



Genetic Studies of Heterosis and Combining Ability for Foliar Disease, Yield and Its Contributing Characters in Faba Bean (*Vicia faba* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present study was carried out in the farm of Sakha Agricultural Research Station, Kafr –El Sheikh, Egypt, during 2019/20, 2020 /21 seasons to produce seed hybrids (F₁ seeds) which evaluated in 2021/22 season. Four parental genotypes namely; Almany, Giza 843, Misr 3 and Najeh were used as testers, while four material genotypes namely; Line 1, Line 2, Line 3 and Line 4

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used as lines which crossed according to Line X tester mating system under insect free cages in the first and second seasons. In the third season the resulted F_1 ,^s sixteen crosses along with their parental genotypes were sown in a randomized complete blocks design with three replications during 2021/22 season. The data subjected to line x tester analysis. Highly significant of genotypes, parents and crosses were found for all traits. The magnitude of genotypes or any of its components i.e., parents, crosses and parents vs. crosses were several times large than corresponding mean squares of error. Mean squares of parent's vs. crosses as an indication to average heterosis over all crosses appeared to be highly significant heterotic effects for almost all traits. Partitioning the crosses mean squares to its components i.e., lines, testers and lines x testers revealed that, lines and testers mean squares seems to be not significant for all traits. While, lines x testers mean squares found to be highly significant for all traits. The ratio of s^2_{gca}/s^2_{sca} was less than unity for all traits, indicating that the non-additive gene effects were of greater important in the inheritance of these traits. The crosses; Line 1 x Tester 1, Line 1 x Tester 2, Line 2 x Tester 2, Line 3 x Tester 1, Line3 x Tester 4, Line 4 x Tester 1 and Line 4 x Tester 2 had significant and /or highly significant mid and better parents heterotic effects for many important traits a result of over-dominance in approximately all studied traits. Tester 4 considered as good combiner parent for plant height, No of pods/plant, No of seeds /plant, seed yield /plant and curd protein percentage. The cross; Line 1 x Tester 2 expressed significant (\hat{S}_{ij}) in favorable direction for rust disease reaction, flowering date, plant height and crude protein percentage. The cross; Line 2 x Tester 3 had significant (\hat{S}_{ij}) in favorable direction for chocolate spot diseases reaction, plant height and No. of branches/plant and the cross; Line 4 x Tester 2 had significant (\hat{S}_{ij}) in positive direction for No of branches/plant, No of pods/plant, No of seeds/plant, seed yield /plant and carbohydrate percentage. Brood sense heritability ranged from 24.6% for No. of seeds/plant to 77.90% for 100-seed weight. While, narrow-sense heritability (h^2), ranged between 0.68% for 100-seed weight to 20.28% for chocolate spot diseases reaction. The predicted genetic advance ranged from 0.18% for 100- seed weight to 6.92% for chocolate spot diseases reaction.

Keywords: *Faba bean; heterosis; combining ability; heritability; genetic advance.*

1. INTRODUCTION

Faba bean is a major winter crop in the Mediterranean area, valued for its high protein content ranged from (24 – 34%). It is an important crop for human animal nutrition in Egypt [1], as well as for improving soil fertility through nitrogen fixation. Also, play a key role as a break crop in cereal rotation system. In the 2023/24 season, Egypt cultivated approximately 130,000 feddan of faba bean, with an average yield of 10.9 ardab/feddan, resulting in total production of about 374,000 tons. However, the country's self-sufficiency rate is only 33.6% [2]. To bridge the gap between production and consumption, it is crucial to develop new high-yielding cultivars and implement proper culture practices.

Combining ability analysis is a useful tool for breeders to identify the most effective parent combinations that can be hybridized to take advantage of heterosis or create synthetic varieties. Bound [3] utilized the relative significance of general combining ability and specific combining ability effects to select parents for hybrid varieties. Induced mutagenesis can

also be employment to increase the genetic diversity of quantitatively inherited traits.

The key factor in selecting appropriate breeding procedures is understanding the type of gene action of quantitative traits in faba bean to enhance seed yield and improve yield characteristics. Various genetic analysis methods such as half and full diallel matings, six-population models, and line x tester analysis have been utilized to determine the most effective breeding scheme. Simply selection superior genotype based on yield alone is ineffective due to the complexity of yield traits, and their interactions with the environment [4]. Successful breeding programs require genetic diversity within the plant collection to enable the section of desirable gene combinations [5,6].

A successful breeding program for faba bean genotypes depending on the genetic variation in the population. Reliable estimates of genetic and environmental variations are essential to determine heritability and predict genetic advance from selection. This study amide to assess variability, hetrosis, general and specific combining abilities, heritability, and genetic

advance for foliar diseases, earliness and yield and yield components traits in sixteen faba bean crosses, via line x tester analysis.

2. MATERIALS AND METHODS

The present study was carried out under field condition in the farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt during the growing winter seasons of 2019/20, 2020/21 to produced hybrid seeds (F₁ seeds) which evaluated in 2021 /22 season. Four parental genotypes namely; Almany, Giza 843 Misr 3 and Najeh were used as testers, while four maternal genotypes namely; Line1, Line2, Line 3 and Line 4 used as lines were which crossed according to lines x testers mating system under insect free cages in the first season of (2019/20). In the second season

(2020/21) the parental genotypes were sown again under wire cages and re-hybridized as done as in the first season to obtain more hybrid seeds. The resulted F₁^s along with their parental genotypes were sown in a randomized complete blocks design with three replications during 2021/22 season. Flowers of F₁ plants grown under wire cage were manually tripped to ensure good pollination. Seeds were sown in single seeded hills, 20 cm apart, each plot consisted of one row for parents as well as their F₁^s. The row was 3 meters long and 60 cm in between. The choice of parents was based on:

a- Genetic diversity, b- Differences in growth habit and disease reactions and c- Differences in yielding ability. The pedigree, disease reactions, agronomical characters and yielding level of parental genotypes are presented in Table 1.

