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Efficiency of three selection methods in two bread wheat populations

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Abstract

A three-seasons study (2021/22–2023/24) were carried out at the Experimental Farm, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt to compare three selection methods i.e., pedigree (PSM), single-seed descent (SSD) and bulk (BM) from F_2 to F_4 generations in two bread wheat populations *i.e.*, Sids14 x Giza 171 (population I) and Sids 14 × Gommiza 11 (population II). The studied characters were grain yield/plant, number of spikes/plant and number of grains/spike. The analysis of variance indicated highly significant differences among the F_3 and F_4 selected families for all the studied characters in both populations, confirming sufficient genetic variation for selection. Across all selection methods and both populations, the mean performance of F_4 selected families consistently surpassed that of F_3 selected families for all the studied characters. The results also revealed minimal differences between the phenotypic and genotypic coefficients of variability for the F_3 and F_4 selected families. This suggests that the environmental effects on these traits were relatively small. High values of broad-sense heritability were observed for all the studied traits in both populations and across all selection methods, indicating that the traits are highly heritable and selection would be effective. Furthermore, a significant and positive phenotypic correlation was found between grain yield/plant and both number of grains per spike and 100-grain weight. This suggests that selecting these component traits could indirectly improve grain yield. The substantial differences observed among families in both populations confirm that selection for grain yield/plant is a feasible and effective strategy for genetic improvement.

Keywords: Wheat, breeding methods, phenotypic and genotypic of variability, heritability, genetic advance.

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1. Introduction

Given its status as a staple in the human diet, wheat (*Triticum aestivum* L.) holds a position of paramount importance as a key strategic cereal crop, extending its essentiality beyond Egypt to encompass the entire globe. The cultivated area, yield and total production of wheat in Egypt were 1.53 million hectares, 6.41 metric tons/hectares and 9.8 million tons, respectively (USDA, 2023). The enhancement of crop productivity (yield) represents a fundamental objective in all plant improvement programs. Achieving this goal necessitates that breeders select methodologies that facilitate the simultaneous genetic improvement of yield and its constituent components. Various selection methods are applicable in the segregating generations following hybridization in self-pollinated crops. A comprehensive understanding of each selection method, including its established relationship with final yield, is crucial for determining the optimal strategy to be applied in a breeding program. This, in turn, allows for the successful development and application of techniques aimed at obtaining high-yielding wheat cultivars. Pedigree Selection (PS) is recognized as the conventional technique for effectively accumulating desirable genetic recombination across successive generations. Research by Khames *et al*. (2017), El-Hosary *et al*. (2020), and Fouad *et al*. (2020) has demonstrated that PS is highly effective in improving both grain yield and its components. Consequently, numerous investigations have been conducted to compare the efficiency of different selection methods within segregating populations of bread wheat (Aref *et al*., 2011; El-Karamity *et al*., 2007; El-Hosary *et al*., 2011; El-Hosary *et al*., 2014; Farag, 2013). Early generation heterozygosity poses a challenge to the efficient selection and identification of superior recombinant genotypes. While Pedigree Selection (PSM) promotes homozygosity, it often demands numerous cycles to stabilize loci governing key agronomic traits. Single Seed Descent (SSD) offers a faster alternative, yielding homozygous inbred lines by accelerating generations; however, its application is constrained by the growth habit of the utilized plant material (Inagaki *et al.,* 1998). Arunachalam *et al*. (2002) and Gehan, Abou-Zaid *et al*. (2023) reported that the PSM and SSD methods were equal efficient, while the bulk method (BM) method turned out to be less effective. The objective of this study was to evaluate the effectiveness and comparison of pedigree, single seed decent and bulk breeding selection methods through estimating genetic variability, broad sense heritability, genetic advance, expected and realized gain from selection, phenotypic and genotypic coefficients of variation and phenotypic coefficient of correlation in two bread wheat populations.

2. Materials and methods

The present study was carried out at the Experimental Farm, Faculty of Agriculture, Al-Azhar University, Assiut, Egypt during three successive winter seasons of 2021/2022, 2022/2023 and 2023/2024. Three bread wheat (*Triticum aestivum* L.) cultivars were used. The name and pedigree of these parents are shown in Table (1). The objective of this study was estimating genetic variability, broad sense heritability, genetic advance, expected and realized gain from selection phenotypic and genotypic of variation and phenotypic correlation coefficient in segregating generations of two bread wheat (*Triticum aestivum* L.) populations *i.e.*, Sids 14 × Giza 171 and Sids 14 × Gommiza 11 under three methods of selection *i.e.*, pedigree (PSM), single seed descent (SSD) and bulk (BM) of the F_2, F_3 and F_4 generations to improve bread wheat yield.

