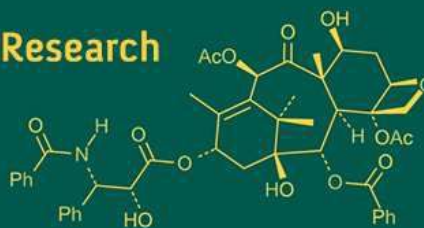


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Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]

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Abstract

Field experiment were conducted at College of Agriculture (Sri Karan Narendra Agriculture University, Jobner) Fatehpur-Shekhawati, Sikar of Eighteen diverse cowpea genotypes were evaluated at the experimental farm during the *kharif* season 2024. The experiment was conduct on randomized block design with three replications. Each genotype was sown in 4 m length with four rows per plot. Rows were spaced 30 cm apart and plants within rows at 10 cm. The presence of single-genotype clusters such as Clusters 4 (G2), 5 (G6), 6 (G10), 7 (G12), 8 (G15), and 9 (G18) reflects high genetic divergence. The highest inter-cluster distances were between Clusters: 8 and 9 (216.68), 3 and 4 (174.03), 4 and 8 (199.88). This variation suggests that crossing genotypes from these clusters may produce maximum heterosis and transgressive segregants. The findings provide valuable insights for selecting diverse parental lines in breeding programs aimed at yield improvement, stress tolerance and adaptability.

Keywords: Cowpea, diversity, legume, cluster and variation

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is a key legume crop in tropical and warm subtropical farming systems. It is a self-pollinating species ($2n = 22$ chromosomes) in the family Fabaceae. Cultivars are typically classified by their primary use: grain, fodder or vegetable. It is commonly known as yard-long bean or snake bean. It is grown for their long green pods harvested before seed maturation. Cowpea is highly drought-hardy, with broad, drooping leaves that create shade, conserving soil moisture and reducing water loss. It is native to Africa and is an important legume crop in eastern, southern, central and western Africa. According to (Vavilov, 1951) ^[1], Africa and India are the centre of origin/native of cowpea. The secondary centre of origin of cowpea is considered China.

Genetic diversity is particularly essential for agricultural productivity and growth (Begna and Begna 2021) ^[3]. Despite its importance, genetic diversity within cowpea remains relatively narrow, highlighting the need for comprehensive studies to elucidate the genetic variation and potential for improvement (Sindhu *et al.*, 2019) ^[4]. This paper aims to investigate the genetic diversity and characterize cowpea accessions to facilitate breeding programs for enhanced crop performance and adaptation.

Genetic diversity refers to the diversity within species and is the basis of the genetic improvement of crops. Genetic diversity serves as a way for crops to adapt to altering environments. Lately, there have been attempts to save and study this variety to progress breeding programs, but more research is still needed (Swarup *et al.*, 2021) ^[5]. The study on genetic diversity in cowpeas is essential for accessing and exploiting genetic variation within the species, thereby justifying introgression and ideotype-breeding programs to enhance crop performance (Tavakol *et al.*, 2017) ^[6]. The first step of any breeding program is to identify crop plants that exhibit exploitable variation for the traits of interest (Zamir, 2001) ^[7]. A quantitative assessment of the genetic divergence among germplasm and the contribution of different traits to genetic divergence provides an essential and effective contribution of different traits to genetic divergence provide essential and effective information to a breeder in his hybridization program and thereby genetic improvement of yield.

The primary objectives of this study are to determine the genetic diversity among eighteen accessions of cowpea under growing conditions and to identify the characters contributing to genetic variation among these accessions.

Materials and Methods

Experimental Site and Details

The experiment was conducted during *kharif*, 2024 at Research farm of College of Agriculture, (Sri Karan Narendra Agriculture University, Jobner) Fatehpur-Shekhawati, Sikar (Rajasthan). It is situated between 27° 57' 04.01" N to 27° 55' 43.59" N latitude and 74° 58' 47.47" E

to 74° 59' 45.97" E longitude with an altitude of 321 to 330 meters above mean sea level. This experiment was conducted on rainfed condition. The experiment was conducted fifteen genotypes with three checks in randomized block design of cowpea crop for estimate genetic variability and correlation analysis. The observation was recorded five randomly selected plant for plant height, number of branches per plant, number of pods per cluster, number of pod per plant, pod length, number of seeds per pod, 100-seed weight and grain yield per plant except days to 50% flowering and days to maturity.

List of genotypes and checks used in experiment

Genotypes					Checks
G1.CPD-229	G4.CPD-273	G7.CPD-307	G10.IC-0650821	G13. CF4-1-4	G16. RC-19(C)
G2.CPD-260	G5.CPD-302	G8.CPD-317	G11. CF1-1-1	G14. CF9-1-9	G17. RC-101(C)
G3.CPD-269	G6.CPD-305	G9.CPD-330	G12.CF2-1-2	G15. CF10-1-10	G18. TC-901(C)

Source:-Department of Genetics and Plant Breeding, ARS, Fatehpur-Shekhawati, Sikar

Statistical Analysis

The ANOVA for Randomized Complete Block Design of experiment were carried out using the method suggested by Panse and Sukhatme (1985) [8]. The genetic divergence in 18 genotypes of cowpea was estimated by Mahalanobis D² statistic as suggested by Rao (1952) [9].

