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RESEARCH ARTICLE

A comparison between pedigree and bulk selection methods for seed yield in a segregating population of faba bean (*Vicia faba* L.)

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Abstract

This study aimed to compare the efficiency of pedigree and bulk methods of selection for improving seed yield in a segregating population of faba bean (Giza 429 × Triple white × Misr 1) × (ILB-938 × Nubariah 1 × Misr 1) in the F_2- F_5 generations. The experiments were conducted at South Valley University Experimental Farm, Qena, Egypt during growing seasons 2014/2015 to 2017/2018. Highly significant differences among the F_5-selected families were observed for the selection criterion; seed yield/plant and all correlated traits either after three cycles of selection (pedigree method) or one cycle selection (bulk method). The genetic variability retained after bulk method was larger and more pronounced than that after pedigree method for the selection criterion; seed yield/plant. While, all studied correlated traits showed smaller genotypic variability after bulk method than that after pedigree method. After three cycles of selection, pedigree selection increased seed yield/plant by 21.82, 20.58 and 53.49% from the bulk sample, the best parent and the check cultivar, respectively. But, after one cycle of selection, bulk method increased seed yield/plant by 8.43, 7.27 and 38.24% from the bulk sample, the best parent and the check cultivar, respectively. Pedigree selection method for improving seed yield was more efficient compared to the bulk method in isolating high yielding genotypes. However, it was accompanied with favorable increased in no. of branches/plant, no. of pods/plant, no. of seeds/plant and 100-seed weight and undesirable delay in flowering date.

***Key words**: Faba bean;* Pedigree selection; Bulk method; Heritability

Introduction

Faba bean *(Vicia faba* L.*)* is one of the most important nutritive seed leguminous crops as a source of plant protein; seed contains a high protein content of 24 - 33% (Winch, 2006). In Egypt and many developing countries, most people depend on faba bean in their nutritive, where it used for making many important popular dishes. Although the importance of faba bean in Egypt, there is a big gap between production and consumption reached to 70%, whereas the total production was 139303 tons resulted from 40298 ha, while the total consumption was about 480.000 tons (FAO, 2018). The limited number of cultivated varieties with their low yield potential is considered the major problem of faba bean production in Egypt. Therefore, selection of high yielding faba bean lines became the main objective of the most breeding programs. Good choosing of the selection methods, which facilitate the improvement of yield and its attributed traits, plays the main role to achieve this goal. Although several breeding methods were used to improve yield and its attributes in faba bean, pedigree selection method has become the most popular by plant breeding procedures. This method is preferred by plant breeders because it is relatively rapid and enables conducting of genetic studies along with the plant breeding work.

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Several studies indicated that pedigree method succeeded for improving seed yield in faba bean (Ahmed *et al*., 2008; Abdel Haleem and Mohamed, 2011; Bakheit and Metwaly, 2011; Ahmed *et al*., 2018 and Abo-Elwafa 2018). The bulk method implemented by harvest all plants in bulk; this method is simple, easy and less expensive. Bulk method could be less costly in breeding for seed yield in faba bean (Omar, 1989). Furthermore, it increased seed yield in faba bean compared with the pedigree (El-Emam, 2005). Many investigations have been conducted to compare the efficiency of selection methods for segregating generations of faba bean (Shalaby *et al.*, 2001; Ashrei, 2006; Abo Mostafa *et al*., 2014 and Ibrahim, 2015).

Therefore, the objective of this study was to compare the effectiveness of pedigree and bulk methods of selection to improve yielding ability of faba been.

Materials and Methods

The present study was carried out at El–Mattana Agric. Res. Sta., Luxor Governorate, ARC, Egypt, during the periods 2014/2015–2017/2018. The basic material was a segregating population of faba bean (*Vicia faba* L.) stemmed from the cross (Giza 429 × Triple white × Misr 1) × (ILB-938 × Nubariah 1 × Misr 1). The pedigree of the parents and their sources are given in Table 1.

