J. Farm Sci., 35(1): (37-39) 2022

RESEARCH PAPER

Assessment of genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm

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(Received: January, 2022 ; Accepted: February, 2022)

Abstract: The present investigation was carried out to understand the extent of genetic diversity in sixty-two cowpea (*Vigna unguiculata* (L.) Walp) genotypes based on eleven quantitative traits. Mahalanobis's D^2 analysis showed the presence of wide genetic diversity among the 62 genotypes by the formation of 5 clusters irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Cluster I had the maximum number of genotypes (39) and cluster IV and V had only one genotype. Intra cluster distance analysis revealed that the minimum intra cluster distance was observed in the cluster IV and V. The inter-cluster distance (D) was found to be the maximum between the clusters III and IV and the same was minimum between clusters I and V. A wider genetic diversity was observed for the different traits studied among the genotypes as evidenced by the formation of five clusters. The results indicated that seed yield per plant (23.59 %) contributed maximum to the total divergence followed by peduncle length (17.29 %), 100 seed weight (15.97 %) and number of pods per plant (10.1 %). The present study identified diverse promising genotypes based on seed yield and agronomic traits such as IC-257449, GC-3, IC-438362, IC- 257428, KBC-9 and IC-390269 and these diverse genotypes could be utilized in breeding programme of cowpea to generate better transgressive segregants for yield and its attributes.

Key words: Cowpea germplasm, Genetic diversity, Phenotypic traits

Introducation

Cowpea is one of the most important legume crop grown in tropical and subtropical regions of the world. In India cowpea is grown as sole, mix-crop and intercrop systems. Cowpea is however, the only pulse suited to both arid and semi-arid regions and adapted better than any other pulses in high rainfall regions. It is a most versatile pulse crop because of its smothering nature, drought tolerant character, soil enrichment properties and multipurpose uses and it is mainly cultivated for seed, also as a vegetable, cover crop and fodder crop. Seeds are rich in quality protein (23.4%), digestible carbohydrate (60.3%) and sufficient amount of calcium (76mg/100g), iron(57mg/100g) and vitamins such as thiamine (0.92mg/100g), riboflavin (0.18mg/100g) and nicotinic acid (1.9mg/100g) (Chatterjee and Bhattacharya, 1986).The crop is gaining popularity in developing and under developed countries, especially in arid regions of the world due to its nutritional and health benefits. Like other legumes, cowpea fixes atmospheric nitrogen, and thus contributes to the available N levels in the soil. The cultivated cowpeas are known by the common names alsandi, black-eyed pea, southern pea, yard long bean, catjang and crowder pea.

The knowledge on the nature and extent of genetic variability present in any crop species plays an important role in designing a suitable breeding method. Genetic diversity is the foremost basic requirement for a successful breeding programme. (Panchata *et al.,* 2021).. Collection and evaluation of genotypes of any crop is a pre-requisite for crop improvement programme, which provides a greater scope for exploiting genetic diversity. A quantitative assessment of the genetic divergence among the collection of germplasm and their relative contribution of different traits towards the genetic divergence provide essential and effective information to breeder in hybridization programme and there by genetic improvement of yield. The necessity for finding out genetic divergence among the genotypes is essential because of two reasons *i.e.,* genetically diverse parents if included in the hybridization programme are likely to produce high heterotic effect and a wide spectrum of variability could be expected in the segregating generation of crosses involving distantly related parents.

Material and methods

Sixty two cowpea genotypes were used in the experiments were collected from different geographical parts of the country and the trial was conducted at ICAR-Indian Institute of Pulses Research, Regional Research Centre, University of Agricultural Sciences, Dharwad and it was laid out in RCBD experimental design with two replications. Individual genotypes were directly sown by dibbling two seeds per hill during *summer* 2021 in a row of 4-meter length with 10 cm of spacing between the plants and 45 cm between the rows. The recommended agronomic practices were adopted uniformly.

The observations were recorded on five randomly selected plants in each replication and the average was worked out and used for statistical analysis. The following quantitative characters were studied, days to 50% flowering, days to physiological maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, peduncle length (cm), pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). The genetic divergence was computed using Mahalanobis (1936) D^2statistics among all the genotypes. Based on genetic distance, all the genotypes were grouped in different clusters (Rao, 1952).

Table 1. Clustering pattern of cowpea genotypes based on D^2 analysis

Cluster	Number of genotypes	Name of the genotypes
I	39	IC-107179, IC-39947, KBC-2, IC-9715499-3, Coll no.NR/18-01, Coll no.NR/18-10, Coll no.NR/18-24, Coll no.NR/18-29, Coll no.NR/18-34, Coll no.NR/18-39, Coll no.NR/18-64, Coll no.NR/18-74, Coll no.NR/18-77, Coll no.NR/18-84, Coll no.NR/18-87, Coll no.NR/18-96, Coll no.NR/18-105, Coll no.NR/18-109 , Coll no.NR/18-112 , DC-15, DC-47-1, RC-101,,CH-46, KM-5, C-152, CRM-01, CRM-01, IC-20664, IT-38956, CO-2,CO-4, GP-37, IC-333208, IC-257428, EC- 724323, EC-724621, EC-724437, GP-1, IC-39922.
II	11	MP-2, RC-19, GP-40, V-578-1, GC-4, CO-7, Alsando, PL-3, GP-36, GC-5, PL-5.
III	10	GC-3, IC-438362, IC- 257428, IC-390269, KBC-9, Coll no.NR/18-44, Coll no.NR/18-51, Coll no.NR/18-25, IC-68768, IC-202784.
IV	1	Coll no.NR/18-44
V	1	IC-257449

