

## Selection Studies in Some Bread Wheat F<sub>3</sub> Crosses at Sakha and Nubaria Locations

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### ABSTRACT

The present experiment was conducted in 2015/16 season at Sakha Agricultural Research station, Kafr Elsheikh and Nubaria Research Station, Egypt. Four parents (Gemmeiza 9, Sids 12, Sids 1 and Cham 4) and three crosses (Gemmeiza 9 × Sids 12, Gemmeiza 9 × Cham 4 and Sids 1 × Cham 4) were used. Sixty families and 300 plants from each cross were evaluated with their parents at Sakha and Nubaria sites, respectively. The two parents of each of the three crosses were different significantly in most cases for plant height and grain yield and yield components at the two sites. There was sufficient genetic variance among the families at Sakha and among the plants at Nubaria in the studied crosses to estimate the genetic parameters. Gemmeiza 9 and Sids 1 were the highest parents for grain yield at the two sites. The overall F<sub>3</sub> means surpassed the parents mean for most studied traits and the ranges of the F<sub>3</sub> families outed the corresponding parents for most characters at the two sites. The genetic variances among the F<sub>3</sub> families exceeded corresponding environmental variances for most characters at Sakha site. The environmental variances were higher than the corresponding genetic variances among plants within families and selection among individual plants within families could be effective for most characters at Sakha site. Relatively medium to high heritability and expected genetic advance estimates for most characters were recorded at the two sites. Based on selection for plants with grain yield higher than the highest parent, medium height, resistant to the three rusts, seventeen plants from 2700 plants and twenty-six plants from 900 plants were selected at Sakha and Nubaria sites, respectively and will be advanced in the F<sub>4</sub>.

**Keywords:** wheat – *Triticum aestivum* - F<sub>3</sub> – selection – rusts -genetic variances.

### INTRODUCTION

Bread wheat (*Triticum aestivum* L.) occupies a prominent position in the farming system in Egypt. Development of new high yielding resistant to rust diseases cultivars is the main objectives of many wheat breeders.

Several studies have been performed to estimate phenotypic and genotypic variances and derived parameters like heritabilities and predicted selection responses utilizing parents and the advanced generations in wheat (Zaazaa *et al* 2012 and Abd El-Rahman, 2013). In addition, considerable genetic variability for plant height, yield and its components in F<sub>2</sub> were obtained by Zaazaa *et al* (2012) and Abd El-Rahman (2013).

In their biometrical studies (analyses) on different generations for agronomic characters, Khan *et al* (2014); Ul Haq *et al* (2016); Abbasi *et al*. (2017); Fellahi *et al* (2017); Hussain *et al*. (2017); Jariko *et al* (2017); Laala *et al*. (2017) and Sowmya *et al*. (2017) indicated the importance of additive and dominance variances, as well as the heritabilities and expected genetic advances were observed to be moderate to high percentages.

The three prominent rust diseases of wheat in Egypt are stem, (black), leaf, (brown) and stripe, (yellow) rusts caused by (*Puccinia graminis* Pers. f. sp. *tritici* Eriks. & Henn), (*P. triticina* Eriks) and (*P. striiformis* f. sp. *tritici*), respectively. (Dubin and Brennan, 2009). According to Moustafa *et al*. (2009) resistant cultivars are the best choice to control the spread of rust diseases. Therefore, Egyptian wheat breeders are continually striving for resistance genes and screening for rust resistance in hotspots. The three rusts are considered very important selection criteria beside the agronomic characters especially grain yield and plant height in wheat breeding in Egypt. In this context, Darwish *et al* (2018) used the resistance to rusts diseases and grain yield plant<sup>-1</sup> to select the best genotypes for wheat breeding.

Therefore, the objectives of this work were to (1) analyze the nature of inheritance of plant height as well as grain yield and its components. (2) develop segregating populations and as well as to select the desirable genotypes for future breeding strategies.

### MATERIALS AND METHODS

#### (1) Experiment sites

This experiment was conducted in 2015/2016 winter season at Sakha Agricultural Research station, Kafr Elsheikh, Egypt (31° 5' 12" North, 30° 56' 49" East) and at Nubaria Research Station, Egypt (30° 66' N latitude and 30° 06' E longitude with an altitude of 15.00 m asl). Sakha site was used as a hotspot for yellow rust and Nubaria as a hotspot for leaf rust.

#### (2) The used materials and evaluation procedures

Four parents were used and their name and pedigree were:

- (1) Gemmeiza 9, Ald"S" / Huac // Cmh74A.630 / Sx.
- (2) Sids 12, BUC // 7C / ALD /5/ MAYA74 / ON // I160.147 /3/ BB / GLL /4/ CHAT"S" /6/ MYA / VUL // CMH74A.630 / 4\*SX.
- (3) Sids 1, HD2172 / PAVON"S" // 1158.57 / MAYA74"S".
- (4) Cham 4, FLK / HORK.

Three crosses i.e. Gemmeiza 9 × Sids 12, Gemmeiza × Cham 4 and Sids 1 × Cham 4 were obtained from preceding studies (Darwish *et al.*, 2018 and Farhat and Darwish, 2016). In 2013/2014 season, 60 plants were randomly selected and their F<sub>3</sub> seed were taken to grow F<sub>3</sub> families.

At Sakha site the parents and the three crosses were planted on 25<sup>th</sup>, November 2015 using the randomized block design. Sixty random families from each cross totaling 180 families from the three crosses were studied in a randomized complete block design (RCBD) with three replications. For a replicate, each cross consisted of 62 rows, one row for P<sub>1</sub> and P<sub>2</sub> and sixty rows for F<sub>3</sub> families (one row for each family).

Each row was 2 meters long and 25 cm apart. Plants within rows were 20 cm spaced. In each row, data were taken on five random competitive plants for P<sub>1</sub>, P<sub>2</sub> and F<sub>3</sub> families. To maintain the identity, each plant was tagged and numbered.

At the Nubaria site, the bulk of the sixty F<sub>3</sub> populations and their parents (P<sub>1</sub>, P<sub>2</sub> and F<sub>3</sub>) were sown on 30 November 2015 in three replications using randomized complete block design (RCBD). The plot of each parent and F<sub>3</sub> cross consisted of 15 rows of 2 meters long, 25 cm apart and plants within rows were 20 cm spaced. Data were taken on random competitive 10 plants from each parent and 100 from each F<sub>3</sub> cross in the replication (30 and 300 plants from each parent and F<sub>3</sub> cross, respectively).

