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Assessment of Genetic Variability, Diversity and Trait Correlation Analysis in Common Bean (*Phaseolus vulgaris* L.) Genotypes

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ABSTRACT

The present investigation was undertaken to study the genetic variability, diversity through cluster analysis and correlation among yield attributing traits. The experimental material is comprised of 63 diverse germplasm accessions including three check varieties were evaluated in augmented design during *Rabi* 2015-16 at IIPR, Kanpur. In this study, totally nine traits, namely, days to fifty per cent flowering (DF), days to maturity (DM), plant height (PH), number of branches per plant (NBP), number of pods per plant (NPP), pod length (PL), seeds per pod (SPP), 100 seeds wt (g) (HSW) and seed yield per plant (g) (SYP) were recorded. The results exhibited that the analysis of variance noticed significant differences among the genotypes for all characters studied. The genetic variability parameter showed that phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits studied. Higher GCV coupled with heritability and genetic advance as % mean was recorded for PH, NPP, HSW and SYP. Likewise, high heritability coupled with high genetic advance as % mean was recorded in DF, PH, NPP, PL, HSW and SYP. Trait association study revealed that the seed yield per plant exhibited significant positive correlation with NBP, NPP, NSP and HSW. In the same pattern, Euclidian clustering analysis displays 63 genotypes were grouped to two major clusters. From this investigation, it was observed that all genotypes showed sufficient genetic variability for the traits studied. The genotype such as EC400414, EC400398, ET8415 and EC540173 were superior to check varieties in terms of morphological and other agronomic traits. These genotypes could be utilized in breeding programme for improvement of specific traits.

Key words: Cluster analysis, Common bean, Genetic variability, Morphological traits.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the most important food legume crops in the world (Broughton *et al*., 2003; Beebe, 2012). It is an important source of nutrients for more than 300 million people, representing 65% of the total protein consumed, 32% of energy and a major source of micronutrients *e.g*., iron (Fe), zinc (Zn), thiamin and folic acid (Welch *et al*., 2000; Broughton *et al*., 2003; Blair *et al*., 2010a; Petry *et al*., 2015). It is one of the main source of dietary protein for human consumption in the world including developed countries like Latin America, Brazil, Africa, the Middle East, China, Canada and Mexico (Ma and Bliss, 1978). Due to its high protein, minerals and vitamins contained in dry seed, it is also popularly called as the “poor men’s meat,” (Blair, 2013). In terms of global production, Latin America is the region of greatest producer of common bean representing about 50% of the world total volume, followed by Africa with 25%. Brazil, Mexico and the United States of America are the three largest producers in the Western Hemisphere. However, it is an extremely diverse crop in terms of cultivation methods, uses, the range of environments to which they have been adapted and morphological variability. They are found from sea level and up to 3000 m above sea level, are cultivated in monoculture, intercropping with maize or any other vegetable crop like potato or amaranths or in rotations that are adapted to many niches, both in terms of agronomic and consumer preference.

In India, it is highly remunerative pulse crop for small and marginal land holding farmers in the hill regions *viz.,* Jammu and Kashmir, Uttarakhand, foothills of Himalayas and Sikkim. It is consumed as tender pods, shelled beans and dry beans. The local vernacular name for grain type common bean is *rajmash or rajma* (Hindi) in northern India. in the recent year this crop has becoming increasingly popular in northern plains as well as central India due to its high yielding potential, good adaptability to different niches with increased cultivating area expansion in Uttar Pradesh, Maharashtra, Andhra Pradesh and Tamil Nadu. The major genetic diversity of this crop exists in the foothills of Himalayan region, Jammu and Kashmir and Sikkim. In these region this crop noticed wide range of genetic diversity for

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seed size, colour and pod types, plant habits from bush to climbing or pole type bean, range of maturities, photoperiod sensitivity and neutrality, adaptation zones, wide range of diseases and stress resistances and different nutritional quality components (Rana *et al*., 2015). This genetic variability should be used by breeders to further enhance the crop improvement. Even though high levels of rajmash genetic diversity exists in the hilly tracts of Himalayan region, but very little information is available on number of rajma landraces exploited, their current situation and their contribution to the farming community. Due to limited research activity and inadequate use of local rajma germplasm in breeding programs could affect the rajma improvement in India.

