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Estimation of some genetic parameters using six populations mean analysis in three faba bean crosses exposed to natural infection of foliar diseases

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ABSTRACT

This investigation was carried out in three winter seasons 2019/20, 2020/21 and 2021/2022at Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Egypt to estimate some genetic parameters of yield and its components as well as the extent of heterosis, inbreeding depression, heritability, genetic advance, and behavior of gene action in three faba bean crosses. The analysis of gene effects was done using means of Six populations (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) of three faba bean crosses were used in this study. These crosses were (Sakha 3 x R V 322), (Nubaria 1 x RV 322) and (Giza 429 x Marina). Analysis of variance showed significant differences among the generations for all traits. Scaling test showed that most studied characters were significant, indicating the presence of non-allelic interactions. Both dominance and additive gene effects were important but mostly dominance higher than additive ones, indicating that dominant genes playing an important role in the inheritance of such traits beside the additive one. The second cross (Nubaria 1 x RV 322) gave a highly significant (aa) with negative values for flowering, maturity, chocolate spot and rust diseases traits, these indicate that the materials used in this study have a decreasing alleles expression which makes it improving through selection in the early generations. Significant positive inbreeding depression and heterotic effect values were detected for most studied traits. Crosses, especially the first cross (Sakha 3 x R V 322) gave the highest heritability in narrow-sense and genetic advance for number of branches, number of pods/plants, number of seeds/pod and seed yield. Therefore, selection in these populations should be effective and satisfactory in the successful breeding purposes.

Keywords: *Vicia faba*, Genetic parameters, Heterosis, Heritability, Genetic advance.

INTRODUCTION

Faba bean (*Vicia faba* L.) has a great role in human nutrition as a major source of protein. The crop is generally included in the crop rotation to keep soil fertility through nitrogen fixation. Faba bean is a partially self-pollinated crop and displays a considerable amount of heterosis and inbreeding depression (Lawes *et al.,* 1983).

The plant breeder is interested in estimating gene effects to formulate the most advantageous breeding procedures for improving his breeding material. Therefore, breeders need information about the nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for given characters. Genetic information from multi populations (P_1, P_2, F_1, F_2, Bc_1 and Bc_2) maybe considered the one of the methods that gives early genetic information of the employed genotypes.

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 (Heiba *et al*., 2022). The losses 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).

Hybrid vigour for seed yield is associated with manifestation of heterotic effects of yield components. The heterotic effects in faba bean are pronounced in F_1 especially among widely divergent parents and less between local varieties (Attia *et al.,* 2002; Attia *et al*., 2006; El-Hady *et al.,* 2009 and Abdalla *et al.,* 2017). Inbreeding depression not only reduces auto fertility and hence yield in the absence of pollinators, but also reduces yield through the loss of heterosis. Poulsen (1979) stated that' the decreased yield after three generations of selfing occurred due to inbreeding depression and reduced auto fertility and he mentioned that inbreeding depression alone-reduced yield by 11%. Moreover, Attia *et al*., (2006), El-Hady *et al.,* (2009) and Abdalla *et al*., (2017) reported that' the F_2's exhibited generally lower values than F_1's for most characters in faba bean with high inbreeding depression.

The success of any breeding program depends on the presence of sufficient genetic variability among used genotypes to permit effective selection. In a systematic breeding program, the genetic variance components analysis in terms of type of gene action, heritability and breeding potentials of genetic entries involved in this program are obviously essential. The low heritability and consequent limited genetic advance for yield in response to selection has led many scientists to search for characters which are associated with yield, but which are relatively highly heritable. Bond (1966) reported that' components of yield were general nearer to additively than yield. Poulsen (1979) stated that' although a major part of the variation in seed yield was detected as additive genetic variance and the dominance effects also play a considerable role in the inheritance of this trait.

The present investigation was undertaken to study the behavior of gene action and other genetic parameters for foliage diseases, yield, and its components in three faba bean crosses and their six populations' i. e., P_1, P_2, F_1, F_2, Bc_1 and Bc_2.

MATERIALS AND METHODS

Field experiments:

The present investigation was carried out during the successive seasons of 2019/20, 2020/21 and 2021/2022, at the Farm Sakha Agricultural Research Station (SARS). Five parental varieties of faba bean (*vicia faba L.*) namly; Sakha 3, Nubaria 1, Giza 429, RV 322 and Marina were used to generate the experimental materials for this study. Three crosses were produced namely, Sakha 3 x R V 322, Nubaria 1 x RV 322 and Giza 429 x Marina are designated in the text as first, second and third cross, respectively.

In 2019 /20 season F_1's and their correspondent parents were sown under wire cages. In 2020/21 season, F_1 plants were selfed and at the same time backcrossed to each parent under the same wire cages to obtain the F_2, BC_1 and BC_2 for each cross.

In 2021/2022 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 rows of three meters length and 60 cm width, distance between one plant and another was 20 cm apart with one seed per hill. Plots varied in size; 18therows for F_2, 8 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. Names, Pedigree, botanical group, disease reaction and agronomic characters of five parental faba bean genotypes used in this investigation.