The soil texture was a clay and calcareous sandy loam to silty clay loam and the recommended cultural practices for wheat cultivation in old and newly reclaimed lands in Egypt were applied at the proper time in Sakha and Nubaria sites, respectively. The experiments were surrounded by mixed wheat

genotypes highly sensitive to yellow, leaf and stem rusts as a spreader of natural infection.

### (3) The collected data and statistical analysis

In each site, the studied characters were plant height (PH, cm), number of spikes plant<sup>-1</sup> (SP), number of kernels spike<sup>-1</sup> (KS), 100 kernel weight (KW, g), grain yield plant<sup>-1</sup> (GY, g), leaf (LR), yellow (YR) and stem (SR) rusts.

For yellow, leaf and stem rusts, the types of the infection were considered resistant (R), moderately resistant (MR), moderately susceptible (MS) and susceptible (S), in addition disease severity for leaf and stem rusts were recorded according to Stakman *et al.* (1962). The rusts results used only for selection of the best plants.

For Sakha site, the “t” test was used to test the significance of difference between means of the two parents in each cross.

Basic generations variances for each cross including three populations (P<sub>1</sub>, P<sub>2</sub> and F<sub>3</sub>) were statistically analyzed on plot mean and individual plant bases according to Hallauer *et al.* (2010). The possible form of the analysis of variance of the F<sub>3</sub> families included in replicated tests for each cross according to Hallauer *et al.* (2010) is shown in Table 1.

**Table 1. Form of analysis of variance for the F<sub>3</sub> families according to Hallauer *et al.* (2010).**

Source of variance	DF	Mean squares	Expected mean squares
Replications (R)	r-1		
Among F <sub>3</sub> Families (F)	f-1	M <sub>1</sub>	$\sigma_e^2 + \sigma_{wg}^2 + n\sigma_1^2 + nr\sigma_{F3}^2$
R × F (Error)	(r-1)(f-1)	M <sub>2</sub>	$\sigma_e^2 + \sigma_{wg}^2 + n\sigma_1^2$
Plants within F <sub>3</sub> Families	(n-1)rf	M <sub>3</sub>	$\sigma_e^2 + \sigma_{wg}^2$

**Where:** r, f and n represent the number of replications, F<sub>3</sub> families and plants within each family, respectively. M<sub>1</sub>, M<sub>2</sub> and M<sub>3</sub> denote the mean squares for F<sub>3</sub> families, replications × F<sub>3</sub> families and the plants within the F<sub>3</sub> families. Meanwhile,  $\sigma_e^2$  denote the average of the within plot variances of non-segregated generations and equal to (VP1 + VP2 + VF1)/3. In addition,  $\sigma_{wg}^2$  equal to the genetic variance among plants within F<sub>3</sub> families. Moreover,  $\sigma_1^2$  represents the environmental effects on the plots of the F<sub>3</sub> families. Meanwhile,  $\sigma_{F3}^2$  denotes the genetic variance among F<sub>3</sub> families. A direct F test was made to determine if the differences among F<sub>3</sub> families were significant; if they are,  $\sigma_{F3}^2 = (M_1 - M_2)/rn = \sigma_A^2 + 1/4\sigma_D^2$  and  $\sigma_{wg}^2 = M_3 - \sigma_e^2 = 1/2\sigma_A^2 + 1/2\sigma_D^2$ . Where,  $\sigma_A^2$  and  $\sigma_D^2$  denote the additive and dominance variances, respectively. To estimate the  $\sigma_A^2$  and  $\sigma_D^2$ , the two equations were solved, then:  $\sigma_A^2 = 2/3(2\sigma_{F3}^2 - \sigma_{wg}^2)$  and  $\sigma_D^2 = 4(\sigma_{F3}^2 - \sigma_A^2)$ .

The estimates of the additive and dominance variance in procedures of Hallauer *et al.* (2010) were used to calculate heritability in the broad ( $h_b^2$ ) and narrow ( $h_n^2$ ) senses for F<sub>3</sub> family means as follows:  $h_b^2 = (\sigma_A^2 + 1/4\sigma_D^2) / (\sigma_A^2 + 1/4\sigma_D^2 + E_2) \times 100$  and  $h_n^2 = (\sigma_A^2) / (\sigma_A^2 + 1/4\sigma_D^2 + E_2) \times 100$ . Where,  $E_2 = (M_2 - M_3)/n$ . The expected genetic advance from selection ( $\Delta g$ ) was computed according to Johanson *et al.* (1955) as follows:  $\Delta g = k\sigma_{ph}h_n^2$ . Where: (K) is a selection differential and equals to 2.06 for selection intensity of 5 % as given by Lush (1943),  $\sigma_{ph}$  is the phenotypic standard deviation among the means of F<sub>3</sub> families and  $h_n^2$  is the heritability in narrow sense.

For the F<sub>3</sub> populations in Nubaria site, the “t” test was used to test the significance of difference between means of the two parents in each cross. The phenotypic ( $\sigma_p^2$ ), genotypic ( $\sigma_g^2$ ) and environmental ( $\sigma_e^2$ ) variances were obtained using parents and their F<sub>2</sub> crosses as

outlined by Cruz *et al.* (2012). F ratio was calculated to test the significance of the differences between F<sub>2</sub> variance and the corresponding environmental variance. Broad sense heritability (H %) was calculated and equal to ( $\sigma_g^2 / \sigma_p^2 \times 100$ ) according to Acquah (2012). Selection differential (S), the expected response to selection (RS), the expected response to selection expressed as % of the base population mean (%RS) and the expected genetic gain (PGG) were calculated using the formulas reported by Cruz *et al.* (2012).  $S = (\bar{X}_S - \bar{X}_O)$ ,  $RS = S * H$ ,  $RS (\%) = 100 * RS / \bar{X}_O$ . The statistical analyses were performed by Microsoft Excel Spreadsheets, 2016.

