E-ISSN: 2618-0618
P-ISSN: 2618-060X

www.agronomyjournals.com
2024; 7(12): 677-683
Received: 25-10-2024
Accepted: 29-11-2024

Girish U Chopade
M.Sc. Agriculture Scholar, Genetics and Plant Breeding, Division of Agricultural Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Dr. LS Shitole
Assistant Professor, Division of Agricultural Botany, College of Agriculture, Pune Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Dr. Basavaraj PS
Scientist, Genetics and Plant Breeding, ICAR-National Institute of Abiotic Stress Management, Baramati, Maharashtra, India

SS Chavan
M.Sc. Agriculture Scholar, Genetics and Plant Breeding, Division of Agricultural Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Dr. MR Bhakre
Junior Research Assistant, Division of Agricultural Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Dr. PY Shinde
Assistant Professor, Division of Agriculture Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Dr. TD Katore
Junior Research Assistant, Division of Agricultural Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Corresponding Author:
Girish U Chopade
M.Sc. Agriculture Scholar, Genetics and Plant Breeding, Division of Agricultural Botany, College of Agriculture, Pune, Mahatma Phule Krishi Vidyapeeth, Maharashtra, India

Genetic analysis and characterization of cowpea genotypes for yield and yield enhancing traits

Girish U Chopade, LS Shitole, Basavaraj PS, SS Chavan, MR Bhakre, PY Shinde and TD Katore

DOI: https://doi.org/10.33545/2618060X.2024.v7.i12i.2238

Abstract
Cowpea is a dual-purpose crop extensively cultivated in semi-arid tropics for food and fodder. Although, crop is resilient to climatic extremes but its yield remains low due to several genetic and agronomic factors. The present study aims to characterisation of novel cowpea accessions for yield and yield enhancing traits. Therefore, the study involved 55 cowpea (genotypes studied for various yield and yield-enhancing traits during the *Kharif* season of 2023 at ICAR-NIASM, Baramati. The results revealed that, there was significant variability was observed among genotypes for key agronomic traits such as days to 50% flowering, plant height, primary branches, pods per plant, seeds per pod, test weight and grain yield. High heritability coupled with high genetic advance estimates indicated additive gene action for these traits, suggesting strong potential for selection in breeding programs. Multivariate analysis using Mahalanobis D^2 statistics grouped the genotypes into distinct clusters, revealing plant height and pods per plant as the primary contributors to genetic divergence. The findings highlighted the potential of specific genotypes for developing high-yielding, stress-tolerant cowpea varieties. This research provides a foundation for future breeding strategies aimed at sustainable agricultural practices in cowpea.

Keywords: Diversity, variability, heritability, genetic advance, clusters

Introduction
Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous crop of the *Leguminosae* family (Mackie and Smith, 1935) [6]. It is a diploid with a chromosome number of 2n=2x=22 (Darlington and Wylie, 1955) [2]. It is also known as southern pea or black-eyed pea and is a highly adaptable leguminous crop with significant agricultural, nutritional and economic importance. It is well adapted to the tropics and is cultivated globally in both tropical and subtropical regions. The crop is native to India and Africa, with China recognized as a secondary center of origin (Vavilov, 1951) [22]. The genome size of cowpea is 620 Mbp. It is primarily used in the form of dry seeds, fodder, green pods, green manure and cover crops. Due to its fast-growing nature and drought-resistant traits, cowpea plays a crucial role in sustainable farming systems by improving soil fertility through atmospheric nitrogen fixation (Ortiz, 1998) [13].
Cowpea's ability to thrive in arid and semi-arid environments, coupled with its versatility and adaptability to marginal soils, makes it an essential crop for resource-limited farmers. Its designation as "vegetable meat" emphasizes its high protein content, providing crucial dietary protein in areas where food resources are limited, particularly as it complements lysine-deficient cereals. The considerable genetic variability present in cowpea, spanning both wild and cultivated accessions, supports breeding programs aimed at improving yield potential. Cowpea's resilience under low-input conditions, including drought, coupled with its compatibility in intercropping systems, enhances its suitability as a resource-efficient crop for sustainable agriculture. A comprehensive understanding of the genetic diversity for key yield-related traits is essential for advancing breeding programs. Therefore, this study aims to analyse genetic variability and diversity among cowpea genotypes using D^2 statistics to assess genetic divergence, providing a scientific basis for selecting superior genotypes for breeding programs aimed at developing high-yielding varieties.

Material and Methods

Experimental setup: The present experiment was carried out during *Kharif* 2023 at ICAR – National Institute of Abiotic Stress Management, Malegaon, Baramati, the experiment was set up in the semi-automated greenhouse (Allice Biotechnology®) at the phenomics facility of ICAR-NIASM, Baramati with temperature of 28±2 ^{0}C and relative humidity of 60-70% was maintained. The experiment was laid out in a completely randomised design with two biological replicates.