Results and Discussions

Genetic Divergence Analysis

The genetic divergence analysis grouped the 18 genotypes into nine distinct clusters, indicating a wide range of genetic variability among the genotypes under study. The maximum number of genotypes (6) were found in Cluster 1, while Clusters 4 to 9 were mono-genotypic, indicating the uniqueness and divergence of these genotypes.

Cluster Pattern and Genetic Diversity, Trait Contribution to Divergence

Cluster 1 consisted of genotypes G3, G4, G5, G7, G8, and G9, suggesting a relatively homogenous group. The presence of single-genotype clusters such as Clusters 4 (G2), 5 (G6), 6 (G10), 7 (G12), 8 (G15), and 9 (G18) reflects high genetic divergence. Maximum inter-cluster distance was observed between Cluster 8 and Cluster 9 (216.68), followed by Clusters 3 and 4, indicating that genotypes in these clusters are highly diverse and may be used in future hybridization programs.

Based on the Singh's statistic and cumulative proportion, the most contributing traits to genetic divergence were: Days to maturity, plant height, grain yield per plant and days to 50% flowering. These traits showed a wide range of variation among the clusters, suggesting that selection based on these can be effective in improving yield and adaptability.

Cluster Means Analysis, Intra-and Inter-Cluster Distances

Cluster 7 recorded the highest mean for number of branches per plant (9.53) and number of pods per plant (21.8). Cluster 5 showed the highest values for pods per plant (20.67) and number of pods per cluster (3.07). Cluster 9 was superior in days to 50% flowering (54.67) and days to maturity (69.33), indicating its potential for late-maturing genotypes. 100-seed weight was highest in Cluster 2 (10.92), while yield per plant peaked in Cluster 7 (14.0).

The lowest intra-cluster distance was observed in Cluster 2 (13.28), indicating close genetic similarity among its members. The highest inter-cluster distances were between Clusters: 8 and 9 (216.68), 3 and 4 (174.03), 4 and 8 (199.88). This variation suggests that crossing genotypes from these clusters may produce maximum heterosis and transgressive segregants.

Similar results were found for genetic diversity Ba *et al.*, (2004) [10], Xiong *et al.*, (2016) [11], Nkhoma *et al.*, (2020) [12] and Ku *et al.*, (2016) [13].

Table 1: Different cluster groups in cowpea genotypes

Cluster groups		
Cluster	Total Genotypes	Genetic material
Cluster 3	3	G1, G16, G17
Cluster 6	1	G10
Cluster 2	3	G11, G13, G14
Cluster 7	1	G12
Cluster 8	1	G15
Cluster 9	1	G18
Cluster 4	1	G2
Cluster 1	6	G3, G4, G5, G7, G8, G9
Cluster 5	1	G6

Table 2: Mean of Different traits for cluster group of cowpea genotypes

Means of traits									
Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Days to 50% flowering	44.33	45.89	48.06	51.33	44.67	48.22	45.00	42.67	54.67
Days to maturity	63.33	67.89	63.72	67.33	70.00	66.22	59.67	58.67	69.33
Plant height	59.75	55.51	36.91	49.96	37.32	53.59	39.41	38.12	40.14
Number of branches per plant	6.33	7.24	7.43	7.07	7.47	7.40	9.53	5.47	6.47
Number of pods per plant	18.47	17.93	19.37	13.67	20.67	19.02	21.80	14.93	19.00
Number of pod per cluster	2.83	2.42	2.69	2.17	3.07	2.87	4.00	2.13	2.60
Pod length	15.87	14.22	12.86	13.93	13.27	12.53	11.60	13.53	15.67
Number of seed per pod	13.93	12.09	12.21	12.47	11.80	10.38	12.40	11.87	10.80
100-seed weight	8.47	10.92	8.31	9.57	10.67	8.80	8.10	8.80	8.70
Grain yield per plant	12.67	13.16	12.60	13.40	11.20	12.60	14.00	10.07	10.20

Contribution of traits			
Traits	Singh statistic	Proportion	Cumulative proportion
Days to 50% flowering	20.12	-435.78	169.01
Days to maturity	-4.36	1646.08	178.75
Plant height	1.69	178.75	534.44
Number of branches per plant	0.59	-66.67	27.92
Number of pods per plant	0.36	-96.76	111.60
Number of pod per cluster	0.17	-19.80	18.45
Pod length	-1.71	-0.78	43.95
Number of seed per pod	-1.42	14.12	29.48
100-seed weight	0.12	-32.30	2.48
Grain yield per plant	2.50	-50.20	-15.11

