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Genetic variability, correlation and path analysis in faba bean (*Vicia faba*) for yield and its attributing traits under semi-arid conditions

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Abstract

The present investigation consisted of 53 genotypes of faba bean that were assessed from various source and raised in randomised block design with three replications in the *rabi* season of 2019-20 at Research Farm of MAP Crop Section, Department of GPB, CCS HAU, Hisar, Haryana. The results of analysis of variance indicated that the substantial genetic variability were present for seed yield and its contributing traits. It was observed that the estimates of PCV had higher in magnitude than that of respective estimates of GCV, which suggested that the environmental factor were also influencing the expression of the genotypes. The high estimates of heritability were reported for no. of pod clusters per plant and seed protein content. Seed yield had positive and significant correlation with almost all the traits except days to 50% flowering and days to maturity. The results of path analysis revealed biological yield, harvest index, pod yield per plant, no. of pod clusters per plant, 100 seeds weight, no. of seeds per pod, no. of branches per plant, no. of pods per cluster, pod breadth, seed protein content and no. of pods per plant had positive direct effect on seed yield, whereas, plant height, days to 50% flowering, days to maturity, weight per pod and pod length had direct negative effect on seed yield. The genotypes namely EC-32905, EC-243036, EC-591784, HB-03, HB-19, HB-61 and Vikrant are selected on the basis of their mean performance for different characters. These genotypes are important for including in crossing programme to further exploit genetic variability among populations, to affect selection of elite superior lines for hybridization programme and/or elite populations for composite varieties.

Keywords: Faba bean, analysis of variance, genetic variability, correlation and path analysis

Introduction

Faba bean (*Vicia faba* L.) is a hardy winter plant, which can tolerate extreme cold temperature. It is widely believed to have originated in the North Africa and South Caspian Sea (Tanno and Willcox, 2006) ^[43] and introduced in India by Arab traders. At Global level, in 2018-19, faba bean got 6th in production, after the common bean, pea, chickpea, cowpea and lentil with total production of 4.5 M tons, with 2.5 M ha area (Khazaei and Vandenberg, 2020) ^[22]. China is leading in faba bean with respect to area and production. In India, the area and production of faba bean is low and that is why it is still categorized as minor crops. The statistics of faba bean with respect to area and production in India is not available (Pradhan and Sinha, 2012) ^[32]. Faba bean is a dual purpose crop, green pod are used as vegetable, whereas, dry seed are used as grain legume. The seeds of faba bean are good source of protein (29.4 per cent), carbohydrate (51 per cent to 68 per cent) and fat (1.5 per cent) (Cerning *et al.*, 1975) ^[9]. Faba bean have many medicinal values as it is used as ingredients and applications to soften stiff limbs. The seeds of faba bean are good source of L-DOPA, a precursor dopamine, which is used as a medicine for the treatments of Parkinson's disease. Faba bean also contain certain anti-nutritional factors in fresh pods as well as in immature seeds such as polyphenols which impart beany flavor which known to cause astringency (Bjerg *et al.*, 1988; Kumar *et al.*, 2019) ^[7, 23].

As we know that variability is prerequisite for any crop improvement programme. If in any crop, sufficient genetic variability is present, help in further improvement as well as development of superior cultivars. Genetic variability is the primary consideration of many investigators. Vavilov (1951) ^[45] realized first that if in a crop wider range of variability is present, provides a better chance for selecting the desirable genotypes. Apart from genetic variability, their mode of transmission to the next generation is also an important factor. In a population, genetic variability is the true measure for access the variability (Ngoc *et al.*, 2019) ^[26].

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The knowledge of inter-relationships among different traits is helpful because the selection of one trait may directly affect the performance of another, which is determining the components of complex traits like yield. However, correlation studies do not provide an exact picture of the direct influence of each of the components traits towards the yield. Path coefficient proves helpful in partitioning the correlation coefficient into direct and indirect effects

Materials and Methods

Experimental materials and design: The present investigation was carried out on 53 genotypes of faba bean that were assessed from various sources and raised in randomised block design with three replications in *rabi* 2019-20 at Research Farm of MAP Crop Section, Department of Genetics & Plant Breeding, CCS HAU, Hisar. All the recommended cultural practices were followed to raise a healthy crop. Seeds of each genotype were sown in paired row of 4 meters length with row to row spacing of 45 cm, whereas, plant to plant spacing of 10 cm. Randomization of each treatment were done while allotting in each replication.

