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HERITABILITY AND GENE EFFECTS FOR DISEASE RESISTANCE, YIELD AND ITS COMPONENTS IN THREE FABA BEAN CROSSES (*Vicia faba* L.)

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ABSTRACT

The genetic parameters controlling the expression of foliage disease resistance, seed yield and its components of faba bean have been studied using the generation mean analysis, during 2012/13, 2013/14 and 2014/15 seasons at Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt. The six population parameters P_1, P_2, F_1, F_2, BC_1 and BC_1 of three faba bean crosses (Giza 3 x Rena Mora , Sakha 1 x Ohshima-Zairai and Sakha 2 x Rena Mora) were used in this study. The obtained results indicated that both additive and dominance types of gene effects were involved in the inheritance of No. of seeds/plant, seed yield/plant, No. of seed/pod, 100-seed weight and reaction to chocolate spot and rust diseases in the three crosses, moreover, additive x additive gene effects were relatively more important than additive effects in the inheritance of these traits but less important than dominance ones.

Significant and negative mid parental heterosis was detected for days to flowering in the second cross, days to maturity in the first and second cross and reaction to chocolate spot and rust diseases in the three crosses as a result of partial dominance towards lower parent but the better parental heterosis did not exceed or reach the performance of the better parent for these traits. Significant negative values of breeding depression were obtained for these traits indicating that the depression were occurred due to inbreeding.

Highly significant positive heterosis over both mid and better parent were detected for No. of branches/plant in the second and third cross, No. of pods/plant in the first and second cross, No. of seeds/plant in the first cross and seed yield /plant in the first and third cross, however, dominance especially over-dominance as the potence ratio seems to be more contributing than epistasis in the expression of this valuable heterosis.

The inbreeding depression estimates were positive and significant and/or highly significant for No. of branches/plant and No. of seeds/plant in the second and third cross, No. of seeds/plant and seed yield/plant in the second cross and chocolate spot and rust diseases reaction in the first cross, while it was negative and significant for chocolate spot and rust diseases reaction in the second and third cross.

High genetic gain upon selection was found to be associated with high narrow sense heritability values and high estimates of GCV% and PCV% for No. of branches/plant, No. of pods/plant and No. of seeds/pod in the three crosses, indicating the effectiveness of selection for these traits.

INTRODUCTION

Faba bean plant has attracted the attention of most plant breeders to improve its yield because of the importance of the crop for both human and animal nutrition. Most of plant breeders assume the absence or decrease of epistatic gene effects. Gamble (1962) reported that epistatic gene effects are present in sufficient magnitude in quantitative traits which may alter the breeder's decision for the breeding method which must be followed. For example, if the additive genetic variance is of major importance, the intra-population selection will be considered as the most effective procedure for gathering the favorable genetic constitutions. If dominant variance especially over-dominance is predominant, then the hybrids programs for commercial purpose may be the appropriate choice. On the other hand, if the epistatic variance is relatively high, more reliance should be placed on selection between families(El Galaly *et al* (2008), El-Hady *et al* (2008), El-Hady *et al* (2009), El-Refaey and Abd El-Razek (2013) and Abo Mostafa *et al* (2014) .

So, 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) is 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 study is to elucidate the relative magnitudes of the different types of gene action for reaction to chocolate spot and rust diseases, seed yield and some of its components of faba bean. Heterosis, inbreeding depression and genetic advance were determined also in this study.

MATERIALS AND METHODS

Field experiments:

The present investigation was carried out during the successive seasons of 2012/13, 2013/14 and 2014/15 seasons at Sakha Agricultural Research Station, ARC, Kafr El-Sheikh. Five faba bean (*vicia faba L.*) varieties namely; Sakha 1,Sakha 2, Giza 3,Ohshima-Zairai and Rena Mora were used to generate the experimental materials for this study. The three initial crosses; Giza 3 x Rena Mora,Sakha1 x Ohshima-Zairai and Sakha 2 x Rena Mora are designated in the text as first, second and third cross, respectively.

The crosses were developed in 2012/13 season under the isolation wirecages of Sakha Agricultural Research Station, ARC, Kafr El-Sheikh Governorate, Egypt. In 2013/14 season, F_1 plants were selfed and backcrossed to each parent under the same wirecages to obtain the F_2, BC_1 and BC_2 for each cross.

In 2014/2015 growing season, the six population seeds ,i.e. P_1,P_2,F_1,F_2,BC_1 and BC_2 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 three meters length and 60 cm width. Hills were spaced 20 cm apart with one seed per hill. Plots varied in size;16 rows for F_2, 9 rows for BC_1 and BC_2 and 3 rows for P_1, P_2 and F_1. 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 five parental faba bean varieties used in the present study.

