Variability and Cluster Analysis of Morphological, Fodder and Seed Yield Attributes of Cowpea *Vigna unguiculata* (L.) Walp; Germplasm for Identification of Donor Sources

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Cowpea is a multipurpose crop grown for fodder, grain and improving soil fertility. For improving cowpea, a set of 168 exotic and indigenous genotypes of cowpea *Vigna unguiculata* including three cultigroups, *i.e. unguiculata, catjang, sesquipedalis,* with three checks and one local control were evaluated at Experimental farm, Crop Improvement Division, Indian Grassland and Fodder Research Institute, Jhansi, during 2004-05 and 2005-06 in augmented block design. Pooling of the data, Non Heirarchical Euclidean Cluster analysis using SPAR-1, formed 12 clusters for 20 trait variables. Genetic variability, and frequency distribution of forage and grain yield, yield attributing characters were also performed for selection. On the basis of clustering in the present study identification of donor sources in respect of forage and grain yield was done, *i.e.,* for higher biomass/plant, IL-1177, IL-3171 and IL-966-B; higher fresh leaf/stem ratios, HY6P52-3, IL893 and IL-99-171; dry matter yield/plant, IL-1177; IL-3171 and IL-449; the maximum pod bearing lines were IL-90, EC240809, IL3117.

Key Words: Cowpea, Variability, Frequency distribution, Cluster analysis

Introduction

Among legumes, cowpea is being grown in almost all parts of India, except high hills. It is a unique pulse crop with manifold uses such as pulse, green vegetable, green fodder and as a cover crop for stopping soil erosion. But due to low yield it is not easy to exploit the crop efficiently. For any crop improvement programme, variability is the first requirement (Anku *et al.*, 2001). For proper utilization of variability in breeding programme an efficient screening, evaluation and documentation of germplasm lines for useful traits is essential so that the potential value of particular germplasm line may be assessed. Therefore, a set of exotic and indigenous germplasm was evaluated and cluster analysis was performed for identification of donor sources of various morphological attributes showing high effect for improving fodder and grain yield.

Materials and Methods

A set of 29 exotic and 139 indigenous genotypes of cowpea *Vigna unguiculata* including three cultigroups, i.e., *unguiculata, catjang, sesquipedalis,* with three checks, Bundel lobia-1, Bundel lobia-2, UPC-5286 and one local control IGFRI-95-1 were evaluated at Experimental farm of Crop Improvement Division of Indian Grassland and Fodder Research Institute, Jhansi, during the years 2004-05 and 2005-06 in augmented block design. The layout consisted of 7 blocks with 24 germplasm lines, 3 checks and 1 control in each block. The observations were recorded according to minimal descriptor for Agri-horti crops.

(Srivastava *et al.,* 2001). The recorded 29 traits were, early plant vigour, plant growth habit, plant height, length of main shoot per branch, number of nodes, number of primary branches, number of secondary branches, number of leaves per plant, leaf length, leaf width, leaf weight per plant, stem weight per plant, biomass per plant, fresh leaf/stem ratio, dry leaf weight, dry stem weight, dry weight per plant and dry leaf per stem ratio, days to flowering initiation, days to 50 per cent flowering, days to maturity initiation and days to total maturity, number of pod clusters/plant, number of pods per plant, pod length, seeds per pod, 100 seed weight, seed weight per plant and number of seeds per plant. Clustering pattern of the germplasm as a whole was analyzed based on average data of two years. Pooling of the data was done by taking out the average value of the trait recorded for the year 2004-05 and 2005-06. Non Heirarchical Euclidean Cluster analysis, performed on the pooled data, formed 12 clusters for 20 trait variables. Table 1 shows morphological character's mean and standard deviation for different clusters of the data pooled for the years 2004-05 and 2005-06. The morphological data of twenty nine forage and yield traits for years 2004-05, 2005-06 and pooled average of both years was analyzed, using statistical package software, SPAR -1. Clustering of 172 germplasm lines was done based on morphological attributes. A study of genetic variability, and frequency distribution of forage and grain yield, yield attributing characters were also performed for selection.

