old land (47.96%) and in cross 2 under new land.

**Table 5. Generations means analysis, heterosis% (MP and BP), components of variation, and GS% for No. of spikes/plant in both crosses under new and old lands conditions.**

Cross	Cross 1		Cross 2	
Conditions	New lands	Old lands	New lands	Old lands
Parameters				
<b>m</b>	<b>6.98**<math>\pm</math>0.13</b>	<b>11.35**<math>\pm</math>0.14</b>	<b>6.45**<math>\pm</math>0.11</b>	<b>9.09**<math>\pm</math>0.12</b>
<b>d</b>	<b>0.37**<math>\pm</math>0.35</b>	<b>0.45<sup>NS</sup><math>\pm</math>0.33</b>	<b>-0.18<sup>NS</sup><math>\pm</math>0.24</b>	<b>-0.40<sup>NS</sup><math>\pm</math>0.32</b>
<b>h</b>	<b>-3.48**<math>\pm</math>0.96</b>	<b>-5.32**<math>\pm</math>0.99</b>	<b>-1.44<sup>NS</sup><math>\pm</math>0.73</b>	<b>-2.09<sup>NS</sup><math>\pm</math>0.83</b>
<b>i</b>	<b>-5.20**<math>\pm</math>0.88</b>	<b>-7.09**<math>\pm</math>0.87</b>	<b>-2.48**<math>\pm</math>0.65</b>	<b>-3.82**<math>\pm</math>0.79</b>
<b>j</b>	<b>0.95<sup>NS</sup><math>\pm</math>0.44</b>	<b>1.32<sup>NS</sup><math>\pm</math>0.53</b>	<b>0.41<sup>NS</sup><math>\pm</math>0.33</b>	<b>0.67<sup>NS</sup><math>\pm</math>0.36</b>
<b>l</b>	<b>8.23**<math>\pm</math>1.69</b>	<b>10.85**<math>\pm</math>1.73</b>	<b>4.34**<math>\pm</math>1.25</b>	<b>6.89**<math>\pm</math>1.45</b>
<b>Epistasis</b>	<b>D</b>	<b>D</b>	<b>--</b>	<b>--</b>
<b>Heterosis (MP)%</b>	<b>30.75**</b>	<b>18.34**</b>	<b>30.83**</b>	<b>21.58**</b>
<b>Heterosis (BP)%</b>	<b>18.38**</b>	<b>8.57**</b>	<b>6.97**</b>	<b>7.33**</b>
<b>ID %</b>	<b>4.35**</b>	<b>0.47<sup>NS</sup></b>	<b>30.70**</b>	<b>6.94**</b>
<b>H</b>	<b>3.66</b>	<b>2.18</b>	<b>0.33</b>	<b>4.86</b>
<b>D</b>	<b>1.12</b>	<b>2.18</b>	<b>1.61</b>	<b>0.54</b>
<b>E</b>	<b>2.53</b>	<b>2.18</b>	<b>1.29</b>	<b>1.64</b>
<b>H/D<sup>1/2</sup></b>	<b>1.81</b>	<b>0.32</b>	<b>0.45</b>	<b>3.01</b>
<b>Heritability (h<sup>2</sup>b)</b>	<b>36.78</b>	<b>50.42</b>	<b>40.76</b>	<b>47.41</b>
<b>Heritability (h<sup>2</sup>n)</b>	<b>13.99</b>	<b>47.96</b>	<b>36.98</b>	<b>8.57</b>
<b>G.S%</b>	<b>8.26</b>	<b>18.28</b>	<b>17.5</b>	<b>3.43</b>

\* & \*\* = Significant at 0.05 & 0.01 levels of probability, respectively. NS = nonsignificant. D = Duplicate

Genetic advance under selection (G.S%) according to Johnson *et al* (1955) was realized as low (< 10%), moderate (> 10% < 20%), and high (> 20%). G.S values were 8.26% and 3.43% in cross 1 under new land and cross 2 under old land, respectively. These values place it in low category, while it was recognized as moderate in cross 1 under old land and in cross 2 under old land with values of 18.28% and 17.50%,

respectively (Table 5). These results are completely in agreement with those reported by Mohammadi *et al* (2022).