Table (1): Pedigree and origin of used cultivars in the two bread wheat populations in this study.

Parent	Pedigree	Origin
Sids-14 (P_1)	BOW"S"/Vee"S"//Bow"S"/TSI/3/Beni Sweef 1 SD293-1SD-2SD-4SD- Osd	Egypt
Giza-171 (P_2)	Sakha93 / Gemmiza 9	Egypt
Gemmiza 11 (P_3)	BOW"S"/KVZ"S"//7C/SERI-82/3/GIZA 168/SAKHA 61 GM7892-2GM-1GM-2GM-1GM-0GM	Egypt

2.1 Season 2021/2022 (F_2 generation)

1200 plants from each F_2 population, their parents and check cultivar (Sids 12) were sown on December 5th in spaced plants and non-replicated plots. Each plot included 15 rows, spacing between rows was 60 cm and plant to plant was 20 cm and one plant per hill was maintained. All agricultural practices were carried out as follows for the wheat over the experiments. Data were recorded on 1000 plants chosen randomly from each population. The best 100 plants (10% selection intensity) from each population were selected according to grain yield/plant, number of spikes/plant and number of grains/spike.

2.2 Season 2022/2023 (F_3 generation)

The 100 selected families from each population and selection method beside bulk plot and local check (Sids 12) were sown on 5th of December in separate experiments in a randomized complete block design with three replications. Recommended agronomic practices and need based plant protection measures were followed. In the pedigree selection method (PSM), the plot size was one row, 4 m long, 60 cm apart and 20 cm between hills within the row. The best 20 F_3 families (20 % selection intensity) from each population were selected for grain yield/plant, number of spikes/plant and number of grains/spike. In the single seed descent method (SSD), one grain taken from 100 F_2 selected plants of each population was planted as F_3 generation. Similarly, 20 families were selected from each population and were harvested individually by using selection intensity at 20%. In the bulk method (BM), five grains) from each 100 F_2 selected plants of each population were bulk harvested. A random sample of bulked grains of each population was space-planted in 5 rows, 4 m long, 60 cm apart and 20 cm between hills within row as F_3 generation.

2.3 Season 2023/2024 (F_4 generation)

The 20 F_3 selected families from each population and selection methods were shown in this season as mentioned in the previous season.

2.4 The studied characters

Grain yield/plant in grams (GY/P), number of spikes/plant (NS/P) and number of grains/spike (NG/S) were recorded on the F_2 individual selected plant and random sample of 10 guarded plants in each plot of the F_3 and F_4 generations.

2.5 Statistical analysis

Analysis of mean squares with a randomized complete block design to compute the significance for genotypes (Table 2) was made according to Snedecor and Cochran 1967. The least significant difference (L.S.D) test at 0.05 and 0.01 levels of probabilities was used to compare among means according to Stell and Torrie (1980)

Table (2): The analysis of variance and expected mean squares.

Source of variance	D.F	M.S	Expected mean square	
			Variance	Covariance
Replications	r–1	M_3	$\sigma^2e + g\sigma^2r$	
Genotypes	g-1	M_2	$\sigma^2e + r\sigma^2g$	Cov.e + r Cov.g
Error	(r-1) (g-1)	M_1	σ^2e	Cov.e

Where: r and g are number of replications and genotypes, respectively, σ^2e and cov.e are error variance and covariance, respectively and σ^2g and cov.g are genetic variance and covariance, respectively.

2.6 Heritability in broad sense (H)

Heritability in broad sense (H) was calculated as follows:

Heritability in the F_2

$$(H) = (VF_2 - ((VP_1 + VP_2) / 2)) / VF_2) \times 100$$

Heritability in the F_3 and F_4

$$(H) = (\sigma^2g / \sigma^2p) \times 100$$

Where: VF_2 = the phenotypic variance of the F_2 population. VP_1 = variance of the first parent. VP_2= variance of the second parent. σ^2g= the genotypic variance of the F_3 and F_4 generations. σ^2p= the phenotypic variance of the F_3 and F_4 generations.

