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### Direct and Indirect Selection for Grain Yield in Bread Wheat (*Triticum aestivum* L.)

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#### ABSTRACT

Direct and indirect selection for grain yield through 1000 grain weight, spikelet fertility and spike density were achieved in bread wheat at the Exper. Farm Fac. Agric., Minia Univ. Egypt during the three successive seasons of 2016/17 to 2018/19. After two cycles of pedigree selection phenotypic variation of grain yield/plant, 1000 grain weight, spikelet fertility and spike density decreased rapidly from F<sub>2</sub> base population to F<sub>4</sub>. Indirect selection through high 1000 grain weight resulted in the highest grain yield/plant (23.62g) followed by direct selection for grain yield/plant (20.66 g). Average direct gain for the ten selected families of direct selection for grain yield showed highly significant increase in percentage of the bulk sample of 62.95% and the better parent of 39.25%. Pedigree selection was effective in detecting the high yielding families. Family No. 145 gave significant ( $P < 0.01$ ) grain yield in percentage of the better parent and bulk sample by 77.09 and 107.23%, respectively. Average direct response in percentage of the bulk sample was significant and reached 21.08% for 1000 grain weight, 31.12% for spikelet fertility and 7.27% for spike density. Three families; No. 15, No. 72 and No. 153 surpassed significantly the bulk sample by 33.83, 43.01 and 29.28%, respectively, when selection practiced for 1000 grain weight. Family No. 145 considered to be a promising line in grain yield and spikelet fertility. High strong positive genotypic correlation was found between grain yield with each of weight of spikes/plant (0.81), no. of grains/spike (0.71), weight of grains/spike (0.91), 1000 grain weight (0.92) and spikelet fertility (0.70).

**Keywords:** fertility; spike density; pedigree selection; genotypic correlation.



#### INTRODUCTION

In Egypt, wheat is the most important grain crop. Wheat constitutes nearly 10% of agricultural production and approximately 20% of all agricultural imports McGill *et al.* (2015). In spite of a lack share of cereals as a source of food energy, wheat still the main food as energy source from daily calories intake in the Egyptian diet. Globally, Egypt is the biggest importer of wheat. So, it's necessary to increase wheat production to decrease the imports. One of the means of increasing unit area productivity is the breeding for high-yielding varieties through pedigree selection method. Khames *et al.* (2017) revealed that the direct pedigree selection for grain yield/plant in wheat was an effective tool for improving the grain yield and could be effective to isolate high yielding lines. El-Hosary *et al.* (2020) found that pedigree method is considered the best breeding method for grain yield/plant, spikes/plant, grains/spike and 1000- grain weight. Meier *et al.* (2019) noted that the heritability of the spike weight, no. of grains/spike, and grain yield/plant may result in greater direct selection gains. El-Hosary *et al.* (2011) evaluated the high selected lines for grain yield/plant and 1000-grain weight, and indicated that indirect selection for 1000-grain weight was more efficient in breeding for superior yielding F<sub>5</sub> lines. Cantrell and Haro-Arias (1986) pointed to the effect of indirect selection for spikelet fertility on grain yield. They found that the group selected for high spikelet fertility exhibited significantly higher number of grains/spikelet and grains/spike than the random group and the groups selected for low fertility. Selection for spikelet

fertility resulted in low significant of 1000 grain weight and grains weight/spike in the groups of families selected for high spikelet fertility. Iftikhar *et al.* (2012) reported that spike characteristics like spike length, spikelets/spike, grains/spike and 1000 grain weight had significantly positive association with improved grain yield in wheat. Yousaf *et al.* (2017) reported that thousand grain weight could be used as selection criteria for selecting high yielding genotypes for future use in hybridization programs. Guo *et al.* (2017) noted that the morphology of the spike is crucial in determining grain yield. The components of the spike affect each other. The number and structure of these spike components involve spike length, spike weight, grains/spike, grain weight/spike, and spikelets/spike, that all share to last grain yield/spike. Guo *et al.* (2018) reported that the traits identified affect spike morphology i.e. spikelet fertility, spikelet density can be used to improve grain yield. This study aimed to compare the efficiency of indirect selection for yield via spike traits compared to direct selection for grain yield in bread wheat, and their effects on phenotypic and genotypic correlations

#### MATERIALS AND METHODS

The field experiments were carried out at the Exper. Farm of Fac. Agric., Minia Univ., Egypt during three successive seasons i.e., 2016-2019. F<sub>2</sub> segregating population derived from the cross Emar1 x Nielain (*Triticum aestivum* L.) was used.

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**Table1. The pedigree of the parents.**

Parental cultivars	Pedigree
Emara 1	Kindly provided from Prof. Dr. Ezzat Mahdy – Prof. of plant breeding in Agronomy Dept. – Fac. of Agriculture. Assiut Univ. S948.A1/7*SANTA ELENA (CMH72A.390-OSDN)
Nielain	

In 2016/2017 season, 600 F<sub>2</sub> individual plants from the population were grown in 3 non-replicated plots. Each plot consisted of 10 rows, 2 m long and 30 cm apart. Grains were sown on November 20<sup>th</sup>, 2016 and spaced 10 cm within a row to give average 20 individual plants/row. The two parents were grown in separate plots. Data were recorded on 200 plants chosen randomly from the population. Pedigree selection was practiced as follows: 1-Direct selection for grain yield (The highest 20 plants in grain yield). 2-Indirect selection for each of the highest 20 plants in 1000 grain weight, the highest 20 plants in spike density and the highest 20 plants in spikelet fertility. An equal number of 2 grains from each plant (600 plants) were bulked to give F<sub>2</sub> random bulk sample for the population.

In 2017/2018 season: the eighty selected plants (F<sub>3</sub>-generation) from the population along with the parents and the bulk sample were sown in rows on November 20<sup>th</sup>, 2017 in a randomized complete block design of three replications. The plot size was one row, 1.5 m long, 30 cm apart and 5 cm between grains within a row. The recommended cultural practices for wheat production were adopted throughout the growing seasons. At the end of the season, the best plant from each of the best 10 families was saved to give 40 selected plants; 10 plants for each selection criterion.

In 2018/2019 season: the forty selected plants (F<sub>4</sub>-generation) from the population along with the parents and the bulk sample were sown on November 20<sup>th</sup>, 2018 in a randomized complete block design of three replications. The same procedures of the previous season were followed. The following characteristics were measured on the basis of ten guarded plants per row from each row, hence the mean of the ten plants was calculated. Plant height [PH, cm], Spike length [SL, cm], No. of spikes/plant [NS/P], No. of spikelets/spike [NST/S], No. of grains/spike [NG/S], Weight of grains/spike [WG/S, g], Grain yield/plant [GY/P, g], 1000-grain weight [1000-GW, g], Spike density SD = [NST/SL], Spikelet fertility SF = [NG/S] / [NST/S]. Data were statistically analyzed according to Steel and Torrie (1980). Means of genotypes were compared using Revised LSD test at 5% and 1% level of probability, according to El-Rawi and Khalafala (1980).

The phenotypic (PCV %) and genotypic (GCV %) coefficients of variability were calculated as outlined by Burton (1952).

Estimates of broad sense heritability (H) in F<sub>2</sub>-generation:

$$\sigma^2 E = (\sigma^2 P_1 + \sigma^2 P_2) / 2,$$

Where P<sub>1</sub> and P<sub>2</sub> are the two parents.  $\sigma^2 G = \sigma^2 F_2 - \sigma^2 E$ ,  $H = \sigma^2 G / \sigma^2 F_2$

Estimates of the expected genetic advance ( $\Delta G$ ) in F<sub>2</sub>-generation  $\Delta G = i \sigma P H$ , where  $i$ =selection intensity,  $\sigma P$  is the phenotypic standard deviation and H is the heritability of the trait.

Estimates of in heritability broad sense F<sub>4</sub>-generation were calculated from variance components according to Walker (1960).

Realized heritability  $h^2 = R$  “response to selection” / S “selection differential” as mentioned by Falconer, 1989.

The significance of the observed direct and correlated response to selection was measured as deviation percentage of families mean from the bulk or the better parent using L.S.D.