Parents	Genotypes	Pedigree	Botanical group	Disease's foliar reaction	Agronomic characters	
					Flowering date	Earliness of maturity
P_1	**Sakha 3**	Giza716 (Giza461x503/453/83)	Equina	Highly resistant	Medium	Late
P_2	**Nubaria 1**	(Reina blanca) introduction from Spain	Major	Resistant	Late	Late
P_3	**Giza 429**	Selection from Giza 402	Equina	Susceptible	Medium	Medium
P_4	**RV 322**	HEL 170, inbred line (China)	miner	Highly susceptible	Early	Very early
P_5	**Marina**	Introduced from Hungary	miner	Highly resistant	Medium	Late

Data of yield and its components were recorded on the base of 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 severity 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).**

Statistical and Genetic Procedures:

Heterosis and inbreeding depression (%) were estimated according to Miller *et al.* (1958). Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula suggested by Dudley and Moll (1969). The analysis was proceeded to estimate the various gene effects using the six parameters genetic model of Jinks and Jones (1958) and Hayman (1958) as follows:

m = Mean effect. d = Additive gene effects.
h = Dominance gene effects. i = Additive x additive epistatic gene effects.
j = Additive x dominance epistatic gene effects.
l = Dominance x dominance epistatic gene effects.

RESULTS

Mean performance:

Data of No. of plants, mean performance, and variance for the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the three crosses for different traits are presented in Table (3). Results revealed significant differences among the tested genotypes for most studied traits, indicating the presence of genetic differences between generations' means among crosses.

In **Table (3),** the cross 1 and cross 2 had the earliest P_1 parent for flowering and maturity plants recording 33.17 and 124.37 days, respectively. Meanwhile, P_1 in the cross 3 had the lowest infected plants to chocolate spot and rust diseases reaction and recorded 2.73 and 2.60, respectively.

Table 3. Number of plants (n), mean of performance ($\bar{X}$) and variance of means($S^2\bar{X}$) for the six populations of the three crosses for studied traits.

Traits	**Crosses**	**Statistical Parameter**	**P_1**	**P_2**	**F_1**	**F_2**	**BC_1**	**BC_2**
		n	**45**	**45**	**45**	**270**	**120**	**120**
Days to flowering	**Cross 1**	$\bar{X}$	33.17	51.67	40.60	48.75	36.13	47.33
		S^2	2.42	5.75	12.52	45.46	23.93	36.31
		$S^2\bar{X}$	0.054	0.128	0.278	0.168	0.266	0.403
	Cross 2	$\bar{X}$	33.17	77.33	57.50	60.13	40.53	67.67
		S^2	2.42	6.04	6.47	27.07	2.41	16.31
		$S^2\bar{X}$	0.054	0.134	0.144	0.113	0.016	0.109
	Cross 3	$\bar{X}$	51.83	42.17	47.17	57.95	52.78	47.56
		S^2	6.01	6.35	6.83	29.21	18.31	19.39
		$S^2\bar{X}$	0.134	0.141	0.152	0.122	0.122	0.129
Days to maturity	**Cross 1**	$\bar{X}$	124.37	157.83	139.03	148.01	129.78	141.73
		S^2	6.79	6.35	16.55	43.28	25.63	35.74
		$S^2\bar{X}$	0.151	0.141	0.368	0.160	0.285	0.397
	Cross 2	$\bar{X}$	124.37	169.5	149.67	153.8	138.33	151.80
		S^2	6.79	5.43	9.61	21.59	16.31	15.84
		$S^2\bar{X}$	0.151	0.121	0.214	0.090	0.109	0.106
	Cross 3	$\bar{X}$	168.33	153.67	158.33	166.06	167.89	161.89
		S^2	4.75	5.06	10.75	58.86	36.24	48.01
		$S^2\bar{X}$	0.106	0.112	0.239	0.245	0.242	0.320
Plant height (cm)	**Cross 1**	$\bar{X}$	63.33	127	115.63	119.34	101.08	122.22
		S^2	24.71	17.14	57.41	91.70	63.52	77.78
		$S^2\bar{X}$	0.549	0.381	1.276	0.340	0.706	0.864
	Cross 2	$\bar{X}$	63.33	125.24	109.38	116.07	99.67	119.26
		S^2	24.71	28.69	59.98	88.71	66.09	69.95
		$S^2\bar{X}$	0.549	0.638	1.333	0.370	0.441	0.466
	Cross 3	$\bar{X}$	145.00	128.33	154.20	139.62	149.00	138.00
		S^2	7.00	55.08	85.71	142.43	120.17	108.17
		$S^2\bar{X}$	1.556	1.224	1.905	0.593	0.801	0.721
No of branches/ plant	**Cross 1**	$\bar{X}$	2.87	3.93	4.88	3.47	3.46	4.28
		S^2	2.05	1.07	3.01	4.36	3.13	3.49
		$S^2\bar{X}$	0.046	0.024	0.067	0.016	0.035	0.039
	Cross 2	$\bar{X}$	2.87	7.81	6.25	5.23	4.40	6.71
		S^2	2.05	1.53	3.76	5.13	4.87	4.4o
		$S^2\bar{X}$	0.046	0.034	0.084	0.021	0.032	0.029
	Cross 3	$\bar{X}$	3.00	4.08	4.16	4.16	4.10	4.00
		S^2	5.71	4.98	6.31	11.21	9.66	8.92
		$S^2\bar{X}$	0.127	0.111	0.140	0.047	0.064	0.059
Chocolate spot disease reaction	**Cross 1**	$\bar{X}$	6.03	3.27	4.07	4.42	4.56	3.13
		S^2	0.24	0.20	0.26	1.02	0.75	0.66
		$S^2\bar{X}$	0.005	0.004	0.006	0.004	0.008	0.007
	Cross 2	$\bar{X}$	6.03	3.13	3.83	4.67	4.41	3.64
		S^2	0.24	0.12	0.24	0.34	0.25	0.29
		$S^2\bar{X}$	0.005	0.003	0.005	0.001	0.002	0.002
	Cross 3	$\bar{X}$	2.73	6.93	4.10	4.08	3.76	5.33
		S^2	0.20	0.17	0.29	0.99	0.68	0.62
		$S^2\bar{X}$	0.004	0.004	0.006	0.004	0.005	0.004
Rust disease reaction	**Cross 1**	$\bar{X}$	5.53	3.13	3.90	3.35	4.75	3.19
		S^2	0.26	0.12	0.27	0.81	0.59	0.59
		$S^2\bar{X}$	0.006	0.003	0.006	0.003	0.007	0.007
	Cross 2	$\bar{X}$	5.53	3.40	4.30	4.93	4.20	3.63
		S^2	0.26	0.25	0.22	0.47	0.16	0.23
		$S^2\bar{X}$	0.006	0.006	0.005	0.002	0.001	0.002
	Cross 3	$\bar{X}$	2.60	7.33	4.43	4.11	3.47	5.31
		S^2	0.16	0.23	0.25	0.65	0.39	0.52
		$S^2\bar{X}$	0.004	0.005	0.006	0.003	0.003	0.003