In 2014/2015 growing season, 750 F_2-seeds were grown individually in a non–replicated trail. Each plot represented by single row 3m long, 60 cm apart and 20 cm between hills on one side of the ridge with one seed/hill. The cultural practices were applied as recommended for faba bean production. The data were recorded on 500 random guarded plants.

At harvest, equal seed from each of the 500 plants were bulked to give an unselected bulk sample. In each generation for each method, seeds of the unselected bulk sample were bulked without selection to be raising the next generation. The cultivar Giza 843 was used as the check cultivar. Furthermore, two methods of selection were applied on each population as follow:

A-Pedigree selection method

From the 500 plants, 100 best plants with high seed yield were selected and seeds of each plant were saved individually for next generation.

In 2015/2016 growing season, the 100 selected plants along with their parents, the bulk sample and the check cultivar were grown in a randomized completed block design with three replications. Each family was represented by single row 3 m long, 60 cm apart and 20 cm between hills on one side of the ridge with one seed/hill in each replication. Data were recorded on five random guarded plants in each plot.

After harvest, the best plant from each of the best twenty families based on seed yield/plant was saved for the next generation.

In 2016/2017 growing season, the 20 F_4–selected families along with their parents, the bulk sample and the check cultivar were grown as in the previous season. The experimental design, number of replications, planting date were adopted as the same in the previous season.

After harvest, the best plant from each of the best ten families based on seed yield/plant and retained to be raise as F_5-generation in the final evaluation trial during 2017/2018 season.

B- Bulk method

Equal number of seeds from each of the 500 plants were bulked and saved to the next season.

In 2015/2016 growing season, a sample of the F_3–bulked seeds along with their parents, the bulk sample and the check cultivar were planted as in the first season. At harvest, seeds from each plant were taken and saved in bulk to the next season.

In 2016/2017 growing season, a sample of the F_4-bulked seeds along with their parents, the bulk sample and the check cultivar were planted as in the first season. After harvest, the seeds of the 10 plants that had the highest seed yield were retained individually to be raise as F_5-generation in the final evaluation trial during 2017/2018 season.

In 2017/2018 growing season, the best ten F_5–selected families for each method along with the original parents, F_5–bulked random sample and the check cultivar were evaluated in a separate experiment. For each experiment, a randomized complete block design with three replications was used. Each family was represented by single row 3 m long, 60 cm apart and 20 cm between hills on one side of the ridge with one seed/hill in each replication. The cultural practices for the two methods and all generations were applied as recommended for faba bean production. The recorded data for the two methods and all generations were days to flowering (DF); days, days to maturity (DM); days, plant height (PH); cm, no. of branches/plant (NB/P), no. of pods/plant (NP/P), no. of seeds/plant (NS/P), seed yield/plant (SY/P); g and 100–seed weight (SI); g.

Statistical analysis

Two separate analyses of variance were done according to Gomez and Gomez (1984). The first includes the entries (10 selected families along with the bulk samples, parents and the check cultivar to measure the variability and the significance of the observed gain. The second included the selected families only to calculate phenotypic (PCV), genotypic (GCV) coefficients of variability and heritability in broad sense.

The phenotypic (σ^2p) and genotypic (σ^2g) variances were calculated according to Al-Jibouri *et al* (1958).

Heritability in broad sense was estimated as (H) = (σ^2g/σ^2p) × 100 according to Walker (1960).

The phenotypic (PCV %) and genotypic (GCV %) coefficients of variability were estimated using the formula developed by Burton (1952).

Comparisons among means were calculated by using revised L.S.D (El-Rawi and Khalafalla 1980).

Results and Discussion

Description of the F_2-population.

1-Range, average and phenotypic variance

The average was 41.49 days, 134.69 days, 114.79 cm, 6.06, 35.03, 97.23, 66.70 g and 67.48 g for days to flowering, days to maturity, plant height, no. of branches/plant, no. of pods/plant, no. of seeds/plant, seed yield/plant and 100–seed weight, respectively. Furthermore, the data of range and phenotypic variance reflects the presence of sufficient variances, which consider as a base to selection (Table 2).

