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Pedigree and Single Seed Decent Selection Methods in Early Segregating Population of Faba Bean (*Vicia faba L.*)

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ABSTRACT

This study was carried out at the experimental farm of the Faculty of Agriculture, Al-Azhar University, Assiut branch during three successive winter seasons of 2020/2021, 2021/2022 and 2022/2023 to improve some yield components of faba bean. The breeding materials used in this experiment were the F₂, F₃ and F₄ generations of one cross (Giza 843 x Misr 3). Pedigree (SP) and single-seed descent (SSD) selection methods were used for days to maturity, number of branches/plant, number of pods/plant, seeds yield/plant and 100 seed weight to study phenotypic (PCV) and Genotypic (GCV) coefficients of variability, expected gain from selection (EGS) and realized gain from selection (RGS). Results indicated that PCV and GCV estimates decreased in sequence generations. EGS and RGS estimates were useful and decreased from generation to generation in most study traits. The EGS% for PS and SSD in F₂ for seed yield/plant was 7.12 and 8.20, respectively, and diseased to 7.11; 8.16 and 6.76; 7.14% in the F₃ and F₄ generations, respectively. The realized gains for selection (RGS %) in PS and SSD were 24.77, 24.27 and 20.43, and 21.35% in the F₃ and F₄ generations, respectively. It was found that pedigree and single-seed decent selection methods have good efficiency in the selection procedures to improve the studied characters.

Keywords: Pedigree, Single seed decent, Heritability.

INTRODUCTION

Faba bean (*Vicia faba L.*) is a globally important legume crop whose main originated between the oriental Mediterranean countries and Afghanistan (O'Sullivan and Angra, (2016). Faba bean is considered the most famous crop in developing countries and the Middle East. It plays a very important role in the economic stability of most countries of the world, and it is the important source of plant protein for both humans and animals in most areas of world. The protein content of faba bean seeds can reach up to 28%. Furthermore, its cultivation contributes to soil fertility and the increase in soil nitrogen and soil fertility after planting the Faba bean is the result of the symbiotic relationship between the bacteria that fix atmospheric nitrogen on the root system. The cultivated area of faba bean in (2023) reached about 23951 hectares produced 100316.46 tons of seed in Egypt (FAO, 2023). 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. Pedigree line selection, a popular approach, has proven effective in enhancing various faba bean traits. Haridy (2017) identified the number of pods/plant as a promising indirect selection criterion. The investigator found that the pedigree method has good efficiency in the selection procedures to improve the studied characters. Born *et al.* (1998) reported high heritability and genetic advance (GA %) for pods/plant and seed yield/plant in faba bean, suggesting significant potential for improvement through selection. The most used selection methods are pedigree selection (PS) and single seed descent (SSD). PS is well known and its success in creatively improving many cultivars has been widely acclaimed (Sarutayophat and Nualsri 2010).

The objective of this study was to compare the effectiveness of pedigree and single seed decent methods of selection to improve yielding ability of faba bean.

MATERIAL AND METHODS

This study was conducted at the Faculty of Agriculture's Experimental Farm. Al-Azhar University, Assiut Branch across three consecutive winter seasons of 2020/2021, 2021/2022, and 2022/2023. In this work, two different selection strategies were used to separate segregated generations of a single broad bean population (*Vicia faba L.*) to determine genetic variability, heritability, and response to selection. The used population was Giza 843 X Misr 3 through its F₂, F₃, and F₄ generations as the breeding materials for this experiment.

Season 2020/2021, F₂, generation

The F₂ plants of the aforementioned population and its parents were sowed on November 6th in spaced plants for the first season of 2020/2021. Plants were spaced 25 cm apart from one another and 60 cm apart between rows. Every slope had a single plant and the recommended agricultural practices were applied for the faba bean, where the population was planted in two experimental plots along with to the parents, one plot for pedigree selection (PS) and the other one for single seed descent selection (SSD). A total of two plots were planted, each containing 2000 plants. From these, the top 400 plants per plot were selected based on their seed yield. This represented 20% selection intensity, and the lineage and numbering of the 400 selected families from each plot were recorded.

