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Genetic Variability Studies for Identification of High Yielding Genotypes with High Protein Content in Grain Cowpea [*Vigna unguiculata* (L.) Walp.]

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ABSTRACT

Background: Cowpea is a major legume crop which has high protein content and provides a powerful tool to combat malnutrition due to its highly nutritional value. Identification of superior genotypes will aid in cowpea breeding program. Genetic variability is the foremost requirement in a breeding population for the selection of high yielding genotypes. To develop a new high yielding variety, it is important to study the genetic variability present in it so that proper and efficient selection could be done and most promising genotypes could be identified.

Methods: Keeping this in mind, studies on genetic variability in grain cowpea was done utilizing 40 diverse exotic and indigenous cowpea genotypes which were evaluated for ten quantitative characters for two consecutive years 2020 and 2021. The experiment was planted in randomized block design with 3 replications at Pantnagar. Data was recorded on ten characters.

Result: Mean squares were found to be highly significant for all the characters. Cluster analysis revealed five genetically diverse clusters. Cluster I had 8 genotypes, cluster II had 9 genotypes, cluster III consisted of 12 genotypes, cluster IV had 6 genotypes and Cluster V consisted 5 genotypes. Cluster I had the greatest intra-cluster distance (2.500) whereas cluster V had the smallest intra-cluster distance (1.701). In the cluster V, one of the genotype Pant Lobia-2 exhibited the highest mean values for all the characters. The highest GCV and PCV was recorded by number of pods per plant (28.87, 29.19) followed by yield (q/ha) (28.72, 29.04). The higher value of phenotypic component compared to the corresponding genotypic component suggest that there was an environmental influence on the performance of the genotypes. Correlation studies revealed positive correlation between pod length, pods per cluster, seeds per pod and yield quintal per hectare. Path coefficient analysis showed the significant 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. The results of the study showed that, out of the 40 genotypes evaluated, Pant Lobia-2 exhibited the best performance. It has attractive red bold seeds with 31% protein content. Therefore it can be used in grain cowpea breeding program.

Key words: Grain cowpea, Iron, Legume crop, Nutrition, Protein content, Seed yield, Short-duration, Vigna**,** Zinc.

INTRODUCTION

Cowpea (*Vigna unguiculata*) is one of the most important grain legume crop. The plant tolerates drought, performs well in a wide variety of soils and replenishes low fertility soils when the roots are left to decay. It also grows and covers the ground quickly and thus aids in preventing erosion. The name "cowpea" probably derives from when it was an important livestock feed for cows in the United States. The global annual production of cowpea is approximately 6.5 million metric tons and the area of cowpea is 14.5 million hectares worldwide (Horn *et al*., 2022). Nigeria is the largest producer of cowpea with 2.4 million tonnes annual production and an area of five million hectares (Rivas *et al*., 2016). Nigeria, the largest producer and consumer, accounts for 61% of production in Africa and 58% worldwide. In India, the area under cowpea is 58000 ha and production is 4.8 lakh tonnes with a productivity of 8.44 t/ha.

Cowpea acts as a means of livelihood and as a source of nutritional well-being for farmers (Bolarinwa *et al*., 2021). Cowpea is mainly grown for grain, fodder, vegetable, green manure and cover crop. It can be consumed as a vegetable in the form of green pods. Cowpea grains contain 20%-32% protein with high content of essential amino acids namely lysine and tryptophan, minerals (zinc, iron, Ca), vitamins (thiamine, riboflavin and folic acid) and fibres (6%) (Boukar *et al*., 2018). Cowpea acts as a cheap source of protein and contributes for the eradication of malnutrition (Ddungu *et al*., 2015).

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According to Sebethaet *al.* (2014), protein content of cowpea is two to four times higher than that of cereal and tuber crops (Trehan *et al*., 2015). Due to its nutritional quality, it is helpful where many people cannot afford animal proteins like meat and fish. The *g*enetic base in legumes, especially cowpea, can be widened through a greater understanding of legume variety and the utilization of wild relatives in breeding (Van *et al*., 2020), (Kilian *et al*., 2021). The most popular breeding technique employed by cowpea breeders is the pedigree selection which has been found successful in creating cultivars with novel combinations of desirable traits and disease resistance (Metwally *et al*., 1988), (Obisesan, 1992).

The knowledge of genetic divergence, genetic advance, heritability and correlation is a need for selection of superior genotypes in cowpea (Addisu and Shumet, 2015). Heritability, genetic advance and correlation aids in exploitation of genetic variability for selection and identification of promising genotypes (Bilgin *et al*., 2010). Cluster analysis is essential for the grouping of genotypes and helps in selecting suitable parents in crossing programme (Koij and Saba, 2015). The present study was conducted to determine the *g*enetic variability, heritability and correlation between yield and associated traits among 40 cowpea genotypes at Pantnagar.