However, under these circumstances assessment of genetic variation present in the prevailing rajma germplasm is paramount in common bean breeding. It would be useful for determining the morphological variation among the gene pool and also reveal patterns of genomic differentiation. This can also provide information on the population structure, allelic richness and diversity parameters of germplasm. This genetic variability provides opportunity for rajma breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (high yield potential, determinate plant type with medium seed size *etc*.) and breeder-preferred traits (pest and disease resistance with cold and drought resistance, *etc*.) (Ashish Kumar *et al*., 2014: Bhandari *et al*., 2017).

Yield improvement is an important breeding objective of most crop improvement programs (Ghobary and Abd-Allah, 2010). Like other pulse crops, yield in common bean is a complex trait and many morphological and physiological traits constitute it. Seed yield is affected by genotype and environmental factors because of its quantitative properties (Park *et al*., 2000; Gonzalez *et al*., 2010; Perez-Vega *et al*., 2010). The relationships between yield and yield contributing traits on one hand and among themselves on the other hand could be measured by correlation coefficient (Bendangkumzuk and Chaturvedi, 2014). It is one of the prerequisites for crop improvement programmes. Hence, it is important to know the extent of existing genetic variations in the germplasm material.

Keeping these in view, the present study was undertaken to assess the magnitude of genetic variability parameters, genetic diversity and correlation coefficient among yield components present in Common bean genotypes.

MATERIALS AND METHODS

Plant genetic materials

The plant genetic materials for investigation comprised of 60 Rajmash genotypes collected from National Gene Bank unit NBPGR, New Delhi and three check varieties such as Uday, Arun and Utkarsh (Table 1).

Field evaluation and data collection

Field evaluation of rajmash genotypes was conducted at the main research farm of ICAR-Indian Institute of Pulse Research, Kanpur, India during *rabi* 2015-16. Seeds were sown on raised bed with 60 cm row to row and 15 cm plants to plant spacing. The experiment was laid out in augmented block design (ABD) and all the recommended agronomic practices were followed for raising a good crop. The data were recorded from randomly selected 5 plants on nine morphological characters, namely, days to fifty per cent flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, pod length (cm), seeds per pod, 100 seeds wt (g) and seed yield per plant (g).

Statistical analysis

Mean values recorded for the quantitative traits were analysed (ANOVA) following standard statistical techniques (SAS Enterprise Guide 4.2 version). To assess the magnitude of genetic variability, diversity available in common bean germplasm, correlation coefficients for the quantitative traits studied were determined using INDOSTAT software 8.1 version.

Table 1: List of Common bean genotypes used for evaluation during *Rabi* 2015-16.

Genotypes	Growth habit	Seed colour	Shape	Hilum colour	SL (mm)	SW(mm)	HSW (gm)
Arun (Variety)	Semi pole	Gulf red	Elliptic	White	15.94	8.07	42.30
Utkarsh (Variety)	Semi pole	Gulf red	Circular to Elliptic	White	10.72	7.29	38.50
Uday (Variety)	Bush	Red mottled	Elliptic	White	15.79	7.91	38.50
EC500232	Bush	Medium red	Elliptic	White	14.18	8.11	31.20
IC14351	Semi pole	Light red	Elliptic	White	15.06	7.54	32.50
IC25537	Bush	Red mottled	Elliptic	White	10.20	5.30	25.00
EC400400	Pole	Light red	Elliptic	White	14.55	7.69	12.50
NO3107	Bush	Red mottled	Elliptic	White	15.14	7.85	49.00
GPR203	Bush	White	Elliptic	White	12.26	6.78	38.50
EC564797	Bush	Red mottled	Elliptic	White	10.23	6.30	46.30
EC500234	Bush	Gulf red	Flat	White	12.30	7.80	35.60
EC400419	Bush	Orange	Elliptic	White	14.30	7.20	52.50
EC565673B	Semi pole	Orange	Elliptic	White	10.60	7.60	42.30

Table 1: Continue...

