International Journal
of
Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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www.agronomyjournals.com
2024; SP-7(12): 88-92
Received: 06-10-2024
Accepted: 08-11-2024

Annu Dahiya
1. Ph.D. Scholar, Department of Genetics and Plant Breeding, CCSHAU Hisar, Haryana, India
2. ICAR-Central Soil Salinity Research Institute, Karnal, Haryana, India

Satyawan Arya
Assistant Scientist, Forage Section, Department of Genetics and Plant Breeding, CCSHAU Hisar, Haryana, India

Ravish Panchta
Department of Genetics and Plant Breeding, CCSHAU Hisar, Haryana, India

Jogender
Ph.D. Scholar, Department of Genetics and Plant Breeding, CCSHAU Hisar, Haryana, India

Corresponding Author:
Satyawan Arya
Assistant Scientist, Forage Section, Department of Genetics and Plant Breeding, CCSHAU Hisar, Haryana, India

Delineating the genetic variability in cowpea [*Vigna unguiculata* (L. Walp)] under the summer season

Annu Dahiya, Satyawan Arya, Ravish Panchta and Jogender

DOI: https://doi.org/10.33545/2618060X.2024.v7.i12Sb.2111

Abstract

The investigation conducted at the Dry Land Research Area of CCS Haryana Agricultural University in Hisar during the summer of 2021 focused on assessing genetic variability among 48 cowpea genotypes through the analysis of 12 quantitative traits, finding significant differences among the genotypes and indicating a high level of genetic variability; the genotypic coefficient of variation (GCV) ranged from 2.6% to 48.34%, while the phenotypic coefficient of variation (PCV) ranged from 4.62% to 49.37%, with the higher PCV compared to GCV across all traits suggesting that environmental factors considerably influence trait expression, and high heritability (h^2) and genetic advance as a percentage of the mean (GAM) were observed for several traits, including days to 50% flowering, number of branches per plant, number of clusters per plant, number of pods per plant, seed yield per plant, and 100-seed weight, indicating a predominance of additive gene action for these traits and suggesting that selection for these traits could be effective in enhancing their performance, contributing valuable insights into the genetic potential of cowpea and emphasizing the importance of selecting genotypes based on their heritable traits for future breeding programs.

Keywords: GCV, PCV, GAM and Heritability

Introduction

Cowpea (*Vigna unguiculata*), an annual leguminous plant with a diploid chromosome 2n=2x=22, is predominantly cultivated in semi-arid regions worldwide and is recognized for its significant economic, nutritional, and ecological importance. This diploid plant has a genome size of approximately 620 million base pairs (Lonardi *et al*., 2019) [8]. This crop supplies essential nutrients for human diets. It serves as forage for livestock, with seeds containing 23% to 32% protein and essential amino acids. It is a crucial food source in many developing countries, particularly in sub-Saharan Africa and parts of Asia and the Americas. Often referred to as "poor man's meat," cowpea complements cereal-based diets and provides dietary fiber, carbohydrates, and vital minerals such as iron and zinc; its starch is digested more slowly than cereals, offering additional health benefits. The leaves and immature pods are also edible, contributing vitamins and minerals, including beta-carotene and iron, essential for addressing micronutrient deficiencies. Cowpea thrives in poor soils and low rainfall, enhancing soil fertility through nitrogen fixation, and can be intercropped with cereals like sorghum and maize, improving agricultural productivity in resource-limited settings. Its ability to fix nitrogen through symbiosis with nodulating bacteria helps maintain soil health. Cowpea is photo-insensitive and can be cultivated throughout the year in all three seasons Summer, Kharif, and Rabi (Peninsular India).In India, cowpea is primarily grown in states such as Rajasthan, Karnataka, and Tamil Nadu, although its cultivation has declined due to monoculture practices focusing on wheat and rice, raising concerns about soil nutrient depletion. This decline underscores the urgent need for high-yielding and drought-tolerant legume varieties to restore soil health and enhance food security. Genetic improvement is achieved by screening appropriate germplasm for various traits of interest. Genetic variability is a pre-requisite for any successful breeding program. The current investigation aimed to study the genetic variability present among the indigenous and exotic genotypes for various traits.

Materials and Methods

In the current experiment, 48 genotypes of cowpea [*Vigna unguiculata (L) Walp]* (Table 1) were evaluated in a Randomized Complete Block Design (RCBD) with three replications at the Forage Research Area of the Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar, during the summer season of 2021. The research site is in a subtropical region with a dry environment characterized by scorching summers, chilly winters, and little rainfall. Each genotype was grown in paired rows of 2-meter length, with row-to-row and plant-to-plant distances of 45 cm and 15 cm, respectively. For recording observations i.e., Plant Height (cm), Days to 50% flowering, Days to maturity, Number of pods per cluster, Number of clusters per plant, Number of pods per plant, Number of seeds per pod, Pod length (cm), Number of branches per plant, 100 Seed weight (g), Seed yield per plant (g), and Crude Protein content (%), five competitive plants from the middle of each row were taken from each genotype/replication.

