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Diversity Analysis for Seed Yield and its Component Traits among Faba Bean (*Vicia faba* L.) Germplasm Lines

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ABSTRACT

Background: Faba bean (*Vicia faba* L.) is one of the oldest cool season food legume crops, stands next to soybean (*Glycine* max L.) and pea (*Pisum sativum* L.). A throughout knowledge of existing genetic variation among seed yield and its component traits is essential for developing high yielding varieties in faba bean. Realizing the importance of genetic diversity in key economic traits, the present investigation planned to assess the genetic diversity in faba bean germplasm for yield improvement in faba bean breeding programme.

Methods: The experimental material comprised of 80 faba bean germplasm lines, grown in RBD with three replications at Research Farm of Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Rabi* 2015-16. The data on 10 quantitative traits was analysed for Mahalanobis D^2 statistic, stepwise multiple regression and principle component analysis (PCA).

Result: The present study has assessed the existed genetic variations traits among faba bean germplasm lines for seed yield and its component traits. This would certainly provide guidelines in the selection of parents as well as effective selection of promising faba bean genotypes in faba bean breeding programmes for developing high yielding varieties.

Key words: Faba bean, Genetic diversity, Mahalanobis D^2, PCA, Regression analysis.

INTRODUCTION

Faba bean (*Vicia faba* L.) is one of the oldest cool season food legume crops in the world. It stands next to soybean (*Glycine max* L.) and pea (*Pisum sativum* L.) in respect to area and production (Mihailovic *et al*., 2005). It is popularly known as broad bean, horse bean, wonder bean, English bean, field bean, tick bean, winter bean, pigeon bean and Bakla in India. It is facultative cross-pollinated diploid (2n=2x=12) plant able to grow in diverse agro-climatic conditions (Kaur *et al*., 2014). Faba bean contains 22-24% protein constituting about 79% globulins, 7% albumins and 6% glutelins which is higher than the many other food legume crops (Burstin *et al*., 2011). It is used as human food in developing countries and also as animal feed in developed countries, as far as India is concerned, it is categorized as underutilized legume (Singh *et al*., 2010).

Assessment of genetic diversity is the fundamental rule of any crop breeding programme. A throughout knowledge of existing genetic variation among seed yield and its component traits is essential for developing high yielding varieties in faba bean. Study of genetic divergence plays a central role in selection of most diverse parents in hybridization programme for more heterotic response, more chances of better transgressive segregants in segregating generations and minimization of duplicates in germplasm conservation. For effective breeding strategy, variability, heritability and genetic advance is in prime importance for analysing the relative contributions of genetic and non-genetic factors to total phenotypic variances in a population. The degree of genetic variability can reflect the level of genetic progress in crop breeding. There is constant search for new diverse genetic resources for improvement and stabilization of faba bean yield as well as quality of produce. From above point of view, the present investigation was planned to assess the genetic diversity in faba bean germplasm.

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MATERIALS AND METHODS

The present investigation was carried out on 80 faba bean germplasm lines (Table 1) selected from MAP (Medicinal, Aromatic and Potential Crops) Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar, Haryana, India. The experiment was conducted in a randomized block design (RBD) with three replications at Research Farm of Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Rabi*, 2015-16.

The 10 quantitative traits were used to assess the genetic variability parameters and study of genetic divergence *viz*., days to 50% flowering, days to maturity, plant height, number of branches/ plant, number of clusters/

Table 1: List of eighty faba bean germplasm lines used for assessment of genetic diversity.