Parent	Genotype	Pedigree	@Disease reaction	Earliness of maturity	Agronomic characters		
					Flowering date	*Seed coat and hilum color	Seed size
P1	Sakha1	Giza 716 x 620/283/85	R	Early	Early	Light brown(BH)	Medium
P2	Sakha2	Rena Blanka x 461/845/83	R	Medium	Medium	Colorless (WH)	Medium
P3	Giza 3	Giza 1 x Dutch 29	MR	Medium	Medium	Light brown(BH)	Medium
P4	Ohshima-Zairai	Introduced from Japan	HS	Very early	Late	Light brown(BH)	Small
P5	Rena Mora	Introduced from Spain	MR	Early	Early	(BH)	Large

@ R= resistant, MR= moderately resistant,HS = Highly susceptible *BH=Black hilum, WH=white hilum

Data of yield and its components were recorded on individual guarded plant for days to flowering , days to maturity, 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 reaction) under the natural infection were the characters registered. The resistance to foliage diseases were determined as in Table (2) with the adjustment of grading system from 1 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).

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 (2).

Table 2: Chocolate spot and rust disease scales according to 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).

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:

$A = \bar{B}c_1 - \bar{p}_1 - \bar{F}_1$

$B = 2\bar{B}c2 - P\bar{2} - F\bar{2}$

$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$

$D = 2\bar{F}_2 - B\bar{C}_1 - B\bar{C}_2$

And

$V(A) = 4V(\bar{Bc}_1) + V(\bar{P}_1) + \bar{V}(F_1)$

$A(B) = 4V(\bar{Bc}_2) + V(\bar{P}_2) + V(\bar{F}_2)$

$A(c) = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_{1)} + \bar{V}(P_2)$

$A\{d\} = 4V(\bar{F}_2) + V(B\bar{C}_1) + V(B\bar{C}_2)$

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 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) type of epistasis. The significance of D scale reveal (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 as three parameter model:

$$m=\tfrac{1}{2}\bar{p}_1+\tfrac{1}{2}\bar{p}_2+4\bar{F}_1-2\bar{BC}_1-2\bar{BC}_2$$

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

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

where, their variances have been computed using following formulae:

$$V_{\bar{m}}=1/4\,\bar{V}\,P_{1+1/4}\,\bar{V}P_2+16\bar{V}\,F_1+4\bar{V}BC_1+4VBC_2$$

$$V_d=1/4\,V\,\bar{P}_{1+1/4}\,V\bar{P}_2$$

And

$$\bar{V}_h=36VBC_1+36VBC_2+64VF_2+V\,F_{1+}\,\bar{9}/4Vp_1+9/4\,Vp_2$$

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

$$t(m)=m/SE(m),\ t\{d\}=d/SE\{d\}\ \text{and}\ t\{h\}=h/SE\{h\}$$

Broad_sense heritability (H) for F_2 – generation was estimated based on the equation:

$$H=\frac{Vg}{Vg+Ve}x100$$

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

$$V_g=V\,F_2-V_e$$

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

Where, ne = $n_{p1}+n_{p2}+n_{f1}$ which represented 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:

$$h^2=2VF_2-(VBC_1+VBC_2)/VF2\,x100$$

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

The expected genetic advance form selection (G_a) 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 F_1 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 :

$\overline{SE}$ for mid parental heterosis $(F_1\text{-}\overline{MP}) = (V\ \overline{F_1} + 1/4V\ \overline{P_{1+}}\ 1/4\ V\overline{P_2})^{1/2}$

SE for better parental heterosis $(\overline{F_1}\text{-}MP) = (\overline{V}\ F_1 + 1/4\overline{V}\ P_{1+}\ 1/4\overline{V}P_2)^{1/2}$

SE for inbreeding depression $(\overline{F_1}\text{-}\overline{F_2}) = (V\ \overline{F_1} + \overline{V}F_2)^{1/2}$

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

Potence ratio: This parameter was calculated as follows: According to Wigan (1944) and Mather and Jinks (1971).

$$\textbf{Potence ratio is (P)} = \frac{\textbf{F1 – M.P}}{\textbf{1/2 (}P_1 - P_2\textbf{)}}$$

Where: F_1 = Mean of the F_1 generation.

$$\textbf{M.P= Mid-parent value} = \frac{P_1 + P_2}{2}$$

P_1= The mean of the better parent, and

P_2= The mean of the second parent.

