


Comparison between three breeding methods in segregating generations of faba bean (*Vicia faba* L.) crosses

Gehan G. Abou-Zaid*¹ , Ramadan A. El-Refeay², Mohamed M. El-Tokhy² and Zeinab E. Ghreeb³

Address:

¹ Field crops Research Institute, Agricultural Research Center, Giza, Egypt.

² Faculty of Agriculture, Tanta University, Egypt.

³ Central Laboratory for Design and Statistical Analysis Research, Agricultural Research Center, Giza, Egypt.

*Corresponding author: **Gehan G. Abou-Zaid**, e-mail: gehangalalabou-zaid@gmail.com

Received: 15-02-2023; Accepted: 07-07-2023; Published: 14-07-2023

DOI: [10.21608/ejar.2023.194043.1355](https://doi.org/10.21608/ejar.2023.194043.1355)



ABSTRACT

This investigation was carried out in four winter seasons: 2017–18 (F₂), 2018–19 (F₃), 2019–20 (F₄), and 2020–21 (F₅) at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt, to study the comparison between three breeding methods: pedigree, bulk, and single pod descent for improving seed yield in segregating generations of faba bean crosses: (1) Triple White x Giza 429; (2) Ohishima-Zaira x Giza 429; (3) Giza 40 x Giza 429; and (4) Ohishima-Zaira x Foul Sbai labiade. The pedigree method had a superiority over the other two breeding methods for almost all studied traits in all crosses of the three generations, except for the cross 1 of the F₄ generation and the cross 4 of the F₅ generation, where the bulk method had a superiority. Narrow-sense heritability estimates were moderate in the four studied crosses of the three generations, with few exceptions. Predicted genetic advance estimates were moderate for the number of branches, pods, seeds, and seed yield per plant in all crosses of the three generations. While the same estimate was low for chocolate spot disease, flowering date, plant height and 100-seed weight in approximately all crosses of the three generations. Comparable predicted genetic advances were observed with respect to the two breeding methods for chocolate spot disease in F₃ and F₄ generations. while bulk exceeded that for single pod descent in the F₅ generation. The bulk method had a superiority over single-pod descent in the three generations for the number of pods and seeds per plant. The bulk method exceeded that for single pod descent in the F₅ generation for seed yield per plant. Broad-sense heritability was moderate under bulk as well as single pod descent methods for plant height, number of branches, pods, and seeds per plant, and seed yield per plant. Predicted genetic advance was considered moderate in most cases, except for chocolate spot disease in the cross 3 and 4 of all generations, rust disease in the cross 3 of F₃ and F₄-generations, and flowering date in all crosses of all generations where the values were considered low.

Keywords: Pedigree, bulk, single pod-descent, narrow-sense heritability, predicted genetic advance, segregating generations.

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most important seed legumes in prone regions of North and East Africa, especially in Egypt, and is common in the northern provinces of Sudan along the Nile Valley. not only because of its high protein content, which ranges from 24 to 33% (Winch, 2006), but also because of its use in preparing several local dishes. It plays an important role in world agriculture owing to its ability to fix atmospheric nitrogen and grow and yield well on marginal lands. The breeder should know the type of gene action of the quantitative traits because this is the main determinant in the choice of selection and breeding procedures. The national faba bean area in the 2020/21 season was about 50.400 hectares with an average productivity of 281.000 tons and an average seed yield of 3.69 tons per hectare, which covers about 41% of our essential human consumption needs (Source: Annual Report of Field Crop Research Institute, ARC, Egypt, 2022). It brings the plant breeder's attention to breed faba beans suitable to grow in arid conditions with high yielding ability, high total protein content, and early maturity. However, successful breeding programs will depend on the magnitude of genetic variation in the population. Moreover, reliable estimates of genetic and environmental variations will be helpful to estimate heritability and, consequently, predict genetic advance from selection. Increasing seed yield and improving its stability, along with resistance to foliar diseases (chocolate spot and rust) are the main objectives of most breeding programs. Several selection procedures (pedigree selection, bulk population breeding, and single pod descent) have been proposed for improving the

seed yield of self-pollinated crops. Knowledge about the relative efficiency of the different methods may immensely help the plant breeder in choosing a better method to adapt of a particular crop.

Since, selection based on single plant basis in F₂ was not effective. Shebeski (1967) suggested that, a large number of F₂ plants may be selected and their F₂ progenies will be based on their actual yields or their yields expressed as percentage of adjacent control. Pedigree selection is the convention method of accumulating genetic recombination in each generation. The heterozygosity in early generations makes the efficient identification and selection of recombinant genotypes more difficult. Repeat pedigree selection can increase homozygosity, but many generation cycles are required to reach homozygosity in loci associated with agronomic traits. The single pod descent method can be used to obtain homozygous inbred by accelerating generation cycles, but its application is dependent on growth habit of plant materials used (Wolf-Quintero, et al. 1998).

Many investigations have been conducted to compare the efficiency of breeding methods for segregating generations of faba bean (Shalaby et al. 2001; Ashrei, 2006; Abo Mostafa et al. 2014; Ibrahim, 2015).

The main objectives of this investigation were to evaluate the effectiveness and comparison of pedigree, bulk and single pod descent (SPD) breeding methods on improving resistance to foliar diseases (chocolate spot and rust), earliness and seed yield and its components in faba bean.

MATERIALS AND METHODS

This investigation was carried out in four winter seasons, i.e., 2017–18 (F₂), 2018–19 (F₃), 2019–20 (F₄), and 2020–21 (F₅), at Sakha Agricultural Research Station, Kafr-El-Sheikh governorate, Egypt, to study the comparison between three breeding methods in segregating generations of faba bean after crossing between parents: Giza 429, Ohishima-Zaira, Giza 40, Triple White, and Foul Sbailabiade, to produce four crosses: (1) Triple White x Giza 429; (2) Ohishima-Zaira x Giza 429; (3) Giza 40 x Giza 429; and (4) Ohishima-Zaira x Foul Sbailabiade. The breeding methods were pedigree selection, bulk, and single-pod descent. The origin, botanical group, and agronomic characteristics of the used parents are shown in Table 1.

Table 1. Names, Origin, botanical group, disease reactions and agronomic characters of the parental faba bean genotypes used in this investigation.

Genotypes	Original	Botanical group	Disease reactions	Agronomic characters	
				Flowering date	Yielding level
Triple Whit	Sudan	miner	Susceptible	Early	Medium
Giza429	Egypt	Equina	Moderately resistant	Early	Medium
Ohishima-Zaira	Japan	Equina	Resistant	Early maturity	High
Giza40	Egypt	Equina	Susceptible	Early	High
Foul Sbailabiade	Morocco	Major	Resistant	Medium	High

Reaction to foliar diseases was recorded in mid - February and mid- March for chocolate spot and rust diseases, respectively, according to the disease scales suggested by Bernier et al. (1984) under natural infection.

Table 2. Rating scale for chocolate spot and rust diseases according to Bernier et al. (1984).

Rate	Chocolate spot scale
1	No disease symptom (highly resistant)
3	Few small discrete lesions (Resistant)
5	Some coalesced lesions with some defoliation (moderately resistant)
7	Large coalesced lesions, 50% defoliations, some dead plants (susceptible)
9	Extensive lesions on leaves, stems and pods, severe defoliation, heavy sporulation, death of more than 80% of plants (highly susceptible)
Rust scale	
1	No pustules or very small non-sporulating flecks (high resistant)
3	Few scattered pustules covering less than 1% of the leaf area, and few or no pustules on stem (resistant)
5	Pustules common on leaves covering 1-4% of leaf area, little defoliation and some pustules on stem (moderately resistant)
7	Pustules very common on leaves covering 4-8% of leaf area, some defoliation and many pustules on stem (susceptible)
9	Extensive pustules on leaves, petioles and stem covering 8–10% of leaf area, many dead leaves and several defoliation (highly susceptible).

Pedigree method (PM):

In the 2017/18 growing season, approximately 200 plants from each F₂ population cross were selected according to their phenotypic performance; each individual plant progeny was kept on a page and sown in a separate row representing F₃ families. Seeds from each individual plant progeny were mixed and sown in a replicated experiment as a pedigree selection method. In the 2018/19 growing season, the seeds were spaced at 20 cm, while row spacing was 60 cm. Selection was practiced in two steps: the first among F₃-families, where the promising family was labeled; and the second step was the selection within each promising family, where the best five plants according to their phenotypic appearance were chosen, and the progeny of the best one was used in the next generation as an F₄ family. The remaining four plants from each selected family were mixed and sown in a replicated experiment, representing the pedigree selection method; the procedure was repeated in each generation. In the 2019/20 season, the same procedures in F₄ were repeated as in F₃ cross-populations. In the 2020–21 season, the selection among and between F₅ cross-populations was done as in the F₄ generation. It is to be noted that, the selection families in each cross-population were reduced from generation to another and in the F₅ cross-population, 15 pure lines were obtained for each cross-population and retained to be raised as the F₅ generation in the final evaluation.

Bulk method (BM):

In the 2017/18 growing season, seeds from each F₂ cross-population were mixed to form the population seed bulk. Samples from the mixed seeds of each cross-population were sown in 10 rows per plot; a row was three meters in length, 60 cm between rows, and 20 cm between hills. A complete randomized block design with three replications was used. The same procedures were practiced and repeated from F₂ to F₅ generations without selection up to the 2020–21 season. Twenty plants were taken from each plot; the required data were collected in each cross-population of F₃, F₄ and F₅ generations and subjected to statistical and genetic analysis.

