PLANT SCIENCE TODAY
Vol x(x): xx–xx
https://doi.org/10.14719/pst.9633

eISSN 2348-1900

RESEARCH ARTICLE

Assessment of breeding potential of determinate and indeterminate vegetable cowpea genotypes through multivariate analysis for ideotype breeding

Monami Sarkar[1*], Amit Ranjan Mandal[1], Subhrajyoti Sengupta[1], Gayatri Sinha[2], Debanjan Baul[1], Ivi Chakraborty[3], Asit Kumar Mandal[4] & Arup Chattopadhyay[1]

[1]Department of Vegetable Science, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia 741 252, West Bengal, India
[2]Indian Council of Agricultural Research-National Institute of Rice Research, Cuttack 753 006, Odisha, India
[3]Department of Post Harvest Technology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia 741 252, West Bengal, India
[4]Department of Plant Pathology, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia 741 252, West Bengal, India

*Correspondence email - msmonamisarkar@gmail.com

Received: 26 May 2025; Accepted: 08 September 2025; Available online: Version 1.0: 04 December 2025

Cite this article: Monami S, Amit RM, Subhrajyoti S, Gayatri S, Debanjan B, Ivi C, Asit KM, Arup C. Assessment of breeding potential of determinate and indeterminate vegetable cowpea genotypes through multivariate analysis for ideotype breeding. Plant Science Today (Early Access). https://doi.org/10.14719/pst.9633

Abstract

The development of a vegetable cowpea variety that is adaptable to diverse agricultural production systems and has a short, non-vining stem, early maturing and constant green pod bearing, medium-long, meaty pods and a high pod protein content is urgently needed. Using both determinate and indeterminate cowpea genotypes, it is necessary to identify genetically diverse parents for the creation of such a cowpea ideotype. Twenty-four vegetable cowpea genotypes involving both determinate and indeterminate types were assessed for 18 quantitative traits. Genetic variability, correlation and genetic divergence through multivariate analysis were estimated as per the standard procedure through software packages. Based on pod yield, Maharani Laffa Barbati, Kashi Nidhi and Lal Laffa were found superior irrespective of genotypes and need to be critically tested before commercialization. Plant height, branch number per plant, total pickings, marketable pod length, number of marketable pods per plant, seeds per pod, marketable pod weight and yield per plant showed high genetic coefficient of variation, heritability and genetic advance and were primarily governed by additive genetic influences. Pod weight and number of marketable pods per plant were identified as important selection indices for improvement of pod yield. Genetic diversity could not be adequately measured by geographic diversity alone. Three principal components, pod length, plant height and pod protein content, accounted for 95.60 % of the variation irrespective of genotypes, with eigenvalues greater than 1. Based on cluster analysis and scatter diagram of principal component analysis, indeterminate genotypes Asutosh, Vayjayanthi, Shweta, Arya Vaibhav Laxmi and determinate genotype Pusa Komal were found most diverse and could be used as potential donors. The future breeding strategies for the development of cowpea ideotype were discussed.

Keywords: cowpea; genetic divergence; genetic variability; vegetable crop; yield component analysis

Introduction

As a member of the Fabaceae family with the diploid chromosome number “2n=2×=22”, the cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important self-pollinated legume vegetable crops in India. The cowpea is indigenous to West Africa, as opposed to Ethiopia and Africa, which are considered the primary and secondary centres of diversification respectively (1). Five subspecies of cowpea were identified (2), they are *unguiculata*, *cylindrica*, *sesquipedalis*, *mensensis* (Schweint.) and *dekindtiana* (Harms.). The last 2 are considered wild species, while the first 3 are cultivated. Cowpeas are a multipurpose crop that can be grown in a range of climates as a quick-growing cover crop, forage, green manure, grain legumes (mainly for dry beans) and green vegetables. Along with a variety of food, fodder and fibre crops, it makes an excellent companion crop.

Cowpeas are a substantial source of protein (23-30 %) and are sometimes called "vegetable meat" because they supplement diets with other proteins. The problem of protein-related malnutrition could be greatly alleviated by this crop. Another important feature is the capacity to fix atmospheric nitrogen by forming a symbiotic relationship with nodule bacteria (*Bradyrhizobium* spp.). The majority of the varieties cultivated in India are open-pollinated due to the crop's intricate flower structure and challenges with crossover fruit formation. The development of high-yielding, stress-resistant varieties must be carefully considered to increase yield.

Cowpea cultivation faces numerous agronomic and environmental challenges that hinder its productivity, including the limited availability of advanced high-yielding genotypes, degraded soil nutrient status, erratic precipitation patterns driven by climatic fluctuations and the widespread occurrence of biotic stressors such as pathogenic infections, insect infestation and parasitic flora (3). Using a broad range of genotypes based on various growth, leaf, root, nodule, flower, pod, seed and stomatal characteristics, detailed characterization and genetic diversity of *Vigna unguiculata* subspecies *unguiculata*, *sesquipedalis* and *cylindrica* were carried out in multiple sets of experiments (4-7).

Vegetable cowpea pod yield is complicated, varies greatly and is linked to several component traits (8). The potential for increasing the protein contents of both pods and seeds was suggested by the significant variation in both pod and seed protein contents among the genotypes of the 3 cultigroups (9). Improving yield through an efficient selection approach requires a thorough understanding of genetic variability and the correlations among traits, particularly the genotypic and phenotypic relationships between yield and its associated agronomic characteristics (10). Several morphological and yield-related traits, including primary leaf area, leaf dry biomass, individual pod weight, number of pods per plant, length of pods and 100 seed weight, have been recognized as key contributors to pod yield, as evidenced by multiple correlation analysis and a simultaneous path coefficient analysis using phenotypic correlation coefficients (11). Therefore, these traits merit careful consideration for the vegetable cowpea pod yield improvement program. Furthermore, the basis for comprehending the structure of diversity in any intraspecific population is provided by the genetic distance between 2 genotypes. In order to help plant breeders with their selection process, it creates an all-to-all matrix that describes the distance between each sequence pair of genotypes (12). Previous researchers have shown that multivariate analysis is a valuable tool for selecting the parents for hybridization (13, 14). In light of the aforementioned considerations, the current study was conducted to study the genetic analysis and to select parental lines for future breeding using multivariate analysis.

Materials and Methods

Experimental site

The study was conducted at "C" Block Farm under the All India Coordinated Research Project (AICRP) on Vegetable Crops at Bidhan Chandra Krishi Viswavidyalaya in Kalyani, West Bengal, India (23.5° N latitude and 89° E longitude with a mean sea level of 9.75 m).

Plant materials and field growing

Twenty-four vegetable cowpea genotypes, collected from Uttar Pradesh, West Bengal, Jharkhand, Chattisgarh, New Delhi, Maharashtra, Kerala, Tamil Nadu, Karnataka, Haryana and Meghalaya of India, were assessed using a randomized complete block design with 3 replications during the spring-summer season of 2023. Following treatment with thiram (3 g/kg of seed), seeds were sown in plots measuring 3.0 × 3.2 m in well-prepared land with sandy loam soil (pH range 6.8-7.0) in the 3rd week of February 2023 at 2.5 cm deep furrows with 50 cm between rows and 40 cm between plants. Before seeding, the soil was fine-tuned by a tractor. In addition to 10 t of FYM/ha, all fertilizers were applied at a basal dose comprising 25 kg nitrogen (as urea) per ha, 60 kg phosphorus (as single super phosphate) per ha and 50 kg potassium (as muriate of potash) per ha. All cultural practices were implemented as per the schedule of the crop (15).

Observations recorded

Ten randomly chosen plants from each genotype were observed and the average was calculated for statistical analysis. For the purpose of recording distinct pod characters, 10 pods (12 days old from anthesis) per genotype per replication were collected. To count the number of seeds in each pod, the pods were divided in half. The quantitative traits recorded included plant height (cm), number of branches per plant, number of trifoliate leaves per plant, number of leaflets per plant, days to 1st flowering, days to 50 % flowering, stem girth (cm), days to first and last picking, total number of pickings, marketable pod length (cm), pod diameter (mm), number of marketable pods per plant, seeds per pod, 100 seed weight (g), marketable pod weight (g) and marketable pod yield per plant (g). The crushed pods were utilized to create a replication-wise composite sample in order to estimate fresh pod protein content in g/100 g (16).

Statistical analysis

Analysis of variance (ANOVA) was performed following the standard procedures (17). Genotype and phenotypic coefficients of variation were estimated (18). Broad-sense heritability (H) was calculated using the standard formula (19). The anticipated genetic gain (GA) was derived using the standard approach (20, 21). Path coefficient analysis, as advocated (22), was employed to dissect the direct and indirect influence of yield contributing traits on marketable pod production. Population clustering was conducted using Tocher's method (23). Hierarchical clustering was carried out on the same set of genotypes to assess the level of similarity among them, utilizing trait data visualized through a dendrogram constructed (24). To select the best-performing genotypes, the varietal information was condensed into a smaller number of factors using principal component analysis (PCA), which was used to determine the factor dimension of the data. Indostat software (8.0 version, Hyderabad, India) and SAS (9.3 Professional Version, SAS Institute, NC) were used to analyse the data.

Results and Discussion

Mean performance of genotypes

The goal of the current study was to investigate differences in 18 traits across 24 genotypes of vegetable cowpeas. The genotypes showed highly significant differences for all the characters except plant girth thickness, even at the 1 % level of significance (Table 1). This clearly supported the rationale for using these genotypes to study the genetic variability of various characters. The character plant height, number of branches per plant and number of trifoliate leaves per plant had a significant impact on the genotypes under the investigation (Table 2a). The highest plant height was recorded by the genotype Arya Vaibhav Laxmi (337.48 cm), followed by Shweta (319.70 cm) and Vanita (25.80 cm) showed the lowest plant height among the genotypes. The genotypes with a determinate growth habit had lower plant height than the indeterminate type. The most vigorous plants are those that are categorized as indeterminate (25). The indeterminate or spreading type plant pattern of Arya Vaibhav Laxmi, Shweta, HACP-3, Vayjayanthi, Asutosh, Lal laffa, Maharani Laffa Barbati and Ankur Gomti supports the aforementioned claim made by the earlier worker (25). Vayjayanthi had the most branches per plant (6.61), followed by Indira Hari (6.16). Studies conducted on cowpea reported that the notable variability in branch number per plant could be ascribed to the inherent genetic diversity among the evaluated cultivars (26, 27).