Absence of dominance is considered when (P) is zero, and partial dominance is assumed when (P) is between +1.0 and -1.0, but not equal zero, and complete dominance is present when the (P) equals either +1 or -1.0 (+1.0= P= -1.0), over dominance is considered when the (P) exceeds either (+1.0) or (-1.0); i.e., (-1<P> +1).

RESULTS AND DISCUSSION

The difference between each two parents were found to be significant in all studied traits in the three crosses except number of branches/plant in the second cross as the t-test indicated. The genetic variance within F_2-population was also found to be significant for all traits in the three crosses under investigation (Table 3). Consequently, the genetic parameters needed in this concern were calculated.

Table 3 :Number of plants (n), mean of performance($\bar{x}$) and variance of mean($S^2_{\bar{x}}$) for studied traits in the three faba bean crosses.

Trait	Cross	Statistical parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
Days to flowering	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	60.18	48.28	55.39	56.17	58.59	53.89
		$S^2_{\bar{x}}$	0.402	0.367	0.650	0.421	0.434	0.458
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	49.17	83.56	62.91	75.89	54.13	70.80
		$S^2_{\bar{x}}$	0.144	0.181	0.434	0.397	0.304	0.501
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	61.14	48.28	53.44	58.20	56.47	49.56
		$S^2_{\bar{x}}$	0.20	0.37	0.65	0.48	0.57	0.48
Days to maturity	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	169.44	151.36	158.14	159.51	160.18	155.29
		$S^2_{\bar{x}}$	0.425	0.515	0.962	0.522	0.501	0.622
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	151.45	139.29	148.10	150.03	150.67	147.34
		$S^2_{\bar{x}}$	0.351	0.436	0.700	0.568	0.634	0.527
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	164.12	151.36	156.75	160.13	159.21	153.49
		$S^2_{\bar{x}}$	0.390	0.515	0.655	0.427	0.469	0.579
Plant height	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	152.45	105.12	136.13	116.95	148.67	120.33
		$S^2_{\bar{x}}$	0.811	0.510	1.076	0.932	0.890	1.227
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	138.15	115.00	129.72	125.80	135.00	120.56
		$S^2_{\bar{x}}$	0.198	0.389	0.701	0.540	0.573	0.677
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	141.13	105.12	125.50	126.09	127.44	114.44
		$S^2_{\bar{x}}$	0.637	0.509	0.970	0.496	0.571	0.534
No. of branches /plant	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	3.02	4.75	3.9	4.04	4	4.24
		$S^2_{\bar{x}}$	0.022	0.022	0.027	0.015	0.015	0.016
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	3.20	3.50	4.18	3.25	3.24	3.61
		$S^2_{\bar{x}}$	0.008	0.010	0.020	0.010	0.011	0.011
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	3.28	4.75	5.10	4.81	3.68	4.86
		$S^2_{\bar{x}}$	0.009	0.010	0.020	0.012	0.012	0.013
No. of pods/plant	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	23.03	10.05	26.3	19.89	27.44	15.13
		$S^2_{\bar{x}}$	0.437	0.128	0.703	0.544	0.607	0.506
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	24.68	17.58	29.43	26.91	25.62	21.64
		$S^2_{\bar{x}}$	0.206	0.362	0.590	0.864	0.807	0.920
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	23.73	10.05	18.85	19.35	24.89	15.53
		$S^2_{\bar{x}}$	0.282	0.128	0.428	0.583	0.653	0.567
No. of seeds/plant	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	67.13	54.10	78.03	60.52	82.78	65.73
		$S^2_{\bar{x}}$	0.791	1.032	1.382	1.042	0.940	1.245
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	90.70	43.43	84.25	60.39	86.58	63.51
		$S^2_{\bar{x}}$	0.278	0.429	0.472	0.399	0.461	0.387

Continue Table 3 :Number of plants (n), mean of performance($\bar{x}$) and variance of mean($S^2_{\bar{x}}$) for studied traits in the three faba bean crosses.

