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RESEARCH ARTICLE

Assessing genetic variation and trait associations in cowpea (*Vigna ungucuilata* (L.) (Walp.) genotypes for yield optimization

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Abstract

The study was conducted at the Horticultural College and Research Station, Vegetable Science Department of TNAU, Coimbatore. Thirty cowpea genotypes, including 2 check varieties, were used to measure genetic variation, heritability and the genetic improvement across 13 key traits. The results suggested that for all traits, phenotypic variation exceeded genotypic variation, indicating that environmental factors played a dominant role in the observed variation. Genetic diversity was observed from the GCV values for several traits. These traits are associated with high heritability and significant genetic improvement, especially for characters such as pod weight, per plant pod yield and pod length, which are mainly controlled by additive genes; thus, they are suitable for use in breeding program to improve yield. The important trait in selecting high-yield cowpea varieties is shown by the strong positive genetic resemblance between the per pod seed number and per plant pod yield. PCA identified 5 main components that showed 77.53 % of the total variation. Traits with positive values in each component were considered the most important for yield, making them key factors for selecting high-yielding cowpea varieties.

Keywords: correlation; cowpea; genetic advance; heritability; pca variability

Abbreviations

DFG: Days for germination; DF50 %: Days for 50 % flowering; DFF: Days for first flowering; DFH: Days for the first harvest; PH: Plant height (cm) ; NB/P: No. of branches per plant; NOF/P: No. of flowers per plant; NOP/P: No. of pods per plant; PL: Pod length (cm); PG: Pod girth (cm); PW: Pod weight (g); NS/P: No. of seeds per pod; PY/P: Pod yield per plant (g)

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.), also known as Poor Man's Meat, Lobiya, Black-eyed pea, Southern pea, Barbati or the Hungry Season Crop, is a leguminous plant valued for its high protein content, which helps address protein deficiency in India (1, 2). Despite its nutritional and farming benefits, cowpea's average yield is relatively low, around 350 kg/ha, compared to other pulses. However, the global cowpea market is projected to grow from USD 7.21 billion in 2023 to USD 9.43 billion by 2028, with an impressive annual growth rate of approximately 5.50 % (3).

Enhancing cowpea yield can boost production, provide protein rich food and improve soil fertility through nitrogen fixation. In vegetable cowpeas, where tender green pods are highly valued, improving yield in the varieties being developed depends on the genetic potential of the plants and the inheritance of specific traits.

For breeders seeking to develop new cultivars or enhance existing ones to meet shifting consumer preferences, evaluating genetic resources is crucial. Given that crop yield is a multifaceted trait, it is critical to understand how yield is related to its contributing factors, as well as to assess the variability within the available germplasm. This genetic variability is the foundation of any breeding program, particularly when considering the various agro-climatic zones from which genotypes may be sourced. Analyzing crop diversity and variability is an essential tool for evaluating genetic variation and heritability within germplasm. Combining heritability estimates with genetic gain offers valuable insights into the potential for selecting superior individuals (4). Developing high-yielding varieties requires a thorough understanding of genetic variability and the relationships between traits. Analytical techniques, such as Principal Component Analysis (PCA), are essential for exploring these relationships and identifying the key traits that should be prioritized for yield improvement.

This study focused on the genetic differences in traits that impact green pod yield, examining factors such as genotypic and phenotypic variation, heritability and genetic gain. Additionally, the research examined the relationships between traits and employed PCA to identify the most significant traits to focus on for yield enhancement.

Material and Methods

A. Agronomic evaluation

The investigation comprised 30 cowpea genotypes, including 2 check varieties, Kashi Kanchan and Kashi Nidhi and was conducted in 2024 at the college orchard in Horticulture College and Research Institute (HC&RI), Coimbatore, Tamil Nadu, India. Seeds were sourced from the National Bureau of Plant Genetic Resources (NBPGR), as listed in (Table 1) and have been sown in well-prepared soil with 30 cm and 40 cm between rows and plants respectively. An experimental design Randomized Block Design (RBD) was adopted in this study, with 3 repetitions. Specifically, a Randomized Block Design (RBD) was adopted in this study, with 3 repetitions to ensure reliable results. Readings were taken on 5 plants at random under each replication for 13 traits (germination days, flowering and harvest timelines, plant height, number of branches, flowers and pods, as well as pod length, weight, girth, seeds per pod and pod yield per plant).