Table 1. ANOVA for 18 quantitative characters of cowpea

Source of variation	Mean sum of square		
	Replication	Treatments	Error
DF	2	23	46
Plant height (cm)	110.74	26959.38**	198.10
Number of branches per plant	1.49	3.22**	0.35
Number of trifoliate leaves per plant	6.94	269.03**	19.61
Number of leaflets per plant	62.45	2421.30**	176.50
Days to 1st flowering	4.50	84.85**	3.40
Days to 50 % flowering	2.01	83.07**	5.37
Plant girth thickness (cm)	0.00	0.04	0.03
Days to 1st picking	4.70	73.34**	5.50
Days to last picking	4.60	191.48**	25.85
Total number of pickings	0.43	8.04**	0.36
Marketable pod length (cm)	21.94	329.17**	10.64
Marketable pod diameter (mm)	0.88	5.88**	0.70
Number of marketable pods per plant	1.96	89.49**	2.79
Number of seeds per pod	2.48	36.81**	0.82
100 seed weight (g)	2.58	2.86**	1.18
Marketable pod weight (g)	1.28	43.63**	2.50
Protein content in pod (g/100 g)	0.02	0.75**	0.02
Marketable pod yield per plant (g)	187.68	6776.11**	805.10

DF = Degrees of freedom; ** Significant at 0.01 level of probability.

Days to 1st flowering and days to 50 % flowering are the primary characteristics used to assess how early a genotype is. The genotype Half Laffa Juli opened its 1st flower in the shortest amount of time (33.46 days). Arka Garima had the longest time to 1st flowering (55.06 days) (Table 2a), followed by Vayjayanthi (49.46 days). The genotype Kashi Kanchan took the shortest time to produce 50 % flowering (38.00 days), followed by Medinipur Local (38.39 days). The genotype with the greatest plant girth thickness was Arya Vaibhav Laxmi (1.19 cm), followed by HACP-3 (1.14 cm). The genotypes Half Laffa Juli and Special Kashi Kanchan took the shortest time to 1st harvest (44.01 and 44.54 days respectively). Arka Garima had the longest time to 1st picking (64.93 days) and Maharani Laffa Barbati had the longest time to last picking (103.29 days) (Table 2a).

The genotype Maharani Laffa Barbati (8.33) had the most pickings overall (Table 2b). Pusa Komal (17.83 cm) and Arka Garima (19.51 cm) had the smallest marketable pod lengths, while Maharani Laffa Barbati (51.38 cm) had the largest. It is proposed that a commercial standard of 20 cm for pod length, as larger pods are advantageous for manual harvesting (28). The genotype Maharani Laffa Barbati displayed the largest marketable pod diameter (12.49 mm). The most marketable pods per plant were produced by the genotype Pusa Komal (25.19), followed by Vanita (24.66) (Table 2b). Medinipur local had the fewest marketable pods per plant (7.31), followed by Half Laffa Juli (8.19).

Asutosh had the most seeds per pod (19.36), followed by Maharani Laffa Barbati (15.84) and Medinipur local (16.57). In Arya Vaibhav Laxmi, the smallest number of seeds per pod was recorded at 5.81. While shorter pods produced fewer seeds per pod, larger pods produced the most. Furthermore, this variation may be the result of distinct genotypes or environmental factors that encourage early maturity, leaving the least amount of time for seed setting and development as observed by previous workers (29, 30). The number of seeds per pod is also influenced by plant height (31). For 100 seed weight, the genotype Maharani Laffa Barbati (12.72 g) displayed the highest value, followed by Bidhan Sadabahar (12.55 g) and the genotype Kashi Kanchan (9.50 g) displayed the lowest value. The time it takes for assimilates to accumulate in the seeds and variations in the genetic composition of various genotypes may be the cause of these variations in seed weight. The genotype Arya Vaibhav Laxmi had the lowest marketable pod weight (5.52 g), while Maharani Laffa Barbati had the heaviest pod (20.99 g).

Protein content is an important parameter for the assessment of the nutritional quality of legumes. The highest pod protein content was recorded by the genotype Medinipur local (4.52 g/100 g), followed by Vayjayanthi (4.41g/100 g). The genotype Maharani Laffa Barbati had the lowest protein content in the pod (2.83g/100 g). Cowpea genotypes assessed in Southern Europe (32) had immature pod protein contents ranging from 2.33 to 3.43 g/100 g, which agreed well with the present study. Maharani Laffa Barbati produced the most marketable pod yield per plant (228.80 g), followed by Kashi Nidhi (217.16 g) and Lal laffa (207.88 g) (Table 2b). The genotype with the lowest marketable pod yield per plant was Medinipur local (74.52g). Variability in pod yield was observed, though and this could be related to the genotypes' genetic composition and the diversity of the climate. Such differences in pod yield of various cowpea genotypes were also reported (33). It is also evident from the study that high-yielding genotypes had low protein content in the pod. The selection of high-yielding genotypes with significant protein content in pods should be promoted as part of the plan to increase protein yield. To ensure successful selection, a large gene pool must be created. Based on pod yield, Maharani Laffa Barbati, Kashi Nidhi and Lal laffa appeared as the most potential in the Gangetic plains of West Bengal and could be recommended for commercial cultivation after critical testing in cowpea-growing zones.

Studies on genetic variability and heritability

Characters with a high genotypic coefficient of variation suggest the possibility of successful selection in genetic studies (34). Nevertheless, heritable variation cannot be quantified using the genotypic coefficient of variation alone (35). The estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as a percentage of mean were calculated for 18 agronomic traits across 24 cowpea cultivars (Table 3). Predicting the degree of variation in a particular collection of genotypes is made much easier with an

Table 2a. Mean performance of cowpea genotypes for different quantitative characters

Genotype	PH	NBP	NTLP	NLP	D1F	D50F	PGT	D1P	DLP
Bidhan Barbati 1	47.50	4.04	39.06	117.18	35.85	40.25	1.10	46.50	79.28
Bidhan Sadabahar	55.85	4.63	39.38	118.14	34.25	39.93	1.07	45.59	76.70
Kashi Kanchan	57.67	4.78	44.74	134.23	34.98	38.00	1.05	45.36	81.04
Medinipur local	59.19	4.55	50.67	152.02	34.67	38.39	0.90	46.40	92.74
Asutosh	134.99	4.00	52.14	156.42	36.23	41.36	1.05	46.39	97.01
Lal Laffa	130.51	4.49	51.94	155.81	36.45	42.01	0.99	45.42	100.73
Maharani Laffa Barbati	134.16	3.84	52.79	158.37	37.51	42.27	0.79	46.60	103.29
Half Laffa Juli	46.45	5.92	59.38	178.14	33.46	39.36	1.02	44.01	96.03
Special Kashi Kanchan	49.17	5.88	42.42	127.27	33.87	38.15	1.08	44.54	78.53
Arka Garima	53.01	5.40	38.64	115.93	55.06	59.39	0.78	64.93	91.66
Indira Lal	32.87	4.52	53.30	159.90	39.16	43.68	0.92	50.15	98.84
Swarna Harita	39.58	5.29	54.68	164.05	36.72	40.92	0.95	46.71	99.37
Ankur Gomti	102.07	2.80	42.21	126.63	39.72	43.19	0.91	50.65	86.28
Vayjayanthi	196.63	6.61	53.55	160.64	49.46	53.74	0.93	57.41	94.05
RCCP-1	57.02	4.27	46.47	139.42	44.73	49.95	0.95	53.76	88.29
Vanita	25.80	2.49	36.22	108.65	42.52	47.32	0.83	51.12	84.02
Shweta	319.70	3.40	67.91	203.72	40.21	42.56	1.02	50.35	97.41
IVRCP-5	63.20	5.39	58.14	174.41	39.39	42.70	1.08	47.01	87.76
Pusa Komal	41.21	3.75	32.95	98.85	40.07	45.85	0.81	49.07	83.19
Arya Vaibhav Laxmi	337.48	4.21	62.23	186.68	45.62	50.85	1.19	54.36	94.38
IVRCP-3	77.55	5.64	42.49	127.47	41.46	46.20	1.04	48.48	89.47
Indira Hari	58.67	6.16	37.52	112.57	37.15	43.32	0.97	44.73	79.08
HACP-3	316.59	4.26	58.18	174.54	45.88	48.74	1.14	55.28	98.79
Kashi Nidhi	34.41	3.95	36.29	108.88	38.69	43.74	0.84	47.43	85.49
Mean	102.97	4.59	48.05	144.16	39.71	44.24	0.98	49.26	90.14
C.D. at 5 %	23.13	0.98	7.28	21.83	3.03	3.81	-	3.86	8.36
CV (%)	13.67	12.94	9.22	9.22	4.65	5.24	17.65	4.76	5.64

PH = Plant height (cm); NBP = Number of branches per plant; NTLP = Number of trifoliate leaves per plant; NLP = Number of leaflets per plant; D1F = Days to 1st flowering; D50F = Days to 50 % flowering; PGT = Plant girth thickness (cm); D1P = Days to 1st picking; DLP = Days to last picking.