Data recorded: The observations for traits like, plant height(cm), no. of pods cluster per plant, no. of branches per plant, no. of pods per plant, no. of pods per cluster, weight per pod(g), pod length (cm), pod breadth (cm), no. of seeds per pod, 100 seeds weight (g), protein content (%), pod yield per plant (g), biological yield (q/ha), harvest index % and seed yield (q/ha) were recorded on randomly selected five competitive plants per paired row in each replication, while for days to 50% flowering and days to maturity observations were recorded on whole paired row basis. The seed protein content was estimated by the Micro-kjeldahl's method suggested by Jackson (1973) [17].

Statistical analysis: The analysis of variation was performed as suggested by Panse and Sukhatme (1967) [30]. The GCV and PCV were estimated according to Burton (1952). The heritability in broad sense was calculated as the ratio of genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was expressed in the form of percentage (Hanson *et al.*, 1955) [16]. Genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955). Genetic advance as per cent of mean for each character was worked out by the following formula:

$$GAM (\%) = \frac{GA}{\bar{X}} \times 100$$

The genetic advance as per cent of mean was categorized below as:

0-10% = Low 10-20% = Moderate >20% = High

Correlation coefficients at phenotypic level and genotypic level were calculated using the variances and co-variances according to Al-Jibouri *et al.* (1958) [3]. Path coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Wright (1921) [47] and further illustrated by Dewey and Lu (1959) [13].

Table 1: List of faba bean genotypes and their sources

Sr. No.	Genotypes	Source
1	HB-01	CCS HAU, Hisar
2	HB-02	CCS HAU, Hisar
3	HB-03	CCS HAU, Hisar
4	HB-05	CCS HAU, Hisar
5	HB-15	CCS HAU, Hisar
6	HB-19	CCS HAU, Hisar
7	HB-21	CCS HAU, Hisar
8	HB-24	CCS HAU, Hisar
9	HB-28	CCS HAU, Hisar
10	HB-30	CCS HAU, Hisar
11	HB-33	CCS HAU, Hisar
12	HB-37	CCS HAU, Hisar
13	HB-58	CCS HAU, Hisar
14	HB-61	CCS HAU, Hisar
15	HB-63	CCS HAU, Hisar
16	HB-65	CCS HAU, Hisar
17	HB-66	CCS HAU, Hisar
18	HB-68	CCS HAU, Hisar
19	HB-71	CCS HAU, Hisar
20	HB-73	CCS HAU, Hisar
21	HB-78	CCS HAU, Hisar
22	HB-79	CCS HAU, Hisar
23	HB-82	CCS HAU, Hisar
24	HB-90	CCS HAU, Hisar
25	NDFB-08	NDUA&T, Ayodha
26	NDFB-12	NDUA&T, Ayodha
27	NDFB-14	NDUA&T, Ayodha
28	EC-25085	NBPGR, New Delhi
29	EC-25192	NBPGR, New Delhi
30	EC-32905	NBPGR, New Delhi
31	EC-32923	NBPGR, New Delhi
32	EC-32976	NBPGR, New Delhi
33	EC-117744	NBPGR, New Delhi
34	EC-243036	NBPGR, New Delhi
35	EC-243596	NBPGR, New Delhi
36	EC-243793	NBPGR, New Delhi
37	EC-287710	NBPGR, New Delhi
38	EC-293820	NBPGR, New Delhi
39	EC-329681	NBPGR, New Delhi
40	EC-331564	NBPGR, New Delhi
41	EC-343691	NBPGR, New Delhi
42	EC-351587	NBPGR, New Delhi
43	EC-361485	NBPGR, New Delhi
44	EC-363781	NBPGR, New Delhi
45	EC-366272	NBPGR, New Delhi
46	EC-591784	NBPGR, New Delhi
47	EC-628925	NBPGR, New Delhi
48	EC-628940	NBPGR, New Delhi
49	EC-628942	NBPGR, New Delhi
50	PRT-12	NBPGR, New Delhi
51	ET-3279	NBPGR, New Delhi
52	VIKRANT	CCS HAU, Hisar
53	HFB-01	CCS HAU, Hisar

Results and Discussion

Range and mean performance: The wide ranges among the genotypes for seed yield and its contributing characters (table 2) indicated the extent of variability present among the genotypes for characters under the investigation; hence the wide range is desirable for breeder's point of views.

