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ESTIMATION OF HETEROSIS AND GENE ACTION FOR YIELD AND YIELD COMPONENTS IN FABA BEAN

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Abstract: Six genotypes of faba bean were crossed in using half-diallel analysis method. During winter season of 2017, to produce fifteen F1 crosses. The parent and crosses were cultivated during winter season of 2018. By using R.C.B.D. with three replications to estimate different heterosis, general and specific combining ability effects, genetic parameters on single cross faba bean hybrids. For growth, yield, yield components and Quality. The analysis of variance showed that significant differences were found among parental and their crosses for all the traits. The results were showed that the hybrid (Turkish x Italian) gave highest for seed yield 116.20g, 100 seed weight 155g, number of seed pod⁻¹ 5.90, number of pod plant⁻¹ 16.30, number of branches⁻¹ 6.30. While the hybrid (Turkish × Italian) gave the highest heterosis 38.58% for seed yield, 100 seed weight 10.24%, number of seed pod⁻¹ 40.47%. Significant general and specific combining ability variance were observed for all traits, the overall study of GSA effect suggested that parent (Turkish) was significant for GCA for yield gave 5.12. However, the crosses (French × Turkish) showed highest SCA effect for seed yield indicates variance of additive gene more than non-additive gene. The significant positive SCA of crosses could be used for commercial variety development. The values of the broad sense heritability were high for all the traits. The average of degree of dominance reduced one for most the traits. The results indicated that some genotypes could be used in breeding program to develop new hybrid with highest seed yield.

Key words: Degree of dominance, Expected genetic advance, Gene action, Heritability, Faba bean.

1. Introduction

Faba bean (*Vicia faba* L.) is one of the most important crop in world, It contains highest protein with average ranging from 25-40% [Beshoni *et al.* (2018), Bishoni *et al.* (2018)]. It is one of the earliest domesticated, combining ability showed important information for Improving seed yield and yield components faba bean breeders do their best to explore the genetic material in order to develop new faba bean genotypes which characterized by high yielding and better quality [Bishoni *et al.* (2018), Alkumer *et al.* (2017)]. Difference of Heterotic effects were obtained in many traits in faba bean and positive desirable heterotic value over better parent for yield and yield components traits GCA and SCA in the inheritance of faba bean were studied by several others [Beshoni *et* al. (2018), Bishoni et al. (2018)]. Highly significant GCA and SCA are very essential in developing plant breeding value for all the studied traits [Abd EL and Mohamed (2015), Alghamdi and Ali (2004), Belitz et al. (2009), Bishoni et al. (2012)]. Half-diallel crosses analysis help the breeders to the estimates several genetic parameters regarding combining ability with genotypes GCA and SCA, degree of dominance and broad sense, narrow sense heritability. Heritability in the broad sense is defined as the ratio of the genetic variance $\delta^2 G$, to the phenotypic variance $\delta^2 P$ narrow sense, broad sense heritability was higher for same studied traits [Alan and Geren (2007), Beshoni et al. (2018)]. This information is helpful to plant breeders depend on the knowledge genetic systems controlling their inheritance and environmental factors that influence their expression.

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for formulating hybrid breeding programs. The objective of this study is to determine heterosis, estimate GCA and SCA among parents for all the studied traits.

2. Materials and Methods

The experimental material consisted of 6 faba bean genotypes originating (Cypriot, French, Turkish, Italian, Dutch and Spanish) which were crossed in half-diallel crosses to obtain 15F1 crosses [Bishoni *et al.* (2012), Griffing (1956)] the parents and their F1 crosses were grown in winter season 2018. In Randomized complete block design with three replications a row length of 5m and distance between rows were 0.40 m, within the raw 0.25 m. Several traits were studied during the growth period of faba bean (plant height, branch plant⁻¹, number of pods plant⁻¹ number of seeds pod⁻¹, 100 seeds weight, protein percentage.

Statistical analysis was performed for each trait using analysis of variance of (RCBD). The treatment means were compared at 5% level of significant difference. Heterosis was calculated by Abdelmula and Abuanja (2007).