2.7 Expected gain from selection (EGS%)

The expected genetic advance (GA) expressed as a percentage of the mean value with an assumed 10 and 20 % intensity of selection pressure was computed by the formula given by Allard (1960) as follow:

$$\text{EGS\%} = k.\,\text{H}\sqrt{\sigma^2 P}$$

Where: k = 1.75 and 1.41 constant for 10 and 20% selection intensity (*i.e.* the highest-performing 10 and 20% are selected), respectively. H = broad-sense heritability. σ^2P= Phenotypic variance of the population.

2.8 Realized gain from selection (RGS%)

Realized gain from selection was calculated as follow:

$$\text{RGS\%} = (\overline{X}_0 - \overline{XP}) \times 100/\overline{XP}$$

Where: RGS% is the realized advance in one generation of selection, $\overline{X}_0$ is the phenotypic mean of the offspring of selected parents and $\overline{XP}$ is the phenotypic mean of the whole parental generation.

2.9 The phenotypic (PCV%) and genotypic (GCV%) coefficients of variation

The phenotypic (PCV%) and genotypic (GCV%) coefficients of variation are computed according to Burton (1952) as follow:

$$\text{PCV} = (\sqrt{VP}/\overline{X}) \times 100$$

$$\text{GCV} = (\sqrt{VG}/\overline{X}) \times 100$$

Where: PCV and GCV are phenotypic and genotypic coefficients of variation, respectively, VP and VG are corresponding variances and $\overline{X}$ is the population mean.

The relative values of these two types of coefficients give an idea about the magnitude of variability presented in a population. Interpretation of variability in terms is given below (Singh and Singh, 1975).

2.9 Phenotypic(rp) correlation

The calculation of phenotypic correlation requires estimates of corresponding variances and covariance (Walker, 1960). Phenotypic correlation: rp_{xy} = cov $p_{xy}/(\sigma p_x.\sigma p_y)$. Where: rp phenotypic correlation coefficient.

3. Results and Discussion

Three selection methods *i.e.*, pedigree (PSM), single seed decent (SSD) and bulk (BM) were achieved by three characters *i.e.*, grain yield/plant (GY/P), number of spikes/plant (NS/P) and number of grains/spike (NG/S) from F_2 to F_4 generations of two bread wheat populations *i.e.*, Sids 14 × Giza 171 (Pop. I) and Sids 14 × Gommiza 11 (Pop. II) during three successive winter seasons at 2021/2022, 2022/2023 and 2023/2024 to improve wheat yielding ability.

3.1 Description of the base populations (F_2 generation)

The characteristics of the two F_2 base populations (Table 3) indicated highly significant (**) differences among the F_2 plants for all the studied characters at all the selection methods in the two populations, as well as sufficient coefficient of variability (CV %) in the Pop. I with 30.18% and in Pop. II with 29.62% for grain yield/plant. As well as, for number of spikes/plant with 26.73 and 26.10% in the Pop. I and Pop. II, respectively. While, for number of grains/spike was moderated in the Pop. I and Pop. II with 19.86 and 16.88%, respectively. This enhanced chance of selection for spike characteristics. Otherwise, the CV % of all the studied characters of the three parents was very low, indicating the high purity at three parents under this study. Broad sense heritability (H) estimates were high for all the studied characters in the two populations. Similar results were reported by El-Mahdy Rasha *et al.* (2012), Khames *et al.* (2017) and Fouad *et al.* (2020).

Table (3): The mean, variance, coefficient of variation (CV%), broad sense heritability (H%) and genetic advance (GA%) of the two F_2 base populations and their parents for the three studied characters in 2021/2022 growing season.

Items			GY/P (g)	NS/P	NG/S
Population I (Sids 14 × Giza 171)					
		Mean	36.78	10.59	69.49
		Variance	123.36**	8.02**	190.58**
		CV%	30.19	26.73	19.86
		H %	89.20	96.20	91.17
		GA%	47.41	45.26	31.87
Parents	Sids 14	Mean	43.53	6.21	70.3
		CV%	7.54	9.65	4.07
	Giza171	Mean	41.43	5.93	64.7
		CV%	9.61	8.42	7.79
Population II (Sids 14 × Gommiza 11)					
		Mean	31.74	11.06	71.64
		Variance	88.39**	8.34**	142.82**
		Cv%	29.62	26.10	16.68
		H %	86.45	90.99	92.42
		GA%	52.13	41.80	27.13
Parent	Gommiza 11	Mean	38.81	9.79	68.85
		CV%	9.34	8.17	5.32

Where: GY/P is grain yield /plant, NS/P is number of spike/plants, NG/S is number of grains/plants, CV% is coefficient of variation, H is broad sense heritability and GA% is genetic advance.