B. Data collection and statistical analysis

Readings were taken from 5 randomly selected plants per replication for 13 traits, including germination days, flowering and harvest timelines, plant height, number of branches, flowers and pods, as well as pod length, weight, girth, seeds per pod and pod yield per plant. Variability analysis, including the Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), (1) broad-sense heritability (h^2), genetic advance (GA) and (2) genetic advance as a percentage of the mean (GAM), as well as genotypic correlations among traits, were analyzed using data processed in R Studio (version 4.3.3) with the *variability* package (3). This approach provided a comprehensive understanding of the genetic architecture of the genotypes studied. Additionally, PCA was performed using the *FactoMineR* and *factoextra* packages in R Studio (5, 6).

Results and Discussion

A substantial difference was observed among the genotypes for every trait studied. Table 2 shows that the average values for each trait varied notably across the genotypes, aligning with the findings of previous studies (7, 8). This variation suggests the potential for utilizing breeding and selection methods to enhance specific traits, such as pod yield and nutritional quality, in cowpea germplasm.

A broad variation was observed among the genotypes for several traits, as presented in Table 3. The number of flowers per plant varied from 56.79 - 28.21, pod weight ranged from 20.25 - 2.07 g and the number of seeds per pod fluctuated between 21.00 and 7.72. Moderate differences were seen in pod length (36.89 - 11.92 cm) and pod yield per plant (290.63 - 1087.83 g). Traits such as days to germination (5.31 - 3.29) and

Table 1. List of germplasm undertaken for evaluation

Accession number	Germplasm	Source of genotypes
Cbe-cp-01	IC-536645	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-02	IC-202803	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-03	IC-202526	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-04	IC-559399	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-05	IC-536635	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-06	IC-202804	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-07	IC-209711	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-08	IC-201075	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-09	IC-97797	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-10	IC-559387	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-11	IC-536572	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-12	IC-202931	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-13	IC-536638	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-14	IC-559406	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-15	IC-337932	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-16	EC-390213	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-17	Kairali	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-18	Lola	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-19	Anaswara	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-20	Geethika	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-21	Kashi Unnati	Indian Institute of vegetable research, Varanasi, UP
Cbe-cp-22	EC-390220	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-23	EC-472272	National Bureau of Plant Genetic Resources, New Delhi
Cbe-cp-24	Local type-1	Coimbatore, Tamil Nadu
Cbe-cp-25	Kashi Nidhi	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-26	Local type-2	Erode, Tamil Nadu
Cbe-cp-27	Kashi Vishan	Indian Institute of Vegetable Research, Varanasi, UP
Cbe-cp-28	Local type-3	Erode, Tamil Nadu
Check 1	Kashi Kanchan	Indian Institute of Vegetable Research, Varanasi, UP
Check 2	Kashi Gauri	Indian Institute of Vegetable Research, Varanasi, UP

Table 2. Mean performance of cowpea genotypes for various growth quantitative traits

