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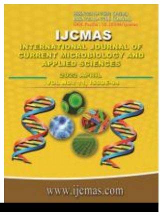

Original Research Article

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Study on Genetic Diversity in Chickpea (*Cicer arietinum* L.) Germplasm under Normal Sown Conditions

Dasari Praneeth*, Padala Chandana and Gaibriyal. M. Lal

Gopalarao Street, Addanki, Prakasam (dt.), Andhra Pradesh, India

**Corresponding author*

ABSTRACT

Chickpea (*Cicer arietinum* L.) also referred to as "poor man's meat and rich man's vegetable" is that the second most significant food legume within the world after beans in terms of area (13.5 million hectares) and production (13.1 million tons). Variability may be a greater need for initiating a breeding program for yield and yield contributing traits. a complete of 35 lines, together with a check, were evaluated in Randomized Complete Block Design (RCBD). Highest seed yield per plant was recorded by IPC-04-01. All the traits except number of branches showed significant variation among the lines. Number of pods per plant, biological yield and number of secondary branches showed high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), whereas number of number of seeds per plant, number of pods per plant and days to maturity, showed moderate GCV and PCV. Supported D2 values, 35 genotypes were grouped into nine clusters. Cluster I with 4 genotypes, cluster II with 13 genotypes had highest number of genotypes, cluster III with 9 genotypes, cluster IV & V with 1 genotypes in each, cluster VI with 4, and cluster VII, VIII and IX with 1 genotype each. The non-hierarchical Euclidean cluster analysis using 13 quantitative characters revealed maximum diversity between cluster V & IX. supported cluster means, cluster distances and as such performance BGD-9977, ICC-1205, RVG-204, IPC-12-100, ICCV-16317, JG-130 were found more diverse among 35 chickpea genotypes which may well be used as parents in hybridization programme for more heterotic response and generation of higher segregants in chickpea breeding.

Keywords

Cicer arietinum, GCV, PCV and Divergence

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Introduction

Chickpea is a self-pollinated, diploid crop with chromosome number 2n=14 that belongs to the leguminaceae family's subfamily Papilionoideae and tribe Cicereae. It is grown on a 12 million acre plot with an annual yield of 8.9 million tons. Chickpeas are important for improving soil fertility because their root nodules fix atmospheric nitrogen. The extent to which yield and quality attributes are heritable from generation to generation and the magnitude of genetic diversity contained in the breeding material are the most important factors in crop development. Estimates of genotypic and phenotypic coefficients are required to comprehend the impact of the environment on various traits. The extent to which yield and quality attributes are heritable from generation to generation and the magnitude of genetic diversity contained in the breeding material are the most important factors in crop development. To understand the impact of the environment on specific traits, estimates of genotypic and phenotypic coefficients are required.

D2 analysis is a valuable method for determining the degree of genotypic divergence between biological populations and determining the relative contribution of different components to overall divergence, both at the inter- and intra-cluster levels. Keeping this in mind, the genetic divergence was calculated using Mahanlanobis's (1936) D2 statistics, which is dependent on many variate analysis of quantitative traits. It's one of the most promising tools for determining genetic divergence within a group of people utilising the statistical distance concept and multivariate measures.

As a result, the current study was conducted to examine the genetic diversity among the parents, the relationship between different features and yield, and the selection of high yielding genotypes with better architecture.

Materials and Methods

The experimental material comprised of thirty five germplasm of chickpea were sown on 4th October 2019 in Rabi, 2019-20 at Field Experimentation Centre of the Genetics and Plant Breeding. The experiment was laid in Randomized Block Design.

Data for 13 quantitative traits were recorded viz; days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of seeds per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100-seed weight and seed yield per plant. Recommended package of practices were followed to raise a healthy chickpea crop. Statistical methods are followed to estimate genetic coefficient of variance, phenotypic coefficient of variance and divergence.

Results and Discussion

Analysis of variance for the thirteen quantitative traits has been revealed that the lines exhibited highly significant differences among thirteen traits. The high genotypic coefficient of variation was found for biological yield (28.46 %) followed by number of seeds per plant (28.15 %) and Number of pods per plant (27.40 %) while high phenotypic coefficient of variation was also found in biological yield (29.23 %) followed by number of seeds per plant (28.53 %) and number of pods per plant (27.73 %). In the present investigation, it is depicted from the table-1 that in general, estimates of phenotypic coefficient of various was found higher than their corresponding genotypic coefficient of variation, indicating that the influence of environment on these traits. Higher amount of phenotypic and genotypic coefficient of variation was reported for seed yield per plant, biological yield, and no. of seeds per plant showing wide variation among the genotypes with respect to these characters and similar results were reported by Deshmukh *et al.*, 2004; Zali *et al.*, 2010.

