Plant Archives Vol. 18, Special Issue (ICAAAS-2018), 2018 pp. 227-231 **ISSN 0972-5210**

MORPHOLOGICAL BASED GENETIC DIVERSITY STUDIES OF COWPEA

Moolendra[1], Triveni Sharma[2], Anjali Malik[3] and Neeraj Tandan[1]

[1]Department of Botany, Shri Venkateshwara University, Gajraula (UP), India
[2]School of Biosciences, Suresh Gyan Vihar University, Jaipur (Rajasthan), India
[3]Department of Microbiology, C.C.S. University, Meerut (UP), India

Abstract

16 cowpea genotypes were used in this investigation. Genetic parameters like range, mean, standard error, variance and standard deviation were calculated among 8 morphological characters of cowpea. Among 16 cowpea genotypes plant height, leaf length, leaf width, pod length, number of pods/plant, number of seeds/pod, days to plant maturity and seed yield/plant ranged from 32.0-85.31 cm, 6.86-12.4 cm, 3.8-7.7 cm, 12.46-19.2 cm, 3.0-30.23, 5.0-13.3, 80-91 days and 1.9-36.5 gm, respectively. Highest variability was found in plant height. Genetic similarity coefficient for 16 cowpea genotypes based on morphological characters ranged from 0.017-0.235. Highest similarity coefficient value occured between IC-559388 *vs* EC-472283 was 23.5% and lowest similarity coefficient value occured between IC-559390 vs EC-528429 was 1.7%. Clustering classified the 16 cowpea genotypes into 6 different clusters *i.e.* cluster A, B, C, D, E and F. Hence, these characters could be considered and exploited for selection purpose. This collection of cowpea accessions provides an opportunity for further exploitation of the cowpea accessions for improvement of this crop.

Key words: Cowpea, *Vigna unguiculata* L., genetic variation, morphological characters, dendrogram.

Introduction

Cowpea (*Vigna unguiculata* L.) is a multi-use crop, providing food for human and feed for livestock and it is a cash generating commodity for farmers, small and medium-size entrepreneurs. Fruits of cowpea are consumed at all stages of growth (e.g., green pods, fresh or dry seeds) and young leaves are often used for soups and stews (Quaye *et al.,* 2009). In addition to its value as human food, cowpea hay is an important source of animal fodder (Tarawali *et al.,* 2002). Cowpea is a food legume of significant economic importance worldwide with high protein and mineral content. It plays a critical role in the lives of millions of people in Africa and other parts of the developing world where it is a major source of dietary protein. Cowpea fixes nitrogen symbiotically with root *rhizobacteria* and helps to restore soil fertility (Carsky *et al.*, 2002; Sanginga *et al.*, 2003).

The characterization will help in the identification of varieties and their future utilization for varietal advancement using conventional techniques *i.e.* selection of new genotypes for direct production and hybridization. Genetic variability is a vital component for every breeding programme desired to develop the characteristics of crop plant. According to diverse studies, various morphological characters are mainly used as markers including number of pod per plants, number of seeds per pod and seed yield per plant which affect on potential yield of cowpea (Sardana *et al.*, 2001; Mishra *et al.*, 2002; Carnide *et al.*, 2007; Siise and Massawe, 2013). Morphological markers are highly dependent on the environment for expression, in fact, several limitations reduce their ability to estimate genetic diversity in plants. Knowledge of genetic diversity in available genotypes is very useful for plant breeders. The objective of this study was to evaluate the diversity and relationships of cowpea accessions based on morphological characters.

Material and Methods

Seeds of 16 cowpea genotypes were obtained from Scientific and Applied Research Centre (SARC), Meerut (UP) (table-1). The genetic material was grown in plot for germination and growth at Scientific and Applied

Research Centre, Meerut with standard agronomical practices and observations were taken for two seasons *viz.*, 2012-13 and 2013-14. Morphological data of 10 plants for each genotype were recorded for the different characters are as follow-

1. **Plant height (cm):** Plant height was measured in centimetres from the ground level to the tip of the plant on average of 10 randomly selected plants recorded at the time of harvesting.
2. **Leaf Length (cm):** Mean length of 10 longest leaf from 10 randomly selected plants.
3. **Leaf Width (cm):** Mean width of 10 leaf measured on the broadest part of 10 randomly selected plants.
4. **Pod Length (cm):** Mean of 10 longest mature pods from 10 randomly selected plants at the time of harvesting.
5. **Number of pods/plant:** Mean number of mature pods from 10 randomly selected plants at the time of harvesting.
6. **Number of seeds/pod:** Mean number of seeds of the 10 longest mature pods from 10 randomly selected plants at the time of harvesting.
7. **Days to Plant Maturity:** Total number of days of 10 randomly selected plants were counted from sowing to harvesting time.
8. **Seed yield/plant:** Mean seed weight in grams from 10 randomly selected plants was recorded at the time of harvesting.

