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UNRAVELING GENETIC DIVERSITY IN CHICKPEA FOR YIELD-ORIENTED BREEDING

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ABSTRACT

The present study was conducted during the Rabi season of 2024–25 at the S.I.F. Farm, C.S.A.U.A.&T., Kanpur (U.P.), with the aim of evaluating genetic diversity among 32 chickpea (*Cicer arietinum* L.) germplasm accessions, along with five check varieties: BG 3043, WR 315, JAKI 9218, PHULE G 405, and JG 74. The experiment was laid out in a Randomized Block Design (RBD). Results revealed that seed yield per plant showed a positive and significant correlation with the number of primary branches, number of pods per plant, number of seeds per pod, and 100-seed weight. Path coefficient analysis indicated that days to 50% podding, number of primary and secondary branches per plant, number of pods per plant, plant height, and seed yield per plant exerted a positive and direct effect on seed yield, suggesting that direct selection for these traits could be beneficial in yield enhancement programs. Cluster analysis grouped the genotypes into four distinct clusters. Cluster IV contained the highest number of genotypes (18), followed by Cluster II (7), Cluster I (5), and Cluster III (2). The maximum inter-cluster distance was observed between Clusters III and IV (5.558), while the highest intra-cluster distance was recorded within Cluster IV (2.786), indicating a high degree of genetic diversity among the accessions.

Key words : *Cicer arietinum* L., Correlation, Path Coefficient analysis, Cluster analysis.

Introduction

Chickpea (*Cicer arietinum* L.), commonly known as Bengal gram, belongs to the genus *Cicer* within the family Leguminaceae and has a chromosome number of $2n = 16$. It is one of the most important rabi pulse crops grown in India. As per FAOSTAT (2024), chickpea is cultivated over approximately 107.40 lakh hectares in India, producing about 135.44 lakh tonnes with an average productivity of 1261 kg/ha. Nutritionally, chickpea is a rich and affordable source of protein (21.2%), fat (11.4%), carbohydrates (57–60%), ash (4.8%), and moisture content (4.9–15.59%) (Huisman and Vander Poel, 1994). The primary goal of any well-structured breeding program is to develop new, high-performing varieties that surpass the existing ones. Chickpea, a vital leguminous crop in India, contributes significantly to nutritional security and soil fertility due to its high protein content and nitrogen-fixing ability. However, despite its economic and

ecological value, chickpea productivity remains relatively low when compared to major cereal crops. Many researchers, including Ramanujam (1975) have suggested that the underutilization of existing genetic variability is one of the major reasons for the limited yield gains in legumes, including chickpea. Upadhyaya *et al.* (2006) noted that less than one percent of chickpea germplasm has been utilized in breeding, reflecting a narrow genetic base in cultivar development. However, since yield is a complex trait influenced by multiple environmental factors, selecting solely based on yield may not be effective. A better approach involves understanding the extent and nature of correlations among yield-contributing traits. While correlation and path coefficient analyses help identify both the direct and indirect effects of different traits on yield, principal component analysis (PCA) and cluster analysis provide insights into the genetic diversity among germplasm lines.

To develop superior transgressive segregants with improved yield and stress resistance, it is essential to use genetically diverse parents. This can be achieved by incorporating a broad range of chickpea germplasm—including landraces, exotic lines, and wild relatives—into recombination breeding programs rather than relying on a narrow genetic base. Therefore, the present study was designed to assess genetic diversity and identify promising traits among chickpea germplasm for their potential use in future crop improvement programs.

Materials and Methods

The experimental material consisted of 32 chickpea germplasm accessions obtained from ICRISAT, Hyderabad, along with five check varieties: BG 3043, WR 315, JAKI 9218, PHULE G 405 and JG 74. The experiment was conducted during the Rabi season of 2024–25 at the Student Instructional Farm (S.I.F.), CSAUA&T, Kanpur (U.P.). The trial was laid out in a Randomized Block Design (RBD) with appropriate replications. All recommended agronomic practices were followed throughout the crop growth period. Data were recorded from five randomly selected plants in each plot to ensure unbiased results. Observations were made on fourteen key traits, including days to 50% flowering, fruit pod initiation, 50% podding, maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant and 100-seed weight.

