GENERATION MEAN ANALYSIS FOR DISEASE RESISTANCE, YIELD AND ITS COMPONENTS IN THREE CROSSES OF FABA BEAN (*Vicia faba* L.)

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ABSTRACT

The present study was conducted during 2011/12, 2012/13 and 2013/14 seasons at Sakha Agricultural Research Station, ARC, Kafr El-Sheikh Governorate, Egypt . Quantitative analyses were done by crossing between four faba bean (*Vicia faba* L.) parental genotypes namely Giza 40, Giza 429, Sakha 1 and Triple white (TW) to produce three crosses namely; Giza 40 x Giza 429 (I), Sakha 1 x Giza 429 (II) and Giza 429 x TW (III). The parental genotypes could be arranged into two groups. The first group included Sakha 1 where it is considered as the most resistant group to foliage diseases i.e, chocolate spot *Botrytis fabae* (Sard) and rust (*Uromyces viciae-fabae,* Pers.) Schrot., and high yielding ability. The second group included Giza 40, Giza 429 and TW as susceptible genotypes with low yielding potentiality. Generation mean analysis was used to estimate genetic variance components in the crosses for nine traits. Heterosis over mid and better parent for all traits were highly significant except plant height in the first (Giza 40 x Giza 429) and second (Sakha 1 x Giza 429 crosses relative to mid parent, in the first cross (Giza 40 x Giza 429) relative to better parent, also the first cross had non-significant for no. of branches/plant and reaction to rust relative to mid parent and for no. of pods/plant relative to better parent. Also, the second (Sakha 1 x Giza 429) and third crosses (Giza 429 x TW) showed non-significance for chocolate spot relative to mid-parent and for 100 seed weight relative to better parent. The inbreeding depressing estimate was positive significant and/or highly significant for no. of branches/plant and no. of pods/plant, while it was negative significant for no. of seeds/pod in the three crosses. Heritability values in broad sense were generally higher than the corresponding values in narrow sense in all crosses for all traits. The additive genes seems to apply an improvement role of the inheritance of most of traits especially no. of pods/plant and no. of seeds/pod in the second cross; (Sakha 1 x Giza 429), where the differences between broad and narrow sense heritability were closes. The indirect selection in the progeny of this cross (Sakha 1 x Giza 429) and direct selection in the progeny of other crosses would be fruitful due to the high values of narrow sense heritability and the prediction genetic advance in these crosses. The additive type (a) was significant positive and negative in all of crosses for most traits except no. of branches/plant and no. of seeds/pod in the first (Giza 40 x Giza 429) and third (Giza 429 x TW) crosses. For dominance effect (d) it was higher in magnitude than that of additive type of gene effects. The additive x additive (aa) gene effect was highly significant in most crosses for all traits, except in a few cases. However, highly significant positive and negative epistatic gene action (ad) was observed in most crosses for most traits. The same trend was found with respect to dominance x dominance (dd) where positive and negative significant were observed for most crosses for most traits.

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the most important grain legumes in prone regions of North and East Africa, especially in Egypt. It play an important role in world agriculture, owing to its high protein content, ability to fix atmospheric nitrogen, capacity to grow and yield well on marginal lands (Al-Ghamdi, 2007).

One of the main reasons is the unreliable yields, mainly due to susceptibility of the crop to pests and diseases. A number of aerial fungi, together with soil-borne pathogens associated with foot and root rot complexes, nematodes, parasitic weeds and viruses may cause severe diseases in faba bean crop (Stoddard et al., 2010).

Faba bean (*Vicia faba* L.) crop has attracted the attention of most plant breeders to its yield because the importance of the crop for both human and animal nutrition. Foliage diseases chocolate spot *Botrytis fabae* (Sard) and rust *Uromyces viciae-fabae* (Pers.) Schrot., are the most destructive leaf disease of faba bean crop in the world. The losses as a result of foliage diseases were estimated to be more than 55% for susceptible cultivar Rebaya40 which was left for natural infection at Sakha (Mohamed *et al.*, 1980).

The plant breeder is interested in estimating gene effects in order to formulate the most advantageous breeding procedures for improving the genetic material (Abdelmula, et al., 1999 and Bond et al., 1994)..

Six population analysis suggested by Gamble (1962) considered as the most important analysis method which supply the breeder by the information about the nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for given characters.

The aim of the present investigation is to obtain useful information about gene action of foliage diseases, yield and its components as well as the extent of heterosis, inbreeding depression, heritability and genetic advance in the three faba bean crosses.

MATERIALS AND METHODS

Field experiments:

The present study was carried out during 2011/12, 2012/13 and 2013/14 seasons at Sakha Agricultural Research Station, ARC, Kafr El-Sheikh Governorate, Egypt. Four faba bean genotypes (Vicia faba L.) were chosen for this study on the basis of genetic diversity and origin (Table 1). These genotypes were Giza40, Giza 429, Sakha1 and Triple white (TW). In 2011/12 growing season, these genotypes were sown and crossed under screen house to produce the F1 seeds of each three crosses: Cross I (Giza 40 x Giza 429), Cross II (Sakha 1 x Giza 429) and Cross III (Giza 429 x TW). In 2012/13 growing season, some of F1 plants for each cross and their parents were backcrossed to corresponding its two parents to obtain the backcrosses BC1 (F1 x P1) and BC2 (F1 x P2) generations. Some of the F1 plants were selfed to produce F_2 seeds and the others kept as F1,s .

In 2013/14 growing season, the six population seeds, i.e. P1, P2, F1, F_2, BC1 and BC2 of the three crosses were sown in a randomized complete block design with three replications, under natural infection of early sowing dates in November 1st (early date). The plants were grown in ridges of two meters length and 60 cm width. Hills were spaced 20 cm apart with one seed per hill. Plots varied in size;25 rows for F_2, 15 rows for BC1 and BC2 and 3 rows for P1, P2 and F1. All cultural practices were done as usual with ordinary faba bean culture. Data were taken on plants of six populations in each cross for the following characters.

Table (1): The pedigree, diseases reaction and agronomic characters of four parental faba bean varieties used in the present study.

