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Genetic analysis of French bean (*Phaseolus vulgaris* l.) germplasm through principal component analysis and D^2 cluster analysis

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Abstract
Seventy four French bean germplasm were evaluated for twenty two quantitative traits to study the genetic diversity during Jan-Feb in G.B. Pant University of Agriculture and Technology. Principal component analysis showed that the first principal component had maximum of 30.85% variation of total variation, while the first seven principal component axes together with explained 83.41% variation, suggesting first seven principal axes are adequate to explain the variation in reduced dimension. Clustering through D^2 analysis revealed maximum inter-cluster distance of clusters V and IX (1405.141) followed by cluster III and IX (1297.298).

Keywords: Principal component analysis, D^2 analysis, Toucher method, Diversity, French bean

Introduction
French bean (*Phaseolus vulgaris* L.), 2n = 22 is the most popular leguminous vegetable crop in many part of the world. It was brought to India from Europe during the 17th century. It is adapted to variety of climatic conditions, being grown from 52° north latitude to 32° south latitude in the humid tropics, semi-arid tropics and even cold climate regions (Schoonhoven and Voysest, 1991) [17]. French bean had evolved from a wild growing vine *viz., Phaseolus aborigineus* distributed in the highlands of middle America and Andes (Brucher, 1988) [4]. India has about 137.54 thousand ha area under bean cultivation and the production is 1370.21 thousand MT with an annual productivity 9.96 MT/ha green pod (NHB, 2015) [1].
The knowledge of genetic diversity is an important pre-requisite to any breeding programme aimed to exploit hybrid vigour. Moreover, the information related to the nature and extent of association among various yield attributes, direct and indirect influence of each of the component traits on yield could prove helpful in formulating effective breeding strategy.

Materials and Methods
The present investigation was conducted at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar (Uttarakhand) during Jan-May, 2014. The experimental material comprised of 74 genotypes. The experiment was laid out in randomized block design with three replications. Each genotype was sown in three meter row length following plant spacing at 30 x 20 cm apart. Observations were recorded on five randomly selected competitive plants per replication for each entry on twenty two quantitative and fourteen quality traits. PCA and D^2 analysis were calculated as per Hotelling (1933) [9] and P.C. Mahalanobis (1936) [12], respectively.

Results and Discussion
The principal component analysis of 74 French bean genotypes based on correlation matrix of yield and yield contributing traits yielded seven eigen roots or eigen values. The percent variation explained by each eigen roots are presented in Table 1 and figure 1.

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Table 1: Latent roots (Eigen values) and variability of Principal Component of French bean genotypes

Principal component	Eigene Value (Root)	% Var. Exp.	Cum. Var. Exp.
PC-1	6.789	30.857	30.857
PC-2	3.360	15.272	46.129
PC-3	2.834	12.884	59.012
PC-4	1.806	8.209	67.222
PC-5	1.440	6.545	73.767
PC-6	1.207	5.488	79.255
PC-7	0.914	4.155	83.410
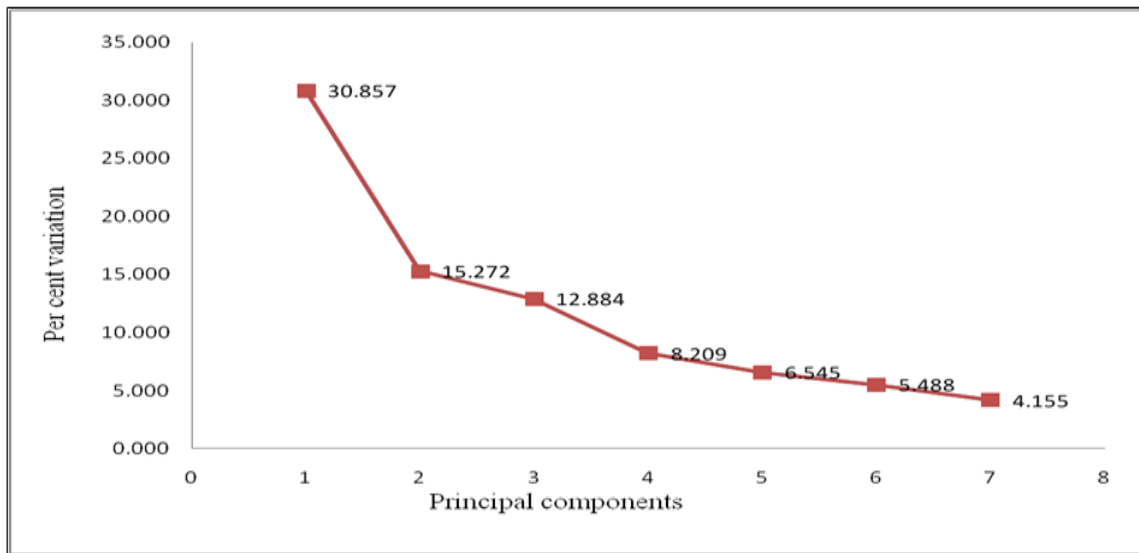
Fig 1: Cattel scree graph for variation explained by variation principal components based on yield attributing traits in French bean genotypes