LSD Family =  $t \cdot \sqrt{\frac{2Mse}{r}}$  to compare families with the better parent and the bulk sample.

LSD Average =  $t \cdot \sqrt{Mse/r + Mse/fr}$  to compare average of the families with the better parent and the bulk sample.

## RESULTS AND DISCUSSION

### 1- Description of the base population.

Means and variances of the F<sub>2</sub>-generation are presented in Table 2. Comparing the population mean of plant height (106.87cm) and NST/S (23.40) with mean of the two parents indicates dominance towards the lower parent Nielain which gave 106.52cm for plant height and 24.13 for NST/S. However, mean spike length (15.21cm) showed nearly no-dominance, where the parental mean was 16.99 cm. Population mean in no. of spikes/plant (12.44), weight of spikes/plant (39.30g) and grain yield/plant (22.14g) showed over dominance with regard to the two parents.

Concerning days to heading, no. of grains/spike, weight of grains/spike, spike density and spikelet fertility showed nearly no dominance in which the population mean was close to the parental mean. Yadav and Singh (2011) found that knowledge of nature of gene action, correlation among traits, heritability and genetic advance help the breeders in determine the most appropriate breeding procedure to enhance the genetic potentialities and to make breakthrough in the productivity of crop.

The coefficient of variation in grain yield was very high (66.42%) ranging from 1.65 to 70.01 g indicating possibility selection for grain yield in F<sub>2</sub>-generation. The coefficient of variability for spike characteristics, 1000-grain weight, spike density and spikelet fertility were 22.95, 23.17 and 32.96%. This enhanced chance of selection for spike characteristics. High values of heritability in broad sense were estimated for all traits and ranged from 74.93 for spike density to 99.81% for weight of spikes/plant. Similar results were reported by Mahdy *et al.* (2012), Rasha, Mahdy *et al.* (2012), Hamam (2014) and Khames *et al.* (2017).

High genetic variance for the studied traits resulted in high heritability in broad sense and high values of expected genetic advance under selection of the highest 10% plants, /from the base population. Expected genetic advance from selection as percentage of population mean reached 54.00% for grains/spike, 57.00% for spikelet fertility, 98% for spikes/plant, 118% for weight of spikes/plant and 112% for grain yield/plant. These high estimates could be the result of high level of heterozygosity in F<sub>2</sub>-generation, dominance and over dominance effects.

**Table 2. Description of base population and the two parents in F<sub>2</sub>-generation (2016/2017 growing season).**

	DH	PH <sub>cm</sub>	SL <sub>cm</sub>	NS/P	WS/P <sub>g</sub>	NST/S	NG/S	WG/S <sub>g</sub>	1000-GW <sub>g</sub>	GY/P <sub>g</sub>	SD	SF
Mean	87.75 ±	106.87 ±	15.21 ±	12.44 ±	39.30 ±	23.40 ±	58.89 ±	2.38 ±	41.33 ±	22.14 ±	1.58 ±	2.53 ±
± S.E.	0.50	1.57	0.18	0.49	1.87	0.25	1.34	0.06	0.67	1.04	0.03	0.06
F <sub>2</sub> -Variance	49.67	490.22	6.50	48.74	701.96	12.54	360.37	0.76	89.99	216.28	0.13	0.69
C.V%	8.03	20.72	16.76	56.12	67.42	15.16	32.24	36.62	22.95	66.42	23.17	32.96
Min.	72.00	48.00	6.00	2.00	5.00	16.00	14.00	0.57	18.50	1.65	0.77	0.50
Max.	103.00	145.00	22.00	41.00	154.00	29.00	109.00	4.98	94.44	70.01	3.50	5.06
Emeral P1	99.89	125.78	23.40	2.98	13.82	27.48	78.64	3.68	54.86	11.72	1.18	2.86
Nielain P2	93.01	106.52	10.58	4.39	10.84	24.13	46.54	1.90	50.90	10.52	2.30	1.93
δ <sup>2</sup> P1	8.61	13.46	2.18	0.09	0.91	0.93	19.44	0.02	6.43	5.25	0.01	0.02
δ <sup>2</sup> P2	15.63	13.70	0.81	0.29	1.70	0.99	11.65	0.15	30.07	12.84	0.06	0.02
H%	75.60	97.23	77.03	99.61	99.81	92.34	95.69	88.62	79.72	95.82	74.93	97.43
GA	9.38	37.89	3.46	12.24	46.54	5.76	31.97	1.36	13.31	24.80	0.48	1.43
Δ GA/mean%	11.00	35.00	23.00	98.00	118.00	25.00	54.00	57.00	32.00	112.00	31.00	57.00

δ<sup>2</sup>= variance, H%= heritability in broad sense, GA= expected genetic advance.

**2. Evaluation of the 2<sup>nd</sup> cycle of pedigree selection, F<sub>4</sub>-generation; season 2018/2019**

**1. Variability and heritability estimates**

Mean squares showed significant differences (p<0.01) among the selected families of the studied traits for each selection criterion in F<sub>4</sub>-generation as presented in Table 3. This refers to presence enough variation for further cycles of selection for these traits. Similar results were obtained by Mahdy *et al.* (2015) and Khames *et al.* (2017).

After two cycles of pedigree selection for grain yield/plant, 1000 grain weight, spikelet fertility and spike density, the PCV% decreased rapidly to 23.87, 12.94, 14.80 and 14.25%, respectively in F<sub>4</sub> (Table 3) compared to 66.42, 22.95, 32.96 and 23.17%, respectively in F<sub>2</sub> base population

(Table 2). The variability was estimated as CV % in the F<sub>2</sub>-generation and as PCV % in the F<sub>4</sub>-generation. Phenotypic coefficient of variability (PCV%) was slightly larger than genotypic one (GCV%) for each selection criterion and the other correlated traits. The same trend for the other correlated traits of each selection criterion was observed. Mahdy *et al.* (2012), Salous *et al.* (2014) and Abd El-Rady (2017) found that the genotypic variance was slightly less than the phenotypic variance and generally decreased from the base population (F<sub>3</sub>) to the F<sub>5</sub>-generation.

The four selection criteria recorded high estimates of broad sense heritability; 92.76% for grain yield/plant, 87.62 for spikelet fertility and 96.16 for spike density, while 1000 grain weight showed moderate heritability 65.74%..

**Table 3. Mean squares, Heritability in broad sense (H%), Realized heritability (h<sup>2</sup>), Genotypic (GCV%) and phenotypic (PCV%) coefficients of variation of the studied traits in selected families for each selection criterion in F<sub>4</sub>-generation (season 2018/19 ).**