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Table 1. Morphological character's mean and standard deviation for different clusters of pooled data for the years 2004-05 and 2005-06

Cluster No.	Days to 50 per cent flower	Days to total flower	Plant height	No. of nodes	No. of primary branch	No. of secondary branch	Stem girth	Leaves/ plant	Leaf length	Leaf width	Leaf weight/ plant	Stem weight/ plant	Dry stem weight/ plant	Dry weight/ plant	Days to total maturity	No. of pod cluster/ plant	No. of pods/ plant	Pod length	No. of seeds/ pod	No. of seeds/ plant
I	49.62 ±6.53	66.78± 6.30	163.78± 20.06	20.29± 3.11	5.24± 0.87	3.82± 1.29	1.14± 0.14	67.15± 11.72	12.86± 0.99	8.67± 1.30	325.11± 59.27	149.51± 28.88	15.65± 3.57	79.42± 10.01	136.07± 4.32	5.74± 2.47	14.99± 6.10	12.47± 1.82	11.57± 2.15	175.46± 74.97
II	59.98 ±9.96	76.10± 10.48	158.92± 30.51	22.28± 2.76	6.62± 1.28	7.87± 3.02	1.32± 0.16	93.89± 23.25	11.54± 1.82	7.48± 1.06	446.90± 104.28	221.25± 57.85	16.15± 4.18	86.90± 9.83	131.14± 7.91	4.76± 2.52	12.35± 7.19	12.99± 2.19	11.71± 2.69	139.72± 77.79
III	46.78± 4.71	63.22± 7.56	151.45± 25.34	19.28± 1.81	5.96± 1.17	4.00± 1.57	1.24± 0.14	69.20± 19.41	11.81± 1.69	7.32± 1.23	365.64± 71.19	175.11± 43.10	15.19± 1.79	76.22± 8.55	133.28± 5.60	6.85± 3.03	19.35± 8.10	15.45± 1.96	16.11± 1.48	07.83± 120.83
IV	47.00± 0.00	84.00± 0.00	205.72± 0.00	27.98± 0.00	8.58± 0.00	2.32± 0.00	1.36± 0.00	185.29± 0.00	14.25± 0.00	8.00± 0.00	503.33± 0.00	277.28± 0.00	16.72± 0.00	116.00± 0.00	135.00± 0.00	12.22± 0.00	28.31± 0.00	18.98± 0.00	20.82± 0.00	90.98± 0.00
V	52.10± 7.42	69.76± 8.33	150.42± 21.32	19.45± 2.78	4.98± 0.99	3.63± 1.69	1.05± 0.14	61.29± 14.80	9.36± 0.77	5.82± 0.70	286.83± 44.46	130.10± 19.21	12.12± 3.54	81.35± 12.15	136.62± 6.40	5.26± 1.75	14.06± 6.10	12.76± 1.85	12.32± 2.31	173.23± 81.91
VI	68.84± 10.47	93.29± 6.08	149.70± 24.33	21.25± 2.48	5.60± 0.80	4.88± 1.92	1.26± 0.16	91.46± 29.88	9.61± 2.19	5.97± 1.38	386.53± 85.17	211.45± 52.65	14.65± 2.22	109.58± 11.94	138.87± 6.22	5.25± 2.62	11.85± 5.72	14.03± 1.70	13.52± 2.20	159.97± 82.28
VII	56.19± 10.73	71.75± 11.55	188.60± 25.06	17.72± 2.82	4.23± 0.89	2.93± 1.75	0.89± 0.10	39.87± 11.71	9.77± 1.93	6.19± 1.08	206.35± 79.23	104.44± 23.40	17.51± 1.64	82.62± 14.83	135.75± 7.69	6.11± 2.10	12.81± 5.52	18.70± 4.18	17.60± 3.10	226.95± 100.67
VIII	48.60± 9.98	82.65± 13.95	148.20± 13.66	20.49± 2.07	5.49± 0.99	2.62± 0.71	1.29± 0.17	70.62± 22.53	11.95± 1.19	7.92± 0.83	382.48± 52.92	176.99± 39.50	16.02± 1.97	100.40± 14.92	138.30± 5.10	15.39± 3.99	35.89± 4.83	16.33± 1.99	14.63± 2.16	524.57± 107.08
IX	49.35± 4.53	66.05± 7.29	172.23± 27.65	19.52± 3.34	4.07± 0.73	2.60± 0.83	1.05± 0.13	50.93± 18.27	11.03± 1.55	7.25± 0.89	237.17± 72.00	115.36± 27.67	11.84± 2.46	78.05± 7.73	120.91± 6.01	8.45± 3.38	23.07± 9.12	12.31± 2.25	11.51± 1.92	269.60± 122.77
X	70.50± 9.19	90.00± 9.19	179.82± 21.59	22.83± 0.74	6.16± 0.37	11.67± 1.53	1.69± 0.28	173.98± 38.29	9.57± 1.53	5.94± 1.83	859.33± 119.08	580.07± 64.26	13.62± 0.28	104.00± 19.80	138.50± 7.78	5.86± 5.52	9.19± 4.36	15.08± 3.32	14.16± 4.99	141.52± 107.08
XI	52.38± 6.18	66.62± 4.33	154.04± 24.38	21.30± 3.17	5.39± 1.30	2.91± 1.06	1.14± 0.11	71.42± 18.04	10.58± 1.00	6.72± 0.82	331.33± 54.19	150.23± 25.44	15.46± 3.19	78.62± 6.25	135.85± 6.95	21.32± 5.59	44.70± 5.38	14.87± 2.92	14.06± 2.82	616.21± 84.97
XII	51.07± 7.11	73.36± 11.39	195.50± 13.77	25.00± 2.67	5.20± 1.04	4.02± 1.33	1.34± 0.23	78.56± 8.97	11.90± 1.71	7.26± 0.86	519.43± 97.66	246.61± 53.58	14.77± 3.26	80.71± 12.34	134.00± 7.66	12.84± 3.66	31.44± 5.50	16.79± 2.76	15.24± 1.93	484.92± 82.65