Table 1. Names, pedigrees', disease reactions and agronomical characters of the parental faba bean genotypes used in this investigation

Genotype	Pedigree	Agronomical characters	
		Flowering date	Characteristics
Lines			
Line 1 520/283/2015	Cross (Giza 843 x Misr 1)	Medium	Resistant to foliar disease and tolerant to <i>Orobanche</i>
Line 2 313/453/2015	Cross (Giza 2 x Misr 1)	Early	Resistant to foliar disease and tolerant to <i>Orobanche</i>
Line 3 249/230/2015	Cross (Giza 843 x Giza 2)	Medium	Resistant to foliar disease and tolerant to <i>Orobanche</i>
Line 4 461/345/2015	Cross (Sakha 3 x Giza 2)	Medium	Moderate resistant to foliar disease and Tolerant to <i>Orobanche</i>
Testers			
Almany	Introduction from Germany	Medium	Resistant to foliar disease and high yield
Misr 3	L667 x (Cairo 241 x Giza 461)	Early	Tolerant to <i>Orobanche</i>
Giza 843	561/2076/85 x 461/845/83	Medium	Tolerant to <i>Orobanche</i>
Najeh	INRAT, Tunisia	Medium	Tolerant to <i>Orobanche</i>

Data were taken on the basis of individual plant as follows:

1- Chocolate spot disease reaction.	2- Rust disease reaction.	3- Flowering date (day).
4- Plant height (cm).	5- No of branches/plant.	6- No of pods /plant.
7- No. of seeds/plant.	8- 100-seed weight.	9- Seed yield / plant.
10- Crude Protein%.	11- Carbohydrates%.	12- Fibers%.

Table 2. Rating scale for chocolate spot and rust diseases reactions

Rate	Chocolate spot scale
1	Highly resistant, no disease symptom.
3	Resistant, few small discrete lesions.
5	Moderately resistant, some coalesced lesions with some defoliation.
7	Susceptible, large coalesced lesions, 50% defoliations, some dead plants.
9	Highly susceptible, extensive lesions on leaves, stems and pods, severe defoliation, heavy sporulation, death of more than 80% of plants.
Rust scale	
1	High resistant, no pustules or very small non- sporulation flecks
3	Resistant, few scattered pustules covering less than 1% of the leaf area, and few or no pustules on stem.
5	Moderately, resistant, pustules common on leaves covering 1-4% of leaf area, little defoliation and some pustules on stem.
7	Susceptible, pustules very common on leaves covering 4-8% of leaf area, some defoliation and many pustules on stem.
9	Highly susceptible, extensive pustules on leaves, petioles and stem covering 8—10% of leaf area, many dead leaves and several defoliation.

Table 3. Mean squares (MS) and expected mean of square (EMS)

S.O.V	d f	MS	EMS
Replication	r-1	M r	
Genotype (G)	(g-1)	MS g	$s^2_e + rs^2_g$
Error	(r-1) (g-1)	MS e	s^2_e

Reaction to foliar diseases was recorded on mid-February and mid-March for chocolate spot and rust diseases, respectively; according to the disease scales suggested by Bernier et al [7] as presented in Table 2.

The statistical procedure was done according to the regular analysis of variance of randomized complete blocks design as outlines by Cochran and Cox [8]. The analysis of variance was done depending on the mean of the individual plant basis. The source of variation and degrees of freedom are shown in Table 3.

Where: r is the number of replications; g is the number of genotypes; s^2_g and s^2_e refer to genotypic and error variances, respectively . The difference between any two means was tested according to the least significant difference (L.S.D) at both 5% and 1% level of significance as follows:

$$L.S.D: P \leq 0.05 = t_{0.05} (d.f) \times Sd$$

$$P \leq 0.01 = t_{0.01} (d.f) \times Sd$$

Where: r is the number of replications and MS_e : is the mean square of error

According to Kempthorne [9], the variance of general and specific combining abilities may be

computed from the covariance of full sib (F.S) and half sib (H.S) families.

Where:

$$s^2_{gca} = Cov H.S = 1 + F/4 \times s^2_A, \text{ with } F=1,$$

$$s^2_A = 2s^2_{gca}$$

$$s^2_{sca} = \{1 + F/2\} s^2_D, \text{ with } F=1, s^2_D = s^2_{sca}$$

Where F is the coefficient of inbreeding that ranged from 0 to 1 with open pollinated varieties to completely pure lines, respectively.

Where: the MS due to lines (M_l) and testers (M_t) were tested against MS due to lines x testers (M_{lxt}) and the latter is , in turn, tested against MS due to error (M_e) [9].

The genetical parameters; genotypic variance (V_g), phenotypic variance (V_{ph}) were computed according to the formula suggested by Burton [10]. For each character, PCV% and GCV% were computed based on the methods given by Burton [10]. Heritability in broad sense (H) was calculated according to lush Jay [11]. The range of heritability was categorized as suggested by Johnson et al [12], where : low (< 30%), moderate (30-60%) and high (> 60%).

Table 4. Line X tester analysis of variance including parents

S.O.V	d f	MS	EMS
Replication	r-1		
Genotype (G)	(g-1)		
Parents	(P-1)		
Parent's vs. crosses	1		
Crosses	(C-1)		
Lines	(l-1)	Ml	$s_e^2 + r s^2 2lt+rs^2l$
Testers	(t-1)	Mt	$s_e^2 + r s^2 lt+rs^2t$
Lines x testers	(l-1) (t-1)	Mlt	$s_e^2 + r s^2 lt$
Error	(r-1) (g-1)	Me	s_e^2

Narrow sense heritability (h^2) estimates were calculated as Acquaah [13]. According to Stansfield [14], the classification of narrow-sense heritability was as follows: Low (< 20%), moderate (20-50%) and high (> 50%). For each character, expected genetic advance (Ga) and predicted genetic advance (Ga%) were estimated in accordance with the methods illustrated by Fehr [15] assuming selection of the superior 5% of the genotype plants and the narrow-sense heritability (h^2) was used to calculate the expected genetic advance (Ga). The range and frequency is as follows: low (less than 10), moderate (10-20) and high (more than 20).

Seed Quality: All seed properties were carried out at Sakha Seed Technology Research section as Follow.

1-Crude Protein (%) Tested seeds were ground to a fine powder to pass through 2 mm mesh and used to determine the crude protein percentage according to methods of A.O.A.C [16].

3-Carbohydrate contents: were calculated by difference: [100-(protein + oil+ ash + fiber +moisture)].

2-Fiber content: was determined according to A.O.A.C [16].

3. RESULTS AND DISCUSSION

Analysis of variance: Highly significant mean squares of genotypes, parents and crosses were found for all studied traits (Table 5), except for parents mean square of No. of branches/plant. The magnitude of genotypes or any of its components i, e., parents, crosses and parents v s crosses were several times larger than corresponding mean squares of error. This would indicate the wide genetic variability between genotypes, therefore, it become statistically valid for the required diversity for the success of the planned crosses. Mean squares

of parent vs. cross as an indication to average heterosis over all crosses appeared to be highly significant heterotic effects for all traits, except for crude protein percentage, carbohydrate percentage and fiber percentage. The latest three traits did not significant heterotic effects over all crosses. Partitioning the crosses mean squares to its three components i.e., lines, testers and lines x testers revealed that, lines and testers mean squares seems to be not significant for all the studied traits, except testers mean squares for plant height and carbohydrate%, where it's at least significant. Regarding to lines x testers mean squares, it's found to be highly significant for all studied traits in view, except, 100-seed weight, where it was only significant. Results presented in Table 5, revealed not significant s^2_{gca} and s^2_{sca} for all studied traits. s^2_{gca} / s^2_{sca} ratio was less than unity for all studied traits indicating the non additive types of gene action controlling these traits.