Accessions	DFG	DFF	DF50 %	DFH	PH	NOB/P	NOF/P	NOP/P	PL	PG	PW	NS/P	PY/P
Cbe-cp-01	4.10	36.81	40.13	50.14	70.44	4.13	34.68	18.60	14.10	2.41	6.80	9.81	1042.41
Cbe-cp-02	4.63	35.16	40.06	50.81	75.13	4.63	49.14	26.13	14.82	2.52	15.61	18.91	1011.36
Cbe-cp-03	4.48	38.03	42.41	53.14	70.83	3.42	48.61	21.14	17.13	1.98	18.21	20.14	290.63
Cbe-cp-04	4.90	39.14	43.06	55.19	69.41	3.14	32.41	16.03	14.08	2.10	2.60	10.12	408.97
Cbe-cp-05	5.10	35.91	40.63	50.83	72.41	4.83	49.48	23.11	21.32	3.62	20.21	18.24	1079.32
Cbe-cp-06	3.86	34.81	39.06	50.06	71.31	4.91	52.10	20.32	16.21	2.51	15.16	16.14	1057.24
Cbe-cp-07	4.08	34.11	39.86	50.14	68.13	5.14	56.18	24.63	17.02	1.24	16.78	15.14	1046.75
Cbe-cp-08	4.36	36.81	41.54	51.08	70.51	5.56	36.14	15.43	15.16	2.61	3.62	8.01	332.41
Cbe-cp-09	3.91	35.13	40.61	51.14	71.16	3.41	40.46	16.14	14.12	3.08	5.43	12.14	322.94
Cbe-cp-10	5.14	37.18	43.14	53.61	68.14	2.91	36.31	14.44	15.80	2.52	2.16	10.32	389.18
Cbe-cp-11	4.16	34.16	39.18	50.16	65.33	3.36	29.13	11.86	23.14	3.68	13.14	16.14	800.67
Cbe-cp-12	3.76	36.10	41.03	51.12	69.43	3.86	48.44	20.13	15.14	3.84	8.14	14.61	549.30
Cbe-cp-13	4.01	35.18	40.41	50.33	72.14	4.12	38.11	14.40	15.01	3.80	4.98	11.42	434.16
Cbe-cp-14	3.38	35.14	40.61	50.63	73.16	5.12	31.33	11.86	14.81	1.81	14.91	17.41	1087.83
Cbe-cp-15	4.16	37.14	41.43	52.14	69.14	4.63	50.10	24.82	16.12	3.04	4.86	11.42	468.42
Cbe-cp-16	4.03	38.18	43.61	52.81	68.41	3.91	32.14	16.34	14.91	3.81	8.91	15.30	503.73
Cbe-cp-17	5.04	35.60	41.16	50.71	78.66	3.07	49.14	17.12	29.14	1.81	8.68	12.91	743.69
Cbe-cp-18	4.36	36.14	43.48	51.43	88.34	2.91	38.61	14.61	18.03	3.08	5.61	12.44	946.41
Cbe-cp-19	4.68	35.33	41.14	50.83	81.64	3.14	32.03	13.06	20.13	1.88	10.81	15.06	825.19
Cbe-cp-20	3.91	36.18	42.14	51.43	70.68	3.91	46.14	16.12	15.81	2.14	6.82	10.43	770.21
Cbe-cp-21	4.15	37.81	43.40	52.61	73.61	3.00	39.19	17.03	23.12	2.32	5.14	11.10	965.51
Cbe-cp-22	3.66	38.16	43.68	53.78	63.81	3.61	35.03	13.82	17.13	2.61	8.10	12.14	908.14
Cbe-cp-23	3.98	36.96	40.03	51.41	72.14	2.81	29.13	14.03	15.14	3.14	9.71	10.46	819.27
Cbe-cp-24	4.13	37.93	41.41	53.61	66.54	3.63	31.10	12.83	36.31	3.70	6.92	11.14	979.52
Cbe-cp-25	4.91	38.06	42.83	54.63	70.86	3.14	36.33	15.08	25.11	1.81	4.14	12.71	643.25
Cbe-cp-26	4.86	37.14	43.06	53.16	69.14	3.91	32.10	11.33	18.41	2.76	9.81	10.37	743.37
Cbe-cp-27	4.91	36.13	42.13	54.11	65.32	3.86	38.14	13.40	26.12	1.28	6.72	13.14	879.63
Cbe-cp-28	4.81	38.43	40.14	53.81	63.88	4.01	37.13	14.81	12.14	2.61	10.92	12.16	959.95
Check 1	4.11	37.16	41.31	52.61	52.14	3.91	48.14	18.31	20.13	3.02	8.14	16.44	1153.93
Check 2	4.18	35.19	40.82	51.48	59.14	3.98	42.13	19.13	19.14	2.61	8.63	14.12	1147.46
SE(m)	*0.070*	*0.590*	*0.614*	*0.699*	*1.045*	*0.048*	*0.593*	*0.218*	*0.303*	*0.044*	*0.138*	*0.198*	*0.035*
CD 5 %	*0.200*	*1.671*	*1.739*	*1.979*	*2.960*	*0.137*	*1.679*	*0.618*	*0.859*	*0.124*	*0.391*	*0.563*	*0.099*
CD 1 %	*0.266*	*2.223*	*2.314*	*2.633*	*3.938*	*0.183*	*2.234*	*0.823*	*1.145*	*0.166*	*0.520*	*0.749*	*0.132*