Sel. criterion	df	Grain yield/Plant											
		DH	PH	SL	NS/P	WS/P	NST/S	NG/S	WG/S	1000-GW	GY/P	SF	SD
Reps	2	19.92	71.72	0.62	1.52	51.67	1.99	24.89	0.34	129.2	7.36	0.01	0
Families	12	120.36**	938.95**	26.71**	2.87**	176.15**	7.98**	508.93**	2.50**	119.07*	72.98**	0.52**	0.21**
Error	24	11.84	66.86	0.67	0.82	10.28	0.5	33.65	0.32	53.9	5.28	0.04	0.01
H %	-	-	-	-	-	-	-	-	-	-	92.76	-	-
G.C.V%	-	5.66	12.48	17.59	14.87	24.48	5.95	16.44	22.53	9.58	22.99	13.87	16.3
P.C.V%	-	5.96	12.94	17.81	17.58	25.23	6.15	17.01	24.11	12.95	23.87	14.45	16.55
h <sup>2</sup>	-	-	-	-	-	-	-	-	-	-	71.54	-	-
1000 grain weight													
Reps	2	13	27.87	1.03	0.97	3.64	0.86	21.31	0.16	9.77	5.62	0.07	0
Families	12	129.08**	1081.88**	23.89**	4.39**	184.77**	10.95**	511.35**	1.48**	132.86*	132.04**	0.73**	0.22**
Error	24	17.42	65.65	0.75	0.64	15.95	0.7	26.63	0.16	45.52	5.21	0.04	0.01
H %	-	-	-	-	-	-	-	-	-	-	65.74	-	-
G.C.V%	-	5.75	12.59	16.78	18.4	22.5	7.08	17.47	18.01	10.49	27.53	17.19	16.75
P.C.V%	-	6.18	12.99	17.05	19.9	23.54	7.32	17.95	19.05	12.94	28.09	17.65	17.04
h <sup>2</sup>	-	-	-	-	-	-	-	-	-	-	45.38	-	-
Spikelet fertility													
Reps	2	7.72	28	0.09	1.29	41.8	1.64	4.8	0.53	221.5	6.13	0	0
Families	12	116.75**	1025.56**	24.01**	2.72**	135.74**	6.68**	503.75**	2.34**	128.53*	59.57**	0.54**	0.21**
Error	24	14.77	76.06	0.48	0.47	8.77	0.46	50.59	0.27	47.23	4.56	0.07	0.01
H %	-	-	-	-	-	-	-	-	-	-	-	87.62	-
G.C.V%	-	5.54	13.19	16.95	16.45	22.85	5.52	16.39	21.77	10.63	21.69	13.85	16.42
P.C.V%	-	5.92	13.71	17.12	18.07	23.62	5.72	17.28	23.13	13.37	22.57	14.8	16.64
h <sup>2</sup>	-	-	-	-	-	-	-	-	-	-	-	34.25	-
Spike density													
Reps	2	16.69	13	1.45	0.89	29.01	3.01	27.09	0.08	15.25	1.8	0.04	0
Families	12	132.49**	913.12**	21.17**	6.34**	137.72**	9.49**	400.87**	0.84**	110.99*	118.20**	0.61**	0.19**
Error	24	12	50.22	0.48	0.91	11.74	0.8	47.56	0.13	50.33	5.45	0.09	0.01
H %	-	-	-	-	-	-	-	-	-	-	-	-	96.16
G.C.V%	-	5.96	12.22	18.61	21.87	23.83	6.86	16.21	14.63	9.32	30.42	15.45	13.98
P.C.V%	-	6.25	12.57	18.82	23.64	24.91	7.17	17.27	15.94	12.61	31.15	16.68	14.25
h <sup>2</sup>	-	-	-	-	-	-	-	-	-	-	-	-	70.00

\*and \*\*; significant at 0.05 and 0.01 level of probability, respectively

The realized heritability of criteria grain yield/plant, 1000 grain weight, spikelet fertility and spike density were 71.54, 45.38, 34.25 and 70.00%, respectively (Table 3).

These values were lower than heritability in broad sense those calculated from variance components. The high values of broad sense heritability in F<sub>4</sub>-generation calculated from

the expected mean squares could be attributed to evaluation the selected families in one location for one season. Other than if the evaluation was done in different years and locations. Furthermore, high values of heritability might be resulted from the effects of dominance and gene interactions. Meier *et al.* (2019) found significant genetic differences in days to flowering, spike weight, spike length, no. of spikelets, kernel weight and no. of kernels in different wheat genotypes. The wheat lines showed a high ability for improving these traits via selection. The wheat lines presented high phenotypic variance for the plant height PH, no. of tillers and no. of kernels, which was mostly attributed to the lower environmental variation. The higher heritability values for SW and KW were more than 70%. The heritability of the spike weight, no. of kernels, and kernel weight reveals that selection of these traits may result in greater direct selection gains.

## 2. Means of the studied traits of each selection criteria

Selection for 1000 grain weight resulted in the highest grain yield per plant (23.62 g.), followed by direct selection for grain yield per plant (20.66 g.). Selection for spikelet fertility recorded the lowest grain yield (19.74 g.) (Table 4). El-Hosary *et al.* (2020) considered that pedigree method is the best method to improve grain yield/plant, spikes/plant, grains/spike and 1000-grain weight.

Regarding the effect of selection criteria on the other correlated traits; selection for 1000 grain weight gave the highest 1000 grain weight 51.42 g., followed by selection for high spikelet fertility 48.97 g. Selection for high grain yield and spikelet fertility almost gave the same value of spikelet fertility (2.88) followed by selection for 1000 grain weight (2.79). Moreover, selection for spike density recorded the lowest spikelet fertility (2.70). Concerning, spike density, results of selection indicated that selection high for spike density gave the highest spike density 1.77, followed by the three other selection criteria (Table 4).

Regarding effect of selection criteria on correlated traits; selection for grain yield gave the highest values of spike length 16.75 cm, no. of spikelets/spike 26.52 and no. of grains/spike 76.55. Selection for 1000 grain weight gave the tallest plant (146.17 cm) and the highest weight of spikes/plant (33.33 g). Also, selection for spikelet fertility gave the highest grains weight/spike (3.82 g). The highest spikes/plant (6.15) recorded from selection for spike density (Table 4). El-Hosary *et al.* (2011) estimated the response to individual plant selection in early generation through direct and indirect selection to increase grain yield. The results indicated that indirect selection was more efficient in breeding forward superior yielding F<sub>5</sub> lines.

**Table 4. Average of studied traits of the selected families in the four selection criteria, means of the two parents and the bulk sample in F<sub>4</sub>-generation, season 2018/19**

Criteria	DH	PH; cm	SL; cm	NS/P	WS/P; g	NST/S	NG/S	WG/S; g	1000 GW; g	GY/P; g	SD	SF
GY/P; g	106.20	136.67	16.75	5.56	30.37	26.52	76.55	3.79	48.65	20.66	1.60	2.88
1000 GW; g	106.10	146.17	16.55	6.08	33.33	26.12	72.75	3.69	51.42	23.62	1.59	2.79
SF	105.33	134.83	16.53	5.27	28.48	26.07	74.98	3.82	48.97	19.74	1.59	2.87
SD	106.30	138.83	14.11	6.15	27.20	24.80	66.94	3.32	48.24	20.16	1.77	2.70
LSD 5%	2.18	4.45	0.40	0.49	1.63	0.42	3.50	0.26	ns	1.28	0.03	0.13
LSD 1%	2.89	5.92	0.53	0.66	2.17	0.56	4.65	0.34	ns	1.70	0.04	0.18
Emara1	110.33	167.00	21.83	3.74	28.03	29.37	77.42	3.36	48.55	14.84	1.34	2.64
Nielain	98.33	128.67	10.63	5.28	27.30	25.60	47.78	2.42	47.37	12.93	2.42	1.87
Bulk	98.33	137.00	15.77	4.93	29.59	25.90	56.58	2.42	42.47	12.68	1.65	2.19

## 3. Observed direct and correlated response of the studied traits

Average direct observed genetic gain for the ten selected families for direct selection criterion; grain yield showed significant increase ( $P \leq 0.01$ ) in percentage of the unselected bulk sample by 62.95% and the better parent (Nielain) by 39.25% (Table 5). These results indicate that pedigree selection was effective in detecting the high yield families. These results agree with those reported by Salous *et al.* (2014), Mahdy *et al.* (2015), Abd El-Rady (2017) and Khames *et al.* (2017). The average correlated genetic gains showed significant increase over the bulk sample for no. of grains/spike (35.31%), weight of grains/spike (56.23%), spikelet fertility (31.71%) and days to heading (8.00%), and significant decrease ( $P \leq 0.01$ ) for plant height (-18.16%), spike length (-23.28), spikelets/spike (-9.69%) and spike density (-33.94%).