Heterosis (%) was estimated over mid-parent and better parent as a percent of the studied trait. Heterosis values over better parent were (18.38, 8.57%), (6.97, and 7.33%) in cross 1 and cross 2 under new and old land, respectively. While the heterosis over mid-parent values were (30.75, 18.34%), (30.83, and 21.58%) in cross 1 and cross 2 under new and old land, respectively. The results revealed that heterosis over better parent was medium with positive sign which means that it tends to better parent direction in both crosses under both conditions. With regard inbreeding depression (ID) with significance and with negative values are desirable; it was highly significant with positive values while it was nonsignificant in cross 1 under old land (Table 5).

These results indicate that the highest heterosis with low inbreeding depression (heterosis = 46.00% and ID = 4.35%) was in cross 1 under new land followed by cross 2 under old land (heterosis = 40.19% and ID = 6.94%). These results are in harmony with those obtained by Busa *et al* (2022).

#### **No. of kernels/spike (K/S)**

The results in Table (6) indicate that K/S trait is controlled by additive effect (d) where it was highly significant with positive values in both crosses under both conditions. Therefore, selection method is effective in improving K/S trait. The inhibitory genes seem to be present in cross 1 under new land and in cross 2 under both conditions, which was confirmed by the significance with negativity of dominance effect (h) in these cases. While it was not present in cross 1 under old land which was clear by its insignificance and positive values. The significance and negative values of additive  $\times$  additive effects (i) refer to the possibility of obtaining transgressive segregations from their parent in late generations in both crosses under both conditions. Additive  $\times$  dominance (j) and dominance  $\times$  dominance (l) were significant with positive values in both crosses under both conditions. Duplicate epistasis was found in all cases, except in cross 1 under old land conditions.

**Table 6. Generations mean analysis, heterosis % (MP and BP), components of variation, and GS% for No. of kernels/spikes in both crosses under new and old lands conditions.**

Cross	Cross 1		Cross 2	
Parameters \ Conditions	New lands	Old lands	New lands	Old lands
m	52.45** $\pm$ 0.86	60.74** $\pm$ 0.90	44.95** $\pm$ 0.64	63.50** $\pm$ 0.93
d	15.26** $\pm$ 2.08	14.34** $\pm$ 2.08	9.02** $\pm$ 1.45	11.55** $\pm$ 2.13
h	-23.86** $\pm$ 5.69	-8.48 <sup>NS</sup> $\pm$ 5.74	-15.29** $\pm$ 4.02	-12.85** $\pm$ 5.90
i	-26.30** $\pm$ 5.89	-16.14** $\pm$ 5.52	-21.55** $\pm$ 3.87	-21.60** $\pm$ 5.66
j	15.88** $\pm$ 2.29	16.00** $\pm$ 2.32	12.91** $\pm$ 1.63	14.94** $\pm$ 2.43
l	54.18** $\pm$ 9.69	49.25** $\pm$ 9.62	38.29** $\pm$ 6.70	38.66** $\pm$ 9.88
Epistasis	D	--	D	D
Heterosis (MP) %	4.72**	12.53**	19.97**	15.09**
Heterosis (BP) %	3.47**	9.55**	5.31**	8.75**
ID %	2.98 <sup>NS</sup>	11.73**	24.31**	4.85**
H	139.43	48.50	23.96	34.04
D	148.06	48.50	120.96	237.41
E	57.60	38.65	26.43	68.46
H/D <sup>1/2</sup>	0.97	0.72	0.45	0.38
Heritability (h <sup>2</sup> <sub>b</sub> )	65.4	73.65	71.55	65.01
Heritability (h <sup>2</sup> <sub>n</sub> )	44.46	58.40	65.10	60.66
G.S %	22.53	26.87	28.76	27.53

\* & \*\* = Significant at 0.05 & 0.01 levels of probability, respectively. <sup>NS</sup> = nonsignificant. D = Duplicate.