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EC565673A	Pole	Gulf red	Elliptic	White	15.68	8.96	42.30
EC564795	Bush	Orange	Elliptic	White	15.90	8.12	26.30
GPR4190	Bush	Red mottled	Elliptic	White	12.30	6.30	41.30
HURG13B	Pole	Medium Red	Elliptic	White	13.48	7.40	45.00
EC400361	Pole	Brown	Circular to Elliptic	White	13.09	8.81	41.50
PL227468	Pole	Red mottled	Kidney	White	13.20	5.50	84.93
GPR118A	Bush	Dark red	Circular to Elliptic	White	13.56	7.50	35.20
HURG0478	Bush	Creamy	Circular to Elliptic	White	14.30	6.30	33.20
HUR53	Bush	White	Elliptic	White	14.34	7.10	37.00
IC31084	Semi pole	Red mottled	Elliptic	White	13.60	7.37	32.50
IC311670	Pole	Red mottled	Elliptic	White	15.58	8.11	36.00
GPR4189	Pole	Gulf red	Elliptic	White	12.65	7.78	41.00
EC150250	Pole	Black	Circular to Elliptic	Black	5.77	3.32	14.14
BD9116291	Pole	Medium red	Elliptic	White	14.09	7.05	28.60
EC400407	Pole	Light red	Elliptic	White	15.54	7.89	35.00
ET8447	Bush	Medium red	Elliptic	White	14.20	5.30	34.50
EC14920	Pole	Pink mottled	Elliptic	White	13.48	7.00	36.00
IC311676	Pole	Red mottled	Elliptic	White	15.30	7.20	28.50
ET8401	Semi Pole	Gulf red	Elliptic	White	8.60	4.30	22.30
EC400445	Bush	Gulf red	Elliptic	White	14.50	7.20	28.50
ET8490	Bush	Brown	Elliptic	White	13.26	7.20	36.50
BLF101	Bush	Medium red	Elliptic	White	14.71	6.54	32.50
EC540173	Semi pole	Brown	Flat	White	13.56	6.30	41.30
EC500407	Semi pole	Gulf red	Flat	White	12.56	7.20	36.50
HUR35	Semi pole	Gulf red	Elliptic	White	14.23	6.50	33.50
ET4515	Semi pole	Gulf red	Elliptic	White	14.23	6.50	34.50
IC84607	Semi pole	Pink mottled	Elliptic	White	13.65	7.30	40.30
ET8494L	Semi pole	Purple	Elliptic	White	9.63	5.60	39.50
EC400414	Bush	Red mottled	Elliptic	White	14.50	8.47	31.20
LD2-1	Bush	Light brown	Elliptic	White	10.25	5.60	42.30
NO3160A	Bush	Medium red	Elliptic	White	15.35	6.81	37.00
NO3127	Bush	Dark brown	Elliptic	White	12.36	6.30	36.50
IC311670	Bush	Light pink	Elliptic	White	10.56	5.30	38.50
PLB438	Bush	Light pink	Elliptic	White	16.30	8.90	34.20
EC400401	Semi pole	Light red	Elliptic	White	17.18	9.16	32.20
EC400407	Semi pole	Brown	Elliptic	White	13.56	7.30	31.20
ET8415	Semi pole	Red	Elliptic	White	14.56	7.20	33.50
ET8482	Semi pole	Light brown	Elliptic	White	12.36	6.30	36.50
BLF101A	Bush	Light brown	Elliptic	White	14.20	7.80	33.50
EC41702	Bush	Red mottled	Elliptic	White	12.60	6.30	35.60
SKUST2-B	Bush	Dark red	Flat	White	10.60	5.20	37.80
ET84030	Bush	White	Elliptic	White	9.60	4.60	36.50
EC400398	Bush	Red mottled	Elliptic	White	15.30	7.30	35.60
ET8447	Bush	Orange	Elliptic	White	12.30	6.30	36.50
BSLR-2	Bush	Light brown	Elliptic	White	14.50	8.10	25.00
ILB101	Bush	Gulf red	Elliptic	White	13.50	5.60	26.30
ET8404	Bush	Grey mottled	Elliptic	White	11.20	5.30	37.50
ET8405	Bush	Red mottled	Elliptic	White	13.20	5.60	40.30
ET8456	Bush	Purple	Elliptic	White	14.50	7.30	33.20
EC541703	Pole	Red mottled	Elliptic	White	15.20	7.30	31.50