Based on the individual families, seven families; No. 2, No. 58, No. 126, No. 137, No. 138, No. 143 and No. 145 significant out yielded ( $P \leq 0.01$ ) the bulk sample by 97.85, 46.88, 86.80, 93.56, 82.75, 46.86 and 107.23%, respectively. From these families, five families; No. 2, No. 126, No. 137, No. 138 and No. 145 significant out yielded ( $P \leq 0.01$ ) the better parent by 69.07, 59.63, 65.40, 56.17 and 77.09%, respectively. Family No. 145 gave the highest significant ( $P \leq 0.01$ ) grain yield in percentage of the better parent and bulk sample by 77.09 and 107.23%, respectively. Grain yield of this family depended on significant increase ( $P \leq 0.01$ ) in

weight of spikes/plant, no. of grains/spike, weight of grains/spike and spikelet fertility by (55.58 and 64.21%), (68.50 and 23.13%), (129.40 and 65.34%) and (54.16 and 27.81%) in percentage the bulk and better parent, respectively. Moreover, this family No. 145 recorded significant ( $P \leq 0.01$ ) decrease in spike density -14.89 and -42.11% in percentage the bulk sample and the better parent, respectively. Family No. 2 recorded second high yielding family by 97.85 and 69.07% in percentage bulk and better parent, its high grain yield depended on the significant ( $P \leq 0.01$ ) increase in number of spikes/plant (41.22 and 32.00%) and weight of spikes/plant (35.52 and 43.04%) in percentage bulk and better parent, respectively (Table 5). In addition to family No. 2 recorded highly significant increase in no. of grains/spike (30.76%), weight of grains/spike (57.78%), 1000-grain weight (29.75%) and spikelet fertility (33.05%) compared to the bulk sample. Family No. 137 recorded third high yielding family compared to bulk (93.56%) and better parent (65.40%). Family No. 137 gave positive significant in weight of spikes/plant (27.11 and 20.43%) compared better parent and bulk, respectively. Furthermore, it showed significant increase compared to bulk sample in plant height (11.92%), number of grains/spike (21.18%), spikelet fertility (20.65%), and highly significant increase in days to heading (15.93%) and weight of grains/spike (59.67%). However, it recorded negative significant ( $P < 0.01$ ) decrease in spike length (-28.40%), spikelets/spike (-11.58%) and spike density (-31.34%).

Family No. 138 gave significant ( $P \leq 0.01$ ) increase in weight of grains/spike (86.16%), spikelet fertility (39.21%), increase ( $P \leq 0.05$ ) in spikelets/spike (6.18%) and 1000 grain weight (32.89%) compared to bulk sample, and weight of grains/spike (34.18%) and spikelet fertility (15.42%) compared better parent. However, it showed significant decrease compared to better parent of plant height (-15.17%), spike length (-21.53%) and spikelets/spike (-6.36%).

The average direct genetic response to selection for 1000 grain weight (Table 6) in percentage of the bulk sample was significant positive (21.08%) but was not significant in percentage the better parent (5.90%). El-Hosary *et al.* (2011) indicated that selection for grain number, number of spikes/plant and 1000-grain weight was efficient in isolating superior yielding  $F_5$  lines.

The average correlated genetic grain of the ten selected families for 1000 grain weight showed significant increase ( $P \leq 0.01$ ) from the bulk sample in days to heading (7.90%), no. of spikes/plant (23.20%), no. of grains/spike (28.58%), weight of grains/spike (52.15%), grain yield/plant (86.27%) and spikelet fertility (27.77%), significant increase for in percentage the better parent in days to heading (7.90%), weight of spikes/plant (18.91%) and grain yield/plant (59.17%). However significant ( $P \leq 0.01$ ) decrease in percentage of better parent for plant height (-12.48%), spike length (-24.20%), no. of spikelets/spike (-11.07%) and spike density (-34.31%) (Table 6).

**Table 5. Observed direct and correlated genetic response to selection for grain yield/plant in percentage of the bulk sample and better parent of the studied traits of the selected families in the  $F_4$ -generation (season 2018/19)**

Families	GY/P		DH		PH		SL		NS/P		WS/P	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
2	97.85**	69.07**	7.12*	7.12*	8.27	-11.18**	-2.96	-29.92**	41.22*	32.00*	35.52**	43.04**
3	27.28	8.76	10.51**	10.51**	7.06	-12.18**	-1.06	-28.55**	-22.97	-28	-21.14*	-16.77
58	46.88**	25.51	10.51**	10.51**	-24.57**	-38.12**	0.21	-27.63**	34.23*	25.47	-28.58**	-24.61*
75	25.08	6.89	5.08	5.08	2.19	-16.17**	-16.91**	-40.00**	22.97	14.95	-27.00**	-22.95*
126	86.80**	59.63**	19.66**	19.66**	11.92*	-8.18	26.64**	-8.55**	13.51	6.11	21.55*	28.30**
137	93.56**	65.40**	15.93**	15.93**	11.92*	-8.18	-0.85	-28.40**	22.97	14.95	20.43*	27.11**
138	82.75**	56.17**	3.05	3.05	3.41	-15.17**	8.67	-21.53**	0.68	-5.89	5.22	11.06
143	46.86**	25.5	2.03	2.03	-5.11	-22.16**	13.74**	-17.86**	-6.08	-12.21	-10.21	-5.23
145	107.23**	77.09**	-1.02	-1.02	3.41	-15.17**	28.33**	-7.33*	2.7	-4	55.58**	64.21**
160	15.19	-1.57	7.12*	7.12*	-20.92**	-35.13**	6.55	-23.05**	18.58	10.84	-24.86**	-20.69*
Average	62.95**	39.25**	8.00**	8.00**	-0.24	-18.16**	6.24	-23.28**	12.78	5.42	2.65	8.35
LSD5% Fam	30.55	26.1	5.9	5.9	10.06	8.25	8.73	6.3	30.88	28.86	18.26	19.27
LSD1% Fam	41.4	35.37	7.99	7.99	13.63	11.18	11.83	8.54	41.84	39.11	24.75	26.12
LSD5% Avg	22.65	19.36	4.37	4.37	7.46	6.12	6.47	4.68	22.9	21.4	13.54	14.29
LSD1% Avg	30.7	26.23	5.93	5.93	10.11	8.29	8.77	6.34	31.03	29.01	18.35	19.37
Families	NST/S		NG/S		WG/S		1000-Gw		SF		SD	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
2	-1.8	-13.39**	30.76**	-4.45	57.78**	13.72	29.75*	13.49	33.05**	10.31	1.01	-31.30**
3	0.64	-11.24**	52.03**	11.09	59.80**	15.17	20.49	5.39	50.72**	24.96**	1.63	-30.88**
58	-2.06	-13.62**	27.57**	-6.78	17.65	-15.2	-8.32	-19.81	29.80**	7.62	-2.48	-33.67**
75	-7.21**	-18.16**	13.06	-17.38**	7.28	-22.68	0.55	-12.05	21.68**	0.89	11.52**	-24.15**
126	14.16**	0.68	50.38**	9.89	71.58**	23.67	23.16	7.72	31.84**	9.3	-9.73*	-38.60**
137	0.26	-11.58**	21.18*	-11.45	59.67**	15.09	24.25	8.69	20.65*	0.03	0.94	-31.34**
138	6.18*	-6.36**	47.89**	8.07	86.16**	34.18*	32.89*	16.24	39.21**	15.42*	-2.38	-33.60**
143	1.42	-10.56**	28.42**	-6.16	52.21*	9.7	15.23	0.79	26.28**	4.69	-10.97*	-39.45**
145	9.27**	-3.63	68.50**	23.13**	129.40**	65.34**	22.76	7.38	54.16**	27.81**	-14.89**	-42.11**
160	3.09	-9.08**	13.25	-17.24**	20.8	-12.94	-15.23	-25.85*	9.75	-9.01	-3.44	-34.32**
Average	2.39	-9.69**	35.31**	-1.13	56.23**	12.6	14.55	0.2	31.71**	9.2	-2.88	-33.94**
LSD5% Fam	4.59	4.05	17.28	12.63	39.12	28.19	29.13	25.48	15.64	12.97	8.23	5.6
LSD1% Fam	6.22	5.49	23.42	17.11	53.01	38.21	39.48	34.53	21.2	17.58	11.15	7.59
LSD5% Avg	3.4	3	12.81	9.36	29.01	20.91	21.61	18.9	11.6	9.62	6.1	4.15
LSD1% Avg	4.61	4.07	17.37	12.69	39.31	28.33	29.28	25.61	15.72	13.03	8.27	5.63

\*and \*\* significant at 0.05 and 0.01 level of probability.