Table 3. A simple analysis of variability among the 30 cowpea genotypes

Character	Grand mean	Range of mean		Coefficient of variability (%)		Heritability in a broad sense (%)	Genetic advance	Genetic advance as a percentage of mean
		Maximum	Minimum	GCV	PCV			
Days for germination	4.23	5.31	3.29	10.72	11.08	93.48	0.92	21.35
Days for first flowering	36.50	40.00	32.84	3.33	4.35	58.59	1.91	5.25
Days for 50 % flowering	41.45	44.91	37.33	2.94	3.90	56.78	1.89	4.56
Days for first harvest	51.96	55.93	48.16	2.55	3.45	54.62	2.02	3.86
Plant height (cm)	70.03	88.47	51.59	9.04	9.41	92.45	12.55	17.92
No. of branches per plant	3.86	5.66	2.77	19.24	19.36	98.73	1.52	39.39
No. of flowers per plant	39.97	56.79	28.21	19.48	19.65	98.29	15.90	39.80
No. of pods per plant	16.86	26.20	11.25	23.80	23.90	99.12	8.23	48.82
Pod length (cm)	18.49	36.89	11.92	28.44	28.58	99.01	10.78	58.29
Pod girth (cm)	2.64	3.93	1.19	27.95	28.10	98.95	1.51	57.28
Pod weight (g)	9.05	20.25	2.07	52.14	52.21	99.74	9.71	107.27
No. of seeds per pod	13.32	21.00	7.72	22.59	22.74	98.71	6.16	46.24
Pod yield per plant (kg)	2.199	3.92	0.97	38.68	38.78	99.49	1.74	79.48

pod girth (3.93 - 1.19 cm) exhibited slight variation. These results revealed more variation among the genotypes, suggesting them to be a good potential for selective breeding.

Variability analysis

From Table 3, it was inferred that the highest PCV and GCV were found for pod weight, with values of 52.21 % and 52.14 % respectively. Pod yield per plant was also high, with values of 38.78 % PCV and 38.68 % GCV. Traits like the number of pods per plant and pod girth had a smaller range, with PCV and GCV between 27 % and 28 %. The lowest PCV and GCV were seen for traits like days to first harvest (2.55 % and 3.45 %, respectively) and days to 50 % flowering (2.94 % and 3.90 %), showing less genetic variation for these traits. These results are consistent with previous findings in terms of the number of seeds per pod, pod yield and pod weight; the number of pods per plant; plant height; and the days to first harvest, where lower variation was also noted (9–12).

The pod weight showed the most significant heritability estimates at 99.74 %, with pod yield per plant at 99.49 % and pod length at 99.12 % coming next. Traits like the number of seeds per pod, pod girth, number of flowers per plant and number of branches per plant showed around 98 % heritability. The strong heritability values suggest that these characters are less prone to environmental variation and have a high potential to be inherited by the next generations. Similar results were noted from the findings of some studies (9, 13). The lowest heritability was observed for traits like days to first harvest (54.62 %) and days to 50 % flowering (56.78 %), which is consistent with the results of another study (10).

Moderate genetic advance (between 11 - 20 %) was observed for the number of flowers per plant (15.90 %), followed by plant height (12.55 %) and pod length (10.78 %). The lowest genetic advance (between 1 - 10 %) was observed for traits such as days to germination (0.92 %), pod girth (1.51 %), number of branches per plant (1.52 %) and pod yield per plant (1.74 %). The ability to achieve genetic improvement through selection is determined by the genetic variation within the population and the heritable nature of the specific trait.