The broad sense heritability includes the contribution of additive gene effects, allelic interactions due to dominance and non-all elided to epitasis. In the present investigation, number of pods per plant (97.6), number of seeds per plant (97.3), number of secondary branches per plant (96.9) followed by, number of primary branches per plant (96.4), number of seeds per pod (95.5) and all other characters showed high estimates of heritability (b.s.). Similar findings were exported by Kumar *et al.*, (2019) and Hahid *et al.*, (2010).

Thus considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as percent of mean, and selection must be done in the characters like number of pods per plant, biological yield, number of secondary branches, seed yield per plant for improving the yield in chickpea.

The cluster mean revealed (Table-2) that clusters II and III varied considerably for most of the characters from those of other clusters. This indicates that the genotypes included in these clusters might have entirely different genetic architecture from the genotypes included in the other clusters. The cluster mean revealed high variability among the clusters for the traits, number of seeds per plant, number of secondary branches, biological yield, and seed yield per plant. Among these traits, number of secondary branches showed highest percent. A study observed that characters like number of seeds per plant, number of secondary branches, biological yield, and seed index contributed maximum to the diversity. Same results reported by Parameshwarappa *et al.,* (2009). Nimbalkar and Harer (2001) reported maximum genetic divergence due to number of pods per plant and number of seeds per plant.

Table.1 Genetic parameters for 13 quantitative characters of 35 genotypes during Rabi 2019-20

Characters	GCV %	PCV %	h^2	GA	GAM
Days to 50% Flowering	**7.28**	**7.83**	**86.4**	**12.04**	**13.94**
Days to 50% Pod Setting	**9.56**	**10.08**	**90.1**	**20.68**	**18.69**
Plant height (cm)	**11.94**	**12.48**	**91.5**	**16.15**	**23.52**
Number of primary branches	**22.78**	**23.20**	**96.4**	**0.93**	**46.07**
Number of secondary branches	**24.60**	**24.99**	**96.9**	**2.79**	**49.87**
Days to Maturity	**9.52**	**10.06**	**89.4**	**25.26**	**18.53**
Number of pods per plant	**27.40**	**27.73**	**97.6**	**35.83**	**55.76**
Number of seeds per pod	**23.03**	**20.50**	**95.5**	**0.63**	**40.32**
Number of Seeds per plant	**28.15**	**28.53**	**97.3**	**51.46**	**57.22**
Biological yield (g)	**28.46**	**29.23**	**94.8**	**23.06**	**57.09**
Seed Index (g)	**18.70**	**19.66**	**90.5**	**7.54**	**36.64**
Harvest index (%)	**16.01**	**16.90**	**89.8**	**13.67**	**31.24**
Seed yield per plant (g)	**26.10**	**26.95**	**93.8**	**9.00**	**52.07**

GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation,h^2 *=heritability (Broad sense), GA= Genetic Advance @ 5%, GAM= Genetic Advance as % mean.*