## RESULTS AND DISCUSSION

### (A) F<sub>3</sub> families' evaluation at Sakha site

#### (1) Analysis of variances and mean performance

The two parents of each of the three crosses (Table 2) were different significantly (at 0.01 or 0.05 probability) for plant height (PH) in Gemmeiza 9 × Cham 4 and Sids 1 × Cham 4; spikes plant<sup>-1</sup> (SP) in Gemmeiza 9 × Sids 12; and grain yield (GY) in the three crosses; revealing the different genetic background of the parents involved. On the other hand, insignificant differences were found in the other cases. Despite the absence of significant differences between the parents for the preceding characters, there were significant differences (0.01 or 0.05 probability) among the F<sub>3</sub> families in all crosses, indicating sufficient differences in their genetic constitution allowing to estimate the genetic variances, heritabilities and genetic advance as well as the possibility of selection among these families. In general, similar trend was obtained by Farhat (2009); Aglan and Farhat (2014a and b); Abbasi *et al.* (2017) and Sowmya *et al.* (2017).

**Table 2. Analysis of variance for the F<sub>3</sub> families and t test significance of differences between parents in the studied crosses for all characters in Sakha site.**

Source of variation	df	Mean of squares				
		Plant height (PH)	No. spikes plant <sup>-1</sup> (SP)	No. kernel spike <sup>-1</sup> (KS)	100-kernel weight (KW)	Grain yield plant <sup>-1</sup> (GY)
<b>Gemmeiza 9 × Sids 12</b>						
Replication (R)	2	457.8	15.0	975.5	0.632	412.1
Among F <sub>3</sub> families (F)	59	2679.1**	147.4**	316.4**	2**	790.9**
R × F (Error)	118	479.7	44.0	93.9	0.669	222.2
Plants within F <sub>3</sub> families	720	198.8	28.3	69.5	0.473	159.2
T test between the two parents		ns	**	ns	ns	**
<b>Gemmeiza 9 × Cham 4</b>						
Replication (R)	2	640.1	325.9	542.0	8.317	923.3
Among F <sub>3</sub> families (F)	59	908.3**	124.6**	337.4**	3.3**	1046.6**
R × F (Error)	118	186.3	40.9	69.1	1.141	274.3
Plants within F <sub>3</sub> families	720	79.4	35.8	69.4	0.602	192.4
T test between the two parents		**	ns	ns	ns	**
<b>Sids 1 × Cham 4</b>						
Replication (R)	2	728.1	49.6	206.2	2.024	240.0
Among F <sub>3</sub> families (F)	59	261.4*	259**	189**	2.3**	633.8**
R × F (Error)	118	169.0	130.3	29.5	1.018	163.7
Plants within F <sub>3</sub> families	720	48.0	52.1	31.9	0.611	136.3
T test between the two parents		**	ns	**	ns	**

\*, \*\* = significant at 0.05 and 0.01 probability levels, respectively and ns = not significant.

For parents as in Table 3, the values of studied characters ranged from 95.7 cm in Cham 4 to 115 cm in Gemmeiza 9; 10.4 spikes plant<sup>-1</sup> in Sids 12 to 23.6 spikes plant<sup>-1</sup> in Gemmeiza 9; 50 kernels spike<sup>-1</sup> in Sids 1 to 65.5 kernels spike<sup>-1</sup> in Sids 12; 3.28 g in Cham 4 to 4 g in Sids 1; and 28.71 g in Sids 12 to 71.7 g in Gemmeiza 9 and Sids 1 for PH, SP, KS, KW and GY, respectively.

**Table 3. Means of the parents and their F<sub>3</sub> families and the ranges of F<sub>3</sub> families means for the studied characters in the three wheat crosses at Sakha site.**

Population		Plant height (cm)	No. of spikes plant <sup>-1</sup>	No. of kernel spike <sup>-1</sup>	100-kernels weight (g)	Grain yield plant <sup>-1</sup> (g)
<b>Parents</b>						
Gemmeiza 9		115.0	23.6	54.7	3.33	71.7
Sids 12		109.0	10.4	65.5	3.84	28.7
Sids 1		115.0	23.6	54.7	3.33	71.7
Cham 4		95.7	23.3	53.9	3.28	38.4
Parents mean		108.7	20.2	57.2	3.445	52.66
<b>F<sub>3</sub> families</b>						
Gemmeiza 9 × Sids 12	Mean	119.1	18.6	54.9	4.109	39.82
	Min.	81.0	12.4	44.9	3.219	22.03
	Max.	142.0	26.2	64.5	5.395	57.67
Gemmeiza 9 × Cham 4	Mean	108.2	24.2	51.9	3.615	39.88
	Min.	85.7	16.7	40.1	2.571	17.50
	Max.	132.3	30.8	61.2	4.651	57.54
Sids 1 × Cham 4	Mean	113.1	23.3	51.8	3.964	37.67
	Min.	95.7	13.5	43.3	3.137	19.47
	Max.	120.0	30.8	60.1	4.850	54.00
F <sub>3</sub> mean		113.5	113.5	22.1	52.9	3.9

Respect to the F<sub>3</sub> families (Table 3), the overall F<sub>3</sub> mean surpassed the parents mean for the studied traits, except for KS and GY. The F<sub>3</sub> means for PH, SP, KS, KW and GY were in the range of 108.2 cm in Gemmeiza 9 × Cham 4 and 119.1 cm in Gemmeiza 9 × Sids 12, 18.6 spikes plant<sup>-1</sup> in Gemmeiza 9 × Sids 12 and 24.2 spikes plant<sup>-1</sup> in Gemmeiza 9 × Cham 4, 51.8 kernels spike<sup>-1</sup> in Sids 1 × Cham 4 and 54.9 kernels

spike<sup>-1</sup> in Gemmeiza 9 × Sids 12, 3.62 g in Gemmeiza 9 × Cham 4 and 4.11 g in Gemmeiza 9 × Sids 12 and 37.67 g in Sids 1 × Cham 4 and 39.88 g in Gemmeiza 9 × Cham 4, respectively. The F<sub>3</sub> family means went in line with the corresponding highest parent for KS in Gemmeiza 9 × Sids 12 and SP in Gemmeiza 9 × Cham 4. Meanwhile, the F<sub>3</sub> family means were in line with the corresponding lowest parent for GY in Gemmeiza 9 ×

Cham 4. Moreover, the  $F_3$  family means went in midway between the two corresponding parents in Gemmeiza 9 x Sids 12 for KS and GY; Gemmeiza 9 x Cham 4 for PH; and Sids 1 x Cham 4 for KW. In addition, the  $F_3$  family means were higher than the highest corresponding parents for PH and KW in Gemmeiza 9 x Sids 12; SP and KW in Gemmeiza 9 x Cham 4; and PH in Sids 1 x Cham 4. Moreover, the  $F_3$  family means were lower than lowest corresponding parent for KS in Gemmeiza 9 x Cham 4 and GY in Sids 1 x Cham 4. In this respect, Farhat (2009) and Aglan and Farhat (2014a and b) found, in general, the average of  $F_3$  populations were lower than the average of their parents for grain yield.