RESULTS AND DISCUSSION

The estimation of genetic diversity in gene pools conserved in the gene banks is important for deciphering the nature and magnitude of variability and genetic relationship between traits for the efficient management and use of germplasm (Stoilova *et al*., 2013; Blair *et al*., 2010; Szilagyi *et al*., 2011). The germplasm evaluation process has been found to be useful for preliminary characterisation and discrimination of accessions to understand the level of genetic diversity existing in gene pool (Foschiani *et al*., 2009; Atilla *et al*., 2010; Szilagyi *et al*., 2011). Keeping above facts in view, the present investigation was carried out to evaluate the genetic variability, association among yield contributing traits and genetic diversity in common bean germplasm. The germplasm noticed a wide range of genetic variability for all traits studied among 63 accessions including three check varieties with the experimental results are discussed below.

Analysis of variance for nine quantitative traits

The analysis of variance revealed significant differences among the genotypes for all characters studied, indicating a high degree of variability in the material (Table 2). The mean sum of squares for all traits for different sources of variation. The block effect (unadjusted) showed only days to 50% flowering was significant while all other traits showed non-significant. On the other hand, the treatment effects (adjusted) were noticed significant for all traits expect days to 50% flowering and number of branches per plant. Likewise, the treatment effects (unadjusted) were noticed non-significant for all the traits studied. Similarly, the effects due to checks showed significant for all traits except days to 50% flowering and pod length and varieties were significant. However, the adjusted block effects were non-significant for all traits except days to 50% flowering, pods per plant, seed per pod and seed yield per plant indicating homogeneity of the evaluation blocks. Similarly, the mean square due to checks v/s Augmented (genotypes) was significant for all the traits except days to 50% flowering, indicating thereby that the test entries were significantly different from the checks except for days to 50% flowering. Similar findings were observed by Sajad *et al*., (2014); Iram Saba *et al*., (2017). In addition to above, the paired t test was estimated to compares the means of two paired groups, to understand the whether there was a difference in mean of traits after two year of germplasm evaluation under open filed condition. The results showed that genotypes were highly significantly different for the mean value of days to fifty percent flowering, days to maturity, number of pods per

Table 2: Analysis of variance for nine quantitative traits in Common bean genotypes.