Expected genetic advance (GA %) from selection as percentage of the F_2 population mean reached to 47.41 and 52.13 % for GY/P, 45.26 and 41.80 % for NS/P and 31.87 and 27.13 % for NG/S in the Pop I and Pop II, respectively. These results are in harmony with those obtained by Khattab *et al* (2010), El-Aref *et al.* (2011), Amin (2013), Abd-El-Rady (2018) and El-Massry *et al* (2018). In a study by Khaled (2013), three crosses showed a moderate to high genetic advance (GA%) for the traits of (NS/P), (NG/S) and (GY/P) indicating significant potential for genetic improvement.

3.2 Variability among the F_3 and F_4 selected families

Data in Table (4) revealed highly significant differences among the F_3 and F_4 selected families of the two populations for the three studied traits at the three selection methods. Similar results were reported by Srivastava *et al*. (1989), El-Aref *et al*. (2011) and Farag (2013).

Table (4): Mean squares of the F_3 and F_4 selected families of the two populations for the studied characters at the three selection methods in 2022/2023 and 2023/2024 growing seasons.

S.O.V / Characters	Population I							
	Selection methods							
GY/P(g)	DF		PSM		BM		SSD	
	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
Replication	2	2	0.38	1.01	2.62	4.19	17.30	2.78
Families	49	19	344.96**	286.50**	123.56**	58.26**	292.38**	101.30**
Error	98	38	1.36	2.11	1.65	3.05	8.88	1.51
NS/P								
Replication	2	2	1.04	0.22	0.09	1.07	0.33	2.46
Families	49	19	18.08**	9.04**	12.75**	3.68**	10.96**	12.55**
Error	98	38	0.56	0.73	0.41	0.44	1.43	0.62
N.K/S								
Replication	2	2	2.29	6.66	0.33	0.82	7.79	2.51
Families	49	19	277.41**	232.31**	225.01**	216.75**	265.64**	63.35**
Error	98	38	2.99	1.93	2.14	1.26	2.07	2.13
	Population II							
GY/P(g)	DF		PSM		BM		SSD	
	F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
Replication	2	2	0.071	0.52	1.14	3.70	0.39	0.822
families	49	19	178.50**	63.11**	112.44**	118.73**	171.05**	114.36**
error	98	38	1.81	2.09	0.89	1.08	1.09	0.82
NS/P								
Replication	2	2	1.49	6.016	0.246	0.066	2.29	0.52
Families	49	19	21.84**	15.70**	12.02**	4.82**	13.79**	14.24**
Error	98	38	1.23	1.01	0.90	1.24	2.57	1.59
N.K/S								
Replication	2	2	2.29	0.60	10.64	4.27	2.52	4.02
Families	49	19	276.84**	82.31**	239.11**	71.87**	261.66**	119.01**
Error	98	38	3.21	3.74	2.94	2.60	2.62	5.84

GY/ P is Grain yield /plant, NS/P is number of spikes/plant, NG/S is number of grains/plant, CV% is coefficient of variation, H is Broad sense heritability, S.O.V is Source of variation, DF is Degree of freedom, PSM is Pedigree selection method, BM is Bulk selection method, SSD is Single seed descent method, * and ** significant at 0.05 and 0.01 levels probability and F_3 and F_4 are the third and F_1 all generation.

3.3 Mean performance of the F_4 selected families

Mean performance values of the 20 F_4 selected families for GY/P, NS/P and NG/S at the three selection methods of the two populations are presented in Tables (5 and 6).

Table (5): Mean performance of the 20 F_4 selected families, their parents and the check variety at the three breeding methods in the first population.