MATERIALS AND METHODS

The present investigation was conducted at Breeder Seed Production Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar (Udham Singh Nagar). Pantnagar is located in the foothills of Shivalik range of Himalayas popularly called as “Tarai” region. Tarai region falls in humid subtropical zone at 290 North latitude, 79.30o East longitude at height of 243.84 m above mean sea level. All genotypes were sown on *kharif,* 25-03-2020 in randomized block design (RBD) with three replications. Each genotypes were accommodated in 4 rows of 4 meters in length having spacing of 45×10 centimeters. The experimental material consists of forty genotypes of grain cowpea (Table 1). The *g*enotypes which are selected were highly distinct from each other and they also showed significant amount of variation for both qualitative and quantitative traits.

Observations were recorded as average of randomly selected five plants from each genotype and than average of five plants were taken for estimation of data.

Data was collected on ten characters namely days to 50% flowering, plant height (cm), peduncle length (cm), number of pods per cluster, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and yield (qtl/hec). Statistical analysis of the mean data was performed. Studies on genetic divergence, heritability, genetic advance, genotypic variance (σ^2g), phenotypic variance (σ^2p), environmental variance, correlation analysis and path coefficient analysis were conducted. Analysis of variance was carried out using the Panse and Sukhatme (1967) approach. Singh and Chaudhary (1985) technique was used to calculate the *g*enotypic coefficient of variation and the phenotypic coefficient of variation. Genetic advance and heritability were calculated using the approach described by (Burton and Devane, 1953). The approach recommended by Dewey and Lu (1959) was used to calculate the correlation coefficient and the path analysis. The following scales were used for path coefficient (Lenka and Mishra, 1973) 0.00-0.09= negligible, 0.10-0.19= low, 0.20-0.29= moderate, 0.30-0.99= high, >1.00= very high. The per cent N in cowpea leaves and seeds was determined using mass spectrometry, as described by Belane *et al*. (2010). The protein in leaves and seeds was estimated as percent N of organ×6.25 (Jones, 1941; Mariotti *et al*., 2008).

Genetic divergence

Mahalanobis (1936) D^2 statistic analysis was used for calculating the genetic divergence between different genotypes in population. The values of D^2 were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952). Group constellations-D^2 is treated as the square of generalized distance, all genotypes were divided into clusters according to Tocher method.

Estimation of variability, heritability and genetic advance

Mean

The general mean was computed by summing the data of all the treatments over all the three replications for each character.

Range

The lowest and highest mean value for each character was taken as range.

Genotypic variance (σ^2g)

The genotypic variance σ^2g is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was:

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{MSt-MSe}}{r}$$

Where,
MSt = Mean square due to genotypes.
MSe = Mean square due to error.
r = Number of replications.

Phenotypic variance (σ^2p)

Phenotypic variance (σ^2p) denotes the total variance present in a population for particular character and was calculated by following formula:

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where:
σ^2g= Genotypic variance.
σ^2e= Mean sum of squares due to error/Environment variance.

Environmental variance

The environmental variance ($\sigma^2 e$) is the variance due to environmental deviation.

$$\sigma^2 e = MSe$$

Estimation of heritability

Heritability in broad sense was calculated for each character as described by Johnson *et al*. (1955) as follows.

$$h^2_{(b)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

$h^2_{(b)}$= Heritability in broad sense.

σ^2_g= Genotypic variance.

σ^2_P= Phenotypic variance.

The genotypic and phenotypic variances are obtained from the expectation of mean squares of analysis of variance of RBD.

Estimation of expected genetic advance

The expected genetic advance from (G.A) straight selection as per Allard (1960).

$$G.A = h^2_{(b)} \times \sigma_p \times K$$

Where,

GA = Expected genetic advance.

$h^2_{(b)}$ = Heritability in broad sense.

σ_P = Phenotypic standard deviation.

K = Constant for which the value is given as 2.06 which is the expected in the case of 5% selection intensity.

Genetic advance was expressed as per cent of population mean.

Genetic advance as per cent of mean=

$$\frac{\text{Genetic advance}}{\text{GM}} \times 100$$

RESULTS AND DISCUSSION

The assessment of variability in a population is a must for any breeding programme. Table 2 (Supplementary table) displays the mean values of ten traits in forty cowpea genotypes evaluated for consecutive two years *i.e*. 2020 and 2021.

All the characters, including days to 50% flowering, plant height (cm), peduncle length (cm), pod length (cm), number of pods per cluster, number of pods per plant, number of seeds per pod, 100-seed weight, protein content and yield (qtl/hec) were subjected to analysis of variance. Mean squares were found to be highly significant Table 3. The mean values showed that Pant Lobia-2 performed the best among all the 40 genotypes. Pant Lobia-2 had the highest mean values for peduncle length (62.02 cm) which is suitable for mechanical harvesting. The maximum pod length (14.95 cm), pods per cluster (3.73), seeds per pod (14.58) and 100 seed weight (13.35g) were also shown by Pant Lobia-2. These characteristics are important contributors to yield. The most critical characteristic for a pulse or legume crop is protein content, Pant Lobia-2 has the highest protein content (31.00%). The highest grain yield (18.76 q/ha) was obtained from Pant Lobia-2 among the 40 genotypes and it has erect and bushy plant (Fig 1). It has attractive large bold red seeds that gives it a glimpse of red kidney bean (Fig 2).