Statistical Analysis

To assess the differences among genotypes, the analysis of variance (ANOVA) was performed individually for each trait, following the approach recommended by Panse and Sukhatme (1984). This method allows researchers to determine if there are significant variations in the expression of specific traits across different genotypes. The Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated using the standard formulas proposed by Burton and Devane (1953) [2]. Heritability (h2) in broad sense that the genetic advance percent mean was calculated by using the formula given by Johnson *et al*., (1955) [7].

Result and Discussion

The analysis of variance for Days to 50 % flowering, Days to Maturity, Plant height, number of branches per plant, number of pods per plant, number of clusters per plant, number of seeds per pod, number of pods per cluster, pod length (cm), 100-seed weight (g), crude protein content (%) revealed that there are high and significant differences among the studied genotypes (Table 2) which indicates that there is sufficient variability exists in the present material selected for the study and it shows the suitable selection for crop improvement. Similar results were also observed by Gupta *et al*. (2019) [5], Nguyen *et al*. (2019) [9], Thangam *et al*. (2020) [18], Ugale *et al*. (2020) [19] and Tambitkar *et al*. (2021) [17] in cowpea. The knowledge of the magnitude of genetic and phenotypic variation in indigenous and exotic lines in cowpeas and the degree of association among characters is important to provide the basis for effective selection. The variation in the germplasm line concerning maturity was wide, with the maximum number of days required to reach physiological maturity being 120 days and the minimum being 72 days. The range for plant height was from 44.33 cm to 151.33 cm, indicating significant genotype viability for this trait. The hundred seed weights ranged from 4.68 g to 23.29 g, while the seed yield per plant varied from 5.33 g to 33.20 g. Additionally, the percent crude protein content in the seeds ranged from 18.85% to 24.97%.

Phenotypic coefficients of variation (PCV) and Genotypic coefficients of variation (GCV)

The genotypic coefficient of variation (GCV) ranged from 2.6% to 48.34%, while the phenotypic coefficient of variation (PCV) ranged from 4.62% to 49.37%. The lowest and highest values for both genetic parameters were recorded for protein content and seed yield per plant, respectively. The highest PCV value was observed for seed yield per plant (49.37%), followed by the number of branches per plant (38.45%), the number of clusters per plant (34.28%), and the number of pods per plant (31.41%), as detailed in the table. The highest GCV (48.34%) was recorded for seed yield per plant, followed by the number of branches per plant and the number of clusters per plant (32.33%). In contrast, low GCV values were recorded for days to maturity (11.12%), days to flowering (12.44%), and crude protein content (3.44%). The higher magnitudes of the phenotypic coefficient of variation (PCV) compared to the genotypic coefficient of variation (GCV) for all traits suggest that environmental factors significantly influence trait expression. This finding emphasizes the importance of considering environmental conditions when evaluating genotypic performance and selecting specific traits. These findings confirmed the results of Nguyen *et al*. (2019) [9] and Thangam *et al*. (2020) [18] for seed yield, and the number of pods per plant. Likewise, similar findings were also reported by Patel *et al*. (2016) [12] for plant height; Havaraddi *et al*. (2018) [6] and Purohit *et al*. (2020) [13] for seed yield and number of pods per plant by Gupta *et al*. (2019) [5] for pods per plant and plant height by Sharma *et al*. (2017) [15] and Sharma *et al*. (2019) [14] for seed yield, plant height and number of clusters per plant.

Estimates of heritability in a broad sense

Heritability values are classified as very high (80%), moderately high (60-79%), moderate (40-59%), and low (40%) according. The estimated heritability for the studied traits was presented (Table 4). Most of the characters expressed high estimates of broad sense heritability. The estimates of heritability help the plant breeder in the selection of genotypes from a diverse genetic population. Therefore, high heritability helps in the effective selection of a particular character. Very high heritability (80%) was computed for no. pods per cluster (96.26%), seed yield per plant (95.88%), days to 50% flowering (95.56%), days to maturity (94.40%), no. of branches per plant (93.14%), and no. of cluster per plant (88.93%). The moderate high heritability (60-79%) was computed for pod length (68.75%) and plant height (60.83%). The moderate heritability (40-59%) was computed for no. of pod per cluster (59.50%) and no. of seed per pod (45.36%). The low heritability values were (31.77%) for crude protein content.

