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ELUCIDATING GENETIC DIVERSITY IN THE ADVANCED CHICKPEA BREEDING LINES FOR SUSTAINABLE CROP IMPROVEMENT

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ABSTRACT

Genetic diversity constitutes the cornerstone for the success of any efficient crop improvement program. Hence, the current study has been undertaken at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, M.P. during the *Rabi* season of 2021-22. Utilizing Mahalanobis D^2 statistics, analysis for genetic diversity classified forty advanced chickpea breeding lines into nine clusters with Cluster I having the highest 16 genotypes, followed by Cluster II (6 genotypes), Cluster III (4 genotypes) and Cluster IV (4 genotypes). The study revealed varying intra-cluster distances, with the maximum observed in Cluster VII (D^2 = 107.20) followed by Cluster IV (D^2 = 102.23) and Cluster III (D^2=99.61). However, the highest inter cluster distance was identified between Cluster VIII and Cluster II (D^2=517.65) succeeded by Cluster VIII and Cluster V (D^2 = 503.29), Cluster VIII and Cluster IX (D^2=452.07). Maximum genetic divergence was contributed by traits including biological yield per plant (23.1%), total number of pods per plant (22.8%) and hundred seed weight (19.8%). Based on inter cluster distances, cluster means and*per se* performance, six superior genotypes, namely JG 2020-1614, PG 205, ICCV 211209 and JG 2020-634958, were identified as potential parents for future chickpea hybridization programs.

Key words : Character, Cluster, Chickpea, Diversity.

Introduction

The genus Cicer encompasses 9 annual and 35 perennial species, with *Cicer arietinum* L. standing out as the most extensively cultivated species on a global scale. Chickpea (*Cicer arietinum* L.) is a significant winter season food legume crop. This diploid pulse crop, characterized by chromosome number of 2n=2x=16, exhibits self-pollination and is classified within the family Leguminoseae and subfamily Papilionoidae. Positioned as the third most important crop following dry bean and field pea, chickpea serves as an economically viable and nutritionally rich source of high-quality protein, predominantly composed of globulin and albumin in comparison to animal protein (Gupta *et al*., 2021; Ningwal *et al*., 2023). Being the oldest and extensively cultivated pulse crop in over 50 countries, chickpea plays a pivotal role in ensuring nutritional security. In India, chickpea cultivation covers an area of 11.20 million hectares, contributing to a production of 13.98 million metric tons and a productivity of 1249 kg/ha. Specifically in Madhya Pradesh, chickpea is cultivated across 2.80 million hectares, yielding 3.61 million metric tonnes, with a productivity of 1291 kg/ha (Annual Report, DPD 2021-22).

The escalating global population, projected to surpass ten billion by 2050 (Godfray, 2010), coupled with the dynamic challenges posed by fluctuating climatic conditions, necessitates innovative approaches for ensuring sustainable food production for future generations. The cultivation of chickpeas, essential for global nutrition, faces formidable constraints due to various biotic and abiotic stresses. In this context, genetic diversity emerges as a crucial cornerstone for the development of resilient crop varieties capable of withstanding diverse

environmental challenges, encompassing pests, diseases, and climatic variations. The integration of diverse genetic materials becomes imperative for plant breeders, serving as a strategic tool to engineer crops with increased adaptability. This not only mitigates the risks associated with crop failure but also augments overall agricultural productivity. Thus, the principal objective of the present study lies in elucidating the gene diversity present in the advanced breeding lines of chickpea, offering a pioneering approach towards sustainable and adaptable crop improvement.

Materials and Methods

An experiment was carried out at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur, M.P. during the *Rabi* season of 2021-22. The experiment comprised 40 advanced breeding lines of chickpea obtained from AICRP chickpea, JNKVV, Jabalpur and ICRISAT, Patencheru, Hyderabad along with three check varieties, namely JG12, JG24 and JG36. The experiment followed a Randomized Complete Block Design (RCBD), with each plot consisting of four rows that were four meters in length. The spacing between rows and plants was maintained at 30cm × 10cm. To ensure the successful growth of the crop the recommended agronomic and plant protection practices were implemented. Observations were recorded for fourteen quantitative traits, including days to 50% flowering (DFF) and days to maturity (DTM), plant height (PH), height of the first fruiting node (HFFN), stem thickness (ST), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), total number of pods per plant (TNPPP), number of effective pods per plant (NEPPP), number of seeds per pod (NSPP), hundred seed weight (HSW), biological yield per plant (BY), harvest index (HI) and seed yield per plant (SYPP) by selecting five competitive random plants from each genotype in each replication. Divergence analysis was executed utilizing Mahalanobis D^2 statistics (1936) and subsequent clustering was performed in accordance with Tocher's method as outlined by Rao (1952).

