
Effectiveness of breeding methods for production of superior genotypes and maintenance of genetic variance in Faba Bean (*Vicia faba*, L.)

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Abstract: The present study was carried out during the period from 2007/ 08 to 2011/2012 at Agricultural Research Station, Faculty of Agriculture, Alexandria University, Alexandria, Egypt. The study aimed at evaluating the effectiveness of pedigree (P), single seed descent (SSD), and mass selection (MS) breeding methods. Two F₂ populations, derived from two crosses, were used. Twenty families derived from each of the three breeding methods in each cross were tested for seed yield (t/ ha), seed yield per plant (g) and its components in F₆ generation. A randomized complete block design with three replications was used. Significant differences existed, within F₆ families of each cross, for seed yield, seed yield per plant and its components by applying either of the three methods. The widest range in seed yield was obtained by the SSD method. The SSD breeding method produced consistently more superior families in either and over the two crosses with 22, 19 and 18 families for (SSD), (P) and (MS) methods, respectively. The genotypic (δ^2_G) and phenotypic (δ^2_{ph}) variances, for seed yield, estimated from SSD method were the highest compared with the other breeding methods over the two crosses. Heritability estimates, in broad sense, and expected genetic advance from selection for higher seed yield indicated that the SSD method recorded higher values ($h^2=0.87-0.93$, $\delta_G=0.51-0.85$) compared with the other two methods. Based on the obtained results, it seems that the SSD breeding method was more effective compared to the other two breeding methods, in producing superior genotypes in seed yield and maintaining genetic variance for further selection and improvement of that character. Considering the partial allogamous nature of the crop, it could be concluded that the SSD method was more efficient and could be less costly in breeding for high seed yield.

Keywords: Faba Bean (*Vicia faba*, L.), Breeding Methods, Genetic Variance

1. Introduction

Faba bean (*Vicia faba* L.) is the most important nutritive popular food crop in Egypt. It plays a major role in the Egyptian diet as a source of protein. The crop is partially allogamous species having an intermediate level of out-crossing (in the 20-25% range). Increasing seed yield and improving the stability of yield are the main objectives of most breeding programs.

Breeding methods employed in faba beans range from single seed descent as proposed by Brim (1966), through pedigree or bulk pedigree approaches to mass selection. Mass selection is the most widely used breeding method in faba bean improvement especially in upgrading local

population following hybridization (Nassib and Khalil, 1981).

However, Emping and Febr (1971) reported that single seed descent method (SSD) of soybean was more effective in maintaining large seeded lines compared to other selection methods. Haddad and Muhllbauer (1981) observed that (SSD) maintained more genetic variation in 15 of 21 lentil characters compared to Bulk population (BP). Similar results were reported by Pawar *et al.* (1986) in wheat. On the other hand, Rahman and Bahl (1985) concluded the Mass selection (MS) excelled (SSD) and Random Bulk (RB) in chickpea breeding for higher seed yield and yield components. Gill *et al.* (1995) found that single seed descent method was suitable for deriving superior lines for seed yield and pods per plant in mungbean compared to pedigree. Mehta and Zaveri (1997) compare three selection methods viz. Pedigree

Selection (PS) SSD AND Mass Selection (MS) in F_5 generation of *vigna unguiculata*. Seed yield/plant was strongly and positively associated with branches/plant, clusters/plant and in all three selection methods. Results revealed the superiority of SSD over PS and MS schemes for the production of high yielding progenies, for the maintenance of high variability and for handling the segregating materials. Gill *et al.* (2000) compared four selection methods and three intervarietal crosses of mungbean. They concluded that considerable variability was present among lines of single seed descent, pedigree selection and bulk methods to conduct effective selection for the improvement of yield and its components. They also reported variability among selection methods and between

varietal crosses in heritability and expected genetic advance for studied yield and yield components. Meena and Kumar (2012) reported that estimates of phenotypic variances for seed yield and its components in F_4 showed that single seed descent method was superior to pedigree method in maintaining relatively high variances over five crosses of chickpea.

The main objective of this investigation was to compare the effectiveness of pedigree, single seed content, and mass selection methods in improvement of seed yield and its components in faba bean.