Parent	Genotype	Pedigree	Disease reaction	Earliness of maturity	Agronomic characters	
					Seed coat color	Seed size
P1	Giza40	Derived from Rebaya 40	*H.S	Medium	Light brown	Medium
P2	Giza429	Derived from Giza402	H.S.	Medium	Light brown	Medium
P3	Sakha1	Giza 716 x 620/283/85	R	Very early	Light brown	Medium
P4	Triple White (TW)	Introduced from Sudan	H.S	Early	White	Small

*HR = Highly resistant , R = resistant, MR = moderately resistant, S = susceptible, H.S. = Highly susceptible

Plant height, no. of branches/plant, no. of pods/plant, no. of seeds/plant, seed yield/plant (g), no. of seeds/pod, 100- seed weight, (chocolate spot and rust severity) under the natural infection were the characters registred. The resistance to foliage diseases were determined as in Table (2) with the adjustment of grading system from 0 to 9 for the increasing lesion percentage of leaf, flower and stem area covered by lesions, according to the scale of Bernier *et al.* (1993).

Table (2):Chocolate spot and rust disease scales by Bernier *et al.* (1993)

	Chocolate spot scale
1	No disease symptoms or very small specks (highly resistance)
3	Few small disease lesions (resistant)
5	Some coalesced lesions, with some defoliation (moderately resistant)
7	Large coalesced sporulating lesions, 50% defoliation and some dead plants (susceptible)
9	Extensive, heavy sporulation, stem girdling, blackening and death of more than 80% of plants (highly susceptible)
	Rust scale
1	No pustules or very small non-sporulating flecks (highly 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 leave, petioles and stem covering 8-10% of leaf area, many dead leaves and several defoliation (highly susceptible).

Disease Assessment:

Reaction to foliar diseases (The disease severity of chocolate spot and rust diseases) was recorded on mid February and mid March for chocolate spot and rust diseases, respectively, according to the disease scales by Bernier *et al.* (1993) presented in table (1).

Statistical analysis.

To determine the presence or absence of non- allelic interaction, scaling test as outlined by Mather (1949) was used. The quantities A, B, C and D and their variances have been calculated to test adequacy of the additive- dominance model in each case.

Where:

$A = \overline{Bc_1} - \overline{p_1} - \overline{F_1}$

$B = 2\overline{Bc2} - \overline{P2} - \overline{F2}$

$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$

$D = 2\overline{F_2} - \overline{BC_1} - \overline{BC_2}$

And

$V(A) = 4V(\overline{Bc_1}) + V(\overline{P_1}) + V(\overline{F_1})$

$A(B) = 4V(\overline{Bc_2}) + V(\overline{P_2}) + V(\overline{F_2})$

$A(c) = 16V(\overline{F_2}) + 4V(\overline{F_1}) + V(\overline{P_1}) + V(P_2)$

$A\{d\} = 4V(\overline{F_2}) + V(\overline{BC_1}) + V(\overline{BC_2})$

The standard error of A,B ,C and D is worked out by taking square root , of respectively variances. The t- values are calculated by dividing the effects of A,B,C and D and D by the respectively standard error . The calculated t-values were compared with tabulated value of t at 5% levels of probability in each test, the degrees of freedom (df) is sum of (df) of various generation involved. The significance of A and B scales indicate the presence of all types of non – allelic gene interactions. The significance of C scale suggests (dd) types of epistasis. The significance of D scale reveals (aa) gene interactions, significance of C and D scale indicates (aa) and (dd) type of gene interactions (Singh and Narayanan, 1993).

Genetic analysis of generation means to give estimates of the types of gene effects were obtained using the relationships given by Gamble (1962).

Jinks and Jones (1958) however, used following formulae to estimate m, a and d components in the absence of non- allelic interactions:

$m = \frac{1}{2}\overline{p_1} + \frac{1}{2}\overline{p_2} + 4\overline{F1} - 2\overline{BC_1} - 2\overline{BC_2}$

$d = = \frac{1}{2}\bar{p}_1 - \frac{1}{2}\bar{p}_2$

$h = 6\overline{BC}_1 + 6\overline{BC}_2 - 8\overline{F}_2 - \overline{F}_1 \frac{1}{2}\bar{p}_1 - 3/2\bar{p}_1 - 3/2\bar{P}_2$

where, Their variances have been computed using following formulae:

$V_m = 1/4 \overline{V} P_{1+} 1/4 \overline{V}P_2 + 16\overline{V} F_1 + 4\overline{VBC}_1 + 4\overline{VBC}_2$

$V_d = 1/4 \overline{V} P_{1+} 1/4 \overline{V}P_2$

And

$\overline{V}_h = 36\overline{VBC}_1 + 36\overline{VBC}_2 + 64\overline{VF}_2 + V \overline{F}_{1+} 9/4Vp_1 + 9/4 Vp_2$

- SE(m)= $(Vm)^{\frac{1}{2}}$, SE{d}= $(Vd)^{\frac{1}{2}}$, and SE {h} =$(Vh)^{\frac{1}{2}}$
- t (m) = m/SE(m), t{d} = d/SE{d} and t{h}=h/SE{h}

Broad + sense heritability (H^2) for F_2 – generation was estimated based on the equation:

$$H_2 = \frac{Vg}{Vg + Ve} \times 100$$

The genetic variance (Vg) and environmental (Ve) were estimated according to Mansur et al.(1993) as follows:

$$V_g = Vf_2 - V_e$$

$$V_e = n_e^{-1} (n_{p1}v_{p1} + n_{p2}v_{p2} + n_{f1}v_{f1})$$

Where, ne = $n_{p1} + n_{p2} + n_{f1}$ and n_{p1}, n_{p2} and n_{f1} are the number of plants of P_1, P_2 and F_1 generations in each cross, respectively .

Narrow-sense heritability (h^2) for F_2 – generation was estimated as proposed by Warner (1952).

Where:

$H^2 = 2VF_2 - (VBC_1 + VBC_2)/VF2 \times 100$

The phenotypic (PCV%) and Genotypic (GCV%) coefficient of variation were estimated as formulae developed by Burton (1952).

The expected genetic advance form selection (G_g) was calculated as the formulae proposed by Johnson et al. (1955), using the selection differential (K) equal 2.06 for 5% selection intensity and heritability in narrow sense.