SN	Genotypes	Sources	SN	Genotypes	Sources	SN	Genotypes	Sources
1.	EC-1072	Bulgaria	28.	ET-4105	Bulgaria	55.	HB-70	CCS HAU, Hisar
2.	EC-3293	Bulgaria	29.	ET-4107	Bulgaria	56.	HB-77	CCS HAU, Hisar
3.	EC-117744	Bulgaria	30.	ET-4108	Bulgaria	57.	HB-80	CCS HAU, Hisar
4.	EC-243596	Bulgaria	31.	ET-5106	Bulgaria	58.	HB-82	CCS HAU, Hisar
5.	EC-267675	Bulgaria	32.	HB-1	CCS HAU, Hisar	59.	HB-83	CCS HAU, Hisar
6.	EC-320729	Bulgaria	33.	HB-2	CCS HAU, Hisar	60.	HB-85	CCS HAU, Hisar
7.	EC-329605	Bulgaria	34.	HB-4	CCS HAU, Hisar	61.	HB-86	CCS HAU, Hisar
8.	EC-329708	Bulgaria	35.	HB-5	CCS HAU, Hisar	62.	HB-176	CCS HAU Hisar
9.	EC-329812	Bulgaria	36.	HB-6	CCS HAU, Hisar	63.	Vikrant	CCS HAU Hisar
10.	EC-361427	Bulgaria	37.	HB-10	CCS HAU, Hisar	64.	DFB-9-1	NBPGR, New Delhi
11.	EC-366272	Bulgaria	38.	HB-12	CCS HAU, Hisar	65.	DFB-9-2	NBPGR, New Delhi
12.	EC-591828	Bulgaria	39.	HB-15	CCS HAU, Hisar	66.	IC-243784	NBPGR, New Delhi
13.	EC-591863	Bulgaria	40.	HB-17	CCS HAU, Hisar	67.	IC-329648	NBPGR, New Delhi
14.	EC-591864	Bulgaria	41.	HB-20	CCS HAU, Hisar	68.	IC-361485	NBPGR, New Delhi
15.	EC-628922	Bulgaria	42.	HB-25	CCS HAU, Hisar	69.	MLMK-7	NBPGR, New Delhi
16.	EC-628929	Bulgaria	43.	HB-26	CCS HAU, Hisar	70.	NDFB-9	NDAUT, Faizabad
17.	EC-628940	Bulgaria	44.	HB-32	CCS HAU, Hisar	71.	NDFB-13	NDAUT, Faizabad
18.	EC-628955	Bulgaria	45.	HB-37	CCS HAU, Hisar	72.	NDFB-14	NDAUT, Faizabad
19.	EC-628957	Bulgaria	46.	HB-41	CCS HAU, Hisar	73.	RFB-6	Ranchi, Jharkhand
20.	ET-3104	Bulgaria	47.	HB-43	CCS HAU, Hisar	74.	RFB-8	Ranchi, Jharkhand
21.	ET-3116	Bulgaria	48.	HB-44	CCS HAU, Hisar	75.	RFB-9	Ranchi, Jharkhand
22.	ET-3118	Bulgaria	49.	HB-53	CCS HAU, Hisar	76.	RFB-10	Ranchi, Jharkhand
23.	ET-3128	Bulgaria	50.	HB-54	CCS HAU, Hisar	77.	RFB-10-1	Ranchi, Jharkhand
24.	ET-3131	Bulgaria	51.	HB-55	CCS HAU, Hisar	78.	RFB-11	Ranchi, Jharkhand
25.	ET-3137	Bulgaria	52.	HB-58	CCS HAU, Hisar	79.	RFB-12	Ranchi, Jharkhand
26.	ET-3160	Bulgaria	53.	HB-63	CCS HAU, Hisar	80.	RFB-13-2	Ranchi, Jharkhand
27.	ET-4101	Bulgaria	54.	HB-65	CCS HAU, Hisar			

plant, number of pods/ plant, pod length, number of seeds/ pod, 100 seed weight and seed yield/ plant. Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated as per the method suggested by Burton and Devane (1953); heritability and genetic advance by Hanson *et al.* (1956) and Johnson *et al.* (1955), respectively; Hierarchical Euclidean cluster analysis by Mahalanobis D^2 statistic (Mahalanobis, 1936) based on minimum genetic distance using Tocher's method as described by Rao (1952). Average intra- and inter-cluster distances were determined using INDOSTAT software as suggested by Singh and Chaudhary (1977). Similarly, regression analysis evaluated by Lush (1940) and principal component analysis (PCA) by Kaiser (1958) and Jeffers (1967) using SPSS software 2.0.

RESULTS AND DISCUSSION

In the present investigation, PCV was not much higher than their corresponding GCV indicated the less influence of environmental factors on the expression of seed yield and its component traits. The GCV and PCV were observed high for 100 seed weight, seed yield/ plant and number of clusters/ plant indicated the presence of wide variations on these traits. High heritability coupled with high genetic advance were observed for traits *viz*., days to 50% flowering, plant height, number of branches/ plant, number of clusters/ plant, pod length, number of pods/ plant, 100 seed weight and seed yield/ plant that these traits are amenable for making efficient selection as well as combination breeding for improvement in seed yield. Similar findings were reported by findings of Ahmad (2016) and Tomas *et al.* (2016). The high GCV and PCV coupled with high heritability and genetic advance were found for traits such as 100 seed weight, number of clusters/ plant and seed yield/ plant, therefore, these traits could be used for selection of parents as well as genotypes of segregation generations in future breeding programme (Table 2).