Plant materials: The experimental material was comprised of 55 genotypes of cowpea including national check and local check varieties. These genotypes/germplasms were collected from different sources, details are provided in Table 1.

Trait measurement: The growth and yield attributes of cowpea were assessed through various parameters such as Days to 50% flowering, plant height, primary branches per plant, pods per plant, number of seeds per pod, test weight and grain yield per plant were recorded.

Statistical analysis

The statical analysis was conducted following the standard procedure outlined for a completely randomized design (CRD) by Panse and Sukhatme (1995). Using completely randomized design (CRD). Genetic variability was assessed through genotypic and phenotypic coefficients of variation (GCV and PCV) as per Burton (1952) [1]. Heritability estimates were computed following Robinson (1949) [17] and genetic advance was calculated using the method of Johnson *et al.* (1955) [4]. Additionally, correlation coefficient analysis (Singh and Chowdhary, 1977) [18]. Multivariate analysis was performed using Mahalanobis D² statistics (Mahalanobis, 1936) [8] and clustering of genotypes was carried out using the Tocher method (Rao, 1952) [16].

Statistical analysis

All the data were subjected to statistical analysis for proper interpretation, focusing on growth, yield and phenotyping parameters of cowpea. The analysis was conducted following the standard procedure outlined for a completely randomized design (CRD) by Panse and Sukhatme (1995). Using completely randomized design (CRD), the study enabled a robust analysis of genotypes influencing cowpea performance. Statistical tools included the analysis of variance (ANOVA) for identifying significant differences among treatments and variability was assessed through genotypic and phenotypic coefficients of variation (GCV and PCV) as proposed by Burton (1952) [1]. Heritability estimates were computed following Robinson (1949) [17] and genetic advance was calculated using the method of Johnson *et al.* (1955) [4]. Additionally, correlation coefficient analysis (Singh and Chowdhary, 1977) [18] evaluated trait interrelations. Multivariate analysis was performed using Mahalanobis D² statistics (Mahalanobis, 1936) [8] and clustering of genotypes was carried out using the Tocher method (Rao, 1952) [16], facilitating the grouping of genotypes based on similarity. This robust statistical framework ensured a comprehensive examination of the factors influencing cowpea traits under different conditions.

Table 1: List of genotypes used in the present study and their sources

Sr. No	Code	Name of the genotype	Source of genotypes
1.	Variety 1	EC240884	NBPGR, New Delhi
2.	Variety 2	EC240877	NBPGR, New Delhi
3.	Variety 3	EC107173	NBPGR, New Delhi
4.	Variety 4	EC117720	NBPGR, New Delhi
5.	Variety 5	EC148709	NBPGR, New Delhi
6.	Variety 6	IC353315	NBPGR, New Delhi
7.	Variety 7	EC24081	NBPGR, New Delhi
8.	Variety 8	EC240900-A	NBPGR, New Delhi
9.	Variety 9	EC240861	NBPGR, New Delhi
10.	Variety 10	EC240920	NBPGR, New Delhi
11.	Variety 11	EC240765	NBPGR, New Delhi
12.	Variety 12	EC240868	NBPGR, New Delhi
13.	Variety 13	EC240826	NBPGR, New Delhi
14.	Variety 14	EC240803	NBPGR, New Delhi
15.	Variety 15	EC240829	NBPGR, New Delhi
16.	Variety 16	IC488084	NBPGR, New Delhi
17.	Variety 17	IC488119	NBPGR, New Delhi
18.	Variety 18	IC488085	NBPGR, New Delhi
19.	Variety 19	EC242128	NBPGR, New Delhi
20.	Variety 20	EC723742	NBPGR, New Delhi
21.	Variety 21	IC488270	NBPGR, New Delhi
22.	Variety 22	IC488222	NBPGR, New Delhi
23.	Variety 23	IC488185	NBPGR, New Delhi
24.	Variety 24	I488239	NBPGR, New Delhi
25.	Variety 25	EC723836	NBPGR, New Delhi
26.	Variety 26	EC244148	NBPGR, New Delhi
27.	Variety 27	EC723744	NBPGR, New Delhi
28.	Variety 28	EC241056	NBPGR, New Delhi
29.	Variety 29	EC23850	NBPGR, New Delhi
30.	Variety 30	EC240830	NBPGR, New Delhi
31.	Variety 31	IC410042	NBPGR, New Delhi
32.	Variety 32	IC402159	NBPGR, New Delhi
33.	Variety 33	IC430632	NBPGR, New Delhi