Based on the individual families, three families; No. 15, No. 72 and No. 153 surpassed significantly the bulk sample in 1000-grain weight by 33.83, 43.01 and 29.28%, respectively. Family No. 15 recorded significant ( $P \leq 0.01$ ) increase over the bulk sample in plant height (14.36%), spikes/plant (39.19%), weight of spikes/plant (40.26%), no. of grains/spike (24.75%), weight of grains/spike (64.51%), grain yield/plant (105.24%) and spikelet fertility (21.97%). Family No. 72 showed significant increase of 1000-grain weight (25.09%) in percentage better parent. All families except No. 111 showed significant or insignificant increase in 1000-grain weight, also showed insignificant ( $P \leq 0.01$ ) increase in grain yield/plant compared to the bulk sample. The same results were found based on the better parent with exception families No. 96 and No. 111.

Average direct gain from two cycles of selection for spikelet fertility showed significant increase of (31.12%) in percentage the bulk sample but compared to the better parent

the ten families recorded insignificant increase (8.71%) (Table 7).

The average genetic gain for the correlated traits showed significant ( $P \leq 0.01$ ) increase in percentage the bulk sample in days to heading (7.12%), number of grains per spike (32.53%), weight of grains/spike (57.54%) and grain yield/plant (55.67%). The average correlated gain in percentage the better parent showed highly ( $P \leq 0.01$ ) significant decrease in plant height (-19.26%), spike length (-24.31%), spikelets/spike (-11.21%) and spike density (-34.30%), with exception the days to heading which recorded increase (7.12%). All the selected families except No. 3 and No. 160 surpassed the bulk sample in spikelet fertility and grain yield. Two selected families No. 3 and No. 145 showed significant ( $P \leq 0.01$ ) increase in percentage the better parent. All selected families exceeded bulk sample in spikelet fertility except families No. 44 and No. 160.

**Table 6. Observed direct and correlated genetic response to selection for 1000 grain weight in percentage of the bulk sample and better parent of the studied traits of selected families 1000 grain weight in F<sub>4</sub>-generation (season 2018/19 ).**

Families	1000 Grain Weight		DH		PH		SL		NS/P		WS/P	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
15	33.83*	17.06	6.1	6.1	14.36**	-6.19	1.48	-26.72**	39.19**	30.11*	40.26**	48.04**
38	22.45	7.11	2.03	2.03	7.06	-12.18**	-3.38	-30.23**	22.3	14.32	20.77	27.47*
72	43.01**	25.09*	12.54**	12.54**	13.14*	-7.19	-4.86	-31.30**	26.35	18.11	13.89	20.21
79	25.82	10.06	-0.34	-0.34	7.06	-12.18**	2.11	-26.26**	45.27**	35.79**	33.38**	40.78**
90	20.64	5.53	4.75	4.75	14.36**	-6.19	0.42	-27.48**	22.97	14.95	-19.23	-14.74
96	8.79	-4.84	7.12	7.12	4.62	-14.17**	1.27	-26.87**	51.35**	41.47**	30.00*	37.22**
111	-18.68	-28.87*	5.42	5.42	-31.87**	-44.11**	-2.96	-29.92**	-31.48*	-35.95**	-55.16**	-52.68**
126	23.16	7.72	19.66**	19.66**	11.92*	-8.18*	26.64**	-8.55*	13.51	6.11	21.55	28.30*
153	29.28*	13.08	3.73	3.73	5.84	-13.17**	1.06	-27.02**	13.51	6.11	7.02	12.96
198	22.45	7.11	17.97**	17.97**	20.44**	-1.2	27.91**	-7.63*	29.05*	20.63	34.06**	41.50**
Average	21.08*	5.9	7.90**	7.90**	6.69	-12.48**	4.97	-24.20**	23.20*	15.16	12.65	18.91*
LSD5% Fam	26.77	23.42	7.15	7.15	9.97	8.18	9.26	6.69	27.25	25.48	22.75	24.01
LSD1% Fam	36.28	31.74	9.69	9.69	13.51	11.08	12.55	9.06	36.93	34.52	30.83	32.54
LSD5% Avg	19.86	17.37	5.3	5.3	7.39	6.06	6.87	4.96	20.21	18.89	16.87	17.81
LSD1% Avg	26.91	23.54	7.19	7.19	10.02	8.22	9.31	6.72	27.39	25.6	22.86	24.13
Families	NST/S		NG/S		WG/S		GY/P		SF		SD	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
15	1.93	-10.10**	24.75**	-8.84	64.51**	18.57	105.24**	75.39**	21.97**	1.13	0.25	-31.82**
38	-6.31*	-17.37**	30.21**	-4.85	58.01**	13.89	139.46**	104.63**	38.69**	14.99*	-3.11	-34.10**
72	7.46**	-5.22*	16.78*	-14.67*	65.66**	19.4	100.60**	71.42**	8.6	-9.96	12.78**	-23.29**
79	4.76	-7.60**	18.54*	-13.38*	35.59*	-2.27	105.65**	75.74**	13.21	-6.14	2.48	-30.30**
90	-2.32	-13.85**	-16.68*	-39.12**	33.31*	-3.92	60.90**	37.49**	-14.69	-29.27**	-2.83	-33.91**
96	-7.85**	-18.73**	39.85**	2.2	50.39**	8.4	111.05**	80.35**	51.73**	25.79**	-9.11*	-38.18**
111	-9.14**	-19.86**	31.16**	-4.16	-4.13	-30.90**	-23.43	-34.57*	44.42**	19.74**	-6.32	-36.28**
126	14.16**	0.68	50.38**	9.89	71.58**	23.67*	86.80**	59.63**	31.84**	9.3	-9.73*	-38.60**
153	0	-11.80**	31.37**	-4	68.04**	21.11*	67.55**	43.18**	31.13**	8.72	-1.21	-32.81**
198	5.66*	-6.81**	59.47**	16.53**	78.50**	28.65**	108.84**	78.46**	50.85**	25.07**	-17.43**	-43.84**
Average	0.84	-11.07**	28.58**	-6.04	52.15**	9.66	86.27**	59.17**	27.77**	5.94	-3.42	-34.31**
LSD5% Fam	5.45	4.81	15.37	11.23	27.45	19.79	30.33	25.92	15.05	12.47	8.72	5.93
LSD1% Fam	7.39	6.52	20.83	15.22	37.2	26.82	41.1	35.13	20.39	16.9	11.82	8.04
LSD5% Avg	4.05	3.57	11.4	8.33	20.36	14.68	22.49	19.22	11.16	9.25	6.47	4.4
LSD1% Avg	5.48	4.83	15.45	11.29	27.59	19.89	30.48	26.05	15.12	12.54	8.76	5.96

\*and \*\* significant at 0.05 and 0.01 level of probability.

**Table 7. Observed direct and correlated genetic response to selection for spikelet fertility in percentage of the bulk sample and better parent of the studied traits of selected families in F<sub>4</sub>-generation (season 2018/19 ).**

