Original research

Pedigree selection for yield and some of its components in bread wheat

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Abstract:

The current study was conducted at Fac. Agric. Farm, Assiut University, Egypt, over three consecutive seasons, 2019/2020, 2020/2021, and 2021/2022. The objective of this study was to examine the effectiveness of two cycles of pedigree line selection for grain yield and one cycle of late selection in a single segregating population of bread wheat (*Triticum aestivum. L*). From the base population to the final early and late cycles of pedigree line selection, the genotypic (GCV) and phenotypic (PCV) coefficients of variation for grain yield/plant and its attributes decreased. Otherwise, from the base population to the end cycles of early and late selection, the heritability values for grain yield/plant and its attributes were increased. The final 10 selections of both early and late selected families outperformed their respective parents and unselected bulk sample, resulting in late selections with a more powerful direct response to selection.

Keywords: bread wheat, pedigree selection, heritability.

1- Introduction

Wheat is one of the most important cereal crops, with 780 million tonnes produced in 2021; it is planted on approximately 220 million hectares worldwide **(FAO 2021).** In Egypt, wheat is the staple grain and the most important cereal crop. Humans consume wheat in the form of grains, and animals consume straw as nourishment. Its area was approximately 1.33 million hectares (3.17 million faddan), and during the 2019–2020 growing season, it generated 8.5 million tonnes at an average yield of 6.4 tons/ha (17.85 Ardab faddan) **(Economic Affairs Annual Report, 2020).** According to **Gharib *et al.*** (2016), the local production of wheat is insufficient to meet the country's annual needs. As a result, improving wheat productivity is the most effective way to close the production-consumption gap. This can be done by paying close attention to growing wheat's area and productivity per unit area. With self-pollinated species, the pedigree selection approach is frequently employed without combining seeds from various pedigree lines **(Allard 1960).**

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The most intriguing selection for yield from early generations based on single plant evaluation should begin in the F2 generation **(Sneep 1977).** One of the key methods for crop development is selection, which should not only be utilized to increase grain production but also take other yield factors into account. The choice of selection criteria for increasing grain production, however, will determine if the selection technique is successful **(Samonte *et al.,* 1998).** Individual plant selection at early segregating generations for quantitatively inherited traits such as grain yield has met with success. This imposition may be due to several factors such as polygenic nature, high heritability of a trait (grain yield, number of spikes per plant, 100-kernel weight, number of kernels/spike, etc.), linkage, additive gene effects, and environmental effects. This is important for selection in self-pollinated crops, as the action of additive genes would be retained through subsequent inbreeding **(Tripathi *et al.*, 2021).** Therefore, the presence of genuine genetic differences between genotypes in these generations and their persistence after selection is necessary for early generations' selection to be effective **(Islam *et al*. 1985).**

The objectives of the current study were to:
1- Estimate the efficiency of single trait selection as grain yield/plant in one segregation population of bread wheat.

2- Determine the relationship between grain yield and its components through the successive generation of study.

2- Materials and Methods

The current study was carried out in the Fac. Agric. Farm, Assiut University, Egypt, during the three successive seasons i.e., 2019/2020, 2020/2021, and 2021/2022 using one population of bread wheat (Misr^2 Sakha 94).

Season 2019/20 (F$_3$-generation).
Six hundred F$_3$ individual plants were grown in four non-replicated plots. Each plot consisted of 20 rows, each 3m long and 15 cm apart. spaced 10 cm within a row to give an average of 30 individual plants/row and grains were sown on November 27th, 2019 Moreover, the two parents were grown in separate plots in four rows. Each parent is in two rows. Data were recorded on 500 plants chosen from the studied population.

Season 2020/2021 (F$_4$-generation).
The F$_3$ - plants that gave sufficient grains for replicated in F$_4$ were 500 families of the population. On December 9th, 2020, populations, their respective parents, and an unselected bulk sample were sown in a randomized complete block design (RCBD) with three replications. The population was represented by an equal number of grains from each family in the unselected bulk sample. The plot was 3 meters long, 20 centimeters apart, and 5 centimeters between grains within the row. At harvest, the following traits were measured on five randomly guarded plants in each plot (row)/replicate.