Results and Discussion

The utilization of genetic diversity is pivotal for selecting parents with significant genetic divergence to be employed in hybridization programs. It quantifies the extent of diversification and establishes the relative contribution of each component character to the overall divergence. Differentiation forces are assessed at two levels: inter-cluster and intra-cluster. This methodology provides reliable estimates of divergence, allowing for the simultaneous evaluation of a considerable number of germplasm lines for genetic diversity.

Composition of clusters

Utilizing Mahalanobis D^2 values, the 40 genotypes were classified into nine clusters (Table 1), revealing significant variation in the advanced breeding lines across all studied traits. Cluster I comprised the largest number of genotypes (16 genotypes), succeeded by Cluster II (6 genotypes), Cluster III (4 genotypes), Cluster IV (4 genotypes), Cluster VII (4 genotypes), Cluster V (2 genotypes), and Cluster VI (2 genotypes), with the remaining clusters characterized by a solitary genotype each. The dominance of sixteen genotypes in Cluster I suggestlimited genetic divergence among them, potentially attributed to a shared genetic background from their common ancestral population. Nevertheless, this genetic

Table 1 : Composition of genotypes into different clusters using Mahanlobis D^2.

Cluster	Number of genotypes	Name of genotypes
I	16	JG 2020-12-16-13, JG 2017-49, ICCV191609, ICCV191616, JG 2016-1411, JG 2020-23, ICCV181109, ICCV 181667, ICCV 211202, ICCV191606, ICCV181602, ICCV 211203, JG 2020-1614, JG 2021-96029, ICCV 191608, ICCV 211208
II	6	RVG-204, ICCV 211210, JG 24, ICCV 211206, ICCV 211205, ICCV 191618
III	4	JG 2020-1614, PG 205, ICCV 211209, JG 2020-634958
IV	4	ICCV 181108-2, ICC181106, JG 2020-15118, JG 2016-36
V	2	ICCV 211204, ICCV 211207
VI	2	ICCV 211201, ICC181612
VII	4	JG 2020-75, JG 2018-51, JG 36, JG 2018-54
VIII	1	JG 2016-14-16-11
IX	1	JG 12

