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Genetic variability and trait association in cowpea (*Vigna unguiculata* L.) genotypes for yield and reproductive efficiency

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Abstract

Cowpea (*Vigna unguiculata* L. Walp.) is a vital food legume cultivated widely in tropical and subtropical regions for its protein-rich seeds, fodder value, and ability to thrive in marginal environments. The present investigation was conducted to assess genetic variability, estimate heritability and genetic advance, and determine trait associations related to yield and reproductive efficiency in 22 diverse cowpea genotypes. Significant differences were observed among genotypes for all 13 traits studied, indicating substantial genetic variation. High genotypic and phenotypic coefficients of variation were recorded for seed yield per plant (GCV: 34.77%, PCV: 36.13%), secondary branches per plant (GCV: 39.00%, PCV: 40.04%), and plant height (GCV: 32.48%, PCV: 33.32%). Broad-sense heritability estimates were high for days to 50% flowering (95.17%), seed yield per plant (92.57%), and number of pods per plant (90.81%), coupled with high genetic advance, suggesting additive gene action. Genotypic correlation analysis revealed strong positive associations of seed yield per plant with number of primary branches (r = 0.988), secondary branches (r = 0.837), pods per plant (r = 0.895), and plant height (r = 0.667). Pollen viability and germination also showed moderate associations with yield, highlighting their relevance for reproductive success. These results emphasize the importance of integrating both agronomic and reproductive traits for selection. The identified high-heritability, high-correlation traits provide a strong basis for improving seed yield and reproductive efficiency in cowpea through targeted breeding strategies.

Keywords: Cowpea, genetic variability, heritability, trait association, seed yield, reproductive traits

1. Introduction

Cowpea (*Vigna unguiculata* L. Walp.), a self-pollinated diploid legume ($2n = 2x = 22$) of the family Fabaceae, plays a crucial role in food and nutritional security across tropical and subtropical regions. It is widely cultivated in Africa, Asia, and Latin America for its high-protein grains, edible leaves, and tender pods, and also serves as an important fodder crop in mixed farming systems. In India, a secondary center of diversity, cowpea is grown under diverse agro-climatic zones and is known by various regional names such as lobia and chawli (Anonymous, 2023) [1, 2]. Its exceptional adaptability to low-input conditions, drought-prone areas, and poor soils makes it an ideal crop for sustainable and climate-resilient agriculture. Owing to its rich protein content, it is often referred to as the "poor man's meat" (Diwaker *et al.*, 2018) [6].

Despite its multifaceted importance, cowpea yields in India remain suboptimal, with national productivity averaging around 625 kg/ha—well below the global average of approximately 900 kg/ha (Anonymous, 2023) [1, 2]. This low yield is primarily due to a narrow genetic base, inadequate breeding for yield stability, and variable environmental conditions. Enhancing cowpea productivity requires a systematic evaluation of genetic variability and identification of superior genotypes through selection. Estimating key genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance enables breeders to quantify trait variability and predict selection efficiency (Vinay *et al.*, 2022) [12]. Traits with high heritability and high genetic advance are often under additive genetic control and respond well to direct selection (Johnson *et al.*, 1955; Meena *et al.*, 2015) [7, 8].

Seed yield, a complex quantitative trait, is governed by numerous morphological and physiological components. Understanding the interrelationships among these yield-contributing traits is essential for efficient selection. Correlation studies help reveal which traits have the strongest direct or indirect influence on yield and thus serve as effective selection indices (Sharma *et al.*, 2019; Dinesh *et al.*, 2017) [11, 5]. Previous studies have consistently reported significant positive associations between yield and traits such as plant height, number of pods per plant, number of branches, and pod length (Nguyen *et al.*, 2019; Bhagwati *et al.*, 2017) [9, 4]. Furthermore, reproductive traits like pollen viability and germination are increasingly recognized as critical contributors to pollination success and seed set, especially under stress-prone environments (Barros *et al.*, 2024; Saidaiah *et al.*, 2021) [3, 10].

In this context, the present study was conducted to assess genetic variability, estimate heritability and genetic advance, and explore trait correlations related to yield and reproductive efficiency in 22 diverse cowpea genotypes. The objective is to identify key traits that contribute to seed yield and offer potential for improvement through breeding. The findings will provide valuable insights for designing effective selection strategies aimed at enhancing cowpea productivity and stability under diverse growing conditions.