Season 2021/2022 (F$_5$-generation).
On December 9th, all of the selected families (10 for each early and late selection), parents, and bulk samples were sown. For this generation, the same procedures and experimental design were used as in the previous season.

Characteristics that were measured during the experiment's seasons.

1- **Plant height (PH)**, the distance from the ground surface to the base of the main culm's spike.

2- **Spike length (SL)**, cm: the distance between the base of the main spike and its tip, excluding awns.

3- **Number of spikes/plant (NSP):** the plant's number of spikes.

4- **Number of spikelets/spike (NSES):** the number of spikelets on a single main spike per plant.

5- **Weight of spikes/plant (WSP)**, g: weight of spikes of the plant

6- **Biological yield/plant (BYP),** g: the air dry weight of the up ground growth/plant was recorded.

7- **Grain yield/plant (GYP)**, g: the weight of grains from each guarded plant was recorded.

8- **Seed index (SI), g:** was recorded as the mean weight of random 100-kernel samples.

9- **Harvest index % (HI):** the ratio of GYP to BYP.

10- **Threshing index % (TI):** the ratio of GYP to WSP.

Statistical analysis:

Estimates of genotypic and phenotypic variance and covariance, as well as heritability, were calculated from the variance and covariance components of selected families for separate analysis using the Expected Mean Square (EMS) **(Steel and Torrie, 1980).**

was calculated as the ratio of genotypic ($\sigma^2 g$) to phenotypic ($\sigma^2 p$) variance according to **Walker (1960).**

3- Results and Discussion

The F3 base population consisted of 500 families with two parents and an unselected bulk sample.

3.1.- Variance and means:

The range, means, standard deviation, phenotypic and genotypic coefficients of variation, and heritability are shown in Table 1. These data revealed that the F3 families in the base population had high differences for studied traits, reflecting genetic differences among the F3 families in the base population. As a result, this sufficient genetic variation could be used for additional pedigree line selection for grain yield/plant. Similar results were observed by **Mostafa (2015), Sharaan *et al.,* 2017, Koubisy (2020), Tripathi *et al.,* (2021),** and **Stojsin *et al.,* (2022).** High values of phenotypic and genotypic coefficients of variation (Table 1) were recorded for biological yield/plant (43.52 and 33.69), the number of spikes/plant (34.86 and 25.99), grain yield/plant (44.36 and 33.93), harvest index (22.81 and 16.76) and seed index (13.54 and 10.59%) in F_3 base population. The moderate estimates of heritability were recorded for biological yield/plant (59.93%), the number of spikes/plant (55.58%), grain yield/plant (58.42%), harvest index (54.03%), and seed index (61.11%). These results were coupled with high estimates of the range recorded for biological yield/plant (8.15 to 95.85 g), the number of spikes/plant (3 to 13), grain yield/plant (3 to 39.53 g), harvest index (7 to 56.23 %) and seed index (2.42 to 6.13 %) in F_3 base population. The results exhibited that ranges of all traits of the F₃ families were scaled outside the average of their both parents and bulk sample, indicating transgressive segregation Moreover, the values of the bulk sample were less and close to the mean of all traits, except seed index, was slightly exceeded it.

Meanwhile, the average of the F₃ families surpassed the better parent for the number of spikes/plant, harvest index, and seed index by 5.64, 3.15, and 2.07%, respectively. The average of both biological yield/plant and grain yield/plant was close to the better parent. Moreover, it is clear results that some families exceeded in high values the bulk sample and both parents for all previously studied traits (Table 1). The obtained results also revealed that the better parent had nearly and possibly complete dominance in biological yield, number of spikes/plant, grain yield/plant, harvest index, and seed index. **Mostafa (2015)** noted that the non-additive acted both of grain yield/plant and biological yield/plant and the complete dominance for harvest index towards the better parent in wheat. **Khalifa *et al.,* (2016), Abd-El-Rady (2017), Koubisy (2020),** and **Mahdy Rasha (2020)** found significant differences in started populations for grain yield and its attributes of wheat.

Table 1: Characterization of main yield traits in the F3 base population and their parents.