2. Materials and Methods

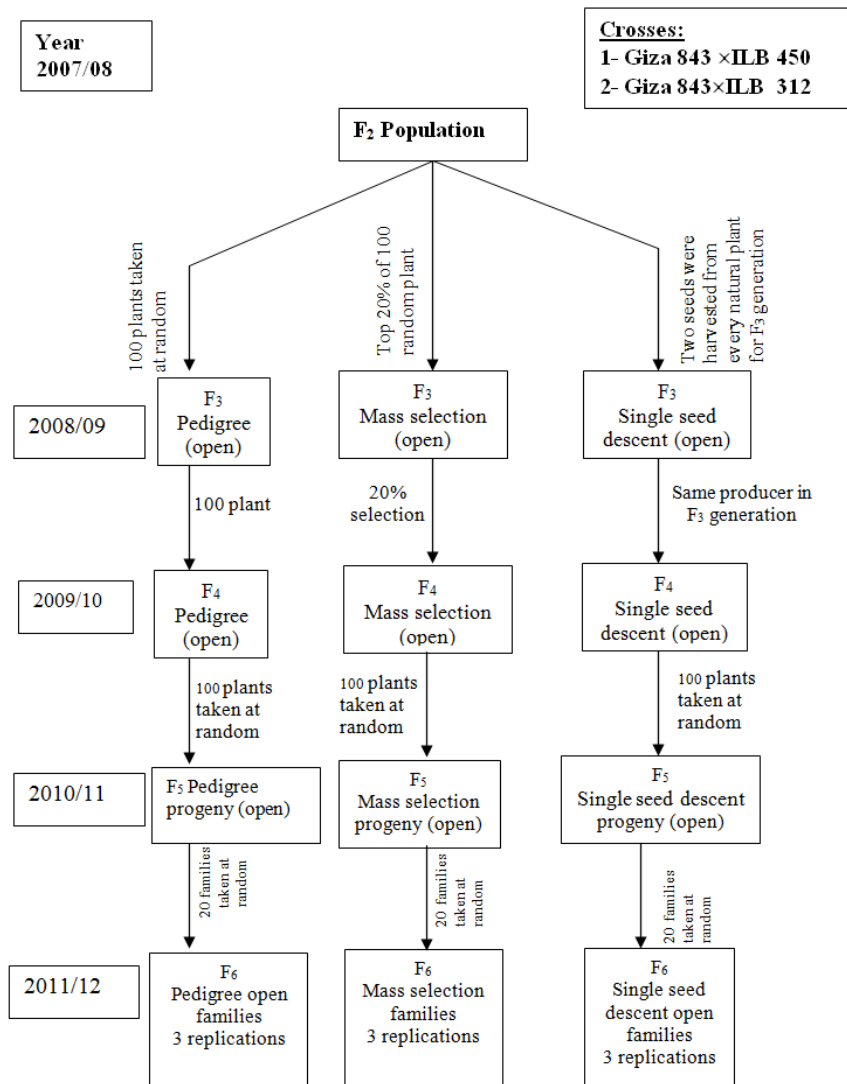


Fig 1. Outline of generation advance for Pedigree selection, Mass selection, and SSD methods

This study was carried out during the five years 2007/ 08 to 2011/2012 at Agricultural Research Station, Faculty of Agriculture, Alexandria University, Alexandria, Egypt.

The parental material consisted of three early maturing, medium seeded genotypes. These were Giza 843 (Egyptian, 100 seed weight 60- 65 g), International Lines of Broad Beans (ILB) ILB- 450 and ILB 312, (introduced from

ICARDA with 100 seed weight of 80 and 90g), respectively).

The study aimed to evaluate the effectiveness of three selection methods in faba bean namely: Pedigree selection (PS), Single Seed Descent (SSD), and Mass selection (MS).

Two populations of the following two crosses were used, i.e., 1- Giza 843 × ILB 450, 2- Giza 843 × ILB 312.

In 2007/08 growing season, approximately 500 plants per

F₂ population were planted in the field, in ridges 60 cm apart with plants 20 cm apart within ridges.

The following characters were recorded, i.e, (1) Seed yield (t/ ha).(SYD), (2) Seed yield per plant (g).(SYD/ pl), (3) 100-seed weight (g).(100-SW), (4) Number of pods per plant (NP/PL), (5) Number of seeds per plant (NS/PL), (6) Number of branches per plant (NB/PL)

The pattern of generation advance for pedigree selection, single seed descent, and mass selection methods is presented in Fig. 1.

2.1. Statistical Analysis

The evaluation of pedigree, Single seed descent, and mass selection breeding methods was determined by planting the

F₆ families for each method in a trial of randomized complete block design. The three trials of each cross were subjected to combined analysis according to the procedure outlined by Gomez and Gomez (1984). The efficiency of the three breeding methods were compared based on the following:

1. The different measured statistics; i.e. ranges, means and number of superior families for all studied characters.
2. The different genetic parameters; i.e. variances (genotypic δ^2_G and phenotypic δ^2_{ph}), heritability (h^2), expected genetic advance (Δ_G) and coefficient of variability for seed yield per ha., Seed yield per plant (g).and 100-seed weight (g).