The predicted genetic advance where the expected genetic gain upon selection was expressed as percentage of F_2 mean (Ga%) was calculated following Miller et al.(1958).

The amount of heterosis was expressed as the percentage deviation of F1 mean performance from mid- parent and better parent. Inbreeding depression was calculated as the difference between the F_1 and F_2 means as

a percentage of F_1. The "t " test was used to determine the significance of these deviations where the standard error (SE) was calculated as follows :

SE for mid parental heterosis $(\overline{F}_1\text{-MP}) = (\overline{V}\ F_1 + 1/4 \overline{V}\ P_{1+}\ 1/4\ \overline{VP}_2\ )^{1/2}$

SE for better parental heterosis $(\overline{F}_1\text{-M}\overline{P}) = (\overline{V}\ F_1 + 1/4\overline{V}\ P_{1+}\ 1/4\overline{V}P_2)\ ^{1/}$

SE for inbreeding depression $(\ \overline{F1}\text{-F2}) = (V\ \overline{F}_1 + VF_2\ )^{1/2}$

Where, the t is the deviation /SE at the corresponding degrees of freedom.

RESULTS AND DISCUSSION

Data in Table (3) showed no. of plants, mean performance and variance of mean for the six populations of the three crosses for different traits. Significantly differences were observed among most genotypes for measured traits. The parental genotypes could be arranged into two groups; the first group included the genotype of Sakha1 which was considered to be the most resistant group to chocolate spot and rust with high yielding ability where the yield value per plant was 101.10 gm, in addition, it has less rating scale values of chocolate spot and rust reaction (3.01 and 3.25), respectively. The second group included Giza40, Giza 429 and Triple white which performed as susceptible genotypes it had high rating scale values of chocolate spot reaction (6.16, 6.23 and 6.15), also had high rating scale values of rust reaction (6.61, 6.56 and 6.97), respectively, accompanied with low yielding ability (91.53, 80.86 and 21.64 g), respectively. The difference between the studied crosses with respect to foliar diseases resistance and yield component traits could be observed in Table (3), also significant genetic variance were detected for all traits in the three crosses and therefore genetic parameters were detected as reported by Khalil *et al.* (1993b) and Attia *et al.* (2006).

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Table (3): Number of plants (n), mean performance (x⁻) and variance of mean (S^2_x) for studied traits in the three faba bean crosses.

Traits	Crosses	Statistical parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
Plant height	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		$\overline{X}$	130	123.33	128.17	126.2	129.12	125.22
		$S^2\overline{X}$	0.632	0.720	0.772	0.381	0.407	0.498
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		$\overline{X}$	136.89	123.33	129.00	126.00	139.33	132.11
		$S^2\overline{X}$	0.979	0.720	1.038	0.585	0.643	0.738
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		$\overline{X}$	123.33	103.50	119.46	120.12	112.35	115.68
		$S^2\overline{X}$	0.720	0.843	0.717	0.501	0.574	0.601
No. of branches /plant	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		$\overline{X}$	3.57	3.13	3.43	2.56	3.41	3.08
		$S^2\overline{X}$	0.010	0.015	0.029	0.008	0.009	0.011
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		$\overline{X}$	3.50	3.13	4.07	3.38	4.62	4.05
		$S^2\overline{X}$	0.010	0.015	0.017	0.010	0.013	0.012
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		$\overline{X}$	3.13	1.50	3.42	3.27	2.72	2.98
		$S^2\overline{X}$	0.015	0.013	0.009	0.017	0.015	0.020
No. of pods/ plant	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		$\overline{X}$	50.33	37.7	52.4	38.9	49.24	39.47
		$S^2\overline{X}$	0.267	0.306	0.376	0.249	0.301	0.281
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		$\overline{X}$	39.97	37.70	45.73	40.10	39.87	46.40
		$S^2\overline{X}$	0.852	0.306	1.105	1.264	1.190	1.261
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		$\overline{X}$	37.7	23.48	43.35	41.25	34.36	33.7
		$S^2\overline{X}$	0.306	0.426	0.704	1.283	1.282	1.475
No. of seeds/ plant	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		$\overline{X}$	141.7	118.01	135.6	120.12	139.13	121.11
		$S^2\overline{X}$	0.587	0.524	0.555	0.301	0.341	0.375
	ss 2 (Sakha1 x Giza429)	Cron $\overline{X}$	30 126.00	30 118.01	30 140.93	250 128.00	150 141.44	150 138.22
		$S^2\overline{X}$	0.600	0.524	0.880	1.017	1.401	1.321
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		$\overline{X}$	118.01	43.56	126.12	131.15	75.18	86.22
		$S^2\overline{X}$	0.524	0.621	0.938	0.521	0.654	0.541
Seed yield/ plant	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		$\overline{X}$	91.53	80.86	94.66	80.2	85.17	82.89
		$S^2\overline{X}$	0.306	0.299	0.471	0.441	0.428	0.521
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		$\overline{X}$	101.10	80.86	113.84	98.40	123.70	103.22
		$S^2\overline{X}$	0.591	0.299	0.539	0.799	0.889	0.814
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		$\overline{X}$	80.86	21.64	82.28	86.30	49.16	52.41
		$S^2\overline{X}$	0.333	0.659	0.706	0.525	0.594	0.641

table 3 cont:

Traits	Crosses	Statistical parameter	P$_1$	P$_2$	F$_1$	F$_2$	BC$_1$	BC$_2$
No. of seeds/ pod	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		X̄	2.82	3.21	2.41	3.09	2.83	3.07
		S^2 X̄	0.004	0.003	0.004	0.005	0.005	0.004
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		X̄	3.15	3.21	3.08	3.19	3.55	2.98
		S^2 X̄	0.004	0.003	0.005	0.003	0.002	0.002
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		X̄	3.21	1.86	3.05	3.18	2.19	2.56
		S^2 X̄	0.003	0.009	0.013	0.012	0.012	0.014
100 seed weight	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		X̄	64.59	68.51	69.81	66.77	68.40	68.44
		S^2 X̄	0.364	0.385	0.419	0.273	0.270	0.348
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		X̄	80.24	68.51	80.78	76.88	87.46	74.61
		S^2 X̄	0.753	0.385	0.606	1.012	0.848	1.260
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		X̄	68.51	49.68	65.24	65.8	65.39	60.79
		S^2 X̄	0.385	0.608	1.435	0.405	0.428	0.476
Chocolate spot	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		X̄	6.16	6.23	6.04	5.92	5.86	5.94
		S^2 X̄	0.010	0.009	0.007	0.009	0.011	0.010
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		X̄	3.01	6.23	4.89	5.75	4.38	5.85
		S^2 X̄	0.006	0.009	0.006	0.005	0.005	0.006
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		X̄	6.23	6.15	5.98	5.91	6.01	6.00
		S^2 X̄	0.009	0.016	0.024	0.006	0.006	0.007
Rust	Cross 1 (Giza40 xGiza429)	n	30	30	30	250	150	150
		X̄	6.61	6.56	6.14	6.18	6.54	6.48
		S^2 X̄	0.005	0.006	0.004	0.004	0.005	0.004
	Cross 2 (Sakha1 x Giza429)	n	30	30	30	250	150	150
		X̄	3.25	6.56	4.93	5.81	4.66	5.92
		S^2 X̄	0.005	0.006	0.006	0.004	0.005	0.004
	Cross 3 (Giza 429 x TW)	n	30	30	30	250	150	150
		X̄	6.56	6.97	6.04	6.00	6.14	6.28
		S^2 X̄	0.006	0.014	0.021	0.005	0.005	0.006

Table (4): Heterosis over mid (MP) and better (BP) parent and potence ratio (PR) for the studied traits in the three faba bean crosses.

Characters	Crosses	MP	BP	PR	ID%	H2	h2(%)	Ga%	PCV%	GCV%
Plant height	1	1.19	-1.41	0.45	1.54	77.72	57.65	9.19	7.74	6.82
	2	-0.85	-5.76**	-0.16	2.33	81.30	58.42	11.56	9.60	8.66
	3	5.33**	3.14**	0.61	-0.55	81.78	59.21	11.36	9.31	8.42
No. of branches/ plant	1	2.39	-3.92	0.36	25.36**	73.23	52.71	60.43	55.66	47.63
	2	22.78**	16.29**	4.08	16.95**	83.98	51.95	50.66	47.34	43.38
	3	47.73**	9.27**	1.36	4.39*	91.25	73.51	94.79	62.60	59.80
No. of pods/ plant	1	19.05*	4.11*	1.33	25.76**	84.73	59.53	24.86	20.27	18.66
	2	17.75**	14.41*	6.07	12.31**	92.84	83.66	76.41	44.347	42.72
	3	41.71//	14.99*	1.79	4.84*	95.52	71.04	63.53	43.41	42.43
No. of seeds/ plant	1	4.42**	-4.30**	0.49	11.42	77.86	57.36	8.53	7.22	6.37
	2	15.51**	11.85**	4.74	9.17	92.12	39.43	10.12	12.46	11.96
	3	56.12**	6.87**	1.22	-3.99	84.00	62.18	11.14	8.70	7.97
Seed yield/ plant	1	9.82**	3.42	1.59	15.28	90.23	70.85	19.10	13.09	12.43
	2	25.13**	12.60**	2.26	13.56	92.85	72.23	21.38	14.37	13.84
	3	60.54**	1.76	1.08	-4.89	87.31	60.96	16.66	13.27	12.40
No. of seeds/ pod	1	-20.07**	-24.92**	-3.33	-28.22**	90.35	74.56	53.07	34.55	32.84
	2	-3.14	-4.05*	-2.00	-3.57**	84.77	79.31	47.77	29.24	27.09
	3	20.32**	-4.98*	0.82	-4.26*	91.72	70.53	79.40	54.65	52.34
100 seed weight	1	4.90*	1.90	-1.66	4.35	82.86	63.82	16.25	12.36	11.25
	2	8.61**	0.67	1.24	4.83	93.11	75.02	31.97	20.69	19.96
	3	10.40**	-4.77*	0.74	-0.86	76.00	66.02	20.79	15.28	13.32
Chocolate spot	1	-2.50	-1.95	-4.43	1.99	89.31	68.35	36.62	26.00	24.58
	2	5.84**	62.46**	0.16	-17.59**	82.49	45.76	17.81	18.89	17.16
	3	-3.39	-2.76	-5.25	1.17	85.75	68.97	28.95	20.37	16.61
Rust	1	-6.76**	-6.40**	-17.80	-0.65	85.71	66.67	22.77	16.58	15.35
	2	0.51	51.69**	0.02	-17.85**	83.33	74.04	26.77	17.55	16.02
	3	-10.72**	-7.93**	-3.54	0.66	83.59	77.34	30.04	18.86	15.55

Heterosis:

Plant breeder have been investigated the possibility of developing hybrid cultivars. Thus the utilization of heterosis in various crops through the world has tremendously increased the production. Heterosis is a complex phenomenon which depends on the balance of different combinations of genotypes effect as well as the distribution of plus and minus alleles in parents. Heterosis is expressed as the percentage deviation of F_1 mean performance from the mid or better parent of the traits. As it will be expected, better parent from seed yield was the highest one. In this concern, percentage of heterosis over mid parent and better parent values is presented in the three crosses in Table (4) which indicated that heterosis over mid and better parent for plant height was significant in the third cross due to partial dominance, no. of branches and seeds/plants had highly significant mid and better parent heterosis in the second and third crosses due to over-dominance in most crosses, highly significant for no. of pods and seeds/plant in three crosses a result of over-dominance, highly significant for seed yield /plant in the first and second crosses due to over dominance, highly significant for no. of seeds/pod in the third cross due to partial dominance and highly significant in negative direction for rust disease in the first and third crosses due to over-dominance. However, the third cross (Giza

429 x TW) showed significant better parental heterosis for plant height, no. of pods/plant, no. of seeds/plant, no. of seeds/pod and resistant to rust disease which give the cross the susceptibility over the other crosses.The differences in heterosis percent might be due to genetic variability of the parents and for non-allelic interactions, which can either increase or decrease the expression of heterosis. Even in the absence of epistasis, multiple alleles at a locus could lead to either positive of negative heterosis (Cress, 1966).