34.	Variety 34	IC488095	NBPGR, New Delhi
35.	Variety 35	IC554413	NBPGR, New Delhi
36.	Variety 36	IC369857	NBPGR, New Delhi
37.	Variety 37	IC471384	NBPGR, New Delhi
38.	Variety 38	IC402182	NBPGR, New Delhi
39.	Variety 39	IC400155	NBPGR, New Delhi
40.	Variety 40	IC402181	NBPGR, New Delhi
41.	Variety 41	IC433448	NBPGR, New Delhi
42.	Variety 42	IC471955	NBPGR, New Delhi
43.	Variety 43	IC488065	NBPGR, New Delhi
44.	Variety 44	IC488063	NBPGR, New Delhi
45.	Variety 45	IC471435	NBPGR, New Delhi
46.	Variety 46	EC724364	NBPGR, New Delhi
47.	Variety 47	IC488280	NBPGR, New Delhi
48.	Variety 48	IC519737	NBPGR, New Delhi
49.	Variety 49	IC548859	NBPGR, New Delhi
50.	Variety 50	C-152	NBPGR, New Delhi
51.	Variety 51	DC 15	UAS, Dharwad, Karnataka
52.	Variety 52	GC 3	ARS, Badnapur
53.	Variety 53	PL 3	ARS, Badnapur
54.	Variety 54	Phule Pandhari	MPKV, Rahuri
55.	Variety 55	Phule Vithai	MPKV, Rahuri

Results and Discussion

The results of the analysis of variance revealed that mean sum of squares due to genotypes were significant for all the traits studied (Table 2). This highlights the presence of substantial variability among the genotypes and confirm the suitability of the test materials used for further study.

Table 2: Analysis of variance for different characters in cowpea

SV	Df	Mean sum of squares						
		DFF	**PH**	**PB**	**PP**	**SPP**	**TW**	**GY**
Genotype	54	361.56	1187.75	2.87	14.19	35.07	18.90	47.19
Replication	1	12.44	1.058	1.10	0.09	0.03	0.78	0.29
Error	54	9.16	0.110	0.15	0.13	0.05	0.015	0.12

Note: DFF; Days to 50% flowering, PH; Plant height (cm), PB; Primary branches per plant, PP; Pods per plant, SPP; Seeds per pod, TW; Test weight (g), GY; Grain yield per plant (g),

The genetic parameters, including genotypic and phenotypic coefficients of variation, heritability in the broad sense, genetic advance, along with the mean and range of different traits, are presented in Table 2. According to Deshmukh *et al.* (1986) [3], a phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) greater than 20% are regarded as high, whereas values less than 10% are considered low and values between 10% and 20% are considered medium. A wide range of variation was observed for traits such as plant height (48.15-184.1 cm), days to 50% flowering (34.50-69.00), pods per plant (5.00-21.00), grain yield per plant (2.12-28.21 g), test weight (5.15-13.9 g), primary branches per plant (3.00-9.00) and seeds per plant (7.00-16.5), indicating substantial variability among the genotypes for these traits.

The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all traits, suggesting the environmental influence on the manifestation of these characters. However, the difference between PCV and GCV values was very low, suggesting the least influence of the environment in trait expression. The genotypic coefficient of variation for various traits ranged from 19.28% to 54.72%. High GCV was observed for grain yield per plant (54.72%), pods per plant (33.68%), days to 50% flowering (23.56%), test weight (23.50%), primary branches per plant (23.38%) and seeds per pod (21.56%), while moderate GCV was observed for plant height (19.28%). The results suggest that, there was high genetic variability among the cowpea genotypes used in the study for various yield and yield enhancing traits and offers an opportunity for selection. Similar results for high GCV were reported by Nwosu *et al.* (2013) [12] and Hasan Khan *et al.* (2015) for grain yield per plant in cowpea and Sapara *et al.* (2014) [23] and Khanpara *et al.* (2015) [5] for number of pods per plant. Moderate GCV for plant height was also reported by Nwosu *et al.* (2013) [12].

The phenotypic coefficient of variation for various characters ranged from 19.35% to 54.92%, with high variability observed for grain yield per plant (54.92%), pods per plant (33.73%), days to 50% flowering (24.24%), test weight (23.50%), primary branches per plant (24.68%) and seeds per pod (21.95%), while moderate variability was observed for plant height (19.35%). High PCV values for similar traits were reported by Mahesh Sharma *et al.* (2017) [9] for primary branches per plant and by Sapara *et al.* (2014) [23] and Khanpara *et al.* (2015) [5] for number of pods per plant and hundred seed weight.