Table 2b. Mean performance of cowpea genotypes for different quantitative characters

Genotype	TNP	MPL	MPD	NMPP	NSPP	100SW	MPW	PCP	MPYPP
Bidhan Barbati 1	3.33	23.56	7.85	17.07	11.18	11.70	7.67	3.95	131.32
Bidhan Sadabahar	4.00	23.46	6.23	16.91	10.71	12.55	9.13	3.58	154.68
Kashi Kanchan	3.67	30.46	7.76	14.06	9.27	9.50	9.86	3.88	138.96
Medinipur local	5.67	38.89	7.58	7.31	16.57	10.15	10.47	4.52	74.52
Asutosh	6.00	51.15	8.33	9.38	19.36	9.76	15.78	3.72	149.24
Lal Laffa	7.33	49.30	7.03	11.21	15.33	10.79	18.51	2.93	207.88
Maharani Laffa Barbati	8.33	51.38	12.49	10.87	15.84	12.72	20.99	2.83	228.80
Half Laffa Juli	6.67	32.33	7.60	8.19	9.16	9.67	10.46	4.30	84.29
Special Kashi Kanchan	3.33	32.75	8.32	13.86	9.84	10.13	10.52	3.74	146.59
Arka Garima	3.00	19.51	7.78	9.50	7.10	9.70	11.25	4.14	106.60
Indira Lal	6.33	31.89	7.05	18.12	9.02	9.56	9.04	3.48	163.67
Swarna Harita	6.67	48.28	6.67	15.39	15.21	10.21	12.66	3.34	194.60
Ankur Gomti	3.33	24.01	5.22	18.03	6.27	10.16	7.94	3.75	144.14
Vayjayanthi	6.00	35.73	7.15	8.64	11.86	10.26	9.08	4.41	77.91
RCCP-1	3.33	25.69	5.98	12.29	8.72	10.18	7.71	4.24	93.56
Vanita	3.33	31.55	7.41	24.66	11.17	10.45	8.35	3.09	206.79
Shweta	6.67	39.05	5.56	14.52	12.73	9.84	12.27	3.38	177.67
IVRCP-5	4.00	44.26	8.16	14.84	13.82	11.99	13.87	3.23	206.66
Pusa Komal	3.33	17.83	7.74	25.19	7.54	10.23	6.53	3.47	164.80
Arya Vaibhav Laxmi	6.00	16.21	6.58	14.28	5.81	10.37	5.52	4.34	79.10
IVRCP-3	4.00	27.69	6.69	24.57	9.46	9.88	6.80	3.40	168.41
Indira Hari	3.33	31.78	6.78	21.31	11.14	11.81	9.28	3.26	197.64
HACP-3	6.33	28.63	6.11	24.17	7.37	10.11	6.44	3.53	156.32
Kashi Nidhi	3.67	42.26	8.24	16.41	11.93	11.93	13.15	2.86	217.16
Mean	4.90	33.24	7.35	15.45	11.10	10.57	10.55	3.64	152.97
C.D. at 5 %	0.98	5.36	1.37	2.74	1.49	1.78	2.60	0.24	46.63
CV (%)	12.21	9.81	11.35	10.81	8.16	10.27	14.98	4.08	12.55

TNP = Total number of pickings; MPL = Marketable pod length (cm); MPD = Marketable pod diameter (mm); NMPP = Number of marketable pods per plant; NSPP = Number of seeds per pod; 100SW = 100 seed weight (g); MPW = Marketable pod weight (g); PCP = Protein content in pod (g/100 g); MPYPP = Marketable pod yield per plant (g).

Table 3. Mean, range and estimates of genetic parameters of 24 cowpea genotypes

Character	Mean	Range	GCV (%)	PCV (%)	GCV:PCV	h^2 in broad sense (%)	Genetic advance as % of mean
Plant height (cm)	102.97	25.80-337.48	91.72	92.74	98.91	97.80	186.89
Number of branches per plant	4.59	2.49-6.61	21.26	24.89	85.42	73.00	37.41
Number of trifoliate leaves per plant	48.05	32.95-67.91	18.98	21.09	89.95	80.90	35.16
Number of leaflets per plant	144.16	98.85-203.72	18.98	21.09	89.95	80.90	35.16
Days to 1st flowering	39.71	33.46-55.06	13.12	13.92	94.27	88.90	25.48
Days to 50 % flowering	44.24	38.00-59.39	11.50	12.64	91.01	82.80	21.57
Plant girth thickness (cm)	0.98	0.78-1.19	5.47	18.48	29.61	8.80	3.34
Days to 1st picking	49.26	44.01-64.93	9.65	10.76	89.68	80.40	17.83
Days to last picking	90.14	76.70-103.29	8.24	9.99	82.53	68.10	14.01
Total number of pickings	4.9	3.00-8.33	32.65	34.85	93.67	87.70	62.99
Marketable pod length (cm)	33.24	16.21-51.38	31.00	32.52	95.34	90.90	60.89
Marketable pod diameter (mm)	7.35	5.22-12.49	17.89	21.19	84.44	71.30	31.13
Number of marketable pods per plant	15.45	7.31-25.19	34.80	36.44	95.50	91.20	68.45
Number of seeds per pod	11.1	5.81-19.36	31.20	32.25	96.75	93.60	62.18
100 seed weight (g)	10.57	9.50-12.72	7.08	12.48	56.76	32.20	8.28
Marketable pod weight (g)	10.55	5.52-20.99	35.08	38.14	91.97	84.60	66.46
Protein content in pod (g/100 g)	3.64	2.83-4.52	13.56	14.16	95.76	91.70	26.75
Marketable pod yield per plant (g)	152.97	74.52-228.80	29.16	34.56	84.38	71.20	50.69

GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2 = Heritability estimate

understanding of the phenotypic (PCV) and genotypic coefficient of variation (GCV). The observed values of PCV and GCV were nearly identical across all traits evaluated in the study; however, PCV was greater than GCV (Table 3). The GCV value varied from 5.47 % (plant girth thickness) to 91.72 % (plant height). Conversely, PCV varied between 9.99 % (days to last picking) and 92.74 % (plant height). Plant height, branches per plant, total pickings, marketable pod length, number of marketable pods per plant, seeds per pod, marketable pod weight and marketable pod yield per plant were all found to have high GCV values (> 20.00 %). The earlier researcher (36) also recorded higher GCV values for these characters, which support these observations.

Moderate GCV values, ranging from 10 % to 20 %, were observed for the number of trifoliate leaves per plant, number of leaflets per plant, days to 1st flowering, days to 50 % flowering, marketable pod diameter and pod protein content. Previous researchers (37) have reported low GCV values for the number of days to 1st flowering. Plant height, number of branches, number of trifoliate leaves, number of leaflets, total number of pickings, marketable pod length, marketable pod diameter, number of marketable pods, number of seeds per pod, marketable pod weight and marketable pod yield per plant also showed high PCV values (> 20.00 %), while days to 1st flowering, days to 50 % flowering, plant girth thickness, days to 1st picking, 100 seed weight and protein content in pod showed moderate PCV values (10-20 %).

In this study, the percentage of GCV to PCV varied from 29.61 % in plant girth thickness to 98.91 % in plant height. Elevated values of both GCV and PCV (> 20 %) were observed for pod width, mature pod weight, number per plant and pod yield per plant, suggesting that the phenotypic expression of these traits is particularly influenced by genotype-environment interactions (38). Characteristics whose expressions are dependent on the environment may not be suitable descriptors for morphological classification (39). However, genetic contribution accounted for a considerable portion of the overall phenotypic expression of most traits in our study. As a result, their use as a substantial discriminatory variable in studies on cowpea classification seems to be rather reliable.

Plant breeders are mainly interested in heritability because it serves as an indicator of transmissibility and a gauge of the importance of selection for a given trait in different kinds of offspring (40). In order to assess the relative strength of the influence of genes and environments on overall phenotypic variability, the concept of heritability is crucial. Heritability is defined as the additive genetic variance expressed as a percentage of the total variance, which indicates that the offspring will resemble their parents (41). For the majority of the characters in the study, high broad sense heritability (60 % and above) was noted with the exception of the traits plant girth thickness and 100 seed weight. Selection based on phenotypic expression could be trusted because genetic constitution played a significant role in the expression of these characters (42). High heritability indicates less environmental influence in the observed variation. However, the broad sense heritability values were likely inflated in this study since it was hard to rule out variance caused by different genetic components and their interactions. However, the amount of genetic advancement that would arise from choosing the best individuals cannot be determined solely by the heritability value.

The performance improvement of selected lines over the original population is known as genetic advance (GA). In order to predict the effect of selection in segregating generation, combining heritability estimates with substantial GA provides a more reliable measure of trait inheritance than considering heritability in isolation. Most of the traits under study showed high magnitude (> 20.00 %) of GA as a percentage of the mean, except plant girth thickness and 100 seed weight. These 2 traits showed low magnitude of genetic advance and days to 1st picking and days to last picking showed moderate genetic advance (Table 3). High GA for the number of pods per plant, pod yield per plant, pod weight, number of days to flower and pod length were also corroborated by earlier research (43). Pod width's low genetic advancement and low heritability suggested that selection based on this trait would be less successful. A combination of high GCV, substantial heritability and elevated GA offered a more reliable basis for identifying superior genotypes than relying solely on heritability estimates. High GCV, heritability and genetic advancement were found in plant height, number of branches per plant, total number of pickings, marketable pod length, number of marketable pods per plant, number of seeds per pod, marketable pod weight and marketable pod yield per plant. Pod yield per plant, pod length, pod width and number of pods per plant exhibited both high heritability and substantial genetic advance, implying that these traits were predominantly controlled by additive genetic influence and could be effectively improved through selection (44). Selection based on these traits could be successful. Some results may differ because previous researchers used genotypes from different cowpea cultigroups that were tested in various environments.

Studies on correlation and path analysis

Both phenotypic and genotypic correlation coefficients were examined in order to examine the relationships between various yield component traits and pod yield (Table 4). For the majority of the traits under investigation, the correlation coefficient between genotype and phenotype was extremely close, which corroborated well with earlier research (45, 46). There were positive, significant, genotypic correlations between marketable pod yield per plant and marketable pod length, marketable pod diameter, number of marketable pods per plant, number of seeds per pod, 100 seed weight and marketable pod weight, which agreed well with the previous findings (47-50).