Two season (2012-13 and 2013-14) pooled morphological data for plant height (cm), leaf length (cm), leaf width (cm), pod length (cm), number of pods/plant, number of seeds/pod, days to plant maturity and seed yield/plant (gm) were analyzed using simple statistics to calculate the genetic parameters like Range, Mean, Standard error, Variance and Standard deviation for 8 morphological traits of 16 cowpea genotypes using statistical package PAST version 2.03 (Hammer *et al.*, 2001). The pooled data for morphological traits were used to construct a dendrogram showing the relations among 16 cowpea genotypes using computer software NTSYS-pc (Numerical Taxonomy and Multivariate Analysis System) version 2.0. Finally, the data were subjected to cluster analysis using the NTSYS-pc version 2.2 (Rohlf, 2000).

Results and Discussion

Morphological character and their mean performance

Genetic variation in 8 morphological characters showed a high variability in 16 cowpea genotypes (table-2). Plant height of 16 cowpea genotypes ranged from 32.00 cm (IC-559388) to 85.31 cm (EC-528410) and the mean was 64.32 cm. Minimum and maximum leaf length was recorded in IC-559399 (6.86 cm) and IC-402166 (12.4 cm), respectively and mean was 9.79 cm. Minimum and maximum leaf width was recorded in IC-559388 (3.8 cm) and IC-402166 (7.7 cm), respectively and mean was 6.33 cm. Pod length ranged from 12.46 cm (EC-472250) to 19.20 cm (EC-390249) and the mean was 15.71 cm. Number of pods per plant of 16 cowpea genotypes ranged from 3.00 (IC-559388) to 30.23 (EC-472283) and the mean was 13.71. Number of seeds per pod varied from 5.0 (IC-559388) to 13.3 (IC-249141) and the mean was 10.8. Days to plant maturity ranged from 80 days (IC-559388) to 91 days (IC-402154 and EC-390249) and the mean was 85.5 days. The highest seed yield per plant of 36.5 gm was obtained in EC-472283 and the lowest was 1.9 gm in IC-559388. The mean of seed yield per plant was 15.62 gm. Among 16 cowpea genotypes, EC-472283 and EC-390249 showed maximum values for number of pods per plant, seed yield per plant and pod length, days to plant maturity, respectively. Similar results reported by Kumar *et al.*, 2013 & 2014 and Sharma *et al.*, 2014.

The range of variability was maximum for plant height (32.0-85.31), followed by seed yield per plant (1.9-36.5), number of pods per plant (3.0-30.23), days to plant maturity (80-91), number of seeds per pod (5.0-13.3), pod length (12.46-19.2), leaf length (6.86-12.4) and leaf width (3.8-7.7). The highest variance recorded for plant height (198.76), followed by seed yield per plant (95.22), number of pods per plant (47.11), days to plant maturity (10.94), whereas the lowest variance were estimated for leaf width (1.29), followed by leaf length (2.04), pod length (4.2), number of seeds per pod (5.15). Maximum variance was observed for most of the characters indicating more involvement of genetic component for the total dissimilarity. Variance revealed that presence of significant amount of genetic variability for yield and its components studied in all the environments. Therefore,

Table 1: List of 16 cowpea genotypes

S. No.	Accessions	S. No.	Accessions
1.	IC-9883	9.	IC-402166
2.	IC-4506	10.	IC-402154
3.	IC-249141	11.	EC-472283
4.	IC-202786	12.	IC-559390
5.	IC-559399	13.	EC-528410
6.	EC-472250	14.	EC-528429
7.	IC-398065	15.	EC-390249
8.	IC-559388	16.	IC-202826

Table 2: Range, mean, standard error, variance and standard deviation for 8 morphological characters in 16 cowpea genotypes.

