

Strategic Approaches for Genetic Enhancement of Quantitative and Physiological Traits in Advanced Breeding Lines of Chickpea

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ABSTRACT

Performance on seed yield and yield attributing traits of 41 advance breeding lines were used to estimate parameters of genetic variability, association analysis and diversity analysis between seed yield and its contributing traits. Traits such as biological yield per plant, number of seeds per pod, seed yield per plant, stem thickness, height of first fruiting node, number of effective pods per plant, total number of pods per plant, harvest index and primary branches per plant revealed high genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean. High magnitude of positive direct effect and significantly positive correlations on seed yield per plant was found with number of effective pods per plant, biological yield per plant, harvest index and number of secondary branches per plant. Clustering analysis based on various morphological

traits assorted 41 desi chickpea genotypes into four clusters. Traits like biological yield, plant height and 100 seed weight contributed most towards the genetic divergence. Genotypes ICCV211103, ICCV211106, ICCV211108, ICCV211111, ICCV211116, RVG 204, JG 24, JG 12, JG 16, Virat and Vishal recorded maximum positive principal component scores for the traits viz., plant height, total number of pods per plant, number of effective pods per plant, days to 50% flowering, days to maturity, stem thickness, biological yield per plant, harvest index, seed yield per plant, 100 seed weight and stem height at first fruiting node, therefore these genotypes will as promising donor lines for chickpea yield improvement.

Keywords Heritability, Genetic advance, Correlation, Path coefficient analysis, D² statistics, PCA.

INTRODUCTION

The rice-wheat cropping system plays a vital role in Indian economy and global food security. But prolong cereal based crop rotation results in deterioration of soil health. Crop diversification by introducing chickpea in such cropping pattern can improve soil nutrients through nitrogen fixation and helps in breaking disease pest cycle. Chickpeas (gram/chana) are major protein providers of vegetarian population of India. Madhya Pradesh alone has about 28% of the country's chickpea area, while contributing 34% in total pulse production followed by Maharashtra (20% and 18%), Rajasthan (19% and 18%) and Karnata-

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ka (10% and 6%) in terms of area and production (Ministry of Agriculture and Farmers Welfare 2022). *Rabi* season presents a greater likelihood opportunity of growing chickpea due to the following factors: (a) Offers security of food products after harvest of paddy, (b) In the absence of erratic rainfall, there is low possibility of waterlogging thus, reducing the damage caused by root rot and flower drop. There is no leaching of fertilizers, allowing for optimal utilization of fertilize thereby reducing cost of cultivation, (c) The amount of infection or infestation by numerous diseases and insect pests is fairly low during the *rabi* season due to the low temperature and humidity, leading to increased yields, (d) Longer daylight (7-9 hrs) enables crops to grow for longer periods of time hence, increasing production. The purpose of this study was to estimate genetic variability and unravel the association of different traits as well as to identify suitable plant type to develop selection criteria for the traits related to crop yield.

MATERIALS AND METHODS

Forty one advanced breeding lines (Table 1) of desi chickpea obtained from, JNKVV, Jabalpur and ICRI-

SAT, Patencheru including two checks (JG 24 and JG 36) were evaluated at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (MP), during the *rabi* season of 2021-2022. The experiment was conducted in Randomized Complete Block Design and standard agronomic practices and recommended fertilizer doses were adopted. Each genotype was raised in four rows of 4.0 meter length with spacing of 30.0 × 8.0 cm between and within the rows respectively. Observations were recorded on five randomly selected plants from each replication viz., days to 50% flowering, days to maturity, plant height (cm), height of first fruiting node (cm), stem thickness (mm), number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per pod, 100 seed weight, biological yield per plant (g), harvest index (%) and seed yield per plant. Physiological traits were also included in the study, Leaf area index (%), light transmission ratio (%), relative water content, water saturation deficit, chlorophyll content, and canopy temperature depression. Standard biometrical techniques were used for analysis of data.

Table 1. List of tested genotypes.