F_1 had the tallest plants (154.20 cm) and had profuse branches in the crosses 1 and 3, respectively, whereas the cross 1 and cross 2 had the shortest plants (63.33 cm) for P_1. The mean of BC_1 was the highest No. of pods/plant (37.22 pods); meanwhile, BC_2 recorded the highest No. of seeds/plant (107.06 seeds) in cross 1.

The mean of F_1 population recorded the highest for No. of pods/plant (33.50 pods) in the second cross, No. of seeds/plant (88.88 and 99.08 seeds) in the cross 2 and cross 3, respectively and seeds yield /plant (68.57 g) in the cross 3. While P_2 had high values for 100-seed weight trait in all crosses, recording the highest mean in the cross 2 (112.44 g).

Continue Table 3.

Traits	Crosses	Statistical Parameter	P_1	P_2	F_1	F_2	BC_1	BC_2
		N0.	45	45	45	270	120	120
No. of pods/plant	Cross 1	$\bar{X}$	17.77	21.93	30.00	35.46	37.22	33.47
		S^2	32.87	30.07	175.71	292.90	197.09	199.86
		$S^2\bar{X}$	0.730	0.668	3.905	1.085	2.190	2.221
	Cross 2	$\bar{X}$	17.77	15.19	33.50	24.21	29.40	23.05
		S^2	32.87	59.86	152.57	197.60	162.18	171.92
		$S^2\bar{X}$	0.730	1.330	3.390	0.823	1.081	1.146
	Cross 3	$\bar{X}$	28.33	23.04	35.60	24.37	36.00	28.80
		S^2	66.52	86.73	98.58	291.78	216.27	241.20
		$S^2\bar{X}$	1.480	1.930	2.190	1.220	1.440	1.610
No. of seeds/plant	Cross 1	$\bar{X}$	50.07	72.67	99.63	102.06	101.97	107.06
		S^2	68.55	51.52	84.55	150.90	126.75	109.45
		$S^2\bar{X}$	1.523	1.145	1.879	0.559	1.408	1.216
	Cross 2	$\bar{X}$	50.07	66.71	88.88	72.68	89.40	70.93
		S^2	68.55	74.31	93.98	176.60	107.83	146.51
		$S^2\bar{X}$	1.523	1.651	2.088	0.736	0.719	0.977
	Cross 3	$\bar{X}$	77.33	52.21	99.08	92.46	88.10	78.80
		S^2	45.38	33.82	68.66	248.94	173.88	142.70
		$S^2\bar{X}$	1.008	0.752	1.526	1.037	1.159	0.951
No. of seeds /pod	Cross 1	$\bar{X}$	3.070	3.460	3.950	2.900	3.140	3.290
		S^2	0.230	0.170	0.280	0.960	0.680	0.660
		$S^2\bar{X}$	0.005	0.004	0.006	0.004	0.008	0.007
	Cross 2	$\bar{X}$	3.070	4.390	2.790	3.030	2.980	3.220
		S^2	0.230	0.190	0.210	0.710	0.290	0.400
		$S^2\bar{X}$	0.005	0.004	0.005	0.003	0.002	0.003
	Cross 3	$\bar{X}$	2.820	2.200	2.760	3.930	2.600	2.950
		S^2	0.270	0.220	0.320	0.990	0.690	0.620
		$S^2\bar{X}$	0.006	0.005	0.007	0.004	0.005	0.004
100-seed weight (gm)	Cross 1	$\bar{X}$	32.45	73.96	56.96	52.31	45.85	59.29
		S^2	17.37	27.18	32.29	89.66	59.19	68.04
		$S^2\bar{X}$	0.386	0.604	0.718	0.332	0.658	0.756
	Cross 2	$\bar{X}$	32.45	112.44	77.85	60.60	48.46	96.68
		S^2	17.37	24.91	26.3	97.62	39.00	62.07
		$S^2\bar{X}$	0.386	0.554	0.584	0.407	0.26	0.414
	Cross 3	$\bar{X}$	56.95	65.11	60.38	58.63	60.93	58.11
		S^2	22.63	34.67	48.72	157.59	102.29	97.89
		$S^2\bar{X}$	0.503	0.770	1.083	0.657	0.682	0.653
Seed yield/plant	Cross 1	$\bar{X}$	19.43	53.21	53.91	53.25	50.37	63.93
		S^2	31.38	51.34	60.62	548.47	289.47	393.77
		$S^2\bar{X}$	0.697	1.141	1.347	2.031	3.216	4.375
	Cross 2	$\bar{X}$	19.43	75.01	65.37	43.43	44.19	53.19
		S^2	31.38	42.94	66.20	233.17	84.64	104.73
		$S^2\bar{X}$	0.697	0.954	1.471	0.972	0.564	0.698
	Cross 3	$\bar{X}$	43.79	34.61	68.57	53.67	54.20	44.20
		S^2	36.14	42.09	55.59	139.10	110.22	86.15
		$S^2\bar{X}$	0.803	0.935	1.235	0.580	0.735	0.574

