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Analysis of combining ability and inheritance of breeding parameters in yield component traits in faba bean (*Vicia faba* L.)

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Abstract
The efficiency and efficacy of the parent selection programmes in most crops including faba bean can be significantly improved by estimating the combining ability and effects. The present study was undertaken with an aim to estimate the combining ability variances and effects in 48 cross combinations constituted by 16 faba bean genotypes for yield and major yield contributing traits. The 16 faba bean genotypes of Indian and exotic origin were crossed in L x T fashion. Four genotypes which were used as females were crossed to 12 pollen parents to obtain 48 cross combinations. The ANOVA indicated presence of significant variability in the genotypes and heterotic effects among F_1s for different traits. The pollen parents were better general combiner as compared to the female parents for all traits except seeds per pod. Highly significant differences among genotypes relative to General Combining Ability (GCA) and Specific Combining Ability (SCA) variances were observed for all the studied traits. The line × tester interactions had greater contribution towards total variance which indicated higher estimates of specific combining ability variance. The estimates of heritability and genetic advance for the studied characters are also presented in the paper. Highly significant GCA effects should be the criteria for parent selection for synthesis of a dynamic population and highly significant SCA effects should be the criteria for parent selection for hybridization. Therefore, phenotypic performance based selection may prove reliable in faba bean hybridization programme for improvement of yield and other characters.

Keywords: Combining ability, gene effects, yield component traits, line x tester, *Vicia faba* L.

Introduction
Legumes have remained an important part of human diet since the early ages of agriculture. Their importance as a source of dietary protein is manifold, especially in the developing countries like India where a significant proportion of the population is vegetarian (Bishnoi, 2016 [9]; Key *et. al.,* 2006) [17]. Faba bean (*Vicia faba* L.) is world's fourth most important legume crop after pea, chickpea and lentil and seventh most produced legume (Kaur *et al.,* 2014; Oliveira *et al.,* 2016) [15, 21]. It is one of the earliest domesticated legumes cultivated widely in the temperate and sub-tropical world for human food, animal feed and fodder. It is an efficient nitrogen fixer and improves soil fertility through symbiotic nitrogen fixation (Bishnoi *et al.,* 2018) [7]. Because of its high seed protein content which ranges from 20 to 40% depending upon the genotype and the growing conditions, it is gaining importance as a grain legume for protein security of demographically expanding and climatically changing world (Bishnoi *et al.,* 2012) [6]. In India, faba bean has been categorized as a potential legume as an alternative source of protein for humans as well as animals (Kumar *et al.,* 2016) [18]. Faba bean is called *Baqla* or *Bakla* in Hindi and its subsidiary dialects which are also its Arabic and Turkish names. Faba bean is a diploid (2n = 2x = 12) autogamous annual plant with partial allogamy ranging from 20 to 80%. The degree of out crossing depends on environmental conditions, spacing, pollinator insect population and the genotype. The increased yield caused by heterozygosity due to outcrossing has been well documented in faba bean. Thus, heterosis, resulting from the combined action and interaction of allelic and interallelic genes is effective and improved yield can be obtained by hybrid combinations. Moreover, exploitation of heterosis in the form of synthetics and hybrids may contribute in the increase as well as stabilization of yield in faba bean (Bishnoi *et al.,* 2012[6]; Ibrahim, 2015) [13]. The identification of better combining genotypes is crucial for successful exploitation of heterosis. Further, evaluation of parental genotypes is essential for recovering better hybrids. The estimates of combining ability and effects provide important insight in selection of parents that could give rise to better hybrids upon crossing. Moreover, the knowledge about the mode of inheritance and nature and magnitude of gene effects is of considerable importance for developing high yielding varieties in faba bean (Ibrahim, 2015; Beyene, 2015) [13, 5].

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The present study involving 16 faba bean parental genotypes of indian and exotic origin was undertaken with the objectives to estimate general and specific combining ability effects, heritability and genetic advance in yield and yield component traits.