Fig.1 Genetic Summary of 13 characters of 35 genotypes

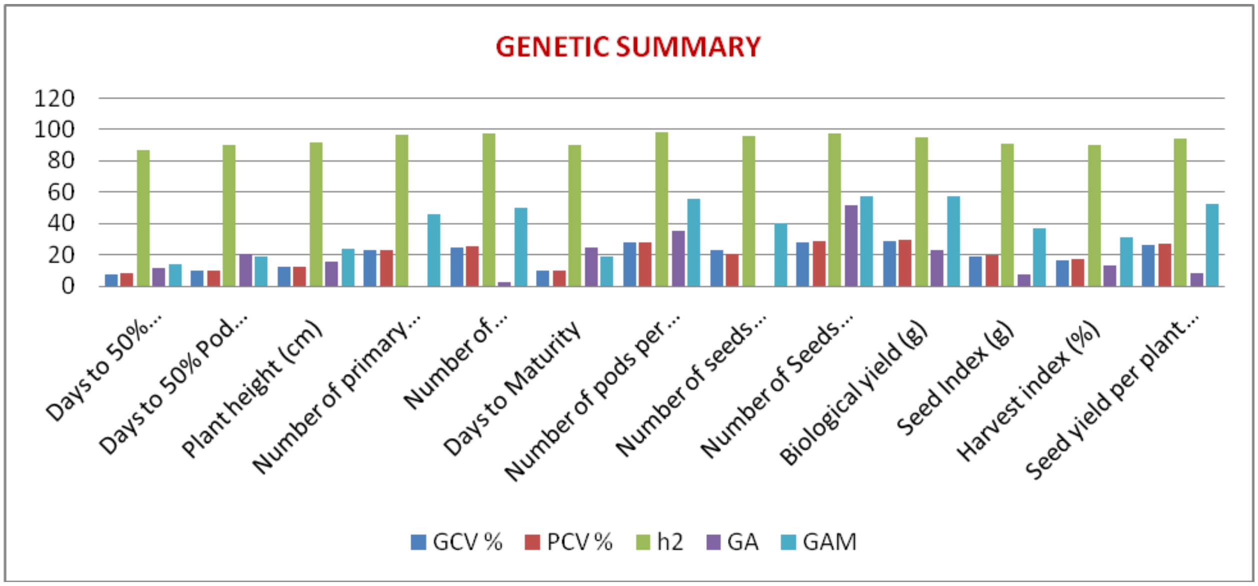

Table.2 Cluster mean of different characters to genetic diversity in chickpea during Rabi 2019-20

	D50F	D50P	PH	NPBP	NSBP	DM	TNPP	NSPO	NSPP	BYP	SW	HI	SYP
Cluster 1	84.08	106.25	60.83	1.92	4.32	123.25	54.72	1.00	55.70	34.30	24.50	48.37	17.02
Cluster 2	86.13	111.00	70.67	2.05	5.64	141.79	58.89	1.78	92.36	37.85	20.46	44.36	16.72
Cluster 3	90.08	108.93	67.88	1.91	5.96	133.33	85.21	1.47	114.44	50.92	18.63	41.15	20.37
Cluster 4	100.0	100.00	69.99	2.00	7.87	147.00	67.53	2.00	116.33	32.87	16.67	40.18	13.20
Cluster 5	84.66	105.67	73.37	3.87	5.33	154.33	66.60	1.80	111.60	53.73	22.67	39.35	21.13
Cluster 6	83.33	126.25	74.72	1.93	5.05	140.20	44.07	1.58	56.13	37.98	25.83	44.80	16.50
Cluster 7	60.33	94.33	65.41	2.53	4.40	124.33	60.67	1.13	69.73	25.17	15.00	53.02	13.34
Cluster 8	81.00	102.00	52.73	1.60	3.20	121.00	33.93	1.47	62.67	11.47	12.00	44.81	5.13
Cluster 9	97.00	117.00	69.40	1.60	10.27	127.00	92.67	1.40	109.33	50.80	18.67	34.23	17.27

D50F= Days to 50% flowering, D50P= Days to 50% pod setting, PH= Plant height, NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, DM= Days to maturity, TNPP= Total number of pods per plant, NSPO= Number of seeds per pod, NSPP= Number of seed per plant, BYP= Biological yield per plant, SW= Seed weight, HI= Harvest index, SYP= Seed yield per plant.

Table.3 Average Intra and Inter cluster D2 values in chickpea during Rabi, 2019-20

	Cluster. 1	Cluster. 2	Cluster. 3	Cluster. 4	Cluster. 5	Cluster. 6	Cluster. 7	Cluster. 8	Cluster. 9
Cluster. 1	9.37	14.98	15.59	21.48	18.21	14.9	13.74	15.02	21.85
Cluster. 2		9.56	12.93	12.96	14.43	13.69	15.18	12.97	18.08
Cluster. 3			11	13.58	17.78	18.6	16.46	15.9	14.69
Cluster. 4				0	18.69	21.07	20.99	16.34	12.89
Cluster. 5					0	17.81	15.92	18.99	24.67
Cluster. 6						12.7	17.57	16.98	23.43
Cluster. 7							0	12.62	23.6
Cluster. 8								0	22.18
Cluster. 9									0

Therefore, while selecting the parents by considering the genetic diversity, the per se performance and cluster mean for the characters also need due consideration in the crop improvement programme. Based on the mean performance of 35 genotypes of chickpea, IPC-04-01 was found superior in terms of seed yield per plant (g) followed by IPCK-1185 and GNG- 1958. Analysis of variance showed significant variation among different genotypes for all the characters. Number of seeds per plant, biological yield, number of pods per plant exhibited high genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV). High heritability was observed in number of pods per plant, number of seeds per plant, high genetic advance and genetic advance as percentage mean was observed in number of seeds per plant. D2 values showed adequate genetic diversity among the genotypes studied. Maximum number of genotypes was grouped into cluster II which included 13 genotypes. Number of seeds per pod, number of secondary branches contributed maximum (16.97%) towards the diversity among all the characters. The cluster II, IV and VIII were found more diverse to each other. Therefore, the genotypes present in these clusters can be used for future hybridization.

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