2.1 Experimental Location and Season

The field experiment was conducted during the *Kharif* 2024 season at the Research Farm of Dr. Sharadchandra Pawar College of Agriculture, Baramati, Pune, Maharashtra. The site is located at an elevation of approximately 538 meters above sea level, characterized by a semi-arid climate and clay loam soils with moderate fertility. Standard agronomic practices were followed throughout the cropping period to ensure optimum growth and development of the cowpea genotypes.

2.2 Experimental Material and Layout

The study comprised 22 cowpea genotypes, including four standard checks. These genotypes were evaluated in a Randomized Block Design (RBD) with three replications to assess genetic variability and yield-related traits. Each entry was sown in a plot consisting of three rows of 4 meters length, spaced at 45 cm between rows and 20 cm between plants within a row. All recommended agronomic inputs such as timely sowing, irrigation (if required), weeding, and plant protection measures were adopted to maintain a healthy crop stand.

2.3 Traits Recorded

Data were recorded on thirteen agronomic and reproductive traits from five randomly selected competitive plants in each plot, excluding border rows to reduce edge effects. The traits studied included days to 50% flowering, days to maturity, plant height (cm), number of primary and secondary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, seed yield per plant (g), seed yield per hectare (kg/ha), pollen viability (%) and pollen germination (%). Pollen viability was estimated using 1% acetocarmine staining, while pollen germination was assessed using the hanging drop method with 15% sucrose solution to stimulate *in vitro* germination.

2.4 Statistical Analysis

The recorded data were subjected to statistical analysis using standard biometrical methods. Analysis of variance (ANOVA) was performed to test for significant differences among genotypes. Genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2), and genetic advance as percent of mean (GAM) were calculated following the procedures of Johnson *et al.* (1955) [7]. Genotypic and phenotypic correlation coefficients were also computed to determine the degree and direction of associations among traits. All statistical analyses were carried out using Microsoft Excel and SPSS software.

3. Results and Discussion

3.1 Analysis of Variance

The results of the analysis of variance (ANOVA) presented in Table 1 revealed highly significant ($p < 0.01$) differences among the 22 cowpea genotypes for all 13 observed traits. This indicates the presence of substantial genetic variability in the experimental material. For instance, the mean sum of squares for seed yield per plant was, while that for seed yield per hectare was, reflecting considerable variation in yield performance among genotypes. Similarly, high variability was also recorded for plant height, number of pods per plant, and number of primary branches per plant. These findings are in agreement with earlier studies conducted by Sharma *et al.* (2019) [11] and Bhagwati *et al.* (2017) [4], who reported significant genotypic variation in cowpea for similar morphological and yield traits, emphasizing the scope for effective selection.

3.2 Genetic Variability, Heritability, and Genetic Advance

Estimates of the genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance for the studied traits are summarized in Table 2. High GCV and PCV were recorded for secondary branches per plant (GCV: 39.00%, PCV: 40.04%), seed yield per plant (GCV: 34.77%, PCV: 36.13%), seed yield per hectare (GCV: 34.88%, PCV: 35.90%), and plant height (GCV: 32.48%, PCV: 33.32%), indicating that these traits are predominantly under genetic control with relatively minor environmental influence. Similarly, number of pods per plant exhibited GCV and PCV of 28.77% and 30.19%, respectively. The minimal differences between GCV and PCV for these traits further support their genetic determinism and selection efficiency (Vinay *et al.*, 2022; Dinesh *et al.*, 2017) [12, 5].

Traits like days to maturity (GCV: 2.99%, PCV: 5.50%) and pollen germination (GCV: 6.33%, PCV: 7.15%) showed lower variability, suggesting a greater environmental influence and limited scope for genetic improvement through simple phenotypic selection.

Heritability estimates ranged from moderate to high for all traits. The highest heritability was observed for days to 50% flowering (95.17%), followed by plant height (95.02%), secondary branches per plant (94.87%), seed yield per hectare (94.38%), and seed yield per plant (92.57%). These traits also showed high genetic advance as a percent of mean (GAM), such as 78.25% for secondary branches, 68.90% for seed yield per plant, 65.22% for plant height, and 55.66% for number of pods per plant. This suggests the preponderance of additive gene action and high effectiveness of selection in the early generations (Johnson *et al.*, 1955; Meena *et al.*, 2015) [7, 8]. In contrast, traits such as days to maturity (heritability: 29.60%, GAM: 3.34%) and pollen germination (heritability: 78.38%, GAM: 11.51%) exhibited moderate to low genetic advance, reflecting the influence of non-additive gene action or environmental interactions.