Material and Method

The present study involving 16 faba bean genotypes was carried out during 2013-14/2014-15 at the research farm of Medicinal, Aromatic and Potential Crops (MAP) Section, CCS Haryana Agricultural University, Hisar. Out of the total 16 genotypes used in the present study 10 genotypes were indigenous and originated from different geographic locations of India, five genotypes were exotic and were procured from the National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi and one genotype was the variety 'Vikrant' released by CCS Haryana Agricultural University, Hisar. Four genotypes viz. HB-85, HB-86, HB-(M)-1 and Vikrant used as female parents were crossed with 12 pollen parents viz. HB-8, HB-14, HB-23, HB-36, HB-43, HB-46, HB-49, EC-117705, EC-321682, EC-247640, EC-628938, EC-591864 in line x tester fashion to raise 48 F_1 hybrids. The experiment was laid out in randomized block design with three replications. The number of rows was kept one for both the parents and F_1 while 15 rows were planted for F_2 of each of the total 48 crosses. The row length was kept 5 m and distance between the rows was kept 45 cm. The interplant distance was kept 20 cm within the rows. The normal recommended package of practices was followed during the growth and developmental period of the crop. The observations were recorded on 10 randomly selected plants for 10 characters viz., days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of pod clusters per plant, pod length (cm), seeds per pod, 100-seed weight (g) and seed yield per plant (g). The analysis of variance for RBD was carried out for individual characters following Panse and Sukhatme (1985). The treatments summed over the replications were arranged in a two-way table (Line×Tester) for conducting the combining ability analysis according to the mathematical model developed by Kempthorne (1957) [16] and adopted by Singh and Choudhary (1985) [24].
which is given below:

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + b_k + e_{ijk}$$

Where,

X_{ijk}	=	Phenotypic values of the ijkth observation
μ	=	General mean
g_i	=	gca effect of ith female parent
g_j	=	gca effects of jth male parent
S_{ij}	=	sca effects of ijth combination
b_k	=	kth replication effect
e_{ijk}	=	Experimental error

Heritability estimate helps in determining the progress under selection. Broad sense heritability ($h^2 = \sigma^2 g / \sigma^2 p$) estimate of each trait was computed as per Falconer (1989) [12]. Genetic advance is the difference between the mean of the progeny of selected individuals and the base population. It depends upon the extant of variability in the base population, heritability of the character under selection and the intensity of the selection. The estimates of genetic advance were obtained as per Singh and Choudhary (1985) [24].

Results and Discussion

Analysis of variance (mean squares) for combining ability is presented in Table 1. The mean squares due to hybrids were highly significant for all the ten studied characters while they were highly significant due to lines for plant height, number of branches per plant, 100 seed weight and seed yield per plant. The mean squares due to testers were significant except for number of days to maturity, number of seeds per pod and 100 seed weight while they were highly significant due to line x tester for all the characters under study. The highly significant mean squares indicated the presence of heterotic effects in the characters under study.

For the traits number of days to maturity, plant height, number of branches per plant, number of pod clusters per plant, 100 seed weight and seed yield per plant, the mean squares due to testers exceeded to those of female parental lines while for number of days to maturity, pod length, number of pods per plant and number of seeds per pod, the mean squares due to lines were higher as compared to those of the testers.