The plant height (cm) ranged from 77.87 cm to 139.30 cm. The days to 50% flowering was ranged from 61.33 days to 66.93 days. The days to maturity was ranged from 142.23 days to 156.53 days. The number of branches per plant was ranged from 2.70 to 4.43. A wide variation in number of pods per plant were observed, which ranged from 20.67 to 50.67. The pod length (cm) ranged from 3.80 cm to 5.53 cm. The mean performance of seeds per pod was ranged from 2.43 to 3.87. A wide variation in 100 seeds weight were observed, which ranged from 22.32 gm. to 43.40 gm. The seeds protein content was ranged from 24.79% to 31.90%. The pod yield per plant was widely ranged from 19.22 to 51.39. The mean performance of seed yield was ranged from 4.18 q/ha to 10.22 q/ha. This indicated that a wide variation in seed yield and its contributing characters were observed for 53 genotypes in present study. The finding of seed yield and other traits was in consonance with Fikreselassie and Seboka (2012) [14], Mulualem *et al.* (2013) [25], Sharifi (2014) [37], Sheelamary and

Shivani (2015) [39], Aziz and Osman (2015) [6], Ahmed *et al.* (2016) [1], Arya (2018) [4] Arya *et al.* (2020) [5] and Raiger *et al.* (2021) [33]. The finding of seeds protein content was in consonance with the finding of Khazaei and Vandenberg (2020) [22]. The variations are helpful in the selection of superior desirable genotypes for further improvement and exploitation through selection, hybridization and combination breeding. In the present investigation, on the basis of mean performance of 53 genotypes, the superior genotypes for seed yield and its contributing characters were shown in table 3. The genetic relationship among all the 53 faba bean genotypes based on Euclidean distance was presented in the dendrogram (Fig. 1). It reflects the genetic variability and divergence among the 53 genotypes used in the present study. Likewise, more or less similar relation was also reported in *Brassica juncea* by Yadav *et al.* (2013) [48] and in cowpea by Ngoc *et al.* (2019) [26].

Table 2: Variability, heritability and genetic advance as per cent of mean for various characters

Sr. No.	Character	Mean±S.E (m)	Range		Coefficient of Variability		H ² (bs) (%)	GAM
			Maximum	Minimum	GCV (%)	PCV (%)		
1	Plant Height (cm)	107.39±5.43	139.30	77.87	11.24	14.25	62.20	18.26
2	Days to 50% Flowering	64.31±0.54	66.93	61.33	1.62	2.17	55.88	2.50
3	Days to Maturity	148.76±2.06	156.53	142.23	1.50	2.83	28.07	1.64
4	No. of Pods Cluster per Plant	10.39±0.51	16.09	6.63	17.81	19.72	81.54	33.13
5	No. of Branches per Plant	3.50±0.14	4.43	2.70	8.98	11.19	64.51	14.87
6	No. of Pods per Plant	33.51±2.27	50.67	20.67	17.25	20.86	68.38	29.38
7	No. of Pods per Cluster	2.15±0.03	2.40	2.00	4.58	5.31	74.48	8.15
8	Weight per Pod (g)	1.16±0.07	1.69	0.84	13.23	16.46	64.63	21.91
9	Pod Length (cm)	4.72±0.13	5.53	3.80	6.59	8.05	66.99	11.11
10	Pod Breadth (cm)	0.75±0.01	0.82	0.65	4.18	5.00	69.89	7.19
11	No. of Seeds per Pod	3.11±0.13	3.87	2.43	10.66	12.78	69.55	18.30
12	100 Seeds Weight (g)	32.38±2.13	43.40	22.32	13.62	17.74	58.99	21.56
13	Seed Protein Content (%)	28.17±0.22	31.90	24.79	7.29	7.41	96.78	14.77
14	Pod Yield per Plant (g)	30.83±2.78	51.39	19.22	23.95	28.58	70.22	41.34
15	Biological Yield (q/ha)	26.36±2.43	35.56	17.79	15.98	22.58	50.11	23.30
16	Harvest Index (%)	25.10±2.24	32.05	18.50	13.27	20.35	42.49	17.82
17	Seed Yield (q/ha)	6.45±0.39	10.22	4.18	18.92	21.57	76.99	34.20

Table 3: Superior genotypes for important characters in faba bean on the basis of their mean performance

Sr. No.	Characters	Genotypes
1	Seed Yield	EC-243036, HB-61, HB-19, EC-32905 and HB-03
2	Biological Yield	HB-61, HB-05, HB-65, EC-243036 and HB-33
3	Pod Yield per Plant	HB-61, HB-19, HB-68 and EC-32905
4	Seed Protein Content	EC-32905, EC-25192 and HB-90
5	100 Seeds weight	EC-243036, EC-293820, EC-32923, HB-65 and HB-19
6	Pod length	EC-591784, EC-25085, EC-293820 and HB-15
7	Weight per Pod	HB-03, EC-293820, HB-33, EC-287710, HB-05 and EC-32905
8	No. of Pod clusters per Plant	HB-19, Vikrant, HB-73, EC-243036 and HB-03