Season 2021/2022, F₃ – generation

In the 2021/2022 season, F₃ plants were planted, where two strips were planted, and in the pedigree selection strip, 400 families were grown in 3 replicates (each family in

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3 lines), with 15 plants in each line, while in the single seed descent selection plot one seed from each plant was planted, selected from the previous generation, with lineage and numbering recorded in both selection methods, in addition to parental cultivation. The best 80 plants in yield were selected using the pedigree selection method and the best 80 plants using the single-seed method.

Season 2022/2023, F₄ – generation

In the 2022/2023 season, F₄ plants were planted, where two strips were planted, and in the pedigree selection plot, 80 families were planted, each family on 3 lines, representing 3 replicates in each line of 15 plants. As for the single-seed descent selection plot, one seed was planted from each plant selected from the previous generation, with the registration of lineage and numbering in both methods of selection, in addition to the cultivation of the parents, and the best 20% of the families, namely 16 families, were selected and then compared between them.

The following characters were recorded on each plant.

- 1- Number of days to maturity (DM).
- 2- Number of branches/plant (NB/P).
- 3- Number of pods/plant (NP/P).
- 4- Seed yield /plant, g (SY/P).
- 5- 100- Seed weight, g (100 W).

Statistical analysis:-

Estimates of genotypic and phenotypic variances and covariance were calculated from the variance and covariance components as presented in Table 1.

Table 1. Mean squares and expected mean squares for genotypic and phenotypic variances and covariance.

E.M.S				
Source of variance	D.F	M.S	Variance	Covariance
Replications	r-1	MS 1	$\sigma^2 E + g\sigma^2 r$	-----
Genotypes	g-1	MS 2	$\sigma^2 E + g\sigma^2 r$	Cov. E + r Cov. g
Error	(r-1)(g-1)	MS 3	$\sigma^2 E$	Cov. E

Where, g and r stand for the number of genotypes and replications, respectively. Error variance and covariance are represented by $\sigma^2 e$ and Cov. e, respectively, while genetic variance and covariance are represented by $\sigma^2 g$ and Cov. g.

The heritability in general was calculated as

$$\text{Heritability in } F_2 (H) = [VF_2 - ((VP_1 + VP_2) / 2)) / VF_2] \times 100$$

$$\text{Heritability in } F_3 \text{ and } F_4 (H) = (\sigma^2 g / \sigma^2 p) \times 100$$

Phenotypic and genotypic variance

The Burton (1952) genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as:

$$\text{Phenotypic coefficient of variation (PCV \%)} = (\sigma P / \bar{X}) \times 100$$

$$\text{Genotypic coefficient of variation (GCV \%)} = (\sigma g / \bar{X}) \times 100$$

Where:

PCV and GCV are phenotypic and genotypic coefficients of variation, respectively, σP = standard deviation of phenotypic families, σg = standard deviation of genotypic families and $\bar{X}$ is the population mean. The relative values of these two types of coefficients provide insight into the amount of variability found in a population.

Expected gain from selection (EGS%)

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

$$EGS = K \cdot H \sqrt{\sigma_p^2}$$

Where:

k = 1.45 constant for 20% selection intensity i.e. H= is the broad-sense heritability and σ_p^2 is the phenotypic variance of the population.

Realized gain from selection (RGS%)

$$RGS\% = (\bar{X}_0 - \bar{X}_P) \times 100 / \bar{X}_P$$

Where:-

$\bar{X}_0$ = the mean phenotype of the offspring of selected parents.

$\bar{X}_P$ = the mean phenotype of the whole parental generation.

RESULTS AND DISCUSSION

1-Evaluation of the base population

Two cycles of pedigree (PS) and single-seed descent (SSD) selection methods were achieved is one population of faba bean (*Vicia faba* L.) derived from cross-breeding between (Giza 843 X Misr 3) in generations F₂, F₃ and F₄. Direct pedigree (PS) and single seed descent (SSD) selection methods were applied to the days to maturity, number of branches/plant, seed yield/plant, the number of pods per plant, and 100-seed weight. A description of the base population (F₂ generation); means, ranges, variation and heritability in a broad sense are presented in Table 2.