The mean performance: The differences between mean performance of the parental lines and testers and their F_1 crosses of faba bean genotypes for studied traits are shown in Table 6. Highly significant difference between genotype was found the parental Line 1, Line 2, Tester 3 (Giza 843) and Tester 4 (Najeh) recorded the lowest values for chocolate spot and Rust diseases reaction. The parental Line 2 and Tester 2 recorded the lowest days of flowering date. While, Line 2, Tester 3 (Giza 843) and Tester 4 (Najeh) registered the best values of plant height. In addition to Line1, Line2, Tester 3 (Giza 843) and Tester 4 (Najeh) had the highest values of number of branches/plant, number of pods /plant, number of seeds/ plant, seed yield/ plant, 100-seed weight and crude protein%. For carbohydrate%, Line 2 and Tester 3 (Giza 843) gave the highest value. While, Line 2 and Tester 2 (Misr 3) showed the highest values for fiber percentage.

Table 5. Analysis of variance for disease reaction, yield and its components of faba bean lines x testers crosses in the F₁ generation

S.O.V	d.f	Chocolate spot diseases reaction	Rust diseases reaction	Flowering date	Plant height (cm)	No .of branches / Plant	No .of pods/ plant	No .of seed/plant	Seed Yield/ plant	100-seed weight	crude protein (%)	Carbo-hydrate (%)	Fiber (%)
Rep	2	0.10	0.40	4.90	19.30	0.70*	3.80	40.00	55.20	41.10	0.70	1.10	0.30
Genotypes	23	2.10**	4.40**	53.1**	448.00**	3.30**	268.90**	2447.90**	1586.60**	130.20	22.3**	27.9**	3.50**
Parents (P)	7	3.30**	3.30**	28.20**	1171.70**	0.60	143.20**	1355.80**	975.8**	64.30**	26.4**	32.3**	6.40**
P vs C	1	8.50**	39.90**	156.30**	270.00**	34.50*	1560.50**	10534.00**	7560.80*	134.00**	14.00	13.60	3.50
Crosses (C)	15	1.20**	2.60**	57.8**	122.20**	2.40**	241.50**	2418.50**	1473.30**	160.80**	20.9**	26.8**	2.20**
Lines (L)	3	1.20	3.30	66.70	162.40	3.90	100.10	1017.30	993.50	32.20	23.90	13.00	0.50
Testers (T)	3	2.00	2.80	80.60	269.90*	0.40	333.00	4313.00	2020.30	104.30	44.50	88.9**	5.40
L x T	9	0.90**	2.30**	47.20**	59.50**	2.60**	258.10**	2254.1**	1450.9**	222.50*	12.0**	10.7**	1.70**
Error	46	0.30	0.30	9.40	11.40	0.20	9.70	830.00	213.00	87.90	0.60	0.60	0.40
s ² gca		0.009	0.010	0.367	2.176	0.007	0.577	5.709	0.778	2.143	0.308	0.559	0.018
s ² sca		0.210	0.690	12.617	16.036	0.802	82.81	723.70	412.6	44.86	3.81	3.367	0.424
s ² gca/s ² sca		0.043	0.014	0.029	0.136	0.009	0.007	0.008	0.002	0.048	0.808	0.166	0.042

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

Table 6. Mean performance of parents and their crosses of faba bean genotypes for studied traits

Crosses	Chocolate spot diseases reaction	Rust diseases reaction	Flowering date	Plant height (cm)	No .of branches/ Plant	No .of pods/ plant
Line 1	3.00	2.00	54.45	111.67	4.23	30.09
Line 2	4.00	3.00	45.11	128.33	3.86	25.53
Line 3	3.00	4.00	50.45	100.07	3.08	21.22
Line 4	5.00	5.00	50.00	117.38	2.91	16.65
Tester 1 (Almany)	5.00	4.00	53.33	110.50	3.10	20.30
Tester 2 (Misr 3)	4.17	3.43	48.33	112.49	3.09	25.30
Tester 3 (Giza 843)	3.33	2.80	53.33	155.00	3.67	38.55
Tester 4 (Najeh)	2.00	2.00	50.00	150.00	3.33	30.07
Line 1 x Tester 1	3.63	2.83	46.67	113.89	5.40	36.72
Line 1 x Tester 2	4.00	3.00	40.00	130.00	4.34	33.00
Line 1 x Tester 3	3.67	4.50	48.33	115.46	4.77	28.00
Line 1 x Tester 4	4.57	6.00	55.00	131.92	5.27	49.50
Line 2 x Tester 1	4.47	5.27	48.33	110.35	4.73	29.93
Line 2 x Tester 2	4.73	4.80	55.00	114.79	4.67	31.85
Line 2 x Tester 3	3.53	4.60	46.67	116.25	6.60	31.76
Line 2 x Tester 4	5.33	6.00	53.33	119.19	4.06	45.46
Line 3 x Tester 1	4.00	5.00	50.00	115.48	4.06	56.04
Line 3 x Tester 2	5.53	5.90	41.67	119.36	3.85	24.04
Line 3 x Tester 3	4.50	4.83	43.33	108.90	3.88	38.71
Line 3 x Tester 4	4.77	5.00	48.33	123.45	4.59	38.34
Line 4 x Tester 1	3.70	4.77	43.33	123.33	4.26	27.51
Line 4 x Tester 2	4.23	4.33	45.00	121.48	6.68	41.44
Line 4 x Tester 3	5.20	5.90	46.67	117.48	4.86	24.55
Line 4 x Tester 4	4.77	5.00	48.33	123.79	6.02	36.56
P LSD 0.05	0.41	0.95	3.44	7.77	1.03	2.78
P LSD 0.01	0.68	1.01	6.12	9.39	1.59	4.98
C LSD 0.05	1.09	0.83	5.89	5.97	0.59	6.15
C LSD 0.01	1.44	1.24	7.54	8.03	1.24	8.26
All LSD 0.05	0.89	0.82	5.03	5.55	0.77	5.12
All LSD 0.01	1.19	1.10	6.72	7.41	1.03	6.83