Trait	Cross	Statistical parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	79.48	54.10	78.78	69.53	94.13	62.28
		$S^2_{\bar{x}}$	0.426	0.587	1.374	0.962	1.064	1.094
Seed yield/plant (g)	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	47.64	66.63	78.63	59.47	69.32	79.13
		$S^2_{\bar{x}}$	0.277	0.423	0.558	0.704	0.655	0.738
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	75.36	23.89	65.58	40.09	69.67	43.70
		$S^2_{\bar{x}}$	0.182	0.261	0.367	0.224	0.256	0.210
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	70.64	66.63	81.85	67.24	89.81	73.86
		$S^2_{\bar{x}}$	0.592	0.423	1.084	1.240	1.312	1.298
No. of seeds/pod	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	2.87	5.38	3.08	3.04	3.02	4.34
		$S^2_{\bar{x}}$	0.005	0.003	0.008	0.004	0.004	0.003
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	3.67	2.40	2.86	2.24	3.37	2.93
		$S^2_{\bar{x}}$	0.004	0.003	0.004	0.003	0.004	0.004
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	3.35	5.38	4.17	3.59	3.78	4.01
		$S^2_{\bar{x}}$	0.005	0.003	0.006	0.007	0.008	0.007
100-seed weight	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	70.97	123.16	100.76	98.27	83.74	120.39
		$S^2_{\bar{x}}$	0.416	0.320	0.496	0.546	0.636	0.523
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	83.09	55.01	77.84	66.39	80.47	68.80
		$S^2_{\bar{x}}$	0.270	0.219	0.428	0.422	0.523	0.387
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	88.87	123.16	103.90	96.71	95.41	118.59
		$S^2_{\bar{x}}$	0.476	0.320	0.745	0.860	0.979	0.847
Chocolate spot disease	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	3.98	5.80	4.16	4.03	4.12	5.14
		$S^2_{\bar{x}}$	0.003	0.004	0.006	0.005	0.004	0.006
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	3.15	6.19	4.24	5.21	3.96	5.10
		$S^2_{\bar{x}}$	0.004	0.005	0.006	0.004	0.004	0.005
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	3.24	5.80	3.89	4.66	3.36	5.25
		$S^2_{\bar{x}}$	0.005	0.004	0.004	0.008	0.009	0.008
Rust disease	Cross 1	n	45	45	45	240	150	150
		$\bar{x}$	5.21	6.01	5.36	5.15	4.39	5.19
		$S^2_{\bar{x}}$	0.003	0.003	0.004	0.004	0.004	0.004
	Cross 2	n	45	45	45	240	150	150
		$\bar{x}$	3.89	6.64	4.65	5.01	4.30	5.25
		$S^2_{\bar{x}}$	0.003	0.004	0.007	0.004	0.005	0.004
	Cross 3	n	45	45	45	240	150	150
		$\bar{x}$	3.60	6.01	4.53	5.38	3.65	5.54
		$S^2_{\bar{x}}$	0.003	0.003	0.003	0.005	0.005	0.006

Cross 1 (Giza 3 x Rena Mora), Cross 2 (Sakha 1 x Ohshima-Zairai) and Cross 3 (Sakha 2 x Rena Mora).

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 interactions. The significance of C scale suggests (dd) type of epistasis. The significant D scale reveal (aa) gene interaction, significance of C and D scales indicates (aa) and (dd) type of gene interactions. 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 4) indicated that, the values of scaling test were significantly differ than zero for all studied traits in all crosses, which mean the presence of non-allelic gene interactions and the six parameter model must be done in all cases.

Table 4 :Estimates of scaling test and type of gene action of the studied traits in three faba bean crosses.