The range of variability was comparatively wider in the F₂ generation as compared with the next generations for studied characters (Table 2), indicating a sufficient coefficient of variability in the F₂ population (11.16, 12.10) in the criterion of selection i.e. SY/P in PS and SSD respectively. The results showed a sufficient coefficient of variability in the F₂ population (17.18, 16.45) in NP/P for PS and SSD respectively. The CV% of the other traits ranged from 2.17 to 23.64% and 2.04 to 26% for days to maturity (DM) and number of branches/plant (NB/P) for PS and SSD, respectively. Similar results were found by, Ahmad (2016), Ahmed *et al.* (2018) and Ahmed and Sakr (2024).

Table 2. The range and mean values in the F₂ population and parents for all studied traits in one faba bean population during the season of 2020/2021.

Families		DM	NB/P	NP/P	SY/P	100 W
Giza 843 × Misr 3 PS	Range	143-162	2-7	11-26	39-74	65.30-83
	Mean	157.33	3.59	17.24	47.58	71.02
	Variance	11.70	0.72	8.77	28.22	8.36
	CV%	2.17	23.64	17.18	11.16	4.07
	Hb	0.84	0.86	0.82	0.92	0.73
	SE	1.35	0.31	1.26	1.46	1.51
Giza 843 × Misr 3 SSD	Range	144-165	3-7.67	12-28	40-81	66.89-85.33
	Mean	160.80	4.00	18.05	49.63	70.94
	Variance	10.74	1.08	8.81	36.09	14.16
	CV%	2.04	26.00	16.45	12.10	5.30
	Hb	0.83	0.91	0.82	0.94	0.84
	SE	1.35	0.31	1.26	1.46	1.51
Giza 843	Mean	148.67	7.52	20.13	69.00	75.33
Misr 3	Mean	147.33	6.31	30.60	83.67	74.00

DM: days to maturity; NB/P: number of branches per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; 100 W: 100 seed weight. CV%: coefficient of variation; H: Broad sense heritability. PS: pedigree selection Method. SSD: single-seed descent Method.

Heritability in broad sense estimates was higher for all in the base population. Also, Ibrahim (2015) estimated high heritability values for NB/P, NP/P and SY/P.

2- Pedigree and single-seed descent selection methods in F₃ and F₄ generations.

The analysis of variance indicates a highly significant (**) among the F₃ and F₄ families for DM, NB/P, NP/P, SY/P,

and 100 W, except NB/P was insignificant in PS and significant (*) in SSD For F₄. This result revealed the available variance for future selection in the current population of faba beans (Table 3).

Table 3. Mean squares of pedigree (PS) and single-seed descent (SSD) selection methods are genotype selection methods for all studied traits in F₃ and F₄ populations (Giza 843 x Mistr 3) in season 2021/2022.

		F ₃					
S.O.V	DF	Selection method	MS				
			DM	N B/P	NP/P	SY/P	100 W
Reps	2	PS	0.83	0.13	0.79	0.21	0.40
		SSD	2.22	0.18	0.45	0.30	0.66
Genotypes	79	PS	18.46**	1.95**	8.73**	77.04**	12.07**
		SSD	27.32**	2.11**	8.53**	100.67**	16.37**
Error	158	PS	2.58	0.36	1.45	2.45	1.03
		SSD	1.92	0.71	1.62	2.86	1.59
		F ₄					
Reps	2	PS	1.27	0.02	0.15	1.93	0.33
		SSD	1.52	0.02	0.44	4.31	0.33
Genotypes	15	PS	17.06**	1.22	5.67**	71.11**	10.44**
		SSD	24.7**	1.55*	5.95**	83.64**	8.54**
Error	30	PS	2.18	0.57	1.52	3.02	0.81
		SSD	2.30	0.55	0.77	5.60	1.07

DM: days to maturity; NB/P: number of branches per plant; NP/P: number of pods per plant; SY/P: seed yield per plant; 100 w: 100 seed weight. S.O.V.: source of variation; REP: Replications; *and ** significant at 0.05 and 0.01 probability levels, respectively.

A- Seed yield/ plant (SY/P)

The averages for DM, NB/P, SY/P, NP/P, and 100 w in the F₃ and F₄ generations of the current population are displayed in Table 4. The averages of the selected families

were greater in the F₄ than in the F₃ generation. Otherwise, for DM, the average was earlier in the F₄ than in the F₃ generation. This result is good to have superior selections in yield and early maturity.