Table 6. Cont

Crosses	No .of seed/ Plant	Seed Yield/ plant	100-seed weight	crude protein (%)	Carbo-hydrate (%)	Fiber (%)
Line 1	89.62	74.16	82.79	25.00	45.00	9.50
Line 2	67.88	57.06	84.05	22.27	50.67	12.50
Line 3	69.40	54.45	78.24	29.00	40.33	9.73
Line 4	47.75	33.52	70.17	24.73	44.00	8.60
Tester 1 (Almany)	52.46	40.20	76.05	26.00	46.00	10.20
Tester 2 (Misr 3)	70.30	51.30	72.92	30.00	41.33	11.00
Tester 3 (Giza 843)	112.41	88.32	78.83	29.67	44.00	8.77
Tester 4 (Najeh)	89.00	69.13	77.60	30.00	41.67	7.93
Line 1 x Tester 1	99.51	81.56	82.21	27.00	46.55	9.07
Line 1 x Tester 2	87.17	73.14	83.96	33.00	42.00	10.00
Line 1 x Tester 3	81.20	63.18	77.73	28.67	45.17	7.97
Line 1 x Tester 4	147.59	121.08	82.01	31.00	42.67	10.00
Line 2 x Tester 1	84.48	72.39	85.69	23.67	51.00	10.00
Line 2 x Tester 2	91.08	83.84	91.89	25.67	44.00	9.47
Line 2 x Tester 3	82.66	63.84	77.33	27.00	46.00	8.00
Line 2 x Tester 4	143.28	82.11	58.07	30.00	42.00	9.00
Line 3 x Tester 1	154.46	129.58	84.02	27.25	47.33	10.33
Line 3 x Tester 2	64.70	50.12	77.78	25.53	45.00	8.67
Line 3 x Tester 3	109.77	85.48	77.92	27.00	46.33	8.33
Line 3 x Tester 4	110.29	96.89	87.86	32.67	38.20	11.00
Line 4 x Tester 1	74.59	59.03	79.22	28.00	46.60	9.60
Line 4 x Tester 2	113.75	88.72	77.99	25.67	47.00	9.67
Line 4 x Tester 3	60.48	51.29	84.80	26.50	47.67	9.00
Line 4 x Tester 4	103.16	81.83	79.11	29.67	43.23	8.90
P LSD0.05	13.15	11.12	5.19	1.43	1.46	1.35
P LSD0.01	15.54	16.35	7.22	2.65	1.98	1.64
C LSD0.05	16.64	28.89	18.41	0.87	1.24	0.91
C LSD0.01	18.87	31.24	25.34	1.99	1.79	1.38
All LSD0.05	14.97	23.98	15.41	1.28	1.31	1.03
All LSD0.01	19.98	32.02	20.57	2.54	175	1.37

The crosses; Line 1 x Tester 1, Line1 x Tester 3, Line2 x Tester 3 and Line4 x Tester 1 were resistant for chocolate spot and rust diseases reaction where showed the lowest values of severity. In addition to the crosses; Line 1 x Tester 2 Line 3 x Tester 2, Line 3 x Tester 3 and Line 4 x Tester 1 were the earliest crosses of flowering date (40.00, 41.67 days, 43.33 and 43.33 respectively). The crosses; Line 1 x Tester 2 and Line 1 x Tester 4 had the highest values of plant height. For No. of branches/ plant, No. of pods/ plant, No. of seeds/ plant, seed yield/ plant and 100 -seed weight the crosses; Line 1 x Tester 4, Line 2 x Tester 2, Line 2 x Tester 4, Line 3 x Tester 1, Line 3 x Tester 3, Line 3 x Tester, Line 4 x Tester 2 and Line 4 x Tester 4) were the highest yielding crosses. Also, five crosses gave the desirable values of crude protein% ranged from (29.67% - 33.00%). On the other hand, seven crosses for carbohydrate% had the highest values ranged from (46.55% - 51.00%).

Heterosis: It is a known fact that, the phenomena of heterosis (hybrid vigour) is of common occurrence in both cross and self-pollinated crops. Faba bean which is often a partially self-fertilized crop also show hybrid vigour when hybridization takes place between homozygous varieties.

The data illustrated in Table 7 show that, highly significant mid and better parents heterotic effects in the cross ; Line 1 x Tester 1 were found for rust disease reaction, flowering date, No. of branches/ plant , No. of pods /plant and No. of seeds/ plant in favourable direction a result of over - dominance as potence ratio pointed out in all cases , except rust disease reaction where partial dominance was controlled the heterotic effect in the trait of view.

Highly significant mid and better parents heterosis in the cross; line 1 x Tester 2 were detected for flowering date, plant height, No. of pods /plant, and protein% in favourable direction due to over – dominance.

Highly significant mid and better parents heterotic effects in the cross; Line 1 x Tester 4 were found for No. of branches / plant, No. of pods /plant, No. of seeds / plant and seed yield /plant in positive direction a result of over-dominance (P > +1). Highly significant mid and better parents heterosis in the cross; line 2 x Tester 2 were observed for No. of branches / plant, No. of pods /plant, No. of seeds / plant and

seed yield / plant, except for No. of branches, No. of pods /plant and seed yield / plant , where the better parent heterosis were only significant , in all cases over – dominance was the main reason of heterotic effects (P> +1).

Significant and / or highly significant mid and better parents heterosis were observed in the cross; Line 3 x Tester 1 for No. of branches / plant, No. of pods /plant, No. of seeds / plant, seed yield / plant and carbohydrate% in positive direction a result of over- dominance in all traits of view. Significant and / or highly significant mid and better parents heterosis were found in the cross; Line 3 x Tester 4 for No. of branches / plant, No. of pods /plant, No. of seeds / plant, seed yield / plant, crude protein% and carbohydrate% in positive direction due to over-dominance in the traits in consideration as potence ratio pointed out.

Highly significant mid and better parents heterosis were detected in the cross; Line 4 x Tester 1 for chocolate spot disease reaction and flowering date in negative direction, plant height; No. of branches / plant, No. of pods /plant, No. of seeds / plant and crude protein% in positive direction due to over- dominance(P > +1) in all traits in question . However, plant height was expressed only significant mid and better parents heterosis in positive direction and the data also shown highly significant mid and better parents heterotic effects in the cross; Line 4 x Tester 2 for No. of branches / plant; No. of pods /plant, No. of seeds / plant, seed yield / plant and carbohydrate%. Over- dominance was the main responsible of the heterotic effect in all traits mentioned, where potence ratio was exceeded plus one.