Mahalanobis D^2 cluster analysis based on Tocher's method grouped 80 faba bean germplasm lines into seven non-overlapping clusters indicated the significant amount of genetic diversity existed among germplasm lines (Fig 1). Dendrogram showing clustering pattern of faba bean germplasm lines using 10 quantitative traits in Fig 1. It revealed that the cluster IV (22) had highest number of genotypes followed by clusters I (15), III (14) and II (11), whereas, lowest number in clusters V, VI and VII (each with six genotypes). The results are broadly in agreement of report of Sharifi and Aminpane (2014) and Rebaa *et al.* (2017).

Table 2: Estimates of genetic variability, heritability and genetic advance using quantitative traits among faba bean germplasm lines.

Quantitative traits	Mean	Range		Coefficient of variation		Broad sense heritability (%)	Genetic advance	
		Min.	Max.	GCV	PCV		Standard	Mean (%)
Days to 50% flowering	63.43	41.67	96.33	19.58	19.83	97.51	25.27	39.83
Days to maturity	163.28	142.00	195.33	7.46	7.69	94.08	24.33	14.90
Plant height (cm)	102.81	66.33	140.11	14.26	15.60	83.55	27.61	26.85
Number of branches/ plant	4.19	2.33	7.22	20.72	25.41	66.46	1.46	34.79
Number of clusters/ plant	9.46	3.67	20.67	40.63	42.37	91.95	7.59	80.25
Number of pods/ plant	37.98	16.33	66.22	28.74	30.20	90.58	21.40	56.35
Pod length (cm)	5.78	4.65	9.67	18.83	20.49	84.47	2.06	35.65
Number of seeds/pod	3.40	2.22	4.89	11.05	14.96	54.48	0.57	16.79
100 seed weight (g)	38.97	23.32	95.67	44.71	45.80	95.30	34.93	89.63
Seed yield/plant (g)	48.76	14.36	147.95	46.09	47.88	92.67	44.58	91.43