Table 1: List of genotypes grain cowpea.

S. no.	Genotype	Details	S. no.	Genotype	Details
1	GCP-234	Pantnagar selection	21	GCP-380	Pantnagar selection
2	GCP-286	Pantnagar selsction	22	GCP-381	Pantnagar selsction
3	GCP-297	Pantnagar selsction	23	GCP-383	Pantnagar selsction
4	GCP-320	Pantnagar selection	24	GCP-380	Pantnagar selection
5	GCP-345	Pantnagar selection	25	GCP-381	Pantnagar selection
6	GCP-346	Pantnagar selection	26	GCP-382	Pantnagar selection
7	GCP-348	Pantnagar selection	27	GCP-383	Pantnagar selection
8	GCP-349	Pantnagar selection	28	GCP-384	Pantnagar selection
9	GCP-350	Pantnagar selection	29	GCP-385	Pantnagar selection
10	GCP-351	Pantnagar selection	30	GCP-386	Pantnagar selection
11	GCP-353	Pantnagar selection	31	GCP-387	Pantnagar selection
12	GCP-354	Pantnagar selection	32	GCP-388	Pantnagar selection
13	GCP-355	Pantnagar selection	33	GCP-389	Pantnagar selection
14	GCP-356	Pantnagar selection	34	GCP-390	Pantnagar selection
15	GCP-357	Pantnagar selsction	35	GCP-392	Pantnagar selsction
16	GCP-358	Pantnagar selection	36	PL-1	Pantnagar selection
17	GCP-359	Pantnagar selection	37	PL-2	Pantnagar selection
18	GCP-360	Pantnagar selection	38	PL-3	Pantnagar selection
19	GCP-362	Pantnagar selection	39	PL-4	Pantnagar selection
20	GCP-378	Pantnagar selection	40	PL-5	Pantnagar selection

Table 2: Mean performance of different genotypes of cowpea for characters studied.

Genotypes	Days to 50% flowering	Plant height (cm)	Peduncle length (cm) cluster	Pod length (cm)plant	Number of pods per	Number of pods per	Number of Seeds per pod	100 seed weight (g)	Protein content (%)	Yield (q/ha)
GCP-234	49.67	38.00	27.43	15.30	3.23	9.70	14.05	11.75	20.20	14.10
GCP-286	48.00	36.20	21.80	13.23	2.73	10.85	11.00	9.63	23.33	12.27
GCP-297	47.67	46.73	20.23	14.60	2.50	9.80	12.30	17.70	19.07	12.53
GCP-320	51.67	45.67	23.50	14.60	2.73	12.75	11.90	12.15	19.40	17.10
GCP-345	49.00	34.50	20.03	10.37	2.50	6.80	12.85	8.10	27.60	3.15
GCP-346	48.33	46.30	27.33	17.00	2.83	7.70	9.85	15.90	19.70	19.00
GCP-348	47.33	36.10	23.63	12.63	2.73	7.40	10.85	15.18	21.80	10.17
GCP-349	43.67	33.93	25.13	11.53	1.73	9.80	10.90	12.03	20.47	9.40
GCP-350	48.33	46.43	27.33	16.63	3.50	13.40	11.85	12.15	19.00	16.00
GCP-351	51.00	45.27	28.17	16.00	3.23	13.95	14.80	12.40	19.60	14.80
GCP-353	49.33	45.53	24.63	13.92	3.27	6.90	13.10	13.00	19.40	10.93
GCP-354	48.00	48.43	30.33	16.70	3.50	12.60	12.95	13.10	19.57	19.10
GCP-355	50.00	39.40	24.23	12.50	2.77	5.27	14.90	13.60	26.80	10.87
GCP-356	40.00	49.23	21.40	13.42	2.73	13.40	12.25	13.80	21.10	12.45
GCP-357	49.00	36.20	21.67	12.80	1.50	9.10	10.85	9.40	22.10	9.40
GCP-358	41.33	44.17	31.00	16.07	3.73	13.17	15.25	11.35	20.80	23.20
GCP-359	43.33	47.03	24.63	14.20	3.50	9.15	13.25	15.40	25.07	15.10
GCP-360	46.33	46.97	21.90	12.33	1.50	4.90	12.80	13.20	26.73	6.02
GCP-362	43.00	56.77	27.00	16.40	2.50	11.80	11.80	11.90	27.97	14.70
GCP-378	43.00	45.30	21.03	13.27	1.73	5.40	7.85	16.15	23.30	4.65
GCP-380	43.00	50.00	26.07	15.07	2.50	7.40	11.25	13.75	24.00	11.35
GCP-381	33.11	48.50	21.23	13.67	2.23	11.17	9.67	10.75	21.20	12.62
GCP-383	34.28	52.67	22.80	12.67	1.73	11.50	11.67	8.63	24.33	12.81
GCP-380	32.80	59.18	28.43	16.83	2.80	11.17	12.00	16.70	20.07	13.87
GCP-381	34.55	55.00	24.50	13.90	1.73	8.17	7.67	11.15	20.40	11.55
GCP-382	37.44	56.02	28.33	13.00	1.50	8.18	15.00	7.10	28.60	13.58
GCP-383	36.08	55.67	23.67	16.42	1.83	6.67	15.00	14.90	20.70	11.91
GCP-384	38.78	50.58	24.63	14.08	2.50	12.17	11.67	14.18	22.80	12.84
GCP-385	35.78	51.02	26.13	14.17	2.73	6.17	12.67	11.03	21.47	12.53
GCP-386	33.97	54.02	25.63	13.33	2.73	8.17	12.00	11.15	20.00	12.43
GCP-387	38.70	52.02	25.33	12.67	2.80	4.67	13.00	11.40	20.60	12.62
GCP-388	36.78	54.00	24.63	14.58	2.50	8.92	11.67	12.00	20.40	12.97
GCP-389	35.44	55.17	27.00	13.50	2.23	8.17	12.67	12.10	20.57	12.22
GCP-390	35.75	63.02	25.23	13.67	2.27	7.17	9.67	12.60	27.80	11.11