Single pod descent method (SPDM):

In this method, one pod was taken from each plant in F₂ for each cross-population, mixed, and sown in the next generation as F₄-generation. The same procedures were followed for F₃-F₅ generations; twenty plants were taken from each plot of each cross-population of F₃, F₄, and F₅ generations to collect the data required. The randomized block design with three replications was used in each generation; 10 rows per plot for each cross were sown, where each row was three meters in length, 60 cm between rows, and 20 cm per part.

Characters studied:

The following characteristics were measured for each breeding method. The data on random sample of 20 guarded plants from each plot for each cross-population of pedigree method, bulk and single pod descent breeding methods were subjected to the statistics and genetic analysis, where the characters were:

- 1-Chocolate spot disease reaction.
- 2- Rust disease reaction.
- 3- Flowering date (day)
- 4-Plant height (cm).
- 5- No. of branches/plant.
- 6- No. of pods /plant.
- 7- No. of seeds/plant.
- 8- Seed yield / plant (g).
- 9- 100-seed weight (g)

Statistical Analysis:

For Pedigree method, narrow-sense heritability estimates were calculated by parent-offspring regression, where mean value of offspring regressed on their parent value for each studied trait were regressed, according to the method outlined by Smith and Kinman (1965). Narrow-sense heritability (h²) according to this method could be calculated between (F₂, F₃), (F₃, F₄) and (F₄, F₅) as in Table (2):

Table 2. Narrow-sense heritability as the regression coefficient of Fn+1 mean on Fn parental value.

Parent-offspring generation	r _{y,x}	h ² = b _{y,x} / 2r _{y,x}
F ₂ , F ₃	3/4	2/3 b F ₃ , F ₂
F ₃ , F ₄	7/8	4/7 b F ₄ , F ₃
F ₄ , F ₅	15/16	8/15b F ₄ , F ₅

Where:

b_{y,x} = Covariance Y X / variance X

r_{y,x} = Covariance Y X / (variance X . Variance Y)^{1/2}

Therefore :

$h^2 (F_2, F_3) = 0.45 b_{y,x} / r_{y,x}$, $b_{y,x}$ = regression coefficient of F_3 progeny mean on F_2 parental value for respective characters.

$h^2 (F_3, F_4) = 0.32 b_{y,x} / r_{y,x}$, $b_{y,x}$ = regression coefficient of F_4 progeny mean on F_3 parental value for respective characters.

$h^2 (F_4, F_5) = 0.28 b_{y,x} / r_{y,x}$, $b_{y,x}$ = regression coefficient of F_5 progeny mean on F_4 parental value for respective characters.

Regression coefficient ($b_{y,x}$) and phenotypic correlation coefficient ($r_{y,x}$) calculated between sequential generation i.e., (F_2, F_3), (F_3, F_4) and (F_4, F_5) generations for each trait.

Expected (Ga) and predicted (Ga%) genetic gain from selection at top 5 % (selection intensity) were calculated according to Hallauer and Miranda (1981), as follows:

$$Ga = K \cdot h^2 \cdot \sigma_{ph}$$

Where:

K: is a constant refers to the selection differential expressed as standard deviation unit at certain selection intensity (K = 2.06 at 5 % selection intensity).

h^2 is the narrow - sense heritability and σ_{ph} is the phenotypic standard deviation.

The predicted genetic advance (Ga %) from selection as percentage of mean was calculated as: $Ga \% = Ga \times 100 / \bar{x}$

The Data of the three methods for the four cross-populations were subjected to statistical analysis of variance according to Gomez and Gomez (1984) in F_3 , F_4 and F_5 - generations. The mean values of each generation for the traits in consideration were compared at 5 % level of probability using least Significant Differences (L.S.D) test. On the other hand, the data of each cross-progeny in the three replications for each generation was subjected to statistical analysis of variance. The heritability in broad - sense estimated as per formula used by Hanson *et al.* (1956).

The expected and predicted genetic gain upon selection were calculated using the values of broad - sense heritability (H) instead of narrow-sense heritability (h^2) in pedigree method according to Miller *et al.* (1958). Phenotypic correlation coefficient (r) was calculated between trait pairs for each generation either in pedigree, bulk or single pod descent methods as outlined by Snedecor and Cochran (1969).

RESULTS

The objective of the present study was to determine the response of some faba bean (*Vicia faba* L.) cross-populations to the breeding methods, i.e., pedigree, bulk, and single pod descent for selection of some earliness attributes, chocolate spot disease, rust disease reaction, and yield and its components in F_3 -generation.

1- F_3 -generation: -

1-a-Cross 1 (Triple white x Giza 429):

The differences between the mean performance of the three breeding methods as shown in Table 3 were highly significant for chocolate spot, rust, flowering date, plant height, and 100-seed weight; significant for number of pods per plant, number of seeds per plant and seed yield per plant; and not significant for number of branches per plant. Data shown in Table 3 revealed that, the pedigree selection method had a superiority over the two breeding methods, i.e., bulk and single pod descent, for all studied traits, except for plant height, where the bulk method and single pod descent surpassed the pedigree method in this concern. However, bulk method was not significantly different from pedigree method for number of seeds per plant, seed yield per plant and 100-seed weight, and –in general– single pod descent came in the second grade after pedigree method with respect to the traits in consideration.

1-b-Cross 2 (Ohishima-Zaira x Giza 429):

The differences between mean performance of the three breeding methods as shown in Table (3) were highly significant for flowering date, plant height, No. of branches/plant, No. of pods /plant, No. of seeds/plant and seed yield/plant. While the same differences were not significant for chocolate spot and rust diseases and 100-seed weight.

Data shown in Table (3) pointed out that, pedigree selection method significantly surpassed the other two breeding methods for all studied traits, except for flowering date and plant height, where the bulk method had the significantly highest values.

1-c-Cross 3 (Giza 40x Giza 429):

As shown in Table 3, the data showed that the differences between the mean performances of the three breeding methods were highly significant for all studied traits without any exceptions. The data revealed that, the pedigree method had a superiority over the two breeding methods for all studied traits except for

flowering data, plant height, and number of branches per plant, where single pod descent was significantly higher in this concern. However, the single-pod descent method did not significantly differ from the pedigree method with respect to the number of seeds per plant and seed yield per plant.

1-d-Cross 4(Ohishima-Zaira x Foul Sbailabiade):

As shown in Table 3, the data revealed that the differences between the mean performance of the three breeding methods were highly significant for chocolate spot and rust disease reactions and flowering date; significant for number of pods and seeds per plant; and not significant for plant height, number of branches per plant, seed yield per plant and 100-seed weight. The pedigree selection method significantly surpassed the other two methods with respect to all studied traits, with no significant difference between single pod descent for number of seeds per plant and the bulk method for the number of pods per plant, where the differences between mean performance in these cases were not significant.

Table 3. Comparison between mean performance of pedigree method, single pod and bulk method for the studied traits in the F₃-generation of faba bean cross-populations.

Crosses	Method	Chocolate disease reaction	Rust disease reaction	Flowering date	Plant height (cm)	No. of branches / plant	No. of pods/plant	No. of Seeds / plant	Seed yield / plant	100-Seed weight
Triple white x Giza429	Pedigree	3.71	3.01	51.10	122.24	3.82	39.59	99.62	70.74	71.72
	Pod	4.18	3.29	55.56	132.44	3.80	24.84	71.38	46.10	68.72
	Bulk	4.30	4.28	42.78	133.89	3.27	33.89	89.64	63.03	70.31
F test		**	**	**	**	ns	*	*	*	**
LSD_{0.05}		-	-	-	-	-	10.2	26.4	19.8	-
LSD_{0.01}		0.49	0.87	5.0	6.0	-	-	-	-	3.6
Ohishima-Zaira x Giza429	Pedigree	3.81	3.22	55.11	133.71	3.36	28.90	77.60	57.99	75.52
	Pod	4.16	3.73	58.13	126.44	3.60	22.49	66.09	50.17	77.53
	Bulk	4.16	4.02	42.22	145.11	2.51	18.73	59.53	42.75	78.40
F test		ns	ns	**	**	**	**	**	**	ns
LSD_{0.05}		-	-	-	-	-	-	-	-	-
LSD_{0.01}		-	-	9.2	10.2	0.9	5.8	20.0	12.6	-
Giza40 x Giza429	Pedigree	3.47	2.65	51.34	130.19	3.33	31.19	86.91	67.60	78.71
	Pod	4.82	4.47	50.89	125.56	4.11	28.36	76.09	55.29	70.96
	Bulk	4.94	4.69	47.89	149.89	2.98	23.53	66.64	45.50	70.42
F test		**	**	**	**	**	**	**	**	**
LSD_{0.05}		-	-	-	-	-	-	-	-	-
LSD_{0.01}		0.8	1.6	2.7	25.50	0.6	2.7	16.1	14.0	7.0
Ohishima-Zaira x Foul Sbailabiade	Pedigree	3.39	2.55	55.66	136.61	4.49	32.98	84.80	73.61	88.96
	Pod	4.27	3.11	68.33	128.44	4.22	25.07	77.16	73.90	93.27
	Bulk	4.24	4.16	70.09	137.83	4.13	27.24	74.64	69.83	94.96
F test		**	**	**	ns	ns	*	*	ns	ns
LSD_{0.05}		-	-	-	-	-	6.0	8.8	-	-
LSD_{0.01}		0.9	1.0	6.9	-	-	-	-	-	-

2-F₄-generation: -

2-a-Cross 1 (Triple white x Giza 429):

As shown in Table (4), the data illustrated that the differences between the mean performance of the three breeding methods were highly significant for flowering date, number of pods per plant, number of seeds per plant and seed yield per plant, but not significant for the rest traits. The bulk method had superiority over two breeding methods for all the significant traits, i.e., flowering date, number of pods and seeds per plant, and seed yield per plant, with no significant differences between bulk and single pod descent methods with respect to seed yield per plant.