Trait	Cross	Scaling test				Six parameters as Gamble procedure					
		A	B	C	D	m	a	d	aa	ad	dd
Days to flowering	1	1.61	4.11*	5.44	-0.14	56.17**	4.7**	1.44	0.28	-1.25	-6.00
	2	-3.82**	-4.87**	45.01**	26.85**	75.89**	-16.67**	-57.16**	-53.7**	0.53	62.39**
	3	-1.64	-2.6*	16.50**	10.37**	58.20**	6.91**	-22.01**	-20.74**	0.48*	24.98**
Days to maturity	1	-7.22**	1.08	0.96	3.55*	159.51**	4.89**	-9.36**	-7.10**	-4.15**	13.24**
	2	1.79	7.29**	13.18**	2.05	150.03**	3.33**	-1.37	-4.10	-2.75*	-4.98
	3	-2.45	-1.13	11.54**	7.56**	160.13**	5.72**	-16.11**	-15.12**	-0.66**	18.70**
Plant height	1	8.76**	-0.59	-62.03**	-35.1**	116.95**	28.34**	77.55**	70.20**	4.68**	-78.37**
	2	2.13	-3.6	-9.39**	-3.96*	125.80**	14.44**	11.07**	7.92*	2.86*	-6.45
	3	-11.75**	-1.74	7.11*	10.30**	126.09**	13.00**	-18.23**	-20.60**	-5.01**	34.09**
No. of branches /plant	1	1.08**	-0.17	0.59	-0.16	4.04**	-0.24	0.34	0.32	0.63**	-1.23
	2	-0.9**	-0.46	-2.06**	-0.35	3.25**	-0.37*	1.53**	0.70	-0.22	0.66
	3	-1.02**	-0.13	1.01	1.08**	4.81**	-1.18**	-1.075*	-2.16**	-0.45**	3.31**
No. of pods/ plant	1	5.55**	-6.09**	-6.12	-2.79	19.89**	12.31**	15.34**	5.58	5.82**	-5.04
	2	-2.87	-3.73	6.52	6.56**	26.91**	3.98**	-4.82	-13.12**	0.43	19.72**
	3	7.2**	2.16*	5.92	-1.72	19.35**	9.36**	5.4	3.44	2.52**	-12.80**
No. of seeds/ plant	1	20.4**	-0.67	-35.21**	-27.50**	60.52**	17.05**	72.36**	54.94**	10.54**	-74.67**
	2	-1.79	-0.66	-61.07**	-29.30**	60.39**	23.07**	75.81**	58.62**	-0.57	-56.17**
	3	30**	-8.32**	-13.02*	-17.40**	69.53**	31.85**	46.69**	34.70**	19.16**	-56.38**
Seed yield/ plant(g)	1	12.37**	13.00**	-33.65**	-29.50**	59.47**	-9.81**	80.52**	59.02**	-0.32	-84.39**
	2	-1.6	-2.07	-70.05**	-33.20**	40.09**	25.97**	82.34**	66.38**	0.23	-62.71**
	3	27.13**	-0.76	-32.01**	-1.82	67.24**	15.95**	71.60**	58.38**	13.95**	-84.75**
No. of seeds/ pod	1	0.09	0.22	-2.25**	-1.28**	3.04**	-1.32**	1.52**	2.56**	-0.06	-2.87**
	2	0.21	0.60**	-2.83**	-1.82**	2.24**	0.44**	3.47**	3.64**	-0.20*	-4.45**
	3	0.04	-1.53**	-2.71**	-0.61**	3.59**	-0.23*	1.03**	1.22**	0.79**	0.27
100-seed w eight	1	-4.25*	16.86**	-2.57	-7.59**	98.27**	-36.65**	18.88**	15.18**	-10.6**	-27.79**
	2	0.01	4.75**	-28.22**	-16.50**	66.39**	11.67**	41.77**	32.98**	-2.37*	-37.74**
	3	-1.95	10.12**	-32.99**	-20.60**	96.71**	-23.18**	39.05**	41.16**	-6.04**	-49.33**
Chocolate spot disease	1	0.1	0.32	-1.98**	-1.20**	4.03**	-1.02**	1.67**	2.40**	-0.11	-2.82**
	2	0.53**	-0.23	3.02**	1.36**	5.21**	-1.14**	-3.15**	-2.72**	0.38**	2.42**
	3	-0.41	0.81**	1.82**	0.71**	4.66**	-1.89**	-2.05**	-1.42**	-0.61**	1.02**
Rust disease	1	-1.79**	-0.99**	-1.34**	0.27**	5.15**	-0.8**	-1.69**	-1.44**	-0.40**	4.22**
	2	0.06	-0.79*	0.21	0.47**	5.01**	-0.95**	-1.56**	-0.94**	0.43**	1.67**
	3	-0.83**	0.54**	2.85**	1.57**	5.38**	-1.89**	-3.42**	-3.14**	-0.69**	3.43**

Cross 1 (Giza 3 x Rena Mora), Cross 2 (Sakha 1 x Ohshima-Zairai) anad Cross 3(Sakha 2 x Rena Mora).

***and * significant at 0.05 and 0.01 levels of probability, respectively.**

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 first cross (Giza 3 x RM) for no. of branches/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) either in positive or negative directions. The values of dominant effect were significant in all crosses for all traits, except for days to flowering date and No. of branches/plant in the first cross, days to maturity and No. of pods/plant in the second cross, and No. of pods/plant in the third 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 genotypes can't be practiced in the early generation but it would be effective in the late ones. Similar results were obtained by Abo Mostafa *et al*. (2009), El-Hady *et al.* (2009), Ashrei *et al.* (2013), El-Refaey and Abd El-Razek (2013) and Abo Mostafa *et al.* (2014).