Source of Variation	df	DF	DM	PH	NBPP	NPP	NSP	PL	HSW	SY/Plt
Block. unadj	5	62.92***	98.46	930.7	1.3209	40.349	0.451	5.325	101.36	138.65
Teatment. adj	62	79.482	70.75***	763.5***	0.4396	42.11***	0.454***	6.541**	138.61***	132.94***
Teatmen. unadj	62	83.9	78.66	838.5	0.5452	44.83	0.448	6.942	146.75	143.85
Block. adj	5	8.09***	0.36	0.9	0.0116	6.71***	0.522***	0.349	0.4	3.42**
Control	2	0.167	337.50***	3939.3***	4.15***	200.68***	0.976***	4.489	501.97***	642.74***
Control + control.VS.Aug.	60	82.125***	61.86***	657.6***	0.3159	36.82***	0.437***	6.609**	126.5***	115.95***
Augmented	59	47.24****	68.27***	743.6***	0.3783	32.28***	0.361***	4.777*	133.31***	89.47***
Control vs augmented	1	2414.59	173.95***	233.7***	3.177**	473.4***	4.549***	139.6**	229.74***	2354.5***
Residuals	10	0.222	1.69	5.7	0.2156	0.08	0.01	1.35	2.3	0.37
CV (%)		1	1.2	3.5	13.7	1.6	2.7	9.3	3.1	2.5

Note: *, **, and *** indicates Significant at P< 0.05, 0.01 and 0.001 respectively.

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPP : Number of pods per plant
NSP : Number of seeds per pod
PL : Pod length (cm)
NBP : Number of branches per plant
HSW : 100 Seed weight (g)
SY : Seed yield per plant (g)

Table 3: Estimates of variance and other genetic parameters in Common bean genotypes.

Characters	Mean	SEm±	Range		PCV	GCV	h^2 (BS)	GAM as % mean
			Lowest	Highest	(%)	(%)	(%)	
Days to 50% flowering	45.98	0.80	32.00	66.00	14.63	13.25	82.10	24.73
Days to maturity	103.17	1.07	65.00	112.00	8.23	7.91	92.30	15.66
Plant height (cm)	39.67	2.12	20.30	118.0	41.36	40.75	97.10	82.71
Number of branches per plant	3.31	0.08	2.00	4.20	47.21	18.44	42.80	14.63
Number of pods per plant	16.52	0.74	8.20	37.00	42.12	34.62	67.20	58.36
Pod length (cm)	11.74	0.28	6.25	18.23	18.52	18.24	97.00	37.00
Number of seeds per pod	3.66	0.07	2.76	5.64	60.86	15.40	64.00	8.03
100 seed weight (g)	48.42	1.43	14.14	84.93	22.51	22.49	99.80	46.29
Seed yield per plant (g)	21.38	1.17	6.32	50.63	46.79	44.09	88.88	85.58

plant and seed yield per plant (g) (Table 6) and these genotypes can be utilized for breeding programme for improvement of specific traits.

Mean, range, variance, coefficient of variance, heritability and genetic advance

Knowledge of genetic variability, heritability and genetic advance of important economic traits and their genotypic and phenotypic correlation coefficient among themselves, plays an important role in the breeding programme of any crop. The success of a breeding programme depends on the genetic variability present in the population. Therefore, partitioning of the phenotypic variation into genetic and environmental variation is necessary. In our investigation, we have estimated simple variance parameters and genetic variation components such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance. The statistical analysis of data on quantitative traits showed a wide range of variability among the genotypes studied (Table 3). The mean numbers of DF were 45.98, but it ranged from 32 for genotype HUR 35 to 66 for ET 8494L. DM had a mean value is 103.17, EC14920 and Arun took longest time of 112 days for maturity as compared IC84607 and HUR35 which matures in 65 days. Likewise, PH has a mean value of 36.97, the highest plant height was recorded in GPR203 which is 118 cm as compared to lowest plant height in GPR4190 which is 20.30 cm. The NBP noticed mean value of 3.31, while higher NBP (4.20) is observed for EC565673B, EC14920, IC311676, EC500407, EC400414 and BLF101. In contrast to this, the lower NBP (2.0) were recorded for IC25537 and EC500232. Similarly, Highest NPP (37.0) were recorded in EC400414, while NPP lowest (8.20) were recorded in HURG0478 and average value of NPP is 16.52. The average value PL is 11.74, higher PL (18.23 cm) is recorded in EC400361 and lowest PL (6.25 cm) is recorded in in ET84030. In addition, NSP has mean value of 3.66, genotype EC150250 were recorded highest NSP (5.64) and lowest NSP (2.76) were recorded in EC41702. In the same manner, highest HSW noticed in PL227468 (84.93 gm) while lowest HSW (14.14) were recorded in EC150250 and average HSW of genotypes were recorded as 48.42 gm. It is observed that variation found in size was significantly wider (14.14-84.93 g/HSW) in the genotypes. These results were in consistent with findings of different researcher who have reported wide variation in seed per pod, shape and size in bean germplasm (Cabral *et al*., 2010; Lioi *et al*., 2012). Further, SYP were noticed mean value of 21.38 gm, highest SYP were recorded in EC400398 (50.63 gm) while lowest SYP were observed in ET8490 (19.32). These results were in agreement with studies conducted by Singh *et al*. (1991) and Bitocchi *et al*. (2012).