2- Correlation study

The correlation coefficients (Table 3) were positive and highly significant between seed yield/plant with each of plant height, number of branches/plant, number of pods/plant, number of seeds/plant and 100–seed weight. These results indicate to importance of these traits for improvement seed yield through selection. In contrast, seed yield/plant showed negative significant correlation with days to flowering. These results were agreement with those obtained by Alghamdi (2007), Turk *et al.* (2008) and Mostafa *et al* (2017) .

Effectiveness of selection methods

A-Pedigree method

a_1- Analysis of variance

There were significant ($p<0.01$) differences among genotypes and F_5-families for seed yield/plant, days to flowering and maturity, plant height, no. of branches/plant, no. of pods/plant, no. of seeds/plant and 100-seed weight after three cycles of selection (Table 4). This indicates that the existence of sufficient variability for further improvement. These results agreed with those reported by Alghamdi (2007), Toker (2009), Abd-Elhaleem and Mohamed (2011) Mulualem (2013), Sheelamary (2015), Mostafa *et al* (2017) and Chaudahary *et al* (2018).

Sufficient genotypic coefficient of variability (Table 4) among the ten selected families was remained for increasing seed yield/plant after three cycles of selection. GCV estimates for seed yield/plant was 10.57%. The small difference between PCV and GCV caused high estimates of broad sense heritability for seed yield/plant (79.22).

Table 1. The origin and pedigree of the parents.

Name	Origin	Pedigree
Giza 429	Egypt	A plant selection from Giza 402
Triple white	Sudan	Introduced from Sudan
Misr 1	Egypt	(Giza 3 × A123/45/76)
ILB-938	International line	Introduced
Nubariah 1	Egypt	Selection from introduction variety

Table 2. The range, means and phenotypic variance (σ^2_P) in the F_2-population for all the studied traits.

Traits	Items		
	Mean ± SE	Range	σ^2_P
Days to flowering(days)	41.49 ± 0.26	26 – 75	34.76
Days to maturity(days)	134.69±0.22	120 – 160	23.58
Plant height (cm)	114.79±0.65	70 – 149	209.30
No. of branches/plant	6.06±0.12	2 – 16	6.79
No. of pods/plant	35.03±0.93	3 – 124	435.35
No. of seeds/plant	97.23±2.78	5 – 375	3857.36
Seed yield/plant (g)	66.70±2.10	3.2 – 267	2203.89
100-seed weight (g)	67.48±1.06	6.67 – 188.89	558.06

Table 3.Simple correlation coefficients in the F_2-population for all the studied traits.

Traits	DH	DM	PH	NB/P	NP/P	NS/P	SY/P	SI
DH		0.09^{*}	0.08	-0.02	-0.04	-0.06	-0.10^{*}	-0.08
DM			0.04	-0.02	-0.01	-0.05	-0.05	-0.02
PH				0.03	0.05	0.12^{**}	0.18^{**}	0.24^{**}
NB/P					0.64^{**}	0.56^{**}	0.55^{**}	0.10^{*}
NP/P						0.89^{**}	0.83^{**}	0.08
NS/P							0.90^{**}	0.07
SY/P								0.41^{**}
SI								

*, **: Significant at 0.05 and 0.01 levels of probability, respectively

Similar results were obtained by Alghamdi (2007); Toker (2009); ; Mulualem (2013); Sheelamary (2015); and Chaudahary *et al* (2018). Fikreselassie and Seboka (2012) found that the genotypic coefficients of variability were high for seed yield/plant followed by number of seeds/plant, while, the values were low for number of seeds/plant. Ghareeb and Helal (2014) reported that heritability in broad sense for seed yield/plant and its components in the F_5–generation were more than 92%. Singh *et al* (2017) found that seed yield /plant and 100–seed weight exhibited wide range of variability maximum genotypic and phenotypic coefficient of variation and broad sense heritability. Tadale *et al* (2019) indicated that the phenotypic and genotypic coefficients of variability for seed yield/plant ranged from 23.05 to 1.08% and 23.26% to 1.20%, respectively.