Results and Discussion

On averaging data of both years, wide range of variation was observed for the various characters recorded. Twelve genotypes were erect type, 53 were semi erect, six were bushy, 27 were viny and 74 genotypes were spreading. The earliest flowering accessions were EC240564 and EC244979 (38 days) and most late flowering genotype was IL-181 in 88 days. Tallest genotypes were, HY-10P-10-2-4 (234.9 cm) followed by IL-99-171 (231.7 cm) and Local-1 (231.2 cm). Shortest were, IL-168 (105.9 cm) followed by NP-3-10 (113.0 cm) and HY 10P- 52-7 (115.3 cm). Accessions having more number of leaves per plant were IL-1177 (201); IL-1057 (185); and IL-1050-3 (158). Higher dry weight per plant was obtained for IL-1177 (625.51 g); IL-3171 (543.63 g); and IL-449 (345.94 g). Genotypes that showed higher dry leaf/stem ratio were [IL-160-A (1.02); IL-99-98-1 (0.97); and (IL-792 (0.94). Genotypes that had higher 100 seed weight were IL-181 (25.2 g); IL-4216 (22.6 g); and IL-156 (22.5 g). Genotypes that showed early maturity initiation in days after sowing were NP-3-10 (60 days); EC240782 (61 days); and EC240887 (62). Genotypes that took lesser number of days for total maturity of pod were EC244979 and IL 99-72 (113 days); EC240884 and IL 99-65 (115 days). The higher biomass was obtained for IL-1177 (943.5 g); IL-3171 (775.1 g); and IL-966-B (663.7 g). Higher leaf/stem ratios were for HY6P52-3 (1.04); IL-893 (1.01); and IL-99-171 (0.95). Genotypes that showed higher number of pods per plant were IL-3168A (53.2); IL-156 (51.3); and IL-2000-180 (50.5). Genotypes that had higher pod length were Local 1 (24.6 cm); IL-2000-182 (24.4 cm); and NP 3-7 (21.8 cm). Genotypes that showed higher number of seeds per pod were Local-2 (22.2); Local-1 (21.1); and IL-1057 (20.8).

The frequency distribution pattern of some morphological traits for the years 2004 and 2005 pooled data, varied from almost symmetrical to asymmetrical types and was in general of unimodal type.

Clustering pattern of pooled data over the years 2004 and 2005, showed 12 clusters for 20 variables as shown in Tables 1 and 2. Cluster V was the biggest with 26 lines and cluster IV was the smallest with only 1 member. The earliest flowering lines were grouped in cluster III. Cluster IV had one genotype with maximum values for plant height, number of nodes, number of primary branches, leaves/plant, leaf length, dry weight/plant, pod length and number of seeds/pod. Cluster X had higher fodder yielding lines with maximum value for number of secondary branches, leaf weight/plant, stem weight/plant and days to 50% flowering. Cluster VI had genotypes with maximum days to total flower and days to total maturity. Cluster XI had genotypes with highest number of pod clusters /plant, number of pods/plant, number of seeds/plant. Genotypes of Cluster VII showed maximum value for dry stem weight/plant. Genotypes of Cluster I showed maximum value for leaf width.

The maximum distance between cluster centroids was between cluster VII and X, *i.e.,* 11.781 followed by between clusters IX and X i.e. 11.589 and 11.054 between cluster X and XI (Table 2). Maximum average distance of cluster members from cluster centroids was 3.711 of cluster II.