The highly significant mean squares due to lines × testers manifested different combining ability effects for the testers and were indicative of both additive and non-additive control of the inheritance of the studied characters. These findings are in agreement with those of Alghamdi (2009) [3]; Sattar and El-Mouhamady (2012) [23]; Obiadalla-Ali et al. (2013) [20]; Ashrei et al. (2014) [4] and Ibrahim (2010) [13] who reported preponderance of both additive and non-additive gene action in the inheritance of above mentioned characters in faba bean. The estimates of general and specific combining ability effects of parents and crosses are given in Table 2 and Table 3 for all the characters under study. The estimates of the gca (general combining ability) effects for number of days to 50% flowering revealed that HB-85 (-2.75%) was best general combiner among lines and EC-591864 (-4.42%) was the best general combiner among testers. Both the parents expressed negative and significant gca effects. Seven parental genotypes expressed significant positive gca effects and seven showed significant negative gca effects for number of days to 50% flowering. The cross HB-(M)-1×EC-628938 (-8.56%) expressed highest significant negative sca (specific combining ability) effects for number of days to 50% flowering. Significant positive sca effects were observed in sixteen crosses while negative significant sca effects were present in thirteen crosses. The best general combiner for number of days to maturity was HB-86 (-1.90%) among the lines and EC-591864 (-6.90%) among the testers. Among all the parents the poorest general combiner for this character was HB-23 (10.18%) as it exhibited maximum positive significant gca effect. Six crosses showed significant positive gca effects and seven showed significant negative gca effects. The cross Vikrant×HB-36 showed highest negative and significant sca effects for number of days to maturity. Significant positive and negative sca effects were observed in a total of 15 crosses each. For plant height, HB-86 had the maximum significant negative gca effect (-4.07%) and thus it was the best combining line while HB-46 expressed maximum significant negative gca effect (-14.42%) among the testers. The genotype EC-117705 was the poorest general combiner with maximum significant positive gca effect (17.27%). Out of the total, six genotypes exhibited significant positive gca effects and nine of them exhibited significant positive gca effects. Significant positive sca effects were observed in ten crosses out of the total 48 while 15 crosses exhibited significant negative sca effects. HB-(M)-1×EC-247640 (-18.53%)

expressed highest significant negative sca effects while HB-86×EC-321682 expressed highest significant positive sca effects (31.26%) for plant height. The estimates of the gca effects for number of branches per plant revealed that HB-(M)-1 (0.55%) was the best general combiner among lines and EC-117705 (2.26%) was best general combiner among the testers for number of branches per plant. Four parents expressed significant positive gca effects and six of them showed significant negative gca effects. The highest significant and positive sca effects for number of branches per plant were observed in the cross Vikrant×EC-628938 (2.24%). Significant positive sca effects were observed in 11 crosses while negative significant sca effects present in 12 crosses. The best general combiner was found to be HB-85 (3.32%) among the lines and EC-117705 (11.65%) among the testers for number of pod clusters per plant. Among parents the poorest general combiner for number of pod clusters per plant was HB-23 (-4.91%) as it exhibited maximum negative significant gca effect. Four parents showed significant positive gca effects and six showed significant negative gca effects. The cross Vikrant×EC-628938, showed highest positive and significant sca effects (10.86%) while maximum negative significant sca effects were present in the cross HB-86×HB-43 (-10.29%). Significant positive and negative sca effects were observed in a total of 11 and 13 crosses respectively. For pod length, HB-(M)-1had the maximum significant positive gca effect (0.30%) among the lines while EC-628938 expressed maximum significant positive gca effect (0.61%) among the testers. The genotype EC-247640 was the poorest general combiner with maximum significant negative gca effect (-0.37%). Out of the total, three genotypes exhibited significant positive gca effects and five of them exhibited significant negative gca effects. Significant positive sca effects were observed in eight crosses while seven crosses exhibited significant negative sca effects. HB-(M)-1×EC-117705 (0.44%) was the best crosses for pod length. The estimates of gca effects for number of pods per plant revealed that HB-85 (6.75%) was the best general combiner among lines and EC-117705 (24.01%) was best general combiner among the testers for number of pods per plant. HB-23 exhibited lowest (-10.72%) gca effects. Four parents expressed significant positive gca effects and five of them showed significant negative gca effects. The highest significant and positive sca effects for number of branches per plant were observed in the cross Vikrant×EC-628938 (22.24%) while HB-86×HB-43 showed highest negative sca effects (-20.89%). Significant positive sca effects were observed in 12 crosses while negative significant sca effects present in 14 crosses. For number of seeds per pod, the best general combiner was HB-(M)-1 (0.30%) among the lines and HB-49 (0.11%) among the testers. Among all the parents, the poorest general combiner was Vikrant (-0.26%) as it exhibited maximum negative significant gca effect. Three crosses showed significant positive gca effects and four showed significant negative gca effects. The cross HB-(M)-1×HB-8 showed highest positive and significant sca effects (0.27%) and maximum negative significant sca effects were present in the cross HB-(M)-1×EC-591864 (-0.37%). Significant positive sca effects were observed in four crosses while negative significant sca effects were present in seven crosses. Among the lines HB-(M)-1 had the maximum significant positive gca effect (0.25%) and thus was the best combining line while EC-247640 expressed maximum significant positive gca effect (1.60%) among the testers for 100 seed weight. The genotype HB-36 was the poorest general