The genetic advance as a percentage of the mean (GAM) represents the projected improvement in a trait through selection, expressed as a percentage of the population's mean. Maximum GAM was observed for pod weight (107.27 %), indicating this trait has a massive impact on the progress achieved via direct selection in breeding programs. The pod yield per plant had a general additive model (GAM) of 79.48 %, further indicating its potential for genetic improvement.

Genetic correlation analysis

Table 4 presents the genotypic correlation coefficients between pod yield per plant and the other characters studied. A positive correlation was found between pod weight and pod yield per plant (0.6747), which is highly significant ($\rho \leq 0.01$). Days to first flowering also had a strong correlation with days to 50 % flowering (0.8540) and days to first harvest (1.0010). Pod weight was significantly correlated with the number of seeds per pod (0.8202) and pod yield per plant (0.6747). The number of seeds per pod also had a significant correlation with pod yield per plant (0.4212). These results are similar to the studies, in which it was noted a positive correlation with the number of seeds per pod (13–15). A negative correlation detected between per plant pod yield and days taken for 50 % flowering (16–18).

The correlation matrix gives essential information for breeding cowpea genotypes with high yield potential. Positive correlations between traits such as the number of seeds per plant, pod weight and number of branches per plant suggest that they should be prioritized in the selection, as they contribute directly to higher pod yields.

Principal component analysis (PCA)

Principal Component Analysis (PCA) is a technique used to reduce the complexity of data by decreasing the number of variables while retaining the majority of the critical information (5). It creates new variables called principal components (PCs), which are combinations of the original traits. These components help identify patterns and show how each trait contributes to the overall differences.

In this study, PCA was used to understand how different traits contributed to the differences among 30 cowpea

Table 4. Genotypic correlation coefficient between different horticultural traits in cowpea genotypes

GENOTYPES	DFG	DFF	DF50%	DFH	PH	NOB/P	NOF/P	NOP/P	PL	PG	PW	NS/P	PY/P
DFG	1 **	0.2613	0. 2694	0.4365*	0.1528	-0.2729	0.0102	0.0140	0.2720	-0.2638	-0.0602	-0.0585	-0.1047
DFF		1 **	0.8540**	1.0010**	-0.2407	-0.3860*	-0.3812*	-0.2101	0.0221	0.0463	-0.4536*	-0.3941*	-0.3148
DF50%			1 **	0.9115**	0.1035	-0.4884**	-0.2896	-0.3100	0.2142	-0.1142	-0.5480**	-0.3410	-0.4868**
DFH				1 **	-0.3910*	-0.4739**	-0.3546	-0.3327	0.2198	-0.1819	-0.463**	-0.2893	0.3252
PH					1 **	-0.1870	-0.0362	-0.0284	-0.0184	-0.1197	0.0391	-0.0246	-0.0563
NOB/P						1 **	0.3930*	0.4391*	-0.2801	-0.038	0.4073*	0.429*	0.4548*
NOF/P							1 **	0.8447**	-0.0707	-0.1731	0.3834*	0.4236*	0.2306
NOP/P								1 **	-0.2190	-0.0460	0.4029*	0.429*	0.2933
PL									1 **	-0.0462	-0.0406	0.0212	-0.0982
PG										1 **	-0.0739	-0.0250	-0.2800
PW											1 **	0.8202**	0.6747**
NS/P												1 **	0.4212*
PY/P													1 **

*: Correlation is significant at the 5 % level (p ≤ 0.05); **: Correlation is highly significant at the 1 % level (p ≤ 0.01).

Table 5. Eigenvalues, percent variation and cumulative percentage of 13 traits toward principal compounds

Variables	Eigenvalue	Variability (%)	Cumulative %
PC1	4.482	34.478	34.478
PC2	1.831	14.085	48.563
PC3	1.460	11.231	59.794
PC4	1.232	9.473	69.267
PC5	1.074	8.260	77.527
PC6	0.889	6.838	84.365
PC7	0.634	4.880	89.245
PC8	0.510	3.924	93/169
PC9	0.399	3.072	96.241
PC10	0.211	1.619	97.860
PC11	0.125	0.962	98.822
PC12	0.097	0.744	99.566
PC13	0.056	0.434	100.00