It is also observed that the estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits studied. It is indicating that environmental factors influencing the characters (Table 3). The highest PCV and GCV were recorded for PH, NBP, NPP, NSP, HSW (g) and SYP (g). Indicating, presence of ample variation for these traits in the present material. These results were in accordance with the findings of Singh *et al.* (1994); Nimbalkar *et al*. (2002). Higher GCV coupled with heritability and genetic advance as % mean was recorded for PH, NPP, HSW and SYP as compared to rest of the traits. These results specify that; GCV alone will not be sufficient for the determination of the magnitude of heritable variation. GCV together with heritability estimates will give a better picture of the expected genetic gain from selection. Hence, selection of genotypes for the breeding programme for these traits was highly effective. Our results were in conformity with the findings of Syed *et al*. (2012) and Asati and Singh (2008). In addition to this, high heritability coupled with high genetic advance as % mean was recorded in DF, PH, NPP, PL, HSW and SYP. This indicated that these traits might be under the influence of additive gene interactions and the use of simple selection methods may bring significant improvement for these traits. Our results were in agreement with the findings of Kumar (2008); Ahmad and Kamaluddin, (2013); Rai *et al*. (2010); Sharma *et al.* (2012).

Table 4: Genotypic correlations coefficients among seed yield and its attributing characters in Common bean.

	DF	DM	PH	NPP	NSP	PL	NBP	HSW	SY/plt
DF	1.000	0.302	0.322	0.294	-0.058	0.029	0.110	0.030	-0.150
DM		1.000	-0.087	0.209	0.038	0.010	-0.119	-0.051	-0.110
PH			1.000	0.436*	0.535**	0.092	-0.102	-0.287	-0.130
NPP				1.000	0.428*	0.479*	0.481*	-0.162	0.556**
NSP					1.000	0.687**	0.124	0.487*	0.438*
PL						1.000	-0.151	0.535**	-0.047
NBP							1.000	0.146	0.456*
HSW								1.000	0.480*

Note: * and ** Significant at 5% and 1% respectively.

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPP : Number of pods per plant
NSP : Number of seeds per pod
PL : Pod length (cm)
NBP : Number of branches per plant
HSW : 100 Seed weight (g)
SY : Seed yield per plant (g)

Correlation studies

To utilize various quantitative characters in a breeding program, interrelationship between the characters are of immense value. The genotypic correlation coefficients between seed yield and its components are presented in Table 4. The seed yield per plant exhibited significant positive correlation with NBP, NPP, NSP and HSW. This suggested that the direct selection of these traits would likely be effective in increasing seed yield. Similar findings were observed by other researchers such as Asati and Singh (2008) and Pandey *et al*. (2013). The significant positive correlation of NPP with NSP, PL and NBP showed that the selection of any of these traits may favour improvement in other traits also whereas negative correlation with HSW may adversely affect the gain. Likewise, HSW and PL having significant positive correlation with NSP. This indicated that indirect selection of these traits was highly effective for crop improvement programmes. Similar results were reported by Ahmed and Kamaluddin (2013); Mudasir *et al*. (2012); Sofi *et al*. (2014).