Earlier study (51) observed that path coefficient values exhibited a substantial positive direct relationship between plant height, peduncle length, pod length, number of pods per cluster, number of pods per plant and number of seeds per pod with yield quintals per hectare. Significant positive genotypic correlations were observed between 100 seed weight and both number of seed per pod and pod length; between seed count per pod and peduncle length; pod length and the number of clusters per plant as well as branch number; number of pods per plant with peduncle length, cluster count and branch number and between the number of clusters per plant and the number of branches per plant which supported earlier finding (52). Marketable pod yield per plant was positively, but not significantly, correlated with the total number of pickings and the days to last picking.

Three characteristics, plant girth thickness, days to 1st picking and pod protein content, showed a significant negative genotypic correlation. Alongside genotypic associations, marketable pod yield per plant exhibited substantial positive phenotypic correlations with marketable pod length, marketable pod weight and the number of marketable pods per plant, which supported earlier findings (53, 54). There were positive but non-significant phenotypic correlations between marketable pod yield per plant and the total number of pickings, marketable pod diameter, number of seeds per pod and 100 seed weight. Additionally, there was a significant negative phenotypic correlation between the marketable pod yield per plant and the protein content of the pod. For the majority of pod yield component and pod quality characters, close values of the genotypic and phenotypic correlation coefficient show that the environment has little influence on the correlated response. Increases in key component traits such as marketable pod length, number of marketable pods per plant and marketable pod weight can boost marketable pod yield per plant, according to the results of the genotypic and phenotypic correlation coefficient. Additionally, an inverse relationship between yield and protein content in the pod was discovered, suggesting that a high-yielding genotype produces a lower amount of protein in the pod than a low-yielding genotype.

The complexity of the relationships between characters and pod yield was highlighted by the fact that the discussion alone did not provide a comprehensive picture of the relative importance of each character's direct and indirect influences on pod yield because these traits were the result of multiple factors that either complemented or counteracted one another. To determine the relative importance of yield components towards cowpea pod yield, the phenotypic correlation coefficients were divided into direct and indirect effects in the current study (Table 5). The marketable pod weight (0.9055) and number of marketable pods per plant (0.8130) had the greatest positive direct effect on marketable pod yield per plant among the yield component traits (Table 5). Marketable pod yield per plant demonstrated a strong, positive correlation with both marketable pod weight and the number of marketable pods per plant. Previous study (55) has also highlighted a substantial direct influence of pod number per plant, followed by pod weight, on marketable pod yield. Hence, selecting directly for these traits could be an effective strategy to enhance pod yield in cowpea.

Studies on genetic diversity through multivariate analysis

The goal of the current study was to use 18 significant quantitative characters to analyze the genetic divergence of 24 cowpea genotypes. Tocher's method could logically group the genotypes with low D^2 values based on the degree of divergence (D^2 values) between any 2 genotypes. By treating estimated D^2values as the square of the generalized distance, all 24 genotypes were categorized into 5 clusters based on the determination of divergence (Table 6). The current results are consistent with the findings of previous reserchers (56-58). With 15 genotypes (Kashi Kanchan, Special Kashi Kanchan, Bidhan Sadabahar, Bidhan Barbati 1, Indira Hari, Indira Lal, IVRCP-5, Swarna Harita, Kashi Nidhi, Ankur Gomti, IVRCP-3, Half Laffa Juli, Medinipur local, Pusa Komal and Vanita), Cluster I was the largest. Cluster IV had 4 genotypes (Arya Vaibhav Laxmi, HACP-3, Shweta and Vayjayanthi) and Cluster II had 3 genotypes (Asutosh, Lal laffa and Maharani Laffa Barbati). The monotypic genotypes found in Cluster V (Arka Garima) and Cluster III (RCCP-1) suggested that the genotypes from these clusters may have originated in breeding programs across the region. Geographic diversity and genetic divergence were not related, as evidenced by the random genotype grouping pattern. Consequently, genetic divergence, not geographic diversity, should be the basis for choosing genotypes for hybridization. Environmental effects on cluster composition were previously documented for cowpea (59). Using squared Euclidean distance, Ward's dendrogram method (Fig. 1) was further examined and it became evident that the cowpea genotypes had strong relationships and high genetic diversity.

The intra- and inter-cluster distances between the 24 cowpea genotypes are depicted in Table 7. Cluster IV had the highest intra-cluster value (105.42) out of the 5 clusters, followed by cluster I (69.21) and cluster II (46.81). Cluster V and IV had the highest inter-cluster value (359.80), followed by Cluster V and II (345.84). Cluster V and III had the lowest inter-cluster value (82.66), followed by Cluster III and I (100.47). It was earlier reported (60) that hybridization involving selected genotypes from genetically distant clusters has a high potential for generating favourable recombinants.

The mean values of the clusters varied for every character (Table 8). For plant height (292.60 cm), number of trifoliate leaves per plant (60.47), number of leaflets per plant (181.40) and plant girth thickness (1.07 cm), cluster IV had the highest cluster mean (Table 8). The marketable pod length (50.61 cm), marketable pod diameter (9.28 mm), number of seeds per pod (16.85), marketable pod weight (18.43 g), marketable pod yield per plant (195.31 g), days to last picking (100.34) and total number of pickings (7.22) all had the highest cluster mean in cluster II. Cluster III displayed the highest

Table 4. Phenotypic and genotypic correlations among 18 characters of cowpea genotypes

Character		PH	NBP	NTLP	NLP	D1F	D50F	PGT	D1P	DLP	TNP	MPL	MPD	NMPP	NSPP	100SW	MPW	PCP	MPYPP
PH	P	**1.000**	-0.128	0.616**	0.616**	0.349*	0.273	0.278	0.331	0.419*	0.475**	-0.025	-0.209	-0.052	-0.095	-0.107	-0.065	0.109	-0.162
	G	**1.000**	-0.157	0.707**	0.707**	0.366*	0.306	0.916**	0.364*	0.503**	0.512**	-0.023	-0.250	-0.041	-0.101	-0.183	-0.060	0.128	-0.170
NBP	P		**1.000**	0.086	0.086	0.052	0.053	0.082	0.009	-0.010	0.030	0.049	0.086	-0.270	0.019	-0.041	-0.063	0.274	-0.277
	G		**1.000**	0.110	0.110	0.030	0.086	0.564**	-0.041	-0.059	0.017	0.053	0.019	-0.315	0.013	-0.063	0.016	0.312	-0.272
NTLP	P			**1.000**	1.000**	0.038	-0.036	0.300*	0.050	0.606**	0.689**	0.339	-0.092	-0.360*	0.206	-0.159	0.228	0.142	-0.111
	G			**1.000**	1.000**	0.021	-0.057	0.845**	0.039	0.819**	0.825**	0.387*	-0.082	-0.443*	0.233	-0.317	0.244	0.184	-0.210
NLP	P				**1.000**	0.038	-0.036	0.300	0.050	0.606**	0.689**	0.339	-0.092	-0.360*	0.206	-0.159	0.228	0.142	-0.111
	G				**1.000**	0.021	-0.057	0.845**	0.039	0.819**	0.825**	0.387*	-0.082	-0.443*	0.233	-0.317	0.244	0.184	-0.210
D1F	P					**1.000**	0.903**	-0.189	0.929**	0.161	-0.121	-0.336	-0.187	0.030	-0.403*	-0.180	-0.254	0.219	-0.246
	G					**1.000**	1.000**	-0.411*	0.998**	0.240	-0.130	-0.413*	-0.201	0.063	-0.454*	-0.337	-0.314	0.260	-0.300
D50F	P						**1.000**	-0.174	0.855**	0.140	-0.118	-0.367*	-0.157	0.070	-0.405*	-0.147	-0.266	0.195	-0.220
	G						**1.000**	-0.551**	0.993**	0.205	-0.158	-0.437*	-0.173	0.050	-0.462*	-0.266	-0.305	0.259	-0.318
PGT	P							**1.000**	-0.157	-0.037	0.056	-0.091	-0.243	0.053	-0.023	-0.022	-0.144	0.122	-0.066
	G							**1.000**	-0.484**	-0.282	0.148	-0.247	-0.703**	0.032	-0.275	-0.166	-0.635**	0.540**	-0.626**
D1P	P								**1.000**	0.205	-0.110	-0.354*	-0.222	-0.047	-0.418*	-0.207	-0.278	0.294	-0.337
	G								**1.000**	0.227	-0.113	-0.481**	-0.237	-0.023	-0.485**	-0.463*	-0.336	0.387*	-0.416*
DLP	P									**1.000**	0.801**	0.467*	0.098	-0.350*	0.299	-0.172	0.372*	-0.040	-0.030
	G									**1.000**	0.934**	0.532**	0.197	-0.379*	0.356*	-0.376*	0.524**	-0.072	0.055
TNP	P										**1.000**	0.543**	0.192	-0.372*	0.436*	-0.033	0.468*	-0.091	0.047
	G										**1.000**	0.604**	0.273	-0.407*	0.466*	-0.060	0.556**	-0.112	0.082
MPL	P											**1.000**	0.381*	-0.381*	0.848**	0.210	0.804**	-0.447*	0.442*
	G											**1.000**	0.480**	-0.395*	0.902**	0.227	0.881**	-0.489**	0.544**
MPD	P												**1.000**	-0.260	0.357*	0.248	0.515**	-0.240	0.205
	G												**1.000**	-0.307*	0.473**	0.602**	0.707**	-0.307	0.361*
NMPP	P													**1.000**	-0.408*	0.056	-0.463*	-0.434*	0.464*
	G													**1.000**	-0.430*	0.105	-0.542**	-0.483**	0.444*
NSPP	P														**1.000**	0.211	0.698**	-0.278	0.299
	G														**1.000**	0.346*	0.784**	-0.305	0.371*
100SW	P															**1.000**	0.264	-0.326	0.332
	G															**1.000**	0.456*	-0.657**	0.683**
MPW	P																**1.000**	-0.453*	0.538**
	G																**1.000**	-0.514**	0.482**
PCP	P																	**1.000**	-0.855**
	G																		-0.989**

PH = Plant height (cm); NBP = Number of branches per plant; NTLP = Number of trifoliate leaves per plant; NLP = Number of leaflets per plant; D1F = Days to 1st flowering; D50F = Days to 50 % flowering; PGT = Plant girth thickness (cm); D1P = Days to 1st picking; DLP = Days to last picking; TNP = Total number of pickings; MPL = Marketable pod length (cm); MPD = Marketable pod diameter (mm); NMPP = Number of marketable pods per plant; NSPP = Number of seeds per pod; 100SW = 100 seed weight (g); MPW = Marketable pod weight (g); PCP = Protein content in pod (g/100 g); MPYPP = Marketable pod yield per plant (g); P = Phenotypic correlation, G = Genotypic correlation;

*,** Significant at 0.05 and 0.01 levels of probability respectively.