Traits	Range		Mean	Std. error	Variance	Stand. dev
	Minimum	Maximum				
Plant height (cm)	32	85.31	64.32	3.52	198.76	14.1
Leaf length (cm)	6.86	12.4	9.79	0.36	2.04	1.43
Leaf width (cm)	3.8	7.7	6.33	0.28	1.29	1.13
Pod length (cm)	12.46	19.2	15.71	0.51	4.2	2.05
Number of pods/plant	3	30.23	13.71	1.72	47.11	6.86
Number of seeds/pod	5	13.3	10.8	0.57	5.15	2.27
Days to plant maturity	80	91	85.5	0.83	10.94	3.31
Seed yield/plant	1.9	36.5	15.62	2.44	95.22	9.76

Table 3: Genetic similarity coefficient of 16 cowpea genotypes derived from morphological characters.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	0.000															
2	0.070	0.000														
3	0.071	0.083	0.000													
4	0.047	0.088	0.058	0.000												
5	0.102	0.058	0.136	0.130	0.000											
6	0.088	0.076	0.136	0.120	0.048	0.000										
7	0.038	0.046	0.069	0.048	0.085	0.084	0.000									
8	0.150	0.122	0.193	0.188	0.073	0.077	0.145	0.000								
9	0.045	0.087	0.105	0.075	0.099	0.068	0.065	0.136	0.000							
10	0.048	0.060	0.057	0.037	0.103	0.098	0.034	0.165	0.070	0.000						
11	0.111	0.116	0.066	0.073	0.170	0.175	0.095	0.235	0.145	0.083	0.000					
12	0.046	0.055	0.099	0.077	0.068	0.055	0.044	0.115	0.043	0.062	0.134	0.000				
13	0.054	0.112	0.075	0.032	0.151	0.136	0.071	0.203	0.081	0.067	0.089	0.092	0.000			
14	0.048	0.052	0.101	0.084	0.058	0.044	0.046	0.105	0.046	0.065	0.140	0.017	0.099	0.000		
15	0.055	0.101	0.112	0.076	0.113	0.081	0.075	0.149	0.027	0.072	0.147	0.056	0.081	0.061	0.000	
16	0.039	0.042	0.068	0.052	0.082	0.083	0.073	0.142	0.066	0.036	0.097	0.042	0.074	0.044	0.077	0.000

Table 4: Distribution of 16 cowpea genotypes into different clusters.

S. No.	Cluster No.	No. of cowpea genotypes	Genotypes
1.	A	04	IC-9883, IC-398065, IC-202826, IC-402154
2.	B	03	IC-559390, EC-528429, IC-4506
3.	C	02	IC-402166, EC-390249
4.	D	02	IC-202786, EC-528410
5.	E	02	IC-249141, EC-472283
6.	F	03	IC-559399, EC-472250, IC-559388

these traits (table-2) could be considered and exploited for selection purpose. Similar results obtained by Khan *et al.,* 2010; Naik, 2012; Doumbia *et al.,* 2013; Ogbuagu and Ndem, 2015 and Dev *et al.*, 2017.

Cluster analysis

The genetic similarity coefficients for the 16 cowpea genotypes based on morphological traits ranged from 0.017 to 0.235 (table-3). The highest similarity coefficient value occurred between IC-559388 *vs* EC-472283 was 23.5% and the lowest similarity coefficient value occurred between IC-559390 *vs* EC-528429 was 1.7%. A dendrogram was constructed by clustering of 16 cowpea genotypes are shown in fig. 1. The resulting dendrogram classified the 16 cowpea genotypes into 6 distinct clusters *i.e.* cluster A, B, C, D, E and F comprising of 4, 3, 2, 2, 2 and 3 cowpea genotypes, respectively (table-4).

Cluster A consisted of 4 genotypes *viz*; IC-9883, IC-398065, IC-202826 and IC-402154, in which the maximum similarity coefficient occured between IC-398065 *vs* IC-202826 with a value of 0.073 and the minimum similarity coefficient occured between IC-398065 *vs* IC-402154 with a value of 0.034. Cluster B consisted of 3 genotypes *viz*; IC-559390, EC-528429 and IC-4506, in which the maximum similarity coefficient occured between IC-4506 *vs* IC-559390 with a value of 0.055 and the minimum similarity coefficient occured