Table 4. Mean squares, phenotypic (PCV%), genotypic (GCV%) coefficients of variability and heritability in broad sense (H%) of the selected families for high seed yield/plant and correlated traits in F_5 –generation.

SOV	df	Selection criterion	Correlated traits						
		SY/P	DF	DM	PH	NB/P	NP/P	NS/P	SI
Reps	2	30.74	75.83*	41.70	76.23	0.59	15.48	128.65	11.05
Genotypes (G)	16	721.05**	164.63**	172.34**	403.48**	3.08**	143.90**	801.74**	469.95**
Selected families (F)	9	334.33**	181.39**	164.07**	232.37**	2.08**	68.59**	489.33**	108.52**
Error (G)	32	61.00	17.89	30.13	43.15	0.39	11.04	63.37	44.70
Error (F)	18	69.46	14.54	25.11	55.27	0.42	11.35	75.18	32.64
PCV%		11.88	18.40	5.92	7.28	14.87	12.15	11.33	6.86
GCV%		10.57	17.64	5.44	6.35	13.28	11.10	10.43	5.74
H%		79.22	91.99	84.70	76.21	79.74	83.46	84.64	69.92

*, **: Significant at 0.05 and 0.01 levels of probability, respectively

a$_2$- Means and direct observed gain of the selected families for seed yield/plant

The average seed yield/plant of F_5-selected families after three cycles of selection ranged from 69.58 g for family no. 225 to 109.89 g for family no. 192 with an average of 88.87 g (Table 5). The average observed gain in seed yield/plant was highly significant and recorded 21.82, 20.58 and 53.49% from the bulk sample, the best parent and the check cultivar, respectively. Most of the selected families showed significant or highly significant highest compared to the bulk sample or the best parent, however, all the selected families were significant (p<0.01) highest from the check cultivar. Five selected families no. 4, 70, 192, 285 and 410 were high significantly surpassed the bulk sample, the best parent and the check cultivar (Table 6).

a$_3$-The correlated selection gains

Three cycles of pedigree selection for increasing seed yield/plant caused desirable decrease in days to maturity by - 10.02, - 2.43 and - 4.66% from the bulk sample, best parent and the check cultivars, respectively (Table 6). Favorable decrease in plant height over the bulk sample and the check cultivar accompanied pedigree selection for seed yield/plant by – 4.30 and – 9.39%, respectively. Desirable increase in no. of pods/plant, no. of seeds/plant and 100-seed weight over the bulk sample, best parent and the check cultivar was resulted from pedigree selection for seed yield/plant by 13.73, 10.20 and 46.19%, 21.04, 9.01 and 34.91% and 14.19, 21.59 and 38.11%, respectively. Unfavorable increase in days to flowering over the bulk sample (1.82%) and the best parent (5.38%) was detected. But, favorable decrease was noticed in days to flowering from the check cultivar accounted to- 2.45%. However, respective desirable increase was observed for no. of branches/plant, which reached 14.51 and 35.58% from the mean bulk sample and the check cultivar. Similar results were reported by Yamni (1998), Bakhiet and Metwali (2011), Abd El-Azize, and Osman (2015) and Abo–Elwafa (2018)

B- Bulk method

b_1- Analysis of variance

After one cycle of selection, mean squares due to among genotypes and F_5-selected families for the selection criterion (seed yield/plant) and other correlated traits; days to flowering, days to maturity, plant height, no. of branches/plant, no. of pods/plant, no. of seeds/plant and 100–seed weight were significant ($p < 0.01$) significant differences. This indicates that the existence of the genetic difference among the selected families (Table 7).

Table 5. Means of seed yield /plant and the correlated response of the other traits of the selected families (F_5 –generation) from pedigree method.

