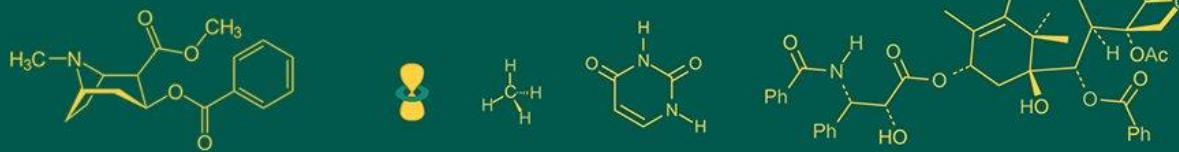


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Assessment of genetic variability and divergence on chickpea (*Cicer arietinum* L.) under late sown conditions

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Abstract

A study was carried out during the Rabi season of 2021-2022 on chickpea crops at the Genetics and Plant Breeding Research Farm of Acharya Narendra Deva University of Agriculture and Technology in Narendra Nagar, Kumarganj, Ayodhya, focusing on late sown conditions. The experiment involved 37 genotypes, including four check varieties (GNG 2299, Pant G 186, BG 372, KPG 59), and employed a Randomized Block Design with three replications. The recorded data subjected to Analysis of variance revealed highly significant differences in days to maturity among replications. Treatments showed significant variations in all observed characteristics. Generally, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits, with the highest values observed in seed yield per plant. The Mahalanobis D^2 cluster analysis categorized the 37 genotypes into six distinct clusters, indicating genetic diversity in the germplasm collection. Divergence analysis identified six clusters with genotypes of diverse origins, suggesting no clear correlation between genetic and geographic diversity. Clusters II and VI exhibited particularly high inter-cluster distances. Results confirm that genotypes BG 4001, Bidhan chana 1, JG 2018-51 in cluster III performing high yields of all the genotypes under late sown conditions. Further PCA analysis revealed that PC1 responsible to maximum percentage in total variation followed by PC2 and PC3. The primary contributors to total genetic divergence were secondary branches per plant, followed by harvest index.

Keywords: GCV, PCV, genetic advance, heritability, principal component analysis, genetic divergence

Introduction

Chickpea (*Cicer arietinum* L.) is often known as gram, Bengal gram or Garbanzo bean, is the most important food grain legume of south Asia and the third most important in the world after common bean and field pea (Ahmad *et al.*, 2015) [1]. Chickpea belongs to the family Fabaceae (Leguminosae) and botanical name is *Cicer arietinum* L. Chickpea is an annual grain legume crop that is self-pollinated and diploid. Legume seeds are an essential element of the human diet since they include a reasonably high quantity of protein, minerals, and vitamins (Kushwaha *et al.*, 2020) [15]. Chickpeas are one such dietary legume and, next to milk, a favored source of protein. It is the world's second most significant pulse crop, and the Indian subcontinent's first (Singh *et al.*, 2022) [25]. Beyond conventional breeding procedures, measures are now being called for to strategically broaden the narrow genetic base of chickpea wild relatives and improve cultivars via advanced breeding approaches with a special emphasis on high yield productivity, biotic and abiotic stresses including climatic resilience, and boosted nutritional values (Singh *et al.*, 2015) [24]. Potential donors with such a wide range of features were found utilizing a core and mini-core collection from the farmed gene pool as well as wild relatives of chickpeas (Sharma *et al.*, 2013) [21]. Late sowing is a common practice in many chickpea-growing regions, as it allows farmers to utilize residual soil moisture after the rainy season, and also enables them to grow other crops during the early season (Korbu *et al.*, 2020) [13]. However, late sowing often exposes the crop to adverse environmental conditions, such as high temperatures and water stress, which can affect the crop's growth and yield.