Results and Discussion

Significant variability was observed across all these traits, consistent with previous reports by Atta *et al.* (2008), Hakim *et al.* (2006) and Khan *et al.* (2011). Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated to assess the extent of variability. Traits such as number of pods per plant and seed yield per plant exhibited high PCV and GCV, reflecting strong genetic control and less environmental influence. The narrow difference between PCV and GCV for days to 50% flowering and maturity indicated that these traits were less influenced by environmental factors, similar to findings by Chavan *et al.* (1994), Vijaylaxmi *et al.* (2000) and Jeena and Arora (2001). High genetic variability in these traits confirms the potential for their effective utilization in selection programs.

Genetic advance as a percentage of mean was also estimated to understand the efficiency of selection. High heritability combined with high genetic advance was observed for seed yield and 100-seed weight, suggesting that these traits are governed by additive genes and can

Table 1 : Analysis of variance for 11 characters of Chickpea genotypes.

Source of variation	DF	50 % flower Initiation [days]	Fruit pod Initiation [days]	Days to 50 % Podding	Days to maturity	Plant height [cm]	No. of primary Branches	No. of secondary Branches	No. of pods/Plant	No. of Seeds/Pod	100 Seed weight [g]	Seed yield/plant [g]
Replication	2	0.50	3.01	0.04	11.45	0.13	1.45	7.82	67.70	0.032	0.34	0.76
Treatment	31	13.79**	19.74**	14.61**	97.57**	62.90**	16.39**	56.00**	732.22**	0.181**	31.80**	27.23**
Error	62	1.38	1.03	0.87	1.07	1.64	0.47	1.10	3.19	0.064	0.90	0.88
Total	95	5.41	7.18	5.34	32.78	21.60	5.68	19.16	242.44	0.101	10.97	9.48

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

Table 2 : Phenotypic correlation co-efficient among the seed yield and its contributing traits in thirty-two genotypes of chickpea.

Traits	50 % flower initiation [days]	Fruit/pod initiation [days]	Days to 50 % podding	Maturity [days]	Plant height [cm]	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	100 seeds weight [g]	Seed yield/ plant [g]
50% flower initiation [days]	1.000	0.831**	0.618**	0.187	-0.260*	0.257*	0.179	0.020	-0.010	-0.046	-0.280**
Fruit pod initiation [days]		1.000	0.751**	0.153	-0.308**	0.328**	0.231*	0.104	0.105	-0.012	-0.240*
Days to 50% podding			1.000	0.152	-0.345**	0.231*	0.217*	0.092	0.037	0.206*	-0.119
Maturity [days]				1.000	0.220*	0.110	0.305**	0.201*	0.092	0.137	-0.251*
Plant height [cm]					1.000	0.095	0.062	-0.319**	0.092	-0.044	-0.061
No. of primary branches						1.000	0.409**	0.190	0.170	0.349**	0.188
No. of secondary branches							1.000	0.338**	0.006	0.336**	0.245*
No. of pods/plant								1.000	-0.070	0.341**	0.558**
No. of seeds/pod									1.000	0.138	-0.206*
100 seeds weight [g]										1.000	0.294**
Seed yield/plant [g]											1.000

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

Table 3 : Genotypic correlation co-efficient among the seed yield and its contributing traits in thirty-two genotypes of Chickpea.

Traits	50 % flower initiation [days]	Fruit pod initiation [days]	Days to 50 % podding	Maturity [days]	Plant height [cm]	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	100 seeds weight [g]	Seed yield/ plant [g]
50% flower initiation [days]	1.000	0.996**	0.774**	0.198	-0.297**	0.312**	0.234*	0.006	0.032	-0.064	-0.353**
Fruit pod initiation [days]		1.000	0.856**	0.158	-0.344**	0.378**	0.251*	0.112	0.036	-0.008	-0.235*
Days to 50% podding			1.000	0.163	-0.397**	0.290**	0.233*	0.103	0.067	0.260*	-0.142
Maturity [days]				1.000	0.235*	0.126	0.318**	0.205*	0.255*	0.138	-0.272**
Plant height [cm]					1.000	0.110	0.067	-0.342**	0.139	-0.052	-0.085
No. of primary branches						1.000	0.450**	0.197	0.241*	0.370**	0.210*
No. of secondary branches							1.000	0.357**	0.030	0.371**	0.267**
No. of pods/plant								1.000	-0.101	0.356**	0.590**
No. of seeds/pod									1.000	0.227*	-0.267**
100 seeds weight [g]										1.000	0.339**
Seed yield/plant [g]											1.000

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

Table 4 : Direct and indirect effects of 10 characters on seed yield of chickpea.