Intra Inter CD									
Cluster Number	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7	Cluster8	Cluster9
Cluster 1	14.76	79.37	137.72	46.43	33.21	32.85	79.45	154.54	47.43
Cluster 2	79.37	13.28	45.31	98.32	67.78	89.55	32.59	33.67	116.64
Cluster 3	137.72	45.31	22.24	174.03	105.23	149.71	31.36	48.72	130.29
Cluster 4	46.43	98.32	174.03	0.00	104.14	105.63	143.72	199.89	57.68
Cluster 5	33.21	67.78	105.23	104.14	0.00	42.09	45.71	101.40	84.60
Cluster 6	32.85	89.55	149.71	105.63	42.09	0.00	84.05	156.60	68.94
Cluster 7	79.45	32.59	31.36	143.72	45.71	84.05	0.00	40.76	114.34
Cluster 8	154.54	33.67	48.72	199.89	101.40	156.60	40.76	0.00	216.68
Cluster 9	47.43	116.64	130.29	57.68	84.60	68.94	114.34	216.68	0.00

Table 3: D² distances of cowpea genotypes

D ² distance																		
Genetic material	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18
G1	0.00	156.01	95.43	115.95	133.31	83.17	112.27	109.27	112.41	125.62	50.51	22.10	60.74	56.77	76.80	22.59	34.24	92.20
G2	156.01	0.00	45.14	21.96	44.88	104.14	37.76	75.96	52.90	105.63	96.30	143.72	89.62	109.04	199.89	175.72	190.36	57.68
G3	95.43	45.14	0.00	10.15	16.11	27.67	5.57	9.36	11.17	31.54	56.81	69.19	82.31	97.76	154.63	123.68	152.93	34.15
G4	115.95	21.96	10.15	0.00	26.17	49.75	11.70	26.92	18.36	46.80	72.33	97.86	82.86	103.52	178.22	149.88	172.19	28.63
G5	133.31	44.88	16.11	26.17	0.00	41.39	8.42	22.33	14.75	44.36	67.77	89.53	90.20	97.06	158.08	149.41	182.28	69.03
G6	83.17	104.14	27.67	49.75	41.39	0.00	29.13	29.77	21.54	42.09	51.80	45.71	69.57	81.97	101.40	109.56	122.96	84.60
G7	112.27	37.76	5.57	11.70	8.42	29.13	0.00	13.74	10.30	30.90	53.28	77.70	71.27	90.04	140.38	127.56	153.60	46.33
G8	109.27	75.96	9.36	26.92	22.33	29.77	13.74	0.00	16.33	14.60	58.09	71.14	95.91	113.77	157.33	133.85	167.19	46.56
G9	112.41	52.90	11.17	18.36	14.75	21.54	10.30	16.33	0.00	28.92	49.79	71.30	67.08	78.82	138.61	132.34	155.41	59.87
G10	125.62	105.63	31.54	46.80	44.36	42.09	30.90	14.60	28.92	0.00	59.15	84.05	96.63	112.88	156.60	145.60	177.91	68.94
G11	50.51	96.30	56.81	72.33	67.77	51.80	53.28	58.09	49.79	59.15	0.00	20.09	12.92	17.29	36.26	36.57	43.29	98.24
G12	22.10	143.72	69.19	97.86	89.53	45.71	77.70	71.14	71.30	84.05	20.09	0.00	42.34	35.34	40.76	31.57	40.41	114.34
G13	60.74	89.62	82.31	82.86	90.20	69.57	71.27	95.91	67.08	96.63	12.92	42.34	0.00	9.61	32.30	41.51	35.12	111.80
G14	56.77	109.04	97.76	103.52	97.06	81.97	90.04	113.77	78.82	112.88	17.29	35.34	9.61	0.00	32.45	43.33	39.93	139.88
G15	76.80	199.89	154.63	178.22	158.08	101.40	140.38	157.33	138.61	156.60	36.26	40.76	32.30	32.45	0.00	43.14	26.22	216.68
G16	22.59	175.72	123.68	149.88	149.41	109.56	127.56	133.85	132.34	145.60	36.57	31.57	41.51	43.33	43.14	0.00	9.91	131.68
G17	34.24	190.36	152.93	172.19	182.28	122.96	153.60	167.19	155.41	177.91	43.29	40.41	35.12	39.93	26.22	9.91	0.00	167.00
G18	92.20	57.68	34.15	28.63	69.03	84.60	46.33	46.56	59.87	68.94	98.24	114.34	111.80	139.88	216.68	131.68	167.00	0.00

Conclusion

The genetic divergence study revealed substantial variability among the 18 genotypes, categorized into nine distinct clusters. The high inter-cluster distances among several clusters (notably Clusters 8 and 9) highlight the potential of

these combinations in breeding programs. Traits such as days to maturity, plant height, and grain yield per plant contributed significantly to the total divergence and can be targeted for future improvement. For hybridization, crosses between genotypes from widely divergent clusters such as

Cluster 3 with Cluster 4 or Cluster 8 with Cluster 9 are recommended to maximize heterosis. The findings provide valuable insights for selecting diverse parental lines in breeding programs aimed at yield improvement, stress tolerance and adaptability.

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