Items		Biological yield/plant, g	Number. of spikes/plant	Grain yield/plant, g	Harvest index, %	100-grain weight, g
F3 600 families	σ_E^2	127.69	2.19	19.03	35.03	0.14
	σ_G^2	190.94	2.74	26.74	41.18	0.22
	σ_P^2	318.62	4.93	45.77	76.21	0.36
	G.C.V.	33.69	25.99	33.93	16.76	10.59
	P.C.V.	43.52	34.86	44.39	22.81	13.54
	H	59.93	55.58	58.42	54.03	61.11
	Min.	8.15	3.00	3.00	7.12	2.42
	Max.	95.85	13.00	39.53	56.23	6.13
	Mean	41.02	6.37	15.24	38.28	4.43
	Bulk	36.37	5.82	11.91	33.70	4.77
P1 (Misr 2) mean		29.34	4.63	10.52	36.11	3.87
P2 (Sakha 94) mean		42.43	6.03	15.65	37.11	4.34

3.2.- Pedigree line selection for grain yield/plant in both F₄ and F₅ generations.

3.2.1- Estimates of variability and heritability:

The analysis of variance of all 500 families, 50 selected families in F4 and F5 generation, and 10 selected families of both early and late pedigree line selection in F5 for grain yield/plant and its correlated traits are presented in Table 2. These analyses were performed twice, once without and once with their parents, and an unselected bulk sample was used for all previous cases.

All 500 families as well as 50 selected families in F₄ (cycle one) and F₅ (cycle two) and the 10 selected families of both early and late pedigree line selection in F₅ exerted highly significant differences for grain yield/plant as a selection criterion and its correlated attributes. The same trend of results was recorded for all genotype

analyses which included families with their parents and unselected bulk samples across both F_4 and F_5 generations for all studied traits. These obtained results are indicating the existence of efficient genetic variation for further cycles of pedigree line selection. Similar results were proposed by **Ali (2012), Mahdy *et al*. (2012), Abd El-Shafi (2014), Ahmed *et al* (2014),** and **Mostafa (2015).**

After two cycles of pedigree line selection, the genotypic (GCV) and phenotypic (PCV) coefficients of variation for grain yield/plant were reduced from 33.92 and 44.42% in the base population (500 F3 families) to 5.46 and 6.34%. (10 F_5 early selected families) as well as to 5.72 and 6.29% after one cycle of late selection (10 F_5 late selected families) respectively (Tables 1 and 2). The same trend of GCV and PCV values as seen before can be recorded for yield attributes in all generations across unselected and selected families. The values of GCV and PCV decreased from 25.99 and 34.86, 33.69 and 43.52, 10.59 and 13.54, and 16.76 and 22.81 in the base population (500 F₃ families) to 21.00 and 21.70, 11.01 and 11.42, 4.10 and 4.60, and 12.37 and 13.01 after two cycles of pedigree line selection (10 F_5 early selected families) as well as to 20.72 and 21.21, 5.87 and 6.52, 4.63 and 5.07, and 5.35 and 6.27% after one cycle of late selection (10 F_5 late selected families) for the number of spikes/plant, biological yield/plant, seed index, and harvest index, respectively (Tables 1and 2). Moreover, the GCV and PCV for the weight of spikes/plant decreased from 12.48 and 14.80% in F_4 (500 F_4 families) to 10.14 and 11.20% after one cycle (50 F_4 selected families) and to 9.21 and 9.94% after two cycles of pedigree line selection (10 F_5 early selected families) as well as to 8.60 and 9.40% after one cycle of late selection (10 F_5 late selected families) (Table 2). **Ahmed (2006)** noted that GCV decreased among families from the base population to the successive selection cycles due to the increase in homogeneity. Grain yield/plant (as a selection criterion) decreased from 28.86 in the base population to 15.82 and 3.08% after two cycles of early and late selections, respectively. Furthermore, **Abd El-Kader (2011)** found that after two cycles (F3-F5) of pedigree selection for the number of spikes/plant (from 26.2 to 4.70) and grain yield/plant (from 28.60 to 3.80%) in two wheat populations, the GCV decreased rabidly. Furthermore, the low differences between PCV and GCV indicated low environmental effects on grain yield and wheat components. (**Mukherjee *et al*., 2008 Mostafa, 2015**). Generally, the moderate and high values of GCV offer the existence of sufficient genetic variation for further improvement. Furthermore, **Abd-El-Rady (2017), Koubisy (2020), Mahdy Rasha (2020),** and **Stojsin et al., (2022)** discovered that the GCV and PCV values of started populations decreased through successive cycles of selection for grain yield and wheat attributes.