Cluster analysis

Every crop breeding programme has been aimed at the improvement of yield, adaptation, resistance to biotic and abiotic stresses and end-use quality. However, breeding

Table 5: Identification of trait specific genotypes in Common bean.

Characters	Promising accessions
Early maturity (< 50 days)	EC400419, GPR4189, EC565673A
No. of primary branches (>3)	EC400414, EC-564797,EC-150250
Pod length (>10 cm)	EC-565673A, PL-227468, GPR4189
No. of seeds per pod (> 5)	HUR-53, EC-500232, BLF-101
Resistance to BCMV	EC150250, GPR203, EC400414
Upright branching	BLF-101, EC-500232
Bold seed type	EC-400414

Table 6: Identification of contrasting genotypes through pairwise comparison between mean value of genotypes in augmented design over two-year evaluation (P value=0.05).

Days to 50% flowering			
Genotypes	Mean value (>67)	Genotypes	Mean value (<40)
ET8494L	67.88a	EC400419	39.88t
Utkarsh	67.33a	GPR4189	39.88t
ET-8404	58.22b	EC565673A	37.22v
ET4515	55.88c	BSLR-2	37.22v
IC84607	55.88c	HUR-35	33.88w
EC500232	55.33c		
Days to maturity			
Genotypes	Mean value (<96)	Genotypes	Mean value (>109)
EC400419	97.66m	EC400361	110.77a
GPR4189	97.44m	EC564797	110.ab
EC565673A	97.44m	ET8482	110.44ab
EC400419	96.77n	Utkarsh	110.00b
		EC400361	109.77bc
Number of pods per plant			
Genotypes	Mean value (>28)	Genotypes	Mean value(<10)
EC400414	35.25a	HUR-35	10.05D
LD2-1	32.45b	NO3127	9.75D
EC540173	29.25c	EC500232	9.75D
IC311676	28.58cd	NO3160A	9.45D
Arun	28.00d	HURG0478	6.45E
Seed yield per plant (g)			
Genotypes	Mean value (>39)	Genotypes	Mean value (<12)
EC400398	51.31a	EC-150250	11.62AB
ET8482	42.98b	BD9116291	11.01ABC
Arun	42.10b	EC400361	10.34BC
EC400414	41.42bc	PLB438	9.16CD
EC14920	39.59cd	IC14351	7.00D

Table 7: Mean value of promising entries for agronomic traits identified during germplasm evaluation.

Genotypes	DF	DM	PH	NBPP	NPP	NSP	PL	HSW	Yield/plt
Arun (Check1)	55.00	112.00	84.70	4.53	28.00	4.32	15.16	38.19	41.70
Utkarsh (Check2)	68.00	109.00	77.63	3.60	22.00	4.80	16.00	62.30	38.20
Uday (Check3)	55.00	98.00	33.60	3.10	16.30	3.60	13.40	56.30	30.30
EC400414	52.00	111.00	27.83	4.20	37.00	4.20	9.18	37.60	42.80
EC400398	43.00	104.00	73.27	4.10	16.30	4.13	11.88	59.54	50.63
ET8415	45.00	109.00	61.23	3.50	10.30	3.92	14.74	56.30	38.06
EC540173	48.00	109.00	44.17	3.00	31.00	5.08	10.16	14.57	41.20

Note:

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height (cm)
NPP : Number of pods per plant
NSP : Number of seeds per pod
PL : Pod length (cm)
NBP : Number of branches per plant
HSW : 100 Seed weight (g)
SY : Seed yield per plant (g)