combiner with maximum significant negative gca effect (-1.34%). Out of the total, three genotypes exhibited significant positive gca effects and five of them exhibited significant negative gca effects for 100 seed weight. Significant positive sca effects were observed in 11 crosses while nine crosses exhibited significant negative sca effects. The best cross was Vikrant×EC-628938 (4.43%). The cross Vikrant×EC-321682 expressed highest significant negative sca effects (-2.99%) for 100 seed weight. For seed yield per plant, the estimates of the gca effects revealed that HB-(M)-1 (5.67%) was the best general combiner among lines and EC-117705 (28.13%) was best general combiner among the testers. HB-23 exhibited lowest (-10.61%) gca effects. Five parents expressed significant positive and eight of them showed significant negative gca effects. The highest significant and positive sca effects for seed yield per plant were observed in the cross Vikrant×EC-628938(35.28%). The cross HB-86×HB-43 exhibited maximum negative sca effect (-22.33%). Significant positive sca effects were observed in 13 crosses while negative significant sca effects were present in 14 crosses. As in the present study highly significant gca effects for number of days to maturity, plant height, number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plant were obtained by El-Bramawy and Osman (2012) [10], for 100-seed weight by Abd-Elrahman et al. (2012) [2] and for plant height and seed yield per plant by Ibrahim (2010) [13]. Abd-Elrahman et al., (2012) [2] obtained highly significant positive gca effects for seed yield per plant, number of pods and seeds per plant and plant height while Ibrahim, (2010) [13] reported highly significant gca effects for number of branches per plant, number of pods per plant, number of days to maturity and 100-seed weight which are in agreement with the findings of the present study. For synthesis of a dynamic population with most favorable genes, the use of above mentioned parents with high gca effects in a multiple crossing programme is advocated. Highly significant differences among genotypes relative to gca and sca variances were observed for all the studied traits which is in agreement with El-Harty et al. (2007) [11]. Non-additive gene action was predominantly present in the studied traits except in pod length and number of seeds per pod which is in agreement with Alghamdi (2009) [3] who observed non-additive gene action for number of days to flowering, plant height, number of branches per plant and seed yield per plant. The preponderance of non-additive gene action is also supported by the studies of El-Harty et al., (2007) [11] and Ibrahim (2010) [13]. The results are also in agreement with Obiadalla-Ali et al., (2013) [20] who reported the presence of predominantly non-additive gene action in yield and yield component traits but in contrast to Sattar et al., (2012) [23]; Abd-Elrahman et al., (2012) [2] and Ashrei et al., (2014) [4] who reported the presence of predominantly additive gene action in yield and yield component traits. The proportional contribution of lines, testers and their interaction to the total variance showed that testers played an important role towards the total variance for all traits except for number of seeds per pod, indicating predominant tester influence (Table 4). The greater contribution of line × tester interactions than testers for number of days to 50% flowering, number of days to maturity, plant height, number of seeds per pod, 100 seed weight and seed yield per plant indicated higher estimates of specific combining ability variance. The values of average degree of dominance were more than unity for all the traits except pod length and number of seeds per pod. The predictability ratio was less than unity for all the characters