The ranges of the performance of the  $F_3$  families exceeded the limits of the minus and plus directions of their parents for all characters, except for SP in Gemmeiza 9 x Sids 12 and PH in Sids 1 x Cham 4, which were close to the lowest corresponding parents and GY in Gemmeiza 9 x Cham 4, which were lowest than the highest parent. These segregation in the  $F_3$  families reflect the amount of the variability produced from the used parents, permitting the selection for extreme types. Similar results were obtained by Farhat (2009) and Aglan and Farhat (2014a and b) in  $F_3$  and  $F_4$  and Darwish *et al.* (2018) in the same crosses in  $F_2$ .

## (2) Genetical analysis

The magnitude of genetic variance (Table 4) among the  $F_3$  families exceeded corresponding environmental variance for all studied characters, except for PH and SP in Sids 1 x Cham 4 cross. In addition, the genetic variance among plants within families was higher than the corresponding environmental variance only for PH in Gemmeiza 9 x Sids 12 cross. The estimates of genetic variance among families were larger than those of within families for KW in all studied crosses; PH in Gemmeiza 9 x Cham 4 and Sids 1 x Cham 4; KS in Gemmeiza 9 x Sids 12; and SP in Sids 1 x Cham 4, suggesting that the selection might be more effective among families rather than within families. Where, GY in all crosses; SP in Gemmeiza 9 x Sids 12 and Gemmeiza 9 x Cham 4; KS in Gemmeiza 9 x Cham 4 and Sids 1 x Cham 4; PH in Gemmeiza 9 x Sids 12 had environmental variance higher than or almost equal to the corresponding genetic variance, suggesting further selection among individual plants within families. In this respect, Farhat (2009) and Aglan and Farhat (2014a and b) found the variances among  $F_3$  families were larger than those within  $F_3$  families for the agronomic characters. Information on the genetic variability and correlation of morpho-agronomic traits with grain yield are helpful for making effective selection (Singh *et al.*, 2016).

**Table 4. Genetic ( $\sigma^2_G$ ) and environmental ( $\sigma^2_E$ ) variance components among  $F_3$  families and among plants within  $F_3$  families for the studied characters in the studied crosses.**

Source		Plant height	No. of spikes plant <sup>-1</sup>	No. of kernels spike <sup>-1</sup>	100-kernel weight	Grain yield Plant <sup>-1</sup>
Gemmeiza 9 x Sids 12						
Among families	$\sigma^2_G$	146.62	6.90	14.83	0.090	37.92
	$\sigma^2_E$	31.98	2.93	6.26	0.045	14.81
Among plants within families	$\sigma^2_G$	171.66	13.52	12.56	0.059	57.14
	$\sigma^2_E$	27.14	14.76	56.95	0.415	102.04
Gemmeiza 9 x Cham 4						
Among families	$\sigma^2_G$	48.13	5.58	17.89	0.142	51.48
	$\sigma^2_E$	12.42	2.72	4.60	0.076	18.29
Among plants within families	$\sigma^2_G$	27.81	6.73	31.33	0.074	88.62
	$\sigma^2_E$	51.55	29.09	38.10	0.527	103.79
Sids 1 x Cham 4						
Among families	$\sigma^2_G$	6.16	8.58	10.63	0.083	31.34
	$\sigma^2_E$	11.27	8.69	1.96	0.068	10.91
Among plants within families	$\sigma^2_G$	4.53	7.98	14.81	0.080	39.66
	$\sigma^2_E$	43.45	44.15	17.12	0.531	96.61

The additive variance components (Table 5) exceeded the dominance portions for all studied characters, except for GY in all crosses 1; KS in Gemmeiza 9 x Cham 4 and Sids 1 x Cham 4; SP in Gemmeiza 9 x Sids 12; and KW in Gemmeiza 9 x Cham 4. In this respect, Farhat (2009) and Aglan and Farhat (2014a and b) obtained similar results and found that both additive and dominance components played an important role in controlling grain yield in the  $F_3$  and  $F_4$  families for some crosses.

The narrow sense heritabilities were not much lower than the broad heritabilities only for KW in all crosses; PH in Gemmeiza 9 x Cham 4 and Sids 1 x Cham 4; and SP in Sids 1 x Cham 4, indicating that the

additive portions were including most of the genetic variations in the  $F_3$  generation for these cases.

Relatively medium to high broad and narrow sense heritability estimates for all studied characters were recorded, except for the narrow sense heritability in Gemmeiza 9 x Sids 12 for PH, SP and GY; Gemmeiza 9 x Cham 4 for KS and GY; and Sids 1 x Cham 4 for PH. The comparatively high environmental and low genetic variance for the excepted characters accounted for their low heritability values. Meanwhile, the high estimates of heritability indicate the importance of the additive component in the inheritance of these characters.