In general, broad sense heritability values for all studied traits increased from the base population (500 F3 families) to the end of two cycles of pedigree line selection (10 F5 early selection) and one cycle of late selection (10 F5 late selection). The increase in heritability values, combined with a decrease in both GCV and PCV estimates, reveals an increase in homogeneity among selected families after one or more cycles of pedigree line selection as presented in Tables 1 and 2.

Table 2. Mean squares for genotypes and families, variance types, heritability estimates, genotypic (g.c.v.%) and phenotypic (p.c.v.%) coefficients of variability of 10 selected families (early and late selection) for grain yield/plant and its attributes in F₅ generation.

	S.O.V.	d.f.	PH	SL	NSP	NSES	BYP	WSP	GYP	SI	HI	TI
						F₅ (Early selection)						
Genotypes	**Rep. SS**	2	3.38	0.93	1.22	1.91	90.75	21.57	2.63	0.02	11.50	56.63
	Genotypes SS	12	152.43**	3.86**	8.05**	8.35**	200.31**	75.87**	22.28**	0.24**	55.28**	67.13**
	Error SS	24	6.75	0.31	0.56	0.63	12.55	5.43	1.55	0.02	3.86	13.57
Families	**Rep. SS**	2	3.76	1.24	1.65	2.66	94.90	30.97	2.91	0.001	8.54	55.91
	Families SS	9	152.57**	4.44**	9.91**	10.42**	169.75**	38.30**	6.52**	0.14**	63.95**	84.74**
	Error SS	18	7.25	0.34	0.64	0.73	11.83	5.43	1.69	0.02	4.75	16.92
	σ_E^2		2.42	0.11	0.21	0.24	3.94	1.81	0.56	0.01	1.58	5.64
	σ_G^2		48.44	1.37	3.09	3.23	52.64	10.96	1.61	0.04	19.73	22.61
	σ_P^2		50.86	1.48	3.30	3.47	56.58	12.77	2.17	0.05	21.32	28.25
	GCV %		6.43	9.47	21.00	25.59	11.01	9.21	5.46	4.10	12.37	13.47
	PCV%		6.6	9.85	21.70	21.33	11.42	9.94	6.34	4.60	13.01	15.05
	H%		95.25	92.34	93.54	92.99	93.03	85.82	74.08	85.71	92.57	80.03
	Average		108.17	12.35	8.37	8.73	65.85	35.94	23.22	4.87	35.49	35.30

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			F$_5$ (Late selection)									
Genotypes	Rep. SS	2	17.48	0.19	2.47	3.42	156.98	34.25	5.36	0.03	13.62	33.67
	Genotypes SS	12	107.80**	4.15**	7.12**	7.44**	191.45**	103.43**	33.04**	0.22**	15.89**	76.01**
	Error SS	24	10.31	0.37	0.41	0.49	13.43	6.50	1.24	0.02	3.42	10.80
Families	Rep. SS	2	19.32	1.28	3.15	4.66	169.42	45.12	5.60	0.01	11.83	40.70
	Families SS	9	107.82**	4.14**	9.21**	9.69**	63.87**	41.00**	7.45**	0.19**	14.91**	96.58**
	Error SS	18	11.83	0.34	0.41	0.42	12.09	6.69	1.29	0.03	4.04	12.38
	σ_E^2		3.94	0.11	0.14	0.14	4.03	2.23	0.43	0.01	1.35	4.13
	σ_G^2		32.00	1.27	2.93	3.09	17.26	11.44	2.05	0.05	3.62	28.07
	σ_P^2		35.94	1.38	3.07	3.23	21.29	13.67	2.48	0.06	4.97	32.19
	GCV %		5.24	10.03	20.72	20.44	5.87	8.60	5.72	4.63	5.35	14.64
	PCV%		5.55	10.47	21.21	20.89	6.52	9.40	6.29	5.07	6.27	15.68
	H%		89.03	92.03	95.55	95.67	81.07	83.68	82.68	84.21	72.90	87.18
	Average		**107.83**	**12.49**	**8.26**	**8.60**	**70.73**	**39.32**	**25.02**	**4.83**	**35.53**	**36.18**

* and **: Significant 0.01 levels of probability; respectively.