Families No.	Selection Criterion	Correlated traits						
	SY/P	DF	SY/P	DF	SY/P	DF	SY/P	DF
4	90.94	45.00	120.33	137.24	6.56	36.97	100.52	92.45
12	87.58	35.33	116.33	121.24	4.83	36.80	107.66	81.54
28	80.54	35.33	121.00	121.90	5.22	35.27	105.42	85.90
70	90.33	36.00	134.67	111.24	5.49	50.20	131.86	90.22
106	82.13	34.00	126.33	114.24	5.76	36.27	98.52	93.56
192	109.89	55.67	138.67	120.90	4.13	36.27	131.12	99.04
225	69.58	49.67	126.00	116.24	5.09	37.07	97.22	81.87
285	96.43	50.00	121.33	130.57	6.55	45.24	120.06	80.59
344	89.45	36.67	116.67	108.90	5.67	39.94	116.79	85.09
410	91.81	45.00	128.67	126.57	6.69	39.37	117.56	86.62
Average	88.87	42.27	125.00	120.90	5.60	39.34	112.67	87.69
Giza 429	65.61	49.22	128.11	121.11	4.57	35.70	103.36	59.74
Nubarihi 1	73.70	55.00	137.78	134.44	6.30	22.76	76.01	72.12
Misr 1	59.40	44.67	135.00	148.89	4.15	27.16	86.95	63.57
Triple white	55.83	42.22	132.78	109.44	3.07	32.49	92.32	56.34
ILB-938	70.88	40.11	128.67	113.61	4.72	30.09	93.10	71.51
Check	57.19	43.33	131.11	133.44	4.13	26.91	83.52	63.49
Bulk' s mean	72.95	41.51	138.92	126.34	4.89	34.59	93.09	76.79
R. L.S.D $_{0.05}$	12.05	6.53	8.87	10.14	1.01	5.13	12.28	10.32
R. L.S.D $_{0.01}$	16.01	8.67	11.79	13.46	1.34	6.81	16.31	13.70
R. L.S.D$_{0.05}$ Average	9.22	4.99	6.81	7.76	0.74	3.92	9.40	7.89
R. L.S.D$_{0.01}$ Average	12.53	6.79	9.34	10.54	1.00	5.33	12.77	10.73

Data in Table 7 indicated that sufficient genotypic coefficient of variability among the ten selected families was remained for increasing seed yield/plant after one cycle of selection. GCV estimates for seed yield/plant was 14.40%. The close estimates of PCV and GCV caused high estimates of broad sense heritability for seed yield/plant (85.84%). These results were obtained by Omar (1989), Shalaby *et al* (2001), Abo-Mostafa *et al* (2014) and EL-Harty (2016).

b_2- Means and direct observed gain of the selected families for seed yield/plant

After one cycle of selection, the average seed yield/plant of F_5-selected families ranged from 66.47 g for family no. 5 to 104.86 g for family no. 10 with an average of 79.06 g (Table 8). The average observed gain (Table 9) in seed yield/plant recorded 8.37, 7.27 and 38.24% from the bulk sample, the best parent and the check cultivar, respectively. Some of the selected families showed significant or highly significant highest compared to the bulk sample or the best parent, however, most of the selected families were significant ($p<0.01$) highest from the check cultivar. Three selected families no. 3, 6 and 10 were high significantly surpassed the bulk sample, the best parent and the check cultivar (Table 9).

b_3-The correlated selection gains

One cycle of selection for increasing seed yield/plant (Table 9) desirable decrease in days to flowering by – 10.62, - 7.50 and – 14.38% from the bulk sample, the best parent and the check cultivars, respectively. Desirable increase in no. of pods/plant, no. of seeds/plant and 100-seed weight over the bulk sample and the check cultivar accompanied pedigree selection for seed yield/plant by 8.26, 3.32 and 3.37.622% and 39.16, 15.16 and 30.17%, respectively. Undesirable increase in plant height over the bulk sample and the best parent accompanied pedigree selection for seed yield/plant by 1.97 and 17.71%, respectively. While, desirable decrease was in plant height over the check cultivar by – 3.46%. However, unfavorable decrease was observed in no. of branches/plant from the bulk sample and the best parent by – 2.93 and - 24.66, respectively.