Materials and Methods

The experiment in the field for the current investigation was carried out in the *Rabi* season of 2021–2022 at the Genetics and Plant Breeding Research Farm, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). Geographically Narendra Nagar is located between 26.47° N latitude, 82.12° E longitude and at an elevation of 113 meters above the mean sea level. The climate of district Ayodhya is Semi-arid with scorching summers and frigid winters. Nearly 80% of total rainfall is received during the monsoon (only up to September) with some showers in the winter. The soil type of the experimental field was saline and inland alkaline with pH=9.1 and EC= 4.3dSm⁻¹. The meteorological data of Ayodhya region comes under a semi-arid zone with scorching summers and frigid winters. The experimental materials for the present investigation consisted of 37 genotypes of chickpea along with four check varieties, namely GNG 2299, Pant 186, BG 372, and KPG 59. These genotypes were procured from the Department of GPB, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya. Experimental materials exhibited a wide spectrum of variation for agronomical and morphological characters. The experiment was conducted on 37 entries including four checks *viz.*, GNG 2299, Pant 186, BG 372, and KPG 59 in Randomized Block Design (RBD) with 3 replications at 30 x 10 cm (row to row and plant to plant distance respectively). The check used in the experiment is well-adopted varieties of the region. Observations on the following characters were recorded based on five plants randomly selected and tagged from each row except for 50% flowering and days to maturity, which were recorded on a plot basis. The field components and observations were days to 50% flowering, days to maturity, primary branches per plant, secondary branches per plant, plant height, seeds per pod, pods per plant, 100 seed weight, biological yield, harvest index, and seed yield.

Results and Discussion

The mean data for eleven characters were subjected to analysis of variance which showed that the mean sum of squares for all the characters due to genotypes were found significant under study, which indicates that considerable amount of variability is present among the genotypes. Mean square due to replications were found non-significant for all these traits except the days to maturity and harvest index. This significant heterogeneity offers a strong opportunity to enhance desirable features in chickpea breeding efforts. Similar results for genetic variability in chickpeas have been reported by Singh *et al.*, 2021^[23], Vijayakumar *et al.*, 2017^[23], Jain *et al.*, 2023^[11] and in a few of their earlier investigations. Hence there is ample scope for the inclusion of promising genotypes in the breeding program for yield and its component's characters.

Heritability and genetic advance

Heritability and genetic advance in percent of mean were estimated for all the eleven characters and are presented in Table 2.

Heritability is a marker for the ability of traits to be transmitted from generation to generation. All the characters estimated high broad sense heritability (>80%) which were recorded for biological yield (97.6%), seed yield per plant (97.6%), 100-seed weight (96.7%), plant height (95.9%),

days to 50% flowering (95.4%), pods per plant (91.1%), days to maturity (88%), secondary branches per plant (82.7%), and moderate (60-80%) harvest index (75.9), seeds per pod (71.7%), primary branches per plant (64.1%).

The high estimates of genetic advance in per cent of mean (>20%) were estimated by seed yield per plant (91.06%), biological yield per plant (77.9%), 100-seed weight (49.53%), plant height (45.76%), pods per plant (43.16%), secondary branches per plant (36.66%), primary branches per plant (21.67) and days to maturity (20.9%). The moderate estimate for genetic advance (10-20%) in per cent of mean was shown by harvest index (17.80%). while the low estimates of genetic advance (<10%) for days to maturity (6.96%).

The phenotypic and genotypic coefficient of variation for all the eleven characters has been given in Table. In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all 11 traits studied in the present experiment. The higher estimates (>25%) exhibited by seed yield per plant (44.73%) for GCV and (45.27%) for PCV. The character which exhibited moderate estimates (10-25%) of GCV and PCV were primary branches per plant (13.14%) for GCV and harvest index (11.38%) for PCV and days to 50% flowering (10.40%) for GCV and (10.65%) for PCV. The characters showed low estimates (<10%) of GCV and PCV were harvest index (9.91%) and days to maturity (3.60%) for GCV and (3.83%) for PCV presented in below Table 2. (Babbar *et al.*, 2012^[2], Jadhav *et al.*, 2012^[10], Kumari *et al.*, 2013^[14], Bala *et al.*, 2015^[3], Srivastava *et al.*, 2017^[26], Singh *et al.*, 2021^[23], Choudhary *et al.*, 2022^[5], Jain *et al.*, 2023^[11]).

Genetic divergence

The genetic divergence existing in 37 chickpea germplasm collections was studied by Mahalanobis, P.C. (1928) employing cluster analysis for 11 quantitative characters. These genotypes were grouped in 6 different non-overlapping clusters is given in Table 3.