Table 2: Continue...

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GCP-392	36.78	54.02	22.40	11.00	1.77	8.00	10.67	12.80	22.10	10.98
PL-1	35.78	58.87	22.67	12.00	2.50	12.00	11.67	10.42	23.10	12.63
PL-2	40.64	62.02	28.90	14.95	3.73	14.58	12.67	13.35	31.00	18.76
PL-3	36.11	59.02	29.17	15.80	3.00	12.17	11.50	13.00	26.07	16.48
PL-4	34.11	48.18	32.00	14.33	2.73	11.33	10.00	12.20	27.73	14.38
PL-5	30.73	61.18	31.33	13.80	2.83	13.17	11.00	13.00	28.97	15.43
Mean	41.47	49.21	25.31	14.07	2.58	9.62	11.96	12.50	22.87	12.95
Min	30.73	33.93	20.03	10.37	1.50	4.67	7.67	7.10	19.00	3.15
Max	51.67	63.02	32.00	17.00	3.73	14.58	15.25	17.70	31.00	23.20
SE(d) ±	1.47	1.71	0.82	0.45	0.09	0.34	0.41	0.43	0.72	0.46
C.D. at 5%	2.94	3.41	1.63	0.91	0.17	0.68	0.82	0.85	1.43	0.92
C.V. (%)	4.36	4.25	3.96	3.95	4.05	4.31	4.23	4.16	3.85	4.34

Table 3: Analysis of variance (mean sum of squares) of different characters of grain cowpea genotypes.

Source of variation	df	Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Pod length (cm)	Number of Pods per cluster	Number of Pods per plant	Number of Seeds per pod	100 seed weight (g)	Protein content (%)	Yield (q/ha)
Repl	2	1.53	5.60	0.29	1.27	0.07	1.13	0.25	0.52	0.23	0.00
Treat	39	118.55**	184.23**	29.88**	8.21**	1.16**	23.32**	9.30**	15.35**	33.67**	41.80**
Error	78	3.26	4.38	1.01	0.31	0.01	0.17	0.26	0.27	0.77	0.32
Total	119	41.02	63.34	10.46	2.91	0.39	7.77	3.22	5.22	11.55	13.91

*, ** significant at 5% and 1% level, respectively.

Genetic divergence

The selection of genotypes that could be used in a hybridization programme for further improvement is supported by knowledge of genetic divergence. Since genetic diversity is necessary to manifest a response to selection pressure, knowledge of the genetic variation available in the genetic material is significant in determining the probability of effective selection and breeding for higher grain yield per plant. In the present investigation, D^2 analysis was used for the study of genetic divergence. Grain cowpea genotypes were grouped into five clusters. The cluster diagram of the forty genotypes has been shown in Fig 3. Clustering pattern of 40 genotypes has been shown in Fig 4. Cluster III has the maximum 12 genotypes namely GCP-381, GCP-383, GCP-381, GCP-382, GCP-385, GCP-386, GCP-387, GCP-388, GCP-389, GCP-390, GCP-392 and PL-1, followed by cluster II with 9 genotypes (GCP-297, GCP-346, GCP-353, GCP-356, GCP-359, Cluster I with 8 genotypes (GCP-286, GCP-345, GCP-348, GCP-349, GCP-355, GCP-357, GCP-360, GCP-378), Cluster IV with 6 genotypes (GCP-234, GCP-320, GCP-350, GCP-351, GCP-354, GCP-358) and Cluster V with 5 genotypes (GCP-362, PL-2, PL-3, PL-4 and PL-5) (Table 4).