Table 6. The observed direct gain and correlated response as percentage from the bulk sample of the selected families (F_5 –generation) from pedigree method.

	Families No.	Selection criterion	Correlated traits						
		SY/P	DF	SY/P	DF	SY/P	DF	SY/P	DF
Bulk sample	4	24.67**	8.41	-13.38**	8.62*	34.15**	6.88	7.99	20.39**
	12	20.05*	-14.88*	-16.26**	-4.04	-1.30	6.40	15.65*	6.18
	28	10.40	-14.88*	-12.90**	-3.51	6.75	1.97	13.25*	11.87
	70	23.83**	-13.27	-3.06	-11.95**	12.20	45.14**	41.64**	17.49*
	106	12.58	-18.09*	-9.06**	-9.58*	17.79	4.86	5.84	21.84**
	192	50.63**	34.10**	-0.18	-4.30	-15.61	4.86	40.86**	28.97**
	225	-4.62	19.65*	-9.30**	-8.00*	4.16	7.17	4.44	6.61
	285	32.19**	20.45*	-12.66**	3.35	34.01**	30.78**	28.97**	4.95
	344	22.62**	-11.67	-16.02**	-13.80**	16.02	15.46*	25.46**	10.80
	410	25.86**	8.41	-7.38*	0.18	36.88**	13.82	26.28**	12.80
	Average	21.82**	1.82	-10.02**	-4.30	14.51	13.73*	21.04**	14.19**
Best parent	4	23.40**	12.19	-6.07	25.40**	4.13	3.56	-2.74	28.19**
	12	18.83*	-11.91	-9.19**	10.78*	-23.39**	3.09	4.16	13.06
	28	9.28	-11.91	-5.55	11.39*	-17.14*	-1.20	2.00	19.11**
	70	22.57**	-10.25	5.12	1.64	-12.91	40.63**	27.57**	25.09**
	106	11.43	-15.23	-1.39	4.38	-8.57	1.60	-4.68	29.73**
	192	49.10**	38.79**	8.24*	10.47*	-34.50**	1.60	26.86**	37.33**
	225	-5.59	23.83**	-1.65	6.21	-19.15*	3.84	-5.94	13.51
	285	30.85**	24.66**	-5.29	19.31**	4.02	26.71**	16.15**	11.75
	344	21.37*	-8.58	-8.93*	-0.49	-9.95	11.87	12.99*	17.98*
	410	24.58**	12.19	0.43	15.65**	6.24	10.28	13.74*	20.10**
	Average	20.58**	5.38	-2.43	10.47**	-11.12	10.20	9.01	21.59**
Check cultivar	4	57.07**	3.85	-8.22*	2.85	58.84**	37.38**	20.36**	45.61**
	12	51.26**	-18.46*	-11.27**	-9.15*	16.87	36.76**	28.90**	28.43**
	28	39.10**	-18.46*	-7.71*	-8.65*	26.39*	31.07**	26.23**	35.30**
	70	56.02**	-16.92*	2.71	-16.64**	32.85**	86.56**	57.87**	42.10**
	106	41.84**	-21.53**	-3.64	-14.39**	39.47**	34.78**	17.96*	47.36**
	192	89.79**	28.47**	5.76	-9.39*	-0.08	34.78**	57.00**	55.99**
	225	20.17*	14.62	-3.90	-12.89**	23.33	37.76**	16.41*	28.94**
	285	66.55**	15.39*	-7.46*	-2.15	58.68**	68.10**	43.75**	26.94**
	344	54.50**	-15.38*	-11.02**	-18.39**	37.37**	48.41**	39.83**	34.02**
	410	58.57**	3.85	-1.86	-5.15	62.07**	46.30**	40.75**	36.43**
	Average	53.49**	-2.45	-4.66	-9.39**	35.58**	46.19**	34.91**	38.11**

*, **: Significant at 0.05 and 0.01 levels of probability, respectively

Table 7. Means squares, phenotypic (PCV%), genotypic (GCV%) coefficients of variability and heritability in broad sense (H%) of the selected families for high seed yield/plant and correlated traits in F_5 –generation.