Genetic variability: To predict the amount of variability in genotypes, the knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is necessary. From the table 2, it were reported that the value of phenotypic coefficient of variation (PCV) was found higher than respective genotypic coefficient of variation (GCV), this results ensured the presence of environmental factor in the expression of genotypes. It was also observed that the value

of PCV was not much higher than the respective value of GCV, this ensured the high heritability and stable nature of genotypes and hence selection through phenotypic performance is also effective as through genotypic performance. Earlier, similar results of higher values of PCV than respective value of GCV were reported by the Mulualem *et al.* (2013) [25], Sharifi (2015) [36], Aziz and Osman (2015) [6], Singh *et al.* (2017) [40] and Kumar *et al.* (2017) [23].

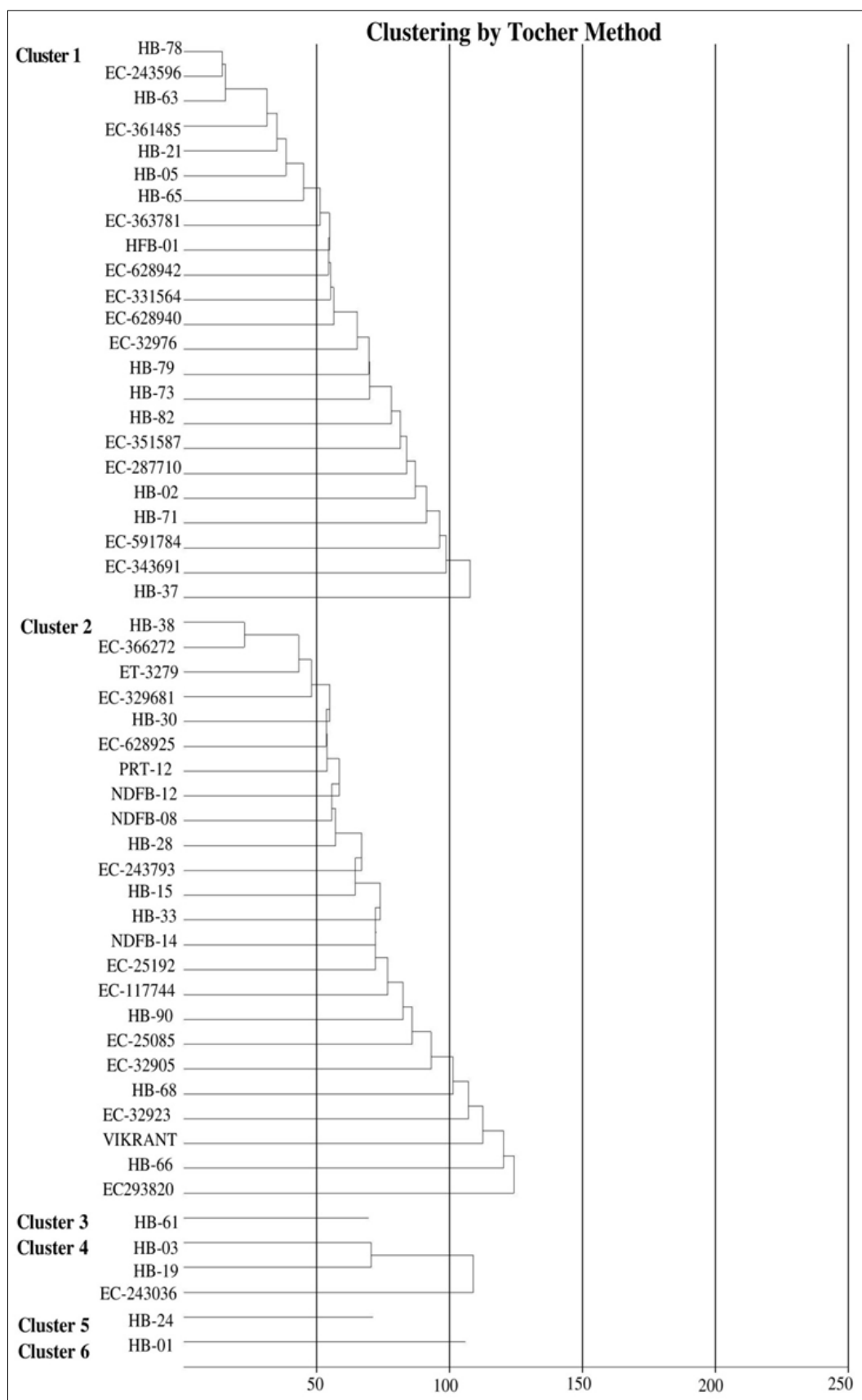


Fig 1: Dendrogram showing the clustering pattern of 53 genotypes of faba bean

High estimate of PCV and GCV were observed for the pod yield per plant, seed yield, biological yield, harvest index, pod per plant and pod cluster per plant. This estimate were in consonance with the finding of Kalia and Sood (2004)^[20] and Solieman and Ragheb (2014)^[41] for pod yield per plant,

Muluaem *et al.* (2013)^[25], Aziz and Osman (2015)^[6] and Sheelamary and Shivani (2015)^[39] for pods per plant and Sanghin (2002)^[35], Reddy *et al.* (2002)^[34], Kalia *et al.* (2003)^[21] and Peksen (2007)^[31] for pod per plant and pod cluster per plant, Singh *et al.* (2017)^[40] for no. of pod per plant and pod

yield per plant and Kumar *et al.* (2017) [23] for seed yield, pod per plant and pod cluster per plant. Moderate estimate of PCV and GCV were observed for plant height, no. of branches per plant, weight per pod, seeds per pod and 100 seeds weight. Earlier similar results for the estimate of PCV and GCV were reported by the Solieman and Ragheb (2014) [41] for seeds per pod, Muluaem *et al.* (2013) [25] for 100-seed weight, Kumar *et al.* (2017) [23] for seeds per pod and Singh *et al.* (2017) [40] for seeds per pod and 100 seeds weight. Low PCV and GCV were observed for the days to 50% flowering, days to maturity, no. of pod per cluster, pod length, pod breadth and seed protein content. The results of these characters were in consonance with the finding of Muluaem *et al.* (2013) [25] for days to maturity and Sheelamary and Shivani (2015) [39] for days to 50 per cent flowering, pod length and days to maturity, Singh *et al.* (2017) [40] for 50% flowering, days to maturity and pod length and Kumar *et al.* (2017) [23] for days to maturity.