Best parent heterosis (%) = $\frac{F1-B.P}{B.P} \times 100$

Genetic parameters is estimated as follow [Abd. and Mohamed (2015), Alkumer *et al.* (2017)]:

Heritability in broad sense $(h^2b.s) = \frac{\delta^2 G}{\delta^2 P} \times 100$.

Heritability in narrow sense $(h^2 n.s) = \frac{\delta^2 A}{\delta^2 P} \times 100$

where,

 $\delta^2 A$ = additive genetic variance

 $\delta^2 D$ = dominance variance

 $\delta^2 E$ = environmental variance,

 $\delta^2 P$ = phenotypic variance

 $\delta^2 E$ = mse the average degree of dominance

$$a = \sqrt{\frac{2\delta^2 D}{\delta^2 A}}$$

% $\Delta G = \frac{H^2 . sk \,\delta P}{x} \times 100$
where, K=20.6

3. Results and Discussion

Estimates of variances due to GCA and SCA and their ratio indicated that SCA were higher for plant height, number of seeds pod⁻¹ seed weight. protein percentage. This shows that additive gene action represents a major portion of the genotypic variance for plant height, branch plant⁻¹, number of pods plant⁻¹, and seed yield. The genotype [Salama and Manal (2001), Salem (2009)] was good GCA effects for seed weight and plant height, while the crosses ($P_1 \times P_3$) and ($P_3 \times P_4$) exhibited desirable SCA effects for plant height and number of pods plant⁻¹. The estimates of phenotypic variance, additive gene, dominance heritability (in broad sense and narrow sense were).

Results in Table 1 show significant difference, among genotypes crosses and parents, according to this significant, the variance of genotypes must be distributed to the GCA and SCA variance [Anonymous (2002),]. Table 2 reveals same crosses over their parents in all the studied traits. The highest seeds yield (116.20 gm plant⁻¹) produced from the plans of the crosses (3×4). While the highest protein% continent the seeds of the crosses (5×6), it was 24.60% [Ghareeb and Helal (2014), Hossam (2010), Yudhvir *et al.* (2017)]. Gene action analysis indicates significant difference of GCA and SCA, means that dominance and additive gene action control the studied traits. The GCA variance was more than the SCA variance value except 100 seeds weight and protein% [Bishoni *et al.* (2018), Farag and

Table1: Analysis of variance of General and specific combining ability, for all studied traits.

Characters SOV	DF	Plant height Cm	branch plant¹ plant¹	Number of pods pod ⁻¹	Number of seeds weight	100 seeds yield	Plant percentage gm	Protein Percenta gm
REP	2	12.55	18.65	21.70	30.11	16.12	34.20	32.16
Geno	20	189.40**	126.15**	26.14**	18.30**	33.20**	48.66**	45.20**
GC.A	5	120.30**	19.30**	18.16**	14.07**	26.05**	70.30**	30.12**
S.C.A	15	66.25**	12.60**	5.40**	10.16**	40.16**	52.40**	25.40**
MSE	40	6.13	0.40	0.60	0.15	3.40	8.15	2.50
δ ² Gca/δ ² Sca		2.04	0.13	0.20	0.05	1.13	2.71	0.83

Afiah (2012)].

Results in Table 3 show significant difference in heterosis%, which calculated according to the beast parent. The highest heterosis (38.58%) had the seeds yield of the crosses (3×4) .

Table 4 indicates the variances of GSA and SCA. It reveals that GCA variance was higher than the SCA variance for the traits branches plant⁻¹, number of pods plant⁻¹ and plant seed yield gram, indicate that there characters under the additive gene action more than dominance, while the other studied traits, dominance [Hossam (2010), Keerthi and Ramesh (2018), Salama and Manal (2001)].

Results in Table 5 show that the GCA effects for

Table 2: Means of parents and their F₁s for different traits in half diallel cross.

