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Principal component analysis and determination of the selection criteria in fodder cowpea (*Vigna unguiculata* (L) Walp.) genotypes

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Abstract

A critical examination of the genetic variability helps to make good decisions in a crossing programme. The present investigation consisted of thirty diverse germplasm lines of cowpea (*Vigna unguiculata* (L) Walp.) in which divergence was studied. On the basis of relative magnitude of cluster distances, all the 30 genotypes of cowpea were grouped into five major clusters. Cluster pattern revealed that cluster II was the largest group consisting of 17 genotypes followed by cluster III (6 genotypes) and cluster I (5 genotypes). Cluster IV and V each had only one genotype where each genotype within a cluster was closest to the cluster mean. The highest intra-cluster distance was observed for cluster II followed by cluster I, cluster III and cluster IV and V. Cluster I had highest mean for dry matter, dry matter per day, plant height and number of branches per plant. Cluster II had highest mean value for leaf length. Similarly cluster III showed highest leaf breadth. Green fodder yield, green fodder per day, days to 50% flowering, leaf weight and straw weight showed highest cluster mean in Cluster IV. The first principal component explained 32.1% of the total variation. The second, third, fourth and fifth principal components explained 17.1, 16.1, 13.6 and 11.7% of the total variance, respectively. It was clear that the first factor expressing the combined effect of stem and leaf weight on green fodder yield can be regarded as green fodder yield factor. PF-2 was associated with dry matter characters, hence can be considered as dry matter yield factor. Similarly PF-3, PF-4 and PF-5 can be regarded as yield contributing factors collectively.

Keywords: Cluster, Cowpea, Divergence, Germplasm

Introduction

Cowpea (*Vigna unguiculata* L. Walp.), an annual legume is a versatile short duration crop commonly grown as grain pulse, vegetable and fodder in semi-arid areas of the country. The worldwide cultivation of cowpea is approximately 12.5 million hectares with an annual production of 3 million tonnes (Fana *et al.,* 2004). Cowpea is one of the most ancient crops known to man and is a major staple crop in Africa. It has also significant production in Brazil, Haiti, India, Myanmar, Sri Lanka, Australia, and the USA (Deshpande *et al.,* 2010). Cowpea, a legume is mainly used as green fodder for animals, seeds as a source of protein rich pulse and pods as vegetable for humans in tropical and sub-tropical countries (Manjunatha *et al.,* 2016). Being a rich source of proteins, vitamins and minerals, it is being looked upon as a good crop for human and livestock consumption. It is a quick growing, highly nutritious, highly palatable forage. In many areas of the world, the cowpea is the only available high-quality legume hay for livestock feed. Digestibility and yield of certain cultivars have been shown to be comparable to alfalfa. It is also used as a green manure crop, a nitrogen fixing crop, or used for erosion control. Cowpea may be used as green or dry fodder. Among the forages, legumes are important in supplying the most demanding and quality nutrients like protein, minerals and vitamins to the animals.

Livestock is an important component in our agricultural production system, playing a vital role in the national economy of the country. But livestock production cannot be sustained due to huge feed shortage which can be overcome by cultivating some potential forage. In the Indian soils, cowpea has several agronomic advantages including drought tolerance, high nutritional value and ability to produce some yield in soils that are too poor for cultivation of other more favoured species.

Genetic variability is available in this crop but a critical examination of the different genotypes helps make good decisions in a crossing programme and more successful and meaningful results can be obtained. Characterization of accessions is necessarily the first step which will benefit plant breeder to facilitate breeding efforts in choosing proper materials. Kumar *et al.* (2015)

characterized twenty genotypes for their better utilization in future breeding programmes. Principal component analyses help researchers to distinguish significant relationship between traits. Present study is planned to determine the extent of variability for green fodder yield and its associated characters among cowpea genotypes.