The additive x additive gene effects was highly significant either in positive or in negative directions in all crosses for all studied traits, except days to flowering and No. of branches in the first cross, days to maturity in the second cross and No. of pods/plant in the third cross. However, significant positive or negative epistatic gene action (ad) was observed in all crosses for all studied traits, except days to flowering, seed yield/plant, No. of seeds/pod and chocolate spot disease reaction in the first cross; and days to flowering, No. of branches/plant and No. of pods/plant, where the values were not significant. The same trend was found with respect to dominance x dominance (dd), where positive or negative significant were observed. However, significant values were detected in all crosses for all studied traits, except No. of days to flowering, No. of branches/plant and No. of pods/plant in first cross and No. of days to maturity, plant height and No. of branches/plant in the second cross and No. of seeds/pod in the third cross where the values did not reach to the level of significant. 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 rays to oss and no. of dmain 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. Nighawan and Yadava (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 and Salem (2006), Al-Ghamdi (2007), El-Galaly *et al*. (2008), El-Refaey and Abd El-Razek (2013) and Abo Mostafa *et al.* (2014).

Results presented in Table (5) indicated that heterosis over mid and better parent for all traits were highly significant in positive or negative direction, except days to flowering in the first and third cross, days to maturity in the third cross and No. of branches/plant in the first cross over mid parents, and also, No. of seeds/plant in the third cross with respect to better parent. Potance ratio were less than unity but not equal zero for most traits concerning yield and its components, indicating partiol dominance. The presence of heterosis over better parent with respect to the first cross for No. of pods/plant, No. of seeds/plant and seed yield/plant in positive direction No. of branches/plant and No. of pods/plant in the second cross and No. of branches/plant and seed yield /plant in the third cross , which would indicate that progeny of these crosses could by used in breeding program for high yielding ability.

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 seeds/pod in the second and third crosses, No of seeds/plant and seed yield/plant in the second cross, chocolate spot and rust diseases reaction in the first cross. On the other hand, negative inbreeding depression values were obtained for chocolate spot and rust diseases reaction in the second and third crosses. 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 of 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).

Table 5 : Estimates of mid(MP) and better(BP) parental, potence ratio(PR),inbreeding depression (ID%), Heritability in broad sense(H) and narrow sense (h^2), expected (Ga) and predicted (Ga%) genetic advance, genotypic coefficient of variation (GCV%) and phenotypic coefficient of variation(PCV%) of the three faba bean crosses for the studied traits.