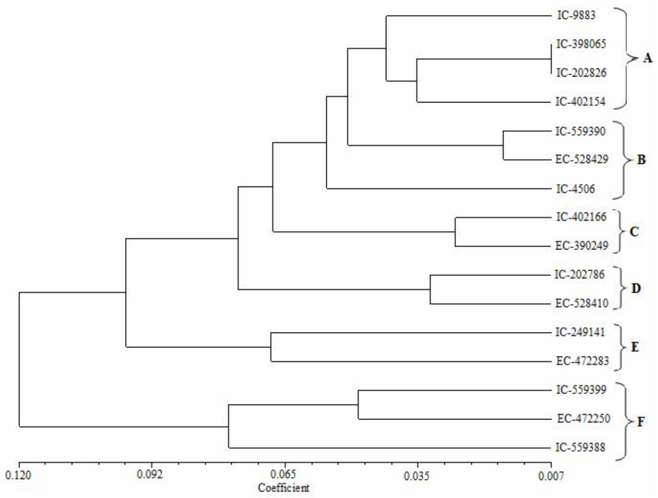

Fig. 1: UPGMA based cluster analysis of 16 cowpea using morphological characters.

between IC-559390 *vs* EC-528429 with a value of 0.017. Only one cowpea genotype (IC-4506) was isolated at the end of cluster B. Cluster C consisted of only two genotypes namely IC-402166 and EC-390249, which showed the similarity coefficient value of 0.027. Cluster D consisted of only two genotypes namely IC-202786 and EC-528410, which showed the similarity coefficient value of 0.032. Cluster E consisted of only two genotypes namely IC-249141 and EC-472283, which showed the similarity coefficient value of 0.066. Cluster F consisted of 3 genotypes *viz*; IC-559399, EC-472250 and IC-559388. In this cluster, the maximum similarity coefficient occurred between EC-472250 *vs* IC-559388 with a value of 0.077 and the minimum dissimilarity coefficient occurred between IC-559399 *vs* EC-472250 with a value of 0.048.

Cluster analysis is extremely helpful in revealing complex relations among populations of different origins in a more simplified mode. It is also effective in representing genotypes with useful characters belong to diverse clusters for hybridization. Clustering indicates the extent of genetic diversity that is of practical use in plant breeding (Sultana *et al.*, 2006). The variation observed among 16 cowpea genotypes suggests that morphological characters can reveal diversity existing among cowpea genotypes. Similar results have also been reported by Upadhyaya *et al.*, 2010; Sharma *et al.*, 2013; Molosiwa *et al.*, 2016; Mafakheri *et al.*, 2017. Current study recommended that crosses are made in breeding programs between IC-559390 and EC-528429. This evaluation could support breeders to choose and identify genotypes with desirable character for addition in cowpea breeding programs.

References

Carnide, V., I. Pocas, S. Martins, amd O. Pinto-Carnide (2007). Morphological and genetic variability in Portuguese populations of cowpea (*Vigna unguiculata* L.). *6th European Conference grain legumes Lisbon Book of Abstracts,* **128:** 12–16.

Carsky, R.J., B. Vanlauwe and O. Lyasse (2002). Cowpea rotation as a resource management technology for cereal-based systems in the savannas of West Africa. In: C.A. Fatokun *et al.* (ed.) Challenges and Opportunities for Enhancing Sustainable Cowpea Production. Proc. of the World Cowpea Conference III held at International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. 4-8 Sept. 2000. IITA, Ibadan, Nigeria., Ibadan, Nigeria, **pp.** 252-266.

Dev, A., P. Verma and B.L. Kumhar (2017). Genetic Character Variability Studies in Desi Chickpea (*Cicer arietinum* L.) Genotypes. *Int.J.Curr.Microbiol.App.Sci.*, **6(4):** 20-25.

Doumbia, I.Z., A. Richard and Y.A. James (2013). Comparative Study of Cowpea Germplasms Diversity from Ghana and Mali using Morphological Characteristics. *J. Plant Breed. Genet.*, **1(3):** 139-147.

Hammer, Ř, D.A.T. Harper and P.D. Ryan (2001). PAST: Paleontological statistics software package for education and data analysis. *Palaeontologia Electronica*, **4(1):** 9pp. http://palaeo-electronica.org/2001_1/past/issue1_01.htm.

Kumar, Ashwani, R.S. Yadav and Rajendra Kumar (2014). Assessment of variability and relationship among some quantitative traits in elite accessions of chickpea (*Cicer arietinum* L.). *Prog. Agric.*, **14(1):** 63-68.