The principal component score based on the correlation of 22 quantitative characters of 74 genotypes of French bean is presented in Table 2.

Table 2: Eigen vector, Eigen root and associated variation for principal component in French bean based on economic traits

S.N.	Traits	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6	PC-7
1.	Days to 1st flowering	0.305	0.142	0.034	0.044	0.134	0.088	0.013
2.	Days to 50% flowering	0.355	0.141	-0.048	0.008	0.069	0.109	0.028
3.	Days to 50% pod setting	0.285	0.091	-0.083	-0.008	0.088	0.156	-0.009
4.	Days to 50% maturity	0.353	0.118	-0.076	-0.044	0.035	0.136	0.060
5.	Days to 1st picking	0.334	0.134	-0.143	-0.022	-0.040	-0.026	0.022
6.	Days to 2nd picking	0.347	0.111	-0.126	-0.007	-0.003	0.114	0.041
7.	Number of pods/ cluster	0.052	0.056	-0.338	-0.101	-0.415	-0.279	0.033
8.	Number of pod clusters/ plant	0.000	-0.058	0.503	-0.013	0.090	-0.286	-0.198
9.	Number of pods/ plant	0.129	0.180	0.102	0.222	0.424	-0.452	-0.188
10.	Pod dia (mm)	0.034	-0.151	0.163	0.523	0.183	0.139	-0.038
11.	Pod length (cm)	0.172	0.047	0.369	-0.232	-0.035	0.196	-0.059
12.	Leaf length (cm)	-0.099	-0.005	-0.250	-0.441	0.373	0.100	-0.115
13.	Leaf width (cm)	-0.211	0.047	-0.040	-0.453	0.281	-0.092	-0.031
14.	Single pod weight (g)	0.124	-0.073	0.388	-0.234	-0.028	0.109	0.049
15.	Plant height (cm)	0.123	-0.099	0.309	-0.163	-0.504	0.026	0.013
16.	Number of seeds/ pod	-0.209	0.316	0.066	-0.039	0.122	0.383	0.207
17.	Seed length (mm)	0.080	-0.466	0.002	-0.113	0.090	0.070	0.057
18.	Seed width (mm)	0.066	-0.407	-0.133	0.202	0.140	0.218	0.221
19.	100 seed weight (g)	0.007	-0.500	-0.130	-0.028	0.043	-0.020	0.097
20.	Seed yield/plant (g)	0.271	-0.155	-0.176	-0.076	-0.048	-0.342	-0.231
21.	Pod yield/ plant (g)	-0.277	0.254	-0.103	0.248	-0.197	0.014	0.039
22.	Pod yield/ ha (q)	0.060	0.067	0.127	-0.064	0.120	-0.392	0.858

The Eigen root of first principal component was accounted approximately 30.857% of total variation followed by second to seven components which accounted 15.272, 12.884, 8.209, 6.545, 5.488 and 4.155% of total variation presented among the genotypes, respectively. The first seven PC axes explained 83.41% of the variation, suggesting considerable diversity among the genotypes for all the characters, the rest of the components not considered. These were interpreted as relative weight of the variables in each component. The important variables are those which have high positive or negative relative weight values.

The first principal component had high positive weight to days to 50% flowering (0.355) followed by days to 50% maturity (0.353) and days to second picking (0.347), while high negative weight to pod yield per plant (-0.277) followed by leaf width (-0.211) and number of seeds per pod (-0.209). The second principal component had high positive weight to number of seeds per pod (0.316) followed by pod yield per

plant (0.254) and number of pods per plant (0.180), while high negative weight to 100 seed weight (-0.500) followed by seed length (-0.466) and seed width (-0.407). The third principal component exhibited high positive weight to number of pod clusters per plant (0.503) followed by single pod weight (0.388) and pod length (0.369), whereas high negative weight to number of pods per clusters (-0.338) followed by leaf length (-0.250) and seed yield per plant (-0.176). Similar studies were reported by Balkaya (2008) [2], Vasic *et al.* (2008) [20], Madakbas *et al.*, (2011) [11] and Stoilova *et al.* (2012) [19].