Heritability estimates, which indicate the heritable portion of variation in a trait, were high for all traits, signifying that these traits are less influenced by environmental factors and have a greater potential for transmission to the next generation. High heritability was observed for traits like days to 50% flowering, plant height, primary branches per plant, pods per plant, seeds per pod, test weight and grain yield per plant, indicating selection would be rewarding for these traits. Singh (2001) [20] noted that if heritability is high (above 70%), selection for such traits could be more effective due to the minimal environmental influence. High heritability for these traits has also been reported by Suganthi and Murugan (2007) [21], Nwosu *et al.* (2013) [12] for hundred seed weight and Ramnarayan Khandait *et al.* (2016) [15] for number of pods per plant.

High genetic advance as a percentage of the mean was observed for pods per plant, grain yield per plant, days to 50% flowering, plant height, seeds per plant, test weight and primary branches per plant. Johnson *et al.* (1955) [4] suggested that high heritability combined with high genetic advance indicates additive gene action, making selection based on these traits more reliable. This study's results align with those of Ramachandran *et al.* (1980) [14], Sreekumar *et al.* (1984) [19], who reported high heritability and genetic advance for these traits. Additionally, similar genetic advance was reported by Ramnarayan Khandait *et al.* (2016) [15] and Khanpara *et al.* (2015) [5] for number of pods per plant and single plant yield in cowpea.

Table 2: Estimates of genetic variability parameters for morpho-physiological and yield traits of cowpea genotypes

Sr. No	Characters	GCV (%)	PCV (%)	h^2bs (%)	GA	GAM
1.	Days to 50% flowering	23.56	24.24	89	24.91	47.18
2	Plant height (cm)	19.28	19.35	91	48.39	39.71
3.	Primary branches per plant	23.38	24.68	91	2.27	45.63
4.	Pods per plant	33.68	33.73	99	8.84	69.27
5.	Seeds per pod	21.56	21.95	96	5.35	43.62
6.	Test weight (g)	23.5	23.52	94	4.61	48.41
7.	Grain yield plant^{-1} (g)	54.72	54.92	90	11.90	61.58

Note: DFF; Days to 50% flowering, PH; Plant height (cm), PB; Primary branches per plant, PP; Pods per plant, SPP; Seeds per pod, TW; Test weight (g), GY; Grain yield per plant (g), GCV; Genotypic coefficient of variation, PCV; Phenotypic coefficient of variation, h^2_{bs}; heritability in broad sense (%), GA; Genetic advance, GAM; Genetic advance as % of Mean.

Genetic diversity studies

Genetic diversity reveals the extent of genetic variation among genotypes, facilitating the identification of diverse genotypes for plant breeding programs. The analysis of genetic divergence has been used to quantify the genetic distance between the genotypes and to identify promising genotypes. Several researchers have proposed various methods to identify genetically diverse genotypes and estimate genetic divergence in crop plants (Murthy and Quadri, 1966; Hussain, 1973) [11]. Among these methods, Mahalanobis generalized distance, estimated by D^2 Statistics (Rao, 1952) [16], stands out for its ability to discriminate populations based on a comprehensive set of parameters, rather than relying on indices derived from morphological similarities and polygenic relationships. This approach provides a more holistic understanding of genetic diversity.

To determine the genetic diversity among 55 genotypes, mean values for the yield and its contributing traits were utilized for estimating the genetic distance between pairs of genotypes by following Mahalanobis D^2 analysis.

Group constellation: Based on Mahalanobis D^2 analysis, 55 genotypes were clustered into eight and nine clusters (Table 3). Clustering pattern revealed that, cluster I was the largest with 28 genotypes, followed by cluster II with 16 genotypes, cluster V (4 genotypes) and cluster VI (3 genotypes). Whereas clusters III, IV, VII and VIII were solitary clusters with one genotype each.

Table 3: Grouping and distribution of cowpea genotypes and checks into different clusters based on Mahalanobis D^2 analysis

Cluster Number	Number of Genotypes	Genotypes
I	28	EC 242128, EC 240830, EC 23850, IC 402181, IC 488270, EC 723742, IC 402182, EC 724364, IC 471955, IC 488085, IC 488185, EC 240826, IC 488119, EC 240765, IC 471384, C-152, IC 488222, IC 369857, PL 3, IC 488084, IC 433448, IC 554413, IC 353315, IC 488239, EC 723836, EC 240900-A, IC 430632, EC240803
II	16	IC 400155, IC 488280, IC 519737, IC 402159, GC 3, IC 548859, IC 488095, EC 241056, IC 410042, IC 488063, EC 240920, IC 471435, EC 723744, EC 240829, DC 15, EC 240868
III	1	EC 148709
IV	1	EC 24081
V	4	EC 240861, Phule Vithai, EC 244148, EC 240877
VI	3	EC 107173, EC 117720, IC 488065
VII	1	EC 240884
VIII	1	Phule Pandhari

Percent contribution of characters towards total divergence:

The percent contribution of traits towards total genetic divergence provides critical insights into the relative importance of each trait in differentiating cowpea genotypes. In this study, 55 genotypes were evaluated based on seven traits and their contributions to divergence were calculated (Table 4).