under study. It indicated the heterozygous makeup of the populations and the presence of non-fixable non-additive gene action resulting from dominance, over dominance, epistatis and other interaction effects. Hence, the breeding strategy for attaining high yield in faba bean would be the full or partial exploitation of heterosis through development of hybrids, synthetics or composite cultivars. The narrow sense heritability was high (>40%) for number of days to flowering (43.75%), number of branches per plant (41.81%), number of clusters per plant (45.34%), pod length (61.10%), number of pods per plant (45.00%) and number of seeds per pod (82.67%). High heritability for different characters was previously reported by Abd-El-Haleem and Mohamed (2011) [1] and Mulualem *et al.* (2013) [19] in faba bean genotypes. The

genetic advance expressed as percent of mean was relatively higher (>5) for number of days to flowering (5.60), plant height (9.54), number of clusters per plant (6.75), number of pods per plant (14.05) and yield per plant (13.98) which indicated that selection could be effective in the improvement of these traits. High genetic advance in number of pods and total yield was previously reported by Solieman and Ragheb (2014) [25]. Moreover, high heritability coupled with high genetic advance for number of clusters per plant (45.34%), pod length (61.10%), number of pods per plant (45.00%) and yield per plant (38.84%) reflected preponderance of additive gene action in the inheritance of these characters. Similar results were reported by Kalia *et al.* (2003) [14].

Table 1: Mean squares for line×tester of quantitative characters in faba bean.

Source	d.f.	No. of days to 50% flowering	No. of days to maturity	Plant height (cm)	No. of branches per plant	No. of Clusters per plant	Pod length (cm)	No. of pods per plant	No. of seeds per pod	100 seed wt (g)	Seed yield per plant (g)
Replications	2	4.52	5.44	15.6	0.05	0.32	0	7.4	0.03	0.01	10.1
Hybrids	47	98.92**	243.33**	684.01**	6.11**	147.51**	0.46**	645.93**	0.28**	9.68**	859.84**
Lines	3	254.41*	198.71	589.69	7.91	286.41*	1.76**	1240.75*	3.19**	2.21	1232.83
Testers	11	157.65*	323.71	1228.52*	13.18**	294.99**	0.89**	1285.27**	0.05	12.2	1658.43**
Line x Tester	33	65.21**	220.60**	511.08**	3.59**	85.73**	0.20**	378.74**	0.08**	9.52**	559.73**
Error	94	4.21	11.91	57.39	0.28	7.8	0.06	29.66	0.03	0.95	29.26
Total	143	35.34	87.88	262.76	2.19	53.62	0.19	231.9	0.11	3.81	301.98

*, **- significant by the f-test at 5% and 1% probability level, respectively

Table 2: Estimates of general Combining Ability Effects for quantitative traits in faba bean