3. Results and Discussion

Table (1). Average F₆ seed yield (t/ha) and other agronomic traits produced by applying three breeding methods in two crosses

	Giza 843 × ILB 450	Giza 843 × ILB 312	Average	LSD at 0.05 for Crosses	LSD at 0.05 for Methods
No. of branches / plant					
Pedigree	3.53	3.57	3.55	—	—
Single seed descent	3.78	3.59	3.69		
Mass selections	3.57	3.63	3.61		
Average	3.63	3.60	6.62		
No. of pods / plant					
Pedigree	13.49	14.82	14.82	0.17	0.04
Single seed descent	15.80	17.10	16.45		
Mass selections	14.69	15.32	15.00		
Average	15.10	15.75	15.43		
No. of seeds / plant					
Pedigree	52.76	52.63	52.71	0.17	1.06
Single seed descent	58.61	59.18	58.90		
Mass selections	55.83	54.80	55.32		
Average	55.73	55.54	55.63		
Seed Yield/ plant (g)					
Pedigree	38.83	42.20	40.52	0.53	0.98
Single seed descent	43.57	46.93	45.25		
Mass selections	40.00	39.99	40.00		
Average	40.80	43.04	41.92		
100-Seed weight (g)					
Pedigree	84.55	86.47	85.51	0.94	1.70
Single seed descent	89.77	93.26	91.52		
Mass selections	83.03	87.84	85.44		
Average	85.78	89.19	87.49		
Seed Yield (t/ha)					
Pedigree	2.35	2.51	2.43	—	0.24
Single seed descent	2.61	3.10	2.86		
Mass selections	2.56	2.70	2.64		
Average	2.51	2.77	2.64		

Analysis of variance for the six trials revealed significant differences between selected F₆families for all studied characters. The homogeneity of error between the two crosses enabled the performance of combined analysis, the results of which are presented in (Table 1). Significant differences were found between the two crosses in seed yield per plant, 100-seed weight, and number of pods per plant, whereas the remaining characters showed insignificant differences. It should be noted that cross. Giza 843 × ILB 312 gave significantly higher mean values for those three characters compared to cross Giza 843 × ILB 450. Meanwhile, single seed descent selection method resulted in significantly higher values, to both or one of the other two

breeding methods (Pedigree and Mass selections), in seed yield per ha, seed yield per plant, 100-seed weight, number of pods per plant and number of seeds per plant. The interaction of crosses × breeding methods was insignificant for all studied characters since crosses performed similarly in the applied selection methods.

Results in (Table 2) indicated that single seed descent selection was comparable, or higher, than the other two selection methods in maintaining variations within population, as shown in the range of studied characters and production of families with superior yield and yield components values. However, single seed descent selection was inferior to Pedigree method in producing families with

high number of pods per plant in the first cross.

Table (2). Range, population means of seed yield and other agronomic traits and number of superior families derived through the three breeding methods

		Range	Population mean	No. of families exceeded	Total No. of tested families	% Families >
Giza843× ILB 450	No. of branches / plant					
	Pedigree	2.97–4.09	3.53	12	20	60
	Single seed descent	3.14–4.18	3.78	11	20	55
	Mass selections	3.04–3.78	3.57	13	20	55
	No. of pods / plant					
	Pedigree	12.72–14.26	13.49	18	20	90
	Single seed descent	11.75–19.97	15.80	13	20	65
	Mass selections	13.63–16.49	14.69	9	20	45
	No. of seeds / plant					
	Pedigree	41.49–61.91	52.76	11	20	55
	Single seed descent	44.80–69.86	58.61	10	20	55
	Mass selections	40.82–66.86	55.83	8	20	40
	Seed Yield/ plant (g)					
	Pedigree	29.03–45.52	38.82	11	20	55
	Single seed descent	38.29–51.77	43.57	9	20	45
	Mass selections	33.43–45.58	40.00	9	20	45
	100-Seed weight (g)					
	Pedigree	78.65–90.86	40.00	8	20	40
	Single seed descent	85.73–92.41	84.55	12	20	60
	Mass selections	84.48–90.05	89.77	9	20	45
Seed Yield (t/ha)						
Pedigree	2.01–2.73	2.35	10	20	50	
Single seed descent	1.97–3.34	2.61	9	20	45	
Mass selections	2.16–3.38	2.56	9	20	45	
Giza843× ILB312	No. of branches / plant					
	Pedigree	3.04–3.78	3.57	13	20	65
	Single seed descent	2.97–4.31	3.59	12	20	60
	Mass selections	3.27–4.05	3.65	11	20	55
	No. of pods / plant					
	Pedigree	12.70–16.91	14.82	9	20	45
	Single seed descent	14.54–18.83	17.10	10	20	50
	Mass selections	12.54–17.57	15.32	10	20	50
	No. of seeds / plant					
	Pedigree	41.80–61.22	52.65	12	20	60
	Single seed descent	49.01–65.80	59.18	11	20	55
	Mass selections	42.43–65.53	54.80	11	20	55
	Seed Yield/ plant (g)					
	Pedigree	37.17–51.18	42.20	11	20	55
	Single seed descent	40.51–52.43	46.93	8	20	40
	Mass selections	33.43–45.58	39.99	9	20	45
	100-Seed weight (g)					
	Pedigree	80.97–90.97	86.47	7	20	35
	Single seed descent	88.91–95.92	93.26	10	20	50
	Mass selections	84.48–90.05	87.84	13	20	65
Seed Yield (t/ha)						
Pedigree	2.14–2.85	2.51	8	20	40	
Single seed descent	2.72–3.54	3.10	13	20	65	
Mass selections	2.22–3.19	2.70	10	20	50	