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It is remarkable results that the estimates of heritability were increased from base population across one cycle to another of pedigree line selection. For instance, i.e the values of heritability for grain yield/plant were recorded at 58.42% in the base population (500 F_3 families), increased to 59.38 after one cycle (50 F_4 selected families), and increased to 74.08% after two cycles of pedigree line selection (10 F5 early selection) and 82.68% after one late selection (10 F5 selected families). For all traits studied, the same conclusion was reached. Furthermore, most heritability estimates for all studied traits were less than 60% in the base population (500 F3 families), but increased to more than 80% after two cycles of pedigree line selection (10 F5 early selection) and one cycle of late selection (10 F5 late selection), except for grain yield/plant after two cycles of pedigree line selection (10 F5 early selection) and harvest index after one cycle of late selection (10 F_5 late selection) recorded 74.08 and 72.90, respectively. **Abd El-Shafi (2014)** exerted that the differences between phenotypic and genotypic variances for grain yield/plant were small, indicating that selection reduced the range and variability in grain yield/plant of F4, which could be related to the high estimates of broad sense heritability in F4 wheat. Furthermore, **Aydin *et al*. (2010)** accounted for low values of heritability for grain yield and plant height of wheat at 46.05 and 43.69%, respectively. Consequently, both traits were most affected by the environmental condition. Otherwise, **Assefa and Lemma (2009)** according that the highest genetic gain (69.7%) with high heritability (88.3%) for grain yield indicated that grain yield relied more on direct selection. Meanwhile, heritability values for grain yield/plant, spike length, number of spikes/spike, harvest index, and plant height were all high values of heritability **(Laghari *et al*., 2010, and Mahdy *et al*., 2012)**. **Mukherjee et al. (2008)** discovered that grain yield had high heritability with moderate genetic advance, owing to non-additive gene action. **Sharma and Sharma (2007),** on the other hand, discovered high heritability (92.27%), indicating additive gene effects for grain yield/plant.

3.2.2-   Mean over cycle one (50 F₄ early selected families) and cycle two (10 F₅ early selected families) of early pedigree line selection as well as one cycle of late selection (10 F₅ late selected families) for grain yield/plant and correlated traits.

For early pedigree line selection cycles one (50 F4 early selected families), two (10 F5 early selected families), and one (10 F5 late selected families) for grain yield/plant and correlated traits, the range and averages of all F4 families and selections, as well as means of their parents and bulk sample, were calculated., are given in Tables 3, 4 and 5, respectively.

The grain yield/plant of all 500 F_4 families ranged from 8.14 to 28.75 with an average of 16.36 g as well as all 500 F_5 families varied from 3.71 to 28.92 with an average of 16.78 g. There are no significant differences recorded among both averages and their parents Misr 2, Sakha 94, and an unselected bulk sample in both generations, except parent Sakha 94 (19.0 g) surpassed significantly the families mean in F_5 (Table 3). Following one cycle of pedigree line selection for grain yield/plant, the means of 50 F4 early selected families ranged from 16.09 to 26.92 with an average of 21.00 g, compared to 16.47, 16.17, and 18.76 g for their parents and unselected bulk sample, respectively (Table 4). It is clear from the results that the average of 50 F4 early selected families (21.00 g) outperformed both their parents and the unselected bulk. Similarly, the means of the 50 F5 selected families (18.85 g) surpassed insignificantly both parents and unselected bulk sample (Table 4).

The mean over the 10 F5 early selected families ranged from 20.79 to 25.74 g after two cycles of pedigree line selection for grain yield/plant, with an average of 23.22 g. This average of 10 F5 **early** selected families surpassed significantly their parents and unselected bulk sample. In addition, the average weight of the 10 F5 **late** selected families was 25.02 g, with a range of 23.48 to 28.44 g. In comparison to their parents and the unselected bulk sample (17.75 = 40.96%), this average of 10 F5 late-selected families outperformed it significantly. (Table 5). It is remarkable results that the late selected families in F_5 recorded increasing means for grain yield/plant by 47.35, 31.68 and 40.96 compared to early selected families in F_5 which yielded 36.75, 22.21 and 30.82% compared to their respective parents and unselected bulk sample, respectively. Moreover, it is a clear conclusion that the selections of both 10 F_5 early and late selected families surpassed significantly their respective parents and unselected bulk sample with a more powerful direct response of selection resulted in late selection at the end of F_5 selections compared to early pedigree line selection for grain yield/plant.