Characters	Plant	branch	Number	Number	100	Plant	Protein
SOV	height	plant ¹	ofpods	of seeds	seed	seed	Percentage
	Cm			plant ¹	pod-1	weight gm	yield gm
1	65.80	4.82	14.30	3.80	148.16	80.23	23.80
2	80.16	5.70	14.70	4.11	130.20	78.66	21.44
3	78.38	4.32	14.20	4.20	140.61	83.85	23.80
4	82.15	5.21	15.40	4.20	140.60	90.55	22.15
5	84.20	3.70	14.00	3.25	132.50	60.16	21.55
6	70.40	3.80	13.00	3.50	132.05	60.51	19.70
1×2	73.13	5.83	14.80	4.90	140.10	78.20	23.90
1×3	86.15	5.60	14.60	4.50	144.00	85.40	21.50
1×4	70.25	6.18	14.90	4.30	145.00	89.60	20.40
1×5	86.55	4.90	13.60	3.40	120.80	55.60	24.15
1×6	80.45	2.80	13.40	4.10	122.00	50.80	21.55
2×3	80.80	3.75	14.61	4.95	145.00	84.90	19.60
2×4	72.11	4.70	15.98	4.80	140.00	91.60	18.90
2×5	86.15	6.19	14.20	4.00	130.60	83.80	23.16
2×6	70.11	5.80	13.50	3.40	133.00	61.15	24.12
3×4	75.20	6.30	16.30	5.90	155.00	116.20	18.16
3×5	74.23	5.66	15.80	3.20	140.00	61.60	24.60
3×6	72.15	5.72	14.70	3.40	120.00	60.12	23.90
4×5	76.80	5.60	14.80	3.60	126.00	66.65	22.30
4×6	85.17	3.30	14.40	4.80	150.80	84.50	21.90
5×6	84.19	5.25	14.20	4.35	140.00	68.20	24.70
means	77.87	5.09	14.54	4.12	137.91	75.34	22.10
L.S.D	4.08	1.04	1.27	0.63	4.30	4.70	2.60

Table 3: Estimates of heterosis over best parent for all studied traits.

Characters	Plant	branch	Number	Number	100	Plant	Protein
SOV	height	plant ¹	of pods	of seeds	seed	seed	Percentage
	Cm			plant ¹	pod-1	weight gm	yield gm
1×2	-13.60	2.28	0.68	19.51	1.44	-2.53	0.42
1 × 3	5.92	16.18	2.09	7.14	2.41	1.84	-9.66
1×4	-14.48	18.61	-3.24	2.38	3.12	-1.04	-14.64
1×5	7.91	1.65	-4.89	-10.52	-13.04	-30.69	1.42
1×6	0.31	-21.16	-6.29	7.89	-11.65	-36.68	-9.45
2×3	-3.94	-34.21	-0.61	17.85	3.57	1.25	-17.64
2×4	-14.27	-17.54	3.18	14.28	-0.42	13.71	-20.58
2×5	2.41	8.59	-3.40	-2.67	-1.43	6.53	7.47
2×6	-16.65	1.75	-8.16	-17.27	-3.62	-22.26	12.50
3×4	-8.46	20.92	5.84	40.47	10.24	38.58	-23.69
3×5	-7.44	31.01	11.26	-23.80	-0.42	-26.53	3.36
3×6	-7.94	30.09	3.52	-19.04	-14.65	-28.30	4.20
4 × 5	-6.51	7.48	-3.89	-14.28	10.24	-17.25	0.67
4×6	3.70	-4.46	-1.00	14.28	7.25	4.90	-1.12
5×6	4.97	38.15	1.42	24.28	5.26	12.70	14.22

Characters SOV	Plant height Cm	branch plant ¹	Number of pods	Number of seeds plant ⁻¹	100 seed pod ⁻¹	Plant seed weight gm	Protein Percentage yield gm
GCA	11.08	1.75	1.14	0.45	1.20	4.25	0.09
SCA	24.58	1.20	1.10	4.20	8.60	2.10	3.16
GCA/SCA	0.45	1.45	1.03	0.10	0.13	2.02	0.02

Table 4: Variance of the GCA and SCA for studied traits

Table 5: Estimates of GCA effects of each parent for all studied traits.