Families / Selection methods		Population I								
		GY/P (g)			NS/P			NG/S		
		PSM	SSD	BM	PSM	SSD	BM	PSM	SSD	BM
1		79.55	62.00	43.76	10.67	10.00	11.33	96.33	98.00	79.00
2		78.81	57.15	43.68	11.00	10.00	11.00	95.67	91.00	76.67
3		67.59	53.53	42.50	13.00	9.67	11.67	92.67	90.33	74.67
4		60.23	52.40	40.80	16.33	9.00	11.67	92.67	87.33	72.33
5		57.15	52.38	40.54	12.00	8.00	10.67	91.00	89.00	73.00
6		53.53	51.48	39.78	14.67	9.00	10.67	91.67	86.67	71.67
7		52.40	51.36	38.44	10.67	9.00	10.00	89.67	87.67	70.00
8		52.38	50.96	38.21	11.00	9.00	10.00	91.67	86.67	70.67
9		51.48	50.42	38.21	11.00	8.67	10.00	92.33	84.33	70.00
10		51.36	50.35	37.91	11.00	8.17	7.00	78.00	85.67	70.67
11		50.96	47.71	37.46	11.67	8.83	10.33	75.33	85.33	68.00
12		50.42	47.40	36.94	11.00	8.50	10.00	105.33	84.00	68.00
13		50.35	47.21	36.81	13.33	8.50	9.33	88.67	84.00	67.33
14		49.37	47.05	34.77	14.67	8.50	9.67	87.67	82.00	68.00
15		48.86	47.00	34.49	13.00	8.00	9.33	79.33	81.33	68.00
16		47.93	46.17	34.31	15.33	8.00	9.00	79.00	80.67	55.00
17		47.71	45.92	34.05	12.67	8.00	9.33	78.00	79.00	54.00
18		47.40	45.29	33.78	11.67	8.00	9.33	75.33	80.00	53.67
19		47.05	43.68	27.77	12.33	8.50	8.67	75.67	81.67	53.00
20		47.00	67.33	27.77	10.33	9.35	9.33	75.67	80.67	51.00
Average		54.58	50.84	37.10	12.36	8.26	9.92	86.58	85.27	66.73
Parents	Sids 14	41.65			9.14			67.00		
	Gommiza 11	38.00			8.81			70.80		
Check	Sids 12	44.55			10.72			74.18		
LSD.05		4.15	3.52	4.96	2.43	2.25	1.88	3.97	4.17	3.20
LSD.01		5.38	4.56	6.45	3.15	2.92	2.44	5.14	5.40	4.14

GY/ P is Grain yield /plant, NS/P is number of spikes/plant, NG/S is number of grains/plant, PSM is Pedigree selection method, BM is Bulk selection method and SSD is Single seed descent method.

At the population I data in Table (5) manifested that 15 families outyielded significantly the check variety and the best of them was No. 1 with 79.55 g at PSM, as well as at SSD 11 families outyielded significantly the check and the best of them was No. 20 with 67.33 g, while none of the families exceeded significantly the check at the BM. For number of spikes/plant, 5 families exceeded significantly the check and the best of them was No. 4 with 16.33 spikes/plant at the PSM, while none of the families exceeded significantly the check at SSD and BM. For number of grains/spike, 14 families exceeded significantly the check and the best of them was No. 12 with 105.33 grains/spike at PSM, as well as at the SSD all the families exceeded significantly the check and the best of them was No.1 with 98.00 grains/spike, while at the BM only No.1 with 79.00 grains/spike exceeded significantly the check**.** These obtained results could be supported with the findings by El-Hosary *et al.* (2011). At the second population, data in Table (6) exhibited that at PSM 11 families outyielded significantly the check variety (Sids 12) and the best of them was No. 20 with 62.33 g. On the other hand, at SSD 4 families outyielded significantly the check and the best of them was No.1 with 62.72 g. While, at BM none of the families outyielded the check. For number of spikes/plant, at PSM 10 families exceeded significantly the check and the best of them was No.1 with 20 spikes plant, as well as 4 families exceeded significantly the check and the best of them was No.2 with 18 spikes/plant, while none of the families exceeded significantly the check at the BM. For number of grains/spike, all families exceeded significantly the check at PSM and SSD, except No.17 at SSD and the best of them was No.1 with 98.67 and 95.00 grains/spike at PMS and SSD, respectively, while at BM only 3 families exceeded significantly the check and the best of them was No. 1 with 92.00 grains/spike. These obtained results could be supported with the findings by El-Hosary *et al.* (2014).

Table (6): Mean performance of the 20 F_4 selected families, their parents and the check variety at the three breeding methods in the second population.