However, the crosses mention before could be used to evaluate faba bean genetic material of the present study through planned breeding program depending upon follow the bulk method in the advanced segregating generations, where according to this method non-additive genetic variance reduced one fourth from generation to another and in the F₅ and F₆ generation this kind of genes approximately disappeared and additive genes would represented almost the genetic variance, hence, effective selection would be done with follow pedigree selection breeding method which allow to obtain some pure lines could be tested through yield trials.

Different values of heterosis might be due to the genetically diversity of the parents with non-

Table 7. Heterotic effects relative to mid (M.P), potence ratios (P) and better (B.P) parent for disease reactions, yield and its components

Crosses	Chocolate spots disease reaction			Rust disease reaction			Flowering date (day)		
	M.P	p	B.P	M.P	p	B.P	M.P	p	B.P
Line 1 x Tester 1	-9.17	-0.37	21.11	-5.56**	-0.17	-29.17**	-13.41**	-12.90	-14.30**
Line 1 x Tester 2	11.63*	0.71	33.33*	10.43	0.40	-12.62	-22.17**	-3.72	-26.54**
Line 1 x Tester 3	15.79	3.00	22.22	87.50**	5.25	60.71**	-10.32*	-9.93	-11.24*
Line 1 x Tester 4	82.67**	4.13	128.33**	200.00**	∞	200.00**	5.31	1.25	1.00
Line 2 x Tester 1	-0.74	-0.07	11.67	50.48**	3.53	31.67**	-1.80	-0.22	-9.38
Line 2 x Tester 2	15.92	7.80	18.33	49.22**	7.31	39.81**	17.72*	5.13	13.79*
Line 2 x Tester 3	-3.64	-0.40	6.00	58.62**	17.00	53.33**	-5.19*	-0.62	-12.5*
Line 2 x Tester 4	77.78**	2.33	166.67**	140.00**	7.00	100.00**	12.15	2.36	6.67
Line 3 x Tester 1	0.00*	0.00	33.33*	25.00*	∞	25.00*	-3.64	-1.31	-6.25
Line 3 x Tester 2	54.42**	3.34	84.44**	58.74**	7.71	47.50**	-15.64**	-7.31	-17.4**
Line 3 x Tester 3	42.11**	8.00	50.00**	42.16*	2.39	20.83*	-16.49**	-5.93	-18.75**
Line 3 x Tester 4	90.67**	4.53	138.33**	66.67*	2.00	25.00*	-3.76	-8.46	-4.19
Line 4 x Tester 1	-26.00**	-∞	-26.00**	5.93	0.53	-4.67	-16.13**	-5.00	-18.75**
Line 4 x Tester 2	-7.64	-0.84	1.60	2.77	0.15	-13.33	-8.47	-5.00	-10.00
Line 4 x Tester 3	24.8**	1.24	56.00**	51.28*	1.82	18.00*	-9.68*	-3.00	-12.5*
Line 4 x Tester 4	36.19**	0.84	138.33**	42.86	1.00	0.00	-3.33	-∞	-3.33
L.S.D(0.05)	0.89		0.77	0.82		0.71	5.03		4.36
(0.01)	1.19		1.03	1.10		0.95	6.72		5.82

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 7. Cont

Crosses	Plant height (cm)			No of branches/plant			No of pods/plant		
	M.P	p	B.P	M.P	p	B.P	M.P	p	B.P
Line 1 x Tester 1	2.53	4.81	1.99	47.37**	3.06	27.62**	45.76**	2.36	22.05**
Line 1 x Tester 2	16.00**	43.73	15.57**	18.66	1.19	2.58	19.26**	2.23	9.77**
Line 1 x Tester 3	-13.40**	-0.82	-25.51**	20.68	2.88	12.60	-18.41	-1.49	-27.36
Line 1 x Tester 4	0.83**	0.06	-12.05**	39.29**	3.30	24.48**	64.58**	2331.04	64.54**
Line 2 x Tester 1	-7.59**	-1.02	-14.01**	35.96*	3.29	22.56*	30.59**	2.68	17.22**
Line 2 x Tester 2	-4.67**	-0.71	-10.55**	34.38*	3.08	20.90*	25.33*	55.43	24.76*
Line 2 x Tester 3	-17.94**	-1.91	-25.00**	75.38**	29.34	70.98**	-0.88*	-0.04	-17.62*
Line 2 x Tester 4	-14.36**	-1.84	-20.54**	12.88	1.76	5.18	63.52**	7.78	51.18**
Line 3 x Tester 1	9.69	1.96	4.51	31.34*	109.33	30.96*	169.93**	76.80	164.08**
Line 3 x Tester 2	12.31*	2.11	6.11*	24.87	363.28	24.79	3.35	0.38	-4.98
Line 3 x Tester 3	-14.61**	-0.68	-29.74**	15.06	1.74	5.88	29.52**	1.02	0.42**
Line 3 x Tester 4	-1.27**	-0.06	-17.70**	42.99**	10.94	37.59**	49.50**	2.87	27.5**
Line 4 x Tester 1	8.24*	2.73	5.07*	41.89**	13.15	37.51**	48.85**	4.95	35.48**
Line 4 x Tester 2	5.70	2.68	3.50	122.8**	41.40	116.38**	97.58**	4.74	63.83**
Line 4 x Tester 3	-13.74**	-0.99	-24.21**	47.70**	4.13	32.41**	-11.05**	-0.28	-36.31**
Line 4 x Tester 4	-7.41**	-0.61	-17.48**	92.95**	13.63	80.63**	56.49**	1.97	21.58**
L.S.D(0.05)	5.55		4.81	0.77		0.67	5.12		4.43
(0.01)	7.41		6.42	1.03		0.89	6.83		5.92