The highest number of genotypes appeared in cluster-III and V, which contained 8 genotypes each followed by cluster-II, cluster-I with found 7 and 6 genotypes respectively and Cluster-VI having 5 entries. Cluster-IV has the minimum number of 3 entries among all the clusters. The estimates of intra and inter-cluster distance for six clusters are presented in Table 4. The highest intra-cluster distance was found for cluster VI (151.19) followed by cluster I (140.48), cluster V (137.14), cluster II (115.68), and the lowest intra-cluster distance was found for cluster IV (62.12). The maximum inter-cluster distance was shown between clusters II and VI (839.82) followed by clusters IV and VI (752.21), clusters III and VI (581.94), clusters I and VI (527.71) and cluster II and IV (397.48). The minimum inter-cluster distance was observed between cluster III and IV (211.89).

The mean performance of clusters for 11 characters is presented in Table 5. The genotypes of cluster V were earlier flowering (X = 59 days) followed by cluster III (X = 62 days). Cluster II was found late in flowering (X = 74 days) followed by cluster IV (X = 68 days). The entries represented in cluster V were comparatively early maturing (X = 124 days) followed by cluster I (X = 131 days), while genotypes in cluster VI were found late in maturity (X = 140 days) followed by cluster IV (X = 134 days). The highest number of primary branches per plant was found in cluster II and III (X = 2.04) followed by cluster VI (X = 2.02) and cluster V (X =

2.00). Cluster IV ($X = 1.82$) appears to possess genotypes having a very low number of primary branches per plant. The genotypes with the high number of secondary branches per plant were concentrated in Cluster V ($X = 10.36$) followed by Cluster II ($X = 9.42$) and Cluster III ($X = 9.25$) whereas, Cluster I ($X = 6.66$) appears to possess genotypes having very low number of secondary branches per plant. The cluster means for plant height varied from 78.21cm (cluster VI) to 43.89 cm (cluster II).

The highest cluster means for the number of pods per plant was observed for cluster VI ($X=73.21$) followed by cluster III ($X = 62.13$) and cluster I ($X = 58.16$) while genotypes for the lowest number of pods per plant were concentrated in cluster II ($X = 36.77$). The genotypes representing the maximum cluster mean for the number of seeds per pod were present in cluster III ($X = 2.04$), while the lowest number of seeds per pod was observed in cluster II ($X = 1.26$). The 100 seed weight of genotypes was the highest among the clusters, cluster III ($X = 27.35$ g) followed by cluster V ($X = 23.68$ g). The lowest 100 seed weight was observed in cluster VI ($X = 14.23$ g). The genotypes with the highest biological yield per plant were found in cluster III ($X = 84.31$ g) followed by cluster I ($X = 54.27$ g). The lowest biological yield per plant was observed in cluster II ($X = 24.24$ g) and the remaining clusters had moderate cluster mean biological yield per plant. The highest cluster mean for harvest index was observed for cluster III ($X = 40.50\%$) followed by cluster I ($X = 40.14\%$), while the lowest harvest index was observed in cluster IV ($X = 35.72\%$) followed by Cluster II ($X = 36.21\%$). The highest cluster mean for seed yield per plant was observed in the case of cluster III ($X = 34.23$ g) followed by cluster I ($X = 21.77$ g). The genotypes with very low seed yield per plant were

exhibited in cluster II ($X = 8.86$). The remaining clusters mean had a medium range of seed yield per plant.

The relative contribution of 11 quantitative characters toward genetic divergence is presented in Table 6. The highest relative contribution towards genetic diversity was recorded by the secondary branches per plant (13.96%) followed by harvest index (13.36%) and primary branches per plant (13.31%) and the lowest contribution towards genetic diversity was found by seed yield per plant (2.10%). These results are corroborative with the findings of Sial *et al.*, 2010 [22], Jadhav *et al.*, 2011 [9], Syed *et al.*, 2012 [27], Devendrappa *et al.*, 2013 [6], Gaikwad *et al.*, 2014 [7], Parhe *et al.*, 2014 [18], Jakhar *et al.*, 2016 [12], Vijayakumar *et al.*, 2017 [23], Gediya *et al.*, 2018 [8], Biswas *et al.*, 2022 [4], Tengse *et al.*, 2022 [29].