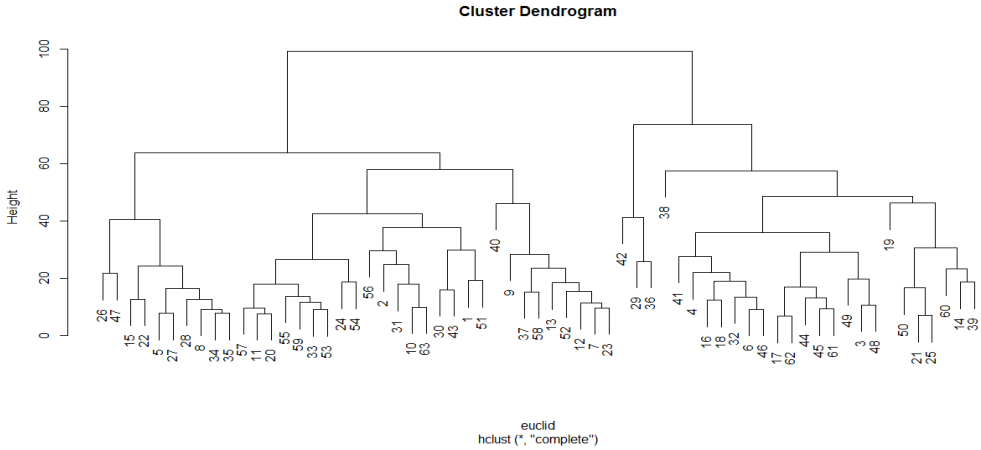


Fig 1: Euclid's dissimilarity coefficient.

objectives have changed over the years beyond yield improvement (Yong, 2015). New cultivars need to be developed with the capacity to achieve high yields in reduced chemical-input systems and with the genetic diversity needed to maintain yield stability under fluctuating climatic conditions (Heinemann *et al*. 2014). Thus, estimation of genetic diversity is a platform for stratified sampling of breeding population and to identify the desired genotypes for hybridization and use of genetically diverse parents is known to provide an opportunity for bringing together gene constellation yielding desirable transgressive segregants in advanced generations. Through Euclidian Clustering method, 63 genotypes were confined to two major clusters. The clustering pattern gave a different picture with cluster I containing 37 genotypes and cluster II consist 26 genotypes. Within cluster I two sub cluster were formed. It might be due to genotypes relatively dissimilar within the same genepool. Similarly, in case cluster II multiple sub cluster were formed (Fig 1). Our results were in conformity with the findings of Gangadhara *et al*. (2014); Boros *et al*., (2014); Ankit *et al*. (2017) and Rana *et al*., (2015) According to the cluster means, cluster II showed better performance in the case of pod length, number of pods per plant, number of seeds per pod and 100 seed weight. This indicated genetic distance and closeness among accessions due to different genetic constitutions. Hence, the genotype of this cluster could be used as parent in future hybridization programme for higher seed yield. Despite this, based on the genetic diversity study, traits specific germplasm accessions were identified from inter cluster group such as early maturity (EC400419, GPR4189, EC565673A), no. of primary branches (EC400414, EC564797, EC-150250), pod length (EC565673A, PL227468, GPR4189), no. of seeds per pod (HUR53, EC500232, BLF-101), resistance to BCMV (EC150250, GPR203, EC400414), upright branching (BLF101, EC500232) and bold seed type (EC-400414) (Table 5). These selected germplasms serve as useful genetic resource for plant breeder for the development of common bean varieties for high yield and BCMV disease resistance. Accordingly, the mean value of selected promising genotypes and checks was indicated in Table 7.

CONCLUSION

From the present investigation, it is concluded that the genotypes used in the present study showed wide range variation for quantitative traits like the number of pods per plant, pod length, seeds per pod, 100 seed weight and seed yield per plant. The genotype such as EC400414, EC400398, ET8415 and EC540173 were superior over check varieties and higher seed yield potential due to their

high seed yield per plant, pods per plant and seeds per pod. Besides this, we have also identified some of the trait-specific genotypes in our study. The promising genotypes could be used for common bean breeding programme in the improvement of specific traits.

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