**Table 5. Estimates of additive ( $\sigma^2_A$ ) and dominance ( $\sigma^2_D$ ) variances, heritability in broad ( $h^2_{(b)}$ ) and narrow senses ( $h^2_{(n)}$ ) and expected genetic advance ( $\Delta g$ ) within  $F_3$  family means for the studied characters in the three studied wheat crosses.**

Parameters	Plant height	No. of spikes plant <sup>-1</sup>	No. of kernels spike <sup>-1</sup>	100-kernel weight	Grain yield Plant <sup>-1</sup>
Gemmeiza 9 × Sids 12					
$\sigma^2_A$	81.06	0.18	11.40	0.08	12.46
$\frac{1}{4}\sigma^2_D$	65.57	6.71	3.43	0.01	25.46
$h^2_{(b)}$	82.09	70.16	70.32	66.95	71.91
$h^2_{(n)}$	45.38	1.84	54.06	60.27	23.63
$\Delta g$	28.62	0.66	7.45	0.54	10.70
Gemmeiza 9 × Cham 4					
$\sigma^2_A$	45.63	2.95	2.97	0.14	9.57
$\frac{1}{4}\sigma^2_D$	2.50	2.63	14.93	0.002	41.92
$h^2_{(b)}$	79.49	67.19	79.53	65.05	73.79
$h^2_{(n)}$	75.36	35.57	13.18	64.04	13.71
$\Delta g$	13.36	4.31	6.62	0.63	9.89
Sids 1 × Cham 4					
$\sigma^2_A$	5.19	6.12	4.30	0.06	15.35
$\frac{1}{4}\sigma^2_D$	0.97	2.46	6.33	0.03	15.99
$h^2_{(b)}$	35.33	49.68	84.41	55.02	74.18
$h^2_{(n)}$	29.76	35.43	34.15	37.85	36.33
$\Delta g$	2.93	4.23	7.95	0.45	11.44

The expected genetic advance values (Table 5) were low for KW in all crosses and SP in Gemmeiza 9 × Sids 12. The remaining characters had medium to high estimates of genetic advance. According to the high estimates of heritability and genetic advance, it could be concluded that selection for plant height would be effective in early segregating generation. In this respect, high expected genetic advance was found for plant height and grain yield and its components (Farhat 2009; Aglan and Farhat, 2014a and b; Sowmya et al., 2017 and Abbasi et al., 2017).

**(3) Advancement of the superior recombinant lines in  $F_3$  to  $F_4$  generation**

In wheat breeding programs in Egypt, wheat breeders, select lines characterized by high yield, medium length and resistance to rusts. Consequently, selected plants had promising high grain yield around the higher parent (Gemmeiza 9 and Sids 1) or higher, medium height (90-110 cm) and resistant or partially

resistant to the three rusts then these plants will be promoted to the  $F_4$  (Table 6). From 2700 evaluated plants, seventeen plants (0.63 %) were selected and were two plants (0.22 % of 900 plants) in Gemmeiza 9 × Sids 12, nine plants (1 % of 900 plants) in Gemmeiza 9 × Cham 4 and six plants (0.67 % of 900 plants) in Sids 1 × Cham 4 (11.33 %). These results were so far in agreement with those obtained from the previous part and these results were summarized in table 10. In this respect, Ragab (2010) and Darwish *et al.* (2018) established selection index containing grain yield and rusts resistance to select the best genotypes. Hussain *et al.* (2017) selected five  $F_3$  populations based on high yielding wheat cultivars. Laala *et al.* (2017) performed direct and correlated responses to  $F_3$  selection and suggested that early generation selection should be restricted to plant height and days to heading while selection to improve grain yield directly or via related traits should be delayed to later advanced generation.

**Table 6. Performance of the selected plants based on grain yield, plant height, rusts reaction from ninety  $F_3$  families in the three studied crosses at Sakha site.**

Family #	Plants #	Plant height (cm)	Grain yield plant <sup>-1</sup> (g)	Stripe rust reaction*	Leaf rust reaction*	Stem rust reaction*
Gemmeiza 9 × Sids 12 (900 plants)						
4	1	100	64.5	0	0	0
17	2	110	60.4	T R	T M S	5 MS
Gemmeiza 9 × Cham 4 (900 plants)						
13	1	95	65.0	0	0	T M S
21	2	100	84.0	0	0	0
23	3	105	75.0	T R	T M S	0
32	4	110	61.0	0	T M S	T M S
41	5	105	67.8	0	0	0
42	6	105	63.8	0	T R	0
42	7	110	60.0	T R	0	0
43	8	110	61.3	0	0	0
47	9	90	66.1	0	0	0
Sids 1 × Cham 4 (900 plants)						
1	1	105	63.1	T R	T M S	0
28	2	105	70.1	0	0	T R
38	3	100	63.0	0	T M S	T M S
41	4	100	68.0	T R	T M S	T R
42	5	110	62.9	0	0	0
43	6	90	79.3	0	0	0

\* T R = trace severity of infection; MR, moderately resistant; MS, moderately susceptible; S, susceptible.

**(B) F<sub>3</sub> bulks evaluation at Nubaria Site****(1) Mean performances**

The data in Table 7 indicate significant (at 0.01 or 0.05 probability) difference between the two parents of each cross for all the studied characters, except for 100-kernel weight in Gemmeiza 9 × Sids 12 and No. of

spikes plant<sup>-1</sup> in Gemmeiza 9 × Cham 4, showing the genetic different background of the used parents. On the other hand, insignificant difference was observed between Gemmeiza 9 and Misr 1 for KS and KW; Gemmeiza 9 and Misr 2 for PH, KW and GY; Gemmeiza 9 and Sids 1 for KS.

**Table 7. Means and variances of parents and their derived F<sub>3</sub> from three wheat crosses in addition to means of the two parents in each cross as well as means and ranges of the crosses for the studied characters at Nubaria site.**

Generation	Parameters	Characters				
		Plant height (cm)	No. of spikes plant <sup>-1</sup>	No. of kernels spike <sup>-1</sup>	100-kernel weight (g)	Grain yield (g)
Parents						
Gemmeiza 9	Mean	101.17	20.20	64.13	4.13	21.05
	Variance	18.42	31.75	29.36	0.27	17.01
Sids 12	Mean	95.67	6.73	52.20	3.60	15.83
	Variance	16.78	1.86	69.82	1.44	6.30
Sids 1	Mean	100.33	14.13	58.53	3.40	21.96
	Variance	11.95	16.81	71.57	0.25	37.60
Cham 4	Mean	84.00	21.93	48.53	2.08	16.26
	Variance	21.38	7.10	22.60	0.35	7.80
Parents means		95.29	95.29	15.75	55.85	3.30
LSD <sub>0.05</sub>		3.71	7.29	9.14	0.83	4.97
F <sub>3</sub> Crosses						
Gemmeiza 9 × Sids 12	T test	**	**	**	ns	**
	Mean	101.82	12.89	61.57	3.84	19.15
	Range	60.00 135.00	5.00 34.00	23.00 102.00	1.16 7.78	8.50 55.33
Gemmeiza 9 × Cham 4	T test	**	ns	**	**	**
	Mean	94.64	19.91	63.01	3.31	21.18
	Range	65.00 125.00	6.00 44.00	23.00 100.00	1.02 5.81	8.63 57.51
Sids 1 × Cham 4	T test	**	**	**	**	**
	Mean	98.52	16.81	56.41	2.78	18.37
	Range	80.00 125.00	5.00 43.00	23.00 100.00	1.05 6.00	8.64 56.94
F <sub>3</sub> means		98.32	16.54	60.33	3.31	19.57
LSD <sub>0.05</sub>		2.14	8.82	11.81	7.96	6.83