Genotypes	No. of Days to flowering	No. of days to maturity	Plant height (cm)	No. of branches per plant	No. of Clusters per plant	Pod length (cm)	No. of pods per plant	No. of seeds per pod	100 seed wt (g)	Seed yield per plant (g)
HB-85	-2.75 **	-1.88* *	-2.39*	0.55* *	3.32* *	-0.22* *	6.75* *	-0.25* *	0.13	4.21* *
HB-86	-1.81* *	-1.90* *	-4.07* *	-0.57* *	-3.45* *	0.01	-7.39* *	0.21* *	-0.32*	-6.36* *
HB-(M)-1	2.31* *	0.82	4.96* *	0.15	0.75	0.30* *	1.55	0.30* *	0.25	5.67* *
Vikrant	2.25* *	2.96* *	1.51	-0.12	-0.63	-0.09*	-0.91	-0.26* *	-0.05	-3.52* *
HB-8	1.17*	3.01* *	8.07* *	0.08	0.69	-0.01	1.05	0	-0.66*	0.92
HB-14	-1.92* *	-5.90* *	-4.88*	-0.51* *	-3.67* *	0.03	-7.69* *	0.02	0.64*	-7.87* *
HB-23	3.17* *	10.18* *	-3.49	-1.23* *	-4.91* *	-0.1	-10.72* *	0.05	0.57*	-10.61* *
HB-36	-0.17	0.18	5.56* *	-0.08	-0.49	0.39* *	-1.34	0.04	-1.34* *	-3.35*
HB-43	-3.42* *	-2.57* *	3.98*	1.53* *	6.36* *	-0.11	12.89* *	0.07	-0.24	15.18* *
HB-46	-0.33	2.35* *	-14.42* *	-1.08* *	-3.86* *	-0.12	-8.80* *	-0.02	0.37	-8.47* *
HB-49	-4.17* *	-3.07* *	13.82* *	0.67* *	3.08* *	-0.18*	7.79* *	0.11*	-0.56*	7.88* *
EC-117705	-2.92* *	-6.32* *	17.27* *	2.26* *	11.65* *	0.04	24.01* *	-0.14* *	1.12* *	28.13* *
EC-321682	6.17**	4.43* *	-4.48*	-0.80* *	-3.90* *	-0.27* *	-7.26* *	-0.02	-0.66*	-9.09* *
EC-247640	5.75**	4.51* *	-8.80* *	-0.76* *	-3.95* *	-0.37* *	-8.07	-0.09*	1.60* *	-9.45* *
EC-628938	1.08*	0.1	0.89	0.03	-0.13	0.61* *	-0.36	-0.02	-1.67* * *	-1.96
EC-591864	-4.42**	-6.90* *	-13.52* *	-0.11	-0.87	0.11	-1.5	-0.01	0.82* *	-1.31
CD 5% GCA (Line)	0.59	1	2.19	0.16	0.82	0.07	1.6	0.05	0.3	1.61
CD 5% GCA (Tester)	1.02	1.73	3.79	0.27	1.42	0.12	2.78	0.08	0.53	2.79
GCA/SCA	0.82	0.30	0.46	0.77	0.89	2.03	0.87	6.32	0.18	0.66

* Significant at 5% ** Significant at 1%

Table 3: Estimates of Specific Combining Ability Effects for quantitative traits in faba bean

S. No	Hybrids	No. of Days to flowering	No. of days to maturity	Plant height (cm)	No. of branches per plant	No. of Clusters per plant	Pod length (cm)	No. of pods per plant	No. of seeds per pod	100 seed wt (g)	Seed yield per plant (g)
1	HB-85 x HB-8	4.08**	4.88**	6.45	-0.06	1.46	-0.15	4.58	0.13	0.22	5.89*
2	HB-85 xHB-14	2.17*	5.46	4.28	0.44	3.37*	-0.17	7.34*	-0.17*	-0.14	6.12*
3	HB-85 xHB-23	-6.58**	-12.29**	2.14	0.03	2.45	0.14	4.43	-0.13	-2.31**	0.34
4	HB-85 xHB-36	1.08	-2.29	-9.40*	-0.38	-1.8	-0.31*	-3.9	-0.15	1.09*	-3.46
5	HB-85 xHB-43	-2	5.13**	-2.86	1.85**	8.93**	0.11	19.03**	-0.01	-0.01	19.16**
6	HB-85 xHB-46	-0.42	-6.13**	0.72	-0.75**	-4.63**	0.02	-9.34**	-0.04	-0.57	-11.68**
7	HB-85 xHB-49	-0.92	-2.71	-10.69**	-1.25**	-6.14**	0.12	-13.98**	-0.09	-0.19	-16.56**
8	HB-85 xEC-117705	-1.83	2.88	-11.28**	-0.54	-4.36**	0.05	-7.81**	0.20*	-1.31*	-10.27**
9	HB-85 xEC-321682	-1.58	-7.54**	-9.71*	0.01	-0.76	-0.18	-1.93	0.01	3.61**	5.37
10	HB-85 xEC-	2.50*	6.04**	11.56**	0.84**	2.97*	0.28*	4.4	0.19*	-0.03	8.43**