The results showed that D and H components were equally contributing in genetic variance for K/S trait in cross 1 under both conditions, therefore population development should take up to develop superior lines with desirable genes. On the other side in cross 2 under both conditions, D component has the largest contribution in genetic variance. These results reveal that improvement should reliance on mass selection method.  $H/D^{1/2}$  was less than unity in both crosses under both conditions; it was 0.97, 0.72, 0.45, and 0.38 in cross 1 under new land, cross 1 under old land, cross 2 under new land, and cross 2 under old land, respectively. These results reveal the presence of partial dominance in all cases for K/S trait; these findings are supported by those concluded by Al-Mfarji *et al* (2023).

Broad sense heritability ( $h^2_b$ ) was high in cross 1 under both conditions and in cross 1 under new land, while  $h^2_n$  was moderate in cross 1 under new and old land. Genetic advance under selection (G.S %) was realized as high, where it was > 20%; it was 22.53%, 26.87%, 28.76, and 27.53% in cross1 under both conditions and cross 2 under both conditions, respectively. These results are in accordance with the findings of Feltaous (2020).

Heterosis based on better parent (%) values were low *i.e.* 3.47, 9.55, 5.31 and 8.75% in cross 1 under new and land, cross 2 under new and old land, respectively; these can be attributed to the negative effects of duplicate epistasis where the opposite sign of dominance and dominance  $\times$  dominance effects neutralize each other (Kumar *et al* 2010). With regard to inbreeding depression (ID), it was highly significant with positive values while it was non-significant in cross 1 under old land. Similar results were reported by Busa *et al* (2022).

#### **100-kernels weight**

The results presented in Table (7) showed that additive effect (d) was highly significant with negative values in both crosses under both conditions; these results indicate that 100-KW is not controlled by additive effect. Dominant effect (h) was highly significant and significant with positive values in cross 1 under both conditions, while it was nonsignificant in cross 2 under both conditions.



**Table 7. Generation mean analysis Heterosis (MP and BP), components of variation, and GS% for 100-kernels weight in both crosses under new and old lands conditions.**

Cross	Cross 1		Cross 2	
Environment Parameters	New lands	Old lands	New lands	Old lands
<b>M</b>	<b>2.80**±0.05</b>	<b>3.87**±0.05</b>	<b>3.00**±0.04</b>	<b>4.12**±0.06</b>
<b>d</b>	<b>-0.79**±0.12</b>	<b>-0.91**±0.13</b>	<b>-0.73**±0.09</b>	<b>-0.93**±0.13</b>
<b>h</b>	<b>1.42**±0.35</b>	<b>1.20*±0.43</b>	<b>-0.02<sup>NS</sup>±0.31</b>	<b>-0.30<sup>NS</sup>±0.38</b>
<b>i</b>	<b>0.47<sup>NS</sup>±0.30</b>	<b>0.35<sup>NS</sup>±0.33</b>	<b>-0.48<sup>NS</sup>±0.24</b>	<b>-1.01**±0.36</b>
<b>j</b>	<b>-0.44<sup>NS</sup>±0.20</b>	<b>-0.73<sup>NS</sup>±0.30</b>	<b>-1.05**±0.20</b>	<b>-1.42**±0.14</b>
<b>l</b>	<b>2.13**±0.62</b>	<b>2.57**±0.78</b>	<b>3.33**±0.55</b>	<b>5.87**±0.61</b>
<b>Epistasis</b>	<b>C</b>	<b>C</b>	<b>--</b>	<b>--</b>
<b>Heterosis (MP) %</b>	<b>30.83**</b>	<b>15.40**</b>	<b>13.80**</b>	<b>15.03**</b>
<b>Heterosis (BP) %</b>	<b>17.39**</b>	<b>15.09**</b>	<b>3.82**</b>	<b>4.16**</b>
<b>ID %</b>	<b>30.70**</b>	<b>4.11**</b>	<b>21.48**</b>	<b>24.22**</b>
<b>H</b>	<b>0.78</b>	<b>0.25</b>	<b>0.35</b>	<b>0.21</b>
<b>D</b>	<b>0.14</b>	<b>0.71</b>	<b>0.29</b>	<b>1.28</b>
<b>E</b>	<b>0.21</b>	<b>0.23</b>	<b>0.11</b>	<b>0.24</b>
<b>H/D<sup>1/2</sup></b>	<b>2.36</b>	<b>0.62</b>	<b>1.09</b>	<b>0.41</b>
<b>Heritability (h<sup>2</sup><sub>b</sub>)</b>	<b>55.73</b>	<b>65.03</b>	<b>68.16</b>	<b>74.26</b>
<b>Heritability (h<sup>2</sup><sub>n</sub>)</b>	<b>14.72</b>	<b>54.46</b>	<b>42.80</b>	<b>68.54</b>
<b>G.S %</b>	<b>7.47</b>	<b>23.48</b>	<b>17.14</b>	<b>33.17</b>