The plant height in the used parents differed from 84.0 cm in Cham 4 to 100.33 cm in Sids 1 and 101.17 cm in Gemmeiza 9. Number of spikes plant<sup>-1</sup> were in the range of 6.73 in Sids 12 and 21.93 in Cham 4 and 20.2 in Gemmeiza 9. The minimum number of the kernels spike<sup>-1</sup> (48.53) were obtained in Cham 4, while the maximum estimate (64.13) was shown by Gemmeiza 9. The lowest values of 100-kernel weight (2.08 g) belonged to Cham 4, while the highest values was (4.13 g) in Gemmeiza 9. Moreover, the highest values of the grain yield plant<sup>-1</sup> were detected in Sids 1 (21.96 g) and Gemmeiza 9 (21.05 g), while the lowest estimate (5.83 g) in Sids 12 and (16.26 g) in Cham 4.

The F<sub>3</sub> mean slightly exceeded the means of the parents for the studied characters. The means of the studied F<sub>3</sub> crosses differed in plant height and ranged from (94.64 cm) in Gemmeiza 9 × Cham 4 to (101.82 cm) in Gemmeiza 9 × Sids 12. The lowest and highest values of number of spikes plant<sup>-1</sup> were observed in Gemmeiza 9 × Cham 4 and Gemmeiza 9 × Sids 12 and were between 12.89 and 19.91, respectively. The lowest number of kernels spike<sup>-1</sup> belonged to Sids 1 × Cham 4 and was 56.41, while the highest values were 63.01 in Gemmeiza 9 × Cham 4 and 61.57 in Gemmeiza 9 × Sids 12. The lightest 100 kernel weight was 2.78 in Sids 1 × Cham 4, while the heaviest values belonged to Gemmeiza 9 × Sids 12 and was 3.84 g. Moreover, the lowest grain yield plant<sup>-1</sup> belonged to Sids 1 × Cham 4 (18.37 g) and Gemmeiza 9 × Sids 12 (19.15 g), while the highest estimates were 21.18 g in Gemmeiza 9 × Cham 4.

Furthermore, the ranges of the F<sub>3</sub> values went out the ranges of the two parents in the three crosses for all the studied characters, indicating the size of the difference among the parents, which were expressed in the amount of the genetic variability produced from segregation in the F<sub>3</sub> crosses. In the study of Farhat (2009); Ragab (2010); Zaazaa *et al* (2012) and Darwish *et al*. (2018), the mean value of the F<sub>2</sub> population comparing with their parents was higher than the highest parent for grain yield and its components in many cases.

**(2) Genetic variability**

The phenotypic variances in the F<sub>3</sub> (Table 8) differed significantly ( $P < 0.01$ ) from the environmental variances in the corresponding parents in the three crosses for all the studied characters. Therefore, there are sufficient variability among the F<sub>3</sub> plants to follow up the estimation of the genetic variances, heritability and genetic advance. In general, similar results were obtained by Farhat (2009); Ragab (2010); Zaazaa *et al* (2012) and Darwish *et al*. (2018) who detected significant genetic variance among F<sub>2</sub> or F<sub>3</sub> plants.

The phenotypic variances in F<sub>3</sub> crosses (Table 8) were between 66.26 (Sids 1 × Cham 4) and 183.9 (Gemmeiza 9 × Sids 12) for PH, 34.77 (Gemmeiza 9 × Sids 12) and 62.07 (Gemmeiza 9 × Cham 4) for SP, 295.23 (Sids 1 × Cham 4) and 473.55 (Gemmeiza 9 × Cham 4) for KS, 1.01 (Gemmeiza 9 × Cham 4 and Sids 1 × Cham 4) and 1.42 (Gemmeiza 9 × Sids 12) for KW and 89.17 (Sids 1 × Cham 4) and 123.08 (Gemmeiza 9 × Cham 4) for GY.

**Table 8. Estimates of phenotypic ( $\sigma_p^2$ ), genotypic ( $\sigma_g^2$ ) and environmental ( $\sigma_e^2$ ) variance components and broad sense heritability ( $h_{bs}^2$ ) for the studied characters of the parents and their F<sub>3</sub> derived from three bread wheat crosses.**

Genetic component	Plant height (cm)	No. of spikes plant <sup>-1</sup>	No. of kernel spike <sup>-1</sup>	100 -kernel weight (g)	Grain yield/plant (g)
Gemmeiza 9 × Sids 12					
$\sigma_p^2$	183.9**	34.77**	406.83**	1.42**	109.26**
$\sigma_e^2$	17.60	16.80	49.59	0.85	11.65
$\sigma_g^2$	166.30	17.97	357.24	0.57	97.61
$h_{bs}^2$ (%)	90.43	51.68	87.81	39.95	89.33
Gemmeiza 9 × Cham 4					
$\sigma_p^2$	125.84**	62.07**	473.55**	1.01**	123.08**
$\sigma_e^2$	19.90	19.42	25.98	0.31	12.40
$\sigma_g^2$	105.94	42.65	447.57	0.70	110.68
$h_{bs}^2$ (%)	84.19	68.71	94.51	69.37	89.92
Sids 1 × Cham 4					
$\sigma_p^2$	66.26**	43.89**	295.23**	1.01**	89.17**
$\sigma_e^2$	16.67	11.95	47.09	0.30	22.70
$\sigma_g^2$	49.60	31.93	248.14	0.71	66.47
$h_{bs}^2$ (%)	74.85	72.76	84.05	70.36	74.54