Table 5. Phenotypic path analysis for seventeen characters of 24 cowpea genotypes

Character	PH	NBP	NTLP	NLP	D1F	D50F	PGT	D1P	DLP	TNP	MPL	MPD	NMPP	NSPP	100SW	MPW	PCP	Phenotypic correlation with MPYPP
PH	**-0.0620**	-0.0018	0.0572	0.0000	-0.0125	0.0095	0.0033	0.0043	-0.0368	-0.0286	-0.0025	0.0160	-0.0421	0.0057	-0.0021	-0.0586	-0.0107	-0.162
NBP	0.0079	**0.0138**	0.0080	0.0000	-0.0019	0.0018	0.0010	0.0001	0.0009	-0.0018	0.0050	-0.0066	-0.2191	-0.0011	-0.0008	-0.0570	-0.0270	-0.277
NTLP	-0.0382	0.0012	**0.0929**	0.0000	-0.0013	-0.0013	0.0035	0.0007	-0.0533	-0.0415	0.0345	0.0070	-0.2930	-0.0122	-0.0031	0.2067	-0.0140	-0.111
NLP	-0.0382	0.0012	0.0929	**0.0000**	-0.0013	-0.0013	0.0035	0.0007	-0.0533	-0.0415	0.0345	0.0070	-0.2930	-0.0122	-0.0031	0.2067	-0.0140	-0.111
D1F	-0.0217	0.0007	0.0035	0.0000	**-0.0359**	0.0315	-0.0022	0.0122	-0.0142	0.0073	-0.0342	0.0144	0.0241	0.0239	-0.0035	-0.2301	-0.0215	-0.246
D50F	-0.0169	0.0007	-0.0034	0.0000	-0.0324	**0.0349**	-0.0021	0.0112	-0.0123	0.0071	-0.0374	0.0120	0.0573	0.0240	-0.0029	-0.2409	-0.0192	-0.220
PGT	-0.0172	0.0011	0.0279	0.0000	0.0068	-0.0061	**0.0118**	-0.0021	0.0033	-0.0034	-0.0092	0.0186	0.0430	0.0014	-0.0004	-0.1300	-0.0120	-0.066
D1P	-0.0205	0.0001	0.0046	0.0000	-0.0334	0.0298	-0.0019	**0.0131**	-0.0181	0.0066	-0.0361	0.0170	-0.0379	0.0247	-0.0040	-0.2521	-0.0290	-0.337
DLP	-0.0260	-0.0001	0.0563	0.0000	-0.0058	0.0049	-0.0004	0.0027	**-0.0880**	-0.0482	0.0476	-0.0075	-0.2849	-0.0177	-0.0033	0.3368	0.0039	-0.030
TNP	-0.0295	0.0004	0.0640	0.0000	0.0043	-0.0041	0.0007	-0.0014	-0.0705	**-0.0602**	0.0554	-0.0147	-0.3027	-0.0259	-0.0006	0.4234	0.0090	0.047
MPL	0.0015	0.0007	0.0315	0.0000	0.0121	-0.0128	-0.0011	-0.0046	-0.0411	-0.0327	**0.1019**	-0.0292	-0.3094	-0.0502	0.0041	0.7278	0.0440	0.442*
MPD	0.0129	0.0012	-0.0085	0.0000	0.0067	-0.0055	-0.0029	-0.0029	-0.0086	-0.0116	0.0388	**-0.0766**	-0.2117	-0.0211	0.0048	0.4663	0.0237	0.205
NMPP	0.0032	-0.0037	-0.0335	0.0000	-0.0011	0.0025	0.0006	-0.0006	0.0308	0.0224	-0.0388	0.0199	**0.8130**	0.0242	0.0011	-0.4193	0.0427	0.464*
NSPP	0.0059	0.0003	0.0192	0.0000	0.0145	-0.0141	-0.0003	-0.0055	-0.0263	-0.0263	0.0864	-0.0273	-0.3321	**-0.0592**	0.0041	0.6321	0.0274	0.299
100SW	0.0066	-0.0006	-0.0148	0.0000	0.0065	-0.0051	-0.0003	-0.0027	0.0152	0.0020	0.0214	-0.0190	0.0451	-0.0125	**0.0194**	0.2389	0.0321	0.332
MPW	0.0040	-0.0009	0.0212	0.0000	0.0091	-0.0093	-0.0017	-0.0037	-0.0327	-0.0282	0.0819	-0.0394	-0.3765	-0.0414	0.0051	**0.9055**	0.0446	0.538**
PCP	-0.0068	0.0038	0.0132	0.0000	-0.0079	0.0068	0.0014	0.0039	0.0035	0.0055	-0.0456	0.0184	-0.3528	0.0165	-0.0063	-0.4105	**-0.0985**	-0.855**

Residual effect = 0.01220, Direct effect = Bold diagonals.

PH = Plant height (cm); NBP = Number of branches per plant; NTLP = Number of trifoliate leaves per plant; NLP = Number of leaflets per plant; D1F = Days to 1st flowering; D50F = Days to 50 % flowering; PGT = Plant girth thickness (cm); D1P = Days to 1st picking; DLP = Days to last picking; TNP = Total number of pickings; MPL = Marketable pod length (cm); MPD = Marketable pod diameter (mm); NMPP = Number of marketable pods per plant; NSPP = Number of seeds per pod; 100SW = 100 seed weight (g); MPW = Marketable pod weight (g); PCP = Protein content in pod (g/100 g); MPYPP = Marketable pod yield per plant (g);

*,** Significant at 0.05 and 0.01 levels of probability respectively.

Table 6. Cluster classification of cowpea genotypes

Number of clusters	Name of the genotype with source of collection
I (15)*	Kashi Kanchan (Utter Pradesh), Special Kashi Kanchan (West Bengal), Bidhan Sadabahar (West Bengal), Bidhan Barbati 1 (West Bengal), Indira Hari (Chhattisgarh), Indira Lal (Chhattisgarh), IVRCP-5 (Utter Pradesh), Swarna Harita (Jharkhand), Kashi Nidhi (Utter Pradesh), Ankur Gomti (Maharashtra), IVRCP-3 (Utter Pradesh), Half Laffa Juli (West Bengal), Medinipur local (West Bengal), Pusa Komal (New Delhi), Vanita (Haryana)
II (3)	Asutosh (West Bengal), Lal Laffa (West Bengal), Maharani Laffa Barbati (West Bengal)
III (1)	RCCP-1 (Meghalaya)
IV (4)	Arya Vaibhav Laxmi (New Delhi), HACP-3 (Tamil Nadu), Shweta (Chhattisgarh), Vayjayanthi (Kerala)
V (1)	Arka Garima (Karnataka)

*Figures in parentheses indicate number of genotypes

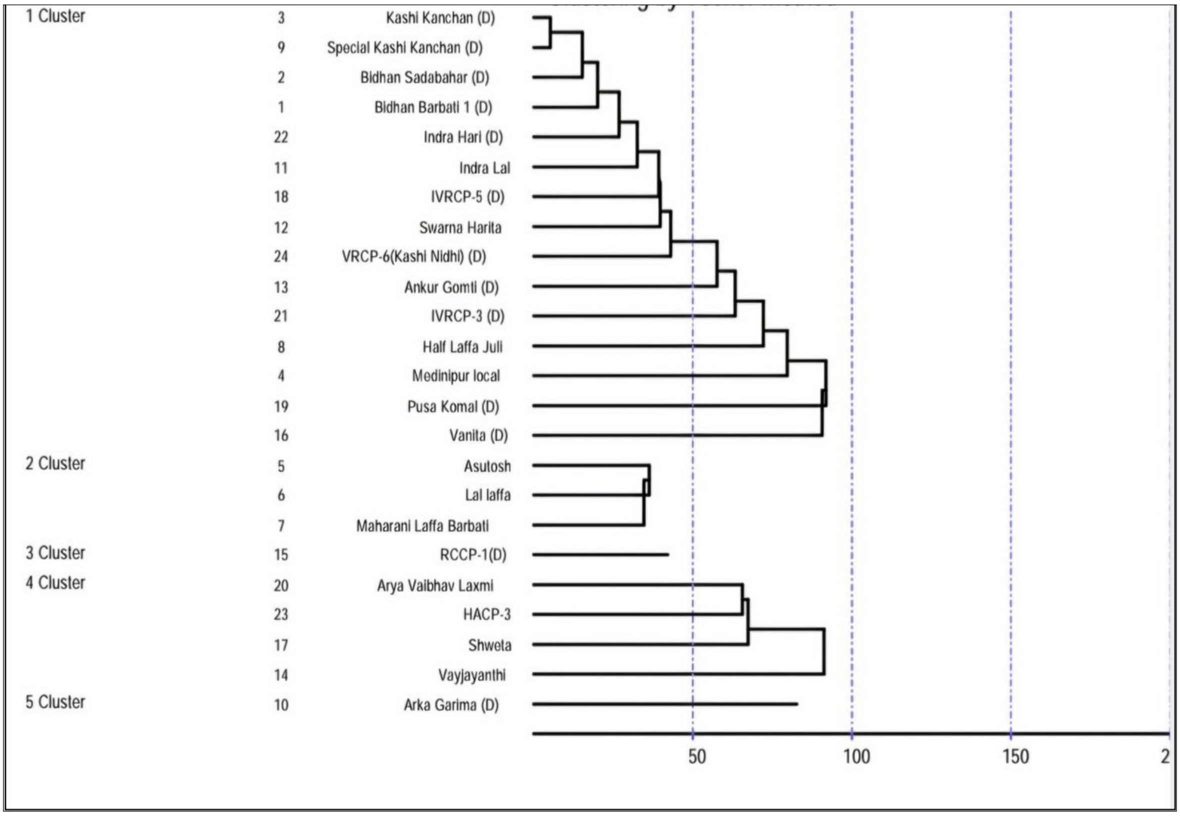

Fig. 1. Dendrogram of cowpea genotypes following Ward's method.