The averages of 50 F_4 selected families for correlated traits such as biological yield/plant, the weight of spikes/plant, and seed index were 47.75, 27.61, and 4.8 g, respectively, and surpassed significantly their both parents and unselected bulk sample which recorded 38.13, 38.20 and 44.80 for biological yield/plant, 20.49, 20.20 and 24.49 for the weight of spikes/plant and 4.18, 4.18 and 4.21 for seed index, respectively (Table 4). This significant increase was 25.23, 25.00, and 6.58 for biological yield/plant, 34.75, 36.68, and 12.74 for the weight of spikes/plant, and 14.83, 14.83, and 14.01% for seed index compared to their parents and unselected bulk sample, respectively

The average of these three correlated traits i.e. biological yield/plant, the weight of spikes/plant, and seed index continued to be significantly high compared to their both parents and an unselected bulk sample in the next cycle of selection i.e. 10 F_5 early pedigree line selection and 10 F_5 late selection (Table 5). The average biological yield/plant yielded 65.85 and 70.73 g in 10 F_5 early pedigree line selection and 10 F_5 late selection and surpassed significantly their parent and unselected bulk sample by 30.22, 10.14 and 17.34% in 10 F_5 early and 39.87, 18.30 and 26.03% in 10 F_5 late selection, respectively. The average weight of spikes/plant gave 35.94 and 39.32 g in 10 F_5 early pedigree line selection and 10 F_5 late selection and surpassed significantly their parent and unselected bulk sample by 43.59, 21.26 and 27.63% in 10 F_5 early and 57.09, 32.66 and 39.02% in 10 F_5 late selection, respectively. In addition, the average harvest index accounted for 35.49 and 35.53% in 10 F_5 early pedigree line selection and 10 F_5 late selection and surpassed significantly the parent Sakha 94 and unselected bulk sample by 11.18 and 11.53% in 10 F_5 early selections and 11.55 and 12.26% in 10 F_5 late selections, respectively (Table 5).

Moreover, plant height for the family's average responses vice versa and reduced significantly compared to both parents and unselected bulk sample. This picture of view for plant height of selected families was clear for a reduction in 10 F_5 early and 10 F_5 late selection and measured 108.17 and 107.83 cm in 10 F_5 early pedigree line selection and 10 F_5 late selection and decreased significantly compared to their parent and unselected bulk sample by -5.68, -8.76 and -5.53% in 10 F_5 early selections and -5.98, -9.04 and 5.83% in 10 F_5 late selections, respectively (Table 5). The last results pronounced that the high-yielding selected families tend to be short compared to the rest families of the current population of wheat.

Table 3.   Range and means of 500 families over F_4 & F_5 as well as means of their parents and bulk sample for grain yield/plant and its attributes.

		PH	SL	NSP	NSES	BYP	WSP	GYP	SI	HI	TI
F4											
500 Families	Min.	71.80	8.80	4.20	5.00	19.28	11.44	8.14	2.96	22.44	7.33
	Max.	146.20	15.00	11.40	12.40	74.24	47.72	28.75	6.10	61.00	49.97
	Average	**108.89**	**11.38**	**7.36**	**7.89**	**39.55**	**21.75**	**16.36**	**4.52**	**41.46**	**24.78**
	Bulk	108.63	12.05	8.07	8.85	44.80	24.49	18.76	4.21	42.48	23.26
P1 (Misr 2)		115.35	11.08	7.19	7.68	38.13	20.49	16.47	4.18	43.23	19.67
P2 (Sakha 94)		117.89	12.92	6.93	7.41	38.20	20.20	16.17	4.18	42.29	19.87
Mid. Parents		116.62	12.00	7.06	7.55	38.17	20.34	16.32	4.18	42.76	19.77
R.L.S.D Genotypes	*0.05*	6.75	1.13	1.42	1.54	10.45	5.22	4.34	0.53	16.12	18.71
	0.01	8.80	1.47	1.86	2.02	13.72	6.83	5.68	0.69	17.45	23.20
R.L.S.D. Families	*0.05*	6.76	1.13	1.42	1.54	10.48	5.24	4.35	0.53	16.17	18.76
	0.01	8.81	1.47	1.86	2.03	13.76	6.85	5.69	0.69	17.50	23.26
F5											
500 Families	Min.	79.60	9.00	4.60	4.80	14.18	6.86	3.71	2.97	21.12	3.26
	Max.	137.40	15.00	13.20	13.80	84.40	48.52	28.92	5.35	53.48	53.59