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 7. Cont

Crosses	No of seeds/plant			Seed yield/plant (g)			100-seed weight (g)		
	M.P	p	B.P	M.P	p	B.P	M.P	p	B.P
Line 1 x Tester 1	40.08**	1.53	11.04**	42.63	1.44	9.98	3.52	0.83	-0.7
Line 1 x Tester 2	9.02*	0.75	-2.74*	16.59	0.91	-1.37	7.84	1.24	1.42
Line 1 x Tester 3	-19.62	-1.74	-27.76	-22.22*	-2.55	-28.46*	-3.81	-1.56	-6.1
Line 1 x Tester 4	65.26**	187.00	64.68**	69.00**	19.68	63.27**	2.27	0.70	-0.93
Line 2 x Tester 1	40.40**	3.15	24.46**	48.87	2.82	26.88	7.04	1.41	1.95
Line 2 x Tester 2	31.84**	18.18	29.57**	54.74*	10.30	46.94*	17.08	2.41	9.33
Line 2 x Tester 3	-8.30	-0.34	-26.46	-12.17*	-0.57	-27.71*	-5.05	-1.58	-8.00
Line 2 x Tester 4	82.66**	6.14	60.98**	30.14	3.15	18.78	-28.16**	-7.06	-30.91**
Line 3 x Tester 1	153.49**	11.04	122.56**	173.81**	11.55	137.98**	8.92	6.28	7.40
Line 3 x Tester 2	-7.37	-11.49	-7.96	-5.22	-1.75	-7.96	2.91	0.83	-0.59
Line 3 x Tester 3	20.76**	0.88	-2.34**	19.75	0.83	-3.21	-0.78	-2.04	-1.15
Line 3 x Tester 4	39.26**	3.17	23.92**	56.81*	4.78	40.15*	12.76	31.47	12.31
Line 4 x Tester 1	48.85**	10.40	42.17**	60.17	6.64	46.85	8.37	2.08	4.18
Line 4 x Tester 2	92.71**	4.85	61.81**	109.2**	5.21	72.93**	9.00	4.68	6.94
Line 4 x Tester 3	-24.47	-0.61	-46.19	-15.81**	-0.35	-41.93**	13.82	2.38	7.57
Line 4 x Tester 4	50.88**	1.69	15.92**	59.43	1.71	18.36	7.07	1.41	1.94
L.S.D(0.05)	14.97		12.97	23.98		20.77	15.41		13.34
(0.01)	19.98		17.31	32.02		27.73	20.57		17.81

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 7. Cont

Crosses	Crud protein%			Carbohydrate%			Fiber%		
	M.P	p	B.P	M.P	p	B.P	M.P	p	B.P
Line 1 x Tester 1	5.88	3.00	3.85	2.31	2.10	1.20	-7.95	-2.24	-11.11*
Line 1 x Tester 2	20.00**	2.20	10.00**	-2.7**	-0.64	-6.67**	-2.44	-0.33	-9.09
Line 1 x Tester 3	4.88	0.57	-3.37	1.50	1.33	0.37	-12.77**	-3.18	-16.14**
Line 1 x Tester 4	12.73	1.40	3.33	-1.54**	-0.40	-5.19**	14.72	1.64	5.26
Line 2 x Tester 1	-1.93**	-0.25	-8.97**	5.52	1.14	0.66	-11.89**	-1.17	-20.00**
Line 2 x Tester 2	-1.79**	-0.12	-14.44**	-4.35**	-0.43	-13.16**	-19.43**	-3.04	-24.27**
Line 2 x Tester 3	3.98**	0.28	-8.99**	-2.82**	-0.40	-9.21**	-24.76**	-1.41	-36.00**
Line 2 x Tester 4	14.80	1.00	0.01	-9.03**	-0.93	-17.11**	-11.91**	-0.53	-28.00**
Line 3 x Tester 1	-0.91**	-0.17	-6.03**	9.65*	1.47	2.90*	3.68	1.57	1.31
Line 3 x Tester 2	-13.45**	-7.93	-14.89**	10.20**	8.33	8.87**	-16.40**	-2.68	-21.21**
Line 3 x Tester 3	-7.95**	-7.00	-8.99**	9.88**	2.27	5.30**	-9.91**	-1.90	-14.38**
Line 3 x Tester 4	10.73**	6.33	8.89**	-6.83**	-4.20	-8.32**	24.53*	2.41	13.01*
Line 4 x Tester 1	10.38**	4.16	7.69**	3.55	1.60	1.30	2.13	0.25	-5.88
Line 4 x Tester 2	-6.21**	-0.65	-14.44**	10.16**	3.25	6.82**	-1.36	-0.11	-12.12*
Line 4 x Tester 3	-2.57**	-0.28	-10.67**	8.33**	∞	8.33**	3.65	3.80	2.66
Line 4 x Tester 4	8.40	0.87	-1.11	0.93	0.34	-1.74	7.66	1.90	3.49
L.S.D(0.05)	1.28		1.11	1.31		1.13	1.03		0.89
(0.01)	1.71		1.48	1.75		1.51	1.37		1.19

*and ** refer to 0.05 and 0.01 levels of probability, respectively.

allelic interactions, which increase or decrease the expression of heterosis [17]. Even in the absence of epistasis, multiple alleles at a locus could lead to either positive or negative heterosis [18]. These results are in good agreement with those obtained in faba bean by Attia et al [19], El-Hady et al [20], El-Metwally et al [21], Abo Mostafa et al [22], Haridy et al [23], Abo-Zaid et al [24], Abdalla et al [25], Abdalla et al [26], Bishnoi et al [27], Fouad [28], Heiba et al [29] and Ibrahim et al [30].

Combining ability: The data presented in Table 6 revealed that, the ratios of s^2_{gca}/s^2_{sca} were less than unity for all studied traits; this might indicate that the non-additive gene effects were of greater importance in the inheritance of these traits. It could be concluded that, selection procedure based on the accumulation of additive would not be successful in improving these traits. To maximize selection advance, procedure which are known to be effective in shifting gene frequency when additive and non-additive genetic variances are involved would be preferred. However, in the case of predominant of non-additive genetic variance in the inheritance of a trait, the selection must be delayed to the later segregating generations and bulk method must be followed.

The data listed in Table 8 revealed the general combining ability effects (\hat{g}_i) of the lines and testers used in the study for the studied traits. The data indicated that, Line 1 considered as good combiner parent for improving the tolerant to rust diseases with respect to the present materials due to its significant (\hat{g}_i) in negative direction. Significant and/or highly significant (\hat{g}_i) in positive direction for plant height and crude protein percentage were found in line 1 and tester 4. The parents; Line 3 and tester 4 showed highly significant (\hat{g}_i) in positive direction for No. of pods/plant, no. of seeds/plant and seed yield /plant in the testers could be used in a suitable breeding program to improve seed yield. The parents line 4, tester 1 and tester 3; had significant (\hat{g}_i) in positive direction for carbohydrates percentage. For tester parent 4 (Najeh) could be used in suitable breeding program to improve yielding potentiality and protein of the present material due to its at least significant (\hat{g}_i) for plant height, No. of pods and seeds/plant and seed yield /plant and crude protein percentage. GCA effects (\hat{g}_i) was previously reported in faba bean by Drwish et al ([31], Ahmad [32], Haridy et al [23], Abo-Zaid et al [24], Abdalla et al [25], Abdalla et al [26],

Bishnoi et al [27], Fouad [28], Heiba et al [29] and Ibrahim et al [30].