Plant height emerged as the most significant contributor to total divergence, accounting for 60%, which underscores its substantial role in distinguishing among genotypes. This high contribution could be attributed to the pronounced variability observed in plant height across genotypes, suggesting its potential as a key trait for selection in breeding programs. Pods per plant ranked second, contributing 11.58%, highlighting its importance in determining yield potential and its utility in genetic differentiation.

Grain yield per plant (3.64%) and test weight (2.34%) also showed notable contributions, reflecting their relevance in assessing productivity-related traits. Days to 50% flowering (2.00%) provided moderate differentiation, signifying its importance in phenological adaptation. Traits like primary branches per plant (1.50%) and seeds per pod (0.47%) exhibited lower contributions, indicating relatively limited variability for these traits in the studied genotypes.

These findings emphasize the potential of traits with higher contributions, such as plant height and pods per plant, as primary targets for selection strategies. Furthermore, traits with moderate to low contributions, while less influential in overall divergence, may still play a role in specific breeding objectives, particularly when combined with other traits. This comprehensive understanding of trait contributions facilitates the prioritization of breeding efforts to maximize genetic gain and improve drought-tolerant cowpea genotypes.

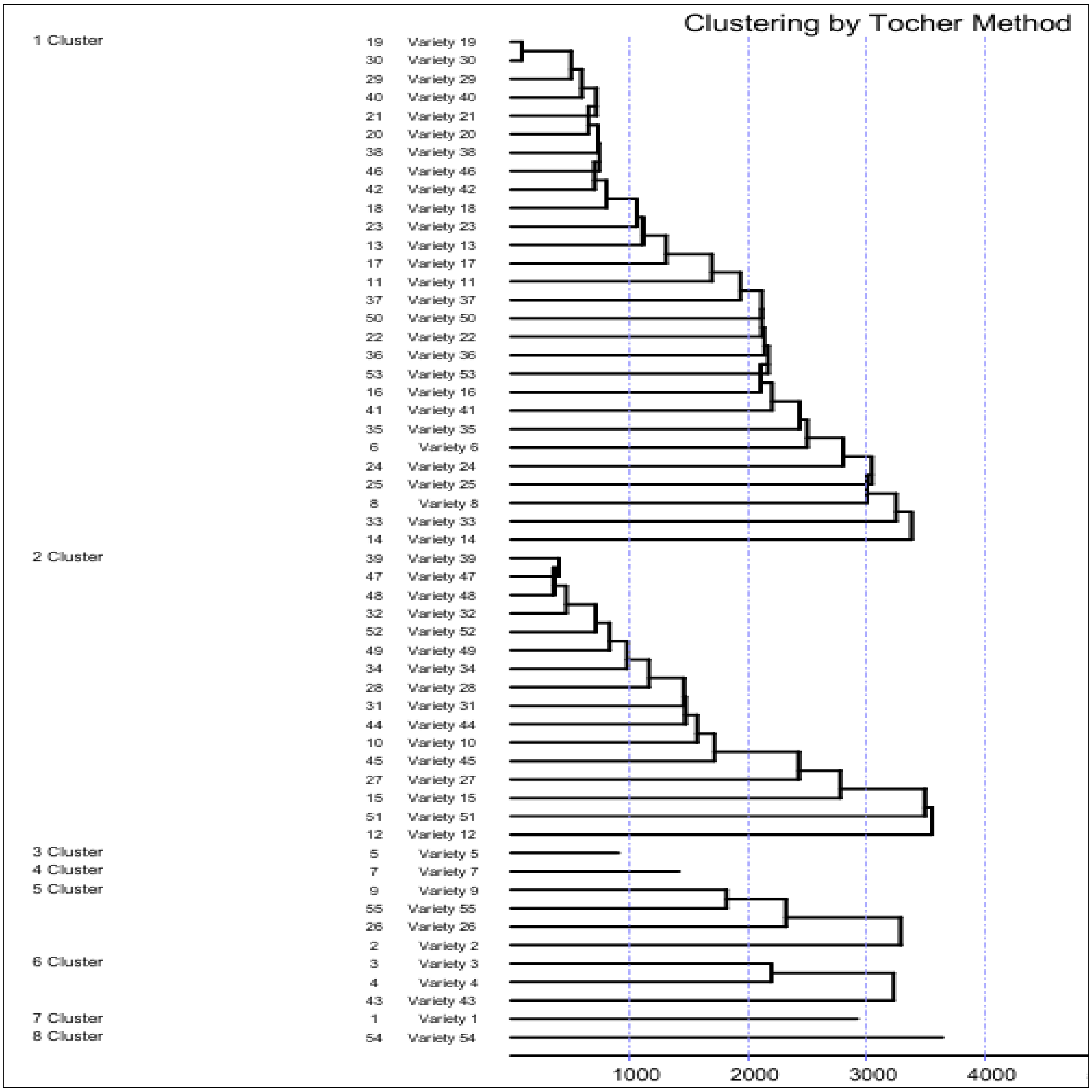
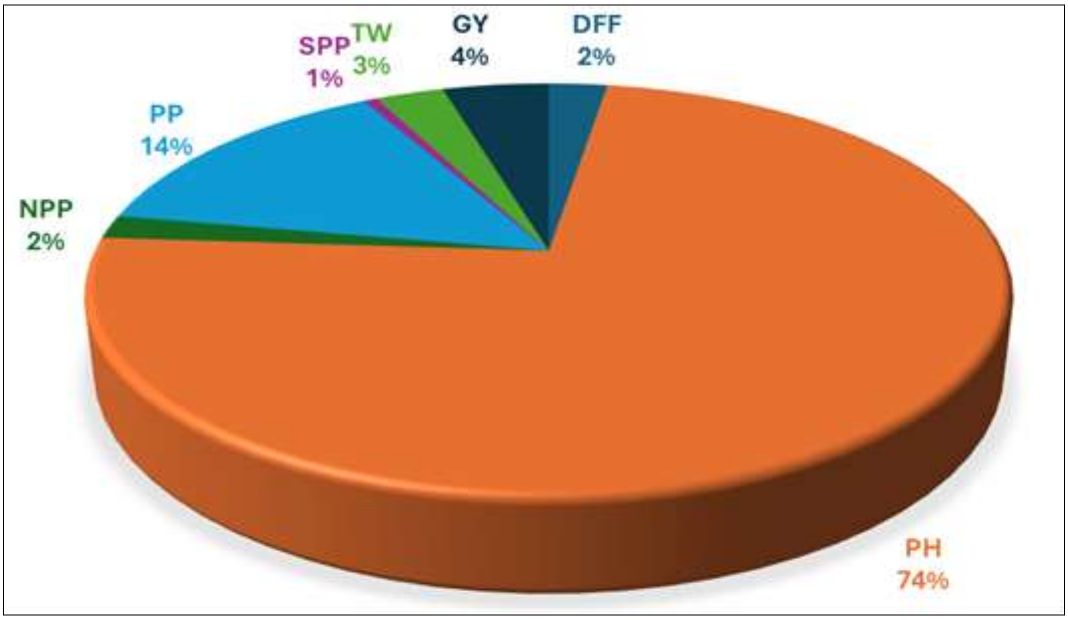


Fig 1: Dendrogram of 55 cowpea genotypes generated by Torcher method