Families		Population II								
		GY/P (g)			NS/P			NG/S		
Selection methods		PSM	SSD	BM	PSM	SSD	BM	PSM	SSD	BM
1		53.56	63.72	41.08	20.00	17.00	12.00	98.67	95.00	92.00
2		53.40	53.19	40.80	18.67	18.00	12.33	91.67	92.33	80.67
3		53.33	50.35	40.54	17.67	13.33	11.67	89.67	90.00	77.67
4		53.25	47.30	39.78	16.33	14.00	12.67	90.67	91.33	74.33
5		51.62	47.08	39.61	16.00	15.67	12.33	92.33	90.00	79.00
6		51.23	45.98	38.44	15.00	12.33	10.67	87.67	93.33	76.67
7		50.73	44.81	38.21	15.33	10.67	10.67	90.33	92.33	78.00
8		50.54	43.60	37.91	14.33	15.33	12.00	82.67	92.00	77.33
9		49.34	43.19	36.94	14.33	10.67	11.67	90.00	92.67	73.00
10		49.18	42.25	24.16	15.67	12.67	12.00	89.67	87.00	76.67
11		47.53	41.60	22.20	12.33	12.00	12.00	85.33	88.00	74.33
12		47.46	41.23	22.19	12.00	11.00	11.67	82.33	90.00	74.67
13		46.94	40.69	45.67	12.00	15.00	9.00	81.67	86.00	73.67
14		46.63	40.30	34.49	15.00	12.33	10.67	82.00	86.67	73.67
15		46.61	40.18	34.31	14.67	12.00	10.33	82.67	84.00	72.00
16		46.29	39.23	34.05	13.33	12.00	10.67	81.33	83.00	70.33
17		46.11	39.00	33.45	12.33	11.00	8.33	80.33	66.33	70.33
18		45.51	38.95	33.44	12.33	11.33	10.00	82.33	83.67	71.00
19		39.72	38.74	33.17	12.00	10.67	8.67	80.67	82.00	71.67
20		62.33	38.70	33.03	14.33	13.67	10.33	80.00	84.67	72.33
Average		49.56	44.00	35.17	14.68	13.03	10.98	86.10	87.52	75.47
Parents	Sids 14	41.65			10.8			67.00		
	Giza 171	43.20			10.3			69.00		
Check	Sids 12	44.55			11.72			74.18		
LS.D.05		4.13	2.59	2.97	2.88	3.60	3.18	5.52	6.90	4.60
LS.D.01		5.35	3.36	3.85	3.73	4.66	4.12	7.15	8.94	5.96

GY/P is Grain yield /plant, NS/P is number of spikes/plant, NG/S is number of grains/plant, PSM is Pedigree selection method, BM is Bulk selection method and SSD is Single seed descent method.

3.4 Mean performance over all the F_3 and F_4 selected families

Means over all the F_3 and F_4 selected families at the two populations for the three studied characters at the three selection methods are presented in Table (7). The obtained results manifested that the mean over all the F_4 selected families surpassed the F_3 selected families for all the studied characters at all the selection methods of both populations.

Table (7): Mean performance values over all the F_3 and F_4 selected families, standard error, phenotypic and genotypic coefficients of variation and broad sense heritability for all the studied characters in the F_3 and F_4 generations of the two populations.

Characters	Pop.	Gen.	SM.	Mean ± SE	σ^2p	σ^2g	PCV%	GCV%	H%
Grain yield/plant (g)	Pop I	F_3	PSM	45.47±0.67	114.98**	114.53**	23.58	23.53	99.60
			SSD	40.21±1.72	97.46**	94.50**	24.55	24.17	96.96
			BM	31.38±0.74	41.18**	40.63**	20.45	20.31	98.66
		F_4	PSM	54.58±0.84	95.50**	94.79**	17.90	17.84	9926
			SSD	50.84±0.71	33.76**	33.26**	11.43	11.34	98.50
			BM	37.10±1.00	19.41**	18.40**	11.87	11.56	94.77
	Pop II	F_3	PSM	42.06±0.78	59.50**	58.89**	23.58	16.38	98.98
			SSD	37.27±0.60	57.01**	56.65**	20.25	20.19	99.36
			BM	30.70±0.54	49.15**	37.18**	22.83	19.85	75.64
		F_4	PSM	49.56±0.83	21.03**	20.33**	9.25	9.09	96.98
			SSD	44.00±0.52	38.12**	37.84**	14.23	13.98	99.27
			BM	35.17±0.60	39.57**	39.21**	17.88	17.80	99.08
No. of spikes/plant	Pop I	F_3	PSM	11.54±0.43	6.02**	5.83**	21.27	20.93	96.88
			SSD	7.29±0.69	3.65**	3.17**	26.21	24.44	86.91
			BM	8.18±0.37	4.25**	4.11**	25.18	24.77	96.81
		F_4	PSM	12.36±0.49	3.01**	2.77**	14.04	13.46	91.98
			SSD	8.26±0.45	4.18**	3.97**	23.43	22.84	95.02
			BM	9.91±0.38	1.22**	1.08**	11.16	10.48	88.17
	Pop II	F_3	PSM	12.27±0.63	7.28**	6.87**	21.98	21.35	94.37
			SSD	11.97±1.33	4.59**	2.81**	17.90	14.00	61.13
			BM	9.97±0.54	4.00**	3.70**	20.07	19.30	92.51
		F_4	PSM	14.68±0.58	5.23**	4.89**	15.58	15.06	93.52
			SSD	13.03±0.73	4.74**	4.21**	16.71	15.75	88.85
			BM	10.98±0.64	1.61**	1.19**	11.54	9.94	74.24
Number of grains/spike	Pop I	F_3	PSM	81.38±0.99	92.47**	91.47**	11.81	11.75	98.92
			SSD	77.44±0.83	88.54**	87.85**	12.15	12.10	99.21
			BM	61.72±0.84	75.00**	74.29**	14.03	13.96	99.05
		F_4	PSM	86.58±0.79	77.43**	76.79**	10.16	10.12	99.16
			SSD	85.27±0.84	21.11**	20.40**	5.38	5.29	96.63
			BM	66.73±0.64	72.25**	71.83**	12.73	12.70	99.42
	Pop II	F_3	PSM	76.75±1.03	92.28**	91.21**	12.51	12.44	98.84
			SSD	79.12±0.93	87.21**	86.34**	11.80	11.74	99.00
			BM	68.57±0.99	79.70**	78.72**	13.01	12.93	98.76
		F_4	PSM	86.10±1.11	27.43**	26.19**	6.08	5.94	95.45
			SSD	87.51±1.39	39.70**	37.75**	7.19	7.02	95.09
			BM	75.46±0.94	23.95**	23.09**	6.48	6.36	96.38