Genetic advance (GA) as a percent of Mean

Genetic advance (GA) is a valuable indicator of the potential improvement in trait performance achievable through selection within a base population, particularly for traits exhibiting both high heritability and high genetic advance, which suggest a greater presence of additive genes. In the current study, the moderate genetic advance was observed for days to maturity, the number of pods per cluster, and pod length while this trait can also be improved, it may require more focused breeding efforts and low genetic advance was noted for crude protein content and the number of seeds per pod. Conversely, high heritability (h^2) and genetic advance as a percentage of the mean (GAM) were recorded for days to 50% flowering, the number of branches per plant, the number of clusters per plant, the number of pods per plant, seed yield per plant, and 100-seed weight, indicating a predominance of additive gene action for these traits and suggesting that selection will be effective in enhancing their performance. Similar findings have been documented by Srinivas *et al*. (2017) [16], Devi and Jayamani (2018) [3], Nguyen *et al*. (2019) [9], and Bamji *et al*. (2020) [1]. Overall, the results highlight the importance of considering both heritability and genetic advancement when developing effective selection strategies for crop improvement programs, as traits with moderate to low GA may require additional selection strategies or hybridization to maximize their performance.

Table 1: Lists of 48 genotypes evaluated during the experiment

S. No.	Genotype	Source	S. No.	Genotype	Source
1.	Pant Lobia 7	GBPUA & T, Pantnagar	25	VCP 12005	NPRC,Vamban
2.	Pant Lobia 3	GBPUA & T, Pantnagar	26.	PMCP 1016	ARS, Pandharpur
3.	GC 3	SDAU, S.K.Nagar	27.	SKUA-WCP-149	SKUAS&T, Srinagar
4.	RC 101	RARI, Durgapura	28.	PGCP 69	GBPUA&T, Pantnagar
5.	GC 1601	SDAU, S.K.Nagar	29.	GC 1805	SDAU, S.K.Nagar
6.	PGCP 71	GBPUA & T, Pantnagar	30.	CPD 340	RARI, Durgapura
7.	PGCP 73	GBPUA & T, Pantnagar	31.	VCP 12006	NPRC,Vamban
8.	PGCP 75	GBPUA & T, Pantnagar	32.	PMCP 1131	ARS, Pandharpur
9.	GC 1802	SDAU, S.K.Nagar	33.	Super 60	PRSS, Samba
10.	VCP 18-032	NPRC, Vamban	34.	PGCP 6	GBPUA&T, Pantnagar
11.	CPD 271	RARI, Durgapura	35.	PGCP 14	GBPUA&T, Pantnagar
12.	PGCP 74	GBPUA & T, Pantnagar	36.	EC 224035	SKUAS&T, Srinagar
13.	PGCP 76	GBPUA & T, Pantnagar	37.	PGCP 4	GBPUA&T, Pantnagar
14.	GC 1906	SDAU, S.K.Nagar	38.	PGCP 1	GBPUA&T, Pantnagar
15.	VCP 17-019	NPRC, Vamban	39.	PGCP 12	GBPUA&T, Pantnagar
16.	CPD 32	RARI, Durgapura	40.	GC 1602	SDAU, S.K.Nagar
17.	HC 46	CCSHAU, Hisar	41.	EC 723909	
18.	Pant Lobia 4	GBPUA & T, Pantnagar	42.	EC 202718	-
19.	KBC 11	UAS, Banglore	43.	EC 224038	-
20.	PCP 1124-1	ARS, Pandharpur	44.	EC 1797K 499-35	-
21.	PGCP 70	GBPUA & T, Pantnagar	45.	EC 528393	-
22.	PGCP 72	GBPUA & T, Pantnagar	46.	CPD 317	RARI, Durgapura
23.	GC 1801	SDAU, S.K.Nagar	47.	VCP 15006	NPRC,Vamban
24.	CPD 331	RARI, Durgapura	48.	GC 1806	SDAU, S.K.Nagar

Table 2: Weather data during the period of experimentation *i.e.*, from March to June 2021

Standard Week	Dates	Temperature		Relative Humidity		Rainfall
		Maximum	Minimum	(%)	(%)	
		°C	°C	M	E	(mm)
1	March 5-11	30.7	14.1	91	43	0.0
2	March 12-18	30.7	13.9	89	40	1.2
3	19-25	31.4	14.5	88	37	4.4
4	Mar 26-Apr 01	33.5	14.3	75	26	0.0
5	Apr 2-8	35.0	13.3	69	18	0.0
6	Apr 9-15	37.2	16.0	54	15	0.0
7	Apr 16-22	35.6	17.2	67	26	0.5
8	Apr 23-29	37.0	17.9	58	23	0.0
9	Apr 30-May 6	40.1	23.1	54	30	1.5
10	May 7-13	38.1	22.7	66	37	5.9
11	May 14-20	34.7	22.9	71	44	0.0
12	May 21-27	36.3	21.1	72	34	20.8
13	May 28-Jun 03	38.4	24.0	75	40	13.2
14	Jun 4-10	40.2	28.1	64	37	0.0
15	Jun11-17	37.9	25.1	80	56	51.8
16	18-24	37.0	26.3	73	45	0.0
17	Jun 25-Jul 01	40.0	26.8	63	35	8.9