\* & \*\* = Significant at 0.05 & 0.01 levels of probability, respectively. <sup>NS</sup> = nonsignificant. C = Complementary.

Additive × additive effects (i) was nonsignificant in all cases, except in cross 2 under old land it was highly significant with negative values. Additive × dominance (j) was non-significant in cross 1 under

both conditions and highly significant with negative values in cross 2 under both conditions. Dominance  $\times$  dominance (I) was highly significant with positive values in both crosses under both conditions. These results refer to lesser magnitude of additive than dominance in improving 100KW therefore, the selection by pedigree or bulk or single seed descent should be delayed to advanced segregating generations in order to reduce heterozygosity in this case. These results are in agreement with those obtained by Sandhu *et al* (2023).

The results showed that the additive component (D) was 0.14, 0.71, 0.29, and 1.28 in cross 1 under new land, cross 1 under old land, cross 2 under new land, and cross 2 under old land, respectively, while dominance (H) was 0.78, 0.25, 0.35, and 0.21 in cross 1 under new land, cross 2 under old land, cross 2 under new land, and cross 2 under old land, respectively. Average degree of dominance ( $H/D^{1/2}$ ) was more than unity in both crosses under new land while, it was less than unity in both crosses under old land. These results indicate presence of over dominance as well as partial dominance. Similar results were obtained by Rady (2022) and Sandhu *et al* (2023).

Broad sense heritability ( $h^2_b$ ) was high in all cases, except in cross 1 under new land, it was moderate. In regards of  $h^2_n$ , it was low in cross 1 under new land (14.72%), high in cross 2 under old land (68.54%), and it was moderate (54.46 and 42.80%) in cross 1 under old land and cross 2 under new land. Genetic advance (GS %) was low (7.47%) in cross 1 under new land and it was moderate (17.14 %) in cross 2 under new land, while it was high (23.48 % and 33.17%) in cross 1 under old land and in cross 2 under new land, respectively. These results are in line with Kumar *et al* (2017).

Heterosis (%) over better parent values were 17.39, 15.09, 3.82, and 4.16% in cross 1 under new land and old lands, cross 2 under new and old lands, respectively. While it was 30.83, 15.40, 13.80, and 15.03% in cross 1 under new land and old lands, cross 2 under new and old lands, respectively. It is notable that heterosis over better parent is high in cross 1 under both conditions compared to cross 2 under both conditions; that can be attributed to the complementary effect of epistasis. Even though, the results revealed that heterosis tend towards

better parent direction in both crosses under both conditions. Regarding ID, it was highly significant and its values were 30.7, 4.11, 21.48, and 24.22%, respectively. These results are in harmony with those obtained by Kumar *et al* (2017).