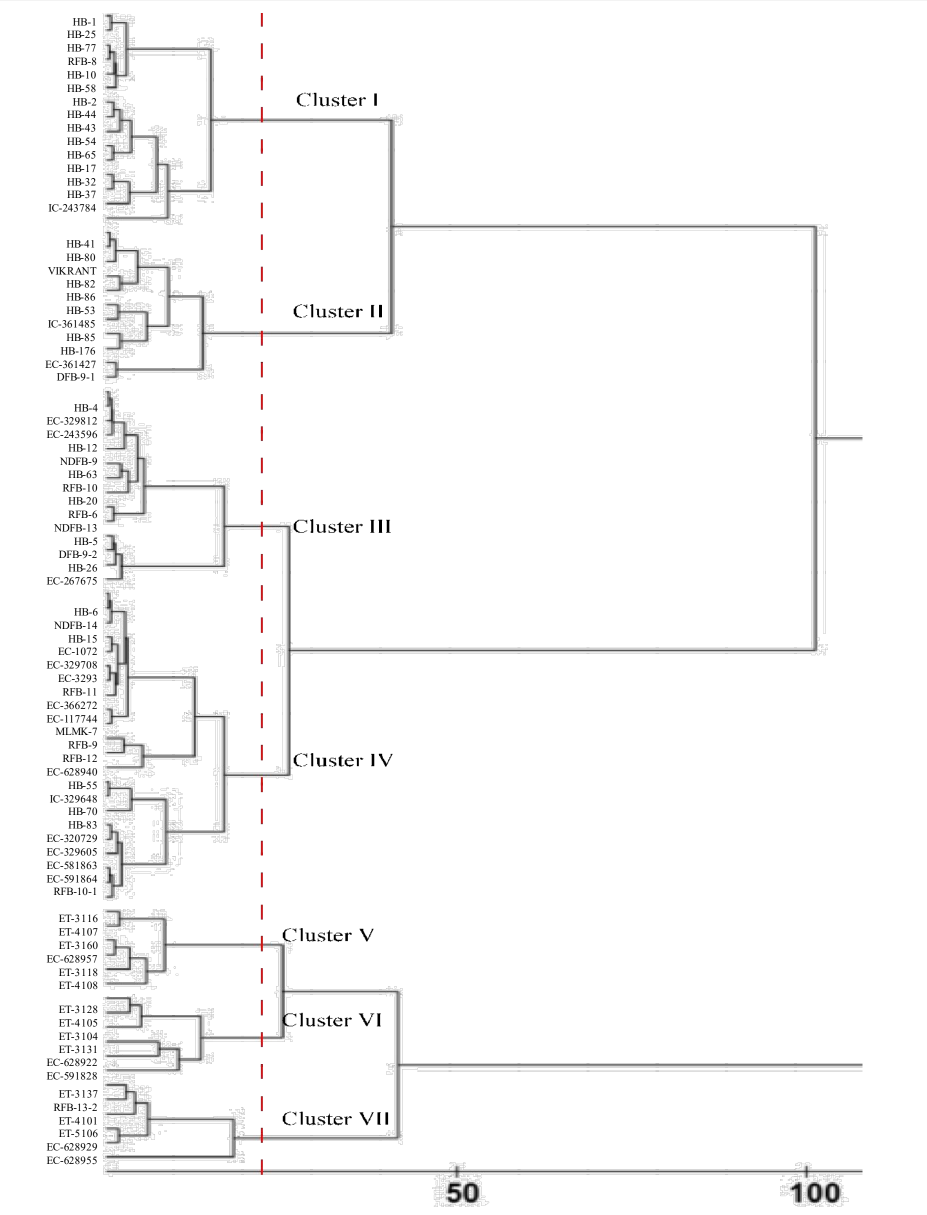

Fig 1: Dendrogram showing Mahalanobis D^2 clustering pattern of eighty faba bean germplasm lines using quantitative traits.

The intra- and inter-cluster distances among seven clusters were presented in Table 3 which exhibited maximum intra-cluster distances for cluster VI (3.964) followed by cluster VII (3.603) and minimum for cluster III (2.529) and VI (2.513), whereas, maximum inter-cluster distances between cluster VI and I (7.29) followed by cluster VI and III (6.80) and minimum in between cluster IV and VI (6.31). The result displayed that the inter-cluster distances were more than their intra-cluster distances which indicated the presence of ample amount of genetic variations between inter-clusters than the narrow variations within cluster. The genotypes found in the clusters I, III, IV and VI were genetically more diverse than the other clusters. The genotypes of these clusters could be used in hybridization programme which is expected to release better segregants for respective traits of clusters in segregation generations through recombination and transgressive breedings. Similar result was reported by Kumar *et al*. (2016) among 65 faba bean genotypes.

The cluster mean values in Table 4 shown considerable difference among seven clusters for various seed yield and its component traits *viz*., lowest mean values for days to 50% flowering (48.489), days to maturity (149.133) and plant height (87.266) were observed in cluster I, whereas, highest for branches/ plant (5.142), clusters/ plant and pods/ plant (56.344) in cluster II; similarly for seed yield/ plant (110.923), pod length (8.332) and number of seeds/ pod (3.871) in cluster VI. Comparative study of cluster mean values suggested that clusters II and VI had highest cluster means for seed yield and its contributing traits, therefore, these clusters may be considered superior for selecting promising parents in hybridization programme. These findings are broadly in agreement from the finding of Chaieb *et al.* (2011). The promising faba bean genotypes identified from both the divergence and cluster mean analysis were EC-591828, EC-628922, ET-3104, ET-3128, ET-3131 and ET-4105 from cluster VI; EC-628957, ET-3160 and ET-4107 from cluster V; EC-628929 and EC-628955 form cluster VII; HB-82 and HB-85 from cluster II, and EC-628940 from cluster IV based on various seed yield and its component traits. The genotypes from most diverse clusters I, IV and VI together with higher cluster mean analysis could be used for hybridization programme for more heterotic response and better segregants in segregating generations.

The diverse and superior genotypes identified from different clusters on the basis of various quantitative traits (Table 5). These genotypes could be used in future faba

Table 3: Average intra- (diagonal) and inter-cluster (above diagonal) distances among faba bean germplasm lines.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
I	2.635	3.664	4.111	3.347	6.488	7.286	5.410
II		2.878	4.771	3.918	6.468	6.505	5.414
III			2.529	3.005	5.160	6.797	4.405
IV				2.513	5.128	6.310	4.343
V					2.845	4.278	4.220
VI						3.964	5.286
VII							3.603

Table 4: Cluster mean values for various quantitative traits among faba bean germplasm lines.