The environmental variance in the two parents of each cross in the F<sub>3</sub> hybrids ranged from 16.67 (Sids 1 × Cham 4) to 19.90 (Gemmeiza 9 × Cham 4) for PH, 11.95 (Sids 1 × Cham 4) to 19.42 (Gemmeiza 9 × Cham 4) for SP, 25.98 (Gemmeiza 9 × Cham 4) to 49.59 (Gemmeiza 9 × Sids 12) for KS, 0.30 (Sids 12 × Cham 4) to 0.85 (Gemmeiza 9 × Sids 12) for KW and 11.65 (Gemmeiza 9 × Sids 12) to 22.7 (Sids 1 × Cham 4) for GY. Moreover, the highest environmental variances in the parents belonged the KS and GY.

For genetic variances, the ranges of values were 49.60 (Sids 1 × Cham 4) and 166.30 (Gemmeiza 9 × Sids 12) for PH, 17.97 (Gemmeiza 9 × Sids 12) and 42.65 (Gemmeiza 9 × Cham 4) for SP, 248.14 (Sids 1 × Cham 4) and 447.57 (Gemmeiza 9 × Cham 4) for KS, 0.57 (Gemmeiza 9 × Sids 12) and 0.71 (Sids 1 × Cham 4) for KW and 66.47 (Sids 1 × Cham 4) and 110.68 (Gemmeiza 9 × Cham 4) for GY. The highest genetic variances in the F<sub>3</sub> crosses resulted by KS and PH.

The broad sense heritabilities ranged from 74.85% (Misr 1 × Sids 1) to 90.43% (Gemmeiza 9 ×

Sids 12) for PH; 51.68% (Gemmeiza 9 × Sids 12) to 72.76% (Sids 1 × Cham 4) for SP; 84.05% (Sids 1 × Cham 4) to 94.51% (Gemmeiza 9 × Cham 4) for KS; 39.95% (Gemmeiza 9 × Sids 12) to 70.36% (Sids 1 × Cham 4) for KW; and 74.54% (Sids 1 × Cham 4) to 89.92% (Gemmeiza 9 × Cham 4) for GY. Generally, the broad sense heritabilities were medium to high in the F<sub>3</sub> crosses. These results were in harmony with those of Abbasi *et al.* (2017); Fellahi *et al.* (2017); Jariko *et al.* (2017); Sowmya *et al.* (2017) and Darwish *et al.* (2018).

**(3) Selection differential, expected response to selection and expected genetic gain**

Based on 5 % of the base population in each F<sub>3</sub> cross the intensity of selection was performed for the studied characters (Table 9). According to the desirable trend, selection differentials, expected response to selection and expected response to selection as a percentage were illustrated by negative values for PH, while the rest characters were vice versa.

**Table 9. Base population mean (X<sub>0</sub>), mean of the selected plants (X<sub>s</sub>), selection differential (S), expected response to selection (RS), expected response to selection expressed as percentage of the base population mean (RS %), and predicted gain genetic (PGG) for the studied characters of the studied three F<sub>3</sub> crosses.**

Parameter	Plant height (cm)	No. of spikes plant <sup>-1</sup>	No. of kernel spike <sup>-1</sup>	100- kernel weight (g)	Grain yield/plant (g)
Gemmeiza 9 x Sids 12					
X <sub>0</sub>	101.82	12.89	61.57	3.84	19.15
X <sub>s</sub>	70.00	27.27	99.33	6.27	46.56
S	-31.82	14.38	37.76	2.43	27.41
RS	-28.77	7.43	33.16	0.97	24.49
RS %	-28.26	57.64	53.85	25.20	127.91
PGG	73.05	20.32	94.73	4.81	43.64
Gemmeiza 9 x Cham 4					
X <sub>0</sub>	94.64	19.91	63.01	3.31	21.18
X <sub>s</sub>	73.00	39.80	100.00	5.41	51.77
S	-21.64	19.89	36.99	2.10	30.59
RS	-18.22	13.66	34.96	1.46	27.51
RS %	-19.25	68.61	55.49	44.15	129.86
PGG	76.42	33.58	97.97	4.77	48.69
Sids 1 x Cham 4					
X <sub>0</sub>	98.52	16.81	56.41	2.78	18.37
X <sub>s</sub>	83.33	34.20	98.53	5.01	46.97
S	-15.19	17.39	42.12	2.23	28.59
RS	-11.37	12.65	35.40	1.57	21.32
RS %	-11.54	75.27	62.76	56.47	116.01
PGG	87.15	29.46	91.82	4.35	39.69

The values of the selection differential were in the range of -15.19 in Sids 1 × Cham 4 and -31.82 in

Gemmeiza 9 × Sids 12 for PH; 14.38 in Gemmeiza 9 × Sids 12 and 19.89 in Gemmeiza 9 × Cham 4 for SP;

36.99 in Gemmeiza 9 × Cham 4 and 42.12 in Sids 1 × Cham 4 for KS; 2.10 in Gemmeiza 9 × Cham 4 and 2.43 in Gemmeiza 9 × Sids 12 for KW; and 27.94 in Gemmeiza 9 × Sids 12 and 30.70 in Gemmeiza 9 × Cham 4 for GY.

The expected responses to selection ranged from -11.37 (Sids 1 × Cham 4) to -28.77 (Gemmeiza 9 × Sids 12) in PH; 7.43 (Gemmeiza 9 × Sids 12) to 13.66 (Gemmeiza 9 × Cham 4) in SP; 33.16 (Gemmeiza 9 × Sids 12) to 35.40 (Sids 1 × Cham 4) in KS; 0.97 (Gemmeiza 9 × Sids 12) to 1.57 (Sids 1 × Cham 4) in KW; and 22.13 (Gemmeiza 9 × Sids 12) to 24.77 (Gemmeiza 9 × Cham 4).