SOV	df	Selection Criterion	Correlated traits						
		SY/P	DF	DM	PH	NB/P	NP/P	NS/P	SI
Reps	2	36.63	10.80	9.63	40.52	1.43	40.43	98.74	13.30
Genotypes (G)	16	522.39**	103.79**	152.96**	387.28**	2.68**	170.70**	487.80**	387.65**
Selected families (F)	9	452.80**	28.74**	162.31*	163.16**	2.91**	117.72**	633.07**	111.93**
Error (G)	32	51.72	11.47	42.19	32.18	0.55	14.75	71.69	21.79
Error (F)	18	64.13	4.91	46.41	38.47	0.74	20.33	77.84	16.77
PCV%		11.88	18.40	5.92	7.28	14.87	12.15	11.33	6.86
GCV%		15.54	8.34	5.53	5.72	20.77	16.73	15.10	7.39
H%		14.40	7.60	4.67	5.00	17.94	15.22	14.14	6.81

*, **; Significant at 0.05 and 0.01 levels of probability, respectively.

Table 8. Means of seed yield /plant and the correlated response of the other traits of the selected families (F_5 –generation) from bulk method.

Families No.	Selection Criterion	Correlated traits						
	SY/P	DF	SY/P	DF	SY/P	DF	SY/P	DF
1	75.03	41.33	137.33	132.18	4.73	31.81	88.58	83.27
2	78.37	43.67	134.00	127.18	6.07	39.81	90.31	84.56
3	92.45	35.67	123.33	127.85	3.87	41.84	97.18	86.76
4	78.41	35.67	139.67	120.85	5.27	37.81	83.85	83.41
5	66.47	36.67	128.67	120.85	5.20	39.11	105.31	73.41
6	86.41	35.33	138.00	130.85	5.00	41.21	113.91	76.01
7	69.53	34.67	130.33	125.18	2.87	30.61	81.58	85.24
8	71.90	37.00	144.00	146.52	4.40	32.91	89.91	79.90
9	67.16	37.33	135.33	131.28	4.07	29.64	85.25	78.75
10	104.86	33.67	120.67	125.52	6.00	49.74	125.91	95.11
Average	79.06	37.10	133.13	128.83	4.75	37.45	96.18	82.64
Giza 429	65.61	49.22	128.11	121.11	4.57	35.70	103.36	59.74
Nubarihi 1	73.70	55.00	137.78	134.44	6.30	22.76	76.01	72.12
Misr 1	59.40	44.67	135.00	148.89	4.15	27.16	86.95	63.57
Triple white	55.83	42.22	132.78	109.44	3.07	32.49	92.32	56.34
ILB-938	70.88	40.11	128.67	113.61	4.72	30.09	93.10	71.51
Check	57.19	43.33	131.11	133.44	4.13	26.91	83.52	63.49
Bulk' s mean	72.95	41.51	138.92	126.34	4.89	34.59	93.09	76.79
R. L.S.D $_{0.05}$	11.10	5.23	11.14	8.75	1.27	5.93	13.69	7.20
R. L.S.D $_{0.01}$	14.74	6.94	15.06	11.63	1.72	7.87	18.18	9.57
R. L.S.D$_{0.05}$ Average	9.45	2.52	9.65	7.32	1.22	5.32	10.95	4.66
R. L.S.D$_{0.01}$ Average	12.85	3.39	13.78	9.95	1.58	7.33	15.01	6.27

Conclusion

Pedigree selection method for improving seed yield was more efficient compared to the bulk method in isolating high yielding genotypes. However, it was accompanied with favorable increase in no. of branches/plant, no. of pods/plant, no. of seeds/plant and 100-seed weight and undesirable delay in flowering date.