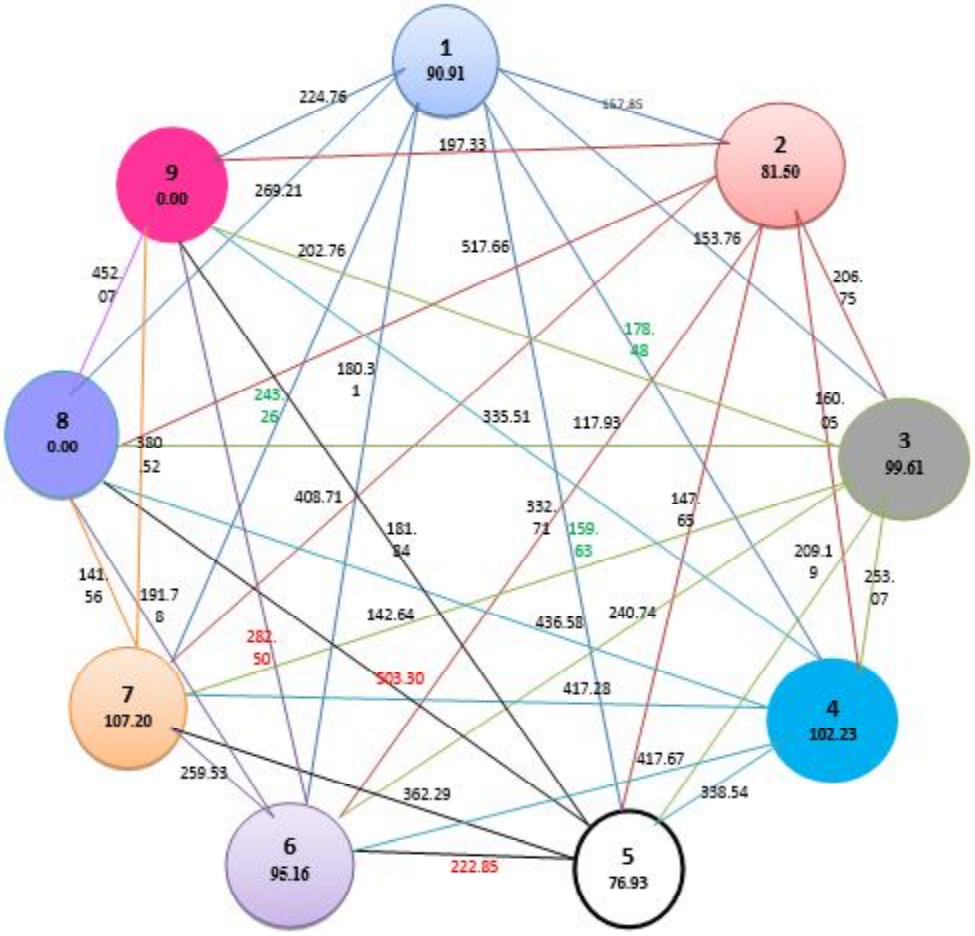

Fig. 1 : Cluster diagram for quantitative traits in the advanced breeding lines of chickpea.

uniformity could also result from unidirectional selection pressures favouring specific traits or linked traits, leading to the convergence of phenotypes into a singular cluster, irrespective of their geographical origin. Similar studies on cluster analysis analogous to the present investigation were undertaken by Pandey *et al.* (2013), Gediya *et al.* (2018), Thakur *et al.* (2018), Aswathi *et al.* (2019), Ponnuru *et al.* (2019), Dar *et al.* (2020), Janghel *et al.* (2020) and Rafiq *et al.* (2020).

Average Intra and Inter Cluster distances

Table 2 offers a comprehensive overview of the computed intra-cluster and inter-cluster distances, encompassing all possible combinations of the nine clusters, with visual representation in Fig. 1. The highest intra-cluster distance was identified in Cluster VII (D^2 =107.20), followed by Cluster IV (D^2 = 102.23) and Cluster III (D^2 = 99.61). Notably, Cluster VIII and Cluster IX exhibited no intra-cluster distance, each comprising only one genotype. The maximum intra-cluster distance values signify the presence of genetic diversity among genotypes grouped within those clusters, suggesting substantial potential for gene exchange. Concerning inter-cluster distance, Cluster VIII and Cluster II demonstrated the highest dissimilarity, with a distance of 517.65, indicating that crossing between these genotypes may yield a significant heterotic response, thereby producing superior recombinants for an effective breeding program. These findings align with observations made by Parhe *et al.* (2014), Naveed *et al.* (2015), Jakhar *et al.* (2016), Aarif *et al.* (2017), Vijaykumar *et al.* (2017), Jayalakshmi *et al.* (2018), Boparai *et al.* (2021) Katkani *et al.* (2022), Thapa *et al.* (2022) and Vikram *et al.* (2023).

Cluster means

To illustrate the clustering pattern among chickpea genotypes, the average performance of the clusters was calculated (Table 3, Fig. 2). Cluster III showed lower performance for stem thickness (2.54mm), whereas exhibited higher recorded values for total pods per plant (81.2) and effective pods per plant (72.2). The genotypes present in the cluster IV displayed superior performance in various attributes including height of first fruiting node (25.3cm), number of primary branches per plant (4.37) and hundred seed weight (33.1g). Cluster V was marked by specific phenological attributes, notably including delayed days to 50 flowering (75), days to maturity (116), tall plant height (70.1cm), increased stem thickness

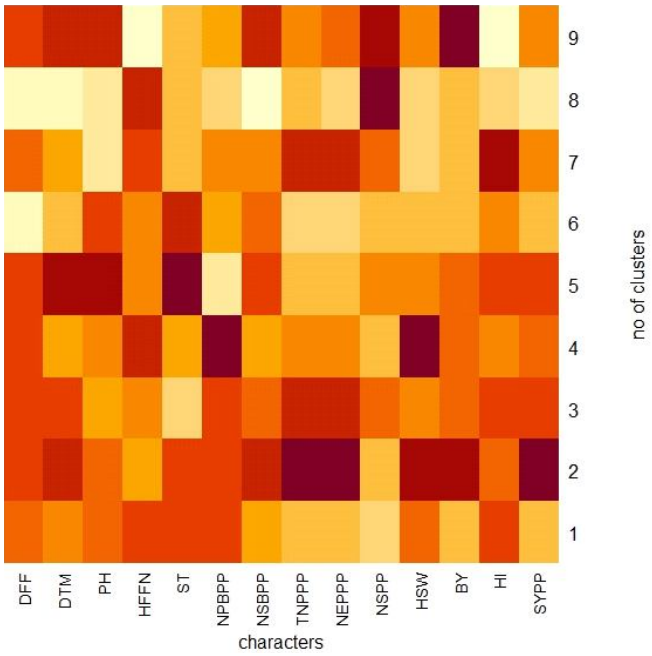

Fig. 2 : Heat map for mean value of quantitative traits in the elite breeding lines of chickpea.