Specific combining ability effects (\hat{S}_{ij}) were estimates of the sixteen crosses for the studied traits. The data presented in Table 9 showed that, the cross; Line 2 x Tester 3 had highly significant (\hat{S}_{ij}) in favorable direction for chocolate spot disease reaction and crosses; Line 1 x Tester1, Line 1 x Tester 2 and Line 3 x Tester 4 had highly significant (\hat{S}_{ij}) in favorable direction for rust disease reaction, indicating that the ability to use these crosses to improve the tolerant to the two diseases. While, cross; Line 1 x Tester 2 recorded negative significant (\hat{S}_{ij}) for flowering date.

For plant height three crosses; Line 1 x Tester 2, Line 2 x Tester 3 and Line 4 x Tester1 exhibited significant positive (\hat{S}_{ij}) and the crosses; Line 2 x Tester 3 and Line 4 x Tester 2 for No of branches/plant. The crosses; Line 1 x Tester 4 and Line 4 x Tester 2 possessed significant and highly significant (\hat{S}_{ij}) in positive direction for No of pods /plant. The crosses; Line 1 x Tester 4, Line 2x Tester 4, Line 3 x Tester 1, Line 3 x Tester 3 and Line 4 x Tester 2 had significant and/ or highly significant (\hat{S}_{ij}) for No of seeds /plant in positive direction.

The crosses; Line 3 x Tester 1 and Line 4 x Tester 2 expressed significant (\hat{S}_{ij}) in positive direction for seed yield /plant. The crosses; Line 1 x Tester 2, Line 3 x Tester 4 and Line 4 x Tester 1 had highly significant (\hat{S}_{ij}) in positive direction for crude protein percentage. The crosses; Line 1 x Tester 4, Line 2 x Tester1, Line 3 x Tester 2 and Line 4 x Tester2 showed significant (\hat{S}_{ij}) in favorable direction for carbohydrate percentage. However, The crosses; Line 1 x Tester 2, Line 1 x Tester 4, Line 3 x Tester 1 and Line 4 x Tester 2 had more significant traits for (\hat{S}_{ij}). These crosses also had significant better parent heterosis for most traits, which might performed that the source of both parameters i.e., heterosis and \hat{S}_{ij} is the non-additive genes. Indicating that these crosses could be used in breeding program to improve the reaction to chocolate spot disease and yielding ability. While, the cross; line 3 x tester 4 showed significant (\hat{S}_{ij}) in favorable direction for fibers percentage. Similar trend are obtained by Abd El-Mohsen [33], El-Metwally et al [21], Ahmad [32], Haridy et al [23], Abo-Zaid et al [24], Bishnoi et al [27], Fouad [28], Heiba et al [29] and Ibrahim et al [30].

Table 8. Estimates of parental lines and testers general combining ability effects for studied traits in the F₁ generation

Genotypes	Chocolate spot diseases reaction	Rust diseases reaction	Flowering date	Plant height (cm)	No .of branches/ Plant	No .of pods/ plant	No .of seed/plant	Seed Yield/ plant	100- seed weight	crude protein (%)	Carbo- hydrate (%)	Fiber (%)
Line												
Line 1	-0.45	-0.78*	0.01	3.75*	0.07	0.97	3.36	4.48	1.01	1.9**	-0.95*	-0.05
Line 2	0.10	0.31	3.33*	-3.92*	0.14	-1.09	-0.14	-4.71	-2.23	-1.43**	0.70	-0.20
Line 3	0.29	0.33	-1.67	-2.27	-0.78*	3.44*	9.29*	10.26	1.42	0.09	-0.83*	0.27
Line 4	0.06	0.14	-1.67	2.45	0.58*	-3.32*	-12.52*	-10.04	-0.2	-0.56	1.08*	-0.02
LSD (gi-gj)	0.445	0.412	2.516	2.777	0.384	2.560	7.485	11.992	7.704	0.639	0.654	0.515
0.05	0.594	0.550	3.358	3.707	0.513	3.417	9.992	16.008	10.284	0.853	0.873	0.687
0.01												
Tester												
Tester 1	-0.46	-0.39	-0.42	-3.31*	-0.26	1.71	2.75	5.39	2.31	-1.54**	2.82**	0.44
Tester 2	0.21	-0.35	-2.08	2.34	0.01	-3.25*	-11.34*	-6.3	2.43	-0.55	-0.55	0.14
Tester 3	-0.19	0.10	-1.25	-4.55*	0.15	-5.09*	-16.9**	-14.3*	-1.03	-0.73*	1.25*	-0.99*
Tester 4	0.44	0.64*	3.75*	5.51*	0.11	6.63**	25.57**	15.22*	-3.71	2.82**	-3.52**	0.41
LSD(gi-gj)	0.445	0.412	2.516	2.777	0.384	2.560	7.485	11.992	7.704	0.639	0.654	0.515
0.05	0.594	0.550	3.358	3.707	0.513	3.417	9.992	16.008	10.284	0.853	0.873	0.687
0.01												

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 9. Estimates of specific combining ability effects for studied traits in the F₁ generation

Crosses	No .of seeds/plant	Seed Yield/ plant	100-seed weight	Protein%	Carbohydrate%	Fiber%
Line 1 x Tester 1	0.13	-0.86*	-0.42	-5.62*	0.72	-1.80
Line 1 x Tester 2	-0.18	-0.73*	-5.42*	4.85*	-0.61	-0.54
Line 1 x Tester 3	-0.11	0.32	2.08	-2.81	-0.33	-3.73
Line 1 x Tester 4	0.16	1.28**	3.75	3.59	0.22	6.06*
Line 2 x Tester 1	0.41	0.49	-2.08	-1.49	-0.02	-6.53**
Line 2 x Tester 2	0.01	-0.02	6.25**	-2.69	-0.35	0.35
Line 2 x Tester 3	-0.79*	-0.67	-2.92	5.65*	1.44**	2.09
Line 2 x Tester 4	0.37	0.19	-1.25	-1.47	-1.06**	4.08
Line 3 x Tester 1	-0.24	0.21	4.58*	1.99	0.23	15.05**
Line 3 x Tester 2	0.62	1.07**	-2.08	0.22	-0.25	-11.99**
Line 3 x Tester 3	-0.01	-0.45	-1.25	-3.35	-0.36	4.51
Line 3 x Tester 4	-0.38	-0.83*	-1.25	1.14	0.38	-7.57**
Line 4 x Tester 1	-0.31	0.16	-2.08	5.12*	-0.93*	-6.72**
Line 4 x Tester 2	-0.45	-0.32	1.25	-2.37	1.22**	12.18**
Line 4 x Tester 3	0.91*	0.80*	2.08	0.50	-0.75	-2.58
Line 4 x Tester 4	-0.15	-0.64	-1.25	-3.25	0.46	-2.58
L.S.D (sij-skij) (0.05)	0.981	0.824	5.031	5.554	0.768	5.120
(0.01)	1.189	1.100	6.716	7.414	1.025	6.834

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 9. Cont.