3.3 Correlation Studies

The genotypic and phenotypic correlation coefficients among all studied traits are presented in Table 3 and 4. At the genotypic level, seed yield per plant exhibited very strong positive correlations with number of primary branches per plant (r = 0.988), number of secondary branches per plant (r = 0.837), number of pods per plant (r = 0.895), and plant height (r = 0.667). These associations suggest that these traits play a critical role in determining yield potential and can be prioritized in selection programs. Moderate positive genotypic correlations were also observed between seed yield and pollen viability (r = 0.299) and 100 seed weight (r = 0.341). These findings highlight the interdependency of morphological and reproductive traits on yield potential, supporting the results reported by Nguyen *et al.* (2019) [9] and Barros *et al.* (2024) [3].

Although phenotypic correlation values were generally lower than their genotypic counterparts likely due to environmental influences—they exhibited similar trends. For example, seed yield per plant was phenotypically correlated with primary branches (r = 0.859), secondary branches (r = 0.769), pods per plant (r = 0.847), and plant height (r = 0.619). These traits are thus confirmed as reliable indicators of yield potential under field conditions. Similar relationships were observed by Saidaiah *et al.* (2021) [10], who also emphasized the utility of branching and reproductive attributes in yield prediction models for legumes.

Tables and figures

Table 1: Analysis of Variance for 13 characters of 22 cowpea genotypes.

Sr. No.	Characters	Mean sum of squares		
		Replications (3)	Treatment (22)	Error (66)
1.	Days to 50% flowering	7.92	181.42**	3.01
2.	Days to maturity	41.87	35.70*	15.76
3.	Plant height (cm)	52.25	1280.51**	21.97
4.	No. of primary branches per plant	2.69	13.34**	1.03
5.	No. of secondary branches per plant	12.02	214.02**	3.79
6.	No. of pods per plant	27.16	346.18**	11.30
7.	Pod length (cm)	1.14	8.73**	0.55
8.	No. of seeds per pod	0.39	5.45**	0.61
9.	100 seed weight	1.97	6.94**	0.68
10.	Pollen viability (%)	31982.68	871.89**	22.71
11.	Pollen viability (%)	66.14	465253.48**	10883.9
12.	Seed yield per plant (g)	23.92	85.17**	15.14
13.	Seed yield per hectare (kg)	28.74	88.62**	11.96

* and ** denotes significant at 5 and 1 percent level of significance, respectively.

Table 2: Estimates of variability parameters for yield and its contributing characters in 22 genotypes of cowpea.

Sr. No.	Character	Mean	Range		GCV (%)	PCV (%)	ECV (%)	Heritability (b.s)%	GA as% of Mean
1	Days to 50% flowering	47.33	37	66	16.29	16.7	3.67	95.17	32.74
2	Days to maturity	86.06	73	96	2.99	5.5	4.61	29.65	3.36
3	Plant height (cm)	63.06	39.8	125.4	32.48	33.32	7.43	95.02	65.22
4	No. of primary branches/plant	12.25	8.4	18.6	16.54	18.5	8.29	79.91	30.46
5	No. of secondary branches/plant	21.47	12	48	39	40.04	9.07	94.87	78.25
6	No. pods per plant	36.72	16.6	56.9	28.77	30.19	9.16	90.81	56.48
7	Pod Length(cm)	13.32	8.46	17.52	12.39	13.6	5.61	82.99	23.25
8	No. of seed per pod	13.43	10.36	18.28	9.46	11.11	5.82	72.53	16.6
9	100 Seed weight (g.)	9.56	5.99	13.34	15.12	17.41	8.63	75.44	27.06
10	Seed yield/plant (g.)	48.39	20.56	91.52	34.77	36.13	9.85	92.57	68.9
11	Seed yield/ha(Kg.)	1117.91	474	2114.4	34.88	35.90	8.51	94.38	69.80
12	Pollen Viability (%)	83.92	67	96	5.76	7.39	4.64	60.65	9.24
13	Pollen Germination (%)	84.88	70	98	5.96	7.22	4.08	68.11	10.12

GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV = Environmental coefficient of variation, GA = Genetic advanc

Table 3: Estimates of genotypic correlation coefficients of yield contributing characters with yield in 22 cowpea genotypes.