exhibited inferior performance in terms of hundred seed weight (18.9g), but show cased a higher harvest index (58.9%). Cluster VIII manifested early onset of flowering (50) and early maturity (98), accompanied by diminished plant height (56.1cm), reduced number of secondary branches per plant (7.3), fewer effective pods per plant (49.4), increased number of seeds per pod (1.66) and diminished seed yield per plant (15.0g). Cluster IX displayed delayed flowering (74) and maturity (114), along with a lower height of the first fruiting node (15.9cm), an elevated number of secondary branches per plant (14.5), higher biological yield per plant (64.8g) and a reduced harvest index (34.6%).

Characters contribution towards Genetic divergence

Per cent contribution of characters towards divergence was analyzed and was found that biological yield per plant (23.1%) contributed highest for divergence followed by total number of pods per plant (22.8%), hundred seed weight (19.8%), days to 50% flowering (16.5%), days to maturity (12.6%) and number of effective pods per plant (10.8%). Subsequently, other traits such as number of secondary branches per plant (9.6%), height of first fruiting node (9.0%) and harvest index (7.2%) displayed comparatively lower levels of

Table 2 : Average intra- and inter- cluster distances in *desi* chickpea genotypes.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**90.91**	157.85	153.76	178.48	159.63	180.31	243.26	269.21	224.76
II		**81.50**	206.75	160.05	147.65	332.71	408.71	517.66	197.33
III			**99.61**	253.07	209.19	240.74	142.64	242.47	202.76
IV				**102.23**	338.54	417.67	417.28	436.58	335.51
V					**76.93**	222.85	362.29	503.30	181.84
VI						**95.16**	259.53	191.78	282.50
VII							**107.20**	141.56	380.52
VIII								**0.00**	452.07
IX									**0.00**

Table 3 : Cluster mean performance for yield and its component traits.

Cluster	DFF	DTM	PH	HFFN	ST	NPBPP	NSBPP	TNPPP	NEPPP	NSPP	HSW	BY	HI	SYPP
I	70	108	64.6	24.3	3.22	3.97	10.8	59.5	53.7	**1.29**	26.3	36.5	54.1	19.4
II	74	115	64.9	21.6	3.26	4.01	13.9	**88.6**	**82.0**	1.35	31.1	61.4	50.8	**31.2**
III	73	112	62.4	22.5	**2.54**	3.99	12.8	81.2	72.2	1.47	24.1	47.2	53.1	24.7
IV	74	106	62.8	**25.3**	2.84	**4.37**	11.4	66.0	59.4	1.33	**33.1**	47.8	50.2	24.1
V	**75**	**116**	**70.1**	22.1	**3.55**	**3.18**	13.4	59.9	54.8	1.45	25.0	47.2	53.9	25.4
VI	51	104	66.2	22.8	3.37	3.54	12.5	**55.0**	50.0	1.34	22.0	**35.9**	49.8	18.1
VII	70	106	56.4	24.3	2.62	3.66	11.9	78.5	71.7	1.50	**18.9**	36.2	**58.9**	21.4
VIII	**50**	**98**	**56.1**	25.1	2.60	3.36	**7.3**	58.1	**49.4**	**1.66**	19.0	36.9	40.7	**15.0**
IX	74	114	69.1	**15.9**	2.65	3.52	**14.5**	66.9	63.3	1.63	24.9	**64.8**	**34.6**	22.4

(3.55mm) and a diminished number of primary branches per plant (3.18). Cluster VI excelled in early flowering (51) and early maturity (104), but demonstrated lower performance for total number pods per plant (55.0), number of effective pods per plant (50.0), biological yield (35.9g) and seed yield per plant (18.1g). Cluster VII