Similarly, Henry and Mathur (2003) studied varietal divergence in cowpea where twenty three varieties of cowpea of different centers were evaluated under rain-fed conditions during monsoon season of 1997 and 1998. In their study, Wards method of hierarchical cluster analysis was applied to group the varieties. The quantum of rainfall received during the cropping season of 1997 and 1998 varied considerably. Twenty three cowpea varieties were classified into 4 clusters in 1997 and into 3 clusters in

Table 2. Distance between centroids of twelve clusters of the pooled data of years 2004-05 and 2005-06

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	0.000											
II	3.390	0.000										
III	2.638	3.602	0.000									
IV	8.384	7.501	7.423	0.000								
V	3.097	4.225	3.203	9.342	0.000							
VI	4.577	3.310	4.462	7.742	3.829	0.000						
VII	4.723	6.105	4.104	9.324	3.933	5.386	0.000					
VIII	4.296	5.004	3.434	6.605	4.921	4.716	5.411	0.000				
IX	3.216	5.132	3.753	9.565	2.949	5.525	4.496	4.968	0.000			
X	10.311	7.642	9.741	9.042	10.460	7.991	11.781	10.009	11.589	0.000		
XI	5.074	5.955	4.128	7.740	5.029	6.002	5.681	2.826	4.746	11.054	0.000	
XII	4.650	4.500	3.690	5.865	5.383	5.144	5.827	3.332	5.269	8.514	3.854	0.000

Table 3. Cowpea genotypes identified as potential parents for hybridization

Traits	Donors	Source
High biomass/plant	IL-1177; IL-3171 and IL-966-B	IGFRI Jhansi
High fresh leaf/stem ratio	HY6P52-3; IL-893 and IL-99-171	IGFRI Jhansi
Dry matter yield/plant	IL-1177; IL-3171 and IL-449	IGFRI Jhansi
Early flowering	EC240564 and EC244979 (38 DAS)	NBPGR New Delhi
High seed test weight	IL-181; IL-4216 and IL-156	IGFRI Jhansi
High number of pods /plant	IL-90; IL 3117 and EC240809	IGFRI Jhansi and NBPGR New Delhi
Long pod	Local 1; IL-2000-182 and NP 3-7	ICAR Research complex Barapani and IGFRI Jhansi
High number of seeds/pod	Local 2; Local-1 and IL-1057	ICAR Research complex Barapani and IGFRI Jhansi
High pod clusters/plant	IL-178-4, IL-622, IL-362	IGFRI Jhansi

1998. The maximum inter cluster distance was between cluster I and IV in 1997 and cluster I and III in 1998. The varieties falling in cluster I in both the environments were early in maturity and some were high yielding in stress environment of 1998. The high yielding varieties with earliness in maturity could be crossed with bold seeded varieties with medium late maturity of cluster IV in 1997 and cluster III in 1998 to get high yielding, early maturing and bold seeded varieties suitable for arid region / rainfed areas.

On the basis of clustering in the present study identification of donor sources in respect of forage was done, *i.e.,* for higher biomass/plant, IL-1177 (943.5 g); IL-3171 (775.1 g); and IL-966-B (663.7 g), higher fresh leaf/stem ratios, HY6P52-3 (1.04); IL-893 (1.01); and IL-99-171 (0.95), dry matter yield/plant, IL-1177 (625.51 g); IL-3171 (543.63 g); and IL-449 (345.94 g), earliest flowering, EC240564 and EC244979(38 days) lines were identified (Table 3).

In respect of grain yield identified donor sources were (Table 3), heaviest seed bearing lines, IL-181 (25.2 g); IL-4216 (22.6 g); and IL-156 (22.5 g), The lines with higher number of pod clusters/plant, IL-178-4, IL-622, IL-362, with a mean value of 15 pod clusters/plant. The maximum pod bearing lines IL-90, EC240809, IL-3117) with a mean value of 45 pods per plant, longest pod bearing lines, Local 1 (24.6 cm); IL 2000-182 (24.4 cm); and NP 3-7 (21.8 cm), highest number of seeds per pod bearing lines, Local-2 (22); Local-1 and IL 1057 (21).

Similarily, Misra *et al.,* (2003) evaluated a set of 740 germplasm accessions of cowpea including both indigenous and exotic origin at IARI during *kharif* 2001. A wide range of variation was observed in almost all the characters under study. Many promising genotypes have been identified which can serve as potential donors for major economic traits.

Thus the characterization of germplasm in to various clusters in the present study resulted in the useful information. Cluster X can be identified as having competent traits that can be utilized for improving fodder yield and cluster number XI has lines with potential for seed yield. Thus cluster analysis helped in drawing representative sample from various segments of genetic stock for further utilization in never ending process of genetic manipulation as earlier reported by (Kohli *et al.*, 2000). Earlier, Shwe *et al.,* (1972) and Kumari *et al.,* (2000) observed better recombinants by crossing parents from clusters of high and low means for the characters under consideration. Therefore, it can be suggested that to have a better heterotic effect the genotypes from diverse clusters (identified sources) could be used for hybridization which may result in desired recombinants.

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