The expected responses to selection varied as a percentage from -11.54% in Sids 1 × Cham 4 to -28.26% in Gemmeiza 9 × Sids 12 for PH; 57.64% in Gemmeiza 9 × Sids 12 to 75.27% in Sids 1 × Cham 4 for SP; 53.85% in Gemmeiza 9 × Sids 12 to 62.76% in Sids 1 × Cham 4 for KS; 25.20% in Gemmeiza 9 × Sids 12 to 56.47% in Sids 1 × Cham 4 for KW; and 117.54% in Gemmeiza 9 × Cham 4 to 127.62% in Sids 1 × Cham 4 for GY.

After one cycle of 5 % selection intensity, the expected genetic gain values will be in the range of 73.05 in Gemmeiza 9 × Sids 12 and 87.15 in Sids 1 × Cham 4 for PH; 20.32 in Gemmeiza 9 × Sids 12 and

29.46 in Sids 1 × Cham 4 for SP; 91.82 in Sids 1 × Cham 4 and 97.97 in Gemmeiza 9 × Cham 4 for KS; 4.35 in Sids 1 × Cham 4 and 4.81 in Gemmeiza 9 × Sids 12 for KW; and 40.76 in Gemmeiza 9 × Sids 12 and 45.84 in Gemmeiza 9 × Cham 4 for GY. Similar results, in general were obtained by Abbasi *et al.* (2017); Fellahi *et al.* (2017); Jariko *et al.* (2017); Sowmya *et al.* (2017) and Darwish *et al.* (2018).

**(4) Advancement of the superior plants in F<sub>3</sub> to F<sub>4</sub> generation**

To select the best plants in the F<sub>3</sub> crosses to advance to as F<sub>4</sub> families, the reaction to yellow, leaf and stem rusts, plant height and grain yield for each plant were considered (Table 10). The selection process based on selecting the plants with grain yield around the higher parent (Gemmeiza 9 and Sids 1) or higher, medium height (90-105 cm) and resistant to the three rusts. From 900 evaluated plants, twenty-six plants (2.9 %) were selected and were five plants (1.7 % of 300 plants) in Gemmeiza 9 × Sids 12, ten plants (3.3 % of 300 plants) in Gemmeiza 9 × Cham 4 and eleven plants (3.7 % of 300 plants) in Sids 1 × Cham 4 (11.33 %). As mentioned above, such selection process was also performed by Ragab (2010); Hussain *et al.* (2017); Laala *et al.* (2017) and Darwish *et al.* (2018).

**Table 10. Performance of the selected plants based on grain yield, plant height, rusts reaction from nine hundred F<sub>3</sub> plants in the three studied crosses at Nubaria station.**

Plant height (cm)	Plant #	Grain yield plant <sup>-1</sup> (g)	Stripe rust reaction*	Leaf rust reaction*	Stem rust reaction*
Gemmeiza 9 × Sids 12 (300 plants)					
95	1	21.34	T R	0	T R
105	2	26.10	0	0	T R
105	3	32.46	0	0	5 R
105	4	34.40	0	0	0
100	5	45.85	0	0	5 R
Gemmeiza 9 × Cham 4 (300 plants)					
95	1	23.15	0	0	5 R
95	2	23.54	0	0	10 R
105	3	24.60	0	0	10 R
95	4	25.98	5 R	0	T R
105	5	27.88	0	5 R	10 R
105	6	29.40	5 R	10 R	5 R
90	7	31.58	0	0	10 R
90	8	33.70	0	0	5 R
90	9	38.15	0	0	5 R
90	10	42.77	5 R	5 R	5 R
Sids 1 × Cham 4 (300 plants)					
100	1	23.27	10 R	0	0
105	2	23.53	R	0	0
100	3	23.86	0	0	0
95	4	24.36	0	0	0
100	5	26.57	0	0	T R
95	6	26.65	10 R	0	T R
105	7	27.15	0	0	T R
90	8	28.00	5 R	0	5 R
105	9	28.11	T R	0	5 R
105	10	28.56	0	T R	5 R
90	11	50.00	0	0	10 R

\* T R = trace severity of infection.

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### دراسات انتخاب في بعض هجن الجيل الثالث لقمح الخبز في موقعي سخا والنوبارية محمد عبد الكريم حسن درويش وثناء حمد عبد الكريم و وليد ذكي اليماني فرحات قسم بحوث القمح – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية – مصر

أجريت هذه التجربة في موسم 2016/2015 في محطتي البحوث الزراعية بسخا والنوبارية بجمهورية مصر العربية. وكانت التراكيب الوراثية المستخدمة هي أربعة أباء (جميزة 9، سدس 12، سدس 1 وشام 4) وثلاث هجن (جميزة 9 x سدس 12، جميزة 9 x شام 4 وسدس 1 x شام 4). وتم تقييم 60 عائلة و300 نبات في محطتي سخا والنوبارية على الترتيب. وفي كلا الموقعين كان الأبوان في كل هجين مختلفين معنويًا في معظم الحالات لصفات الطول ومحصول الحبوب ومكوناته. وقد أظهرت عائلات ونباتات الجيل الثالث في سخا والنوبارية على الترتيب فروقًا وراثية كافية لحساب المعالم الوراثية في كل الصفات في الهجن الثلاث. وكان صنفى جميزة 9 وسدس 1 الأعلى محصولًا في كلا الموقعين. وقد تفوقت متوسطات الجيل الثالث على الأباء المناظرة وتعدت حدود الجيل الثالث حدود الأبوين المناظرين في معظم الصفات المدروسة تحت الموقعين. وكان التباين الوراثي أعلى من التباين البيئي بين عائلات الجيل الثالث وكذلك كان التباين البيئي أعلى من الوراثي بين النباتات داخل العائلات مما يسمح بالانتخاب بين هذه النباتات تحت ظروف سخا. وكانت قيم المكافئ الوراثي والتحسين الوراثي المتوقع متوسطة إلى مرتفعة في معظم الحالات في الموقعين. وقد تم انتخاب النباتات المتوقعة بناءً على محصول الحبوب الأعلى من الأب الأعلى وذات الطول المتوسط والمقاومة للأصداء الثلاثة وكان نتيجة ذلك الحصول على 17 نبات من 2700 نبات في محطة بحوث سخا و26 نبات من 900 نبات في محطة بحوث النوبارية حيث يمكن الدفع بهذه النباتات لتقييمها كعائلات في الجيل الرابع.