	Average	**110.19**	**11.44**	**8.56**	**9.10**	**52.12**	**25.85**	**16.78**	**4.58**	**32.28**	**34.77**
	Bulk	114.50	12.15	9.52	9.73	56.12	28.16	17.75	4.43	31.82	36.57
P1 (Misr 2)		114.69	11.57	8.45	8.80	50.57	25.03	16.98	4.42	33.71	31.76
P2 (Sakha 94)		118.55	13.09	8.39	8.65	59.79	29.64	19.00	4.49	31.92	35.77
Mid. Parents		116.62	12.33	8.42	8.73	55.18	27.33	17.99	4.45	32.81	33.77
R.L.S.D	*0.05*	5.00	0.84	1.27	1.30	5.74	3.47	2.16	0.26	4.00	7.08
Genotypes	*0.01*	6.53	1.09	1.66	1.70	7.49	4.53	2.82	0.34	5.23	9.26
R.L.S.D.	*0.05*	5.01	0.84	1.27	1.30	5.74	3.47	2.16	0.26	4.01	7.09
Families	*0.01*	6.54	1.10	1.66	1.71	7.50	4.54	2.83	0.34	5.24	9.28

Table 4.   Range and means of 50 families over F_4 & F_5 as well as means of their parents and bulk sample for grain yield/plant and its attributes.

		PH	**SL**	**NSP**	**NSES**	**BYP**	**WSP**	**GYP**	**SI**	**HI**	**TI**
						F_4					
50 Families	Min.	87.80	9.20	4.60	5.20	38.38	20.20	16.09	3.34	**33.18**	10.72
	Max.	126.00	15.00	11.00	12.40	63.34	47.72	26.92	6.10	**54.25**	48.10
	Average	**108.48**	**12.17**	**7.94**	**8.39**	**47.75**	**27.61**	**21.00**	**4.80**	**44.19**	**23.46**
	Bulk	108.63	12.05	8.07	8.85	44.80	24.49	18.76	4.21	42.48	23.40
P1 (Misr 2)		115.35	11.08	7.19	7.68	38.13	20.49	16.47	4.18	43.23	19.67

P2 (Sakha 94)		117.89	12.92	6.93	7.41	38.20	20.20	16.17	4.18	42.29	19.87
Mid. Parents		116.62	12.00	7.06	7.55	38.17	20.35	16.32	4.18	42.76	19.77
R.L.S.D	*0.05*	4.70	1.17	1.34	1.45	5.00	3.51	4.08	0.42	8.10	10.73
Genotypes	*0.01*	6.18	1.53	1.65	1.91	6.55	4.60	5.64	0.56	11.46	14.82
R.L.S.D.	*0.05*	4.71	1.19	1.37	1.48	3.35	3.78	3.04	0.43	4.82	8.53
Families	*0.01*	6.18	1.56	1.70	1.96	4.45	4.69	4.03	0.57	6.40	11.31
F$_5$											
	Min.	94.40	9.60	4.60	4.80	40.70	19.04	12.10	3.94	24.84	3.48
	Max.	129.40	15.00	12.40	12.80	81.68	46.46	26.72	5.34	52.25	49.44
50 Families	Average	**109.47**	**12.10**	**8.21**	**8.69**	**56.21**	**28.50**	**18.85**	**4.78**	**33.76**	**33.16**
	Bulk	114.50	12.15	9.52	9.73	56.12	28.16	17.75	4.43	31.82	36.57
P1 (Misr 2)		114.69	11.57	8.45	8.80	50.57	25.03	16.98	4.42	33.71	31.76
P2 (Sakha 94)		118.55	13.09	8.39	8.65	59.79	29.64	19.00	4.49	31.92	35.77
Mid. Parents		116.62	12.33	8.42	8.73	55.18	27.34	17.99	4.46	32.82	33.77
R.L.S.D	*0.05*	3.81	0.85	1.25	1.35	4.31	3.13	2.05	0.23	4.50	9.82
Genotypes	*0.01*	5.02	1.12	1.65	1.78	6.36	4.62	3.01	0.30	5.61	13.22
R.L.S.D.	*0.05*	3.85	0.86	1.26	1.36	4.30	3.19	2.08	0.23	4.59	10.04
Families	***0.01***	5.06	1.14	1.67	1.80	6.33	4.70	3.07	0.30	5.72	13.52