Families	Spikelet fertility		DH		PH		SL		NS/P		WS/P	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
1	27.59**	5.78	1.36	1.36	-12.41*	-28.14**	8.67*	-21.53**	-20.95	-26.11*	-11.45	-6.54
3	50.72**	24.96**	10.51**	10.51**	7.06	-12.18**	-1.06	-28.55**	-22.97	-28.00*	-21.14*	-16.77
44	14	-5.48	17.63**	17.63**	9.49	-10.18*	-18.82**	-41.37**	8.54	1.46	-25.54**	-21.40*
56	39.08**	15.31	4.07	4.07	11.92*	-8.18	2.75	-25.80**	30.18*	21.68	2.97	8.68
58	29.80**	7.62	10.51**	10.51**	-24.57**	-38.12**	0.21	-27.63**	34.23**	25.47*	-28.58**	-24.61**
137	20.65*	0.03	15.93**	15.93**	11.92*	-8.18	-0.85	-28.40**	22.97	14.95	20.43*	27.11**
138	39.21**	15.42	3.05	3.05	3.41	-15.17**	8.67*	-21.53**	0.68	-5.89	5.22	11.06
143	26.28*	4.69	2.03	2.03	-5.11	-22.16**	13.74**	-17.86**	-6.08	-12.21	-10.21	-5.23
145	54.16**	27.81**	-1.02	-1.02	3.41	-15.17**	28.33**	-7.33**	2.7	-4	55.58**	64.21**
160	9.75	-9.01	7.12*	7.12*	-20.92**	-35.13**	6.55	-23.05**	18.58	10.84	-24.86**	-20.69*
Average	31.12**	8.71	7.12**	7.12**	-1.58	-19.26	4.82	-24.31**	6.79	-0.18	-3.76	1.58
LSD5% Fam	19.93	16.52	6.59	6.59	10.73	8.8	7.38	5.33	23.33	21.81	16.87	17.81
LSD1% Fam	27	22.39	8.93	8.93	14.54	11.93	10	7.22	31.62	29.55	22.86	24.13
LSD5% Avg	14.78	12.25	4.89	4.89	7.96	6.53	5.47	3.95	17.3	16.17	12.51	13.21
LSD1% Avg	20.03	16.6	6.62	6.62	10.78	8.84	7.42	5.36	23.45	21.92	16.96	17.9
Families	NST/S		NG/S		WG/S		GY/P		1000-GW		SD	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
1	0.64	-11.24**	28.50*	-6.1	77.43**	27.88*	28.86*	10.11	39.95**	22.42	-7.56	-37.13**
3	0.64	-11.24**	52.03**	11.09	59.80**	15.17	27.28	8.76	20.49	5.39	1.63	-30.88**
44	-9.78**	-20.43**	2.87	-24.83**	30.49	-5.95	33.16*	13.79	13.58	-0.65	10.92**	-24.56**
56	-2.96	-14.42**	35.08**	-1.29	41.81*	2.21	74.96**	49.51**	7.61	-5.87	-5.74	-35.89**
58	-2.06	-13.62**	27.57*	-6.78	17.65	-15.2	46.88**	25.51*	-8.32	-19.81	-2.48	-33.67**
137	0.26	-11.58**	21.18	-11.45	59.67**	15.09	93.56**	65.40**	24.25	8.69	0.94	-31.34**
138	6.18**	-6.36**	47.89**	8.07	86.16**	34.18*	82.75**	56.17**	32.89*	16.24	-2.38	-33.60**
143	1.42	-10.56**	28.42*	-6.16	52.21**	9.7	46.86**	25.50*	15.23	0.79	-10.97*	-39.45**
145	9.27**	-3.63	68.50**	23.13**	129.40**	65.34**	107.23**	77.09**	22.76	7.38	-14.89**	-42.11**
160	3.09	-9.08**	13.25	-17.24*	20.8	-12.94	15.19	-1.57	-15.23	-25.85*	-3.44	-34.32**
Average	0.67	-11.21**	32.53**	-3.16	57.54**	13.55	55.67**	33.03**	15.32	0.87	-3.4	-34.30**
LSD5% Fam	4.4	3.88	21.19	15.48	35.9	25.87	28.39	24.26	27.27	23.86	7.58	5.16
LSD1% Fam	5.96	5.26	28.71	20.98	48.65	35.06	38.47	32.87	36.96	32.33	10.27	6.99
LSD5% Avg	3.26	2.88	15.71	11.48	26.62	19.19	21.05	17.99	20.23	17.69	5.62	3.82
LSD1% Avg	4.42	3.9	21.29	15.56	36.08	26	28.53	24.38	27.41	23.97	7.62	5.18

\*and \*\* significant at 0.05 and 0.01 level of probability.

One of the main goals of this study was develop high yielding lines combined with high spikelet fertility from the first parent Emaral (long spike) and the second parent Nielain (short spike). Therefore, two families No. 138 and No. 145 surpassed the bulk sample which represented the base population (Emaral × Nielain) in spikelet fertility and grain yield, the superior in grain yield for these families depended on superiority in spike length (8.67 and 28.33%), no. of spikelets/spike (6.18 and 9.27%), grains/spike (47.89 and 68.50%) and weight of grains/spike (86.16 and 129.40%) in percentage the bulk sample for families No. 138 and No. 145, respectively. Families No. 3 and No. 145 showed highly significant increase in spikelet fertility by 24.96 and 27.81% compared the better parent Emaral (Table 7). Family No. 145 also gave the highest grain yield 77.09% over the better parent Emaral. This family considered a promising in grain yield and spikelet fertility.

Average direct genetic response after two cycles of selection for spike density resulted in significant ( $P \leq 0.05$ ) increase in spike density over the bulk sample by 7.27% but it decreased ( $P \leq 0.01$ ) compared to the better parent by -27.04 (Table 8).

Selection for spike density significant ( $P \leq 0.05$ ) increased of days to heading (8.10%), no. of spikes/plant (24.64%), grains/spike (18.31%), weight of grains/spike (36.99%), grain yield/plant (58.94%) and spikelet fertility (23.62%), while spike length showed significant ( $P \leq 0.05$ ) decrease by -10.49% compared to the bulk sample. Genetic gain in percentage the better parent showed significant ( $P \leq 0.01$ ) increase in days to heading (8.10%) and grain yield/plant (35.82%). Furthermore, highly significant ( $P \leq 0.05$ ) decrease was found for traits plant height (-16.87%), spike length (-35.36%), spikelets/spike (-15.56%) and no. of grains/spike (-13.54%). Four selected families surpassed ( $P \leq 0.05$  or  $P \leq 0.01$ ) the bulk in spike density. Family No. 37 gave the highest grain yield (161.76%) compared to the bulk sample, its high grain yield resulted from significant ( $P \leq 0.01$ ) increase of number of spikes/plant (79.28%), weight of spikes/plant (51.18%), weight of grains/spike (52.31%) and 1000-grain weight (46.47%) compared to the unselected bulk sample. However, all the selected families showed significant ( $P \leq 0.01$ ) decrease for spike density compared to the better parent.

**Table 8. Observed direct and correlated genetic response to selection for spike density in percentage of the bulk sample and better parent of the studied traits of selected families in F<sub>4</sub>-generation (season 2018/19 ).**

Families	Spike density		DH		PH		SL		NS/P		WS/P	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
37	12.81**	-23.27**	9.15**	9.15**	7.06	-12.18**	-13.11**	-37.25**	79.28**	67.58**	51.18**	59.57**
44	10.92*	-24.56**	17.63**	17.63**	9.49*	-10.18**	-18.82**	-41.37**	8.54	1.46	-25.54*	-21.40*
45	10.66*	-24.74**	12.20**	12.20**	2.19	-16.17**	-13.95**	-37.86**	40.25*	31.10*	-11.57	-6.66
104	7.28	-27.04**	7.46*	7.46*	5.84	-13.17**	-11.42**	-36.03**	12.84	5.47	-26.21*	-22.12*
106	-1.39	-32.93**	5.42	5.42	-5.11	-22.16**	-4.44	-30.99**	4.73	-2.11	-12.69	-7.85
156	6.06	-27.86**	9.15*	9.15**	9.49*	-10.18**	-2.75	-29.77**	32.43	23.79	10.85	17
167	24.68**	-15.20**	14.92**	14.92**	-2.68	-20.16**	-19.66**	-41.98**	38.39*	29.36	-18.21	-13.67
169	-2.91	-33.96**	10.17**	10.17**	18.00**	-3.19	3.38	-25.34**	48.99**	39.26*	13.11	19.38
251	1.43	-31.01**	0.34	0.34	-29.44**	-42.12**	-17.12**	-40.15**	7.34	0.33	-37.93**	-34.48**
255	3.19	-29.81**	-5.42	-5.42	-1.46	-19.16**	-6.98	-32.82**	-26.35	-31.16*	-23.85*	-19.62
Average	7.27*	-27.04**	8.10**	8.10**	1.34	-16.87**	-10.49**	-35.36**	24.64*	16.51	-8.08	-2.98
LSD5% Fam	8.74	5.95	5.94	5.94	8.72	7.15	7.39	5.34	32.64	30.51	19.52	20.6
LSD1% Fam	11.85	8.06	8.04	8.04	11.81	9.69	10.02	7.23	44.24	41.35	26.45	27.92
LSD5% Avg	6.49	4.41	4.4	4.4	6.47	5.3	5.48	3.96	24.21	22.63	14.47	15.28
LSD1% Avg	8.79	5.98	5.97	5.97	8.76	7.19	7.43	5.37	32.81	30.67	19.61	20.7
Families	NST/S		NG/S		WG/S		GY/P		1000-GW		SF	
	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P	Bulk	B.P
37	-1.8	-13.39**	5.16	-23.16**	52.31**	9.78	161.76**	123.69**	46.47**	28.12*	7.07	-11.23
44	-9.78**	-20.43**	2.87	-24.83**	30.49*	-5.95	33.16*	13.79	13.58	-0.65	14	-5.48
45	-4.63	-15.89**	13.01	-17.42*	21.04	-12.76	53.07**	30.80*	3.85	-9.17	18.43	-1.81
104	-4.76	-16.00**	14.06	-16.66**	21.25	-12.61	21.32	3.68	8.48	-5.12	20.2	-0.34
106	-5.66	-16.80**	58.90**	16.12*	53.44**	10.6	54.77**	32.25*	1.26	-11.43	68.30**	39.53**
156	3.35	-8.85**	23.49*	-9.76	62.63**	17.22	86.66**	59.51**	31.87*	15.35	19.21	-1.16
167	0.26	-11.58**	4.08	-23.95**	8.01	-22.15*	19.68	2.27	-8.79	-20.22	3.72	-14
169	0.64	-11.24**	25.49*	-8.3	40.35**	1.16	124.61**	91.94**	17.27	2.57	24.89*	3.54
251	-15.83**	-25.77**	-3	-29.12**	20.5	-13.15	20.59	3.05	4.95	-8.2	15.17	-4.52
255	-4.38	-15.66**	39.07**	1.62	59.89**	15.24	13.74	-2.8	17.03	2.37	45.17**	20.36*
Average	-4.26	-15.56**	18.31*	-13.54*	36.99**	-1.26	58.94**	35.82**	13.59	-0.64	23.62**	2.49
LSD5% Fam	5.84	5.15	20.54	15.01	25.28	18.22	31.02	26.51	28.15	24.63	22.65	18.78
LSD1% Fam	7.91	6.97	27.84	20.34	34.26	24.7	42.04	35.93	38.15	33.37	30.7	25.45
LSD5% Avg	4.33	3.82	15.24	11.13	18.75	13.51	23.01	19.66	20.88	18.26	16.8	13.93
LSD1% Avg	5.86	5.17	20.65	15.09	25.41	18.31	31.18	26.64	28.3	24.75	22.77	18.88