Results and discussion

Genetic relationship existing among genotypes can be measured by similarity or dissimilarity of any number of quantitative characters assuming that the differences between characters of genotypes reflect the divergence of genotypes. The Mahalanobis D^2 analysis revealed that 62 genotypes were distributed into 5 clusters (Table 1). Cluster I was largest comprising of 39 genotypes followed by cluster II with 11 genotypes, cluster III had 10 genotypes, cluster IV and V are solitary in nature. The genotypes from different geographic regions falling into one cluster could be due to free exchange of genetic material from one place to another or due to the fact that unidirectional selection practiced in different places might have had a similar effect and therefore, varieties evolved under similar selection pressure might have clustered together irrespective of their geographic origin (Dwevedi and Lal, 2009; Walle *et al.,* 2019). Previous studies on D^2 statistic in various pulses crops also revealed the lack of parallelism between genetic divergence and geographic diversity (Walle *et al.,* 2019).

The inter and intra cluster D^2 values among five clusters are represented in Table 2. Inter cluster average D^2 values ranged from 102.18 to 450.82 units. The inter cluster distance analysis showed that the maximum divergence was observed between cluster III and cluster V (450.82) followed by cluster II and cluster III (358.5) indicating wide diversity among these genotypes. Hence, genotypes belongs to these clusters could be utilized as parents for hybridization programme which would result in high heterotic combinations for yield components. Minimum inter cluster distance was observed between cluster I and cluster IV indicated that most of the characters had similar values in these clusters. The highest intra-cluster distance was observed in cluster III followed by cluster II and lowest intra cluster distance was observed in cluster IV and cluster V, where in closely related genotypes were grouped into each cluster and indicates less divergence among them.

Table 2. Average intra (bold) and inter cluster distance (D^2) values of clusters in cowpea genotypes

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
1	66.82	175.93	155.6	102.18	185.57
2		92.56	358.5	161.27	175.76
3			113.47	251.68	450.82
4				0	116.73
5					0

* Diagonal values indicate intra cluster distances

* Above diagonal values indicate inter cluster distance

The data on the mean values of quantitative characters are presented in Table 3. The highest cluster mean value for days to 50 % flowering, days to physiological maturity, plant height, number of branches per plant, number of clusters per plant, peduncle length and pod length were in cluster V. For seed yield per plant, test weight, number of pods per plant the highest cluster mean value was in cluster II. For number of seeds per pod the highest cluster mean value was in cluster IV. Accordingly, cluster II and V had most promising genotypes in them. Similar results also reported previously in different pulses crops (Bamji *et al.*, 2020; Srinivas *et al.,* 2016: Walle *et al.,* 2019).

Among the quantitative characters studied, the most important character contributing to the divergence was seed yield per plant followed by peduncle length, test weight and number of pods per plant (Table.4). There is always difference in opinion in specifying the trait that is contributing high or low towards the genetic diversity. The contribution mainly depends upon the genotypes included in the study and the

Table 3. Cluster mean analysis for quantitative characters in cowpea genotypes

Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
I	57.12	83.79	26.98	3.52	3.13	4.08	9.18	14.3	10.44	12	13.29
II	57.86	84.82	24.06	3.45	4.58	12.54	13.7	12.83	11.73	17.87	19.1
III	57.65	83.8	24.9	3.13	3.52	6.26	9.58	9.85	10.05	9.92	11.82
IV	53	81	28.65	3.5	4	5.49	17	12.42	12.5	15.09	14.88
V	62.5	89.5	31.45	3.5	5.5	10.39	19.5	17.25	10.25	14.13	15.2

Table 4. Per cent contribution of each character towards genetic divergence in cowpea genotypes

Characters	Contribution (%)
Days to 50% flowering	8.14
Days to physiological maturity	5.18
Plant height (cm)	6.77
Number of branches per plant	0.48
Number of clusters per plant	1.00
Number of pods per plant	10.1
Peduncle length (cm)	17.29
Pod length (cm)	6.61
Number of Seeds per pod	5.87
Test weight(100 seeds in g)	15.97
Seed yield per plant (g)	23.59

environment influences over the character. Regarding the least contribution, number of branches per plant and number of clusters per plant contributed the least. The minimum contribution by this trait reveals that this trait was least affected in course of evolution. Similar reports were given by Nagalakshmi *et al.* (2010) for seed yield per plant contributed maximum followed by test weight and days to 50 % flowering, Srinivas *et al.* (2016) for number of seeds per pod contributed maximum followed by pod length, plant height and test weight and Purohit *et al.* (2020) for maximum contribution of test weight followed by number of seeds per pod while least contribution shown by pod length towards total divergence in cowpea.

Conclusion

Considering Mahalanobis D^2 diversity analysis and cluster mean performance, the genotypes identified as most diverse were IC-257449, GC-3, IC-438362, IC- 257428, IC-390269, KBC-9, Coll no.NR/18-44, Coll no.NR/18-51 which could be utilized in hybridization programme of cowpea to generate transgressive segregants.

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