Heritability and Genetic Advance: The knowledge of heritability helped in the study of inheritance of quantitative characters (Nagoc *et al.*, 2017). The high estimates of heritability were reported for no. of pod clusters per plant, weight per pod, pod length, pod breadth, seeds per pod, seed protein content, pod yield per plant and seed yield. The finding of heritability was in consonance with the finding of Alghamdi (2007) for no. branches per plant, Toker (2004) [44] for plant height, Sharifi (2015) [36] for pod length, Hanna and Hayes (1966) [15] for pods per plant, Kalia and Sood (2004) [20] for pod yield per plant, Muluaem *et al.* (2013) [25] for pods per cluster and Bora *et al.* (1998) [8] for seed yield per plant. Moderate estimate of heritability were observed for days to 50% flowering, 100 seeds weight, biological yield and harvest index, whereas, low estimate of heritability was observed days to maturity.

Earlier, the breeding approaches were based on the phenotypic performance of the genotypes. The high heritability estimates were effective for such breeding approaches, where prime concern was on phenotypes. Later Jain *et al.* (1999) [18] reported that for selecting the superior genotypes, heritability value along with genetic advance was a better approach rather than heritability value alone. The finding of Panse (1957) [29] that the high estimate of heritability coupled with high genetic advance, showed the additive gene effects, supports the Jain's finding. The high estimate of genetic advance as per cent of mean (GAM) were observed for no. of pod clusters per plant, no. of pods per plant, weight per pod, 100 seeds weight, pod yield per plant, biological yield and seed yield. The moderate estimate of genetic advance as per cent of mean (GAM) were observed for plant height, no. of branches per plant, pod length, no. of seeds per pod, seed protein content and harvest index, whereas, low estimate of genetic advance as per cent of mean (GAM) were observed for days to 50% flowering, days to maturity, no. of pod per cluster and pod breadth. The finding was in agreement with the finding of Solieman and Ragheb (2014) [41] for pods per plant seed yield, and weight per pod.