\*and \*\* significant at 0.05 and 0.01 level of probability.

**4. Effect of selection on genotypic and phenotypic correlation**

After two cycles of pedigree selection for grain yield, high strong positive genotypic correlation between grain yield with each of weight of spikes/plant (0.81), no. of grains/spike

(0.71), weight of grains/spike (0.91), 1000 grain weight (0.92) and spikelet fertility (0.70). The same trend was found for phenotypic correlation (Table 9). Grain yield showed weak positive phenotypic and genotypic correlations with DH (0.23 and 0.29), PH (0.37 and 0.38), SL (0.37 and 0.38) and NST/S

(0.26 and 0.33). Moderate positive genotypic 0.40 and phenotypic 0.42 correlation was estimated between grain yield and spikes/plant. Negative genotypic and phenotypic correlations between GY and spike density -0.42 was recorded. These results were confirmed by selection for grain yield which indicated that average correlated gains of the ten selected families showed significant increase over the bulk sample for no. of grains/spike 35.31, weight of grains/spike 56.23 and spikelet fertility 31.71% (Table 5). The average correlated gains in percentage of the better parent recorded significant decrease ( $P < 0.01$ ) for plant height -18.16, spike length -23.28, spikelets/spike -9.69 and spike density -33.94% (Table 7). EL Ameen and Ebrahim (2017), Meier *et al.* (2019) and Rahimi *et al.* (2017) found significant positive correlation between grain yield with each of number of grains and 1000 grain weight.

Selection for 1000 grain weight resulted in positive genotypic correlation between it and DH (0.44), PH (0.97), NS/P (0.87), WS/P (0.90), NST/S (0.60), WG/S (0.91) and grain yield (0.93). 1000 grain weight showed low negative phenotypic and genotypic correlations with SF (-0.24) and (-0.12), respectively and low positive with each of SL (0.13, 0.10) and SD (0.07, 0.11) (Table 9).

**Table 9. Phenotypic (r p) and genotypic (r g) correlation coefficients between selection criteria and other traits in F<sub>4</sub>-generation.**

Criteria	GY/P		1000-GW		SF		SD	
	r p	r g	r p	r g	r p	r g	r p	r g
R	0.23	0.29	0.11	0.44	0.01	0.03	-0.03	-0.07
DH	0.37	0.38	0.74	0.97	0.16	0.26	-0.34	-0.33
PH	0.37	0.38	0.13	0.10	0.57	0.57	-0.89	-0.85
SL	0.42	0.4	0.54	0.87	-0.17	-0.13	0.27	0.32
NS/P	0.82	0.81	0.67	0.90	0.32	0.41	-0.02	0.01
WS/P	0.26	0.33	0.54	0.60	0.31	0.3	-0.2	-0.25
NST/S	0.68	0.71	0.01	0.14	1.00	0.95	-0.71	-0.68
NG/S	0.85	0.91	0.92	0.91	0.89	0.86	-0.5	-0.52
WG/S	0.74	0.92	-	-	0.31	0.59	0.01	-0.12
1000GW	-	-	0.67	0.93	0.66	0.78	-0.14	-0.13
GY/P	-0.42	-0.42	0.07	0.11	-0.66	-0.69	-	-
SD	0.69	0.70	-0.24	-0.12	-	-	-0.63	-0.59
SF								

The average correlated grains of the ten selected families for 1000 grain weight showed significant increase ( $P < 0.01$ ) of the bulk sample in DH (7.90), NS/P (23.20), NG/S (28.58), WG/S (52.15), GY/P (86.27) and SF (27.77%). Moreover, significant increase for the percentage of better parent in DH (7.90), WS/P (18.91) and GY/P (59.17%). Moreover, highly significant decrease in percentage better parent for PH -12.48, SL -24.20, NST/S -11.07 and SD -34.31% (Table 6). Meier *et al.* (2019) found a positive and strong correlation for spike weight with grain weight (0.958) and a moderate correlation with spikes/plant (0.479).

Concerning the effect of selection for spikelet fertility on the correlation among traits, high strong positive phenotypic and genotypic correlations were found between spikelet fertility and each of NG/S 1, 0.95 and WG/S 0.89 and 0.86, also positive correlation were stated between SF and the remained other traits except negative phenotypic and genotypic correlation with NS/P -0.17, -0.13 and SD -0.66, -0.69 (Table 9). The average gain for correlated traits showed significant increase in percentage the bulk sample in NG/S 32.53%, WG/S 57.54% and GY/P 55.67%. The average

correlated gain in percentage of the better parent showed highly significant decrease in spike density -34.30% (Table 7).

After two cycles of selection for spike density, negative phenotypic and genotypic correlations were observed between spike density and the most other correlated traits with except weak positive correlations between SD and no. of spikes/plant. Average correlated gain was significant ( $P < 0.05$ ) decrease by -10.49% of spike length compared to the bulk sample after two cycles of selection for spike density (Table 8). Average correlated gain in percentage the better parent showed highly significant decrease for PH -16.87, SL -35.36, NST/S -15.56 and NG/S -13.54% (Table 8).

## CONCLUSION

Pedigree selection was the most effective method in detecting the high yield families. Average direct response in percentage the bulk sample was significantly increased for 1000 grain weight, spikelet fertility and spike density. Three families; No. 15, No. 72 and No. 153 surpassed significantly the bulk sample in criteria 1000 grain weight. Family No. 145 considered to be a promising in grain yield and spikelet fertility.