Characters	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm.)**	**No. of primary branches/ plant**	**No. of secondary branches/ plant**	**No. pods per plant**	**Pod Length (cm)**	**No. of seeds/ pod**	**100 seeds weight (g.)**	**Pollen Viability (%)**	**Pollen Germination (%)**	**Seed yield/ plant (g.)**
Days to 50% flowering	1	0.864 **	-0.184	0.057	-0.076	0.147	-0.061	-0.147	0.304	0.033	-0.006	0.147
Days to maturity		1	-0.202	-0.152	-0.195	0.119	0.170	-0.273	0.147	0.05	0.168	0.109
Plant height (cm)			1	0.702 **	0.877 **	0.579 **	0.709 **	0.679 **	0.122	0.577 **	0.376	0.667 **
No. of primary branches/plant				1	0.906 **	0.863 **	0.516 *	0.796 **	0.259	0.290	0.107	0.988 **
No. of secondary branches/plant					1	0.669 **	0.584 **	0.740 **	0.248	0.376	0.239	0.837 **
No. pods per plant						1	0.538 **	0.660 **	0.139	0.292	0.216	0.895 **
Pod Length(cm)							1	0.459 *	0.277	0.403	0.318	0.554 **
No. of seed per pod								1	-0.184	0.212	0.224	0.684 **
100 Seed weight (g.)									1	0.367	0.295	0.341
Pollen Viability (%)										1	0.676 **	0.299
Pollen Germination (%)											1	0.224
Seed yield/plant (g.)												1

*, ** denotes significance at 5 per cent and 1 per cent levels respectively.

Table 4: Estimates of phenotypic correlation coefficients of yield contributing characters with yield in 22 cowpea genotypes.

Characters	**Days to 50% flowering**	**Days to maturity**	**Plant height (cm.)**	**No. of primary branches/ plant**	**No. of secondary branches/ plant**	**No. pods per plant**	**Pod Length (cm)**	**No. of seeds/ pod**	**100 seeds weight (g.)**	**Pollen Viability (%)**	**Pollen Germination (%)**	**Seed yield/ plant (g.)**
Days to 50% flowering	1	0.481 **	-0.176	0.072	-0.067	0.125	-0.052	-0.122	0.223	0.046	0.042	0.129
Days to maturity		1	-0.098	0.025	-0.090	0.072	0.010	-0.143	0.097	0.098	0.067	0.057
Plant height (cm)			1	0.625 **	0.833 **	0.520 **	0.64 **	0.569 **	0.111	0.441 **	0.302 *	0.619 **
No. of primary branches/plant				1	0.807 **	0.730 **	0.420 **	0.575 **	0.224	0.241	0.133	0.859 **
No. of secondary branches/plant					1	0.623 **	0.524 **	0.577 **	0.164	0.283 *	0.192	0.769 **
No. pods per plant						1	0.485 **	0.590 **	0.139	0.214	0.109	0.847 **
Pod Length(cm)							1	0.319 **	0.211	0.336 **	0.210	0.468 **
No. of seed per pod								1	-0.090	0.170	0.197	0.591 **
100 Seed weight (g.)									1	0.304 *	0.175	0.361 **
Pollen Viability (%)										1	0.51 **	0.261 *
Pollen Germination (%)											1	0.157
Seed yield/plant (g.)												1