Inbreeding depression:

Inbreeding depression measured the extent of reduction of the F_2 generation due to inbreeding. Significant positive values were obtained for no. of branches/plant and no. of pods/plant in the three crosses. On the other hand, negative inbreeding depression values were obtained for no. of seeds/pod in the three crosses, reaction to chocolate spot and rust disease in the second cross (Sakha1 x Giza 429). The rest of traits over all crosses were non-significant. Significant effects for the both heterosis and inbreeding depression seem logic since the expression of heterosis in F_1's was followed by considerable reduction in the F_2 performance. Also, reduction in values of non-additive genetic components is expected caused by means of inbreeding depression. In addition, the conflicting estimates heterosis and inbreeding depression were associated in most traits. Similar conclusion were reviewed by El-Refaey and Radi (1991), El-Hady *et al.* (1998), Darwish *et al.* (2005), Attia and Salem (2006), Attia (2007), El-Hady *et al.* (2008), Abo Mostafa *et al.* (2009) and El- Hady *et al.* (2009).

Heritability estimates:

The highest broad sense heritability was obtained for no. of pods/plant in the third cross (Giza429 x TW) being (95.52%) and 100-seed weight in the second cross (Sakha1 x Giza429) where the value was (93.11%) (Table 4). Meanwhile, the lowest estimates was resulted for no. of branches/plant in the first cross (Giza40 x Giza 429) with value of 73.23%. Heritability in narrow sense as estimated by using F_2 and backcrosses data were low for no. of branches/plant, no. of seeds/plant and reaction to chocolate spot in the scond cross (Sakha1 x Giza429) with value of 51.95%, 39.43% and 45.76%, respectively. Meanwhile, high narrow sense values for number of pods/plant and no. of seeds/pod in the second cross (Sakha1 x Giza 429) with values 83.66% and 90.80%, respectively. These results were in harmony with those obtained by Abdalla *et al.* (1999), Mansour *et al.* (2001), Darwish *et al.* (2005), El-Hady *et al.* (2007), El-Hady *et al.* (2009), Abou Mostafa *et al.* (2009) and Ashrei *et al.* (2013).

Genetic advance:

The genotypic coefficient of variability (GCV%) and phenotyhpic coefficient (PCV%), the predicted genetic advance upon selection as a percentage of F_2 generation for the studied characters are presented in Table (4). Number of branches/plant, no. of pods/plant and no. of seeds/pod in the three crosses exhibited high PCV% and GCV% and predicted genetic advance with high heritability. The highest genetic advance as mean percent (Ga%) were detected for no. of branches/plant in the three crosses being (60.43, 50.66 and 94.79%), respectively. Meanwhile, low predicted genetic advance values were obtained for plant height in the three crosses being

(9.19, 11.56 and 11.36%), and for no. of seeds/plant in the three crosses 8.53, 10.12 and 11.14%, respectively. Johanson *et al.* (1955) reported that, heritability estimates along with genetic advance are usually more useful than the heritability values alone in predicting the results of selecting the best individuals. In the present works high genetic advance was associated with high heritability values in narrow sense and PCV% for no. of branches per plant, no. of pods/plant and no. of seeds/pod in the three crosses. Therefore, selection in these populations may be effective and satisfactory in the early generation (El-Refaey, 1999 and El-Hady *et al.* 2009). Also, moderate or low genetic advance was found to be associated with moderate or low heritability and PCV% estimates. Therefore, it could be suggested that, the selection for faba bean seed yield in subsequent generation will be relatively more effective than in the early F_2 generation.

Gene effects:

The estimated values of different scaling test according to Mather (1949) and Hayman and Mather (1955), as well as six parameters describing the nature of gene action and their test of significance according to Gamble (1962), for all studied traits are presented in Table (5). (A) and (B) and tests provides evidence the presence of all types of non-allelic gene interaction. The significance of C scale suggests (dd) type of epistasis. The significant D scale reveals (aa) gene interaction, significance of C and D scales indicates (aa) and (dd) type of gene interaction. The test of adequacy of scales is important because in most cases the estimation of additive and dominance components of the variance are made assuming absence of gene interaction. The values of A, B, C and D should significantly differ than zero within the limits of their standard error. However, the results (Table 5) indicated that, the values of scaling test were significantly differ than zero for all studied traits in all crosses, except plant height and 100-seed weight of the first cross, no. of seeds/pod of the second cross and reaction to both chocolate spot and rust diseases of the third cross, and the reaction of chocolate spot in the first cross indicating that the additive dominance model is inadequate to interpret the gene effects (Mather, 1949), and simple additive- dominance model was adequate for estimating the genetic components of variance of these traits.

The estimated mean effect parameter (m), which reflect the contribution due to the overall mean plus the locus effects and interaction of the fixed loci were highly significant in the three crosses of all traits. The additive gene effect (a) was significant in positive or negative direction in all crosses for all traits except in the third cross (Giza429 x TW) for no. of branches/plant, no. of pots and seeds/pod, and reaction to both chocolate spot and rust. In the second (Sakha1 x Giza 429) for no. of seeds/plant. For dominant effect (d) where its high in magnitude than that of additive type, because it gives high values comparing with additive gene (a) where were positive or negative directions. The values of dominant effect were significant in all crosses for all traits, except for no. of branches/plant, 100 seed weight and reaction to both chocolate and rust diseases in the third cross and for plant height and chocolate spot reaction in the first cross .These results indicated the importance role of dominance gene effects in the inheritance of these traits. On the other hand, significant of additive (a) and dominance (d) components indicated that, both additive and dominance gene

effects are important in the inheritance of these traits. Also, selecting desirable characters may be practiced in the early generation but it would be effective in the late ones. Similar results were obtained by El-Hady *et al.* (2009), Abo Mostafa *et al.* (2009) and Ashrei *et al.* (2013) and El-Refaey and Abd El-Razek (2013). The additive x additive gene effects was highly significant either positive or negative directions in all crosses for all studied traits except no. of seeds/pod in the first cross.

Table (5): Scaling test and gene action parameters of the studied traits in three faba bean crosses.