## REFERENCES

- Abd El-Rady, A.G. (2017). Selection efficiency for grain yield under normal irrigation and water stress conditions in bread wheat. *Assiut J. Agric. Sci.* 48(5): 1-20.
- Burton, G.W. (1952). Quantitative inheritance in grasses. 6<sup>th</sup> *Internet Grassland Cong. Proc.* 1: 227-283.
- Cantrell, R.G. and E.S. Haro-Arias. (1986). Selection for spikelet fertility in a semidwarf durum wheat population. *Crop Sci.* 26(4): 691-693.
- El Ameen, T. and E.M.A. Ebrahim (2017). Selection for heat tolerance in bread wheat (*Triticum aestivum* L.). *Global Adv. Res. J. Agric. Sci.* 6(10): 347-353.
- El-Hosary, A.A., E.M.H Shoker, M.E.R Gomaa, M.A. Abo Shrif, A.A.A. El-Hosary and M.M.M. Hamouda. (2011). Selection for earliness, yield and its components in bread wheat. *J. Plant Prod., Mansoura Univ.* 2(12): 1655-1666.
- El-Hosary, A.A., S.A. Sedhom, M.K. Khelifa, A.A.A. El-Hosary and K.A. Bayoumi. (2020). Efficiency of three breeding methods on three bread wheat populations. 5<sup>th</sup> *Inter. Conf. on Biotech. App. Agric.*, Benha Univ. Moshtohor and Hurgada. 8-11 April 2020, 1-17.
- El-Rawi, K. and A.M. Khalafala. (1980). Design and analysis of agricultural experiments. *El-Mousel Univ. Iraq.* 79-80.
- Falconer, D.S. (1989). *Introduction to quantitative genetics.* 3<sup>rd</sup> Ed. Longman, Hong Kong. 438.
- Guo, Z., D. Chen, A.M. Alqudah, M.S. Roder, M.W. Ganai and T. Schnurbusch. (2017). Genome-wide association analyses of 54 traits identified multiple loci for the determination of floret fertility in wheat. *New Phytol.* 214: 257-270.



- Guo, Z., Y. Zhao, M.S. Roder, J.C. Reif, M.W. Ganal, D. Chen and T. Schnurbusch. (2018). Manipulation and prediction of spike morphology traits for the improvement of grain yield in wheat. *Sci. Rep.* 8:14435: 1-10.
- Hamam, K.A. (2014). Late and early pedigree selection for grain yield with three selection criteria in two populations in bread wheat. *J. Plant Prod., Mansoura Univ.* 5(11): 1831-1847.
- Khames, K.M., A. Abo-Elwafa, A.M. Mahmoud and A. Hamada. (2017). Efficiency of two cycles of pedigree line selection in bread wheat (*Triticum aestivum* L.) under late sowing date. *Assiut J. Agric. Sci.* 48(1-1): 1-25.
- Mahdy, E.E., A.E. El-Karamity, S.A. Mokadem and H.M. Fouad. (2012). Selection for grain yield and its components in two segregating populations of bread wheat, *Triticum aestivum* L. *Minia Inter. Conf. Agric. Irri. Nile Basin Cou., El-Minia, Egypt.* 595-604.
- Mahdy, E.E., A.E. El-Karamity, Sh.A. Mokadem, A.L. Abd-Elmawgood and H.M. Fouad. (2015). Selection for grain yield in bread wheat under normal irrigation and drought stress conditions. *J. Plant Prod., Mansoura Univ.* 6(4): 547-562.
- McGill, J., D. Prikhodko., B. Sterk and P. Talks. (2015). Egypt wheat sector review. Food and agriculture organization. 1 – 112.
- Meier, C., D. Meira, V.S. Marchioro, T. Olivoto, L.A. Klein and V.Q. Souza. (2019). Selection gain and interrelations between agronomic traits in wheat F<sub>5</sub> genotypes. *Rev. Ceres, Viçosa.* 66(4): 271-278.
- Rahimi, L.G., B. Heidari and A. Dadkhodaie. (2017). Construction and efficiency of selection indices in wheat (*Triticum aestivum* L.) under drought stress and well-irrigated conditions. *Plant Breed. Biotech.* 5(2): 78-87.
- Iftikhar, R., I. Khaliq, M. Ijaz and M.A. Rashid. (2012). Association analysis of grain yield and its components in spring wheat (*Triticum aestivum* L.). *J. Agric. Environ. Sci.* 12(3): 389-392.
- Rasha, E. Mahdy, B.R. Bakheit, K.A. Kheiralla and A.A. Ismail. (2012). The relative merits of pedigree selection for grain yield of bread wheat under drought stress and sensitivity to environments. *Assiut J. of Agric. Sci.* 43(3): 55-72.
- Salous, M.Sh., M.A. El-Morshidy, K.A. Kheiralla and M.Kh. Moshref. (2014). Selection for grain yield in bread wheat (*Triticum aestivum* L.) under normal and heat stress conditions. *Assiut J. Agric. Sci.* 45(2): 1-18.
- Steel, R.G.D. and J.H. Torrie. (1980). Principle and procedures of statistics. A biometrical approach 2<sup>nd</sup>. Ed., McGraw-Hill Book Co., New York. U.S.
- Walker, T.T. (1960). The use of a selection index technique in the analysis of progeny row data. *Emp. Cott. Rev.* 37: 81-107.
- Yadav, H.K. and S.P. Singh. (2011). Inheritance of quantitative traits in opium poppy (*Papaver somniferum* L.). *Genetica.* 43(1): 113-128.
- Yousaf, M.I., N. Akhtar, A. Mumtaz, W. Akbar, H.M. Javeed, M.H. Bhatti and A. Mehmood. (2017). Contribution of spike-related traits for grain yield in spring wheat. *J. Agric. Basic Sci.* 2(2): 30-36.

### الانتخاب المباشر والغير مباشر لمحصول الحبوب في قمح الخبز

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أجري الانتخاب المباشر والغير مباشر لمحصول في مزرعة التجارب بكلية الزراعة – جامعة المنيا – مصر خلال 3 مواسم متتالية من 2016/2017 حتى 2018/2019. بعد دورتين من الانتخاب بطريقة تسجيل النسب انخفض التباين المظهري لمحصول الحبوب للنبات ووزن 1000 حبة وخصوبة السنبيلة وكثافة السنبيلة بسرعة من العشيرة الاصلية في الجيل الثاني حتي الجيل الرابع. وكانت درجة التوريث المحققة للاربع صفات المنتخبة السابقة 71,54 و 45,38 و 34,25 و 70% علي التوالي. أعطي الانتخاب الغير مباشر من خلال وزن 1000 حبة أعلى محصول حبوب للنبات (23,62 جرام) يليه الانتخاب المباشر لمحصول الحبوب للنبات (20,66 جرام). أظهر متوسط الاستجابة المباشرة للعشيرة عائلات المنتخبة في الانتخاب المباشر لمحصول الحبوب زيادة عالية المعنوية كنسبة مئوية من العينة المجمعة (12,95%) والأب الأفضل (نيلين) (39,25%)، ووجد ان الانتخاب بطريقة تسجيل النسب كان فعال في اكتشاف العائلات عالية المحصول. وأعطت العائلة رقم 145 محصول حبوب عالي المعنوية كنسبة مئوية من الأب الأفضل والعينة المجمعة بنسبة 77,09 و 107,23%. وزاد متوسط الاستجابة المباشرة معنويا كنسبة مئوية من العينة المجمعة بمقدار 21,08% لوزن 1000 حبة و 31,12% لخصوبة السنبيلة و 7,27% لكثافة السنبيلة. كما حدث انخفاض معنوي لكثافة السنبيلة مقارنة بالأب الأفضل (-27,04%). وتوقفت ثلاث عائلات ارقام (15، 72، 153) معنويا عن العينة المجمعة بمقدار 33,83 و 43,01 و 29,28% علي التوالي عند الانتخاب لصفة وزن 1000 حبة. أظهرت العائلة رقم 3 والعائلة رقم 45 زيادة عالية المعنوية في الصفة الانتخابية خصوبة السنبيلة بمقدار 24,96 و 27,81% مقارنة بالأب الأفضل (عمارة 1). العائلة رقم 145 يمكن ان تكون سلالة واعده في محصول الحبوب وخصوبة السنبيلة حيث تفوقت علي العينة المجمعة والأب الأفضل في هذه الصفات. ووجد ارتباط وراثي موجب وقوي بين محصول الحبوب وكل من وزن سنابل النبات (0,81) وعدد حبوب السنبيلة (0,71) ووزن حبوب السنبيلة (0,91) ووزن 1000 حبة (0,92) وخصوبة السنبيلة (0,07).