The grouping of genotypes in clusters reflects the relative divergence of clusters and allows a convenient selection group of genotypes with their overall phenotypic similarity for formulating breeding programme. Generally parents belonging to most divergent clusters are beneficial for selection or development of new variety and create wide variability in genetic architecture. However, for a practical plant breeder, the objective is not only obtaining high yield but also to achieve high level of production with the shortest possible time.

Cluster analysis by Tocher method based on principal component analysis was found to be more useful measure for estimating divergence. The importance of genetic diversity in several crops has been studied by many workers *viz.,* Murty and Arunachalam (1989) [14], Prasad and Singh (1993) [15] etc. Distribution of genotypes in each cluster is presented in Table 3. Cluster number II had highest number of genotypes (*viz* FB-254, FB-256, FB-237, FB-215, FB-259, FB-252, FB-260, FB-250, IIHR-909, Chitra, FB-257, FB-249, FB-208, FB-228, FB-217, FB-230, FB-206, FB-216, FB-218, FB-235, Contender, FB-220, FB-203, FB-224.) followed by cluster I (18), cluster V (17), cluster IV (8), cluster VIII (3), cluster III, cluster VI, cluster VII and cluster IX (1 each).

Table 3: Distributing pattern of seventy four genotypes of French bean into nine clusters

Cluster number	Number of genotypes	Genotype included
I	18	FB-211, FB-213, Pant Anupama, FB-243, FB-240, FB-242, FB-241, FB-247, FB-245, VL Bean-2, Pant Bean-3, FB-246, FB-222, Arka Komal, Pant Bean-2, FB-239, FB-225, Arka Anoop
II	24	FB-254, FB-256, FB-237, FB-215, FB-259, FB-252, FB-260, FB-250, IIHR-909, Chitra, FB-257, FB-249, FB-208, FB-228, FB-217, FB-230, FB-206, FB-216, FB-218, FB-235, Contender, FB-220, FB-203, FB-224
III	1	VLFB-510
IV	8	FB-212, FB-233, FB-234, FB-204, FB-244, FB-210, FB-236, FB-209
V	17	Arka Suvidha, VLFB-130, VLFB-628, FB-229, FB-251, FB-219, FB-253, FB-231, VLFB-629, FB-255, FB-226, FB-227, FB-201, FB-223, FB-202, FB-248, FB-238
VI	1	FB-221
VII	1	FB-207
VIII	3	FB-205, FB-214, FB-258
IX	1	FB-232

Cluster analysis by Tocher method was done to study divergence in seventy four genotypes in respect of various economic traits. The genotypes were grouped into 9 clusters and the averages inter and intra-cluster distances have been presented in Table 4 and figure 2. Maximum intra-cluster distance was noted in cluster V (314.619) followed by cluster VIII (301.516), cluster IV (233.564), cluster II (185.279), cluster I (143.385), while minimum intra-cluster distance was recorded in cluster III, cluster VI, cluster VII and cluster IX (0.000).