However, genotypes of Sakha 3, Nubaria 1 and Marina which recorded the lowest infection to chocolate spot and rust diseases reaction with highest yielding was considered as the most parental resistant genotypes. Meanwhile, Giza 429 and RV 322 were the susceptible ones. The mean of F_1 population recorded values higher than their respective parents. Data cleared that the F_2 variance followed by BC's variance were larger than the non-segregated generations of P_1, P_2 and F_1 for all traits. This indicates that environmental fluctuation has marked effects on the expression of these traits.

Scaling test:

Scaling test A, B, C and D presented in **Table (4)** were significant for all the studied traits in the three crosses, except No of branches/plant in the third cross, indicating the presence of non-allelic interactions and the inadequacy of the simple model in interpreting the differences between population means. Also, the scaling test estimates for insignificant ones (number of branches/plant in the third cross) indicated that, the absence of non-allelic interactions and the additive-dominance model is adequate in this case. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction. Hence, data indicate the presence of non-allelic interaction for all the studied characters. Scaling test and genetical analysis of generation means to give estimates of additive, dominance and three epistatic effects interaction additive x additive, additive x dominance and dominance x dominance according to the relationships illustrated by Gamble (1962) are presented in Table (4). Scaling tests were significantly different from zero for all traits in the three crosses, except for No. of branches/plant in the cross 3, where the significance is absence for all scales indicating that the additive-dominance model is adequate to interpret the gene effects.

Estimates of the six parameters **Table (4**) revealed that' the estimated mean effects (m) for all studied traits which reflect the contribution due to the overall mean plus the locus effects and interactions of the fixed loci were highly significant in the three crosses. Additive gene effect (a) was positive and significant for most desired seed yield traits plant height, No. of pods/pant, No. of seeds/pant, 100-seed weight and seed yield/plant in the cross 3 and No. of seeds/pant in the cross 2. While the desired negative and significant (a) was noticed for chocolate spot and rust diseases in the cross 3 and days to flowering and maturity in the crosses 1 and 2.

The estimates of dominance effects (d) were positive and significant for No. of branches/pant, No. of pods/pant, No. of seeds/pant, 100- seed weight and seed yield/plant in the cross 2; plant height and No. of pods/pant in the cross 3; No. of branches/pant, No. of seeds/pant, No. of seeds/pod and seed yield/plant in the cross 1. Meanwhile, negative and significant dominance effects were recorded for days to flowering and maturity in the all crosses and chocolate spot and rust diseases in the cross 1 and cross 2. These results indicated the importance role of dominance gene effects in the inheritance of these traits.

Table 4: Scaling test and gene action parameters of the studied traits in three faba bean crosses.