Table 6. Relative contribution of 13 characters towards divergence in the extracted PCs for 30 cowpea genotypes

Variables	PC1	PC2	PC3	PC4
Days for germination	0.136	0.456	0.297	0.108
Days for first flowering	0.339	0.262	-0.332	-0.054
Days for 50 % flowering	0.350	0.237	-0.055	0.160
Days for first harvest	0.355	0.384	0.218	-0.177
Plant height (cm)	-0.014	-0.082	0.590	0.429
No. of branches per plant	-0.313	-0.030	-0.320	0.010
No. of flowers per plant	-0.398	0.311	-0.140	0.417
No. of pods per plant	-0.301	0.298	-0.248	0.414
Pod length (cm)	0.103	0.179	0.381	-0.318
Pod girth (cm)	0.023	-0.394	-0.226	-0.065
Pod weight (g)	-0.371	0.199	0.116	-0.313
No. of seeds per pod	-0.311	0.255	0.083	-0.249
Pod yield per plant (kg)	-0.304	0.179	0.013	-0.361

genotypes. The variation was spread across 13 principal components. Table 5 shows the percentage contribution of each element and Table 6 highlights the extent to which each trait contributed to the differences in the components.

The PCA analysis showed that the first 5 eigenvectors had eigenvalues than 1, together accounting for 77.53 % of the total variation in yield and related characters among the 30 genotypes. This matches the findings of the study, in which it was suggested that a variation percentage above 75 % is ideal for characterizing and evaluating cowpea genotypes(19, 20). The results indicate that the first 5 principal components contribute the most variance in the data, while each subsequent component explains less variance and is not related to the previous ones. Thus, the dataset could be simplified, keeping the vital feature static.

The results in Table 5 indicate that different traits contribute differently to the variation observed in the cowpea genotypes. Traits with higher values have a more significant impact on the main components. Positive means that as the main component increases, the trait also tends to increase, while negative means the trait decreases as the main component increases. In this study, the scores are more significant than ± 0.3, showing that these traits play a key role in the variation (21). In PC1, which accounts for 34.478 % of the total variation, characters *viz.*, days to first harvest (0.355), days taken for 50 % flowering (0.350) and days taken for first flowering (0.339) are the main contributors. These traits have higher values, indicating they strongly influence PC1, whereas traits like plant height (-0.014) and pod girth (0.023) have values close to zero, suggesting they contribute very little to the variation in PC1.

In PC2, which accounts for 14.085 % of the total variation, the traits with the highest values are days to germination (0.456), days to first harvest (0.384) and number of flowers per plant (0.311), all of which contribute significantly to this component. In PC3 (11.231 % variability), plant height (0.590) is the main contributor, accounting for most of the variation in this component. For PC4 (9.473 % variability), traits such as plant height (0.429), the number of flowers per plant (0.417) and pod numbers per plant (0.414) play key roles in explaining the variation contributed by this component.

The biplot (Fig. 1) of the first 2 principal components (PC1 and PC2) shows the relationships between the 30 cowpea genotypes and their traits. Genotypes closer to the origin are more similar, while those far away show more significant genetic differences (22). Genotypes such as Cbe-cp-15, Cbe-cp-19, Cbe-cp-20 and Cbe-cp-30 are located near the origin, indicating that they are more similar to each other. Traits such as plant height, pod length, number of flowers per pod, number of pods per plant, number of seeds per pod, pod yield per plant and number of branches are also close to the origin, indicating that these traits are more similar across the studied genotypes. On the other hand, traits like pod girth, days to germination, days to first harvest and days to 50% flowering are farther from the origin, showing more significant differences among the genotypes for these traits. The genotypes furthest from the origin, such as Cbe-cp-7, Cbe-cp-3, Cbe-cp-2, Cbe-cp-6, Cbe-cp-13, Cbe-cp-10, Cbe-cp-25 and Cbe-cp-4, are spread across the biplot, indicating more genetic diversity among them.