Characters SOV	Plant height Cm	branch plant ¹	Number of pods	Number of seeds plant ¹	100 seed pod ⁻¹	Plant seed weight gm	Protein Percentage yield gm
1	-5.30	1.35	-1.25	0.19	-2.60	-2.12	-4.12
2	-1.34	-0.16	0.18	0.85	-1.20	4.55	-0.05
3	3.42	2.20	1.19	-1.02	3.55	5.12	-2.95
4	2.31	0.81	-0.40	1.13	1.72	-8.40	0.16
5	-0.54	-1.19	0.08	-0.20	-0.82	1.80	-0.44
6	1.85	-3.40	-1.16	0.26	-0.72	0.72	1.25
S.E (gi)	1.65	0.82	0.75	0.48	1.12	2.44	1.05

Table 6: Estimates SCA effects of each parent for all studied traits

Characters	Plant	branch	Number	Number	100	Plant	Protein
SOV	height	plant ¹	ofpods	of seeds	seed	seed	Percentage
	Cm			plant ¹	pod-1	weight gm	yield gm
1×2	-2.4	0.82	-2.78	0.62	1.10	-4.16	-2.14
1 × 3	1.52	1.36	0.35	-1.53	-2.05	0.28	0.19
1 × 4	-3.22	-0.21	3.16	2.21	-0.32	-0.19	0.28
1 × 5	1.60	-0.35	-2.92	-2.41	2.06	0.25	-1.04
1 × 6	-9.20	0.13	-4.15	1.07	0.80	-2.22	1.53
2×3	1.66	1.22	0.44	-2.05	-1.26	4.25	-1.02
2×4	-4.13	-0.60	3.16	-3.15	0.83	-5.66	2.14
2×5	2.58	1.24	0.25	-4.01	1.35	2.16	-3.02
2×6	-1.44	2.92	-1.34	2.28	-0.19	-2.40	2.40
3×4	1.58	-2.16	5.60	-0.28	6.14	1.60	0.19
3×5	2.24	0.15	-2.26	1.18	-0.70	0.11	-1.14
3×6	-3.40	1.54	2.44	-3.25	-0.98	0.88	-2.15
4×5	0.52	-0.32	0.19	3.20	-0.50	-0.66	-2.50
4×6	0.90	-1.04	-2.70	-2.14	3.14	-2.19	4.11
5×6	2.25	2.05	-2.40	-6.20	1.14	0.82	-2.72
S.E (si-sik)	4.12	1.76	0.98	1.16	2.80	3.82	4.41

 Table 7: Estimates of genetic parameters for all studied traits.

Characters SOV	Plant height Cm	branch plant ¹	Number of pods	Number of seeds plant ¹	100 seed pod ⁻¹	Plant seed weight gm	Protein Percentage yield gm
$\delta^2 A$	22.08	3.50	2.28	0.90	2.40	8.50	0.18
δ²D	24.58	1.20	1.10	4.20	8.60	2.10	3.16
δG	46.75	4.70	3.38	5.10	11.00	10.60	3.34
δΈ	6.13	0.40	0.60	0.15	3.40	8.15	2.50
δ²P	52.87	5.10	3.98	5.25	14.40	18.75	5.84
H ² n.s	41.91	68.62	57.28	17.14	16.66	45.33	3.08
H ² b.s	88.40	92.15	84.92	97.14	76.38	56.53	57.19
a	1.48	0.82	0.98	3.05	2.67	0.70	5.92
%ΔG	8.06	62.72	16.19	19.63	0.94	5.36	0.69

the parents 3 were higher than other parents for all the studied traits except protein percentage.

Results in Table 6 show that SCA effect for seed yield plant⁻¹ was highest for the cross (2×3) .

Table 7 shows that the additive variance represent a major portion of the genotypic variance for most of traits. The degree of dominance exceeded one for plant height, number of seeds pod, 100 seed weight and protein percentage [Khashe and Khalafallah (1980)]. Heritability in broad sense was higher for all studied traits while the heritability in narrow sense was higher for all studied traits except seed yield and protein percentage. Advance genetic ranged from 0.94% for 100 seed weigh to 62.72% for branch per plant. These results suggested that both additive and non-additive gene action played greater role in these traits, parent [Abd. EL and Mohamed (2015), Alan and Geren (2007)] have the highest number of desirable traits scored for GCA effects. The crosses (1×3) and (3×4) have the highest number of desirable traits for SCA effects [Abdelmula and Abuanja (2007), Sherwan et al. (2016), Yudhvir et al. (2017). These promising crosses could be used for developing faba bean hybrids. The present study reveals that several combinations of crosses are highly promising to breeding faba bean genotypes.

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