According to Table 5, the inter-cluster distance ranged from 2.665 (between cluster II and cluster III) to 5.245 (between cluster I and cluster V). The intra-cluster distance ranged from 1.701 to 2.500. Cluster I (2.500) had the greatest intra-cluster distance, whereas cluster V had the smallest intra-cluster distance (1.701). The range for the mean days to 50% flowering was 35.70 days (cluster III) to 48.33 days (cluster IV), while the range for the mean plant height was 38.57 cm (cluster I) to 57.43 cm (cluster V)(Table 5). The mean values for peduncle length ranged from 22.43 cm (cluster I) to 29.68 cm (cluster V), for pod length from 12.33 cm (cluster I) to 15.88 cm (cluster IV), for number of pods per cluster from 2.15 cm (cluster I) to 3.32 cm (cluster IV), for number of pods per plant from 7.44 cm (cluster I) to 12.6 cm (cluster V), for number of seeds per pod from 11.39 cm (cluster V) to 13.47 (cluster IV), for 100-grain weight, it varied between 10.93 gm (cluster III) to 15.04 gm (cluster (II) for protein % it varied between 19.76% (cluster IV) to 28.35 % (cluster V), for yield quintals per hectare it varied between 8.24 qtl (cluster I) to 17.38 qtl (cluster V) as shown in Table 6. It was found that Cluster V had the genotypes with the highest mean values for the characters namely plant height, peduncle length, pod length, pods

Fig 1: Crop canopy of Pant Lobia-2.

Fig 2: Seed of Pant Lobia-2.

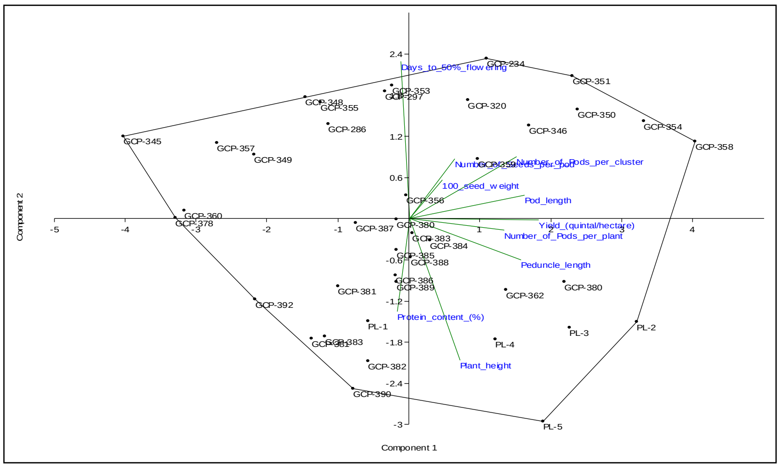

Fig 3: Cluster diagram of 40 genotypes.

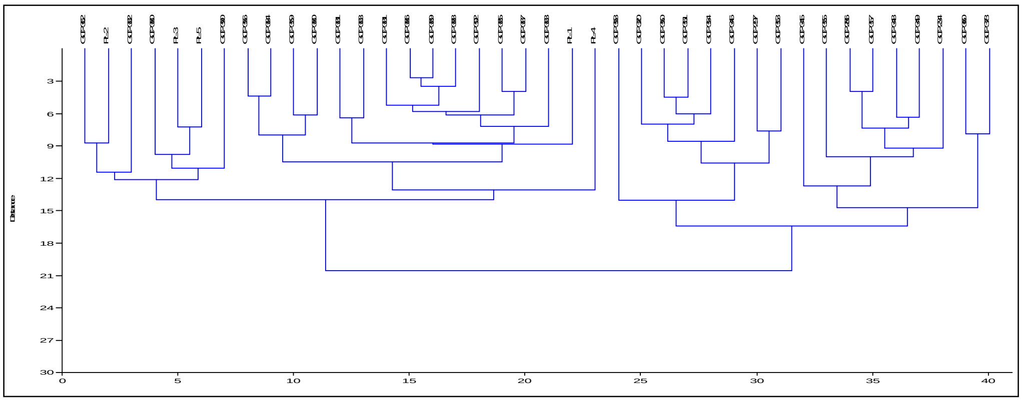

Fig 4: Clustering pattern of 40 grain cowpea genotypes.

Table 4: Clusters showing the distribution of forty grain cowpea genotypes.

Clusters	No. of genotypes	Genotypes
I	8	GCP-286, GCP-345, GCP-348, GCP-349, GCP-355, GCP-357, GCP-360 and GCP-378
II	9	GCP-297, GCP-346, GCP-353, GCP-356, GCP-359, GCP-380, GCP-380, GCP-383 and GCP-384
III	12	GCP-381, GCP-383, GCP-381, GCP-382, GCP-385, GCP-386, GCP-387, GCP-388, GCP-389, GCP-390, GCP-392 and PL-1
IV	6	GCP-234, GCP-320, GCP-350, GCP-351, GCP-354 and GCP-358
V	5	GCP-362, PL-2, PL-3, PL-4 and PL-5

Table 5: Inter and Intra cluster distance for forty grain cowpea genotypes.