Correlation Coefficient Analysis: Correlation is a measure that determines the mutual relationship among various plant traits as well as it also determines the components on which selection will lead to the improvement. For increase the efficiency of selection, a plant breeder must have knowledge

about correlations between different traits. With the knowledge of significant correlation coefficients among various plant traits, the selection procedure to improve the yield is simplified. The results of genotypic and phenotypic correlation of seed yield with component traits were shown in table 4. The results of genotypic and phenotypic correlation revealed that the Seed yield had positive and significant correlation with no. of pods cluster per plant (0.456** and 0.452**), no. of branches per plant (0.247** and 0.279**), no. of pods per plant (0.667** and 0.636**), no. of pods per cluster (0.163*), weight per pod (0.424** and 0.394**), pod length (0.215** and 0.181*), no. of seeds per pod (0.485** and 0.414**), 100 seeds weight (0.405** and 0.359**), pod yield per plant (0.906** and 0.822**), biological yield (0.716** and 0.580**) and harvest index (0.518** and 0.376**), while negative and significant correlation with days to 50% flowering (-0.270** and -0.172*) and days to maturity (-0.353** and -0.210*). From the results of correlation coefficient, it was also reported that the estimates of genotypic correlation coefficient had more value than that of phenotypic correlation coefficient which indicated strong inherent relationship among the studied traits. The above results were in consonance with the research worked of Ahmed *et al.* (2008) [2] for days to 50% flowering and days to maturity, Osman *et al.* (2013) [28] for number of pods per plant, Verma *et al.* (2013) [46] for no. of branches per plant, no. of pods per plant, no. of seeds per pod, biological yield and harvest index, Muluaem *et al.* (2013) [25] and Sharifi and Aminpane (2014) [38] for number of branches per plant, clusters per plant, pods per plant, pod length, number of seeds per pod and 100 seed weight, Singh *et al.* (2017) [40] for no. of pods per plant, no. of pods per cluster, pod length, 100 seeds weight, pod yield per plant, and harvest index and Kumar *et al.* (2017) [23], Dewangan *et al.* (2019) [12] and Raiger *et al.* (2021) [33] for no. of branches per plant, no. of pods per plant, pod length, no. of seeds per pod and 100 seeds weight

Path Coefficient Analysis: The studies on correlation coefficients merely show the nature of association between two traits which alone does not provide exact idea about the relative effect of each component traits towards the major economic product under experiment. Knowledge of direct and indirect effects of different traits on desired traits is essential for selection to improve the population as it may be possible that a component trait may have no direct effect on concerned economic trait but it may influence through other related components. The results of direct and indirect effects of various traits on seed yield were presented in table 5. The results of direct effects of various traits on seed yield revealed that the biological yield had maximum direct positive effect on seed yield (0.762) followed by harvest index (0.684), pod yield per plant (0.163), no. of pod clusters per plant (0.097), 100 seeds weight (0.047), no. of seeds per pod (0.042), no. of branches per plant (0.035), no. of pods per cluster (0.026), pod breadth (0.021), seed protein content (0.017) and no. of pods per plant (0.009). It was also observed that the plant height (-0.050), days to 50% flowering (-0.052), days to maturity (-0.023), weight per pod (-0.0561) and pod length (-0.035) had direct negative effects on seed yield. The similar results were in found in the research worked carried by Tadesse *et al.* (2011) [42], Chaubey *et al.* (2012) [10], Verma *et al.* (2013) [46], Cokkizgin *et al.* (2013) [11], Kumar *et al.* (2017) [23] and Dewangan *et al.* (2019) [12] for one or more traits in

their respective genetic materials. The residual effects were calculated 0.079, which revealed that the traits under investigation contributed 92.1 per cent in total variance in

faba bean, whereas, only 7.9 per cent variance remained unaccounted. Hence, sufficient amounts of variation were present.

Table 4: Genotypic and Phenotypic Correlation Coefficient of yield and its components in Faba bean