Cluster	DF	DM	PH	BP	CP	PP	PL	SP	100SW	SY
I	48.489	149.133	87.266	4.614	12.488	42.615	5.369	3.296	30.238	39.903
II	59.818	161.000	106.677	5.142	14.939	56.344	5.306	3.545	28.337	56.806
III	64.286	164.452	108.960	3.579	6.695	31.032	5.178	2.944	29.850	26.685
IV	63.136	163.439	96.156	3.929	8.939	35.944	5.254	3.455	30.157	38.249
V	80.111	182.278	111.073	3.834	5.463	22.796	7.974	3.537	76.033	61.189
VI	87.944	182.222	113.630	4.778	8.148	38.908	8.332	3.871	74.462	110.923
VII	65.333	161.611	125.592	3.499	5.556	30.629	6.245	3.686	61.332	71.621
Mean	63.433	163.283	102.813	4.187	9.463	37.978	5.779	3.403	38.970	48.761

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BP = Number of branches/plant, CP = Number of clusters/ plant, PP= Number of pods/ plant, PL=Pod length (cm), SP=Number of seeds/ pod, 100SW = 100 seed weight (g), SY = Seed yield/ plant (g).

Table 5: Diverse and superior faba bean genotypes selected from different clusters for various quantitative traits.

Earliness	Number of branches/ plant	Number of clusters/ plant	Number of pods/ plant	Seed yield/ plant
HB-70 (IV)	EC-243784 (I)	HB-85 (II)	HB-41 (II)	ET-4105 (VI)
HB-17 (I)	EC-361427 (II)	HB-176 (II)	HB-85 (II)	EC-591828 (VI)
HB-25 (I)	DFB-9-1 (II)	HB-37 (I)	HB-176 (II)	EC-628955 (VII)
HB-1 (I)	HB-32 (I)	HB-32 (VI)	DFB-9-1 (II)	ET-3131 (VI)
HB-32 (I)	HB-43 (I)	HB-54 (I)	EC-361485 (II)	ET-3128 (VI)

bean breeding programme for selection, hybridization and recover of transgressive segregants with highest yield potential.

Principal component analysis (PCA)

PCA provides information related to extent of genetic diversity in germplasm and also helps in identification and ranking of genotypes and important economic traits contributing in genetic diversity. In present investigation, PCA was performed for yield and its component traits in faba bean in which principal components (PCs) greater than one Eigen value were selected for interpretation. Out of 10, only two PCs exhibited greater than 1.0 Eigen value *viz*., 4.305 and 2.275, respectively and explained 65.788% variability of the total variation among 80 faba bean germplasm lines (Table 6). Therefore, these two PCs were given important for further explanation and shared 43.053% and 22.735% of total variability, respectively (Table 6). The PC 1 accounted for maximum proportion of total variability (43.053%) in yield contributing traits which could be used for selection of faba bean genotypes in future breeding programme for developing superior hybrid.

Further, principal factor analysis was carried out with Varimax roation method (Kaiser, 1985) to derive interaction among yield component traits with respective principal factors (correlation values > ±0.5). Principal factor-1 (PF-1) mostly correlated to yield contributing traits *viz*., 100 seed weight, pod length, seed yield/ plant, days to 50% flowering, days to maturity, number of seeds/ pod and plant height, whereas, principal factor-2 (PF-2) dominated by number of pods/ plant and number of clusters/ plant (Table 7). Thus, PF-1 had shown maximum genetic variation to seed yield and its component traits which could be used for selection of promising faba bean genotypes to bring out rapid improvement in yield. Screen plot explained the percentage of variation associated with each PC obtained by drawing a graph between Eigen value and PCs (Fig 2). These results are in support from the findings of Tiwari and Singh (2019).

Table 6: Total variability explained by principal components among faba bean germplasm lines.

Principal components	Eigen values	Variability (%)	Cumulative variability (%)
1	4.305	43.053	43.053
2	2.273	22.735	65.788

Table 7: Factor loading of yield component traits with respect to two principal factors (Varimax rotation).