Gen is generations, SM is selection methods, SE is standard error, σ^2g is the genotypic variance, σ^2p is the phenotypic variance, PCV % and GCV % are phenotypic and genotypic coefficients of variation, respectively, H is broad sense heritability and F_3 and F_4 are three and four generation.

The PSM possessed the highest means of both the F_3 and F_4 families for all the studied characters at both populations, except number of grains/spike at the Pop. II, where the SSD possessed the highest means. While, the BM possessed the lowest means of both F_3 and F_4 families for all the studied characters at both populations, except number of spikes/plant at both F_3 and F_4 families at Pop. I, where followed the PSM. Therefore, the PSM consider the most efficiency for improvement yield at both populations, followed by the SSD. Thes obtained results could be supported with the findings by Srivastava *et al*. (1989), El-Karamity *et al*. (2007), and El-Hosary *et al*. (2011).

3.5 Genetic parameters

Phenotypic (PCV%) and genotypic (GCV%) coefficients of variability and broad sense heritability (H%) of the F_3 and F_4 selected families at both population for grain yield/plant, number of spikes/plant and number of grains/spike at selection methods are presented in Table (7). The obtained results manifested that small differences between values of phenotypic and genotypic coefficients of variability at the F_3 and F_4 selected families at both populations for all the studied characters at all selection methods. Also, phenotypic and genotypic coefficients of variability values decreased in F_4 than F_3 selected families of both populations for all the studied characters at all selection methods. Similar results were found by Mahdy *et al*. (2012), Zaazaa *et al*. (2012), Khan and Verma (2015), Khames *et al*. (2017), Fouad *et al*. (2020) and Ahmad and Gupta (2023). Heritability in broad sense values (Table 7) were high for all the studied traits of both populations in the F_3 and F_4 generations at all the selection methods. Generally, high estimates of heritability showed that the environmental effects were small compared to the genetic effects. These results are in according with those of El-Aref *et al*. (2011), Amin (2013), Abd El-Rady (2018), Balkan (2018), El-Gammaal and Yahya (2018), Elmassry and El-Nahas Marwa (2018), Bazai *et al*. (2020) and Fouad *et al*. (2020).

3.6 The expected (EGS%) and realized (RGS%) gain from selection in the three selection methods

The expected (EGS%) and realized (RGS%) gain from selection at PSM, SSD and BM in the F_3 and F_4 generations for all the studied characters of both populations are presented in Tables (8, 9 and 10). The obtained results cleared that the EGS% values were decreased from the Next generation than the previous at all the selection methods generations, studied characters and populations, except NS/P and SSD. On the other hand, the RGS% values were increased at F_4 than F_3 of both populations for all the studied characters at all selection method, while decreased at F_4 than F_3 of both populations for all the studied characters at all selection method. These results are in general agreement with those reported by Kattab *et al*. (2010), El-Aref *et al*. (2011), Sultan *et al*. (2011), Amin (2013), Abd El-Rady

(2018), Balkan (2018) and El Massry *et al*. (2018). On the other hand, Kuobisy (2011) reported that the GA% was generally small for all studied characters in the two hybrids, except NG/S in two hybrids and two environments and GY/P in hybrid 1 for two environments it was had moderate of genetic advance values. On the opposite side (Budak, 2002), and Kashif and Khaliq (2004) found the lowest heritability and genetic advance for GY/P.