The screen plot (Fig. 2) illustrates the contribution of each of the first 10 principal components (PCs) to the total variation. PC1 contributes a substantial amount of variation,

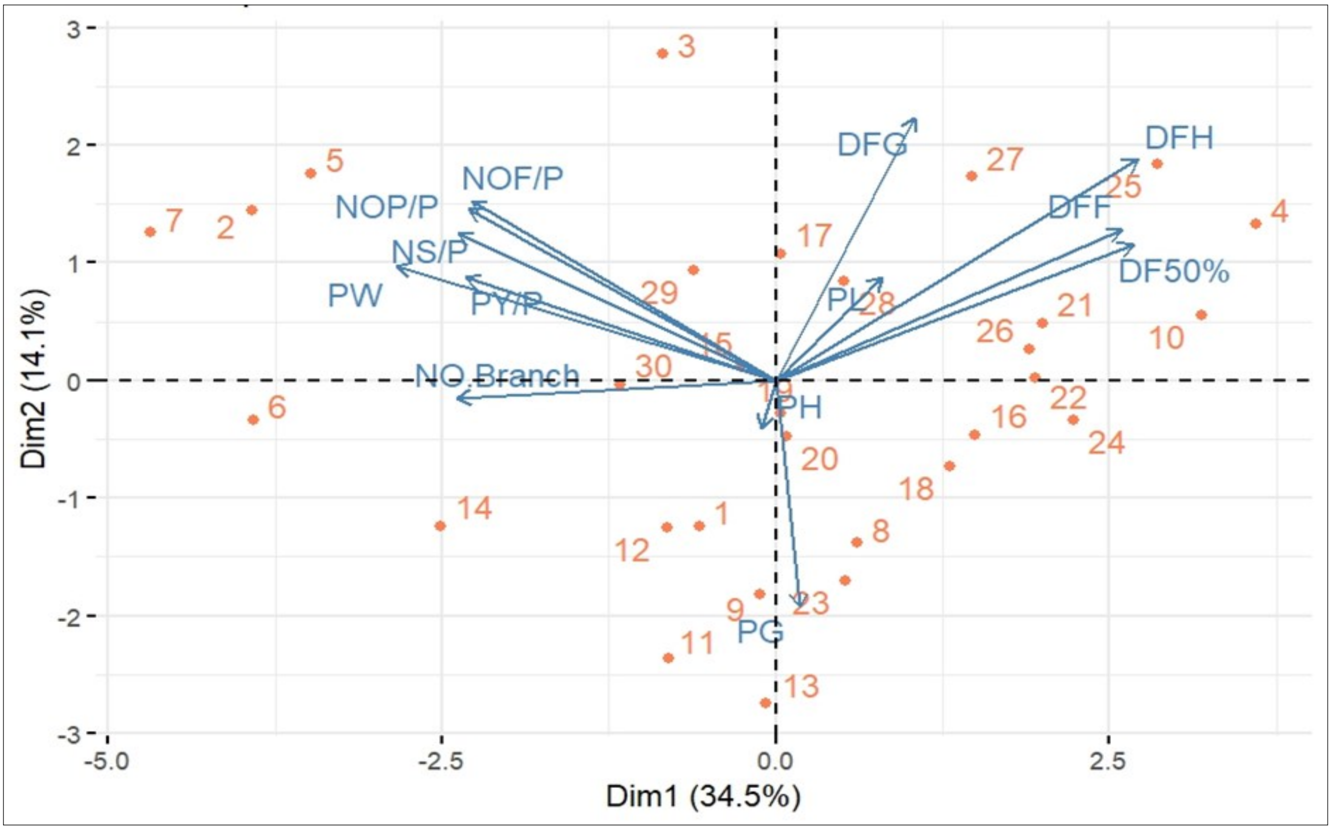

Fig. 1. PCA Biplot between the Principal compound 1 and 2 (PC1 &PC2).