Materials and Methods

Plant materials: The present investigation was carried out at Forage Research Farm, CCS Haryana Agricultural University, Hisar. The experimental material consisted of 30 diverse germplasm lines of cowpea (*Vigna unguiculata* (L) Walp.). All the genotypes were evaluated in randomised block design with three replications during *kharif* 2014. Each plot consisted of six rows of 4 m length, spaced 30 cm apart. All the recommended agronomic practices were followed to raise a good crop. Observations were recorded on ten characters. Observations on plant height (PH), branches/plant (BP), leaf breadth (LB), leaf length (LL) were recorded on randomly selected five plants in each plot and in each replication, whereas observations on days to 50% flowering (DF) and green fodder yield (GFY) were recorded on plot basis. Data on leaf weight (LW), stem weight (SW) and leaf: stem ratio (LSR) was taken out of a sample of 500 g from each plot in each replication. Dry matter yield was recorded on drying up of this sample calculated on plot basis. Per day productivity (GFY/day and DMY/day) was also calculated by dividing the green fodder yield and dry matter yield with number of days to 50% flowering.

Statistical analysis: Hierarchical cluster and principal factor analyses of phenotypic observations were done using SPSS software (Version 20). UPGMA with City Block distance was used for clustering the genotypes. The method of Romesburg (1990) was used to determine the number of clusters. Principal component method of factor extraction was used. Factor axes were rotated using Varimax rotation. The genotypes were plotted using their individual principal factor scores.

Results and Discussion

Genetic divergence analysis: In the present study UPGMA (Unweighted pair-group method using arithmetic averages) method of hierarchical cluster analysis was utilized with city block distances to classify 30 genotypes and dendrogram was prepared using the rescaled distances. Based on the method suggested by Romesburg (1990) the dendrogram was cut to form five clusters containing one to 17 genotypes (Table 1). Cluster pattern revealed that, cluster II was the largest group consisting of 17 genotypes followed by cluster III (6 genotypes) and cluster I (5 genotypes). Cluster IV and V had only one genotype each. No correspondence was observed between the geographical and genetic diversity. This implies that geographic diversity is not the only factor determining genetic divergence and is one among the several factors determining the genetic divergence. Therefore, parental selection for hybridization should be based on the criteria of genetic diversity rather than geographic diversity. Similar findings were also reported earlier (Kapoor *et al.*, 2000; Anbumalarmathi and Nadarajan, 2007; Bertini *et al.,* 2010; Tigga and Tandekar, 2013; Jogdhande *et al.,* 2016).

Inter-and intra-cluster distances: The inter-and intra-cluster distances among 30 genotypes were recorded (Table 2). The results showed that inter-cluster distances were more than intra-cluster distances for all the clusters indicating narrow genetic variation within a cluster. When diversity was studied among the clusters based on the inter-cluster distance, it showed a range of 562.06 to 3414.63. The average inter-cluster distance was found to be highest between cluster IV and V (3414.63) followed by cluster III and IV (3234.84) and cluster I and IV (2742.71) whereas the lowest inter-cluster distance was observed between clusters I and III (562.06). The higher inter-cluster distance indicated the presence of more diversity among the genotypes included among these cluster I had highest mean for dry matter, dry matter yield

Table 1. Distribution of cowpea genotypes in different clusters

Cluster	#Genotypes	Genotypes
I	5	1:BL-1; 8:GFC-1; 17:EC 249141; 22:IT 38952; 25:SK 57
II	17	2:CO 2; 3:CO 4; 4:CO 5; 5:CO FC-7; 6:COFC-8; 10:GFC-3; 11:UPC 5287;12:UPC 625; 13:EC 4216; 14:EC 3914-1-5; 15:EC 10198; 16:EC 528408; 19:IC 201098; 27:TVv 92-2; 28:TVv 3531-1-5; 29:CS 88; 30:HC 46
III	6	7:KBC 2; 9:GFC 2; 18:EC 528491; 20:IC 536626; 24:NDFC 6; 26:SRM 194
IV	1	21:IC 201095
V	1	23:NDFC 15

clusters. Hybridization among the genotypes belonging to distant clusters is likely to produce heterotic hybrids and desirable transgressive segregants in further generations. Similar studies were also reported by Nagalakshmi *et al.* (2010).