Table 5.   Range and means of 10 families (early and late selection) over F_5 as well as means of their parents and bulk sample for grain yield/plant and its attributes.

		PH	SL	NSP	NSES	BYP	WSP	GYP	SI	HI	TI
F5 (10 Early selections)											
Families	Min.	96.33	10.93	5.67	5.93	52.56	31.20	20.79	4.58	31.09	27.36
	Max.	115.87	13.80	10.27	10.53	71.15	41.63	25.74	5.22	42.99	42.22
	Average	**108.17**	**12.35**	**8.37**	**8.73**	**65.85**	**35.94**	**23.22**	**4.87**	**35.49**	**35.30**
	Bulk	114.50	12.15	9.52	9.73	56.12	28.16	17.75	4.43	31.82	36.57
P1 (Misr 2)		114.69	11.57	8.45	8.80	50.57	25.03	16.98	4.42	33.71	31.76
P2 (Sakha 94)		118.55	13.09	8.39	8.65	59.79	29.64	19.00	4.49	31.92	35.77
Mid. Parents		116.62	12.33	8.42	8.73	55.18	27.34	17.99	4.46	32.82	33.77
R.L.S.D Genotypes	*0.05*	4.26	0.92	1.23	1.30	5.81	3.82	2.04	0.26	3.22	6.74
	0.01	5.83	1.25	1.68	1.78	7.95	5.23	2.79	0.37	4.41	9.65
R.L.S.D. Families	*0.05*	4.62	0.99	1.38	1.47	5.90	4.09	2.58	0.24	3.74	7.76
	0.01	6.59	1.42	1.97	2.10	8.43	6.09	3.92	0.34	5.34	10.75
F5 (10 Late selections)											
Families	Min.	96.33	10.93	5.67	5.93	63.17	33.47	23.48	4.51	31.91	28.80
	Max.	116.13	13.80	10.73	11.27	76.43	46.35	28.44	5.22	39.02	45.23

	Average	**107.83**	**12.49**	**8.26**	**8.60**	**70.73**	**39.32**	**25.02**	**4.83**	**35.53**	**36.18**
	Bulk	114.50	12.15	9.52	9.73	56.12	28.16	17.75	4.43	31.65	37.00
P1 (Misr 2)		114.69	11.57	8.45	8.80	50.57	25.03	16.98	4.42	33.60	32.10
P2 (Sakha 94)		118.55	13.09	8.39	8.65	59.79	29.64	19.00	4.49	31.85	35.84
Mid. Parents		116.62	12.33	8.42	8.73	55.18	27.34	17.99	4.46	32.82	33.77
R.L.S.D Genotypes	*0.05*	**5.51**	**1.05**	**1.09**	**1.13**	**6.28**	**4.37**	**1.84**	**0.27**	**3.49**	**5.90**
	0.01	**7.87**	**1.50**	**1.56**	**1.62**	**8.98**	**6.24**	**2.58**	**0.40**	**5.20**	**8.59**
R.L.S.D. Families	*0.05*	**6.18**	**1.00**	**1.10**	**1.11**	**6.56**	**4.65**	**2.15**	**0.29**	**3.99**	**6.32**
	0.01	**8.99**	**1.37**	**1.57**	**1.59**	**9.68**	**6.76**	**2.97**	**0.43**	**5.99**	**9.19**

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