*, ** denotes significance at 5 per cent and 1 per cent levels respectively

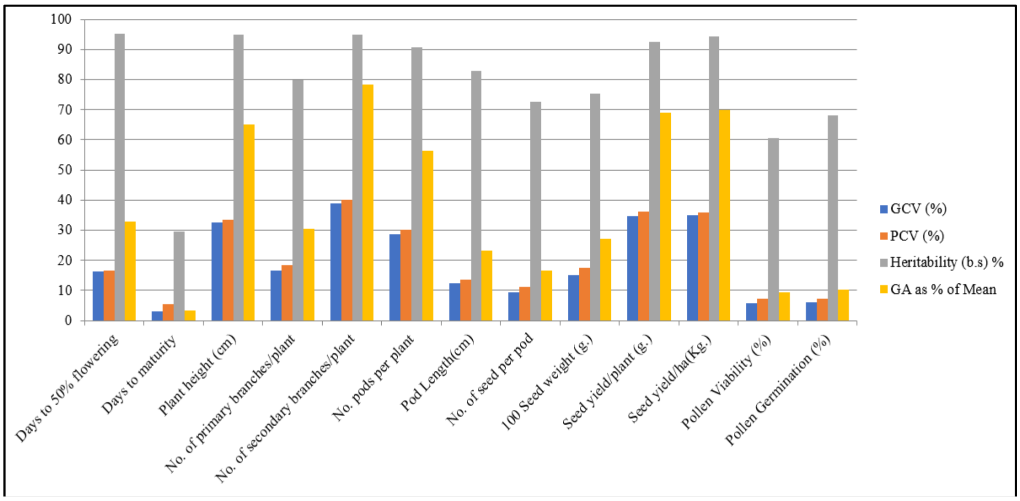