Traits	50 % flower initiation [days]	Fruitpod initiation [days]	Days to 50 % podding	Maturity [days]	Plant height [cm]	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	100 seeds weight [g]	Seed yield/ plant [g]
50% flower initiation [days]	-0.1312	-0.4438	0.2557	-0.0845	-0.0492	0.0670	0.0329	0.0041	-0.0054	0.0009	-0.353**
Fruit pod initiation [days]	-0.1307	-0.4455	0.2830	-0.0676	-0.0569	0.0810	0.0353	0.0725	-0.0062	0.0001	-0.235*
Days to 50% podding	-0.1015	-0.3814	0.3305	-0.0698	-0.0659	0.0622	0.0327	0.0665	-0.0115	-0.0037	-0.142
Maturity [days]	-0.0260	-0.0705	0.0540	-0.4272	0.0389	0.0270	0.0447	0.1324	-0.0434	-0.0020	-0.272**
Plant height [cm]	0.0390	0.1530	-0.1313	-0.1004	0.1657	0.0235	0.0094	-0.2210	-0.0236	0.0007	-0.085
No. of primary branches	-0.0410	-0.1682	0.0959	-0.0537	0.0182	0.2144	0.0634	0.1276	-0.0409	-0.0053	0.210*
No. of secondary branches	-0.0307	-0.1117	0.0769	-0.1356	0.0111	0.0965	0.1408	0.2307	-0.0052	-0.0053	0.267**
No. of pods/plant	-0.0008	-0.0499	0.0340	-0.0875	-0.0567	0.0423	0.0503	0.6464	0.0172	-0.0051	0.590**
No. of seeds/pod	-0.0042	-0.0162	0.0222	-0.1089	0.0230	0.0516	0.0043	-0.0652	-0.1701	-0.0032	-0.267**
100 seeds weight [g]	0.0084	0.0038	0.0858	-0.0591	-0.0087	0.0794	0.0523	0.2304	-0.0387	-0.0142	0.339**

Residual effects- 0.288

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

Table 5 : Grouping of Thirty-two chickpea genotypes into four clusters on the basis of D² analysis.

Clusters	No of genotypes	Genotypes
I	5	IC 440, IC 19114, WR 315, JAKI19218 and JG 74.
II	7	IC 15435, IC 11121, IC 5845, IC 14831, IC 8350, IC 138 and IC 4495.
III	2	IC 4491 and IC 6294
IV	18	IC 227, IC 15510, IC 107, IC 2720 IC 16795, IC 26911, IC 10341, IC 14815, IC 14778, IC 8195, IC 6816, IC 10466, IC 867, IC 19165, IC 1431, IC 19164, BG 3043, PHULE G 405.

Table 6 : Cluster mean among four clusters for eleven characters for thirty-two genotypes of chickpea.

Clusters		50 % flower initiation [days]	Fruit pod initiation [days]	Days to 50 % podding	Maturity [days]	Plant height [cm]	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	100 seeds weight [g]	Seed yield/ plant [g]
I	Mean	73.93	79.33	87.07	123.13	33.27	6.20	18.33	58.47	2.00	19.16	19.25
	± SE	1.32	1.49	1.26	4.48	3.22	1.89	3.92	7.41	0.00	4.83	2.44
II	Mean	74.57	79.67	87.43	111.76	34.05	4.95	11.57	32.00	2.00	15.37	17.29
	± SE	1.46	1.19	1.27	3.92	4.75	0.59	3.35	5.13	0.00	1.04	1.15
III	Mean	72.50	77.83	85.17	106.67	31.33	4.67	14.50	57.17	1.50	13.86	27.34
	± SE	1.65	1.65	3.06	1.89	0.47	1.41	1.18	1.18	0.71	0.52	1.75
IV	Mean	77.69	83.80	89.87	115.83	30.04	6.76	16.61	52.61	1.94	16.44	19.13
	± SE	0.73	1.04	1.74	4.09	4.68	2.76	4.03	16.00	0.24	3.17	2.28

be improved through direct selection. Conversely, traits such as plant height and number of primary branches exhibited high heritability but low genetic advance, implying a greater role of non-additive gene action. Similar results were reported by Sharma and Maloo (1988), Singh and Rao (1991) and Patil (1996).