Traits	Crosses	A	B	C	D	m	a	D	aa	ad	dd
Days to flowering date	1	-1.51	2.39	28.96**	14.04**	48.75**	-11.20**	-29.90**	-28.08**	-1.95**	27.20**
	2	-9.61	0.51	15.02**	12.6**	60.13**	-27.14**	-21.87**	-24.12**	-5.06**	33.22**
	3	6.56	5.78	43.46**	15.56**	57.95**	5.22**	-30.95**	-31.12**	0.39	18.78**
Days to maturity	1	-3.84**	-13.40**	31.78**	24.51**	148.01**	-11.95**	-51.09**	-49.02**	4.78**	66.26**
	2	2.62*	-15.57**	21.99**	17.47**	153.8**	-13.47**	-32.20**	-34.94**	9.09**	47.89**
	3	9.12**	11.78**	25.58**	2.34	166.06**	6.00**	-7.35**	-4.68	-1.33**	-16.22**
Plant height	1	23.20**	1.81	55.77**	15.38**	119.34**	-21.14**	-10.29**	-30.76**	10.69**	5.75
	2	26.63**	3.90	56.95**	13.21**	116.07**	-19.59**	-11.32**	-26.42**	11.36**	-4.11
	3	-1.2	-6.53*	-23.25**	-7.76**	139.62**	11.00**	33.05**	15.52**	2.66**	-7.79
No. of branches/ plant	1	-0.83	-0.25	-2.68**	-0.80*	3.47**	-0.82**	3.08**	1.60*	-0.29	-0.52
	2	-0.32	-0.64	-2.26*	-0.65	5.23**	-2.31**	2.21*	1.30	0.16	-0.34
	3	1.04	-0.24	1.24	0.22	4.16**	0.10	0.18	-	-	-
No. of pods /plant	1	26.67**	15.01**	42.14**	0.23	35.46**	3.75	9.69	-0.46	5.83**	-41.22**
	2	7.53*	-2.59	-3.12	-4.03	24.21**	6.35**	25.08**	8.06	5.06**	-13.00
	3	8.07*	-1.04	-25.09**	-16.06**	24.37**	7.20**	42.03**	32.12**	4.55**	-39.15**
No. of seeds/plant	1	54.24**	41.82**	86.24**	-4.91*	102.06**	-5.09**	48.08**	9.82*	6.21**	-105.88**
	2	39.85**	-13.73**	-3.82	-14.97**	72.68**	18.47**	60.43**	29.94**	26.79**	-56.06**
	3	-0.21	6.31*	42.14**	18.02**	92.46**	9.30**	-1.73	-36.04**	-3.26**	29.94**
Seed yield/plant	1	27.40**	20.74**	32.54**	-7.80*	53.25**	-13.56**	33.19**	15.60*	3.33*	-63.74**
	2	3.58	-34.00**	-51.46**	-10.52**	43.43**	-9.00**	39.19**	21.04**	18.79**	9.38
	3	9.02**	-1.80	25.10**	8.94**	53.67**	10.00**	-1.49	-17.88**	10.82**	10.60
No. of Seeds./Pod	1	-0.74**	-1.01**	-3.01**	-0.63**	127.00**	-0.15	1.85**	1.26**	0.13*	0.49
	2	0.10	-0.74**	-0.92**	-0.14	127.00**	-0.24**	-0.66*	0.28	0.42**	0.36
	3	-0.38	0.94**	5.18**	2.31**	127.00**	-0.35**	-4.37**	-4.62**	-0.66**	4.06**
100 –seed weight	1	2.29	-12.34**	-11.09**	-0.52	52.31**	-13.44**	4.79	1.04	7.31**	9.01
	2	-13.38**	3.07**	-58.19**	-23.94**	60.6**	-48.22*	53.28**	47.88**	-8.22**	-37.57**
	3	16.19**	2.39	15.02**	-1.78	58.63**	2.82	-8.75*	3.56	13.80**	-22.14**
chocolate spot disease reaction	1	-0.98**	-1.08**	0.24	1.15**	4.42**	1.43**	-2.88**	-2.30**	0.05	4.36**
	2	-1.04**	0.32*	1.86**	1.29**	4.67**	0.77**	-3.33**	-2.58**	-0.68**	3.30**
	3	0.69**	-0.37	-1.54**	-0.93**	4.08**	-1.57**	1.13**	1.86**	0.53**	-2.18**
Rust disease reaction	1	0.07	-0.65**	0.94**	0.76**	4.35**	1.56**	-1.95**	-1.52**	0.36**	2.10**
	2	-1.43**	-0.44**	2.19**	2.03**	4.93**	0.57**	-4.22**	-4.06**	-0.49**	5.93**
	3	-0.09	-1.14**	-2.35**	-0.56**	4.11**	-1.84**	0.58*	1.12**	0.52**	0.11

Positive and significant additive x additive (aa) epistatic gene effects were detected for No. of seeds/pant,100-seed weight and seed yield/plant in the second cross; No. of branches/pant, No. of seeds/pant, No. of seeds/pod and seed yield/plant in the first cross and pant height and No. of pods/pant in the third cross. Positive and significant additive x additive (aa) epistatic gene effects were detected for No. of seeds/pant, 100-seed weight and seed yield/plant in the second cross; No. of branches/pant, No. of seeds/pant, No. of seeds/pod and seed yield/plant in the cross1 and pant height and No. of pods /pant in the cross 3. Estimates of dominance x dominance (dd) gene effects were positive and significant for No. of seeds/pant and No. of seeds/pod. Values of additive x dominance (ad) were positive and significant for No. of pods/pant and yield/plant in the three crosses, also, No. of seeds/pant and No. of seeds/pod in the cross 1 and cross 2 and 100-seed weight in the crosses 1 and 3. These results indicated that the inheritance of these traits was affected by the duplication effect of epistatic genes. Meanwhile, negative and significant dominance effects were recorded for chocolate spot and rust diseases in the second cross.