Sl. No.	Entry	Parentage	Sl. No.	Entry	Parentage
1	ICCV 211101	ICCV 93952 × ICCV 11601	21	H 12-55	HC 1 × H 00-216
2	ICCV 211102	ICCV 96970 × ICCV 11601	22	JG 62	Local Bulk Selection
3	ICCV 211103	ICCV 97105 × ICCV 11601	23	Phule G 12	GW 5/7 × Ceylon 2
4	ICCV 211104	ICCV 97105 × ICCV 11601	24	Chaffa	Selection from Niphad (MS)
5	ICCV 211105	ICCV 97105 × ICCV 11601	25	JG 130	(Phule G × Narsinghpur bold) × JG 74
6	ICCV 211106	ICCV 10 × ICCV 11601	26	Pant Gram 5	PG 035 × HC 5
7	ICCV 211107	ICCV 10 × ICCV 11601	27	Vishal	K 850 × ICCL 80074
8	ICCV 211108	ICCV 92944 × ICCV 96836	28	Vikas	Kanpur 6 × AF 7-10
9	ICCV 211109	(ICCV 96836 × GG 2) × (ICC 4958 TM × ICCV 93954)	29	JG 6	(ICCV 10 × K 850) × (H 208 × RS11)
10	ICCV 211110	(ICCV 96836 × ICCV 97105) × (ICC 4958 TM × GG 2)	30	Phule G 0405	Digvijay × WCG 2000-2
11	ICCV 211111	(ICCV 96836 × ICCV 97105) × (ICC 4958 TM × GG 2)	31	Dahod Yellow	Selection from local germplasm
12	ICCV 211112	ICCV 93954 × ICCV 96836	32	Pant G 114	G 130 × G 1540
13	ICCV 211113	ICCV 93954 × ICCV 05113	33	Pant G 186	ILG 613 × Pant G 114
14	ICCV 211114	ICCV 93952 × ICCV 05113	34	Pratap Chana 1	ICC 10301 × ICC 1 (ICC 11522)
15	ICCV 211115	ICCV 10 × ICCV 05113	35	Radhey	197 × 76
16	ICCV 211116	ICCV 93954 × ICCV 05103	36	Virat	(ICC-7676×ICCC 32 × (ICCC 49 × FLRP-82-IC) × ICCV 3)
17	ICCV 211117	ICCV 93954 × ICCV 05103	37	RVG 204	ICCV 10 × ICCL87322
18	ICCV 211118	ICCV 96970 × ICCV 05103	38	JG 24	(JG 74 × ICC 4958)- 21

Table 1. Continued.

Sl. No.	Entry	Parentage	Sl. No.	Entry	Parentage
19	GCP 101	GCP 2 × ICCV 2	39	JG 36	JG 12 × JG 16
20	RVG 202	(JAKI 9226 × DCP 20) × JG 412	40	JG 12	(N. Bold × PG 5) × PG 5
			41	JG 16	ICCV 4 × ICCV 10

RESULTS AND DISCUSSION

The analysis of variance showed that all fourteen traits mean squares were highly significant. Greater variability in the breeding materials ensures better chances of producing desired recombinants for improvement of the crop.

Genetic parameters: Maximum percentage of phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) (Table 2) was found for seed yield per plant (38.5% and 36.5%) followed by biological yield (33.7% and 32.9%), number of effective pods per plant (33% and 29.1%), total number of pods per plant (33.2% and 29.1%), harvest index (26.4% and 23%), height of first fruiting node (23.5% and 21.9%), stem thickness (22.6% and 21.1%), number of secondary branches (23.1% and 18.5%) and number of primary branches (22.6% and 18.8%). Moderate (PCV and GCV) values were ob-

served for 100 seed weight (17.8% and 17.1%), plant height (17.3% and 16.7%) and number of seeds per pod (11.7% and 11.3%). In the current study, it was discovered that for all of the traits, the phenotypic coefficient of variation (2.0% to 38.5%) was larger in terms of magnitude than the genotypic coefficient of variation (1.4% to 36.5%). This shows that the apparent variation is not only caused by genotypes, but also by the influence of the environment. However, in the current study, the difference between PCV (%) and GCV (%) is very small, indicating that the influence of unrelated factors is minimal, and therefore, selection for such traits based solely on phenotype could also be fruitful. Mohammed *et al.* (2019) had low GCV% and PCV% for days to maturity, while the high for grain yield, Katkani *et al.* (2022) observed high GCV% and PCV% for total number of pods per plant, number of effective pods per plant, biological yield per plant and 100 seed weight.