Table (8): The EGS% and RGS% estimates for all studied characters in F_2, F_3 and F_4 generations at PSM method in both populations.

Characters	Generations	PSM			
		Population I		Population II	
		EGS	RGS	EGS	RGS
Grain yield/plant	F_2	47.41	-------	52.13	-------
	F_3	41.34	23.62	25.77	32.51
	F_4	20.65	20.02	12.56	17.83
No. of spikes/plant	F_2	45.26	-------	41.80	-------
	F_3	36.27	8.97	36.52	10.43
	F_4	18.20	7.16	20.54	20.91
Number of grains/spike	F_2	31.87	-------	27.13	-------
	F_3	20.57	17.11	21.77	7.11
	F_4	8.18	6.39	14.20	12.18

EGS% is expected genetic advance % and RGS% is realized gain from selection.

Table (9): The EGS% and RGS% estimates for all studied characters in F_3 and F_4 generations at SSD method in both populations.

Characters	Generations	SSD			
		Population I		Population II	
		EGS	RGS	EGS	RGS
Grain yield/plant	F_2	41.89	27.40	35.42	29.85
	F_3	25.87	26.43	19.64	18.06
	F_4	40.10	5.04	19.26	6.68
No. of spikes/plant	F_2	15.44	28.25	20.94	9.21
	F_3	21.21	7.79	20.56	16.06
	F_4	9.64	6.39	7.56	9.80
Number of grains/spike	F_2	41.89	27.40	35.42	29.85
	F_3	25.87	26.43	19.64	18.06
	F_4	40.10	5.04	19.26	6.68

EGS% is expected genetic advance % and RGS% is realized gain from selection.

Table (10): The EGS% and RGS% estimates for all studied characters in F_3 and F_4 generations at BM method in both populations.

Characters	Generations	BSM			
		Population I		Population II	
		EGS	RGS	EGS	RGS
Grain yield/plant	F_2	35.51	-------	30.39	-------
	F_3	24.61	18.21	22.23	14.56
	F_4	42.90	-------	32.68	------
No. of spikes/plant	F_2	13.84	15.04	12.08	10.34
	F_3	24.45	-------	22.63	-------
	F_4	8.81	8.12	17.56	11.67
Number of grains/spike	F_2	35.51	-------	30.39	-------
	F_3	24.61	18.21	22.23	14.56
	F_4	42.90	-------	32.68	------

EGS% is expected genetic advance % and RGS% is realized gain from selection.

3.7 Phenotypic correlation coefficient

Phenotypic correlation coefficient among GY/P and their two components *i.e.*, NS/P and NG/S in the F_4 generation at PSM, SSD and BM for both populations is presented in Table (11). The obtained results manifested that positive significant phenotypic correlation was detected between GY/P and their two components *i.e.*, NS/P and NG/S at three selection methods and both populations, except NS/P at PSM in Pop. I and NG/S at PSM and BM in Pop. II, indicting that NS/P and NG/S are good selection criteria to improve GY/P. These results were in agreement with those obtained by Fouad (2018), Shrief *et al.* (2019), Ahmed *et al.* (2020) and Bazia *et al.* (2020).

Table (11): Estimates of phenotypic correlation coefficient for GY/P and their two components at PSM, SSD and BM in F_4 generation in population I and population II.

Characters	GY/P		
Selection methods	PSM	SSD	BM
POP.I			
NS/P	-0.13	0.45*	0.56**
N.G/S	0.85**	0.55**	0.82**
POP.II			
N.S/P	0.46*	0.61**	٠,٦٦**
NG/S	0.36	0.46*	0.31

GY/P is grain yield /plant, NS/P is number of spike /plant, NG/S is number of grains/plant, PS is pedigree selection, BM is bulk selection, SSD is single seed descent method and * and ** significance at 0.05 and 0.01 levels of probability.

In conclusion, the PSM and SSD methods were expressed the best for improving grain yield and its components, where by these two methods it could be separated many families which showed superior values for most traits over parents and F_4 generation. As well as, the breeder may utilize such selected families in breeding programs to improve yield and its components.

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