### **Grain yield/plant**

The results in Table (8) revealed that additive effect (d) was significant or highly significant with positive values in all cases except in case of cross 1 under new land it was nonsignificant. The dominance (h) and additive  $\times$  dominance (j) were nonsignificant in both crosses under both conditions. These results pointed out that additive effects is controlling GY trait and selection methods is effective in improving it. Additive  $\times$  additive effects (i) was nonsignificant in all cases, except in cross 2 under old land; it was highly significant with negative values. The significance and positivity of additive  $\times$  additive reveals possibility of obtaining transgressive segregations in late segregating generations *i.e.* cross 2 under old land. Dominance  $\times$  dominance (l) was significant or highly significant with positive values in both crosses under both conditions. These results are in agreement with those shown by Sandhu *et al* (2023).

The additive (D) component has the majority contribution than the dominance component in variance of GY trait. These results indicate that the additive effect is very important for GY trait, as we mentioned above. Average degree of dominance ( $H/D^{1/2}$ ) for GY was more than unity in cross 2 under both conditions and it was less than unity in cross 1. Similar results were concluded by Attri *et al* (2021). Broad sense heritability ( $h^2_b$ ) was high in both crosses under both conditions; similarly narrow sense heritability ( $h^2_n$ ) was high in cross 1 under both conditions. While  $h^2_n$  was low and medium in cross 1 under new and old land conditions, respectively. These results indicate that the additive variance has the largest contribution in genetic variance. Genetic advance (G.S %) was ranged between moderate to high in cross 1 and cross 2 under both conditions. These findings are in accordance with Salous *et al* (2023).

**Table 8. Generations mean analysis, Heterosis% (MP and BP), components of variation, and GS% for grain yield / plant in both crosses under new and old lands conditions.**

Cross	Cross 1		Cross 2	
Environment Parameters	New lands	Old lands	New lands	Old lands
<b>m</b>	21.53**±0.85	26.11**±1.05	20.20**±0.60	28.27**±0.91
<b>d</b>	2.19 <sup>NS</sup> ±1.84	4.08**±2.09	3.17**±1.58	4.22*±2.19
<b>h</b>	0.37 <sup>NS</sup> ±5.09	-7.81 <sup>NS</sup> ±5.98	-1.05 <sup>NS</sup> ±4.00	-9.90 <sup>NS</sup> ±5.72
<b>i</b>	-1.26 <sup>NS</sup> ±5.01	-9.65 <sup>NS</sup> ±5.93	-3.86 <sup>NS</sup> ±3.96	-12.03**±5.70
<b>j</b>	2.62 <sup>NS</sup> ±1.91	3.13 <sup>NS</sup> ±2.20	1.76 <sup>NS</sup> ±1.65	3.16 <sup>NS</sup> ±2.23
<b>l</b>	14.19*±8.30	35.33**±9.46	21.23**±6.83	46.48**±9.55
<b>Epistasis</b>	--	--	--	--
<b>Heterosis (MP) %</b>	6.88**	15.09**	12.7**	6.51**
<b>Heterosis (BP) %</b>	4.98**	2.94	5.95**	3.16**
<b>ID %</b>	14.77**	4.85**	19.15**	19.09**
<b>H</b>	125.78	16.57	259.54	384.37
<b>D</b>	242.08	478.57	26.69	168.79
<b>E</b>	9.94	6.7	2.97	6.19
<b>H/D<sup>1/2</sup></b>	0.72	0.19	3.12	1.51
<b>Heritability (h<sup>2</sup><sub>b</sub>)</b>	93.88	97.32	96.35	96.68
<b>Heritability (h<sup>2</sup><sub>n</sub>)</b>	74.52	95.67	16.43	45.21
<b>G.S %</b>	90.85	79.37	15.10	45.01

\* & \*\* = Significant at 0.05 & 0.01 levels of probability, respectively. <sup>NS</sup> = nonsignificant

Heterosis (%) was highly significant with positive values in all cases. Its values over better parent were 4.98, 2.94, 5.95 and 3.16% in cross 1 under new and lands, cross 2 under new and old lands, respectively. The results of heterosis over mid-parent showed that its values were 6.88, 15.09, 12.70, and 6.51% in cross 1 under new and land, cross 2 under new and old lands, respectively. The findings of positivity heterosis indicate that it tends towards better parent direction in both cross under both conditions. Regarding inbreeding depression (ID), it was highly significant with positive values in all cases. These results exhibit the importance of inbreeding depression and heterosis jointly in positive selection process. These results are in agreement with Salous *et al* (2023).