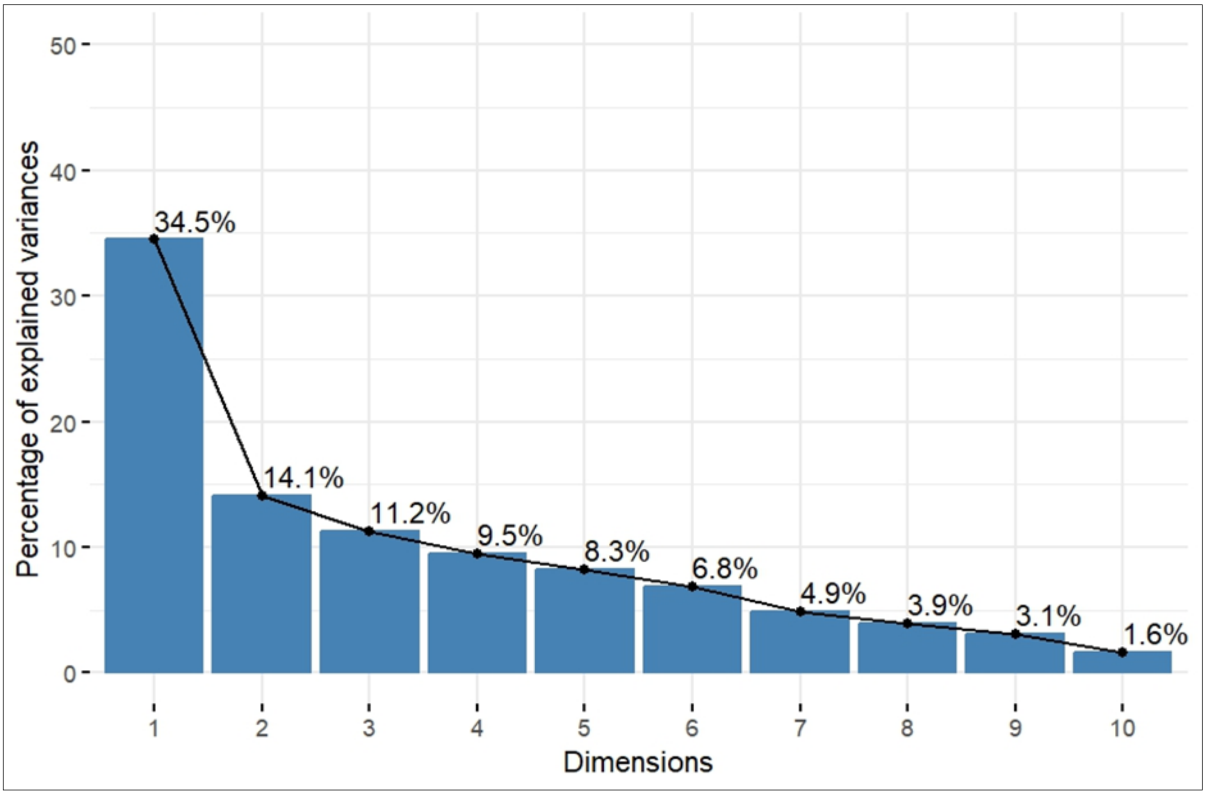

Fig. 2. Screen plot depicting the contribution of various Principal compounds toward the divergence.

indicating that focusing on genotypes based on traits associated with PC1 would yield the most beneficial genetic improvements. This suggests that the traits associated with PC1, which account for 34.5 % of the variability, should be prioritized in breeding decisions to improve desired traits.

Conclusion

This study highlighting the significant variation of characters such as pod weight, pod yield per plant and pod length, which are essential for crop improvement. Environmental factors had a more significant impact than genetic variation for all characters, indicating the more substantial role of the environment. Characters such as pod weight, pod yield per plant and pod length showed high heritability and genetic advancement, suggesting they are essential for developing high-yield varieties. The number of seeds per pod was strongly correlated with pod yield, making it a key trait for enhancing overall yield. Breeding programs should focus on genotypes with higher seed yields per pod to increase yield potential. The PCA analysis grouped traits into four components and traits with positive values should be prioritized in selection for breeding purposes.

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Authors' contributions

RM wrote the original draft and resources collection. Supervision, validation and resources were contributed by CIR, AS, BKS, RN, KG and MS. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Ethical issues: None

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors utilized ChatGPT 4 to enhance the language. After using this tool, the authors reviewed and edited the content as needed and takes full responsibility for the content of the publication.

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