2-b-Cross 2 (Ohishima-Zaira x Giza 429):

Highly significant differences between mean performance of the breeding method referred before for flowering date, plant height, No. of branches/plant, No. of seeds/plant and seed yield /plant; only significant for 100-seed weight and not significant for chocolate spot and rust diseases and No. of pods/plant (Table 4). Pedigree selection method was significantly surpassed the other two breeding methods for plant height, No. of branches/plant, No. of seeds/plant and seed yield /plant. The differences between the mean performance of pedigree method and that for bulk method was not significant for plant height and No. of branches /plant.

2-c-Cross 3 (Giza 40x Giza 429):

Highly significant differences between mean performance of the three-breeding method used for chocolate spot disease reaction, plant height, No. of pods/plant, No. of seeds/plant, seed yield/plant and 100-

seed weight; only significant for rust disease reaction and not significant for flowering date and No. of branches/plant (Table 4). Pedigree selection method revealed a superiority over the two breeding methods for chocolate spot disease, plant height, No. of pods/plant, No. of seeds/plant and seed yield /plant, where its mean performances were significantly highest than the other mean performances of the other breeding methods.

2-d-Cross 4 (Ohishima-Zaira x Foul Sbailabiade):

The listed data in Table 4 pointed out that, highly significant differences between the mean performance of the three breeding methods were observed for plant height, number of branches per plant, number of pods per plant, number of seeds per plant and 10-0seed weight; they were only significant for seed yield per plant and not significant for chocolate spot disease, rust disease reaction and flowering date. The pedigree method significantly surpassed the other two methods for four traits out of six, i.e .,plant height, number of pods per plant, number of seeds per plant and seed yield per plant. while the bulk method had significantly the highest values for plant height, number of branches per plant and 100-seed weight.

Table 4. Comparison between mean performance of pedigree method, single pod and bulk method for the traits in the F₄-generation of faba bean cross-populations

Crosses	Methods	Chocolate Spot disease reaction	Rust disease reaction	Flowering date (day)	Plant height (cm)	No. of branches /plant	No. of Pods / plant	No. of Seeds /plant	Seed yield /plant	100-Seed Weight (gm)
1-Triple white xGiza429	Pedigree	4.47	4.45	56.89	138.27	2.91	23.84	72.60	49.38	69.00
	Pod	4.47	4.51	60.00	130.78	3.73	25.13	75.00	51.50	67.57
	Bulk	4.44	4.36	42.44	135.67	3.27	35.69	99.49	71.58	69.12
F test		ns	ns	**	ns	ns	**	**	**	ns
LSD_{0.05}		-	-	-	-	-	-	-	-	-
LSD_{0.01}		-	-	3.4	-	-	8.9	29.1	21.9	-
2-Ohishima-Zaira xGiza429	Pedigree	3.83	3.81	57.52	128.90	3.69	22.95	74.41	54.90	75.12
	Pod	4.16	3.71	58.24	127.67	3.56	19.98	54.58	45.21	84.44
	Bulk	4.20	4.07	41.89	143.67	2.42	19.09	52.78	41.84	73.64
F test		ns	ns	**	**	**	ns	**	**	*
LSD_{0.05}		-	-	-	-	-	-	-	-	8.8
LSD_{0.01}		-	-	10.2	15.1	1.1	-	14.0	7.2	-
3-Giza40 xGiza429	Pedigree	4.39	4.33	59.33	139.44	3.43	25.53	78.65	55.26	71.08
	Pod	4.82	4.22	50.89	124.22	3.67	20.89	52.47	40.44	78.01
	Bulk	4.92	4.56	48.56	149.22	3.07	15.91	47.89	40.48	84.36
F test		**	*	ns	**	ns	**	**	**	**
LSD_{0.05}		-	0.3	-	-	-	-	-	-	-
LSD_{0.01}		0.5	-	-	19.10	-	7.4	16.70	16.7	10.9
4-Ohishima-Zaira x Foul Sbailabiade	Pedigree	4.03	3.44	62.36	136.94	3.47	21.02	62.08	50.88	83.31
	Pod	4.04	3.04	70.00	129.44	4.00	18.33	50.29	46.75	95.54
	Bulk	3.87	3.20	68.43	139.38	3.51	16.33	46.13	45.42	100.57
F test		ns	ns	ns	**	**	**	**	*	**
LSD_{0.05}		-	-	-	-	-	-	-	5.9	-
LSD_{0.01}		-	-	-	3.4	1.1	4.3	10.0	-	14.7

3- F₅-generation: -

3-a-Cross 1 (Triple white x Giza 429):

The data shown in Table (5) revealed that, highly significant differences between the mean performance of the three breeding methods were found for flowering date (favorable), plant height, 100-seed weight; only significant for rust disease reaction and not significant for chocolate spot disease reaction; number of branches per plant; number of pods and seeds per plant; and seed yield per plant. The pedigree selection method had the significantly lowest values for rust disease reaction and flowering date, with no significant difference between pedigree and bulk methods for rust disease reaction. The pedigree method had the significantly highest value for 100-seed weight, with no significant difference from single-pod descent in this concern. For number of branches, single pod descent and bulk methods had the highest values, without significant differences between both methods.

3-b-Cross 2 (Ohishima-Zaira x Giza 429):

The differences between mean performance of the three breeding methods were highly significant for flowering date, No. of branches/plant and No. of pods/plant; only significant for No of seeds/plant, seed yield/plant and 100-seed weight and not significant for chocolate and rust disease reactions and plant height.

The data listed in Table (5) shown that, pedigree method significantly surpassed the other two breeding methods with respect to all significant traits, with no significant differ than single pod descent with respect to No. of branches/plant, No. of pods and seeds/plant and seed yield /plant.

Table 5. Comparison between mean performance of pedigree method, single pod and bulk method for the studied traits in the F5-generation of faba bean cross-populations

Crosses	Methods	Chocolate Spot disease reaction	Rust disease reaction	Flowering date	Plant height (cm)	No. of branches / plant	No. of pods/ plant	No. of Seeds / plant	Seed yield / plant	100-Seed weight
1-Triple white x Giza429	Pedigree	3.56	1.96	43.56	98.13	4.06	24.77	74.88	65.50	88.51
	Pod	3.48	2.25	45.77	122.17	4.39	22.03	63.16	50.55	83.93
	Bulk	3.68	2.15	46.00	124.80	3.68	21.88	67.44	49.02	73.67
F test		ns	*	**	**	ns	ns	ns	ns	**
LSD_{0.05}		-	0.22	-	-	-	-	-	-	-
LSD_{0.01}		-	-	0.3	26.7	-	-	-	-	5.4
2-Ohishima-Zaira x Giza429	Pedigree	3.70	2.37	52.97	111.55	4.27	22.16	67.32	59.69	88.83
	Pod	3.45	2.38	53.80	111.60	4.13	25.12	73.36	59.34	79.32
	Bulk	3.41	2.41	53.51	110.60	3.07	20.80	59.57	45.28	81.36
F test		ns	ns	**	ns	**	*	*	*	*
LSD_{0.05}		-	-	-	-	-	-	11.2	12.2	6.7
LSD_{0.01}		-	-	0.4	-	0.7	4.1	-	-	-
3-Giza40 x Giza429	Pedigree	4.56	2.58	51.45	120.77	4.34	26.33	75.26	63.81	85.57
	Pod	4.57	2.56	48.00	115.20	3.76	21.01	54.43	42.60	78.26
	Bulk	4.51	2.39	47.33	123.53	3.15	23.59	71.60	52.95	72.98
F test		ns	ns	**	**	*	**	**	**	**
LSD_{0.05}		-	-	-	-	0.8	-	-	-	-
LSD_{0.01}		-	-	1.2	6.1	-	4.5	11.7	9.0	4.5
4-Ohishima-Zaira x Foul Sbailabiade	Pedigree	3.47	2.43	60.23	116.38	4.20	19.70	57.32	52.09	94.32
	Pod	3.49	2.24	64.13	121.33	4.21	26.11	66.92	67.60	91.88
	Bulk	2.92	2.38	63.83	113.43	3.97	23.29	65.67	65.74	103.04
F test		*	**	**	ns	ns	ns	ns	*	**
LSD_{0.05}		0.4	-	-	-	-	-	-	14.1	-
LSD_{0.01}		-	0.1	0.5	-	-	-	-	-	26.7

3-c-Cross 3 (Giza 40x Giza 429):

The data shown in Table (5) revealed that, highly significant differences were found between mean performance of the three breeding methods for flowering data, plant height, No. of pods and seeds/plant, seed yield/plant and 100-seed weight; significant for No. of branches/plant and not significant for chocolate spot and rust disease reactions. Pedigree selection method had a superiority over the two breeding methods used for plant height, No. of branches/plant, No. of pods and seeds/plant, seed yield /plant and 100-seed weight, with no significant differ than bulk method for flowering data, plant height, No. of pods/plant and No. of seeds/plant.