Table 4: Average distance of intra and inter-cluster centroids.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	(143.385)								
II	416.010	(185.279)							
III	205.233	482.642	(0.000)						
IV	305.500	475.676	493.731	(233.564)					
V	339.879	414.385	319.626	614.217	(314.619)				
VI	409.254	338.490	583.866	357.602	648.004	(0.000)			
VII	673.280	283.195	596.048	733.913	486.652	692.887	(0.000)		
VIII	726.867	373.414	849.178	777.408	537.846	820.646	304.711	(301.516)	
IX	1049.301	715.481	1297.298	628.848	1405.141	315.828	986.414	1244.472	(0.000)
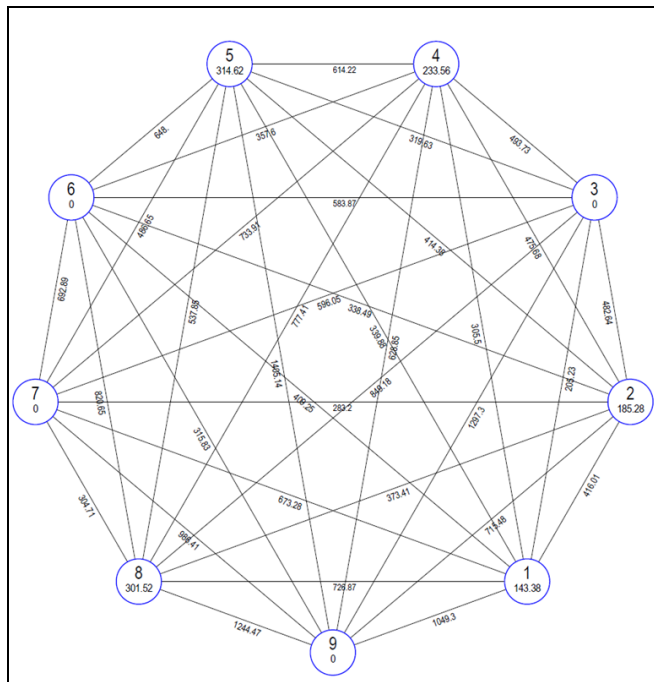
Fig 2: Average distance of intra and inter-cluster centroids based on various traits in 74 French bean genotypes

Maximum inter-cluster distance was calculated between cluster V and IX (1405.141) followed by cluster III and IX (1297.298), cluster VIII and IX (1244.472), cluster I and IX (1049.301), cluster VII and IX (986.414), cluster III and VIII (849.178), cluster VI and VIII (820.646), cluster IV and VIII (777.408), cluster IV and VII (733.913), cluster I and VIII (726.867), cluster VI and VII (692.887), cluster I and VII (673.280), cluster V and VI (648.004), cluster IV and IX (628.484), cluster IV and V (614.217), cluster III and VII (596.048), cluster III and VI (583.866), cluster V and VIII (537.846), cluster III

and IV (493.731), cluster V and VII (486.652), cluster II and III (482.642), cluster II and IV (475.676), cluster I and II (416.010), cluster II and V (414.385), cluster I and VI (409.254), cluster II and VIII (373.414), cluster IV and VI (357.602), cluster I and V (339.879), cluster II and VI (338.490), cluster III and V (319.626), cluster VI and IX (315.828) and cluster I and IV (305.5000), however, minimum distance was found between inter-cluster I and III (205.233) followed by inter-cluster II and VII (283.195) and cluster VII and VIII (304.711).

The cluster means for all the characters are given in Table 5, highest mean value for days to second picking (63.00), days to 50% maturity (59.00) and days to first picking (58.333) and lowest mean value for number of pods per cluster (1.833), seed yield per plant (3.440) and single pod weight (3.667 g) were calculated in cluster IX. Cluster VIII had the highest mean value for pod yield per hectare (94.658 q), days to second picking (71.111) and days to 50% maturity (69.667), while lowest mean value for number of pods per cluster (2.256), number of pods per cluster (4.278), number of seeds per pod (5.256) and single pod weight (5.256 g). Cluster VII had the highest mean value for plant height (85.400 cm), pod yield per hectare (78.813 q) and days to second picking (64.667), while lowest mean value for number of pods per cluster (1.767), number of seeds per pod (3.800) and number of pod clusters per plant (3.833). Highest mean value for days to second picking (63.333), days to 50% maturity (60.333) and days to first picking (58.667) and lowest mean value for number of pods per cluster (2.000), single pod weight (2.800 g) and number of seeds per pod (3.067) were calculated in cluster VI. The genotypes with highest mean value for pod yield per hectare (77.099 q), days to second picking (67.490) and days to 50% maturity (65.098), while number of pods per cluster (1.980), number of pod clusters per plant (3.951) and number of seeds per pod (4.263) were grouped into cluster V.