Note: DFF; Days to 50% flowering, PH; Plant height (cm), PB; Primary branches per plant, PP; Pods per plant, SPP; Seeds per pod, TW; Test weight (g), GY; Grain yield per plant (g)

Fig 2: Percent contribution of characters to the total Diversity

Intra and inter-cluster distances: The analysis of intra- and inter-cluster distances is crucial for understanding genetic diversity among cowpea genotypes, providing insights into variability within and between clusters. The average intra- and inter-cluster divergence values are summarized in Table 4 and Figure 3. Among the eight clusters, the highest intra-cluster distances were observed in cluster VI (3958.67), followed by cluster V (3653.28), cluster I (2338.49) and cluster II (2278.17). These elevated intra-cluster values indicate the presence of substantial genetic variability within these clusters, making them valuable for selecting diverse genotypes for breeding programs. In contrast, clusters III, IV, VII and VIII had an intra-cluster distance of zero, as these clusters were solitary, each comprising only one genotype. The solitary nature of these clusters reflects their unique genetic composition and highlights their potential as distinct sources of variability.

The inter-cluster distance was highest between clusters VI and VIII (102481.40) under control conditions, followed by clusters V and VI (65841.43), indicating substantial genetic divergence between these clusters. Such large inter-cluster distances suggest the existence of highly distinct genotypes, which can serve as potential parents for hybridization to exploit heterosis or broaden the genetic base. The lowest inter-cluster distance was recorded between clusters III and I (4340.67), implying relatively lower genetic divergence between these clusters.