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## طبيعة التوارث للمحصول ومكوناته في هجينين من قمح الخبز تحت ظروف

### الاراضى القديمة والجديدة في مصر العليا

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الهدف الرئيسى لمربى القمح هو إستنباط أصناف عالية المحصول متأقلمة لتخفيف التأثيرات البيئية الناتجة عن تغير المناخ، لذا يجب إستجاء نظام التوارث لصفة المحصول ومكوناته. أجريت الدراسة الحالية فى موقعين يمثلان الأراضى القديمة والجديدة فى محافظة قنا خلال ثلاث مواسم زراعيه ٢٠١٩/٢٠٢٠ حتى ٢٠٢١/٢٠٢٢ لصفة المحصول ومكوناته (عدد السنابل/نبات، عدد الحبوب/سنبله، وزن اله - ١٠٠ حبه، محصول الحبوب/نبات). أظهر تحليل التباين أختلافات معنويه بين الستة عشائر للهجينين لكل الصفات المدروسة. أظهرت النتائج أن الجيل الأول تفوق على الأب الأعلى فى كلا الهجينين فى كلا الموقعين لكل الصفات المدروسة. وأشارت قيم *PR* الى وجود سيادة فائقة فى كلا الهجينين فى كلا الموقعين لكل الصفات المدروسة. أظهر أختبار الـ *Scaling test* عدم كفاية موديل الثلاث مقاييس لكل الصفات المدروسة فى كلا الهجينين فى كلا الموقعين، فى حين أن موديل الستة عشائر نجح فى شرح وجود التفاعلات غير الأليية. كما أظهرت النتائج أن التأثير المضيف والتأثير السيادةى كان معنوى أو على المعنويه بإشارة موجبة فى معظم الحالات لكل الصفات تحت الدراسة، فى حين أن التأثير المضيف  $\times$  المضيف كان معنويًا بإشارة سالبة فى كل الحالات ما عدا فى حالة الهجين الأول تحت ظروف الاراضى القديمة حيث كانت غير معنوية. أيضا وجد أن التأثير المضيف  $\times$  السيادةى غير معنويًا فى كل الحالات فى حين أن التأثير السيادةى  $\times$  المعنويًا بإشارة موجبة فى كل الحالات. وقد وجد تأثير للسيادة الفائقة "Duplicate epistasis" فى الهجين الأول فى كلا الموقعين لصفة عدد السنابل/نبات فى حين انه ظهرت تأثيرها فى صفة عدد الحبوب/سنبله تحت ظروف الاراضى الجديدة فقط، ولكن السيادة الفائقة "Complementary epistasis" وجدت فقط فى الهجين الأول تحت كل الظروف. بالنسبة لقيم قوة الهجين لأعلى الابوين فقد كانت عاليه وموجبه فى معظم الحالات مما يعنى اتجاه قوة الهجين تميل الى الاب العالى. كفاءة التوريث العامة والخاصة والتقدم الوراثى بالانتخاب عامة تراوحت من المتوسطة الى عالية ماعدا بعض الحالات القليلة، وتراوح تأثير التربية الداخلية ما بين (٠,٤٧ - ٣٠,٧٠%) و (٢,٩٨ - ٢٢,٣١%) و (٤,١١ - ٣٠,٧٠%) و (٤,٨٥ - ١٩,١٥%) لصفات عدد السنابل/نبات و عدد الحبوب/سنبله و وزن اله - ١٠٠ حبه ومحصول الحبوب/نبات على التوالى. أظهرت الدراسة أن فهم طبيعة التوارث للمحصول ومكوناته يمكننا من تحديد طريقة التربية والانتخاب المناسبة فى برامج التربية.

المجلة المصرية لتربية النبات ٢٨(٢): ٢٣٩ - ٢٦٢ (٢٠٢٤)