Heterosis and genetic parameters:

Different gene action, heterosis and inbreeding depression percentage for the four studied traits are presented in **Table (5).** The results revealed significant positive heterotic effect to mid-parents for all traits' except for No. of branches/plant and 100-seed weight in the cross 3. However, desired negative heterotic effects that found for days to flowering, days to maturity, chocolate spot and rust diseases was significant in all cases' except for days to flowering in the cross 2 and cross 3 and days to maturity in the cross 2.

Regarding heterosis over the better parent, desired significant heterotic effects and highest values were obtained for No. of pods and seeds/plant in all crosses. These results indicated that' dominance direction was toward the best respective parent.

Potence ratio:

The potence ratio presented in Table (5) revealed that' values with less than unity was obtained for days to flowering, days to maturity, 100-seed weight, chocolate spot and rust diseases in all crosses, indicating partial dominance effects for these traits in the all crosses. Also, partial dominance was estimated for plant height in the cross 1 and cross 2; No. of branches/plant in the cross 2 and cross 3; No. of seeds/pod in the cross 3 and seed yield/plant in the cross 2. Meanwhile, No. of pods/plant and No. of seeds/plant in all crosses and seed yield/plant in the cross 1 and cross 3.

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

	Cross	**MP**	**PR**	**BP**	**ID**	**H**	**h^2**	**Ga**	**Ga%**	**GCV %**	**PCV %**
Days to flowering	**1**	-4.29**	-0.20	22.40**	-20.07**	84.83	67.49	9.37	19.23	12.74	13.83
	2	4.07**	0.10	73.35**	-4.57	75.20	56.90	5.25	8.73	6.46	7.45
	3	0.36	0.04	11.86**	-22.85**	78.10	70.93	7.90	13.63	8.24	9.33
Days to maturity	**1**	-1.47**	-0.12	11.79**	-6.46	77.13	58.20	7.89	5.33	3.90	4.44
	2	1.86**	0.12	20.34**	-2.76	64.66	43.86	4.10	2.67	2.37	2.95
	3	-1.66**	-0.36	3.03**	-4.88	88.36	56.86	8.99	5.41	4.34	4.62
Plant height	**1**	21.50**	0.64	-8.95**	-3.21	63.92	45.91	9.06	7.59	6.42	8.02
	2	16.01**	0.49	-12.66**	12.17	51.98	27.16	4.96	5.17	6.66	9.23
	3	12.83**	2.10	6.34**	9.46	50.67	39.68	9.76	6.99	6.08	8.55
NO. of branches / plant	**1**	43.53**	2.79	24.17**	28.89**	53.13	48.17	2.07	59.71	43.86	60.17
	2	17.04**	0.37	-19.97**	16.32**	52.31	19.30	0.90	17.22	31.32	43.31
	3	-8.37	-0.70	1.96	2.40	49.45	34.26	2.36	58.19	57.99	82.47
No. of pods/plant	**1**	51.13**	4.88	36.80**	-18.20	73.30	66.75	23.73	66.93	41.67	48.67
	2	42.60**	5.44	32.25**	-3.02	58.62	30.92	8.95	36.98	44.46	58.06
	3	38.60**	3.75	25.66**	31.54	71.23	43.21	15.21	62.40	59.16	70.09
No. of seeds/plant	**1**	62.34**	3.39	37.10**	-2.44	54.80	43.47	11.00	10.78	8.91	12.04
	2	52.22**	3.66	33.23**	18.23	60.96	50.32	13.77	18.95	14.28	18.28
	3	52.97**	2.73	28.13**	6.68	80.20	72.83	23.67	25.60	15.28	17.06
Seed yield/ plant	**1**	48.43**	1.04	1.32	1.22	91.29	75.43	36.39	68.34	42.02	43.98
	2	38.44**	0.65	-12.85**	33.56*	81.78	54.87	16.50	38.00	30.40	33.62
	3	74.92**	6.40	56.59**	21.73	67.93	58.83	14.29	26.63	18.11	21.98
No. of seeds/ Pod	**1**	17.73**	2.09	8.52**	26.58**	76.39	60.42	1.22	42.05	29.53	33.79
	2	-25.20**	1.42	-36.45**	-8.60**	70.42	53.52	0.93	30.66	23.34	27.81
	3	9.96*	0.81	-2.13**	-42.39**	72.73	67.68	1.39	35.30	21.59	25.32
100 –seed weight(gm)	**1**	7.06**	0.18	-22.99**	8.16	71.43	58.10	11.33	21.66	15.30	18.10
	2	7.46**	0.14	-30.76**	22.16**	80.00	62.66	12.75	21.05	14.58	16.30
	3	-1.07	-0.16	-7.26**	2.90	77.57	72.97	18.87	32.19	18.86	21.41
Chocolate spot disease reaction	**1**	-12.47**	-0.42	24.46**	-8.60**	77.12	61.76	1.29	29.07	20.07	22.85
	2	-16.38**	-0.52	22.36**	-21.93**	54.55	31.82	0.43	9.31	10.49	14.20
	3	-15.11**	-0.35	50.18**	0.49	77.78	68.69	1.41	34.51	21.51	24.39
Rust disease reaction	**1**	-9.93**	-0.36	24.60**	-11.54**	73.25	54.32	1.01	23.15	17.71	20.69
	2	-3.70*	-0.15	26.47**	-14.65**	52.25	40.54	0.51	10.30	8.92	12.34
	3	-10.78**	-0.23	70.38**	7.22**	67.18	60.00	1.080	24.25	16.08	19.62