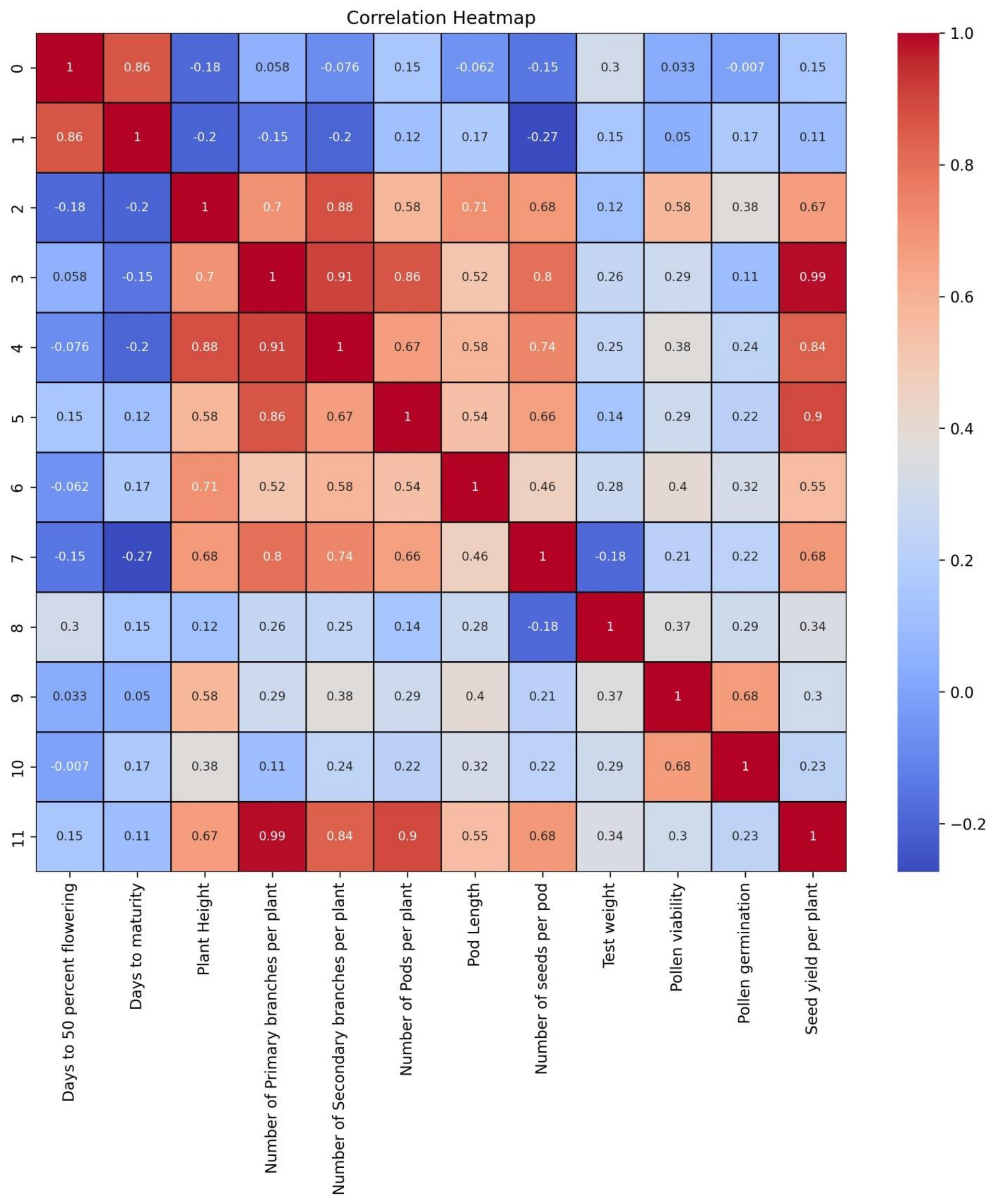
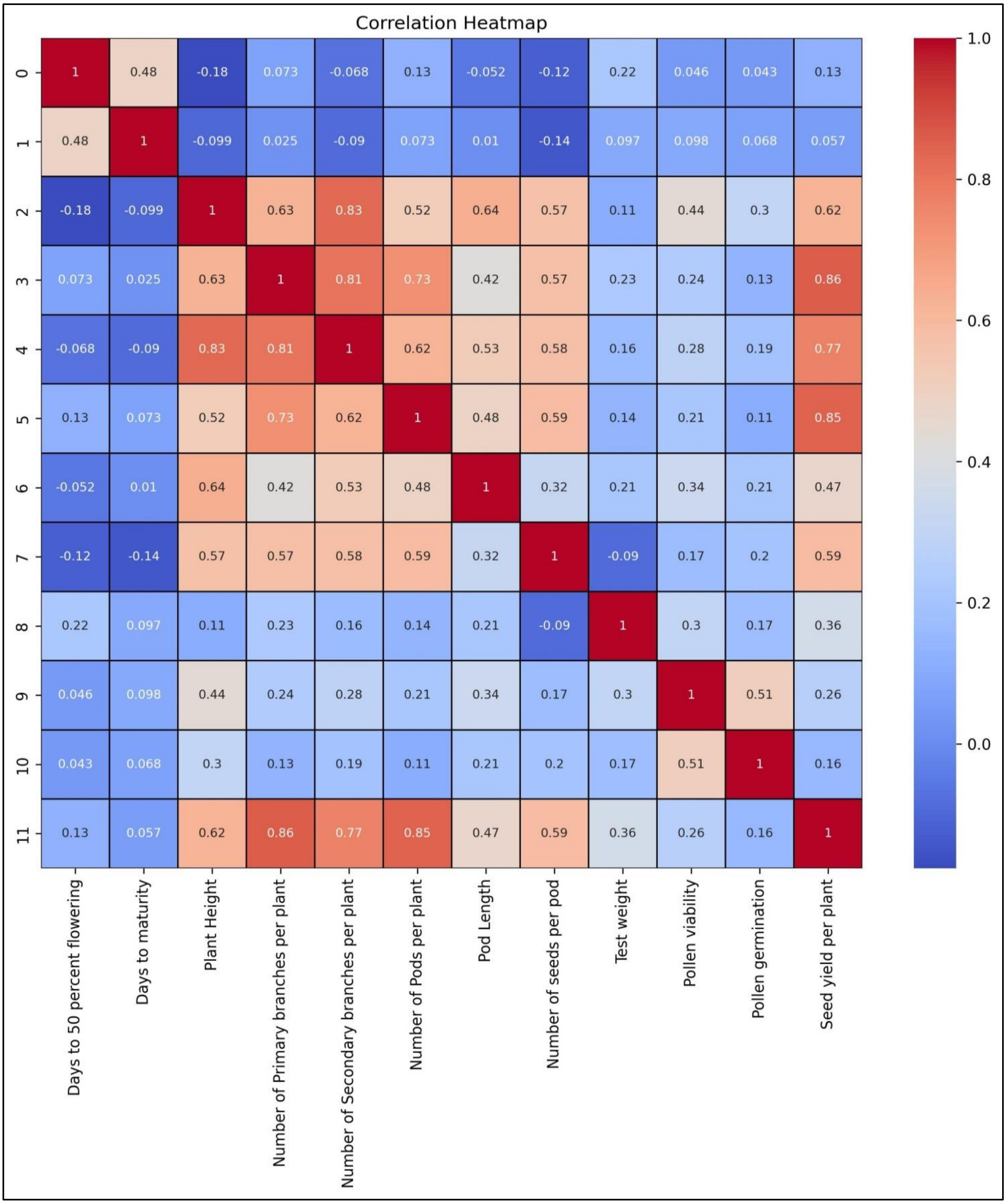