These findings were further emphasized through the data presented in (Table 3) for seed yield of tested F₆ families in the two crosses. Single seed descent selection showed almost double the values of phenotypic and genotypic variances compared to pedigree and mass selection methods, higher genetic advance from selection and heritability values in both crosses, The same trend of results could be observed for Seed yield per plant and 100-seed weight , where SSD method recorded considerable genotypic and phenotypic variances , higher genetic advance and heritability values , in addition to higher mean values compared to the pedigree and

mass selection methods .

Several investigators pointed out that a successful selection method should maintain a high level of genetic variability among the lines of the population after successive generations (Brim, 1966). Develop varieties of high yielding ability (Cooper, 1982), cost-saving (Haddad and Muehlbauer, 1981) and saves time, space and labour (Rahman and Bahl, 1985). The single seed descent selection method seemed to fulfill these requirements, as revealed by the results obtained from this study. Single seed descent was superior, compared to pedigree selection and mass selection, in seed yield and

yield components overall the two crosses. That method also resulted in higher number, or comparable, of high yield lines depending on the cross. At the F_6 generation SSD maintained higher genotypic and phenotypic variances compared to PS and MS methods, gave higher heritability and expected genetic advance estimates for seed yield as an average of the two crosses. Similar findings were reported by Gill *et al.* (2000) and Meena and Kumar (2012). Dahiya *et al.* (1986) emphasized the superiority of single seed descent as a

selection method for the production of high yielding progenies, maintaining high variability and for handling the segregating material in mungbean.

In conclusion, the findings of the present investigation indicate the superiority of single seed descent selection method over mass selection and pedigree selection methods and could be recommended for application in faba bean breeding in local breeding programs.

Table (3). The genetic parameters estimated for seed yield and other agronomic trait of the F_6 families derived through the three breeding methods for the two crosses

	Giza 843 × ILB 450			Giza 843 × ILB 312		
	Pedigree	Single seed descent	Mass selection	Pedigree	Single seed descent	Mass selection
Seed Yield (t/ha)						
Genotypic variance (δ^2G)	0.12	0.25	0.12	0.07	0.10	0.07
Phenotypic variance (δ^2Ph)	0.14	0.27	0.13	0.12	0.11	0.10
Heritability (h^2)	0.86	0.93	0.89	0.54	0.87	0.70
ΔG	0.57	0.85	0.57	0.33	0.51	0.39
Ph. C.V. %	15.9	19.90	14.29	13.80	10.89	11.71
G.C.V. %	14.7	19.15	13.50	10.50	10.20	9.8
Mean	2.35	2.61	2.56	2.51	3.10	2.70
Seed Yield/ plant (g)						
Genotypic variance (δ^2G)	13.85	11.40	10.20	7.88	9.30	7.77
Phenotypic variance (δ^2Ph)	16.29	12.33	11.09	13.40	10.24	11.09
Heritability (h^2)	0.83	0.92	0.88	0.64	0.87	0.70
ΔG	6.69	6.46	5.86	4.68	5.57	4.66
Ph. C.V. %	15.9	8.06	14.29	8.67	6.81	8.32
G.C.V. %	10.39	7.74	13.50	6.65	6.50	7.09
Mean	38.82	43.57	40	42.2	46.93	39.99
100-Seed weight (g)						
Genotypic variance (δ^2G)	3.15	3.20	2.18	2.04	3.20	1.67
Phenotypic variance (δ^2Ph)	3.41	3.48	2.38	2.66	3.57	2.38
Heritability (h^2)	0.89	0.95	0.88	0.79	0.88	0.74
ΔG	3.29	3.54	2.72	2.58	3.33	2.28
Ph. C.V. %	4.61	2.21	1.72	3.08	2.02	1.76
G.C.V. %	4.43	2.12	1.64	1.71	1.92	1.47
Mean	40	84.55	89.77	86.47	93.26	87.84

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