Table 2. Parameters of genetic variability for yield and its component traits. Where, DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height (cm), HFFN: Height of first fruiting node (cm), ST: Stem thickness (mm), PB: Number of primary branches per plant, SB: Number of secondary branches per plant, TNPPP: Total number of pods per plant, NEPP: Number of effective pods per plant, NSPP: Number of seeds per pod, 100 SW: 100 Seed weight, BY: Biological yield per plant (g), HI: Harvest index (%), SYPP: Seed yield per plant (g), GCV: Genotypic coefficient of variability, PCV: Phenotypic coefficient of variability, h^2 (bs): Broad sense heritability.

Sl. No.	Traits	Range		Grand mean	Coefficient of variation		h^2 (bs) %	Genetic advance as % of mean
		Minimum	Maximum		GCV %	PCV %		
1	DTF	67	74.3	70.3	3.5	3.9	77.8	6.3
2	DTM	108	116	113.5	1.4	1.96	51.2	2.1
3	PH	42.3	74.9	57.8	16.7	17.3	93.1	33.2
4	HFFN	17.3	33.2	25.01	21.9	23.5	86.2	41.8
5	ST	2.1	4.1	2.9	21.1	22.6	87.2	40.7
6	PB	2.9	6.3	4.0	18.8	22.03	72.7	33.0
7	SB	7.3	17.3	11.3	18.5	23.1	64.4	30.6
8	TNPPP	38.3	110.3	65.9	29.1	33.2	76.5	52.4
9	NEPP	34.4	99.3	60.1	29.1	32.96	78.2	53.1
10	NSPP	1.04	1.9	1.2	11.3	11.7	92.5	22.4
11	100 SW	16.3	31.5	24.1	17.1	17.8	91.5	33.6
12	BY	18.8	80.4	38.5	32.9	33.7	95.1	66.1
13	HI %	28.0	76.7	44.8	23.0	26.4	75.9	41.3
14	SYPP	9.6	37.7	17.03	36.5	38.5	89.9	71.3

Heritability is a reliable indicator of how traits are passed down from parents to offspring. High heritability (above 60%) (Table 2) was examined for biological yield per plant (95.1%), plant height (93.1%), number of seeds per pod (92.5%), 100 seed weight (91.5%), seed yield per plant (89.9%), stem thickness (87.2%), height of first fruiting node (86.2%), number of effective pods per plant (78.2%), total number of pods per plant (76.5%), harvest index (75.9%) and primary branches per plant (72.7%). High heritability helps plant breeder in effective selection for a particular trait. Although the presence of high heritability values suggests that phenotypic performance based selection is effective, but does not determine the amount of genetic progress for selection of best individuals. It is possible by using the estimates of genetic advance. High genetic advance as percentage of mean was examined for biological yield per plant (66.1%), plant height (33.2%), number of seed per pod (22.4%), 100 seed weight (33.6%), seed yield per plant (71.3%), stem thickness (40.7%), height of first fruiting node (41.8%), number of effective pods per plant (53.1%), total number of pods per plant (52.4%), harvest index (41.3%) and primary branches per plant (33.0%). The results of heritability and genetic advance is in accordance to earlier findings of Hussain *et al.* (2017) observed high heritability coupled with high genetic advance for biological yield per plant, harvest index, number of effective pods per plant, 100 seed weight and total number of pods per plant, Tschaye *et al.* (2020) examined high heritability and genetic advance for number of pods per plant, grain yield and number of secondary branches per plant and Katkani *et al.* (2022) observed high heritability coupled with high genetic advance for 100 seed weight.