The F₃ generation averages SY/P (59.37 and 61.68 g) in PS and SSD respectively. It was evident that sufficient differences across families within the current population were found and support the possibility of effective selection for seed yield. Moreover, the averages of the selected families for seed yield/plant, number of pods/plant, number of branches/plant and 100 seed weight were higher in F₄ than F₃ generations in pedigree and single seed descent methods (Table 4).

The coupled PCV% and GCV% for SY/P in the F₃ selected families were 19.58 and 19.56% and reduced to 17.52 and 17.40 in F₄, respectively (Table 4). This diversity raises the possibility of the selection of seed yield/plant within the F₃ families. Haridy *et al.* (2021) and Hiywotu *et al.* (2022) found similar outcomes. Waly *et al.* (2021) reported additive genes influence SY/P with higher heritability and high genetic advance (GA %) as a percentage of the average. In general, GCV% was less than PCV%. Abo-Elwafa *et al.* (2022) and Ahmad (2016) discovered similar outcomes for the results of seed yield/plant.

The high estimates of heritability were recorded and accounted 96.82 and 95.75% in F₃ and F₄ for SP, respectively. On the other hand, there were 97.16 and 93.31% in SSD for F₃ and F₄, respectively. The high values of (H) generally revealed to the effects of the environment were smaller than the influences of heredity. These findings are consistent with those of Bakhiet *et al.* (2015), Hiywotu *et al.* (2022) and Prateek and Mishra (2022).

Table 4. Mean, VP, VG, PCV, GCV and heritability for all studied treats after two cycles in pedigree (PS) and single seed descent (SSD) selection methods in one population (Giza 843 X Mistr 3).

Selection methods		Fam	Mean ± SE	VP	Vg	PCV%	GCV%	H%
DM	PS	F ₃	150.78 ± 0.93	6.15	5.29	1.64	1.53	86.02
		F ₄	145.67 ± 0.84	5.33	4.62	1.59	1.48	86.69
	SSD	F ₃	154.18 ± 0.80	9.11	8.47	1.96	1.89	92.98
		F ₄	147.90 ± 0.87	8.23	7.47	1.94	1.85	90.69
NB/P	PS	F ₃	5.26 ± 0.35	0.65	0.53	15.32	13.85	81.70
		F ₄	7.42 ± 0.44	0.41	0.22	8.58	6.27	53.33
	SSD	F ₃	6.38 ± 0.48	0.70	0.47	13.14	10.71	66.47
		F ₄	8.46 ± 0.44	0.52	0.33	8.50	6.81	64.25
NP/P	PS	F ₃	22.94 ± 0.69	2.91	2.43	7.44	6.80	83.45
		F ₄	27.02 ± 0.71	1.89	1.38	5.09	4.35	73.11
	SSD	F ₃	23.55 ± 0.73	2.84	2.30	7.16	6.45	80.98
		F ₄	26.88 ± 0.50	1.98	1.73	5.24	4.89	87.04
SY/P	PS	F ₃	59.37 ± 0.90	25.68	24.87	8.54	8.40	96.82
		F ₄	71.50 ± 1.00	23.70	22.70	6.81	6.66	95.75
	SSD	F ₃	61.68 ± 0.98	33.56	32.60	9.39	9.26	97.16
		F ₄	74.85 ± 1.37	27.88	26.01	7.05	6.81	93.31
100 W	PS	F ₃	75.77 ± 0.58	4.02	3.68	2.65	2.53	91.44
		F ₄	79.72 ± 0.52	3.48	3.21	2.34	2.25	92.25
	SSD	F ₃	78.32 ± 0.73	5.46	4.93	2.98	2.83	90.31
		F ₄	84.39 ± 0.60	2.85	2.49	2.00	1.87	87.46

B- Number of branches/plant (NB/P)

The families' average number of branches/ plant of the selected families were higher in F₄ than in the F₃ generations for both PS and SSD (Table 4). It was evident that there was sufficient variation among families, as done for NB/P. But the average in SSD was 5.26 and 7.42 in F₃ and F₄, respectively.

The GCV provides a measure for comparing genetic variability in various metrical characters. For the number of

branches/plants, in the pedigree selection method (SP), the PCV estimates were 15.32 and 8.58 and GCV estimates were 13.85 and 6.27 for F₃ and F₄, respectively. In the single-seed descent selection method (SSD), for the same trait, the PCV estimates were 13.14 and 8.50 and GCV estimates were 10.71 and 6.81 for F₃ and F₄, respectively (Table 4), indicating little influence of the environment on the characters' expression. The coupled PCV% and GCV% with high heritability for

NB/P in the F₃ and F₄ for selected families gave chance for future selection of this trait.