	247640										
11	HB-85 xEC-628938	4.50**	6.13**	15.17**	-0.51	-2.84	0.23	-5.74*	-0.05	0.56	-7.25*
12	HB-85 xEC-591864	-1	0.46	3.62	0.32	1.36	-0.15	2.92	0.13	-0.91	3.91
13	HB-86 xHB-8	-7.19**	-4.43*	8.41*	2.00**	9.46**	0.36**	19.21**	-0.22**	0.32	19.60**
14	HB-86 xHB-14	2.22*	3.82*	-4.2	0.62*	2.67	-0.31*	6.75*	0	-0.9	6.88*
15	HB-86 xHB-23	5.47**	1.74	1.51	0.37	1.6	-0.36**	3.71	0.11	1.48**	6.53*
16	HB-86 xHB-36	-3.53**	-7.93**	-16.37**	-0.44	-2.68	-0.09	-5.86*	0.02	0.11	-5.87*
17	HB-86 xHB-43	6.06**	4.49*	-1.75	-1.79**	-10.29**	-0.15	-20.89**	0.1	-0.08	-22.33**
18	HB-86 xHB-46	3.31**	5.57**	1.68	1.02**	3.39*	0.26*	6.63*	0.09	1.75**	10.25**
19	HB-86 xHB-49	-5.19**	-4.01*	-1.68	-0.96**	-4.29**	0.13	-8.44**	-0.05	-2.39**	-12.13**
20	HB-86 xEC -17705	-3.44**	3.90*	-7.92*	-0.36	-1.24	-0.21	-3.9	0.05	0	-2.19
21	HB-86 xEC-321682	-1.19	-1.18	31.26**	0.09	1.82	-0.03	4.29	0.05	0.37	3.84
22	HB-86 xEC-247640	-0.11	-3.60*	-3.28	0.64*	2.8	-0.09	5.79*	-0.18*	0.43	5.44
23	HB-86 xEC-628938	6.56**	6.82***	1.02	-0.5	-1.4	0.29*	-3.42	-0.07	-2.87***	-9.39**
24	HB-86 xEC-591864	-2.94**	-5.18**	-8.68*	-0.70*	-1.84	0.2	-3.86	0.11	1.78**	-0.62
25	HB-(M)-1 xHB-8	-1.64	-6.49**	0.64	-0.69*	-4.02**	0.19	-7.62**	0.27**	0.62	-5.26
26	HB-(M)-1 xHB-14	-6.22**	-7.90**	0.62	-1.22**	-5.90**	0.32*	-12.65**	0.22**	1.37*	-10.97**
27	HB-(M)-1 xHB-23	4.03**	-3.32	9.66*	-0.04	-1.03	-0.04	-1.97	-0.04	1.61**	-0.32
28	HB-(M)-1 xHB-36	7.03**	23.35**	19.29**	1.02**	5.74**	0.05	13.79**	0.06	-2.42***	12.12**
29	HB-(M)-1 xHB-43	0.61	1.1	-3.52	-0.59*	-0.11	-0.05	-2.24	-0.22*	-0.36	-3.5
30	HB-(M)-1 xHB-46	-1.47	2.51	-9.02*	1.35**	6.39**	-0.37**	13.95**	0.1	0.36	16.45**
31	HB-(M)-1 xHB-49	-1.97	-8.40**	23.95**	0.71*	3.96**	-0.17	8.31**	0.16	1.86**	18.87**
32	HB-(M)-1 xEC-117705	3.44**	0.51	1.1	0.82**	5.26**	0.44**	9.23**	-0.30**	0.23	7.73**
33	HB-(M)-1 xEC-321682	3.03**	0.43	-13.10**	0.06	-1.01	0.08	-2.58	0.09	-0.99	-3.63
34	HB-(M)-1 xEC-247640	-1.22	1.01	-18.53**	-0.51	-4.06**	-0.02	-7.60**	0.06	-0.55	-11.39**
35	HB-(M)-1 xEC-628938	-8.56**	-3.90*	-18.29**	-1.23**	-6.62**	-0.38**	-13.08**	-0.03	-2.12*	-18.64**
36	HB-(M)-1 x EC-591864	2.94**	1.1	7.19	0.33	1.39	-0.04	2.46	-0.37**	0.4	-1.44