Table 2. Inter and Intra clusters (underlined) of cowpea genotypes

Cluster	1	2	3	4	5
I	<u>399.62</u>	1057.86	562.06	2742.71	960.37
II		<u>486.89</u>	655.73	933.18	644.90
III			<u>284.77</u>	3234.84	823.23
IV				<u>0.00</u>	3414.63
V					<u>0.00</u>

The association among the different genotypes is presented in the form of dendrogram prepared using rescaled distances (Fig 1). The dendrogram also showed the relative magnitude of resemblance among the different clusters. The cluster means for the 10 quantitative traits studied in cowpea genotypes revealed considerable differences among the entire clusters (Table 3).

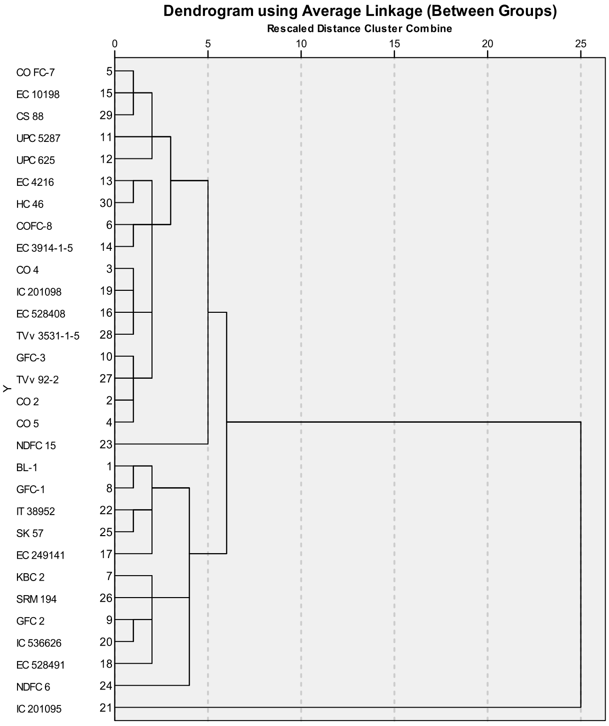

Fig 1. Dendrogram showed the clustering pattern in 30 cowpea genotypes using Ward's minimum variance method of Non-hierarchical Euclidean cluster analysis

per day, plant height and number of branches per plant. Cluster II had highest mean value for leaf length whereas, it had the lowest mean values for plant height and stem weight. Similarly, cluster III showed highest leaf breadth whereas, it had the lowest mean values for days to 50% flowering. Green fodder yield, green fodder per day, days to 50% flowering, leaf weight and straw weight showed highest cluster mean in Cluster IV whereas it had the lowest mean values for leaf length, leaf breadth and leaf stem ratio. Cluster V had highest mean value for leaf stem ratio only whereas, it had the lowest mean values for a number of characteristics *viz.,* green fodder yield, dry matter yield, green fodder per day, dry matter yield per day, branches per plant and leaf weight. This comparison indicated that cluster I and IV had higher cluster means for most of the characters and their inter-cluster distance was also more, therefore, these might be better option for selecting genotypes for hybridization.

In the present study principal factor analysis was carried out using principal component method, which unlike other methods did not require assumption of multivariate normal distribution of population. Initially the data was analyzed without any rotation to derive clear picture of interaction of variables among themselves and with the principal factors. But it failed to provide much information regarding the idea of correlation between the variables and the principal factors. Principal components with Eigen values greater than one were selected for interpretation (Kaiser, 1958). The total cumulative variance explained by the five components having Eigen values >1 amounted to 90.64% of total variability (Table 4). The first PC accounted for maximum proportion of total variability in the set of all variables and remaining components accounted for progressively lesser and lesser amount of variation. In our study, the first principal component explained 32.11% of the total variation and the second, third, fourth and fifth principal components explained 17.12%, 16.06%, 13.63% and 11.71%, respectively. Gerrano *et al.* (2015) studied genetic variability among the cowpea genotypes and found that five principal components showed 79.30% of the total variability among the genotypes.