Traits	Cross	M.B	P. R	B.P	I.D	Heritability		Genetic advance		GCV %	PCV%
						H	h^2	Ga	Ga%		
Days to flowering	1	2.14	0.19	14.34**	-1.41	84.21	67.73	14.03	24.98	15.91	17.90
	2	-5.21**	-0.2	27.94**	-20.63	88.06	63.97	12.87	16.96	12.07	12.87
	3	-2.32	-0.2	10.69**	-8.91	84.15	63.28	13.99	24.04	16.92	18.44
Days to maturity	1	-1.41*	-0.25	4.48**	-0.87	77.21	65.47	15.09	9.46	6.16	7.01
	2	-0.87	-0.21	3.45**	-1.30	83.63	72.21	17.36	11.57	7.12	7.78
	3	-0.63	-0.16	3.56**	-2.16	77.18	46.64	9.73	6.08	5.56	6.32
Plant height	1	5.70**	0.31	-10.71**	14.09	83.92	58.02	17.88	15.29	11.72	12.79
	2	2.48**	0.27	-6.16**	3.02	85.10	55.48	13.02	10.35	8.35	9.05
	3	1.93*	0.13	-11.07**	-0.47	73.36	60.87	13.69	10.86	7.41	8.66
No. of branches /plant	1	0.39	0.02	-17.89**	-3.59	76.21	67.90	2.62	64.95	38.72	45.64
	2	24.78**	5.53	19.43**	22.25**	76.68	65.84	2.11	65.06	42.00	47.96
	3	27.02**	1.48	7.37**	5.69**	80.07	67.01	2.35	48.96	31.73	35.47
No. of pods/ plant	1	59.01**	1.5	14.20**	24.37	85.43	72.16	16.98	85.39	53.10	57.45
	2	39.28**	2.34	19.25**	8.56	91.62	75.00	22.25	82.66	51.21	53.50
	3	11.60**	0.29	-20.56**	-2.65	91.02	69.28	16.88	87.25	58.32	61.13
No. of seeds/ plant	1	28.73**	2.67	16.24**	22.44	80.78	68.99	22.48	37.14	23.49	26.13
	2	25.62**	0.73	-7.11**	28.32**	81.52	67.05	13.51	22.37	14.62	16.20
	3	17.95**	0.94	-0.88	11.74	84.48	59.74	18.70	26.89	20.08	21.85
Seed yield/ plant(g)	1	37.62**	2.26	18.01**	24.37	88.13	68.53	20.43	34.36	20.60	21.20
	2	32.15**	0.62	-12.98**	38.87**	77.39	69.94	10.56	26.34	16.08	18.28
	3	19.25**	6.59	15.87**	17.85	89.42	68.46	24.33	36.19	24.27	25.66
No. of seeds/ pod	1	-25.33**	-0.83	-42.75**	1.30	83.39	56.47	1.18	38.95	25.55	30.33
	2	3.46*	0.17	-14.44**	21.68**	81.30	54.88	1.02	45.70	36.45	40.43
	3	-4.47*	-0.19	-22.49**	13.91**	87.27	60.61	1.60	44.67	33.43	35.78
100-seed weight	1	3.81**	0.14	-18.19**	2.47	85.90	67.36	15.88	16.16	10.80	11.65
	2	12.73**	0.63	-6.32**	14.71	86.40	65.17	13.51	20.34	14.08	15.15
	3	-2.00*	-0.12	-15.64**	6.92	88.80	67.42	19.96	20.64	14.00	14.86
Chocolate spot disease	1	-14.93**	-0.8	4.52**	3.13**	83.04	67.54	1.49	36.86	24.14	26.49
	2	-9.21**	-0.28	34.60**	-22.88**	75.89	56.38	1.13	21.61	16.21	18.61
	3	-13.94**	-0.49	20.06**	-19.79**	90.00	63.68	1.81	38.81	28.06	29.58
Rust disease	1	-4.46**	-0.62	2.88**	3.92**	85.61	73.68	1.48	28.73	17.51	18.93
	2	-11.68**	-0.45	19.54**	-9.68**	77.78	67.71	1.37	26.80	17.25	19.21
	3	-5.72**	-0.23	25.83**	-18.76**	87.65	51.85	1.11	20.63	18.08	19.32

Cross 1 (Giza 3 x Rena Mora), Cross 2 (Sakha 1 x Ohshima-Zairai) anad Cross 3(Sakha 2 x Rena Mora).

***and * significant at 0.05 and 0.01 levels of probability, respectively.**

Heritability estimates:

The high broad sense heritability values were obtained for No. of pods/plant in the second and third cross being (91.62% and 91.02% respectivily) and chocolate spot disease reaction in the third cross (Table 5).

Meanwhile, the lowest estimates was resulted for plant hight in the third cross with value of 73.36%. Heritability in narrow sense as estimated by using F_2 and backcrosses data were low for days to maturity and rust disease reaction in the third cross with value of 46.64% and 51.85%, respectively. Meanwhile, high narrow sense heritability values for No. of pods/plant in the second cross and rust disease reaction in the first cross with values 75.00% and 73.68%, 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), Abou Mostafa *et al*. (2009), *El-Hady et al. (2009) and Ashrei et al. (2013).*

Genetic advance:

The genotypic coefficient of variability (GCV%), phenotypic coefficient(PCV%),the genetic advance and the expected and predicted genetic advance upon selection as a percentage of F_2 generation for the studied characters are presented in Table (5). No. of branches/plant, No. of pods/plant and No. of seeds/pod in the three crosses exhibited high GCV% and PCV% and predicted genetic advance with high heritability. The highest genetic advance as mean percent (Ga%) were detected for No. of pods/plant in the three crosses being (85.39, 82.66 and 87.25%), respectively. Meanwhile, low predicted genetic advance values were obtained for days to maturity in the three crosses being (9.46, 11.57 and 6.08%), and for plant height in the three crosses (15.29, 10.35 and 10.86%, 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 work, high genetic advance was associated with high heritability values in narrow sense and GCV% and PCV% for No. of branches / 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 GCV% 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.

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

Abo Mostafa, R.A.I, E.A.D. Sarhan and Zeinab, E. Gareeb (2014). Generation mean analysis for disease resistance, yield and its components in three crosses of faba bean (*Vicia faba* L.).j.Plant Production, Mansoura Univ., 5 (8): 1375-1390.

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, K, 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., S.B. Hanounik, M.M. Hussein and H.A. Mohamed (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.

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. 46(2): Ag. 131-140, (2008).