Table 7. Inter- and intra-cluster distances of 24 genotypes of cowpea

Clusters	I	II	III	IV	V
I	**69.21**[a]	134.78	100.47	302.80	196.14
II		**46.81**	191.83	239.32	345.84
III			**0.00**	211.85	82.66
IV				**105.42**	359.80
V					**0.00**

[a]Bold diagonal values indicate intra-cluster distance; the remainder of the values indicate the inter-cluster distances.

mean value for the trait protein content in the pod (4.24 g/100 g). These clusters may contain genes that can be used to increase pod yield and quality at the same time. Cluster V displayed the highest mean value for the trait number of branches per plant (5.40), while Cluster I displayed the maximum mean value for the trait number of marketable pods per plant (17.06). However, cluster I showed the shortest number of days to 1st flowering (37.46), while cluster II showed the shortest number of days to 50 % flowering (41.88) and days to 1st picking (46.14). Using genotypes from cluster II and III as parents, a high-yielding crop with superior pod quality and high pod protein content could be produced.

The estimated number of times each character ranked 1st, which represents the relative contribution of each character to genetic divergence, is presented in Table 8. The highest contribution to diversity among the 18 characteristics was expressed by the protein content in the pod (25.72 %), which was followed by plant height (21.74 %), marketable pod length (15.58 %), number of leaflets per plant (8.7 %), number of marketable pods per plant (8.33 %), marketable pod yield per plant (6.52 %) and number of seeds per pod (5.43 %). In cowpea, the contribution of different characters to divergence was previously documented for the number of pods/plant (61). For the determination of genetic diversity in cowpeas, the biochemical variable (pod protein concentration) was just as significant as certain morphological traits.

Variable loadings for components PC1 (protein content in pod), PC2 (plant height) and PC3 (marketable pod length) were estimated using PCA, which provided a simplified view of the relationship between the characters, protein content in pod, plant height and marketable pod length. This approach explained nearly 95.60 % of the contribution to divergence (Tables 9 & 10). These characters were picked because they accounted for nearly 95.60 % of the variance and had eigenvalues greater than 1.0. Plant height decreases and marketable pod length increases when the protein content of the pod decreases, as the 1st component (PC1) accounted for 39.77 % of the variance. An additional 30.72 % of the variation in the relationship between plant height and marketable pod length

Table 8. Cluster means of 18 characters of cowpea genotypes

Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	% contribution towards divergence
Plant height (cm)	52.75	133.22	57.02	292.60	53.01	21.74
Number of branches per plant	4.65	4.11	4.27	4.62	5.40	1.45
Number of trifoliate leaves per plant	44.63	52.29	46.47	60.47	38.64	0.36
Number of leaflets per plant	133.89	156.87	139.42	181.40	115.93	8.7
Days to 1st flowering	37.46	36.73	44.73	45.29	55.06	0.36
Days to 50 % flowering	42.07	41.88	49.95	48.97	59.39	0.00
Plant girth thickness (cm)	0.97	0.94	0.95	1.07	0.78	0.00
Days to 1st picking	47.18	46.14	53.76	54.35	64.93	0.00
Days to last picking	86.52	100.34	88.29	96.16	91.66	0.72
Total number of pickings	4.31	7.22	3.33	6.25	3.00	1.45
Marketable pod length (cm)	32.07	50.61	25.69	29.91	19.51	15.58
Marketable pod diameter (mm)	7.29	9.28	5.98	6.35	7.78	1.81
Number of marketable pods per plant	17.06	10.49	12.29	15.41	9.50	8.33
Number of seeds per pod	10.82	16.85	8.72	9.45	7.10	5.43
100 seed weight (g)	10.66	11.09	10.18	10.14	9.70	0.36
Marketable pod weight (g)	9.72	18.43	7.71	8.33	11.25	1.45
Protein content in pod (g/100 g)	3.59	3.16	4.24	3.92	4.14	25.72
Marketable pod yield per plant (g)	159.62	195.31	93.56	122.75	106.60	6.52

Table 9. Results of principal component analysis (PCA) for characters contributing to divergence in cowpea

Principal components	Eigenvalue %	% Variance	% Cumulative variance
Eigenvalues and variance accounted for (%) by PCA based on correlation matrix			
PC_1	2.78388969	39.77	39.77
PC_2	2.15073563	30.72	70.49
PC_3	1.75743940	25.11	95.60

$PC_{1\text{-}3}$ = principal components 1-3.

Table 10. Contribution of diverse traits in the principal components of cowpea

Variables	PC_1	PC_2	PC_3
Factor loadings due to PCs with eigenvalues greater than 1			
Protein content in pod (g/100 g)	-0.525602	0.167204	-0.282213
Plant height (cm)	-0.128589	0.493470	0.494120
Marketable pod length (cm)	0.483800	0.324102	-0.216730

$PC_{1\text{-}3}$ = principal components 1-3.

and protein content was explained by the 2nd component (PC2). A further 25.11 % of the variance was explained by the 3rd component (PC3), which states that a decrease in marketable pod length causes the protein content of the pod to decrease and plant height to increase. PCA has proven to be an effective method for identifying factors that have a greater impact on genotype differentiation and grouping (62, 63).

Morphological relationships between cowpea genotypes were ascertained using PCA (64). The significance of a trait coefficient for every PC is not clearly defined. A significant coefficient is defined earlier (65) as over 50 % of the coefficient value was normalized by the square root of the eigenvalue's standard deviation for the respective PC. In PCA, accessions positioned in proximity are considered genetically similar, while accessions that are farther apart are seen as more diverse.

In a PCA scatter diagram, close genotypes are viewed as similar, while distant genotypes are seen as more diverse. According to the PCA (Fig. 2), which summarized the data differences, the genotypes Asutosh, Vayjayanthi, Shweta, Arya Vaibhav Laxmi and Pusa Komal were quantitatively different from the others. The remaining genotypes formed a distinct cluster based on similar features. Based on multivariate analysis and average values for horticultural traits, genotypes Asutosh, Vayjayanthi, Shweta, Arya Vaibhav Laxmi and Pusa Komal are decent choices for future use in breeding programs of vegetable cowpea.

Conclusion

The current study showed that cowpea genotypes differed significantly in terms of growth, yield components and quality parameters. After thorough testing in various cowpea-growing zones, promising genotypes like Maharani Laffa Barbati, Kashi Nidhi and Lal Laffa might be used commercially. Correlation and path analysis indicate that variables such as marketable pod weight and the number of marketable pods per plant serve as the key determinants for selection decisions for boosting the productivity of vegetable cowpea. Considering outcomes of multivariate estimates along with mean performance values, diverse determinate cowpea genotypes, Pusa Komal and indeterminate genotypes, Asutosh, Vayjayanthi, Shweta and Arya Vaibhav Laxmi were identified as potential donors. We suggest using a modified backcross-pedigree approach to progress generations from highly heterotic cross combinations (Determinate × Indeterminate). The F_1 of such a cross combination will be backcrossed once with an indeterminate parent before being subjected to pedigree selection for up to 6 generations (Fig. 3). High-protein parents should be retained as females in hybridization programs since maternal inheritance for the protein content of several legumes has been well documented. To achieve a suitable balance between pod yield and protein content, the segregates in the suggested modified backcross-pedigree breeding strategy must be examined for plant frame, pod yield and protein content.