Association analysis: Correlations among traits are of great interest because the changes brought by selection for one trait may bring simultaneous changes in other correlated trait, and correlation studies provide a clear picture of the extent of association between a pair of traits, which is typically due to linkage and pleiotropy. Significant positive correlation of seed yield per plant was found with number of effective pods per plant (0.544), biological yield per plant (0.744), total number of pods per plant (0.523), number of primary branches per plant (0.329), number of secondary branches per plant (0.514) and harvest

index (0.467). Accordingly, In order to increase yield, selection based on these features will be effective. Days to 50% flowering and 100 seed weight exhibited negative association with the trait seed yield per plant. This indicates that increasing the number of days to 50% flowering will reduce seed yield per plant as well as large seeded genotypes will yield less and vice versa. As a result, genotype showing least days for 50% flowering and are small seeded should be selected for obtaining high yield. Earlier researchers, Babbar *et al.* (2015), Kuldeep *et al.* (2014) reported significant positive association of grain yield per plant with total number of pod and number of effective pod. Hence selection of these traits would be effective. Total number of pods per plant showed positive and significant correlation with number of effective pods per plant (0.983). Number of secondary branches per plant exhibited positive and significant association with biological yield per plant (0.390), seed yield per plant (0.514), harvest index (0.184), total number of pods per plant (0.438), number of effective pods per plant (0.445) Additionally, these traits were strongly positively correlated with seed yield. Therefore, while developing the selection process to increase seed production, these traits should be given the weightage.

Correlation coefficient was estimated for seed yield and physiological traits. Seed yield per plant had significant positive correlation with leaf area index (0.497), light transmission ratio (0.573), relative water content (0.425), chlorophyll content (0.456) and canopy temperature depression (0.256). Correlation between number of effective pod per plant and chlorophyll content (0.304) was positive and significant. Leaf area index and light transmission ration were positively correlated with each other but negatively correlated with water saturation deficit. Water saturation deficit exhibited negative and significant correlation with chlorophyll content (-0.444) and seed yield per plant (-0.425). The water saturation defect and relative water content of plant can reflect the degree of water deficiency and also the degree of drought. Less water saturation defect or high relative water content represents the higher ability to resist drought. In the present investigation water saturation defect associates negatively with seed yield and relative water content has positive association with seed yield. These findings indicate that genotypes will

have more seed yield if selection pressure for low water saturation defect or high relative water content is applied. Present research also reveals that cooler canopy (or positive canopy temperature depression) was associated with increase in grain yield. According to Kumar *et al.* (2017) canopy temperature depression and canopy greenness associated with variation in seed yield of soybean. Chlorophyll content revealed positive and significant correlation with traits such as effective pods per plant (0.304), harvest index (0.247) and seed yield per plant (0.456). Since chlorophyll plays essential functions in photosynthesis, it is directly related to production of seed yield of crop. Hence genotypes with large canopy temperature depression and high chlorophyll content are advantageous for high yield in water deficit condition.

Using path analysis, an effort has been made to comprehend the impact of yield attributing traits on seed yield per plant. The path coefficient analysis at genotypic level revealed that days to maturity (0.1795), height of first fruiting node (0.1455), number of secondary branches per plant (0.2141), number of effective pods per plant (2.4401), harvest index (0.4526) and biological yield per plant (0.6702) showed high positive direct effect and days to 50% flowering and 100 seed weight had high negative direct effect on seed yield. The residual effect of the genotypes on seed yield per plant was 0.1750, which suggested that the current study needs to incorporate a few additional traits. Correlation analysis also shows negative association of days to 50% flowering and 100 seed weight with seed yield. It was noted that these two traits had positive association with one another, suggesting that earliness in 50% flowering and large seeds size are key traits for developing the chickpea plant ideotype. The outcome are consistent with the conclusions of Dhuria and Babbar (2015) for number of effective pods per plant, harvest index and biological yield per plant, Paneliya *et al.* (2017) for harvest index and biological yield per plant, Jain *et al.* (2022) for biological yield, harvest index. On the bases of correlation and path studies, early flowering, high biological yield and harvest index, more number of secondary branches with effective pods having optimum seed size would be appropriate for ideal plant type.