These results underscore the importance of clusters with high intra- and inter-cluster distances as reservoirs of genetic diversity. Incorporating genotypes from these clusters into breeding programs can enhance genetic variability, improve drought tolerance and contribute to the development of high-yielding cowpea varieties.

Table 4: Average Intra and Inter-cluster Distance of cowpea genotypes

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	2338.49	7920.33	4340.67	18661.23	34202.89	8045.25	13556.13	60667.84
Cluster II	7920.33	2278.17	4946.48	5192.75	13339.04	24869.64	4833.49	29821.73
Cluster III	4340.67	4946.48	0.00	9128.14	23690.46	14651.81	7670.54	47578.96
Cluster IV	18661.23	5192.75	9128.14	0.00	4738.08	43019.89	4787.28	15655.18
Cluster V	34202.89	13339.04	23690.46	4738.08	3653.28	65841.43	11727.92	6491.46
Cluster VI	8045.25	24869.64	14651.81	43019.89	65841.43	3958.67	33110.35	102481.40
Cluster VII	13556.13	4833.49	7670.54	4787.28	11727.92	33110.35	0.00	25721.62
Cluster VIII	60667.84	29821.73	47578.96	15655.18	6491.46	102481.40	25721.62	0.00

Diagonal and bold values indicate intra-cluster distance. All other values are inter-cluster distance.

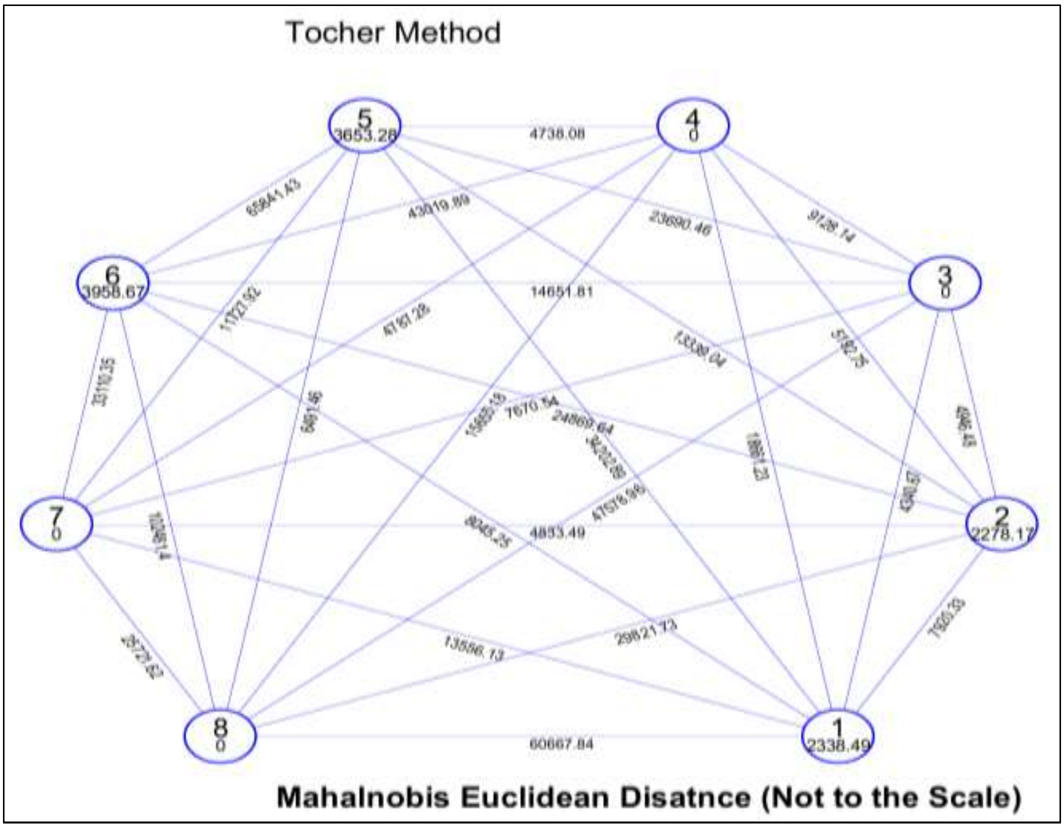


Fig 3: Average Intra and Inter-cluster Distance of cowpea genotypes by Torcher method

Conclusion

The study demonstrated significant genetic variability among the 55 cowpea genotypes for yield and its contributing traits, emphasizing the potential for genetic improvement through targeted breeding programs. High heritability and genetic advance for traits such as grain yield, pods per plant and plant height indicate their amenability to selection and improvement. The clustering analysis revealed substantial genetic diversity with plant height and pods per plant contributing significantly to genetic divergence. These results underscore the importance of these traits as key selection criteria in breeding programs. Additionally, the identified superior genotypes offer a valuable genetic resource for developing high-yielding and drought-tolerant cowpea varieties, contributing to sustainable agricultural systems. The insights gained from this study can inform breeding strategies to enhance productivity and resilience in cowpea cultivation.