Crosses	No .of seeds/plant	Seed Yield/ plant	100-seed weight	Protein%	Carbohydrate%	Fiber%
Line 1 x Tester 1	-7.10	-8.57	-1.58	-1.38*	-0.37	-0.63
Line 1 x Tester 2	-5.36	-5.30	0.05	3.63**	-1.55*	0.60
Line 1 x Tester 3	-5.69	-7.25	-2.72	-0.52	-0.17	-0.30
Line 1 x Tester 4	18.15*	21.12	4.24	-1.73**	2.09**	0.33
Line 2 x Tester 1	-18.64**	-8.54	5.13	-1.38*	2.43**	0.45
Line 2 x Tester 2	2.04	14.60	11.22	-0.37	-1.20*	0.21
Line 2 x Tester 3	-0.73	2.60	0.11	1.14	-1.00	-0.13
Line 2 x Tester 4	17.33*	-8.66	-16.47*	0.6	-0.23	-0.53
Line 3 x Tester 1	41.9**	33.67**	-0.19	0.68	0.29	0.31
Line 3 x Tester 2	-33.77**	-34.1**	-6.55	-2.03**	1.33*	-1.05*
Line 3 x Tester 3	16.95*	9.27	-2.94	-0.39	0.87	-0.26
Line 3 x Tester 4	-25.08**	-8.85	9.68	1.74**	-2.5**	1.00
Line 4 x Tester 1	-16.16*	-16.57	-3.37	2.08**	-2.35**	-0.13
Line 4 x Tester 2	37.09**	24.8*	-4.72	-1.24*	1.42*	0.24
Line 4 x Tester 3	-10.53	-4.62	5.55	-0.23	0.30	0.70
Line 4 x Tester 4	-10.40	-3.61	2.54	-0.61	0.63	-0.80
L.S.D(sij-skij) (0.05)	14.971	23.985	15.408	1.278	1.308	1.030
(0.01)	19.984	32.017	20.568	1.706	1.747	1.375

*and ** refer to 0.05 and 0.01 levels of probability, respectively

Table 10. Means (X), Phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability (H) in broad-sense and narrow sense (h²), expected (Ga) and predicted genetic advance (Ga%) for all studied traits

Traits	_X	PCV	GCV (%)	Heritability		Genetic advance	
				H (%)	h ² (%)	G a	Ga%
Chocolate-spot disease reaction	3.93	16.56	14.42	75.94	20.28	0.27	6.92
Rust disease reaction	4.59	16.37	14.12	74.33	0.71	0.01	0.24
Plant height(cm)	134.86	8.40	6.83	66.72	9.48	2.20	1.63
No .of branches/ plant	4.22	34.33	26.75	60.69	4.95	0.15	3.50
No .of pods/plant	22.56	30.87	24.01	60.49	1.06	0.15	0.67
No .of seeds/plant	65.16	24.93	12.36	24.60	3.37	1.14	1.73
Seed Yield/ plant	53.38	27.54	19.39	49.56	6.76	2.05	3.83
100-seed weight	80.94	12.67	11.12	77.90	0.68	0.14	0.18

IV- Heritability and genetic advance: The heritability is one of the most important parameter for determination the genetic behavior of a metric character. The heritability estimates is usually connected with breeding methods and many practical decisions about the techniques followed depends on its magnitude.

Phenotypic and genotypic coefficient of variation, heritability in broad and narrow-senses and expected and predicted genetic gain from selection are presented in Table 10. In this respect, phenotypic (PCV) and genotypic (GCV) coefficients of variation ranged from 8.4% to 34.33% and 6.83% to 26.75% for plant height and No. of branches/plant, respectively. Broad sense heritability (H) ranged from 24.6% for No. of seeds/plant to 77.90% for 100-seed weight. According to categorized suggested by Johanson [30], low (H) was detected for No. of seeds/plant, moderate values were noticed for No. of pods/plant, No. of branches/plant and seed yield /plant. The other traits had (H) values more than 60% which considered as high broad – sense heritability values. However, the values of (H) were considered as relatively low, which could be attributed to that the present genetic material is more affected by environmental conditions.

With respect to narrow- sense heritability (h^2), the range is between 0.68% for 100-seed weight to 20.28% for chocolate spot diseases reaction. According to the classification of narrow-sense heritability by Stansfield [14], all estimates are considered as low (< 20%).

The low estimates of narrow- sense heritability in the present material could be expected results, because all studied traits were mainly controlled by non-additive gene effects as mentioned before and the additive genes considered as low constitution of the genetic variance and subsequent lowering the narrow-sense heritability.

The expected genetic advance (Ga) or predicted (Ga%) genetic gain upon selection are listed in Table 9. The predicted (Ga%) genetic gain upon selection ranged from 0.18% for 100-seed weight to 6.92% for chocolate spot disease reaction, which considered as low values. This is an expected result due the low values of h^2 and (PCV) which are the main component of (Ga) equation. These results are in the same line with those obtained by El-Metwally et al [21], Abo Mostafa et al [22], Haridy et al [23], Abo-Zaid et

al [24], Abdalla et al [25], Abdalla et al [26], Bishnoi et al [27], Fouad [28], Heiba et al [29] and Ibrahime et al [30].

4. CONCLUSION

Overall, the study revealed significant genetic variability among the parental genotypes and their crosses for various important traits in faba bean. The results indicated the presence of both additive and non-additive gene effects in the inheritance of these traits. Tester 4 was identified as a good combiner parent for several traits, while the crosses Line 1 x Tester 1, Line1 x Tester 3, Line2 x Tester 3 and Line4 x Tester 1 were resistant for chocolate spot and rust diseases reaction showed significant effects in favorable directions for disease resistance. Whilst the crosses; Line 1 x Tester 4, Line 2 x Tester 2, Line 2 x Tester 4, Line 3 x Tester 1, Line 3 x Tester 3, Line 3 x Tester, Line 4 x Tester 2 and Line 4 x Tester 4) were the highest yielding crosses. The heritability estimates varied among traits, with moderate to high values observed for some traits. The study provides valuable insights into the genetic control of important traits in faba bean and highlights the potential for developing high-yielding and disease-resistant hybrids through appropriate breeding strategies.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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