3-d-Cross 4 (Ohishima-Zaira x Foul Sbailabiade):

The data listed in Table (5) illustrated that, highly significant differences between mean performance of the three breeding methods for rust disease reaction, flowering date and 100-seed weight; significant for chocolate spot disease reaction and seed yield/plant and not significant for plant height, No. of branches/plant and No. of pods and seeds/plant. Bulk method was surpassed the other breeding method for chocolate spot, seed yield /plant and 100-seed weight; with no significant differences between bulk and single pod descent methods for seed yield/plant. Pedigree method for flowering date and single pod descent for rust disease reaction and seed yield/plant.

Narrow-sense heritability and genetic advance:-

Narrow-sense heritability is calculated by regression of the mean value of offspring on their parental value for each two subsequent generations, i.e., regression of F_{n+1} on F_n , where n is the number of generations: Firstly, it could be considered that the values of narrow-sense heritability higher than 60% are high ones, those between 30 and 60% are considered moderate ones, and those lower than 30% are considered low values. Narrow-sense heritability is the proportion of additive variance to phenotypic variance as a percentage. But why additive variance? That is because additive variance is expressed by the additive genes that are inherited from the parent to its progeny, while non-additive genes (dominance, additive x dominance, and dominance x dominance) are not inherited. So, narrow-sense heritability is the most important measurement of heritability. The expected genetic advance calculated by using narrow-sense heritability is a real and commonly used method in pedigree breeding. While broad-sense heritability is calculated from the expected mean square in the analysis of variance table. Broad-sense heritability is the proportion of genetic variance

(additive and non-additive) to phenotypic variance as a percentage. So, it logic that narrow-sense heritability values would be less than the corresponding values of broad-sense heritability, and the latest is involved in the calculation of the expected genetic advance in both bulk and single-pod descent breeding methods; therefore, it is not fair to compare between pedigree methods and both bulk and single-pod descent methods on the basis of genetic advance.

The values of narrow-sense heritability listed in Table (6) were considered moderate in the four crosses of the three generations i.e., F₃, F₄ and F₅ones for chocolate spot disease reaction.

For rust disease reaction, the values of narrow-sense heritability are consider moderate ones in all crosses of F₃-generation, crosses 1,3 and 4 of the F₄- generation and in the cross 1 of the F₅-generation. For flowering date the values were considered moderate ones in the four crosses of F₃ and F₄- generations and in the cross1 of F₅-generation. For plant height, the values of narrow-sense heritability were considered moderate ones in the four crosses of F₃ and F₄-generations and in the cross1 and cross 4 of F₅-generation. The values of narrow-sense heritability were considered moderate ones in all crosses of F₄- generation, in the crosses 1,3 and 4 of the F₃-generation and in the crosses 3 and 4 of the F₅-generation for No .of branches /plant . For No. of pods and seeds /plant, the values of narrow-sense heritability were considered moderate ones in the crosses 1,3 and 4 of the F₃ and F₄-generation and in the cross 3 of F₅-generation. For seed yield /plant, the values of narrow-sense heritability were considered moderate ones in all crosses of F₄-generation, in the crosses 1, 3 and 4 of the F₃-generation and in the cross3 of the F₅-generation. For 100-seed weight, moderate values of narrow-sense heritability were detected in the crosses 1, 3 and 4 of the three generations under test and in the cross 2 of F₄-generation. The other estimates of narrow-sense heritability shown in Table (6) were considered low values.

Table 6. Narrow-sense heritability (h²%), expected (Ga) and predicted (Ga%) genetic advance in 4 faba bean cross-progenies for pedigree method.

Crosses	Genetic parameters	Chocolate spot disease reaction			Rust disease reaction			Flowering date (day)		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	h ² %	38.21	34.35	37.22	39.27	35.83	35.99	66.00	52.30	35.20
	Ga	0.31	0.30	0.27	0.52	0.47	0.37	5.00	5.33	2.82
	Ga %	8.51	7.07	7.33	17.50	12.03	16.49	9.68	9.69	6.09
2-Ohishima-Zaira x Giza429	h ² %	34.73	44.86	34.26	42.87	27.37	18.96	52.84	51.93	7.61
	Ga	0.30	0.44	0.28	0.62	0.26	0.08	5.31	6.76	0.16
	GA %	8.01	11.34	7.53	20.26	6.66	3.52	9.86	11.70	0.30
3-Giza40 x Giza429	h ² %	57.13	56.58	42.11	46.79	56.44	29.13	41.97	47.29	25.95
	Ga	0.42	0.57	0.26	1.03	0.86	0.19	2.44	11.76	2.17
	Ga %	12.24	14.57	5.83	39.46	26.81	7.15	4.76	21.46	4.06
4-Ohishima-Zaira x Foul Sbailabiade	h ² %	38.11	51.83	36.59	30.83	45.83	26.44	36.52	40.19	16.56
	Ga	0.22	0.42	0.60	0.15	0.87	0.15	2.99	7.44	0.65
	Ga %	6.61	11.20	17.28	5.76	27.87	6.25	5.36	12.61	1.08

The data in the Table (6) illustrated that, narrow-sense heritability estimates were moderate in the cross2 (Ohishima-Zaira x Giza429) for chocolate spot disease reaction in the three generations, rust disease reaction in the F₃, flowering date in the F₃ and F₄-generations, plant height in the F₃ and F₄-generations, No. of branches/plant in the F₄-generation, seed yield/plant in the F₄-generation and 100-seed weight in the F₄-generation. While, narrow-sense heritability estimates were low in the cross2for rust disease reaction in the F₄ and F₅-generations, flowering date in the F₅-generation, plant height in the F₅-generation, No. of branches/plant in the F₃-generation.

From the data presented in Table (6) it could be observed that, low estimates of narrow-sense heritability were detected in the F₅-generation for most studied traits, except that for100-seed weight. This may be attributed to the high genetic variability among pure lines in this generation, where each pure line represented a new genotype with high homozygosity, therefore, the phenotypic variance would be raised in each cross-progeny, which cause low narrow-sense heritability estimates in this generation.

Expected and predicted genetic gain from selecting of higher 5% plants in the populations were shown in Table (6). Expected genetic advance was expressed as the unit of the trait, while predicted genetic advance was expressed as the percentage of the mean of the generation used.

Table 6. Cont.

Crosses	Genetic parameter	Plant height(cm)			No. of branches/plant			No. of pods/plant		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	h ² %	37.24	49.46	37.33	40.47	40.18	26.91	38.26	42.95	20.69
	Ga	5.51	10.63	6.63	0.83	0.97	0.39	6.28	10.36	2.34
	Ga %	4.50	7.98	5.95	21.61	28.08	9.61	16.14	31.76	9.06
2-Ohishima-Zaira x Giza429	h ² %	46.94	31.40	9.19	17.16	31.61	23.48	29.07	23.03	15.96
	Ga	7.25	3.75	0.31	0.25	0.45	0.35	2.99	1.99	1.01
	GA %	5.44	2.96	0.28	7.47	11.46	8.27	10.20	8.03	4.46
3-Giza40 x Giza429	h ² %	56.06	43.94	28.93	34.24	35.33	36.77	39.41	33.98	39.33
	Ga	9.24	8.35	3.32	0.43	0.62	0.45	4.53	5.34	2.47
	Ga %	7.10	6.27	2.72	13.23	18.22	10.36	14.56	17.38	9.33
4-Ohishima-Zaira x Foul Sbailabiade	h ² %	50.71	38.70	43.88	50.00	41.41	48.05	48.08	46.67	24.00
	Ga	7.88	5.39	5.31	1.04	1.08	0.90	6.40	10.28	2.27
	Ga %	5.75	3.85	4.57	21.63	25.17	20.25	18.57	34.65	11.22

Table 6. Cont.

Crosses	Genetic parameter	No. of seeds/plant			Seed yield/plant (g)			100-Seed weight (g)		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	h ² %	46.49	45.00	22.05	57.21	43.65	19.76	34.40	34.44	49.63
	Ga	21.94	29.01	7.06	21.85	23.31	4.70	4.93	4.96	7.99
	Ga %	22.29	30.15	9.11	31.52	34.39	7.47	6.92	7.08	9.60
2-Ohishima-Zaira x Giza429	h ² %	22.89	28.01	17.10	18.77	32.95	19.90	26.34	59.04	10.27
	Ga	7.34	7.30	3.38	4.64	8.00	3.77	2.79	10.75	0.77
	GA %	9.35	9.15	4.93	7.99	13.53	6.24	3.76	14.41	0.87
3-Giza40 x Giza429	h ² %	37.46	36.67	40.52	36.45	38.65	49.11	49.99	40.07	53.94
	Ga	12.85	19.71	7.77	10.09	16.10	8.96	3.87	5.80	6.39
	Ga %	14.80	21.30	10.52	14.93	22.85	14.42	4.90	7.55	7.53
4-Ohishima-Zaira x Foul Sbailabiade	h ² %	53.28	44.99	26.47	45.64	42.25	26.74	54.37	33.19	32.27
	Ga	17.78	26.34	6.84	13.72	17.99	5.13	11.55	6.91	16.46
	Ga %	20.01	31.59	11.87	17.58	25.94	9.76	12.80	8.02	17.41

The data pointed out that, both expected and predicted genetic advance were correlated with narrow-sense heritability values, where moderate to low values were observed. Chocolate spot disease reaction had low predicted genetic advance in the four crosses of the three generations, except for cross3 in F₃ and F₄ generations, where the values were moderate. Flowering date showed low predicted genetic advance in all crosses of all generations, except for cross 3 in F₄-generation, where the value was moderate. Plant height expressed low values of predicted genetic advance in all crosses of all generations. No. of branches/plant had moderate values of predicted genetic advance, except for cross1 in the F₅-generation and cross 2 in all generations, where the values were low. No. of pods/plant exposed moderate values of predicted genetic advance, except for all crosses in F₅-generation, where the values were low, No. of seeds/plant showed moderate values of predicted genetic advance, except in the cross2 of all generations, and the crosses 1, 3 and 4 in the F₅-generation, where the values were low. Seed yield/plant had moderate values of predicted genetic advance in cross1, cross3and cross 4 of F₃ and F₄-generations, while in the cross 2 of all generations and crosses 1 and 4 of F₅-generation, the values were low. For 100-seed weight, the values of predicted genetic advance were low in all crosses of all generations, except for cross 2 of F₄-generation and the cross 4 of F₅-generation where the values tended to be moderate.