Characters	Crosses	Scaling test				Gambles parameters					
		A	B	C	D	(m)	(a)	(d)	(aa)	(ad)	(dd)
Plant height	1	0.07	-1.06	-4.87	-1.94	126.20**	3.90*	5.38	-	-	-
	2	12.77**	11.89	-14.22**	-19.44**	126.00**	7.22**	37.77**	38.88**	0.44	-63.54**
	3	-18.09**	8.4*	14.73**	12.21	120.12**	-3.33*	-18.38**	-24.42**	-13.25**	34.11**
No. of branches/ plant	1	-18	-0.4	-3.32**	-1.1**	2.56**	0.33	2.82**	2.74**	0.11	-2.16**
	2	1.67**	0.9*	-1.25**	-1.91**	3.38**	0.57*	4.58**	3.82**	0.38ns	-6.39**
	3	-1.11**	1.04*	1.61**	0.84	3.27**	-0.26	-0.5s	-1.68*	-1.08**	1.75
No. of pods/ plant	1	-4.25*	-11.16**	-37.23**	9.09**	38.90**	9.77**	30.21**	21.82**	3.46*	-6.41
	2	-5.96	9.37**	-8.73	-6.07**	40.10**	-6.53*	19.04**	12.14*	-7.67**	-15.55
	3	-12.33**	0.57	17.12**	14.44**	41.25**	0.66	-16.12*	-28.88**	-6.45**	40.64**
No. of seeds/ plant	1	0.96	-11.39**	-50.43**	-20.00**	120.12**	18.02**	45.75**	40.00**	6.18**	-29.57**
	2	15.95**	17.5**	-13.87**	-23.66**	128.00**	3.22	66.25**	47.32**	-0.77	-80.77**
	3	-93.77**	2.76	110.79**	100.9**	131.15**	-11.04**	-156.47**	-201.80**	-48.27**	292.81**
Seed yield/ plant	1	4.15*	-0.94**	-40.91**	-17.66**	80.20**	12.28**	43.79**	35.32**	6.95**	-29.73**
	2	32.46**	11.74**	-16.04**	-30.12**	98.40**	20.48**	83.10**	60.24**	10.36**	-104.44**
	3	-64.82**	0.9	78.14**	71.03**	86.30**	-3.25*	-111.03**	-142.06**	-32.86**	205.98**
No. of seeds/ pod	1	0.43	0.52*	1.51**	0.28	3.09**	-0.24	-1.17**	-0.56	-0.0	-0.39
	2	0.87	-0.33	0.24	-0.15	3.19**	0.57**	0.20	-	-	-
	3	-1.88**	0.21	1.55**	1.61**	3.18**	-0.37	-2.71**	-3.22**	-1.05**	4.89**
100 seed weight	1	2.4	-1.44	-5.64	-3.30	66.77**	-0.04	9.86**	-	-	-
	2	13.9**	-0.07	-2.79	-7.77*	76.88**	12.85**	23.03**	16.62**	6.99**	-30.45**
	3	-2.97	6.66**	14.53**	5.42*	65.80**	4.60**	-4.69	-10.84**	-4.82**	7.15
Chocolate spot	1	-0.48	-0.39	-0.79	0.04	5.92	-0.08	-.23	-	-	-
	2	0.86**	0.58	3.98**	1.27**	5.75	-1.47**	-2.27**	-2.54**	0.14	1.10
	3	-0.19	-0.13	-0.7	-0.19	5.91	0.01	0.17	-	-	-
Rust spot	1	-.48	-.39	-0.79	-0.66	6.18	0.06	0.88*	1.32**	0.03	-1.91*
	2	1.14**	0.35	3.57**	1.04**	5.81**	-1.26**	-2.06**	-2.08**	0.40**	0.-59
	3	-0.32	-0.45	-1.61	-0.42	6.00**	-0.14	0.11	-	-	-

1= Giza40 x Giza 429, 2 = Sakha1 x Giza 429, 3= Giza429 x TW

However, significant positive epistatic gene action (ad) was observed in all crosses for all studied traits, except no. of branches/plant, no. of seeds/pod and reaction to rust disease in the first cross and plant height and no. of seeds/plant in the second cross where the values were not significant. The same trend was found with respect to dominance x dominance (dd). While, positive or negative significant were observed for the remaining of the studied characters in these crosses. The absolute relative magnitude of the epistatic gene effects to the mean effects was somewhat variable depending on the cross and the studied traits. With regard to negative values observed either with main effects ; (a) and (d) or the non-allelic interactions i.e. (aa), (ad) and dd), this might indicate that, the alleles responsible for values traits was over dominant over the alleles controlling high value. Generally, the absolute magnitude of the epistatic effects was larger than additive or dominance effects in most cases. Therefore, it could

be concluded that, homozygous x homozygous and heterozygous x homozygous non-allelic interactions were more important than the heterozygous x heterozygous interaction in the inheritance of most studied traits. The epistatic gene effects were important than additive and dominance gene effects for most of the traits. The failure in detecting epistatic gene effects based on the generation mean analysis does no necessarily indicate that non-allelic interactions did not play role in the determination of phenotypic value. Nighawan *et al.* (1969) reported the importance of the three types of gene action in oats. Thus, the employed breeding system in exploiting any character depends on the involved gene action in its expression for predicted gain in selection progress (Abul-Naas *et al.*, 1993). These results are in agreement with those reported by El-Hady *et al.* (1997), El-Refaey (1999), Kalia and Sood (2004), Attia *et al.* (2006), Al-Ghamdi (2007), El-Galaly *et al.* (2008) and El-Refaey and Abd El-Razek (2013).

REFERENCES

Abdalla, M.M.F.; M.M. El-Hady and E.H. El-Harty (1999). Investigations on faba bean (*Vicia faba* L.). 12 diallel crossed materials grown under cages.Proceed. First Plant Breed Conf., Egypt.J.Plant Breed., 3: 213-229.

Abdelmula, A.A., Link, W., Kittlitz, E., von Stelling, D., (1999). Heterosis and inheritance of drought tolerance in faba bean (*Vicia faba* L). Plant Breed. 118, 485–490.