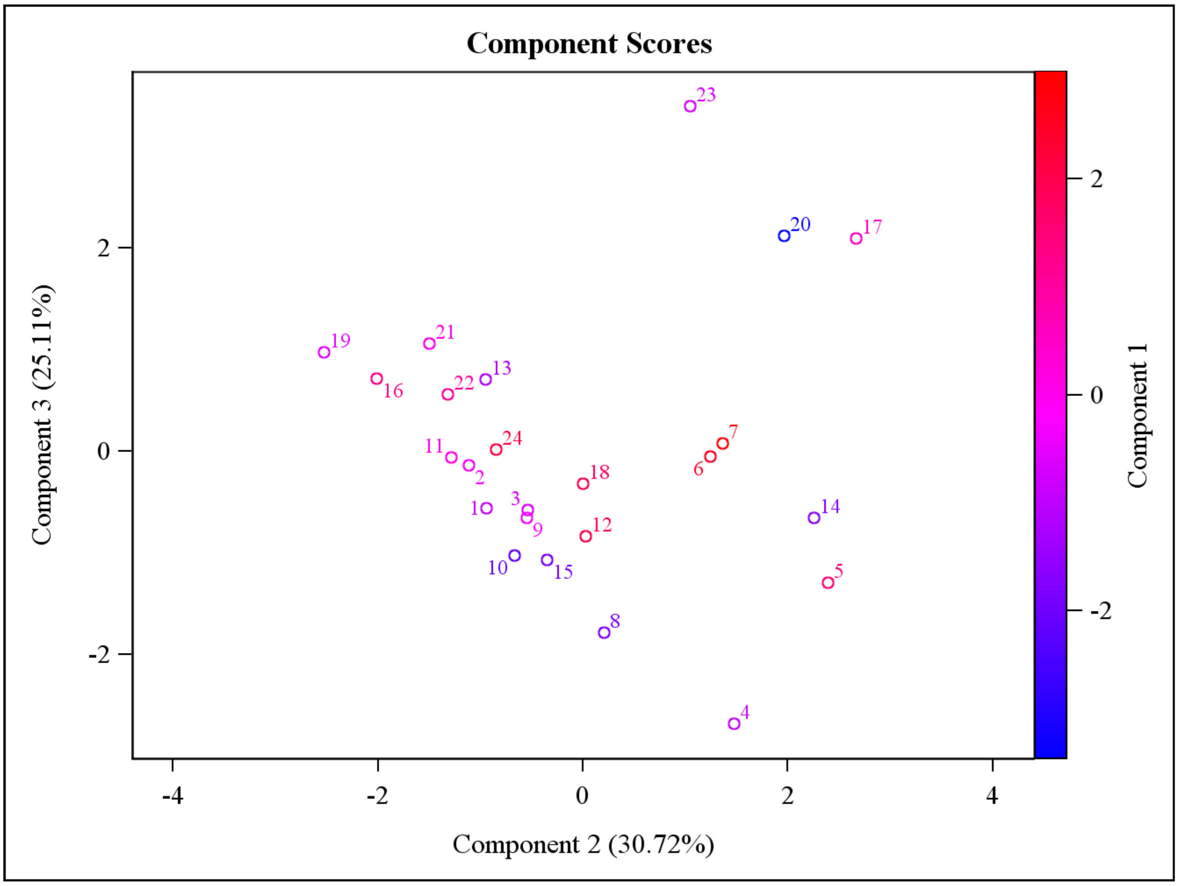

Fig. 2. Scatter diagram of regression factor scores for the first, second and third components as determined by principal component analysis. Points in the diagram closest to the intersection of 0 on the X- and Y-axes indicate similarity. Outliers on the X-axis, that is, 5 = Asutosh; 14 = Vayjayanthi; 17 = Shweta; 20 = Arya Vaibhav Laxmi; 19 = Pusa Komal; indicate genotypic diversity. Numbers correspond to the name of the genotypes in Figure 1.

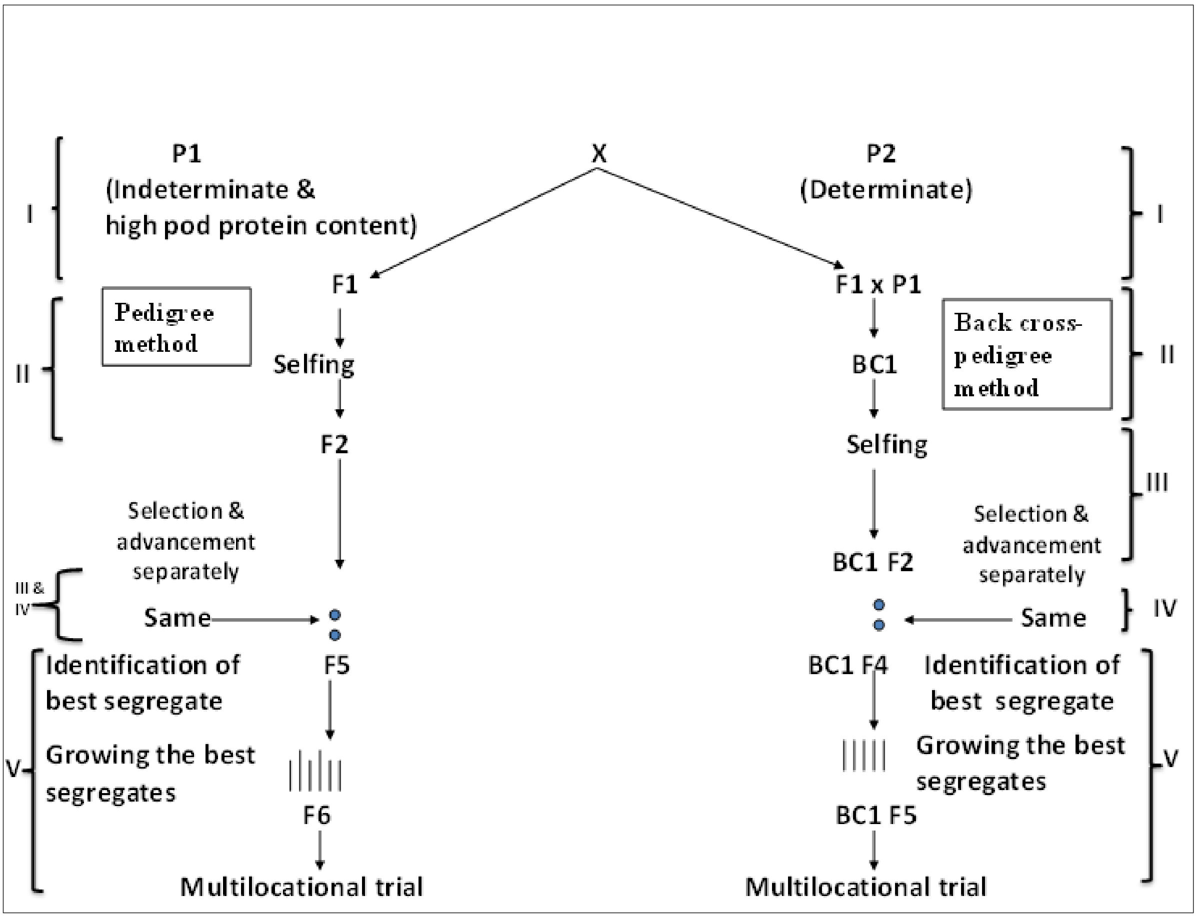

Fig. 3. Breeding scheme for developing cowpea ideotype.

Acknowledgements

The authors thank the Project Coordinator, All India Coordinated Research Project on Vegetable Crops, ICAR-Indian Institute of Vegetable Research, Varanasi, India, for providing planting materials to carry out this research.

Authors' contributions

MS conducted the research. ARM, AKM and AC designed the research program and did the review and editing. AC and MS did the data analysis. MS, SS, GS, DB and IC arranged the data and wrote the main manuscript text. All the authors reviewed and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: The authors have no competing interests to disclose.

Ethical issues: None

References

1. Vavilov NI. The origin, variation, immunity and breeding of cultivated plant. Crom Bot. 1951;13:364.
2. Verdcourt B. Studies in the Leguminosae-Papilionoideae for the 'Flora of Tropical East Africa': IV. Kew Bulletin. 1970; p. 507–69.
3. Dolinassou S, Noubissié TJB, Djirantal AK, Njintang YN. Genotype × environment interaction and kernel yield-stability of groundnut (*Arachis hypogaea* L.) in northern Cameroon. J App Biol Biotech. 2016;4(1):1–7. https://doi.org/10.7324/JABB.2016.40101
4. Chattopadhyay A, Rana NP, Seth T, Das S, Chatterjee S, Dutta S. Identification of selection indices and choosing of parents for vegetable cowpea (*Vigna unguiculata* cv-gr. sesquipedalis) breeding programme. Legume Res. 2014;37(1):19–25.
5. Nkhoma N, Shimelis H, Laing MD, Shayanowako A, Mathew I. Assessing the genetic diversity of cowpea [*Vigna unguiculata* (L.) Walp.] germplasm collections using phenotypic traits and SNP markers. BMC Genet. 2020;21:1–16. https://doi.org/10.1186/s12863-020-00914-7
6. Edema R, Adjei EA, Ozimati AA, Tusiime SM, Badji A, Ibanda A, et al. Genetic diversity of cowpea parental lines assembled for breeding in Uganda. Plant Mol Biol Report. 2023;41(4):713–25. https://doi.org/10.1007/s11105-023-01394-6
7. Diallo S, Badiane FA, Kabkia BNPA, Diédhiou I, Diouf M, Diouf D. Genetic diversity and population structure of cowpea mutant collection using SSR and ISSR markers. Sci Rep. 2024;14(1):31833. https://doi.org/10.1038/s41598-024-83087-y
8. Ullah MZ, Bashar MK, Bhuiyan MSR, Khalequzzaman M, Hasan MJ. Interrelationship and cause-effect analysis among morpho-physiological traits in biroin rice of Bangladesh. Int J Plant Breed Genet. 2011;5:246–54. https://doi.org/10.3923/ijpbg.2011.246.254
9. Hazra P, Chattopadhaya A, Dasgupta T, Kar N, Das PK, Som MG. Breeding strategy for improving plant type, pod yield and protein content in vegetable cowpea (*Vigna unguiculata*). Acta Hortic. 2007;752:275–80.
10. Fraser J, Eaton GW. Application of yield component analysis to crop research. Field Crops Abstr. 1983;36:787–97.
11. Chattopadhyay A, Dasgupta T, Hazra P, Som MG. Character association and path analysis in vegetable cowpea. Madras Agric J. 1996;84:153–6.
12. Adewale BD, Adeigbe OO, Aremu CO. Genetic distance and diversity among some cowpea (*Vigna unguiculata* L. Walp) genotypes. Int Res J Plant Sci. 2011;1(2):9–14.
13. Hazra P, Som MG, Das PK. Leaf characters as pod yield component of cowpea. Phytobreedon. 1992;8:68–72.
14. Nath V, Lal H, Rai M, Rai N, Ram D. Hierarchical clustering and character association studies in cowpea [*Vigna unguiculata* (L.) Walp.]. Indian J Plant Genet Res. 2009;22:22–5.
15. Chattopadhyay A, Dutta S, Bhattacharya I, Karmakar K, Hazra P. Dolichos bean. In: Technology for Vegetable Crop Production. All India Coordinated Research Project on Vegetable Crops. Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal; 2007. p. 218–30.
16. Lowry OH, Rosbrough NJ, Farr AL, Randall RJ. Total protein estimation by Lowry's method. J Biol Chem. 1951;193(1):265–75.
17. Panse VG, Shukhatme PV. Statistical Methods for Agricultural Workers. 2nd ed. ICAR Publications; 1967.
18. Burton GW. Quantitative inheritance in grasses. In: Proceedings of the 6th International Grassland Congress. Washington; 1952. p. 277–83.
19. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating population of Korean lespedza. Agron J. 1956;48:268–72.
20. Lush JL. Heritability of quantitative characters in farm animals. Proceedings of the 8th International Congress of Human Genetics. 1949. p. 356–75.
21. Johnson HW, Robison HF, Gomostock HE. Estimate of genetic and environmental variability in soyabean. Agron J. 1955;47:314–18.
22. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass. Agron J. 1959;51:515–18.
23. Rao CR. Minimum variance estimation in distributions admitting ancillary statistics. Sankhya: Indian J Stat. 1952; p. 53–6.
24. Ward JH Jr. Hierarchical grouping to optimize an objective function. J Am Stat Assoc. 1963;58(301):236–44.
25. Egbadzor KF, Yeboah M, Gamedoagbao DK, Offei SK, Danquah EY, Ofori K. Inheritance of seed coat colour in cowpea (*Vigna unguiculata* (L.) Walp.). Int J Plant Breed Genet. 2014;8:35–43. https://doi.org/10.3923/ijpbg.2014.35.43
26. Ali B, Izge AU, Odo PE, Aminu D. Varietal performance of dual purpose dry season cowpea (*Vigna* unguiculata L. Walp) under varying plant spacing in the Fadama in northeastern Nigeria. Am-Eurasia J Sustain Agric. 2009;3(1):13–8.
27. Ichi JO, Igbadun HE, Miko S, Samndi AM. Growth and yield response of selected cowpea (*Vigna unguiculata* (L.) Walp) varieties to irrigation interval and sowing date. Pac J Sci Technol. 2013;14 (1):453–63.
28. Silva PSL, Oliveira CN. Rendimentos de feijão verde e maduro de cultivares de caupi. Hortic Bras. 1993;11:133–5.
29. Muhammad G, Ramazan CM, Aslam M, Chaudhry GA. Performance of cowpea cultivars under rainfed conditions. J Agric Res. 1994;32 (1):119–22.
30. Amanullah A, Mir Hatam MH, Naeem Ahmad NA. Performance and distinguishing characters of promising cowpea germplasm. Sarhad J Agric. 2000;16(4):365–75.
31. Damarany AM. Testing and screening of some cowpea genotypes under Assiut conditions. Assiut J Agri Sci. 1994;25(4):9–19.
32. Carvalho M, Carnide V, Sobreira C, Castro I, Coutinho J, Barros A, et al. Cowpea immature pods and grains evaluation: An opportunity for different food sources. Plants. 2022;11:2079. https://doi.org/10.3390/plants11162079
33. Ram T, Ansari MM, Sharma TVRS. Relative performance of cowpea genotypes in rainfed condition of Andaman and their genetic parameter analysis for seed yield. Indian J Pulses Res. 1994;7 (1):72–5.