Table 5: Cluster mean for different economic traits in French bean genotypes

S. No.	Characters	Cluster mean								
		I	II	III	IV	V	VI	VII	VIII	IX
1	Days to 1st flowering	44.204	43.389	42.667	47.083	45.941	43.333	43.333	47.000	43.667
2	Days to 50% flowering	47.981	46.583	44.667	50.917	49.275	44.333	46.000	53.000	45.000
3	Days to 50% pod setting	51.815	50.542	48.667	55.083	53.118	48.667	49.333	56.889	48.333
4	Days to 50% maturity	64.167	62.097	59.000	66.583	65.098	60.333	62.667	69.667	59.000
5	Days to 1st picking	62.333	60.444	57.000	64.042	62.216	58.667	59.333	67.222	58.333
6	Days to 2nd picking	66.870	65.278	62.333	68.458	67.490	63.333	64.667	71.111	63.000
7	Number of pods/ cluster	2.007	2.126	2.033	2.321	1.980	2.000	1.767	2.256	1.833
8	Number of pod clusters/ plant	4.193	3.786	4.867	4.692	3.951	3.167	3.833	4.278	4.067
9	Number of pods/ plant	8.270	7.735	9.800	10.558	7.551	6.400	6.800	9.522	7.133
10	Pod dia (mm)	9.546	10.493	13.687	9.083	11.204	11.960	10.140	9.790	11.080
11	Pod length (cm)	10.825	10.187	13.840	12.054	10.769	9.600	14.100	11.084	11.500
12	Leaf length (cm)	9.146	9.246	8.433	9.737	8.461	5.233	9.200	11.322	6.633
13	Leaf width (cm)	7.124	6.725	6.133	7.100	6.369	4.300	7.167	7.333	4.200
14	Single pod weight (g)	4.904	4.617	5.233	4.650	5.229	2.800	6.100	5.256	3.667
15	Plant height (cm)	38.606	39.325	45.867	39.150	51.865	41.733	85.400	45.431	43.933
16	Number of seeds/ pod	4.513	4.572	4.767	5.025	4.263	3.067	3.800	5.256	3.833
17	Seed length (mm)	13.319	13.780	15.080	11.643	15.450	10.140	15.680	15.853	8.240
18	Seed width (mm)	6.613	6.838	6.560	5.624	7.459	6.780	6.920	7.427	4.813
19	100 seed weight (g)	31.833	34.312	32.600	21.413	39.406	22.367	32.400	35.800	12.467
20	Seed yield/plant (g)	11.957	12.428	15.187	11.433	13.145	4.397	8.427	16.493	3.440
21	Pod yield/ plant (g)	37.926	34.719	48.433	46.562	38.550	17.890	39.407	47.329	26.223
22	Pod yield/ ha (q)	75.853	69.439	96.867	93.123	77.099	35.780	78.813	94.658	52.447

Cluster IV had the highest mean value for pod yield per hectare (93.123 q), days to second picking (68.458) and days to 50% maturity (66.583), while lowest mean value for

number of pods per cluster (2.321), single pod weight (4.650 g) and number of pod clusters per plant (4.692). Maximum value for pod yield per hectare (96.867 q), days to second

picking (62.333) and days to 50% maturity (59.000), while minimum value for number of pods per cluster (2.033), number of seeds per pod (4.767) and number of pod clusters per plant (4.867) found in cluster III. The genotypes with highest mean value for pod yield per hectare (69.439), days to second picking (65.278) and days to 50% maturity (62.097), while lowest value for number of pods per cluster (2.126), number of pod clusters per plant (3.786) and number of seeds per pod (4.572) found in cluster II. Cluster I had the highest mean value for pod yield per hectare (75.853 q), days to second picking (66.870) and days to 50% maturity (64.167), while lowest value for number of pods per cluster (2.007), number of pod clusters per plant (4.193) and number of seeds per pod (4.513).

Considering group distances and other agronomic performance, the inter-genotypic crosses between the members of cluster V with that of cluster IX would exhibit high divergence and facilitate the selection of genotype with desired traits. Therefore, more emphasis should be given on cluster V and IX in selecting inbreds for development/selection of variety in breeding programme. The results presented here are in conformity with the findings of Gangadhara et al. (2014) [7], Mishra et al. (2010) [13], Walling (2014) [22], Boros et al. (2014) [3], Javadian et al. (2014) [10], Sharma et al. (2009) [18], Rai et al. (2010) [16], and Verma et al. (2014) [21] in French bean.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Table 6 and figure 3). Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the first rank. The present study showed that, pod yield per hectare (47.20%) contributed maximum to the total genetic diversity among the genotypes followed by seed length (25.84%), seed width (8.22%) and

plant height (5.26%). Hence, pod yield per hectare, seed length, seed width, plant height, days to first picking and 100 seed weight were considered to be important traits contributing towards genetic divergence. Similarly divergence studies were carried out by Dalsaniya et al. (2009) [6], Waliing et al. (2014) [22], Govanakoppa et al. (2002) [8], Gangadhara et al. (2014) [7]. and Chaubey et al. (2003) [5].