	PH	50% FI.	D.M	PC/P	B/P	PD/P	PD/PC	W/P	P.L	P.B	SD/PD	100 SW	PC%	PY/P	BY	HI	SY
PH	1	0.161*	-0.047	0.012	0.009	0.028	0.094	-0.189*	-0.171*	-0.076	-0.138	-0.136	-0.234**	-0.052	0.196*	-0.131	-0.079
50% FI.	0.153	1	0.331**	0.031	-0.044	0.077	0.02	-0.091	-0.174*	0.003	-0.182*	0.052	0.179*	-0.182*	-0.160*	0.051	-0.172*
D.M	-0.143	0.638**	1	0.117	0.009	-0.012	-0.002	0.033	0.003	0.07	-0.181*	0.011	0.107	-0.215**	-0.286**	0.121	-0.201*
PC/P	-0.073	-0.029	0.314**	1	0.320**	0.439**	0.084	0.215**	0.028	-0.132	0.06	0.15	-0.015	0.352**	0.239**	0.160*	0.452**
B/P	-0.072	-0.175*	-0.062	0.298**	1	0.359**	-0.207**	0.114	0.025	-0.187*	-0.004	0.077	-0.191*	0.146	0.199*	0.071	0.279**
PD/P	-0.009	0.049	-0.063	0.406**	0.329**	1	0.018	0.240**	0.045	-0.103	0.225**	0.164*	-0.133	0.623**	0.376**	0.279**	0.636**
PD/PC	0.053	0.003	0.057	0.032	-0.332**	-0.101	1	0.076	0.049	0.062	0.069	0.212**	0.264**	0.271**	0.13	-0.021	0.163*
W/P	-0.439**	-0.138	-0.021	0.248**	0.023	0.258**	0.092	1	0.284**	0.172*	0.287**	0.330**	-0.009	0.467**	0.311**	0.108	0.394**
P.L	-0.246**	-0.242**	0.145	0.088	-0.006	-0.01	0.063	0.296**	1	0.129	0.409**	0.097	-0.049	0.201*	0.025	0.197*	0.181*
P.B	-0.155	0.088	0.06	-0.12	-0.233**	-0.157*	0.149	0.219**	0.156*	1	0.143	0.178*	0.132	0.021	0.073	-0.091	0.004
SD/PD	-0.247**	-0.239**	-0.147	0.09	0.046	0.308**	0.111	0.401**	0.527**	0.087	1	0.153*	-0.093	0.379**	0.204**	0.225**	0.414**
100 SW	-0.270**	0.102	0.034	0.151	0.061	0.15	0.207**	0.339**	0.138	0.345**	0.067	1	0.180*	0.376**	0.235**	0.086	0.359**
PC%	-0.301**	0.232**	0.186*	-0.017	-0.240**	-0.162*	0.333**	-0.008	-0.062	0.162*	-0.112	0.244**	1	0.006	-0.033	0.047	0.032
PY/P	-0.178*	-0.346**	-0.378**	0.310**	0.019	0.661**	0.254**	0.508**	0.219**	0.027	0.487**	0.469**	0.006	1	0.583**	0.213**	0.822**
BY	-0.048	-0.359**	-0.502**	0.283**	0.153	0.538**	0.068	0.375**	0.075	0.111	0.366**	0.310**	-0.03	0.799**	1	-0.476**	0.580**
HI	-0.167*	0.176*	0.073	0.238**	0.181*	0.352**	-0.018	0.126	0.247**	-0.210**	0.306**	0.109	0.063	0.283**	-0.183*	1	0.376**
SY	-0.253**	-0.270**	-0.353**	0.456**	0.247**	0.667**	0.103	0.424**	0.215**	-0.017	0.485**	0.405**	0.041	0.906**	0.716**	0.518**	1

*: Significance at 5 per cent, **: Significance at 1 per cent.

PH: Plant height (cm), 50% FI: Days to 50% flowering, D.M: Days to maturity, PC/P: Number of clusters per plant, B/P: Number of branches per plant, PD/P: Number of pods per plant, PD/PC: Number of pods per cluster, W/P: Weight per pod (g), PL: Pod length (cm), PB: Pod breadth (cm), SD/PD: Number of seeds per pod, 100 SW: 100 seeds weight (g), PC%: Seed protein content (%), PY/P: Pod yield per plant (g), BY: Biological yield (q/ha), HI: Harvest index, SY: Seed yield (q/ha).

Above diagonal: Phenotypic Correlation Coefficient

Below diagonal: Genotypic Correlation Coefficient

Table 5: Path coefficients analysis of seed yield with its component characters in 53 genotypes of faba bean (direct effects: on diagonal and indirect effects: off diagonal)