D² analysis: When it comes to selection, traits that contributed the most towards genetic divergence should be prioritized. Using multivariate analysis (D²), the divergence for a group of traits was evaluated. The highest percent contribution of selected traits to total divergence was found for biological yield (32.44%), plant height (23.53%) and 100 seed weight (16.34%) (Table 3). These traits expressed majority of the genetic divergence. On the bases of genetic divergence 41 desi chickpea genotypes were grouped into four clusters. Cluster I is polygenotypic with 38 genotypes, this implied that there isn't much

Table 3. Contribution of various traits towards clustering in chickpea genotypes.

Sl. No.	Traits	Times ranked 1 st	Contribution towards divergence (%)
1	DTF	2	0.24
2	DTM	3	0.37
3	PH	193	23.54
4	HFFN	2	0.24
5	ST	15	1.83
6	PB	18	2.2
7	SB	1	0.12
8	TNPPP	40	4.88
9	NEPP	1	0.12
10	NSPP	85	10.37
11	100SW	134	16.34
12	BY	266	32.44
13	HI %	42	5.12
14	SYPP	18	2.2

divergence amongst them and have been previously subjected to similar breeding procedures of selections. The genotypes grouped in cluster I revealed a general genetic resemblance between them, whereas, the other three clusters namely cluster II (Pant Gram 5), cluster III (JG 12) and cluster IV (ICCV211108) were monogenotypic. The inter cluster distance was highest between cluster III and cluster IV (D² = 330.24) followed by cluster II and cluster IV (D² =

Table 4. Average intra (diagonal) and inter-cluster distance (D²) values.

	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	53.80	102.08	154.36	162.25
Cluster II		0.00	56.64	178.67
Cluster III			0.00	330.24
Cluster IV				0.00

Table 5. Cluster mean for yield and its component traits of chickpea genotypes: Tocher's method.

	DTF	DTM	PH	HFFN	ST	PB	SB	TNPPP	NEPP	NSPP	100 SW	BY	HI %	SYPP
Cluster I	70	113	57.9	25.1	2.97	3.96	11.22	66.3	60.3	1.21	24.55	37.0	45.0	16.46
Cluster II	68	108	51.5	20.00	2.43	4.30	14.20	65.8	62.4	1.35	16.48	62.2	39.3	24.48
Cluster III	67	116	50.1	20.8	2.23	6.30	14.07	78.1	74.4	1.11	18.15	80.4	46.9	37.73
Cluster IV	73	114	67.8	31.1	3.32	3.00	8.22	38.8	35.4	1.94	21.48	29.1	37.0	10.73

178.67), cluster I and cluster IV ($D^2 = 162.5$), cluster I and cluster III ($D^2 = 154.36$), cluster I and cluster II ($D^2 = 102.08$) and lowest inter cluster distance had between cluster II and cluster III ($D^2 = 56.64$) (Table 4). The D^2 values of various genotypes and the clustering arrangement showed that material is moderately diverse. Research finding of Babbar *et al.* (2015) also depicted comparatively high intra cluster distance than inter cluster distance depicting presence of some kind of homology between nearly placed clusters and heterology among distantly placed clusters.

Analysis of cluster mean (Table 5) revealed that days to maturity recorded lowest value (108 days) in cluster II but contains highest mean value for number of secondary branches per plant (14.2). Days to 50% flowering (67 days) and plant height (50.1 cm) were lowest in cluster III, whereas, it contains highest mean value of number of primary of branches per plant (6.3), total number of pods per plant (78.1), number of effective pods per plant (74.43), biological yield

(80.4), harvest index (46.9%) and seed yield per plant (37.73). Number of seeds per pod (1.94), stem thickness (3.32 mm) and height of first fruiting node (31.1 cm) recorded highest mean value in cluster IV. Cluster I recorded highest mean value for 100 seed weight (24.55 g). Cluster II and cluster III represents that genotype in this cluster is related to earliness. Days to maturity were strongly and positively associated with days to 50% flowering, according to correlation and path analysis. Short-duration varieties are useful in crop rotation and for demonstrating pest tolerance by escaping or avoiding attack during the reproductive phase of the plant since they require fewer days to mature. Researchers supporting the present findings were Dhuria and Babbar (2016), Tiwari and Babbar (2017), Shivwanshi and Babbar (2019), Rafiq *et al.* (2020) and Tengse *et al.* (2022). Elite genotypes can be selected based on these traits and used as donor parents in future hybridization programs.