Principal component analysis

A multivariate principal component analysis (PCA) was conducted, encompassing all traits simultaneously in Table 7. The resulting principal components (PCs) collectively explained over 85.69% of the total variation. First three PCs indicating eigen value >1 of all five PCs which is discussed further. The PC1 responsible for 37.00% of the total variation, was primarily influenced by days to 50% flowering, with the highest positive value attributed to this component. PC2, which explained 18.94% of the total variation, was strongly associated with secondary branches per plant and 100-seed weight. Lastly, PC3, accounting for 14.10% of the variation, was primarily influenced by primary branches per plant, days to 50% flowering, and seeds per pod, all of which exhibited positive weights. (Malik *et al.*, 2014, Rafiq *et al.*, 2020, Qadeer *et al.*, 2021, Talekar *et al.*, 2022) [17, 20, 19, 28].

Table 1: Analysis of variance for eleven characters in chickpea

Source of variation	d.f.	Mean of squares										
		Days to 50 percent flowering	Days to maturity	Primary branches per plant	Secondary branches per plant	Plant height (cm)	Pods per plant	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant
Replications	2	4.945	31.279**	0.001	0.369	15.579	6.405	0.015	0.237	20.581	18.573*	0.188
Treatments	36	152.186**	72.673**	0.240**	7.237**	662.29**	424.361**	0.279**	80.035**	999.304**	46.287**	201.445**
Error	72	2.418	3.149	0.037	0.471	9.31	13.368	0.032	0.896	8.179	4.429	1.611

Table 2: Range, mean, coefficient of variation (%), heritability, and genetic advance for eleven characters of chickpea germplasm

Characters	Parameters							
	Range	Mean	Coefficient of Variation (%)			Heritability in broad sense (%)	Genetic advance 5%	Genetic advance in percent of mean 5%
			GCV	PCV	ECV			
Days to 50% flowering	58 – 83	67.9	10.407	10.656	2.29	95.4	14.215	20.938
Days to maturity	125 -142	133.6	3.602	3.839	1.328	88.00	9.305	6.963
Primary branches per plant	1.40 - 2.87	1.976	13.144	16.42	9.842	64.10	0.428	21.673
Secondary branches per plant	4.40 - 11.42	7.674	19.571	21.518	8.944	82.70	2.814	36.668
Plant height (cm)	39.5 - 89.7	65	22.687	23.167	4.692	95.90	29.762	45.767
Pods per plant	33.33-79.67	53.32	21.95	22.996	6.857	91.10	23.015	43.16
Seeds per pod	1.00 - 2.27	1.602	17.917	21.161	11.26	71.70	0.501	31.249
100 seed weight (g)	12.19-30.89	21.004	24.453	24.865	4.507	96.70	10.405	49.539
Biological yield per plant (g)	19.72-93.12	47.458	38.299	38.771	6.026	97.60	36.988	77.938
Harvest Index (%)	29.37-43.03	37.661	9.918	11.384	5.588	75.90	6.704	17.801
Seed yield per plant (g)	6.20-40.02	18.243	44.738	45.276	6.958	97.60	16.613	91.066

Table 3: Clustering pattern of 37 chickpea genotypes based on D² analysis of eleven characters

Cluster number	Number of genotypes	Genotypes
I	6	BG 4000, PBC 538-18, BG 3046, BGD 3038, BG 3045, CSJ 564
II	7	PG 0109, RKG 12-297, GJG 1010, Pant G 186©, KPG 59©, BG 372©, GNG2299©
III	8	BG 4001, Bidhan chana 1, JG 2018-51, RVSSG 68, PBC 546-18, RG 2016-134, BRC 6, H 15-27
IV	3	GNG 434, RKG 13-22, JG 2018-52
V	8	CSJ 1065, GL 15017, NBeG 798, RKG 18-1, BDNG 2017-1, Phule g 16109, DBGV 217, PG 215
VI	5	DC 16-2, GL 13001, GNG 2372, RLBG 4, ICCV 171105

Table 4: Estimates of average intra and inter-cluster distance for six clusters in chickpea germplasm