Table 9. The observed direct gain and correlated response as percentage from the bulk sample of the selected families (F_5 –generation) from bulk method.

	Families No.	Selection Criterion	Correlated traits						
		SY/P	DF	SY/P	DF	SY/P	DF	SY/P	DF
Bulk sample	4	2.86	-0.43	-1.14	4.63	-3.20	-8.05	-4.84	8.44
	12	7.43	5.20	-3.54	0.67	24.06	15.08	-2.98	10.12*
	28	26.74**	-14.08*	-11.22**	1.20	-20.93	20.96*	4.39	12.99**
	70	7.48	-14.08*	0.54	-4.35	7.70	9.30	-9.93	8.62
	106	-8.89	-11.67	-7.38	-4.35	6.34	13.06	13.13	-4.41
	192	18.45*	-14.88*	-0.66	3.57	2.25	19.13*	22.37**	-1.01
	225	-4.68	-16.49*	-6.18	-0.92	-41.38**	-11.52	-12.36	11.00*
	285	-1.44	-10.86	3.66	15.97**	-10.02	-4.87	-3.41	4.05
	344	-7.94	-10.06	-2.58	3.91	-16.84	-14.31	-8.43	2.56
	410	43.74**	-18.90**	-13.14**	-0.65	22.70	43.80**	35.26**	23.86**
	Average	8.37	-10.62**	-4.17	1.97	-2.93	8.26	3.32	7.62
Best parent	4	1.81	3.05	7.20	20.78**	-24.87*	-10.91	-14.30*	15.46**
	12	6.34	8.87	4.60	16.21**	-3.70	11.50	-12.62	17.25**
	28	25.45**	-11.08	-3.73	16.82**	-38.62**	17.20*	-5.98	20.30**
	70	6.39	-11.08	9.02*	10.43*	-16.40	5.90	-18.88**	15.65**
	106	-9.81	-8.58	0.43	10.43*	-17.46	9.54	1.89	1.78
	192	17.24*	-11.91	7.72	19.56**	-20.63*	15.42	10.21	5.40
	225	-5.65	-13.57*	1.74	14.39**	-54.50**	-14.27	-21.07**	18.19**
	285	-2.44	-7.75	12.40**	33.88**	-30.16**	-7.82	-13.01	10.78*
	344	-8.88	-6.92	5.64	19.96**	-35.45**	-16.97*	-17.52**	9.20
	410	42.28**	-16.06*	-5.81	14.69**	-4.76	39.33**	21.82**	31.88**
	Average	7.27	-7.50*	3.92	17.71**	-24.66*	4.89	-6.95	14.59**
Check cultivar	4	31.20**	-4.61	4.75	-0.94	14.61	18.20	6.06	31.16**
	12	37.04**	0.78	2.20	-4.69	46.89**	47.93**	8.13	33.19**
	28	61.66**	-17.69**	-5.93	-4.19	-6.38	55.48**	16.36	36.66**
	70	37.10**	-17.69**	6.53	-9.43**	27.52	40.49**	0.39	31.37**
	106	16.22	-15.38*	-1.86	-9.43**	25.91	45.32**	26.09**	15.62**
	192	51.09**	-18.46**	5.26	-1.94	21.07	53.13**	36.39**	19.73**
	225	21.58*	-19.99**	-0.59	-6.19	-30.59*	13.74	-2.32	34.26**
	285	25.72*	-14.61*	9.83*	9.80**	6.54	22.28*	7.65	25.84**
	344	17.43	-13.84*	3.22	-1.62	-1.53	10.14	2.07	24.04**
	410	83.35**	-22.30**	-7.97	-5.94	45.28**	84.84**	50.76**	49.81**
	Average	38.24**	-14.38**	1.54	- 3.46	14.93	39.16**	15.16*	30.17**

*, **: Significant at 0.05 and 0.01 levels of probability, respectivel

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