Table 6. Eigen value and percentage variability of seed yield and yield attributing traits of chickpea.

Traits	Principal component (PC)	Eigen value	Variability (%)	Cumulative variability (%)
DTF	PC 1	5.392	38.517	38.517
DTM	PC 2	3.088	22.056	60.573
PH	PC 3	1.302	9.303	69.876
HFFN	PC 4	1.187	8.480	78.357
ST	PC 5	0.953	6.806	85.162
PB	PC 6	0.711	5.077	90.239
SB	PC 7	0.489	3.491	93.730
TNPPP	PC 8	0.316	2.259	95.989
NEPP	PC 9	0.227	1.623	97.612
NSPP	PC 10	0.160	1.143	98.755
100 SW	PC 11	0.113	0.810	99.565
BY	PC 12	0.046	0.330	99.895
HI %	PC 13	0.009	0.063	99.958
SYPP	PC 14	0.006	0.042	100.000

In an attempt to evaluate and simplify the inter-relationship between a large set of variable without losing any important information of the original set of data. Principal Component Analysis (PCA) is found to be more appropriate for genetic improvement of desirable traits. Results obtained by rotated component matrix (Table 6) revealed that PC1 had highest variation (38.5%) and loaded with phenological and yield related traits such as days to 50% flowering (0.80), plant height (0.827), stem thickness (0.841),

Table 7. Interpretation of rotated component matrix for the traits having value >0.5 in each PCs.

PC1	PC2	PC3	PC4
DTF (0.800)	TNPPP (0.735)	DTM (0.689)	HI% (0.769)
ST (0.841)	NEPP (0.718)		
PH (0.827)	SYPP (0.736)		
HFFN (0.674)	BY (0.501)		
100 SW (0.595)			

Table 8. Positive PC score (>1.0) of genotypes in each PCs.

PC1	PC2	PC3	PC4
ICCV 211101 (3.491)	ICCV 211103 (1.727)	ICCV 211106 (1.713)	ICCV 211103 (1.578)
ICCV 211102 (2.348)	ICCV 211105 (3.178)	ICCV 211108 (1.294)	ICCV 211116 (1.030)
ICCV 211103 (1.464)	ICCV 211109 (3.143)	Chaffa (1.142)	Vishal (1.068)
ICCV 211104 (2.368)	ICCV 211111 (1.279)	Vishal (1.109)	JG 24 (2.987)
ICCV 211106 (1.262)	ICCV 211116 (3.745)	Virat (1.612)	JG 36 (1.856)
ICCV 211107 (3.073)	ICCV 211117 (4.232)	JG 12 (2.886)	
ICCV 211108 (3.415)	JG 62 (1.830)	JG 16 (1.748)	
ICCV 211110 (2.969)	Virat (1.382)		
ICCV 211111 (2.531)	RVG 204 (1.104)		
ICCV 211112 (3.203)	JG 24 (1.008)		
ICCV 211113 (2.586)	JG 12 (2.404)		
ICCV 211115 (2.661)			
ICCV 211118 (3.333)			
RVG 204 (1.406)			
JG 24 (2.721)			
JG 16 (2.993)			

stem height at first fruiting node (0.874) and 100 seed weight (0.595) contributing in positive direction. Yield contributing traits such as total number of pods per plant (0.735), number of effective pods per plant (0.718), biological yield per plant (0.501) and seed yield per plant (0.736) contributed 22.1% of total variability in second principal component (PC2). PC3 is loaded with phenological traits i.e. days to maturity (0.689) and contribute 9.3% of total variability and PC4 had harvest index (0.769) having 8.4% of total variability. The first and second principal components were more important because they contribute more than 50% of the total variation. Biswal and Babbar (2022) reported that first PC contributes more towards variation loaded with traits such as days to pod initiation followed by plant height, number of primary branches per plant and seed yield per plant.