Abo Mostafa, R.A.I.; W.M. El-Rodeny and Aziza, M. Hassanein (2009). Generation mean analysis of earliness and chocolate spot disease resistance and quantitative variation in the storage proteins of three *Vicia faba* L. Crosses J. Agric. Sci., Mansoura Univ., 34(2): 925-943.

Abul-Naas, A.A.; M.A. Mahrous and A.A. El-Hosary (1993). Genetical studies on yield and some of its components in barley (*Hordum vulgare* L.). Egyhpt. J. Agron. 18(1-2): 33-46.

Al-Ghamdi, S.S. (2007). Genetic behavior of some selected faba bean genotypes. Proc. 8th African Crop Science Society Conference, El-Minia, Egypt. pp. 709–714.

Ashrei, A.A.M.; Zeinab, E. Ghareeb; Kha, M.M. Ymani; Rehab, A.M. Abd Elrahman and A. Al-Garhy (2013). Statistical and genetical analysis of yield and some related components in faba bean. Egypt J. Plant Breed., 17(5): 57-67.

Attia, Sabah, M. (2007). Gene action and some genetic parameters for seed yield and its components in faba bean (*Vicia faba* L.). Egyptian J. of Appl. Sci., 22(6B): 487-499.

Attia, Sabah, M. and Manal Salem (2006). Analysis of yield and its components using diallel matings among five parents of faba bean. Egypt. J. Plant Breed., 10(1): 1-12.

Bernier, C.C., Hanounik, S.B., Hussein, M.M. and Mohamed, H.A. (1993). Field manual of common faba bean diseases in the Nile Valley. International Center for Agricultural Research in the Dry Areas (ICARDA) *Information Bulletin No. 3.*

Bond, D.A., G.J. Jellis, G.G. Rowland, J. Le Guen, L.D. Robertson, S.A. Halil, and L. Li Juan. (1994). Present status and future strategy in breeding faba beans *(Viciafaba* L.) for resistance to biotic and abiotic stresses. Euphytica 73:151 -166.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proceedings of the 6th International Grassland Congress, August 17-23, 1952, Pennsylvania State College, USA, pp. 277-283.

Cress, C.E. (1966). Heterosis of the hybrid relative to gene frequency differences between two populations. Genetics, 53: 269-274.

Darwish, D.S.; M.M.F. Abdalla; M.M. El-Hady and S. El-Emam (2005). Investigation on faba beans, *Vicia faba*, L. 19-diallel and triallel matings using five parents. Proc. 4th Plant Breed. Conf. March 5 (Suez Canal Univ.). Egypt. J. Plant Breed., 9(1): 197-208.

EL-Galaly, Ola_.A.M.; R.A.I. Abo Mostafa , and W.M. EL- Rodeny (2008), Evaluation of eight promising lines of faba bean *(Vicia faba* L.) for diseases resistance (chocolate spot and rust) and yield in North Delta . Annals of Agric . Sc., Moshtohor, Vol. 46(2): Ag. 131-140, (2008).

El-Hady, M.M.; A.M.A. Rizk; M.M. Omran and S.B. Ragheb (2007). Genetic behavior of some faba bean (*Vicia faba,* L.) genotypes and its crosses. Annals of Agric. Sci. Moshtohor, 45(1): 49-66.

El-Hady, M.M.; Gh.A. Gad El-Karim and M.A. Omar (1997). Genetical studies in faba bean *(Viciafaba* L.). J. Agric. Sci. Mansoura Univ. 22: 3561-3571.

El-Hady, M.M.; M.A. Omar; S.M. Naser; K.A. AH and M.S. Essa (1998). Gene action on seed yield and of some yield components in F] and F2 crosses among five faba bean *(Viciafaba* L.) genotypes. Bull. Fac. Agric., Cairo University, 49: 369-388.

El-Hady, M.M.; Sabah, M. Attia; A.A. Ashrei; E.A.A. El-Emam and M. Shaaban (2009). Heterosis, combining ability and genetic variability and some relative components in faba bean using six populations model. Minia J. Agric. Res. and Develop 29(3): 4187-431.

El-Hady, M.M.; Sabah, M. Attia; E.A.A. El-Emam; A.A.M. Ashrei and EM. Rabie (2008). Diallel mating among eight parents of faba bean (*Vicia faba* L.) and performance of F_1 and F_2.Egypt.J. of Appl.Sci.,23(5):95-114.

El-Refaey, R.A. (1999). Generation mean analysis of earliness, yield and some of its components in three faba bean crosses. Minufiya J. Agric. Res. 24: 409-424.

El-Refaey, R.A. and M.M.Radi (1991) Genetic analysis of seed yield and its related character in soybean. II- Inbreeding depression and interrelationships among traits in the Fl and F2 generations. J.Agric. Res.Tanta Univ., 17(2):334-345.

El-Refaey, R.A. and U.A. Abd El-Razek (2013). Generation mean analysis for yield, its components and quality characteristics in four crosses of Egyptian cotton (*Gossypium barbadense* L.). Assion J. Crop Sci., 5(2): 153-166.

Gamble, E.E., (1962).Gene effects in corn *(Zea mays L.).* I- Separation and relative importance of gene effects for yield.Can. J.of Plant Sci., 42: 339-348.

Hayman, B.I. and K. K. Mather (1955). The description of genetic interaction in continuous variation. Biometrics, 11: 69-82.

Hendawy,F.A (1994). Heterosis and inheritance of some quantitative characters in two intervarietal crosses of field bean *(Viciafaba* L.) Minufiya j.Agric .Res. 19:1957-1971

Jinks, J.L. and R.M. Jones (1958). Estimation of the components of heterosis. Genetics, 43: 223-234.

Johanson, H.W.; H.F. Robinson, and R.E. Comstock,(1955). Estimating of genetic and environmental variability in soybeans. Agron.J.,47: 314-318.

Kalia, P. and S. Sood (2004). Genetic variation and association analyses for pod yield and other agronomic and quality characters in an Indian himalayan collection of broad bean *(Vicia Faba* L.) . sabrao journal of breeding and genetics 36(2) 55-61.