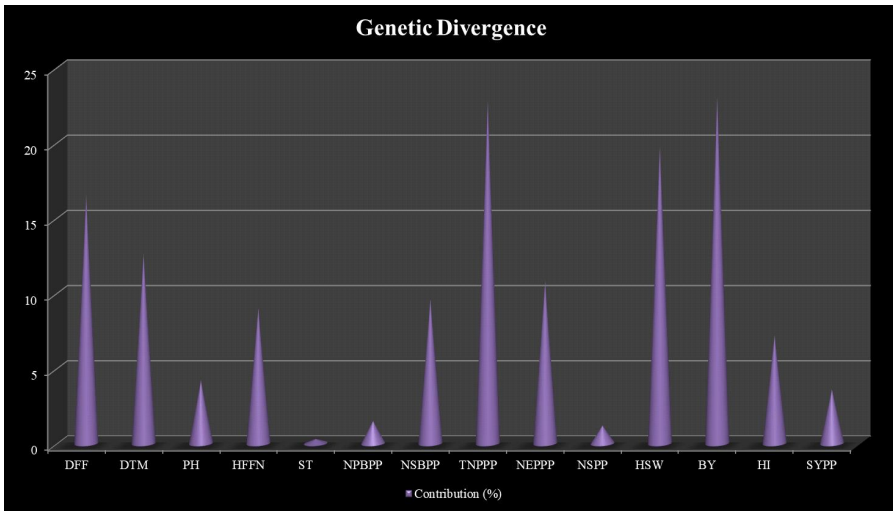

Fig. 3 : Graphical representation of contribution (%) of quantitative traits towards genetic divergence.

Table 4 : Contribution (%) of quantitative traits to genetic divergence.

Source	Times Ranked 1st	Contribution (%)
Days to 50% flowering	55	16.5
Days to maturity	42.0	12.6
Plant height (cm)	14.0	4.2
Height of first fruiting node (cm)	30.0	9.0
Stem thickness (mm)	1.0	0.3
Number of primary branches per plant	5.0	1.5
Number of secondary branches per plant	32.0	9.6
Total number of pods per plant	76.0	22.8
Number of effective pods per plant	36.0	10.8
Number of seeds per pod	4.0	1.2
Hundredseed weight (g)	66.0	19.8
Biological yield per plant (g)	77.0	23.1
Harvest index (%)	24.0	7.2
Seed yield per plant (g)	12.0	3.6

contribution. The remaining characters exhibited minimal or negligible influence on genetic divergence illustrated in the Table 4 and Fig. 3. Similar studies on maximum contribution of character towards genetic divergence was performed by Jayalakshmi *et al.* (2014) for 100 seed weight and number of pods, Parhe *et al.* (2014) for 100 seed weight, number of pods per plant and days to 50% flowering, Gediya *et al.* (2018) for 100-seed weight and pods per plant, Thakur *et al.* (2018) for days to 50% flowering and 100-seed weight, Babbar and Jain (2021) for biological yield per plant.

Identification of promising genotypes

The identified superior breeding lines based on the per se performance and inter cluster distance can be utilized as a parent in the future hybridization programme. Based on the mean performance of fourteen quantitative traits Cluster III displayed higher seed yield per plant, total number of pods per plant, number of effective pods per plant, number of primary branches per plant, number of secondary branches per plant, biological yield per plant and hundred seed weight along with delayed days to 50% flowering and days to maturity containing the four genotypes. D^2 analysis is an important technique which not only represents the percentage contribution of traits but also describes the diversity present in the breeding lines by grouping them into diverse clusters. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study the four genotypes *viz*. JG 2020-1614, PG 205, ICCV 211209, JG 2020-634958 were found to be superior and can be used as a potent parents for improvement of chickpea.

Conclusion

In the investigation of genetic divergence, the predominant contribution was discerned for biological yield per plant, subsequently followed by the total number of pods per plant and the hundred-seed weight, emphasizing the selection for these traits is deemed efficacious. Based on D^2 values, 40 advanced chickpea breeding lines were grouped into nine clusters, with seven being polygenotypic and the remaining two being monogenotypic, highlighting significant diversity in the material. The most pronounced inter-cluster divergence was identified between the genotypes of cluster VIII and cluster II, indicating that the crossing of genotypes from these highly divergent clusters has the potential to generate the maximum number of recombinants in the chickpea breeding material. Based on evaluations involving inter-cluster distances, cluster means, and *per se* performance, certain genotypes have been identified as superior parents for integration into the chickpea hybridization program.

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Conflicts of interest

The authors declare no conflict of interest.

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