Clusters	I	II	III	IV	V
I	2.500				
II	3.400	2.284			
III	3.166	2.665	2.073		
IV	4.914	2.929	4.321	1.757	
V	5.245	3.456	3.475	3.873	1.701

per cluster, seeds per pod, 100 seed weight, protein content and yield. Among the genotypes in cluster V, Pant Lobia-2 showed the highest mean values for all characters and therefore it may be used as a parent in the breeding programme to obtain the better genotypes with desirable traits. The results also resembled those of research on genetic diversity conducted by Aswathi *et al*. (2015), Chandrakar *et al*. (2016) and Patel *et al.* (2017).

The peduncle length (13.57%) made the largest contribution to divergence, followed by plant height (13.38%), days to 50% flowering (12.64%), pod length (11.81%) and number of seeds per pod (10.06%)(Table 7). In the current study, mean cluster values revealed that the peduncle length, followed by plant height, days until days to 50% flowering (the no. of days in which 50% of plants have started flowering), pod length (cm) and number of seeds per pod, contributed most to divergence.

[DF= Days to 50% flowering, PH= Plant height (cm), Pe= Peduncle length (cm), Po= Pod length (cm), POC= Pods per cluster, POP= Pods per plant, SP= Seeds per pod, SW=100 seed weight (g), PC= Protein content (%),Y= Yield (q/ha)]

The coefficient of variation, which gives information about the type and scope of variation, is another way to observe variability. Phenotypic variances was found to be greater than genotypic variances for all the characters (Table 7). The highest values of genotypic variance was found for plant height (59.95), followed by days to 50% flowering (38.43). The largest amount of phenotypic variance was found for plant height (64.33) followed by days to 50% blooming (41.69). The GCV values ranged from 11.53 (Pod length (cm) to 28.87 (number of pods per plant). The PCV values for the number of pods per plant remained (29.19), yield (29.04), pods per cluster (24.36). Nwofia *et al*. (2006) also reported similar results.

Heritability and genetic advance

Heritability varied from 89.51% (pod length) to 97.82% (number of pods per plant). High heritability estimates were observed for yield (97.77) and number of pods per cluster

Table 6: Cluster mean values for various quantitative characters in grain cowpea.

Clusters		Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Pod length (cm)	Number of pods per cluster	Number of pods per Seedsplant	Number of seed per pod	100 weight (g)	Protein content (%)	Yield (q/ha)
I	Mean	47.04	38.57	22.43	12.33	2.15	7.44	11.50	12.16	24.02	8.24
	SE±	2.55	4.96	1.73	0.96	0.58	2.26	2.07	2.90	2.68	3.24
II	Mean	42.15	50.03	24.56	15.06	2.72	9.37	12.30	15.04	21.32	13.33
	SE±	5.73	4.62	2.61	1.35	0.48	2.44	1.43	1.53	2.14	2.47
III	Mean	35.70	54.53	24.66	13.18	2.23	8.52	11.50	10.93	22.55	12.34
	SE±	1.58	3.73	2.07	0.99	0.45	2.16	1.90	1.63	2.93	0.77
IV	Mean	48.33	44.66	27.96	15.88	3.32	12.60	13.47	12.15	19.76	15.95
	SE±	3.72	3.56	2.66	0.81	0.35	1.50	1.46	0.59	0.64	3.35
V	Mean	36.92	57.43	29.68	15.06	2.96	12.61	11.39	12.69	28.35	17.38
	SE±	4.94	5.56	2.01	1.06	0.47	1.29	0.99	0.61	1.81	1.77

Table 7: Genetic parameters of variation for various characters in grain cowpea.

	Mean	Min	Max	var (g)	var (p)	GCV (%)	PCV (%)	% contribution	Heritability (%)	GA	GA% mean
DF	41.47	30.73	51.67	38.43	41.69	14.95	15.57	12.64	92.18	12.26	29.57
PH	49.21	33.93	63.02	59.95	64.33	15.73	16.30	13.38	93.20	15.40	31.29
PeL	25.31	20.03	32.00	9.63	10.63	12.26	12.88	13.57	90.53	6.08	24.02
PoL.	14.07	10.37	17.00	2.63	2.94	11.53	12.19	11.81	89.51	3.16	22.47
POC	2.58	1.50	3.73	0.38	0.39	24.02	24.36	9.75	97.24	1.26	48.79
POP	9.62	4.67	14.58	7.71	7.89	28.87	29.19	6.37	97.82	5.66	58.83
SP	11.96	7.67	15.25	3.01	3.27	14.51	15.12	10.06	92.16	3.43	28.70
SW	12.50	7.10	17.70	5.03	5.30	17.93	18.41	9.24	94.90	4.50	35.99
PC	22.87	19.00	31.00	10.97	11.74	14.48	14.98	6.89	93.41	6.59	28.82
Y	12.95	3.15	23.20	13.83	14.15	28.72	29.04	6.30	97.77	7.57	58.49