The failure of principal factor analysis without rotation to draw sensible conclusions prompted to go for analysis with rotation. Varimax method of orthogonal rotation (Kaiser, 1958) was utilized in the present study to rotate the factor axes. This rotation accentuated the larger loadings in the extracted factors and suppressed the minor loadings thus improving the opportunity of achieving meaningful interpretation of factors (Table 5).

Table 3. Cluster means of cowpea genotypes

Cluster	GF	DM	GFD	DMD	DF	PH	BP	LL	LB	LW	SW	LSR
1	670.0	**93.6**	10.67	**1.49**	62.8	**244.6**	**5.6**	9.2	7.5	214.0	444.0	0.49
2	208.8	52.5	3.38	0.84	62.5	171.9	3.8	**9.3**	7.7	69.3	134.1	0.57
3	460.0	75.5	7.86	1.27	59.3	211.7	5.2	8.9	**8.0**	161.7	298.3	0.58
4	**2000.0**	80.0	**26.67**	1.07	**75.0**	234.0	4.0	7.0	6.5	**400.0**	**1600.0**	0.25
5	100.0	33.0	1.49	0.49	67.0	210.0	2.0	9.0	6.8	45.0	550.0	**0.82**
Mean	**687.8**	**66.9**	**10.01**	**1.03**	**65.3**	**214.4**	**4.1**	**8.7**	**7.3**	**178.0**	**605.3**	**0.54**

GFY- green fodder yield; GFD- green fodder yield/day; SW- stem weight; LW - leaf weight; DM- dry matter yield; DMD- dry matter yield/day; LL- leaf length; LB - leaf breadth; BP - branches/plant; PH- plant height; LSR- leaf: stem ratio and DF- days to 50% flowering

Table 4. Total variance explained by different principal components in cowpea genotypes

Principal component	Extraction sums of squared loadings			Rotation sums of squared loadings		
	Total	% of variance	Cumulative (%)	Total	% of variance	Cumulative (%)
1	4.550	37.914	37.914	3.853	32.111	32.111
2	2.425	20.207	58.121	2.054	17.119	49.231
3	1.608	13.403	71.524	1.928	16.063	65.293
4	1.272	10.598	82.122	1.636	13.636	78.929
5	1.022	8.520	90.642	1.405	11.712	90.642

Data clearly indicated that GFY, GFD, SW and LW were highly loaded on PC-1 (Table 5). Similarly, PC-2 showed a strong and positive relation with traits DM and DMD. LL and LB were loaded high on PC-3. PC-4 showed diversity among accessions based on BP and PH. Similarly LSR and DF were loaded high on PF-5. Nwofia *et al.* (2014) studied genetic and varying population density effect on growth and yield characters of 12 cowpea varieties. The principal components that determined yield were number of pods/plant, dry matter yield/plant, number of seeds/plant and pod length, hence, the traits demand special attention during breeding and selection of cowpea. Sood *et al.* (2016) also studied genetic diversity among 25 *Trifolium* genotypes. *T. alexandrinum* genotypes were in one group with positive loadings for PC 1 and PC 2. Similarly different collections from different places were placed in separate groups.

Table 5. Factor loading of different characters with respect to different principal factor (varimax rotation)

Characters	Principal component				
	1	2	3	4	5
GFY	0.959*	0.097	-0.081	0.134	0.165
GFD	0.945*	0.105	-0.079	0.240	0.054
SW	0.928*	0.024	-0.105	0.023	0.250
LW	0.919*	0.155	0.032	0.227	-0.150
DM	0.139	0.978*	0.117	0.085	0.019
DMD	0.103	0.977*	0.119	0.116	-0.034
LL	-0.145	0.035	0.950*	-0.025	0.068
LB	-0.007	0.214	0.925*	-0.035	-0.170
BP	0.202	0.210	-0.206	0.839*	-0.096
PH	0.402	0.036	0.188	0.764*	0.151
LSR	-0.025	0.052	0.156	-0.192	-0.877*
DF	0.285	0.060	0.122	-0.401	0.673*