El-Hady, M.M., Gh.A. Gad El-Karim and M.A. Omar (1997). Genetical studies in faba bean *(Vicia faba* 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.

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.

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.

Mather, K. and J.L. Jinks (1971). Biometrical genetics. Cornell Univ. Press. Ithaca,N.Y.,231pp.

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

Nighawan, 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.

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

Wigan, L.G. (1944). Balance and potence in natural populations. J. Genet. 46: 150-160.

المكافىء الوراثى والتأثير الجينى للمقاومة للأمراض والمحصول ومكوناته فى ثلاثة هجن للفول البلدى

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تم دراسة المقايس الوراثية المتحكمة فى صفات المقاومة لأمراض المجموع الخضرى والمحصول ومكوناتة للفول البلدى باستخدام تحليل متوسط الأجيال خلال المواسم ١٣/٢٠١٢ و ١٤/٢٠١٣ و١٥/٢٠١٤ فى محطة البحوث الزراعية بسخا – كفر الشيخ – مصروقد تم استخدام مقاييس العشائر الستة (P_1, P_2, F_1, F_2, BC_1 and BC_1) لثلاثة هجن من الفول البلدى (جيزة ٣ x رينامورا) و(سخا ١ x أوشيما زايارا) و(سخا ٢ x رينا مورا) لهذة الدراسة

ويمكن تلخيص النتائج المتحصل عليها فيما يلى:

أوضحت النتائج أن كلا من التأثيرين الوراثين المضيف والسيادى لهما معنوية عالية لصفات عدد البذور للنبات ، ومحصول النبات، وعدد البذور فى القرن،وزن ١٠٠ بذرة ،والحساسية للتبقع البنى والصدأ فى الهجن الثلاثة بما يشير الى أهمية كلاهما فى وراثة هذة الصفات وهذا الى جانب وجود تأثير للفعل الجينى التفوقى وخاصة المضيف x المضيف (aa) والذى يتفوق فى تأثيرة على الفعل الجينى المضيف ولكنة يقل فى تأثيرة عن الفعل الجينى السيادى.

أشارت النتائج الى أن قوة الهجين على اساس متوسط الأبوين معنوية وسالبة لصفات التزهير فى الهجين الثانى والنضج فى الهجينين الأول والثانى والحساسية للتبقع البنى والصدأ فى الهجن الثلاثة وترجع قوة الهجين هذة الى السيادة الجزيئية تجاة كلامن الأب المبكر فى التزهيروالنضج والمقاومة للأمراض بينما قوة الهجين بناء على الأب الأفضل (المبكر والأكثر مقاومة للأمراض) فلم تصل اى من الهجن تحت الدراسة لصفات التزهير والنضج والمقاومة للتبقع البنى والصدأ الى القيم السالبة المعنويةوالمفيدة من وجة نظر المربى حيث كانت جميع القيم موجبة وعالية المعنوية وبالنسبة لصفة المحصول ومكوناتة فقد كانت قوة الهجين سواء على أساس متوسط الأبوين أو الأب الأفضل موجبة وعالية المعنوية لصفات عددالفروع للنبات فى الهجينين الثانى والثالث وعدد القرون للنبات فى الهجينين الأول والثانى وعدد البذورللنبات فى الهجين الأول ومحصول النبات فى الهجينين الأول والثالث ويبدو ان قوة الهجين العالية ترجع الى تعاظم الفعل الجينى السيادى وخصوصا السيادة المتفوقة تجاة الأب الأعلى (P> +1) الى جانب وجود الفعل الجينى التفوقى.

أظهرت النتائج أن التدهور الراجع الى التربية الداخلية معنويا وفى الإتجاة الموجب لصفات عدد الفروع للنبات وعدد البذور للقرن فى الهجينين الثانى والثالث وعدد البذور للنبات ومحصول النبات فى الهجين الثانى والحساسية للتبقع البنى والصدأ فى الهجين الأول بينما كانت سالبة ومعنوية للحساسية للتبقع البنى والصدأ فى الهجينين الثانى والثالث.

وتشير الدراسة كذالك الى ان النسبة المؤية للتحسين الوراثى المتوقع من الإنتخاب كانت عالية لصفات عدد الفروع للنبات وعدد القرون للنبات وعدد البذور فى القرن فى الهجن الثلاثة وذلك لارتباطها بالقيم العالية لكل من المكافى الوراثى فى معناة المحدود ومعامل الإختلاف الوراثى لذا توصى النتائج بالإنتخاب فى الأجيال الإنعزالية المبكرة ليكون فعالا لتحسين هذه الصفات.