Yield component traits	PF-1	PF-2
100 seed weight (g)	0.898	-0.155
Pod length (cm)	0.852	-0.140
Seed yield/plant (g)	0.840	0.385
Days to 50% flowering	0.808	-0.329
Days to maturity	0.726	-0.323
Number of seeds/pod	0.486	0.188
Plant height (cm)	0.484	-0.155
Number of pods/plant	-0.148	0.897
Number of clusters/plant	-0.286	0.852
Number of branches/plant	0.090	0.765

Stepwise multiple regression analysis

The results of stepwise multiple regression analysis was presented in Table 8. The seed yield/ plant considered a dependent variable, while other traits as independent variables. Firstly, 100 seed weight entered in the model and explained 56.70% of total observed variations followed by number of pods/ plant, number of seeds/ pod and days to 50% flowering. The cumulative variations explained by combination of traits such as number of pods/ plant with 100 seed weight by 84.50%; number of seeds/ pod together with number of pods/ plant and 100 seed weight by 89.80% and only little amount of variation added in cumulative variation by days to 50% flowering (90.50%). Thus, stepwise multiple regression analysis identified the most important

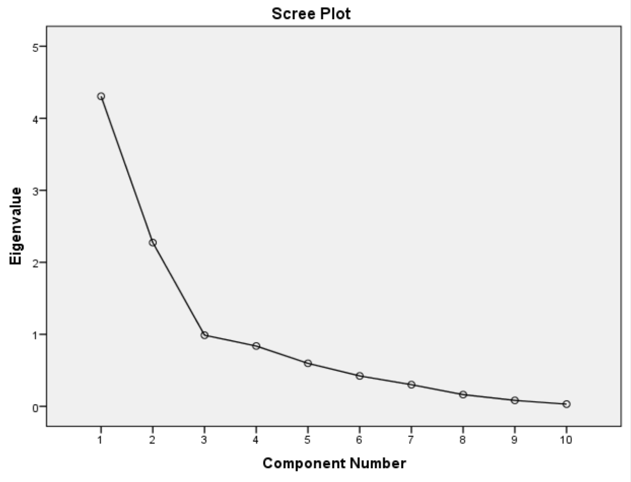

Fig 2: Scree plot constructed based on ten principal components and their Eigen values.

Table 8: Summary of stepwise multiple regression analysis for yield and its component traits.

Steps	Entered variables	b_i	R^2 value	Adjusted R^2	SE	t value
1	100 seed weight	0.757	0.572	0.567	17.150	10.22**
2	Number of pods/plant	0.921	0.849	0.845	10.270	11.85**
3	Number of seeds/pod	0.950	0.902	0.898	8.320	6.44**
4	Days to 50% flowering	0.954	0.910	0.905	8.040	2.70**

**Significant at 1% level of significance, b_i = Regression coefficient, SE= Standard error.

economic traits *viz*., 100 seed weight, number of pods/ plant and number of seeds/pod contributing to faba bean seed yield which could be used for effective selection of promising faba bean genotypes in segregating generations. These findings are in accordance with the reports of Tiwari and Singh (2019). The PCA together with stepwise multiple regression analysis identified most variants and yield contributing traits *viz*., 100 seed weight, number of pods/ plant and number of seeds/pod which could be used in yield enhancement of faba bean.

CONCLUSION

The results obtained from present investigation would provide valuable guidelines in selection diverse genotypes, prediction of possible merits for genetic recombination and also be valuables in formulating ideal plant type. Available knowledge of genetic diversity in faba bean germplasm helps in selection of parents for hybridization programme and effective in germplasm conservation as well. Mahalanobis D^2 cluster analysis and PCA have been used successfully for assessment of genetic diversity in 80 faba bean germplasm lines. On the basis of cluster mean values and genetic divergence study 14 promising genotypes *viz*., EC-591828, EC-628922, EC-628929, EC-628940, EC-628955, EC-628957, ET-3104, ET-3128, ET-3131, ET-3160, ET-4105, ET-4107, HB-82 and HB-85 identified for seed yield and its component traits which could be used in hybridization programme for higher heterotic response and expected to release better segregants in faba bean breeding programmes for yield enhancement. The PCA together with stepwise multiple regression analysis identified most variants and yield contributing traits *viz*., 100 seed weight, number of pods/ plant and number of seeds/ pod which could be used for effective selection of parents and promising faba bean germplasm lines in future faba bean breeding programme.

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