The data presented in Table (7) showed the comparison between bulk and single pod descent breeding methods in F₃, F₄ and F₅-generations over the four cross-progenies with respect to expected and predicted genetic advance for the studied traits of faba bean. Comparable predicted genetic advance was observed for chocolate spot disease reaction in F₃ and F₄-generations, while the bulk method exceeded that for single pod descent method in the F₅-generation by 11.21%. For rust disease reaction, comparable predicted genetic advance was detected in the F₃and F₄- generations, while, in the F₅- generation, bulk method exceeded that for single pod descent method by 6.25%. Comparable predicted genetic advance was noticed in the three generations for flowering date. For plant height, the data revealed that, nearly equal predicted genetic advance was observed in the F₃ and F₅-generations with respect to single pod descent, while single pod descent had superiority over bulk method by 3.38% in the F₄-generation.

Table 7. Expected (Ga) and predicted (Ga %) genetic advance of single pod descent and bulk methods in the F₃, F₄ and F₅ generations over four cross-progenies for the studied traits.

Traits	Generations		F ₃ generation	F ₄ generation		F ₅ generation	
	Methods	Bulk	(SPD)	Bulk	(SPD)	Bulk	(SPD)
Chocolate spot disease reaction	Ga	0.89	0.94	0.82	0.90	1.20	0.87
	Ga%	20.55	21.92	19.41	20.60	34.83	23.62
Rust diseases reaction	Ga	0.96	0.88	0.90	0.82	1.02	0.89
	Ga%	22.60	24.87	22.23	21.46	44.08	37.83
Flowering date (day)	Ga	6.21	7.52	5.92	7.29	4.86	4.37
	Ga%	12.32	12.85	11.64	12.21	8.96	8.09
Plant height (cm)	Ga	13.23	13.56	10.73	14.09	10.04	9.37
	Ga%	9.42	10.58	7.58	10.96	8.59	8.22
No. of branches / plant	Ga	1.54	1.46	1.23	1.79	1.84	1.90
	Ga%	48.06	37.11	39.27	45.70	52.39	45.98
No. of Pods/plant	Ga	12.13	10.16	9.77	7.43	11.14	10.34
	Ga%	45.23	39.86	41.57	35.94	49.53	43.78
No. of Seeds/plant	Ga	29.26	24.72	22.19	19.29	31.17	25.07
	Ga%	40.10	34.01	36.91	33.43	47.18	38.87
Seed yield/plant (gm)	Ga	19.73	17.09	18.06	16.27	23.60	19.75
	Ga%	35.03	31.53	37.07	35.57	42.77	38.35
100-Seed weight(gm)	Ga	12.86	9.20	9.62	10.28	22.33	13.39
	Ga%	16.75	12.11	11.93	12.67	24.45	16.28

Bulk method exceeded that for single pod descent method in the F₃ and F₅-generations by 10.92% and 6.41%, respectively with respect to predicted genetic advance for No. of branches/plant, while single pod descent exceeded that for bulk method by 6.43% for the trait in view in the F₄-generation. Bulk method had a superiority over single pod descent in the F₃, F₄ and F₅-generations by 5.37%, 5.63% and 5.75%, respectively for No. of pods/plant. For No. of seeds/plant, the results exposed superiority of bulk method over single pod descent method with respect to predicted genetic advance by 6.06%, 3.48 and 8.31% in the F₃, F₄ and F₅-generations, respectively. Bulk method exceeded that for single pod descent method by 4.42%, predicted genetic advance in the F₅-generation, for seed yield /plant, while comparable values were detected for the trait in question in the F₃ and F₄-generations. Bulk method exceeded that for single pod descent method in the F₃ and F₅-generations by 4.56% and 8.17% predicted genetic advance values, respectively for 100-seed weight, while in the F₄-generation, the values were nearly equal.

Heritability in broad-sense:-

1-Bulk method:

The data shown in Table (8) exposed heritability in broad-sense in four faba bean cross-progenies of the three generations i.e., F₃, F₄ and F₅, for bulk method. The data could be handled suggesting that, the broad-sense heritability values higher than 80% is considered high values, from 80% to 40% is moderate values and less than 40% is low values.

According to this assumption, the data pointed out that, chocolate spot disease reaction had high values of broad-sense heritability in the four faba bean cross-progenies of the three generations i.e., F₃, F₄ and F₅ except in cross 2 of F₄-generation; rust disease reaction had high values of broad-sense heritability in the crosses 1, 3 and 4 of the three generations, while in the cross 2 the values were moderate in the three generations. For flowering date, high values of broad-sense heritability were detected in the cross 1 of F₃ and F₄-generations and in the cross 3 of F₃-generation, while moderate values were found in the rest of cross-progenies of the other generations.

Generally, following bulk method moderate values of broad-sense heritability were observed in the four cross-progenies of the three generations for plant height, No. of branches/plant, No. of pods/plant, No. of seeds/plant, seed yield/plant and 100 seed weight.

2-Single pod descent method:

The data listed in Table (9) revealed that, high values of broad-sense heritability were found for chocolate spot disease reaction in the cross 1 of F₃ and F₄-generations; in the cross 1 of F₃-generation for flowering date; in the cross 3 of F₃ and F₅-generations and in the cross 4 of the three generations for chocolate spot disease

reaction; in the cross3 of the three generations and in the cross 4of F₄and F₅-generations for rust disease reaction. However, the other broad-sense heritability values in the four cross-progenies of the three generations studied were considered as moderate values for the other studied traits.

Genetic advance:

1-Bulk method:

The data presented In the Table (8) revealed that, the predicted genetic advance considered high values for chocolate spot disease reaction in the cross 1 of the three generations; No. of branches/plant in the cross 1 of the three generations and in the cross 3 of F₃ and F₅-generations;No.of pods/plant in the cross 1 of the three generations, cross 2 in F₃ and F₄-generations and cross 4 in F₃ and F₅ generations; No. of seeds/plant in the cross 4 of F₃ and F₅ –generations; seed yield/plant in the cross 1 of F₃ and F₅-generations and in cross 4of F₄and F₅ –generations. The values of predicted genetic advance were considered moderate ones for chocolate spot disease reaction in the crosses1 and 2 of the three generations; rust disease reaction in the crosses 1and 2 of the three generations, in the cross3 of F₅-generatiion and in the cross 4 of the F₄ and F₅-generations ; No. of branches/plant in the crosses 2 and 3 of F₄-generation and in the cross 4 of the three generations; No. of pods/plant in the cross 2 of F₅-generation, in the cross 3 of the three generations and in the cross 4 of F₄-generation; No. of seeds/plant in the crosses 1, 2 and 3 of the three generations and in the cross 4 of F₄-generation;seed yield/plant in the crosses 1,2 and 3 of the three generations and in the cross 4 of the F₃-generation.

The predicted genetic advance values were considered low ones for chocolate spot disease reaction in the crosses 3 and 4 of the three generations; rust disease reaction in the cross 3 of F₃ and F₄-generations and in the cross 4 of F₃-generation; flowering date in all crosses of all generations; plant height in all crosses of all generations and 100-seed weight in all crosses of all generations.

Table 8. Broad-sense heritability (H), expected (Ga) and predicted (Ga%) genetic advance in 4 faba bean cross-progenies for Bulk method.

Crosses	Genetic parameter	Chocolate spot disease reaction			Rust disease reaction			Flowering date (day)		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	80.13	84.15	86.54	83.07	87.10	79.26	84.92	83.04	69.23
	Ga	1.29	0.88	1.42	1.27	0.88	1.28	5.53	5.10	4.29
	Ga %	30.04	19.90	38.62	29.75	20.21	29.56	12.93	12.02	9.32
2-Ohishima-Zaira x Giza429	H%	87.38	77.06	83.70	78.06	71.53	72.69	73.49	75.32	67.77
	Ga	1.03	1.17	0.87	1.13	0.97	0.75	3.89	3.84	3.22
	Ga %	24.77	27.77	25.37	28.05	23.90	31.16	9.20	9.16	6.02
3-Giza40 x Giza429	H%	88.89	89.01	81.66	81.69	84.15	80.05	87.88	78.28	63.64
	Ga	0.41	0.49	0.85	0.80	0.88	0.81	7.75	6.39	3.32
	Ga %	8.28	10.05	18.83	17.04	19.41	34.00	16.19	13.17	7.02
4-Ohishima-Zaira x Foul Sbailabiade	H%	88.71	82.83	96.01	84.09	83.12	85.38	68.89	70.19	70.11
	Ga	0.81	0.75	1.65	0.65	0.86	1.23	7.69	8.36	8.61
	Ga %	19.10	19.92	16.49	15.58	25.38	31.60	10.97	12.21	13.49

Table 8. Cont.