Table 6: Relative contribution of different characters to the total divergence in French bean

S.N.	Source	Contribution %
1	Days to 1st flowering	0
2	Days to 50% flowering	0
3	Days to 50% pod setting	0
4	Days to 50% maturity	1.3
5	Days to 1st picking	3.26
6	Days to 2nd picking	0.48
7	Number of pods/ cluster	0.07
8	Number of pod clusters/ plant	0.04
9	Number of pods/ plant	0
10	Pod dia (mm)	1.44
11	Pod length (cm)	1.52
12	Leaf length (cm)	0.89
13	Leaf width (cm)	0.04
14	Single pod weight (g)	1.11
15	Plant height (cm)	5.26
16	Number of seeds/ pod	0
17	Seed length (mm)	25.84
18	Seed width (mm)	8.22
19	100 seed weight (g)	2.59
20	Seed yield/plant (g)	0.63
21	Pod yield/ plant (g)	0.11
22	Pod yield/ ha (q)	47.2
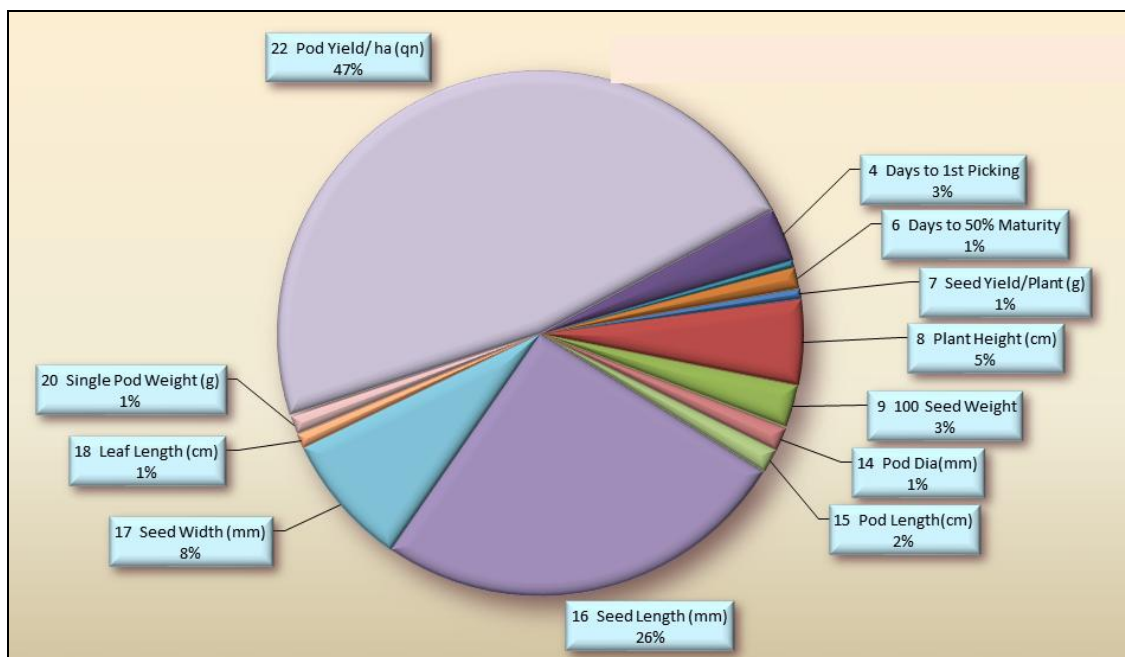
Fig 3: Contribution percent of different characters towards genetic divergence

Summary and conclusion
The eigen root of first principal component was accounted approximately 30.857% variation of total variation, while the first seven principal component axes explained 83.41% variation, suggesting considerable diversity among the characters. Cluster analysis for yield and yield contributing traits classified all seventy four genotypes into 9 clusters. The

analysis revealed the maximum inter-cluster distance was found between clusters V and IX having 17 genotypes and 1 genotype, respectively in the cluster. Therefore, more emphasis should be given on cluster V and IX in selecting inbreds for development/selection of variety in breeding programme. Pod yield per hectare contributed maximum towards genetic diversity, followed by seed length, seed

width, plant height and days to first picking, hence these characters were considered to be important traits contributing toward genetic divergence.

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