34. Sadiq SM, Saleem IJ. Genetic variability and selection in hexaploid triticale. Proceedings of the International Symposium, Sydney. Australian Institute of Agricultural Science. 1986. p. 182–5.

35. Singh HN, Singh RR, Mital RK. Genotypic and phenotypic variability in tomato. Indian J Agric Sci. 1974;44(12):807–11.

36. Vidya C, Oommen SK, Kumar V. Genetic variability and heritability of yield and related characters in yard long bean. J Trop Agric. 2002;40:11–3.

37. Sreekumar KK, Inasi KA, Antony A, Nair RR. Genetic variability, heritability and correlation studies in vegetable cowpea (*Vigna unguiculata* var. sesquipedalis). South Ind Hort. 1996;44:15–8.

38. Saidaiah P, Pandravada SR, Geetha A, Kamala V. Investigations on per se performance, genetic variability and correlations in vegetable cowpea [*Vigna unguiculata* (L.) Walp.] germplasm for yield and its attributing traits. Legume Res. 2021;44(11):1267–77. https://doi.org/10.18805/LR-4645

39. Pandey S, Kumar S, Rai M, Mishra U, Singh M. Assessment of genetic diversity in Indian ash gourd (*Benincasa hispida*) accessions using RAPD markers. In: Cucurbitaceae 2008: Genetics and Breeding of Cucurbitaceae. Proceedings of the IXth EUCARPIA, INRA, Avignon, France; 2008 May 21–24.

40. Hayes HK, Immer FR, Smith DC. Methods of plant breeding. 2nd ed. New York: McGraw-Hill; 1955. p. 551.

41. Robinson HF, Comstock RE, Harvey PH. Estimation of heritability and the degree of dominance in corn. Agron J. 1949;41:353–9.

42. Songsri P, Joglloy S, Kesmala T, Vorasoot N, Akkasaeng CPA, Holbrook C. Heritability of drought resistant traits and correlation of drought resistance and agronomic traits in peanut. Crop Sci. 2008;48:2245–53.

43. Sobha PP. Variability and heterosis in bush type vegetable cowpea [*Vigna unguiculata* (L.) Walp]. M.Sc. Thesis. Kerala Agricultural University, Thrissur; 1994.

44. Panse VG. Genetics of quantitative characters in relation to plant breeding. Indian J Genet Plant Breed. 1957;17:318–35.

45. Venkatesan M, Prakash M, Ganesan J. Correlation and path analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. Legume Res. 2003;26 (2):105–8.

46. Pathak S, Jamwal RS. Variability and correlations for economic traits in powdery mildew-resistant genotypes of garden pea (*Pisum sativum* L.). Himachal J Agric Res. 2002;28(1–2):34–9.

47. 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. J Plant Breed Crop Sci. 2012;4(5):80–6. https://doi.org/10.5897/JPBCS12.007

48. Thorat A, Gadewar RD. Variability and correlation studies in cowpea (*Vigna unguiculata*). ESSENCE Int J Environ Rehabil Conserv. 2013;4 (1):44–9.

49. Sapara GK, Javia RM. Correlation and path analysis in vegetable cowpea (*Vigna unguiculata* L.). Int J Plant Sci (Muzaffarnagar). 2014;9(1):138–41.

50. Patel UV, Parmar VK, Patel PB, Malviya AV. Correlation and path analysis study in cowpea [*Vigna unguiculata* (L.) Walp]. Int J Sci Environ Technol. 2016;5(6):3897–904.

51. Nautiyal MK, Massey P, Bhatt L. Genetic variability studies for identification of high yielding genotypes with high protein content in grain cowpea [*Vigna unguiculata* (L.) Walp.]. Legume Res. 2024. https://doi.org/10.18805/LR-5269

52. Singh OV, Shekhawat N, Singh K, Gowthami R. Assessment of genetic variability and inter-character association in the germplasm of cowpea (*Vigna unguiculata* L. Walp) in hot arid climate. Legume Res. 2018;43(3):332–6. https://doi.org/10.18805/LR-3983

53. Anbumalarmathi J, Sheeba A, Deepasankar P. Genetic variability and interrelationship studies in cowpea [*Vigna unguiculata* (L.) Walp.]. Res Crops. 2005;6(3):517–9.

54. Samaee SM, Shobbar ZS, Ashrafi H, Hosseini-Mazinani M. Molecular characterization of olive germplasm in Iran using random amplified polymorphic DNA (RAPD): Correlation with phenotypic studies. Acta Hortic. 2003;623:169–75.

55. Udensi O, Ikpeme EV, Edu EA, Ekpe DE. Relationship studies in cowpea (*Vigna unguiculata* L. Walp) landraces grown under humid lowland condition. Int J Agric Res. 2012;7(1):33–45. https://doi.org/10.3923/ijar.2012.33.45

56. Vavilapalli SK, Celine VA, Sreelathakumai I. Genetic divergence analysis in vegetable cowpea [*Vigna unguiculata* subsp. unguiculata (L.) Walp.] genotypes. Legume Genom Genet. 2014;5(2):4–6. https://doi.org/10.5376/lgg.2014.05.0002

57. Srinivas J, Kale VS, Nagre PK, Meshram M. Genetic divergence studies in cowpea. Int J Agric Res. 2016;6(3):97–104.

58. Praveena VS, Abraham M, Kumar V. Genetic divergence studies in fodder cowpea [*Vigna unguiculata* (L.) Walp.] using D^2 statistics. Forage Res. 2019;44(4):230–6.

59. Hazra P, Som MG, Das PK. Genetic divergence for pod yield and its components in cowpea. Haryana J Hort Sci. 1993;22:296–302.

60. Kalloo K, Singh VP, Dudi BS, Partap PS. Analysis of variation and genetic divergence in garden peas (*Pisum sativum* L.). Haryana Agric Univ J Res. 1980;10(4):540–6.

61. Jain P, Saini ML, Arrora RN. Genetic divergence in cowpea. Forage Res. 2006;32:12–4.

62. Nogueira APO, Sediyama T, de Sousa LB, Hamawaki OT, Cruz CD, Pereira DG, et al. Análise de trilha e correlações entre caracteres em soja cultivada em duas épocas de semeadura. Biosci J. 2012;28 (6):877–88.

63. Vianna VF, Unêda-Trevisoli SH, Desidério JA, Santiago SD, Charnai K, Ferreira Júnior JA, Mauro AD. The multivariate approach and influence of characters in selecting superior soybean genotypes. Afr J Agric Res. 2013;8(30):4162–9.

64. Chipeta MM, Kafwambira J, Yohane E. Cowpea genetic diversity, population structure and genome-wide association studies in Malawi: insights for breeding programs. Front Plant Sci. 2025;15:1461631. https://doi.org/10.3389/fpls.2024.1461631

65. Johnson RA, Wichern DW. Applied Multivariate Statistical Analysis. New Jersey: Prentice-Hall; 1988.

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

Publisher information: Plant Science Today is published by HORIZON e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.