Correlation analysis provided insights into the interrelationships among various traits. Seed yield showed significant positive correlation with number of primary branches, number of pods per plant, number of seeds per pod, and 100-seed weight. These results are consistent with earlier studies by Ali *et al.* (2011), Arora and Jeena (1999), Berger and Turner (2000) and Narayana and Reddy (2002), indicating that selection for these component traits can indirectly enhance seed yield. Pods per plant, in particular, emerged as a reliable indicator of yield potential due to its strong association with final yield. Similar conclusions were drawn by Mishra *et al.* (1994), Singh *et al.* (1995), Rao and Kumar (2000), and Pratap *et al.* (2002).

Path coefficient analysis was employed to partition the correlation coefficients into direct and indirect effects, providing a more nuanced understanding of trait contributions to seed yield. The analysis revealed that pods per plant and 100-seed weight had strong positive direct effects on yield, supporting the findings of Reddy and Rao (1988), Rao *et al.* (1994) and Arora and Jeena (1999). Plant height also exhibited a positive direct effect, although to a lesser extent. Interestingly, the number of primary branches showed a negative direct effect on yield despite its positive correlation, suggesting its influence is mediated indirectly through other traits.

To assess the genetic divergence among genotypes, Mahalanobis D² statistics were employed. The genotypes were grouped into four clusters using Tocher's method (Rao, 1952), revealing a considerable degree of diversity. Cluster IV contained the highest number of genotypes (18), followed by Clusters II (7), I (5) and III (2). The maximum inter-cluster distance was observed between Clusters III and IV (5.558), suggesting that crossing between these groups could yield superior heterotic combinations. High intra-cluster distances within Cluster IV also indicate a rich source of variability.

Interestingly, several genotypes from different geographical regions were grouped into the same cluster, while others from the same region were scattered across different clusters. This confirms that geographic origin does not necessarily determine genetic relatedness, a conclusion also drawn by Veerabadhiran and Kennedy (2002), Arora (1992), Jeena and Arora (2002). Traits such

as number of pods per plant and 100-seed weight contributed most to genetic divergence, consistent with earlier findings by Katiyar (1978), Anil Kumar *et al.* (1993), Kumar (1997) and Jeethava *et al.* (2000).

The cluster mean analysis provided valuable information on trait performance within each group. Cluster IV was notable for its high means for seed yield, 100-seed weight, and number of primary branches. Cluster I showed higher values for plant height and days to maturity. The presence of such trait-based variation among clusters offers opportunities for selecting contrasting parents for hybridization. Munshi *et al.* (2005) emphasized the importance of combining cluster means and coefficient of variation to optimize diversity-based selection.

Conclusion

The study concluded that significant genetic variability and divergence exist among chickpea germplasm, offering substantial scope for yield improvement through both direct and indirect selection strategies. It recommended using genetically diverse parents from clusters with high inter-cluster distances for crossing, particularly between Clusters III and IV, to maximize heterosis. Additionally, the study highlighted the need to incorporate exotic germplasm and broaden the genetic base, thereby addressing the limitations posed by narrow genetic variability in current cultivars.

In summary, the findings from this research provide a solid foundation for chickpea improvement programs. They underscore the necessity of exploiting existing genetic variation, carefully selecting parental lines based on both performance and divergence and applying advanced genetic tools such as path coefficient and D² analysis for efficient selection. With traits like pods per plant, 100-seed weight and seed yield showing strong genetic control and high heritability, these parameters can serve as reliable selection indices in future breeding programs aimed at developing high-yielding and resilient chickpea varieties suitable for subtropical climates of India.

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