Crosses	Genetic parameter	Plant height(cm)			No. of branches/plant			No. of pods/plant		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	75.00	71.63	68.47	67.40	63.09	56.29	69.76	64.07	61.45
	Ga	15.66	13.21	9.01	2.24	1.85	1.81	20.62	18.92	13.87
	Ga %	11.69	9.74	7.22	68.53	56.62	49.19	60.85	53.02	63.39
2-Ohishima-Zaira x Giza429	H%	78.16	68.60	61.14	64.21	44.19	66.13	65.16	61.36	56.15
	Ga	11.69	9.77	11.26	1.01	0.64	1.53	8.26	8.47	6.58
	Ga %	8.05	6.80	10.18	40.15	26.36	50.01	44.10	44.37	31.62
3-Giza40 x Giza429	H%	60.66	62.95	65.06	63.92	60.45	60.10	59.97	61.74	61.08
	Ga	10.86	10.67	8.34	1.39	1.24	1.43	6.84	5.12	8.15
	Ga %	7.25	7.19	6.75	46.74	38.67	45.30	29.06	30.34	34.57
4-Ohishima-Zaira x Foul Sbailabiade	H%	62.01	60.37	65.06	76.18	51.52	73.98	66.42	59.71	60.90
	Ga	14.71	9.26	11.56	1.52	1.19	2.58	12.78	6.58	15.96
	Ga %	10.67	6.61	10.19	36.81	35.42	35.06	46.91	38.57	68.53

Table 8. Cont.

Crosses	Genetic parameters	No. of seeds/plant			Seed yield/plant (g)			100-Seed weight (g)		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	63.59	61.16	62.38	73.75	60.11	60.01	60.90	59.86	59.02
	Ga	34.52	32.53	33.20	27.80	23.51	20.92	11.16	8.11	12.19
	Ga %	38.51	32.70	49.22	44.11	32.84	42.67	15.87	11.73	16.54
2-Ohishima-Zaira x Giza429	H%	58.17	61.56	60.23	64.76	61.33	54.90	60.84	58.70	57.98
	Ga	23.18	21.74	21.02	13.46	16.38	16.34	14.47	11.90	13.83
	Ga %	38.93	41.19	35.28	31.48	39.15	36.08	18.46	16.16	17.00
3-Giza40 x Giza429	H%	60.31	61.77	60.63	60.45	59.27	58.86	61.01	65.10	59.36
	Ga	21.72	16.54	24.75	13.90	14.67	14.69	15.07	6.76	7.06
	Ga %	32.60	33.99	34.57	30.55	35.58	27.75	21.39	7.98	9.68
4-Ohishima-Zaira x Foul Sbailabiade	H%	65.91	63.34	65.95	61.81	59.16	60.13	59.90	50.03	67.38
	Ga	37.61	17.95	45.73	23.74	17.68	42.45	10.72	11.72	56.23
	Ga %	50.38	39.78	69.64	34.00	40.72	44.57	11.29	11.86	14.57

VI-b-2- Single pod descent method:

The data listed in Table (9) pointed out that, the values of predicted genetic advance were considered high ones for rust disease reaction in the cross 1 of F₅-generation; No. of branches/plant in the cross 1 of F₄ and F₅-generations, in cross 2 of all generations, in the cross 3 of F₄ and F₅-generations and in the cross 4 of F₃ and F₄-generations; No. of pods/plant in the cross 1 of F₅-generation, in the cross 2 of F₅- generations, in the cross 3 of F₃-generation and in the cross 4 of F₄ and F₅- generations; No. of seeds/plant in the cross 1 of F₄ and F₅-generations; seed yield/plant in the cross 1 of F₄ and F₅- generations and in the cross 2 of the F₅-generation.

Table 9. Broad-sense heritability (H%), expected (Ga) and predicted (Ga%) genetic advance in 4 faba bean cross- progenies for single pod-descent method.

Crosses	Genetic parameters	Chocolate spot disease reaction			Rust disease reaction			Flowering date (day)		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	83.33	83.73	73.56	76.83	58.67	77.74	81.84	70.51	63.15
	Ga	0.85	0.89	0.97	0.81	0.59	1.18	7.84	8.90	3.65
	Ga %	20.45	19.82	27.73	24.55	13.07	52.55	14.11	14.83	7.98
2-Ohishima-Zaira x Giza429	H%	73.62	77.24	73.81	79.23	70.35	70.59	74.72	69.72	71.47
	Ga	1.09	0.99	0.77	0.74	0.67	0.71	8.08	6.36	3.20
	Ga %	26.25	23.93	22.31	19.86	18.08	30.00	13.90	10.93	5.95
3-Giza40 x Giza429	H%	85.71	59.57	84.43	83.73	87.93	84.35	69.43	66.56	68.24
	Ga	0.70	0.47	0.88	0.89	0.78	0.88	5.33	4.89	3.49
	Ga %	14.44	9.83	19.14	19.82	18.41	34.31	10.47	9.73	7.27
4-Ohishima-Zaira x Foul Sbailabiade	H%	81.25	85.13	84.19	76.64	83.83	86.18	70.45	68.08	75.69
	Ga	1.13	1.24	0.88	1.10	1.26	0.77	8.84	9.01	7.15
	Ga %	26.52	28.81	25.31	35.25	36.27	34.44	12.93	13.36	11.15

The predicted genetic advance values were considered moderate ones for chocolate spot disease reaction in the crosses 1,2 and 4 of all generations under test ; rust disease reaction in the cross1 of F₃-generation, in the crosses 2 and 3 of F₅-generation and in cross4 of the three generations; No. of branches/plant in the crosses 1 and3 of F₃-generation and in the cross 4 of F₅-generation; No. of pods/plant in the crosses 1 and 2 of F₃ and F₄-generations, in the cross 3 of F₄ and F₅- generations and in the cross 4 of F₃-generation; No. of seeds/plant in the crosses 2,3 and 4 of the three generations and in the cross 1 of F₃ and F₄-generations; seed yield/plant in the cross 1 of F₃- generation, in the cross 2 of F₃ and F₄-generations, in the cross3 of the three generations and in the cross 4 of F₄ and F₅- generations.

The predicted genetic advance values were considered low for chocolate spot disease reaction in the cross3 of all generations; rust disease reaction in the cross 1 of F₄-generation and in the crosses 2 and 3 of F₃ and F₄-generations; flowering date in all crosses of all studied generations; plant height in all crosses of all generations; seed yield /plant in cross 4 of F₃-generation and 100-seed weight in all crosses of all generations.

Table 9. Cont.

Crosses	Genetic parameter	Plant height(cm)			No. of branches/plant			No. of pods/plant		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	75.70	73.99	60.94	62.22	62.07	60.73	58.81	60.02	64.25
	Ga	11.99	14.20	10.74	1.18	2.03	2.17	6.72	8.78	11.65
	Ga %	9.05	10.86	8.79	30.99	54.28	49.55	27.07	34.95	52.91
2-Ohishima-Zaira x Giza429	H%	69.03	65.01	69.72	64.93	58.38	59.90	64.04	60.57	60.14
	Ga	10.96	11.10	6.40	1.57	1.50	2.07	8.93	6.22	10.61
	Ga %	8.67	8.70	5.74	43.51	42.15	50.00	39.73	31.14	42.26
3-Giza40 x Giza429	H%	66.52	69.54	77.13	61.39	59.41	66.27	63.96	65.16	61.79
	Ga	12.83	13.95	9.11	1.22	1.66	1.71	15.11	6.41	7.29
	Ga %	10.22	11.02	7.91	29.72	42.43	45.51	53.28	30.65	34.70
4-Ohishima-Zaira x Foul Sbailabiade	H%	73.58	74.76	69.30	66.13	67.21	60.01	62.32	63.01	67.36
	Ga	18.45	17.11	12.66	1.87	1.97	1.64	9.87	8.31	11.81
	Ga %	14.36	13.27	10.43	44.23	43.93	38.85	39.37	47.02	45.25

Table 9.

Crosses	Genetic parameter	No. of seeds/plant			Seed yield/plant			100-Seed weight		
		F ₃	F ₄	F ₅	F ₃	F ₄	F ₅	F ₃	F ₄	F ₅
1-Triple white x Giza429	H%	59.02	58.55	64.75	61.72	65.52	61.56	60.99	61.35	60.87
	Ga	27.91	26.61	28.90	16.00	20.91	22.36	7.38	9.68	10.89
	Ga %	39.10	35.48	45.75	34.72	40.61	45.62	10.80	14.33	12.98
2-Ohishima-Zaira x Giza429	H%	60.41	60.73	60.42	59.45	58.01	60.50	70.38	57.02	74.37
	Ga	20.55	17.34	27.55	17.12	11.29	23.81	10.13	5.13	19.10
	Ga %	31.09	31.78	37.55	34.12	24.98	52.57	13.06	6.08	24.08
3-Giza40 x Giza429	H%	57.96	55.68	63.59	55.14	53.55	57.21	60.84	65.61	65.21
	Ga	27.97	14.88	19.42	21.02	14.74	14.42	11.58	10.95	12.92
	Ga %	36.76	30.01	35.68	38.02	38.61	27.24	16.32	13.83	16.51
4-Ohishima-Zaira x Foul Sbailabiade	H%	63.89	60.77	60.40	59.60	56.06	56.09	62.13	58.69	57.07
	Ga	22.45	18.34	24.41	14.24	18.15	18.39	7.71	15.36	10.62
	Ga %	29.10	36.45	36.48	19.26	38.08	27.97	8.27	16.44	11.56

DISCUSSION:

1-Mean performance:

With respect to average overall crosses, the present study revealed that pedigree selection method was most efficient method in the three generations i.e., F₃, F₄ and F₅, where the shift in means in negative direction for chocolate spot and rust disease reactions and flowering date and positive direction for No. of branches/plant, plant height, No. of pods/plant, seeds/plant, seed yield /plant and 100-seed weight, were better achieved through pedigree method as compared to single pod descent or bulk method; Juang and Lu (1991) studied the effects of three breeding methods i.e., pedigree, bulk and single seed descent in two which applied from F₂ to F₅ generations of soybean crosses. They found the superior of the pedigree method than the other two methods. Satyawati *et al.* (2000) evaluated three cross-progenies of urdbean advanced through pedigree selection, bulk population and single pod descent methods. They stated that, the progenies developed through pedigree selection were superior over the other two methods. Arunachalam *et al.* (2002) reported in cowpea that, pedigree and single seed descent populations were equally efficient, but the bulk method turned out to be less efficient. El-Hosary and El-Badawy (2003) estimated the response of faba bean to different methods of plant breeding i.e., pedigree, bulk and single pod descent in two crosses of faba bean. They reported that, pedigree method produced more superior lines compared to the overall mean in the first and second cross, respectively. Ahmed *et al.* (2008) evaluated three cross-populations of faba bean for selection by mass selection, pedigree method and picking pod methods from F₂ to F₄-generations. Results indicated differences (P<0.01) among the three methods for most measured traits in the three crosses. The mean values for most traits in the three crosses were higher by pedigree selection method than by the other two methods, therefore, pedigree selection method was found to be the best method in faba bean breeding for higher yield compared to the other methods.

However, the superiority of pedigree selection method relative to single pod descent or bulk population, as the results of the present investigation pointed out, this was an expected result, because the

genetic analysis of the present materials in the F_1 - generation revealed that, the largest part of total genetic variability was due to additive and additive x additive types of gene action for most studied traits. Abou-Zaid *et al.* (2017), indicated that, selection procedure based on the accumulation of additive gene effects, would be very successful in improving these genetic materials. This may be due to the additive genes are the only part of genetic variance which inherited from the parents to its off-spring, but the dominant genes were not so do. Pedigree selection method, where the selection was done among and within families of early segregating generations would be more effective when additive genes played an important role in the inheritance of the traits in consideration. Whereas, the additive genes could express itself, meanwhile, each phenotype appearance is usually linked with genotypic constitution, which led to an effective selection in the early segregating generations.

2-Narrow-sense heritability and genetic advance:-

It could be observed that, there were some differences between narrow-sense heritability values measured by parent-offspring regressions for the same trait during F_3, F_4 and F_5 -generations. These differences may be accounted for by different variances of the trait in question in selected plant as parent and their mean of progeny rows as offspring due dissimilar unit used. Besides, the seasonal effects as it was necessary to grow parent and offspring in different seasons, differences in environmental factors within season were liable to affect the magnitude of regression coefficient in certain cases. Bartly and Weber (1952) and EL-Refaey (1992) found the same trend of results.

It could be observed also that, narrow-sense heritability values in the cross 3 (Giza 40 x Giza 429) were somewhat higher than that in the other cross-progenies i.e., cross 1 (Triple white x Giza429), cross2 (Ohishima-Zaira x Giza 429) and cross 4 (Ohishima-Zaira x Foul Sbailabiade), where the parents of the latest crosses were wide divergence. While for the cross3 where the close divergent between parents was noticed, as they belong to the equena type, which may. Increase the proportion of additive and additive x additive variance than non-additive ones, resulting the increase of narrow-sense heritability values in all generations for approximately all traits in consideration. El-Refaey (1992) studied faba bean cross-progenies in the F_5, F_6 and F_7 - generations using pedigree method. He indicated that, heritability in narrow-sense as estimated by parent-offspring regression was high for plant height; 100-seed weight and No. of branches/plant, indicating that selection for these traits would be effective. He found also that, narrow-sense heritability for seed yield/plant, No. of pods and seeds/plant in the F_5 and F_6 were lower than that for other traits, indicating that these traits were influenced by non-heritable factors. El-Refaey and Radi (1997) utilized pedigree method in F_3 and F_4 of six soybean cross-progenies. They showed that, plant height, 100-seed weight and No. of seeds/pod in F_4 -generation had relatively high narrow-sense heritability values (41-64%), while the other traits i.e., No of branches/plant, No. of pods and seeds/plant and seed yield/plant recorded low estimates. Also, Padi and Jeffrey (2008) found that, narrow-sense heritability estimates were low but different from zero for seed yield, while the estimate for seed size was large. Abo-Mostafa *et al.*, (2009) indicated that indirect and direct selection in the progeny of the two crosses would be fruitful due to high values of narrow-sense heritability and predicted genetic advance. Sarutayopht and Charassri (2010) estimated narrow-sense heritability (h^2) for yield and its components of yardlong bean through regression analysis of the F_4 -progenies on F_3 -parental plants. They found low estimates for pod yield per plant in both studied populations.

3-The comparison between bulk and single pod descent breeding methods:

In F_3, F_4 and F_5 -generations over the four cross-progenies with respect to expected and predicted genetic advance for the studied traits of faba bean. However, single pod descent is a modification of bulk populations which eliminate the effect of sampling error of bulk method. The superiority of bulk against single pod descent may be attributed to the natural selection done in bulk populations which discard the inferior and undesirable plant types especially in early segregating generations and delaying stringent artificial selection until later generations, while, single pod descent method is usually reduce a loss of genotypes during the segregating generations and natural selection has no effect (Jinks and Pooni, 1984). These results are in agreement with that proposed by Thomas *et al.* (1997). Where they, comparing between bulk and single pod descent. They reported that, progenies derived from bulk method had higher ranged for all characters. Satyawan *et al.* (2000) stated that, the variation was higher in the progenies developed through bulk population. Shalaby *et al.* (2001) recorded that, heritability estimates and expected genetic advance were higher in bulk method compared with single pod descent

4-Heritability in broad-sense, genetic advance and genetic advance as percentage:-

The results of broad-sense heritability and genetic advance following bulk and single pod descent methods of breeding in the four faba bean cross-progenies are in agreement with those reported by Chettsi *et al.* (2005) where they found that, plant height and seed yield per unit area exhibited high estimates of heritability, genetic advance and genetic advance as

percentage of mean along with appropriate broad –sense heritability values. The number of seeds/pod and 100-seed weight showed high heritability values but low genetic advance expected and predicted, indicating the presence of poor genetic variance in the materials. Dev Vert *et al.* (2005) found high heritability for all characters, except for pods/plant, where predicted genetic advance was higher for clusters/plant and lowest for days to maturity. Malik *et al.* (2006) recorded high heritability for 100-seed weight, No. of days to maturity, No. of days to 50% flowering, seed yield /plant and plant height. Goncalves-Vidigal *et al.* (2008) found that, the mean estimates of broad-sense heritability varied from 11.5% to 64.2%. Ahmed (2016) found high broad-sense heritability estimates for seed yield/plant and 100-seed weight in F₄-generation. Ahmed *et al.* (2018) found that, broad-sense heritability values ranged from 87.57% for plant height to 99.12% for seed yield/plant in the two segregating populations of faba bean.

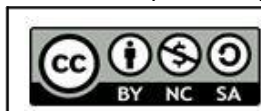
CONCLUSION

It could be concluded from the present study that, pedigree selection breeding method had a superiority over the two breeding methods i.e., bulk and single pod descent and considered as the Best breeding method in faba bean breeding for higher yield compared to the other methods.