(97.24%) (Table 7). Heritability estimates for other traits were found as follows: 100 seed weight exhibited 94.90% heritability. The heritability for protein content was found to be 93.41%, Other traits like plant height showed 93.20% and days to 50% flowering showed 92.18% heritability. The trait number of seeds per pod exhibited 92.16% heritability. According to Singh (2001) selection could be fairly easy if heritability is greater than 70 %. Nonetheless, it is important to add that a high heritability alone is not enough for an efficient selection in advanced generations unless that it is accompanied by substantial genetic advanced (Johnson *et al*., 1955). Therefore, high heritability coupled with high genetic advanced observed for most of the yield components indicate that, promising lines could be selected for further evaluation, selection and release. High heritability was also discovered by Pravin *et al*. (2013) for seed yield per plant, 100-seed weight, pod weight, pod length and number of pods per plant. Genetic advance quantifies genetic improvement made due to selection. Plant height (15.40) and days to 50 % flowering showed high values for genetic advance. Protein content (6.59), peduncle length (6.08), number of pods per plant (5.66), 100-seed weight (4.50) and number of seeds per pod showed moderate genetic advance (3.43). Similar findings were also reported by Sabale *et al*. in 2018.Direct phenotypic selection may be efficient for improving traits with high heritability and high genetic advance.

Correlation

Since yield is a complex trait, choosing genotypes based on yield alone makes it exceedingly difficult to improve. Therefore, identifying the characters which are closely related and which have contributed to yield becomes highly essential. Correlation is a useful factor in this context for determining the direction and intensity of the relationship between various component characters and seed yield. In the current study, the correlation between nine. characteristics and seed yield was assessed. The correlation analysis showed a positive and significant correlation between yield (q/ha), plant height, peduncle length, pod length, number of pods per cluster, number of pods per plant and number of seeds per pod, indicating that these characters are the primary yield determinants in cowpea. The study revealed that there was a positive significant correlation between yield per hectare and pod length (0.722 genotypic, 0.657 phenotypic), number of pods per cluster (0.658 genotypic, 0.640 phenotypic), number of pods per plant (0.649 genotypic, 0.639 phenotypic) and

Table 8: Genotypic and Phenotypic correlations.

Characters		Days to 50% flowering	Plant height (cm)	Peduncle length (cm) cluster	Pod length (cm)plant	Number of Pods per	Number of Pods per	Number of Seeds per pod	100 seed weight (g)	Protein content (%)	Yield (q/ha)
Days to 50% flowering	GC	1.000	-0.742**	-0.225*	0.087	0.266**	-0.055	0.273**	0.111	-0.207*	-0.072
	PC	1.000	-0.724**	-0.206*	0.039	0.256**	-0.050	0.235**	0.113	-0.223*	-0.038
Plant height (cm)	GC			0.355**	0.265**	-0.012	0.189*	-0.090	0.094	0.288**	0.314**
	PC			0.335**	0.267**	-0.022	0.180*	-0.084	0.076	0.280**	0.282**
Peduncle length (cm)	GC				0.608**	0.522**	0.416**	0.224*	0.034	0.177	0.714**
	PC				0.530**	0.497**	0.367**	0.238**	0.007	0.153	0.667**
Pod length (cm)	GC					0.540**	0.423**	0.179	0.416**	-0.262**	0.722**
	PC					0.493**	0.399**	0.151	0.396**	-0.246**	0.657**
Number of pods per cluster	GC					0.470**	0.362**	0.240**	-0.105	0.658**	
	PC						0.449**	0.353**	0.224*	-0.092	0.640**
Number of Pods per plant	GC						0.067	-0.059	0.007	0.649**	
	PC							0.042	-0.049	0.002	0.639**
Number of seeds per pod	GC							-0.108	-0.012	0.272**	
	PC								-0.136	0.000	0.261**
100 seed weight (g)	GC									-0.211*	0.096
	PC									-0.230*	0.092
Protein content (%)	GC										-0.123
	PC										-0.129
Yield (q/ha)	GC										1.000
	PC										1.000

(GC= Genotypic correlation, PC= Phenotypic correlation).

*, ** significant at 5% and 1% level, respectively.

Table 9: Path analysis (Genotypic path and phenotypic path).