The PCV and GCV% in the F₃ and F₄ families are lower than those of the F₂ families (23.64%). According to Ibrahim (2015), Ahmed (2016), Salwa Mostafa *et al.* (2017), Afeta *et al.* (2019), and Waly *et al.* (2021), the PCV% value was greater than the GCV% and H values that were provided for NB/P.

C- Number of pods/plant (NP/P)

The number of pods/plant average for (SP) was 22.94 and 27.02 in F₃ and F₄, respectively. In the single-seed descent selection method (SSD), it was 23.55 and 26.88 in F₃ and F₄, respectively (Table 4). It was evident that there was sufficient variation among families as done for NP/P. For the number of pods/plant in the first selection method (SP), the PCV estimates were 7.44 and 5.09 and the GCV estimates were 6.80 and 4.35 for F₃ and F₄, respectively. In the second selection method (SSD), the PCV estimates were 7.16 and 5.24 for the same trait, while the GCV estimates were 6.45 and 4.89 for F₃ and F₄, respectively.

These variations imply that selection within the F₃ families could result in a shift in the population's average number of pods per plant. PCV% was generally slightly greater than GCV%. According to Prateek and Mishra (2022), the number of pods per plant had modest values for both genotypic and phenotypic coefficients of variability.

D- 100 Seed weight

The average of 100 seeds weight for the first method (SP) increased from 75.77 in F₃ to 79.72 g in F₄. In the second selection method (SSD), it was 78.32 g in F₃ and 84.39 g in F₄ (Table 4). Otherwise, the PCV% was 2.65 and 2.34% in F₃ and F₄, and the GCV% were 2.53 and 2.25% in F₃ and F₄ for (SP). In (SSD), the PCV% was 2.98 and 2.00% in F₃ and F₄, while the GCV% was 2.83 and 1.87% in F₃ and F₄ under the 100 seed weight selection. According to estimates of PCV and GCV%, selection among the F₃ families may be the primary cause of most of the variability.

High heritability estimates were found of 91.44% in F₃ and 92.25% in F₄. For (SP), in (SSD) there were 90.31% in F₃ and 87.46% in F₄, revealing high genetic variability for 100 seed weight in the current population. Afeta *et al.* (2019) and Waly *et al.* (2021) reported similar findings that the PCV value was greater than the GCV% and H values for 100 seed weight.

Actual (RGS %) and predicted (EGS %) gains from selection

The actual (RGS %) and predicted (EGS %) gains from selection are presented in Table 5. The expected (EGS %) and realized (RGS %) gains from selection, as Johnson *et al.* (1955) defined genetic advance of low (<10%), moderate (10–20%), and high (>20%) as a percentage of the mean.

The EGS% for DM in the current population of faba bean in the F₂ generation was 4.19 then it was 3.09 in F₃ and 2.90 in the F₄ generations for (SP), in the (SSD) was 3.95 in the F₂ generation, 4.07 in F₃ and 3.77 in F₄ generations. In the F₂ generation for (SP) and (SSD), the EGS% for the number of branches/plant was 1.06 and 1.37, which decreased to 0.95; 0.81 and 0.49; 0.67 in F₃ and F₄, respectively.

For the number of pods/plant in the PS and SSD, the EGS% of F₂ was 3.52 and 3.53, respectively; however, it dropped to 2.06; 1.98 and 1.46; 1.78% in the F₃ and F₄ generations, respectively. Mishra *et al.* (2021) reported high heritability and GA% for all characteristics except for

pods/plant. Moreover, the EGS% for PS and SSD in F₂ for seed yield/plant was 7.12 and 8.20, respectively, and diseased to 7.11; 8.16 and 6.76; 7.14% in the F₃ and F₄ generations, respectively. The outcomes of Tadele *et al.* (2019) and Abo-Hegazy (2022) are consistent with this one.