Table 3: Analysis of variance for different traits in 48 genotypes of cowpea

Source of variation	DF	Mean sum of sources											
		DF 50%	DM	PH	NBPP	NPPP	NCPP	NPPC	NSPP	PL	100-SW	CPC	SYPP
Replication	2	4.88	19.11	44.3	0.29	6.46	6.33	0.01	7.48	3.27	0.22	0.66	1.58
Genotypes	47	73.14**	343.32**	1485.97**	37.30**	312.42**	72.45**	1.19**	14.72**	17.90**	23.52**	2.27**	121.27**
Error	94	1.15	6.65	262.2	0.89	3.99	2.88	0.139	4.12	2.35	0.62	0.95	1.711
CV%	-	2.68	2.71	15.25	10.07	6.08	11.41	16.83	16.21	11.05	5.62	3.81	10.02
CD 5%	-	1.71	4.19	26.27	1.53	3.24	2.75	0.61	3.33	2.49	1.29	1.58	2.12

** Significant at 1% levels, Days to 50% flowering (DF 50%), Days to maturity (DM), Plant Height (PH) No of branches per plant (NBPP), No. of pods per plant (NPPP), No. of cluster per plant (NCPP), No. of pods per cluster (NPPC), No of seed per pod (NSPP), 100 Seed weight (100-SW), Crude Protein content (CPC), Seed yield per plant (SYPP)

Table 4: Mean, range, phenotypic and genotypic coefficient of variation, heritability, and genetic advance as % of mean for various traits in cowpea

Characters	Mean ± SE(m)	Range	Coefficient of variation		Heritability (%)	Genetic Advance as % of mean
			GCV	PCV		
Days to 50% flowering	39.40±0.86	30-48	12.44	12.72	95.56	25.04
Days to maturity	95.40±2.11	72-120	11.12	11.44	94.40	22.25
Plant height (cm)	106.27±13.23	44.3-151.3	19.00	24.36	60.83	30.53
No. of branches per plant	9.39±0.77	3.7-17.67	37.11	38.45	93.14	73.77
No. of pods per plant	32.90±1.63	16-56	30.82	31.41	96.26	62.28
No. of clusters per plant	14.90±1.39	5.77-34.33	32.33	34.28	88.93	62.80
No. of pods per cluster	2.22±0.31	1.00-3.33	20.4	26.45	59.50	32.42
No. of seeds per pod	12.67±1.68	8.00-18.00	14.77	21.94	45.36	20.50
Pod length (cm)	13.90±1.25	9.00-19.00	16.38	19.76	68.75	27.98
100-seed weight (g)	14.11±0.65	8.2-20.40	19.57	20.37	92.38	38.76
Crude protein content (%)	25.58±0.80	22-27.30	2.6	4.62	31.77	3.02
Seed yield per plant (g)	13.06±1.07	5.3-33.20	48.34	49.37	95.88	97.51

Conclusion

Since genetic variability is necessary to materialize the response to selection, understanding the genetic differences inherent in the genetic material is significant in determining the likelihood of effective selection and breeding for higher grain yield. Analysis of variance confirmed highly significant genotypic variation for most of the studied traits, indicating the ample scope for improvement of these traits through plant breeding. High broad-sense heritability estimates for various traits such as days to 50% flowering, days to maturity, number of branches per plant, number of pods per plant, number of clusters per plant, 100-seed weight, and seed yield per plant indicate that these traits are less influenced by environmental factors and demonstrate greater stability across different conditions.

This stability makes them suitable candidates for direct selection in breeding programs. Furthermore, traits exhibiting both high GCV and high heritability, such as seed yield per plant and number of pods per plant, suggest a strong potential for improvement through targeted selection strategies. The genetic advance as a percentage of the mean (GAM) was found to be high for several traits, including seed yield per plant, number of branches per plant, number of pods per plant, number of clusters per plant, number of pods per cluster, 100-seed weight, plant height, days to 50% flowering, and days to maturity. This indicates that these traits can be effectively enhanced through selection, providing a pathway for breeders to improve cowpea varieties.

The combination of high heritability and high genetic advance for key traits such as seed yield per plant, 100-seed weight, number of clusters per plant, number of pods per plant, number of branches per plant, days to 50% flowering, and days to maturity indicates the presence of predominantly additive genetic variation. This suggests that these traits can be successfully improved through direct selection, making them prime targets for breeding programs aimed at enhancing cowpea productivity. By leveraging this genetic diversity and focusing on traits with favorable heritability and genetic advances, breeders can enhance cowpea production, contributing to food security and agricultural sustainability.

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