REFERENCES

- Abo Mostafa, R.A.I., Sarhan, E.A.D., Atwa, Marwa A.M., & Ghareeb, Zeinab E. (2014). Evaluation of some breeding methods on faba bean improvement. *Journal of Plant Production, Mansoura University*, 5(7), 1225-1237.
- Abou-Zaid, G. G.A., Mostafa, S. M., El-Refaei, R.A., & Mohamed, A. M. (2017). Estimation of combining ability and heterosis via half diallel cross in faba bean (*Vicia faba* L.) for yield, its components and seed quality. *Journal of Plant Production, Mansoura University*, 8(11), 1191-1198.
- Ahmed, A. A., Bakheit, M. A., Sayed, M. A., Mahdy, Rasha E., & Abo Elwafa, Shahat S. (2018). Pedigree selection to improve the seed yield in two segregating populations of faba bean (*Vicia faba* L.). *Assiut Journal Agriculture Science*, 49 (2), 15-37.
- Ahmed, M. S. H. (2016). Studies on genetic variability, heritability & genetic advance in segregating generations of faba bean (*Vicia Faba*L.). *Middle East Journal Agriculture Research*, 5(1), 82–89.
- Ahmed, M. S. H., Abd-ElHaleem, S. H. M., Bakheit, M. A., & Mohamed, S. M. S. (2008). Comparison of three selection methods for yield and components of three faba bean (*Vicia faba* L.) crosses. *World Journal of Agricultural Sciences*, 4(5), 635-639.
- Arunachalam, A., Viswanatha, K.P., Chakravarthy, K.K., Manjunath, A., & Jayashree, M.K. (2002). Efficiency of breeding methods in early segregating generations in cowpea (*Vigna unguiculata* L.) *Walp. Indian Journal of Genetics*, 62(3), 228-231.
- Ashrei, A. A. M. (2006). Expected genetic advance in faba bean (*Vicia faba* L.) through different breeding methods (Doctoral dissertation, *Faculty of Agricultural, Al-Azhar University*).
- Bartly, B. G., & Weber, C. R. (1952). Heritable and non-heritable relationships and variability of agronomic characters in successive generations of soybean crosses. *Agronomy Journal*, 44, 487-493.
- Bernier, C. C., Hanounik, S. B., Hussein, M. M., & Mohamed, H. A. (1984). Field manual of common faba bean diseases in Nile Valley. Information Bulletin No. 3. ICARDA, P.O Box 5466, Aleppo, Syria.
- Chettsi, M., Mondal, S., & Nath, R. (2005). Studies on genetic variability in soybean, *Glycine max* (L.) Merrill in the mid hills of Darjeeling District. *Journal of Interacademia, India*, 9(2), 175-178.
- El-Hosary, A. A., & EL. M EL-Badawy, M. (2003). Evaluation of breeding methods and direct and indirect selection to increase seed yield in faba bean (*Vicia faba* L.) Proc. 10th Conference Agronomy Sues Canal University. *Faculty. environmental, Agricultural, Sciences, El-Arish, Egypt*, 820-837.
- El-Hosary, A. A., Omar, S. A., Naggar, H. M., Hassan, A. I., & Hassan, W. A. (2002). Diallel crosses for improving faba bean (*Vicia faba* L.) under rain-fed condition. 1-Yield and yield component. *Egyptian Journal of Desert Research*, 52(1), 37-53.
- El-Refaei, R. A. (1992). Heritability & advanced generation selection for yield in faba bean cross-progenies. *Egyptian Journal of Applied Sciences*, 7(3), 689-706.
- El-Refaei, R. A., & Radi, M. M. (1997). Selection for yield in early segregating generations of soybean crosses. *Journal of Agriculture Research Tanta University*, 23(2), 153-164.
- Gomez, K. A., & Gomez, A. A. (1984). Statistical procedures for Agriculture Research. Wiley International science publication. *John Wiley and Son*, increase. New York, USA.
- Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating population of Korean lespedeza. *Agronomy Journal*, 48, 286-272.
- Hallauer, A. R., & Miranda, J. B. (1981). Quantitative Genetics in Maize Breeding. Iowa state University Press, Ames.

- Ibrahim, H. M. (2015). Effectiveness of breeding methods for production of superior genotypes & maintenance of genetic variance in faba bean (*Vicia faba*, L.). *American Journal of Life Sciences*, 3(1), 11-16.
- Jinks, J. L., & Pooni, H. S. (1980). Comparing predication of mean performance & environmental sensitivity of recombinant inbred lines based upon F3 and triple test cross families. *Heredity*, 45(3), 305-312.
- Juang, J. R., & Lu, Y. C. (1991). A comparison of soybean breeding populations under different breeding methods. *Journal of Agriculture and Forestry*, 40(2), 1-9.
- Malik, M. F. A., Qureshi, A. S., Ashraf, M., & Abdul Ghafoor. (2006). Genetic variability of the main yield related characters in soybean. *International Journal of Agriculture and Biology*, 8(6), 815-819.
- Merril, P. A., Williams, J. C., Robinson, H. F., & Comstock, R. E. (1958). Estimates of genotypic & environmental variances & covariance in up- Land cotton & their implications in selection. *Agronomy Journal*, 50, 126-131.
- Miller, P. A., Williams, J. C., & Robinson, H. F. (1958). Estimates of genotypic & environmental variances & covariances in soybeans & their implications in selection. *Agronomy Journal*, 50, 126-131.
- Mohamed, H. A., & Bernier, C. C. (1987). Breeding for resistance to faba bean diseases in the Nile Valley Region. *FABIS Newsletter*, 15, 12-14.
- Padi, K. F., & Jeffrey, E. (2008). Effectiveness of early generation selection in cowpea for grain yield in a semi-arid West Africa. *Crop Science*, 48(2), 533-540.
- Satyawan, A., Ramdhari, R., & Tomer, Y. S. (2000). Comparison of selection methods in urd bean [*Vigna mungo* (L.) Hepper]. *International Journal of Tropical Agriculture*, 18(1), 75-80.
- Shalaby, F. H., Attia, S. M., Ibrahim, H. M., Saleeb, S. R., Al-Assily, Kh. A., & Mokhtar, S. A. (2001). Evaluation of some breeding methodology in faba bean (*Vicia faba* L.). *Journal of Agriculture Science Mansoura University*, 26(9), 5205-5215.
- Shebeski, L. H. (1967). Wheat And Breeding. In K. F. Nelson (Ed.), *Proc. Canadian Centennial Wheat Symp*, (pp. 255-272). Modern Press.
- Smith, J. D., & Kinman, L. (1965). The use of parent offspring regression as an estimate of heritability. *Crop Science*, 5, 595-596.
- Snedecor, G. W., & Cochran, W. G. (1980). *Statistical Methods* (6th ed.). *The Iowa State University Press*.
- Thomas, G., Solanki, I. S., & Singh, V. P. (1997). Evaluation of selection methods in lentil (*Lens culinaris Medik.*). *Crop Improvement*, 24(2), 239-243.
- Vart, D., Hooda, J. S., & Malik, B. P. S. (2005). Variability and association studies in soybean (*Glycine max* (L.) Merrill). *Crop Research Hisar*, 29(2), 247-251
- Winch, T. (2006). *Growing food: A guide to food production*. Springer.
- Wolf-Quintero, K., Inagaki, S., & Kim, H. Y. (1998). *Second language development in writing: Measures of fluency, accuracy, and complexity*. University of Hawaii Press.



Copyright: © 2023 by the authors. Licensee EJAR, EKB, Egypt. EJAR offers immediate open access to its material on the grounds that making research accessible freely to the public facilitates a more global knowledge exchange. Users can read, download, copy, distribute, print or share a link to the complete text of the application under [Creative Commons BY-NC-SA International License](https://creativecommons.org/licenses/by-nc-sa/4.0/).



مقارنه بين ثلاث طرق تربيه في الاجيال الانعزالية لهجن الفول البلدى

جيهان جلال عبدالغفار ابوزيد¹، رمضان على الرفاعي²، محمد محمد الطوخي² وزينب غريب³

¹قسم بحوث المحاصيل البقولية ، معهد المحاصيل الحقلية، مركز البحوث الزراعية ، مصر

²قسم المحاصيل، كلية الزراعة، جامعة طنطا، مصر

³المعمل المركزى للتصميم والتحليل الاحصائى ، مركز البحوث الزراعية ، مصر

بريد المؤلف المراسل: gehanqalalabou-zaid@gmail.com

أجريت هذه الدراسة خلال اربعة مواسم شتويه متتالية وهى 2018/2017، 19/18، 20/2019 و 21/2020 أقيمت التجارب الحقلية بمزرعة محطة البحوث الزراعيه بسخا- كفر الشيخ-جمهورية مصر العربيه لمقارنة ثلاث طرق تربية وهى: سجلات النسب، طريقة التجميع وطريقة القرن لكل نبات . وذلك لتحسين محصول البذور خلال الأجيال الانعزالية لأربعة هجن من الفول البلدى وهى:

1-Triple white x Giza429 2- Ohishima-Zaira x Giza429

3-Giza40 x Giza429 4-Ohishima-Zaira x Foul

تم تقدير درجة التورث بمعناها الضيق والتقدم الوراثى المتوقع والمنتبأ به وأوضح النتائج أن: الانتخاب بطريقة سجلات النسب كانت أفضل من الطريقتين الأخرين لمعظم الصفات المدروسة فى كل لهجن خلال الثلاث أجيال ماعدا الهجين الأول فى الجيل الرابع والهجين الرابع فى الجيل الخامس حيث كانت طريقة التجميع هى الأفضل. كانت قيم المكافئ الوراثى فى معناه المحدود متوسطة فى الأربع هجن خلال الثلاث أجيال ماعدا بعض الحالات القليلة. كانت قيم التقدم الوراثى المنتبأ به متوسطة لصفات عدد الفروع، عدد القرون، عدد البذور ومحصول البذور للنبات لكل الهجن فى الثلاث أجيال. بينما كانت القيم منخفضة لصفات مرض التبقع البنى، ميعاد التزهير، طول النبات ووزن ال100 بذرة فى كل الهجن خلال الثلاث أجيال الأنعزاليه .

لوحظ أن التقدم الوراثى المنتبأ به كان متقاربا لكلا من طريقتى التجميع وقرن لكل نبات لصفة مرض التبقع البنى فى الجيلين الثالث والرابع. بينما تفوقت طريقة التجميع فى الجيل الخامس . تفوقت طريقة التجميع على طريقة قرن لكل نبات فى الأجيال الثلاثة لصفات عدد القرون والبذور للنبات وفى الجيل الخامس لصفة محصول البذور. كان المكافئ الوراثى فى معناه الواسع متوسطا للطريقتين لصفات طول النبات، عدد الأفرع والقرون والبذور ومحصول البذور للنبات. أظهر التقدم الوراثى المنتبأ به قيما متوسطة فى معظم الحالات ماعدا صفة مرض التبقع البنى فى الهجينين الثالث والرابع لجميع الأجيال وصفة مرض الصدأ فى الهجين الثالث للجيل الرابع وصفة التزهير فى جميع الأجيال حيث أعتبرت القيم منخفضة.

الكلمات المفتاحية: طريقة سجلات النسب، التجميع ، قرن لكل نبات، درجة التورث بمعناها المحدود، التقدم الوراثى المنتبأ به، الأجيال الأنعزاليه المتقدمه .