Inbreeding depression:

Inbreeding depression, measured as reduction in performance of F_2 generation compared to F_1 generation due to inbreeding. Results (Table 5) revealed that' highly significant positive inbreeding values were obtained for No. of branches/plant in the cross 1 and cross 2; seed yield /plant and 100-seed weight in the cross 2; No. of seeds/pod in the first cross and rust disease in the cross 3. Some cases obtained recorded significant heterosis and insignificant inbreeding depression for No. of pods/plant and No. of seeds/plant in all crosses.

Heritability and genetic advance:

Estimation of broad and narrow-sense heritability estimates (Table 5) depend on magnitudes of its genetic variance components of additive and dominance. The obtained broad-sense heritability ranged from 91.29 to 49.45% for seed yield/plant in the cross 1 and No. of branches in the cross 3, respectively. Meanwhile, the narrow-sense heritability ranged from 75.43 to 19.30% for seed yield/plant in the cross 1 and No. of branches in the cross 2, respectively. Heritability in narrow-sense was high for some cases of traits as No. of pods/plant, No. of seeds/pod, 100-seed weight, and chocolate spot and rust diseases. These results indicate that' selection may be more effective for improving traits of genotypes in early generations. On contrary, low narrow sense heritability were estimated for plant height and No. of branches/pant. These results indicate that environmental and non-additive effects have a larger contribution of the genetic effects for these traits.

Expected genetic gain for all studied traits in the three crosses are shown in Table (5). The expected genetic advance percent ranged between (2.95 to 82.47%) for days to maturity in cross 2 and number of branches/pant in cross 3, respectively.

DISCUSSION

Genetic variances were detected for all traits in the three crosses and-therefore: - a suitable amount of genetic diversity valid for further assessments. Genetic parameters were detected as reported by (Abo Mostafa *et al.,* (2014), Ibrahim *et al*., (2015), Abou-Zaid (2018), Abou Zied and El-Gendy (2019) and Heiba *et al*., (2022). Selection could be effective in the improvement of the studied traits. These results are in harmony with those obtained by Koumber and El-Gammaal (2012). Therefore, parents are precisely selected to find the desired recombination in the segregating generations. The parental differences with response to their genetic background were found to be significant in most traits under investigation. The F_2 populations had also significant differences for all studied traits in the three studied crosses (Attia *et al*., (2006), Abo Mostafa *et al*., (2014) and Ibrahim *et al*., (2015).

Scaling tests were significantly different from zero for most cases, where the significance is absence for most scales indicating that the additive-dominance model is adequate to interpret the gene effects. These results are similar trend to those reported by, Moussa (2010), Zaazaa *et al.,* (2012), Abo Mostafa *et al.,* (2014), Ibrahim *et al*., (2015), Abou-Zaid (2018) and Abou Zied and El-Gendy (2019)..

The desired negative and significant (a) was noticed for chocolate spot and rust disease reactions in the cross 3 and days to flowering and maturity in the crosses 1 and 2. These results indicate that' improving the performance of chocolate spot and rust disease resistance may be more effective by using the pedigree selection program (Ashrei *et al*., (2013), El-Refaey and Abd El-Razek (2013), and Abo Mostafa *et al.,* (2014).

The significance of additive (a) and dominance (d) components indicated that, both additive and dominance gene effects were important in the inheritance of these traits and selecting desirable traits may be practiced in the early generations but it would be effective in the late ones. Similar trend of results was obtained by Ashrei *et al*., (2013), El-Refaey and Abd El-Razek (2013), Abo Mostafa *et al.,* (2014) and Abd El-Hamid and Ghareeb (2018).

Positive and significant results confirm the importance role of dominance x dominance (dd) gene interactions in the genetic system which controls most yield traits. Similar trend of results was reported by Ashrei *et al.,* (2013), El-Refaey and Abd El-Razek (2013) and Abou Zied and El-Gendy (2019).

Generally, the dominance and dominance x dominance effects were important as additive x additive (aa) with more additive gene effect in the expression of the most studied traits in the three crosses. These results are in line with those previously obtained by Sheikh *et al*., (2009) Aykut *et al*., (2011). Novoselovic *et al.,* (2004) identified that significant additive and additive x additive type gene effects could be fixed in their studied populations. Besides, opposite values of dominance and dominance x dominance gene effects indicated the presence of duplicate epistatic effects. This situation complicates using epistatic gene effects in breeding programs. Similar trend of findings were pointed out by Ashrei *et al.,* (2013), El-Refaey and Abd El-Razek (2013), Abo Mostafa *et al.,* (2014) and Ibrahim *et al*., (2015) who reported that' selection in early segregating generations can be advisable to improve the traits governed by additive gene effects but dominance would be effective in the late ones.