***Higher loading**

GFY- green fodder yield; GFD- green fodder yield/day; SW- stem weight; LW - leaf weight; DM- dry matter yield; DMD- dry matter yield/day; LL- leaf length; LB - leaf breadth; BP - branches/plant; PH- plant height; LSR- leaf: stem ratio and DF- days to 50% flowering

It was clear that the first factor expressing the combined effect of stem and leaf weight on green fodder yield was considered as green fodder yield factor. PC-2 was associated with dry matter characters, hence could be considered as dry matter yield factor. Similarly, PC-3, PC-4 and PC-5 could be regarded as yield contributing factor collectively. Identification of the right agro-morphological traits of high discriminating capacity is essential, before embarking on any genetic diversity; as it was revealed that some traits discriminated more efficiently among the accessions than others (Ajayi and Adesoye, 2013).

Figure 2 revealed that genotype no. 24 *i.e.* NDFC 6 showed a very high dry matter and dry fodder yield per day which were loaded on PC-2. So it can be utilized in programmes for developing of genotypes with high dry matter. Genotype UPC 5287 also behaved in the similar way. Similarly genotype no. 21 *i.e.* IC 201095 can be utilized for making crosses with a very high green fodder yield, green fodder yield per day, straw weight and leaf weight which were loaded on principal factor 1. Genotype EC 249141 also behaved in the similar way. Rest of the genotypes behaved almost similar for these two principal factors.

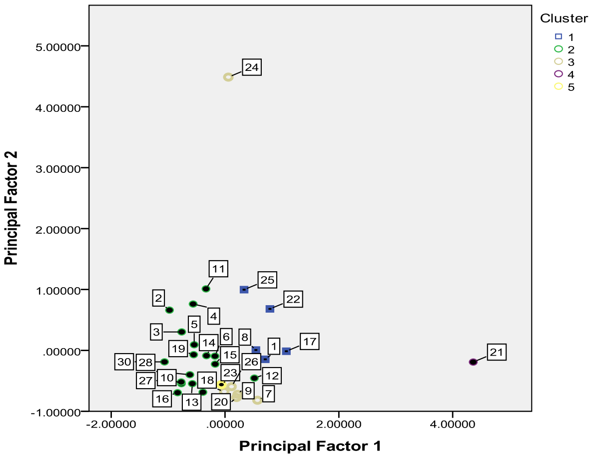

Fig 2. Clustering of genotypes based on principal factors

Conclusion

Thirty genotypes of cowpea were studied for genetic divergence amongst them. On the basis of relative magnitude of cluster distances, all the 30 genotypes of cowpea were grouped in five major clusters. Cluster pattern revealed that cluster II was the largest group consisting of 17 genotypes followed by cluster III (6 genotypes) and cluster I (5 genotypes). The results showed that inter cluster distances were more than intra-cluster distances for all the clusters which indicated the presence of narrow genetic variation within a cluster. Cluster I and IV had higher cluster means for most of the characters. Therefore, these might be considered better for selecting genotypes. Principal component analysis (PCA) and factor analysis were used for understanding the data structure and trait relations. The total cumulative variance of the five factors amounted to 90.64%. The first factor expressing the combined effect of stem and leaf weight on green fodder yield was regarded as green fodder yield factor. PF-2 was associated with dry matter characters, hence could be considered as dry matter yield factor. Similarly PF-3, PF-4 and PF-5 could be regarded as yield contributing factor collectively. The genotype NDFC 6 showed a very high dry matter and dry fodder yield per day which was loaded on principal factor two. So it can be utilized in programmes for developing of genotypes with high dry matter. Similarly genotype IC 201095 can be utilized for making crosses with a very high green fodder yield, green fodder yield per day, straw weight and leaf weight which were loaded on principal factor one.

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