	PH	50% FI.	D.M	PC/P	B/P	PD/P	PD/PC	W/P	P.L	P.B	SD/PD	100 SW	PC%	PY/P	BY	HI
PH	-0.0503	-0.0081	0.0024	-0.001	-0.001	-0.001	-0.0047	0.0095	0.0086	0.0038	0.0070	0.0069	0.0118	0.0026	-0.005	0.0066
50% FI.	-0.0083	-0.0517	-0.0171	-0.002	0.0023	-0.004	-0.0011	0.0047	0.0090	-0.0002	0.0094	-0.0027	-0.0093	0.0094	0.0083	-0.0026
D.M	0.0011	-0.0074	-0.0225	-0.003	-0.001	0.0003	0.0001	-0.001	-0.0001	-0.0016	0.0041	-0.0003	-0.0024	0.0048	0.0064	-0.0027
PC/P	0.0011	0.0031	0.0114	0.0974	0.0312	0.0428	0.0082	0.0209	0.0028	-0.0129	0.0059	0.0146	-0.0015	0.0343	0.0233	0.0156
B/P	0.0003	-0.0015	0.0003	0.0113	0.0352	0.0127	-0.0073	0.0040	0.0009	-0.0066	-0.0002	0.0027	-0.0067	0.0052	0.0070	0.0025
PD/P	0.0003	0.0007	-0.0001	0.0039	0.0032	0.0090	0.0002	0.0022	0.0004	-0.0009	0.0020	0.0015	-0.0012	0.0056	0.0034	0.0025
PD/PC	0.0025	0.0005	-0.0001	0.0022	-0.005	0.0005	0.0262	0.0020	0.0013	0.0016	0.0018	0.0056	0.0069	0.0071	0.0034	-0.0006
W/P	0.0106	0.0051	-0.0018	-0.012	-0.006	-0.014	-0.0043	-0.056	-0.0159	-0.0097	-0.0161	-0.0185	0.0005	-0.026	-0.016	-0.0061
P.L	0.0061	0.0061	-0.0001	-0.001	-0.001	-0.002	-0.0017	-0.010	-0.0353	-0.0046	-0.0144	-0.0034	0.0018	-0.007	-0.001	-0.0070
P.B	-0.0016	0.0001	0.0015	-0.003	-0.004	-0.002	0.0013	0.0037	0.0027	0.0212	0.0030	0.0038	0.0028	0.0005	0.0015	-0.0019
SD/PD	-0.0058	-0.0076	-0.0076	0.0025	-0.001	0.0094	0.0029	0.0120	0.0171	0.0060	0.0419	0.0005	-0.0039	0.0159	0.0085	0.0094
100 SW	-0.0064	0.0025	0.0005	0.0071	0.0036	0.0078	0.0100	0.0156	0.0046	0.0084	0.0006	0.0473	0.0085	0.0178	0.0111	0.0040
PC %	-0.0039	0.0030	0.0018	-0.001	-0.003	-0.002	0.0044	-0.001	-0.0008	0.0022	-0.0016	0.0030	0.0168	0.0001	-0.001	0.0008
PY/P	-0.0085	-0.0295	-0.0349	0.0572	0.0238	0.1013	0.0441	0.0759	0.0327	0.0035	0.0616	0.0611	0.0010	0.1626	0.0948	0.0346
BY	0.0735	-0.1218	-0.2176	0.1820	0.1517	0.2865	0.0993	0.2372	0.0187	0.0556	0.1554	0.1787	-0.0252	0.4444	0.7622	-0.3631
HI	-0.0898	0.0347	0.0827	0.1093	0.0487	0.1908	-0.0145	0.0738	0.1347	-0.0620	0.1538	0.0585	0.0320	0.1455	-0.326	0.6838
R _{p(Sy)}	-0.079	-0.172*	-0.201*	0.452**	0.279**	0.636**	0.163*	0.394**	0.181*	0.004	0.414**	0.359**	0.032	0.822**	0.580**	0.376**

Residual Effect = 0.079

PH: Plant height (cm) 50% FI: Days to 50% flowering, D.M: Days to maturity, PC/P: Number of clusters per plant, B/P: Number of branches per plant, PD/P: Number of pods per plant, PD/PC: Number of pods per cluster, W/P: Weight per pod (g), PL: Pod length (cm), PB: Pod breadth (cm), SD/PD: Number of seeds per pod, 100 SW: 100 seeds weight (g), PC%: Seed protein content (%), PY/P: Pod yield per plant (g), BY: Biological yield (q/ha), HI: Harvest index, r_{p(Sy)}: phenotypic correlation coefficient of seed yield.

Conclusion

The present investigation would help in the selection of parents in further crop improvement programme. As the sufficient genetic variability was found in the studied faba bean genotypes accompanied with desirable heritability and genetic advance. The combined analysis of correlation coefficient analysis and path coefficient analysis revealed that the traits, namely, number of pods cluster per plant, number of branches per plant, number of pods per plant, number of

pods per cluster, number of seeds per pod, 100 seeds weight, pod yield per plant, biological yield and harvest index were the major seed attributing traits and hence; emphasis should be given to this traits while programming any plant breeding programme with this 53 genotypes.

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