37	Vikrant xHB-8	4.75**	6.04**	-15.50**	-1.25**	-6.90**	-0.40**	-16.18**	-0.17*	-1.16*	-20.23**
38	Vikrant x HB-14	1.83	-1.38	-0.7	0.16	-0.15	0.16	-1.43	-0.05	-0.33	-2.02
39	Vikrant xHB-23	-2.92**	13.88**	-13.32**	-0.35	-3.02*	0.26*	-6.17*	0.07	-0.78	-6.55*
40	Vikrant xHB-36	-4.58**	-13.13**	6.47	-0.2	-1.25	0.35**	-4.03	0.08	1.22*	-2.78
41	Vikrant xHB-43	-4.67**	-10.71**	8.13*	0.52	1.47	0.09	4.1	0.13	0.46	6.68*
42	Vikrant xHB-46	-1.42	-1.96	6.62	-1.61**	-5.15**	0.09	-11.24**	-0.14	-1.54	-15.02**
43	Vikrant xHB-49	8.08**	15.13**	-11.57**	1.50**	6.47**	-0.08	14.11**	-0.02	0.72	9.82**
44	Vikrant xEC-117705	1.83	-7.29**	18.10**	0.08	0.34	-0.29*	2.47	0.06	1.08*	4.73
45	Vikrant xEC-321682	-0.25	8.29**	-8.45*	-0.16	-0.06	0.13	0.22	-0.15	-2.99**	-5.58*
46	Vikrant xEC-247640	-1.17	-3.46	10.25**	-0.97**	-1.71	-0.17	-2.59	-0.08	0.16	-2.48
47	Vikrant x EC-628938	-2.50*	-9.04**	2.1	2.24	10.86**	-0.14	22.24**	0.15	4.43**	35.28**
48	Vikrant xEC591864	1	3.63*	-2.13	0.05	-0.91	-0.02	-1.51	0.13	-1.27*	-1.85
	CD (5%) SCA	2.05	3.47	7.57	0.54	2.85	0.25	5.56	0.16	1.05	5.58

* Significant at 5% ** Significant at 1%

Table 4: Proportional Contributions of Lines, Testers and Line×Tester to the total variance

S. No.	Character	Percent contribution of Line	Percent contribution of Tester	Percent contribution of Line×Tester
1.	Number of days to 50% flowering	16.41	37.29	46.28
2.	Number of days to maturity	5.21	31.13	63.65
3.	Plant height	5.50	42.04	52.46
4.	Number of branches per plant	8.26	50.48	41.25
5.	Number of pod clusters per plant	12.40	46.80	40.80
6.	Pod length	24.29	44.84	30.85
7.	Number of pods per plant	12.26	46.57	41.17
8.	Number of seeds per pod	73.93	4.66	21.41
9.	100 seed weight	1.45	29.49	69.05
10.	Seed yield per plant	9.15	45.14	45.70

Conclusions

The estimates of heritability were higher than the estimates of genetic advance for all the studied characters indicating that they were least influenced by environmental component and that the phenotypes were the true representative of their genotypes. The study concluded that the selection based on phenotypic performance, preceding the hybridization, should be reliable in faba bean yield improvement.

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