On the bases of PC scores maximum positive score (Tables 7–8) was found in PC1 for ICCV211101, ICCV211108, ICCV211118, JG 16, JG 24, ICCV211110, ICCV211113, ICCV211111, ICCV211107, ICCV211112, ICCV211102 and ICCV211104, these genotypes exhibits maximum variability for phenological and yield traits namely days to 50% flowering, stem thickness, plant height, stem height at first fruiting node and hundred seed weight. PC2 reported that genotypes viz., ICCV211117, ICCV211116, ICCV211105, ICCV211109 and JG 12, were related to yield re-

lated traits such as, total number of pods per plant, number of effective pods per plant, biological yield per plant and seed yield per plant. PC3 is related to days to maturity and include genotypes JG 12, JG 16 and Virat. However, PC 4 includes JG 24 and JG 36 and was related to harvest index. Dhanushasree and Hemavathy (2022) and also documented that first principal component is responsible for maximum variation in pigeonpea.

CONCLUSION

The existence of genetic variation and the inheritance of desired traits and association between them are key factors in the success of crop breeding programs. In the present study maximum percentage of phenotypic and genotypic coefficient of variability was found for seed yield per plant followed by biological yield, number of effective pods per plant, total number of pods per plant, harvest index, height of first fruiting node, stem thickness, number of secondary branches and number of primary branches, indicating high level of variability in the studied trait. High heritability along with high genetic advance as % of mean was examined for biological yield per plant, plant height, number of seed per pod, 100 seed weight, seed yield per plant, stem thickness, height of first fruiting node, number of effective pods per plant, total number of pods per plant, harvest index and primary branches per plant indicating predominance of additive gene

action and are less influenced by environment in their expression, therefore direct selection of such traits may be fruitful.

Results of association analysis concluded that simple selection of traits having high positive direct effect as well as positive correlation towards seed yield per plant viz., number of effective pods per plant, biological yield per plant, harvest index and number of secondary branches per plant, had the true relation between them and direct selection based on these traits will be rewarding for the yield improvement. Hence, according to correlation and path coefficient analyses the plants producing more number of secondary branches with large number of effective pods, greater biological yield and harvest index must be considered when selecting for any improvement in seed yield.

Finding of cluster analysis imply that intercrossing genotypes from distantly placed clusters having good mean performance may aid in development of high yielding genotypes with better seed yield. The genotype JG 12 from cluster III, Pant Gram 5 from cluster II and ICCV 211108 from cluster IV can be utilized as parents in crossing program to develop genetically segregating population, which helps in establishing new inbred lines.

Four components in principal component analysis had Eigen values greater than 1 having cumulative variation of 78.36%. It suggests that the traits within these four components had a significant impact on the genotypes' morphology. PC1 dominates with yield contributing traits such as stem thickness, plant height, stem height at first fruiting node and hundred seed weight, it allows for simultaneous selection of yield attributing traits for the production of multiple high yielding genotypes. PC1 and PC3 are loaded with high positive phenological traits such as days to 50% flowering and days to maturity respectively. Genotypes ICCV211101, ICCV211108, ICCV211118, JG 16, JG 24, ICCV211110, ICCV211113, ICCV211111, ICCV211107, ICCV211112, ICCV211102 and ICCV211104 exhibits high PC scores in PC1. Direct selection of these genotypes will lead to the development of late maturing varieties having high yield attributing attributes. However, low PC score

of phenological traits will lead to development of early maturing variety. PC2 and PC4 are mostly related to yield components. The genotypes exhibiting maximum positive PC scores and common in PC1, PC2, PC3 and PC4 were ICCV211103, ICCV211106, ICCV211108, ICCV211111, ICCV211116, RVG 204, JG 24, JG 12, JG 16, Virat and Vishal for the traits viz., plant height, total number of pods per plant, number of effective pods per plant, days to 50% flowering, days to maturity, stem thickness, biological yield per plant, harvest index, seed yield per plant, 100 seed weight and stem height at first fruiting node.

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