Kumar, Ashwani, R.S. Yadav and Rajendra Kumar, (2013). Estimation of genetic parameters and correlation between morphological traits in selected chickpea (*Cicer arietinum* L.) Accessions. *Plant Archives,* **13(2):** 719-723.

Lambot C. (2002). Industrial potential of cowpea. In: C.A. Fatokun *et al.* (ed.) Challenges and opportunities for enhancing sustainable cowpea production. Proc. of the World Cowpea Conference III held at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. 4-8 September 2000. IITA, Ibadan, Nigeria. **pp.** 367-375.

Mishra, S.K., B.B. Singh, D. Chand and K.N. Meene (2002). Diversity for economic traits in cowpea. In A. Henry, D. Kumar and N.B. Singh (Eds.), Recent advances in arid legumes research for food, nutrition security and promotion of trade (**pp.** 15–16). Hissar: CCS Haryana Agricultural University.

Molosiwa, O.O., G. Chiyapo, M. Joshuah and M.C. Stephen (2016). Phenotypic variation in cowpea (*Vigna unguiculata* [L.] Walp.) germplasm collection from Botswana. *Int. J. Biodivers. Conserv.*, **8(7):** 153-163.

Naik, A. (2012). Characterization of fenugreek (*Trigonella foenumgraecum* L.) genotypes through morphological characters. *International Journal of Agriculture, Environment & Biotechnology*, **5(4):** 445-449.

Ogbuagu, U.U. and E.E. Ndem (2015). Evaluation and Identification of Genetic Variation Pattern in Cowpea [*Vigna unguiculata* (L.) Walp] Accessions Using Multivariate Analyses. *Journal of Basic & Applied Sciences,* **11:** 149-158.

Quaye, W., K. Adofo, Y.E. Madode and A.R. Abizari ((2009)). *Afr J Agric Res.*, **4:** 311-320.

Rohlf, F.J. (2000). NTSYS-pc Numerical Taxonomy and Multivariate Analysis System. Version 2.0. Exeter Software, Setauket, New York.

Sanginga, N., K.E. Dashiell, J. Diels, B. Vanlauwe, O. Lyasse, R.J. Carsky, S. Tarawali, B. Asafo-Adjei, A. Menkir, S. Schiz, B.B. Singh, D. Chikoye, D. Keatinge and R. Ortiz (2003). Sustainable resource management coupled to resilient germplasm to provide new intensive cereal-grainlegume-livestock systems in the dry savanna. *Agric. Ecosyst. Environ.*, **100:** 305-314.

Sardana, S., R.K. Mahajan, D. Kumar, M. Singh and G. D. Sharma (2001). Catalogue on cowpea (*Vigna unguiculata* L. Walp.) germplasm, (**pp.** 80). New Delhi: National Bureau of Plant Genetic Resources.

Sharma, Triveni, Ashwani Kumar, S.C. Dwivedi and R.P. Vyas (2013). Assessment of genetic diversity of maize inbred lines using morphological traits. *Plant Archives*, **13(1):** 477-480.

Sharma, Triveni, Ashwani Kumar, S.C. Dwivedi and R.P. Vyas (2014). Estimate of genetic factors and correlation analysis in maize (*Zea mays* L.). *Plant Archives*, **14(1):** 19-21.

Siise, A. and F.J. Massawe (2013). Microsatellites based marker molecular analysis of Ghanaian bambara groundnut (*Vigna subterranea* (L.) Verdc.) landraces alongside morphological characterization. *Genetic resources and crop evolution*, **60:** 777–787.

Sultana, T., A. Ghafoor and M. Ashraf (2006). Geographic pattern of diversity of cultivated lentil germplasm collected from Pakistan asassessed by protein assays. *Acta Biologica Cracoviensia, Series Botanica, Poland*, **48:** 77-84.

Tarawali, S.A., B.B. Singh, P.M. Kormawa and M. Tamo (2002). Challenges and Opportunities for Enhancing Sustainable Cowpea Production. *Intl. Inst. Tropical Agric., Ibadan, Nigeria*, **pp.** 22–40.

Upadhyaya, H.D., S. Sharma, B. Ramulu, R. Bhattacharjee, C.L.L. Gowda, V. G. Reddy and S. Singh (2010). Variation for qualitative and quantitative traits and identification of trait-specific sources in new sorghum germplasm. *Crop and Pasture Science*, **61:** 609-618.