Acknowledgement
The authors are grateful to ICAR-NIASM and MPKV Rahuri for permitting to carry out research at ICAR-NIASM. Further, the corresponding author is thankful to ICAR-NICRA for funding the project “Phenotyping of Pulses for Enhanced Tolerance to Drought and Heat”.

References
1. Burton GN, Devane EM. Estimating heritability in tall fescue (*Festuca arundinacea* L.) from replicated clonal material. Agronomy Journal. 1953;45:478-81.
2. Darlington CD, Wylie AP. Chromosome atlas of flowering plants. London: George Allen and Unwin Ltd.; c1955. Available from: http://dspace.bits-pilani.ac.in:8080/xmlui/handle/123456789/7109
3. Deshmukh SN, Basu MS, Reddy PS. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences. 1986;56:816-821.
4. Johanson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-315.
5. Khanpara SV, Jivani LL, Vachhani JH, Kachhadia VH. Genetic variability, heritability and genetic advance studies in vegetable cowpea (*Vigna unguiculata* (L.) Walp.). Electronic Journal of Plant Breeding. 2015, 7(2).
6. Mackie WW, Smith FL. Evidence of field hybridization in beans. Journal of the American Society of Agronomy. 1935;27:903-908.
7. Mahalanobis PC. A statistical study of head measurement. Journal of the Asiatic Society of Bengal. 1928;25:201-277.
8. Mahalanobis PC. On generalized distance in statistics. Proceedings of the National Academy of Sciences, India. 1936;2:49-55.
9. Sharma M, Sharma PP, Sharma H, Meghawal DR. Genetic variability in cowpea (*Vigna unguiculata* (L.) Walp.) germplasm lines. Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1384-1387.
10. Manggoel W, Uguru MI, Ndam ON, Dasbak MA. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea (*Vigna unguiculata* (L.) Walp) accessions. Journal of Plant Breeding and Crop Science. 2012;4(5):80-86.
11. Murty BR, Quadri MT. Analysis of divergence in some self-compatible forms of *Brassica campestris* L. var. Brown Sarson. Indian Journal of Genetics and Plant Breeding. 1966;26:45-58.
12. Nwosu DJ, Olatunbosun BD, Adetiloye IS. Genetic variability, heritability and genetic advance in cowpea (*Vigna unguiculata* (L.) Walp.) genotypes in two agro-ecological environments. Greener Journal of Biological Sciences. 2013;3(5):202-207.
13. Ortiz R. Cowpea from Nigeria: A silent food revolution. Outlook on Agriculture. 1998;27:125-128.
14. Ramachandran C, Peter KV, Gopalakrishnan PK. Variation in selected varieties of cowpea (*Vigna unguiculata* L. Walp.). Agricultural Research Karale. 1982;18(1):94-97.
15. Khandait R, Jain PK, Prajapati S, Solanki P. Genetic variability studies of diverse cowpea (*Vigna unguiculata* (L.) Walp.) genotypes. Journal of Functional and Environmental Botany. 2016;6(2):114-122.
16. Rao CR. Advanced statistical methods in biometrical research. New York: John Wiley and Sons; 1952.
17. Robinson HF, Comstock RF, Harvey PH. Estimates of heritability and degree of dominance in corn. Agronomy Journal. 1949;41:353-359.
18. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Ludhiana: Kalyani Publishers; c1977.
19. Sreekumar K, Inasi KA, Alice A, Nair RR. Genetic variability, heritability and correlation studies in vegetable cowpea (*Vigna unguiculata* var. *sesquipedalis*). South Indian Horticulture. 1996;44(1&2):15-18.
20. Singh BD. Plant breeding: Principles and methods. New Delhi: Kalyani Publishers; 2001. 896 p.
21. Suganthi S, Murugan S. Variability studies in cowpea (*Vigna unguiculata* (L.) Walp.). Crop Research. 2007;33(1/3):195-197.
22. Vavilov NI. The origin, variation, immunity and plant breeding of cultivated plants. Chronica Botanica. 1951;13:364.
23. Sapara A, Birchwood M, Cooke MA, Fannon D, Williams SC, Kuipers E, *et al*. Preservation and compensation: the functional neuroanatomy of insight and working memory in schizophrenia. Schizophrenia research. 2014 Jan 1;152(1):201-209.