Fig 1: Distribution of GCV, PCV, genetic advance as a percentage of the mean and heritability for various traits across 22 Cowpea [*Vigna ungiculata* (L.) Walp] genotypes.



	Days to 50 percent flowering	Days to maturity	Plant Height	Number of Primary branches per plant	Number of Secondary branches per plant	Number of Pods per plant	Pod Length	Number of seeds per pod	Test weight	Pollen viability	Pollen germination	Seed yield per plant
0	1	0.86	-0.18	0.058	-0.076	0.15	-0.062	-0.15	0.3	0.033	-0.007	0.15
1	0.86	1	-0.2	-0.15	-0.2	0.12	0.17	-0.27	0.15	0.05	0.17	0.11
2	-0.18	-0.2	1	0.7	0.88	0.58	0.71	0.68	0.12	0.58	0.38	0.67
3	0.058	-0.15	0.7	1	0.91	0.86	0.52	0.8	0.26	0.29	0.11	0.99
4	-0.076	-0.2	0.88	0.91	1	0.67	0.58	0.74	0.25	0.38	0.24	0.84
5	0.15	0.12	0.58	0.86	0.67	1	0.54	0.66	0.14	0.29	0.22	0.9
6	-0.062	0.17	0.71	0.52	0.58	0.54	1	0.46	0.28	0.4	0.32	0.55
7	-0.15	-0.27	0.68	0.8	0.74	0.66	0.46	1	-0.18	0.21	0.22	0.68
8	0.3	0.15	0.12	0.26	0.25	0.14	0.28	-0.18	1	0.37	0.29	0.34
9	0.033	0.05	0.58	0.29	0.38	0.29	0.4	0.21	0.37	1	0.68	0.3
10	-0.007	0.17	0.38	0.11	0.24	0.22	0.32	0.22	0.29	0.68	1	0.23
11	0.15	0.11	0.67	0.99	0.84	0.9	0.55	0.68	0.34	0.3	0.23	1

Fig 2: Genotypic correlation heat map of twelve characters of Cowpea for twenty two genotypes



	Days to 50 percent flowering	Days to maturity	Plant Height	Number of Primary branches per plant	Number of Secondary branches per plant	Number of Pods per plant	Pod Length	Number of seeds per pod	Test weight	Pollen viability	Pollen germination	Seed yield per plant
0	1	0.48	-0.18	0.073	-0.068	0.13	-0.052	-0.12	0.22	0.046	0.043	0.13
1	0.48	1	-0.099	0.025	-0.09	0.073	0.01	-0.14	0.097	0.098	0.068	0.057
2	-0.18	-0.099	1	0.63	0.83	0.52	0.64	0.57	0.11	0.44	0.3	0.62
3	0.073	0.025	0.63	1	0.81	0.73	0.42	0.57	0.23	0.24	0.13	0.86
4	-0.068	-0.09	0.83	0.81	1	0.62	0.53	0.58	0.16	0.28	0.19	0.77
5	0.13	0.073	0.52	0.73	0.62	1	0.48	0.59	0.14	0.21	0.11	0.85
6	-0.052	0.01	0.64	0.42	0.53	0.48	1	0.32	0.21	0.34	0.21	0.47
7	-0.12	-0.14	0.57	0.57	0.58	0.59	0.32	1	-0.09	0.17	0.2	0.59
8	0.22	0.097	0.11	0.23	0.16	0.14	0.21	-0.09	1	0.3	0.17	0.36
9	0.046	0.098	0.44	0.24	0.28	0.21	0.34	0.17	0.3	1	0.51	0.26
10	0.043	0.068	0.3	0.13	0.19	0.11	0.21	0.2	0.17	0.51	1	0.16
11	0.13	0.057	0.62	0.86	0.77	0.85	0.47	0.59	0.36	0.26	0.16	1

Fig 3: Phenotypic correlation heat map of twelve characters of Cowpea for twenty two genotypes

4. Conclusion

In this study, significant genetic variability was observed among 22 cowpea genotypes across key agronomic and reproductive traits. Traits such as plant height, primary and secondary branching, pod number, and seed yield exhibited high heritability and genetic advance, indicative of additive gene action and suitability for phenotypic selection. The strong positive correlations between these traits and seed yield reinforce their value as selection markers in cowpea breeding. In addition, moderate associations of pollen viability and germination with seed yield highlight the relevance of incorporating reproductive efficiency into breeding strategies. The superior genotypes characterized and their favorable trait combinations offer a robust genetic foundation for developing high-yielding, drought-resistant cowpea cultivars tailored to rainfed and semi-arid agro-ecological regions.

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6. Conflict of Interest

The authors declare that they have no conflict of interest related to the publication of this manuscript.

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