Clusters	I	II	III	IV	V	VI
I	140.484	249.618	328.122	375.290	262.263	572.716
II		115.688	308.230	397.489	354.442	839.827
III			108.330	211.896	213.186	581.940
IV				62.12	355.458	752.219
V					137.146	365.360
VI						151.199

Table 5: Cluster means for six clusters in chickpea germplasm

Number of clusters	Days to 50% flowering	Days to maturity	Primary branches per plant	Secondary branches per plant	Plant height (cm)	Pods per plant	Seeds per pod	100-seed weight (g)	Biological yield per plant (g)	Harvest index (%)	Seed yield per plant (g)
I	63.53	131.70	1.92	6.66	70.27	58.16	1.64	23.30	54.27	40.14	21.77
II	74.00	132.66	2.04	9.42	43.89	36.77	1.26	19.53	24.24	36.21	8.86
III	62.93	132.40	2.04	9.25	73.66	62.13	2.04	27.35	84.31	40.50	34.23
IV	68.04	134.45	1.82	6.78	73.58	48.54	1.60	19.14	40.37	35.72	14.53
V	59.33	124.66	2.00	10.36	47.03	39.00	1.53	23.68	37.42	37.59	14.08
VI	67.55	140.33	2.02	6.72	78.21	73.66	1.57	14.23	43.33	37.92	16.31

Table 6: Contribution of 11 quantitative characters towards divergence in chickpea germplasm

S.No.	Source	Times Ranked 1st	Contribution %
1	Days to 50% flowering	53	7.96%
2	Days to maturity	53	7.96%
3	Primary branches/ plant	82	12.31%
4	Secondary branches/ plant	93	13.96%
5	Plant height (cm)	49	7.36%
6	Pods/ plant	59	8.86%
7	Seeds/ pod	73	10.96%
8	100 seed weight (g)	63	9.46%
9	Biological yield/ plant	36	5.71%
10	Harvest index (%)	89	13.36%
11	Seed yield/ plant (g)	14	2.10%

Table 7: Principal component analysis of eleven traits with eigenvalue and variance

Traits	PC1	PC2	PC3	PC4	PC5
Days to 50% flowering	0.29	0.09	0.49	0.09	0.34
Days to 50% maturity	-0.04	-0.49	0.29	0.37	0.35
Primary branches/plant	-0.04	0.05	0.60	0.14	-0.71
Secondary branches/plant	-0.13	0.53	0.05	-0.31	0.17
Plant height(cm)	-0.22	-0.43	-0.32	0.23	-0.12
Pods/Plant	-0.30	-0.37	0.12	-0.50	-0.13
Seeds /Pod	-0.30	-0.24	0.35	-0.49	0.23
100 Seed weight(g)	-0.33	0.17	0.23	0.32	-0.02
Biological yield / Plant (g)	-0.45	0.14	-0.09	0.18	-0.06
Harvest index (%)	-0.41	0.18	0.10	0.25	0.35
Seed yield/Plant (g)	-0.43	0.14	-0.10	0.00	-0.06
Eigen Value (Root)	4.07	2.08	1.55	1.00	0.73
% Variance	37.00	18.95	14.11	9.05	6.64
Cumulative variance	37.00	55.95	70.05	79.10	85.74

Conclusion

Genetic variability is regarded as an essential criterion for crop development. Based on the outcomes of this study, it is determined that all analyzed characteristics had substantial variable estimations. The PCV was greater than the GCV for

all evaluated characteristics, indicating that the environment influenced their expression. For seed yield per plant, biological yield, 100-seed weight, plant height, and pods per seed, strong heritability was seen in conjunction with a high GA percent mean. Because these characteristics were within

the influence of additive gene effect, the high heritability combined with rapid genetic progress indicated that they may be enhanced by selection. Cluster analysis distributed the genotypes into six distinguished clusters. Results indicate that the members of cluster-III (BG 4001, Bidhan chana 1, JG 2018-51) are more diverse in performance of different traits and high yielding as well. The clustering of genotypes might aid chickpea breeders in identifying and choosing the genotypes. Our analysis of principal component analysis reveals that the greatest genetic variability is predominantly attributed to the first three components. Consequently, selecting parental types based on these components would yield more advantageous outcomes. These genotypes with economically essential qualities might be utilized to integrate desirable traits in a single line with a broad genetic base.

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