Characters		Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Pod length (cm)	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Protein content (%)	R with yield (q/ha)
Days to 50% flowering	GP	0.0004	-0.1123	-0.0638	0.0229	0.0602	-0.0153	0.0169	-0.0110	0.0303	-0.072
	PP	0.0646	-0.1297	-0.0629	0.0073	0.0561	-0.0160	0.0140	-0.0076	0.0360	-0.038
Plant height (cm)	GP	-0.0003	0.1513	0.1007	0.0695	-0.0026	0.0521	-0.0056	-0.0093	-0.0421	0.314**
	PP	-0.0468	0.1790	0.1024	0.0502	-0.0049	0.0575	-0.0050	-0.0051	-0.0452	0.282**
Peduncle length (cm)	GP	-0.0001	0.0537	0.2838	0.1595	0.1181	0.1148	0.0138	-0.0033	-0.0259	0.714**
	PP	-0.0133	0.0600	0.3055	0.0995	0.1089	0.1172	0.0141	-0.0005	-0.0247	0.667**
Pod length (cm)	GP	0.0000	0.0401	0.1727	0.2622	0.1224	0.1167	0.0111	-0.0411	0.0384	0.722**
	PP	0.0025	0.0478	0.1618	0.1879	0.1079	0.1274	0.0090	-0.0267	0.0397	0.657**
Pods per cluster	GP	0.0001	-0.0017	0.1481	0.1417	0.2264	0.1297	0.0224	-0.0237	0.0154	0.658**
	PP	0.0165	-0.0040	0.1519	0.0926	0.2190	0.1434	0.0210	-0.0151	0.0148	0.640**
Pods per plant	GP	0.0000	0.0285	0.1179	0.1108	0.1063	0.2762	0.0041	0.0059	-0.0010	0.649**
	PP	-0.0032	0.0322	0.1120	0.0749	0.0983	0.3196	0.0025	0.0033	-0.0004	0.639**
Seeds per pod	GP	0.0001	-0.0136	0.0635	0.0470	0.0820	0.0185	0.0618	0.0107	0.0018	0.272**
	PP	0.0152	-0.0150	0.0726	0.0284	0.0774	0.0135	0.0595	0.0092	0.0000	0.261**
100 seed weight (g)	GP	0.0000	0.0142	0.0096	0.1092	0.0543	-0.0164	-0.0067	-0.0988	0.0309	0.096
	PP	0.0073	0.0135	0.0020	0.0744	0.0491	-0.0158	-0.0081	-0.0674	0.0372	0.092
Protein content (%)	GP	-0.0001	0.0436	0.0503	-0.0688	-0.0239	0.0019	-0.0008	0.0209	-0.1463	-0.123
	PP	-0.0144	0.0501	0.0467	-0.0463	-0.0201	0.0007	0.0000	0.0155	-0.1615	-0.129

Resi = 0.02068 (For genotypic path), Resi = 0.0250 (For phenotypic path).

*, ** Significant at 5% and 1% level, respectively.

number of seeds per pod (0.272 genotypic, 0.261 phenotypic) (Table 8). Patel *et al*. (2017), Nkoana *et al*. (2019) and Nwofia *et al*. (2006) reported similar findings. For all the traits, the amount of genotypic correlation was greater than the phenotypic correlation, indicating an inherent connection among the characters.

Path coefficient analysis

The results of path coefficient analysis revealed that there is a positive direct effect of the number of pods per plant, number of clusters per plant and 100 seeds weight with the yield. Traits such as number of clusters per plant, number of pods per cluster and plant height at the genotypic level, as well as traits such as number of branches per plant and pod length at the phenotypic level, were directly positively affecting the amount of seeds produced by each plant (Table 9.The highest positive direct relationship between yield and pods per cluster (0.640), number of pods per plant (0.639) and number of seeds per pod (0.261) was found by path coefficient analysis. The findings were similar with Walle *et al* (2018). The path coefficient analysis results revealed that traits like pod length, number of pods per plant and plant height should be taken into account for the selection of high-yielding genotypes because these traits had a significant positive direct impact or we can say directly and positively associated with the seed yield.

CONCLUSION

The results of this investigation indicates that Pant Lobia-2 can be used in crossing programme to obtain the genotypes with desirable traits. Pant Lobia-2 is profitable for farmers and seed producers. It has attractive large bold red seeds that gives it a glimpse of red kidney bean. According to the analysis, Pant Lobia-2 performed the best among the 40 genotypes. It displayed early flowering (40.64 days), a plant height of 62.02 cm, pod length 14.95 cm , pods per cluster 3.73, seeds per pod 14.58, a protein content of 31%, and a yield of 18.76 q/ha. It has bushy determinate growth pattern. Pant Lobia-2 exhibits synchronous maturity which makes it convenient for single harvesting to save farmers time and labour. Pant Lobia-2 may be considered as the first option for farmers and consumers in order to tackle the problem of malnutrition. Pant Lobia-2 is able to withstand both biotic and abiotic stress and it also contributes to improved soil fertility by biologically fixing nitrogen. It can be recommended for cultivation and grain cowpea breeding programmes. It can be employed as a parent in cowpea quality improvement programme and will improve the production of legumes.

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Ethical statement

Research has been conducted ethically and in compliance with relevant guidelines and regulations.

Conflict of interest

The authors declare no conflict of interest.

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