Khalil, S.A.; M.M.El-Hady; R.F. Dissouky; M.I.Amer and S.A. Omer (1993). Breeding for high yielding ability with improved level of resistance to chocolate spot (*Botrytis faba*) diseases in faba bean *(Vicia faba* L.). J Agric. Sci . Mansoura Univ. 18(5) : 1315-1328.

Mansour, S.H.; Sabah, M. Attia; Manal M. Salem and M.M. El-Hady (2001). Genetic analysis of shedding and some yield characters in faba bean. J. Agric. Sci. Mansoura University, 26(4): 1875-1887.

Mansur, L.M.; A.L. Carriquiry and A.P. Rao-Arelli (1993). Generation mean analysis of resistance to race-3 of soybean cyst-nematode. Crop Sci., 33: 1249-1253.

Mather, K. (1949). Biometrical Genetics. Dover Publications, Inc., London Miller, P.A., J.C. Williams, H.F. Robinson and R.E. Comstock (1958). Estimates of genotypic and environmental variances and covariance in upland cotton and their implications in selection.Agron.J., 50: 126-131.

Miller, P.A.; J.C. Wiliams; H.F. Robinson and R.E. Comstock (1958). Estimates of genetic and envnironmental variance and covariance in upland cotton and their implication in selection. Agron. J., 50: 126-131.

Mohamed, H.A.; M.E. El-Rafei; N.M. Abou Zeid; S.A. Omer; Wadaia F. Habib.; LA. Ismail, ; M. Raof.; and H. Khidr; (1980). Plant pathobgy research studies ICARDA/IFAD Nile Valley Project on faba beans Annual coordination Meeting 1979-1980, Cairo, Mimeograph, 49pp.

Nighawan, Dechan and T.D. Yadava (1969). Detection of gene effect of some quantitative characters in oats (*Avena sateral,*L.).Indian J.Hered, 1: 145.

Singh, P. and S.S. Narayanan (1993). Biometrical Techniques in Plant Breeding. 1st Edn. Kalyani Publishers, New Delhi, India, p. 182.

Stoddard, F.L; Nicholas, A; Rubiales, D; Thomas, J and Villegas-Ferna´ndez, A.M (2010). Integrated pest, disease and weed management in faba bean. Field Crops Res. 115, 308–318.

Warer, J.N. (1952). A method for estimating heritability. Agron. J. 44: 427-430.

تحليل متوسط الأجيال لصفات المقاومة للأمراض والمحصول ومكوناتـه فى ثلاثـة هجن من الفول البلدى

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- أقيم هذا البحث خـلال المواسم بـي 2011/2012 ، 2012 /2013 ، 2013/2014 بمزرعـة محطـة البحوث الزراعية بسخا بمحافظة كفرالشيخ.

- أجرى التحليل الكمى بالتهجين بين 4 تراكيب وراثية أبوية للفول البلدى وهى جيزة 40 ، جيزة 429 ، سخا1 ، TW لإنتاج 3 هجن وهى: الهجين الأول (جيزة 40 × جيزة 429) ، الهجين الثانى (سـخا1 × جيزة429) ، الهجين الثالث (جيزة 429 ، TW).

- ويمكن تقسيم التراكيب الوراثية الأبوية إلى مجموعتين.

- المجموعة الأولى تشمل سـخا 1 والـذى يعتبر أكثر الأصناف مقاومة للتبقع البنى والصـدأ إلـى جانب المحصول العالى.

- المجموعـة الثانيـة تشمل جيزة 40 ، جيزة 429 ، TW وهـى أصـناف قابلـة للاصـابة بالمرضين مـع إنخفاض محصولهما.

- استخدم تحليل متوسط الأجيال لتقدير مكونات التباين الوراثى فى الهجن الثلاثة والتسعة صفات.

- كانت قوة الهجين بناء على متوسط الأبوين والأب الأفضـل عاليـة المعنوية لجميـع الصـفات ماعدا طـول النبات فى الهجن الأول والثانى بالنسبة لمتوسط الأبوين وفى الهجين الأول نسبة إلـى الأب الأفضـل وكـان الهجين الاول غير معنوى فى عدد الأفرع للنبات ، والمقاومـة لمرض الصـدأ نسـبة إلـى متوسـط الأبـوين ولصفة عدد القرون/نبات ، بالنسبة للأب الأفضل.

- وقد أظهر الهجينين الثانى والثالث عدم معنوية للتبقع البنى بالنسبة إلى متوسط الابوين ووزن 100 بـذرة نسبة إلى الأب الأفضل.

- كانت التدهور الراجع إلى التربية الداخلية معنويا وفى الاتجاه الموجب لصفتى عدد الأفرع والقرون/نبـات بينما كانت سالبة ومعنوية لصفة عدد البذور/قرن فى الهجن الثلاثة.

- كانت قيمة المكافىء الوراثى فى معناه الواسع بصفة عامة أكبر من مثيلاتها فى المعنى الضيق فى جميـع الهجن ولكل الصفات .

- كانت الجينات المضيفة ذات أهمية كبرى فى توريث معظم الصـفات وبخاصـة عدد القرون/نبـات وعدد البذور/قرن فى الهجين الثانى.

- وبذا فإن الانتخاب المباشر والغير مباشر فى نسل هذا الهجين سـوف يكـون فعـالا ويرجع ذلـك إلـى القيم العالية للمكافىء الوراثى فى معناه المحدود أو الضيق وإلى القيم العالية للتقدم الوراثى المتنبأ به.

- كان الفعل الجينى المضيف معنويا موجبا أو سالبا فى كل الهجن فى معظم الصفات عدا عدد الأفرع/نبـات ، عدد البذور /قرن فى الهجينين الأول والثالث.

- كان الفعل الجينى السيادى أعلى قيمة من نظيره المضيف فى معظم الحالات.

- كان الفعل الجينى الاضافى × الاضافى عالى المعنوية فى معظم الهجن وفى كـل الصـفات ماعدا حـالات قليلة.

- كان الفعل الجينى الاضـافى × السيادى عـالى المعنويـة فـى الاتجـاه الموجب أو السـالب لمعظم الهجن ومعظم الصفات ونفس الاتجاه لوحظ بالنسبة للفعل الجينى السيادى × السيادى.