The realized gains for selection (RGS %) in PS and SSD, were -4.16, -4.12 and -3.39, -4.08; 46.45, 59.56 and 41.12, 32.59; 33.03, 30.48 and 17.80, 14.14; 24.77, 24.27 and 20.43, 21.35; and 6.68, 10.41 and 5.22, 7.20% for DM; NB/P; NP/P; SY/P and 100W in the F₃ and F₄, respectively (Table 5). This outcome agrees with the findings of Ahmad (2016) and Mishra *et al.* (2021).

Table 5. The EGS% and RGS% gains were attained using pedigree (SP) and single-seed decant (SSD) methods for all study treats in the F₂, F₃ and F₄ generations of the cross (Giza 843 x Misr 3).

Treat	Selection cycle	PS Pop2		SSD Pop2	
		EGS%	RGS%	EGS%	RGS%
DM	F2	4.19	----	3.95	----
	F3	3.09	-4.16	4.07	-4.12
	F4	2.90	-3.39	3.77	-4.08
NB/P	F2	1.06	----	1.37	----
	F3	0.95	46.45	0.81	59.56
	F4	0.49	41.12	0.67	32.59
N P/P	F2	3.52	-----	3.53	-----
	F3	2.06	33.03	1.98	30.48
	F4	1.46	17.80	1.78	14.14
SY/P	F2	7.12	-----	8.20	-----
	F3	7.11	24.77	8.16	24.27
	F4	6.76	20.43	7.14	21.35
100 W	F2	3.04	-----	4.57	-----
	F3	2.66	6.68	3.06	10.41
	F4	2.50	5.22	2.14	7.75

CONCLUSION

Pedigree selection method for improving no. of branches/plant and no. of pods/plant was more efficient compared to the single seed decent selection method in isolating high yielding genotypes. However, single seed decent selection method was very effective for days to maturity, seed yield/plant and 100 seed weight.

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انتخاب النسب والتحدر من بذرة واحدة في الأجيال الانعزالية المبكرة لعشيرة من الفول البلدي

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المخلص

أجرى هذا البحث في مزرعة كلية الزراعة جامعة الأزهر فرع اسيوط خلال المواسم الشتوية الثلاثة ٢٠٢٠/٢٠٢١ و ٢٠٢١/٢٠٢٢ و ٢٠٢٢/٢٠٢٣ لتحسين صفات المحصول في الفول البلدي حيث استخدمت طريقتي انتخاب (انتخاب النسب والتحدر من بذرة واحدة) في عشيرة للجبل الثاني من الهجين جيزة ٨٤٣ x مصر 3. وتم الانتخاب من الجيل الثاني وحتى الجيل الرابع وذلك بانتخاب النباتات الفردية المتميزة في الصفات محل الدراسة لطريقتي الانتخاب. وقد تم حساب المقاييس الوراثية في كل طريقة لكل جيل وهي معامل الاختلاف المظهري ومعامل الاختلاف الوراثي ودرجة التوريث بالمعنى الواسع والتقدم المتوقع للانتخاب والتقدم الحقيقي. وقد أظهرت النتائج وجود فروق معنوية بين متوسطات الأجيال الثلاثة لكل طريقة من طرق الانتخاب في كل الصفات المدروسة. ووجود قيم ملحوظة لمعامل الاختلاف المظهري ومعامل الاختلاف الوراثي حيث بلغت بالجيل الرابع لصفة عدد الأفرع/ نبات ٨,٥٨، ٦,٢٧ في طريقة النسب و ٨,٥٠، ٦,٨١ لطريقة التحدر من بذرة واحدة لنفس الصفة وبلغت لصفة وزن محصول النبات ٦,٨١، ٦,٦٦ في طريقة النسب و ٧,٠٥، ٦,٨١ لطريقة التحدر من بذرة واحدة لنفس الصفة. كما كانت تقديرات درجة التوريث بالمعنى الواسع مرتفعة لكل الصفات المدروسة في كلتا الطريقتين. ووجود قيم ملحوظة للتقدم المتوقع للانتخاب والتقدم الحقيقي في كل الصفات المدروسة لطريقة النسب والتحدر من بذرة واحدة. ومن خلال الدراسة تبين أنه يمكن تحسين صفات ميعاد النضج ووزن محصول النبات ووزن ١٠٠ بذره من خلال طريقة انتخاب التحدر من بذرة واحدة. في حين ان طريقة انتخاب النسب كانت مناسبة جدا لصفات عدد القرون / نبات وعدد الفروع / نبات.