The significant heterotic effect might be due to the dominance and/or dominance × dominance effects, confirming the previous results. Absence of significant heterosis in some cases could be due to the internal cancellation of heterosis components. These results are in the same time as those obtained by Ashrei*et al.* (2013), El-Refaey and Abd El-Razek (2013), Abo Mostafa *et al*., (2014) and Ibrahim *et al*., (2015), Abou-Zaid (2018) and Abdalla *et al*., (2021). The feasibility of growing hybrid cultivars depends on the significant superiority in yield as well as best performance of hybrids compared to the current commercial cultivars (Mahrous 1998*).* Then, heterosis over better parent may be useful in identifying the best hybrid combinations (Prasad *et al*., 1988*).*

Potence ratio greater than unity, indicating over-dominance effect towards the higher parent. These results suggested that' the selection must therefore be delayed to late generations. These results agree with those obtained by Hendawy (2003), Mahgoub and Hammad (2006), Abdel-Nour and Moshref (2006), Koumber and El-Gammal (2012), Sultan *et al.* (2011) and Abd El-Rahman (2013). However, these results for Iinbreeding depression are logic and expected since the expression of heterosis in F_1 will be followed by a considerable reduction in F_2 due to homozygosity. The results are at the same time as those obtained by Koumber and El-Gammaal (2012) and Zaazaa *et al.,* (2012).

Comparison between broad and narrow-sense heritability estimates revealed equal importance of additive and non-additive effects in genetic control of traits. Considerable differences were observed between broad-sense and narrow-sense heritability in all crosses. These results suggest that dominance gene action was primarily responsible for the inheritance of most traits in these crosses. These results were similar to these obtained by Farshadfar *et al*., (2013) and Abd El Rahman (2013).

The expected genetic advance percent ranged from low to high percentage for days to maturity and number of branches/pants. These results indicated the possibility of practicing selection in early generations for some traits/crosses to realize high yielding genotypes. Dixit *et al.* (1970) pointed out that, high heritability is not always associated with high genetic advance, but to make effective selection, high heritability should be associated with high genetic gain.

CONCLUSION

Generally, the most genetically parameters resulted from the first and second crosses were higher in magnitude than those obtained from the third one and confirmed that the introduced resistant genotype with susceptible one was the good donor. Consequently, it could be concluded that the cross (Nubaria 1 x RV 322) followed by (Sakha 3 x R V 322) would be of interest in a breeding program for improvement of faba bean yield. The traits examined in the present study have shown complex genetic behavior. The complex genetic behavior particularly dominance components could be successfully exploited in later generations. It is suggested that selection for the improvement of the yield traits should be delayed to later segregated generations in these faba bean crosses.

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تقدير بعض المكونات الوراثية باستخدام تحليل متوسطات العشائر الستة فى ثلاثة هجن من الفول البلدى المعرضة للإصابة الطبيعية بأمراض الأوراق

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أقيمت هذة التجربة فى محطة البحوث الزراعية بسخا – محافظة كفرالشيخ خلال مواسم الزراعة 20/2019 ، 21/2020 و 2022/22021 لدراسة قوة الهجين، التربية الداخلية، وطبيعة الفعل الجينى الذى يتحكم فى النظام الوراثى لبعض صفات الفول البلدى.

استخدم نظام العشائر الستة لثلاثة هجن من الفول البلدى وهى (سخا 3 RV322 X) و(نوبارية1 RV322 X) و(جيزة 429 X مارينا).

-أظهر تحليل التباين الوراثى فروق معنوية بين الأجيال لكل الصفات .

- أظهر اختبار Scaling test فروقا معنوية لمعظم الصفات المدروسة وهذا يدل علي وجود تفاعل بين الجينات الغير الِلية (التفوق).

- كان كل من الفعل الجينى السيادى والمضيف لهما اهمية ولكن الغالب أن الفعل السيادى أعلى من المضيف، وهذا يدل على ان الجينات السائدة تلعب دور مهم فى توريث هذة الصفات بجانب الفعل المضيف.

- أعطى الهجين الثانى (نوبارية 1 X RV 322) قيما سالبة عالية المعنوية للفعل (الإضافي X الإضافي) لصفات التزهير، ميعاد النضج، مقاومة مرضى التبقع البنى والصدأ وهذا يدل على ان هذه الهجن المستخدمة فى هذه الدراسة أظهرت ثباتها فى التعبير عن الجينات الأليلية والتى تعمل على أن يكون التحسين من خلال الانتخاب فى الأجيال المبكرة.

- أظهرت قوة الهجين والتربية الداخلية قيما معنوية موجبة لمعظم الصفات المدروسة.

- أعطى الهجين الأول (سخا 3 RV322 X) قيما عالية لدرجة التوريث على النطاق الضيق والتقدم الوراثى لصفات عدد الفروع ، عدد القرون للنبات، عدد البذور بالقرن ومحصول البذور.

لذلك الانتخاب فى هذة العشائر سيكون اكثر كفاءة فى تحقيق اهداف التربية بنجاح.

الكلمات المفتاحية: الفول البلدي، المقايس الوراثية، قوة الهجين، درجة التوريث، التقدم الوراثي