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 D² 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) [23]. 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 replications were found non-significant under study, which indicates that considerable amount of variability is present among the genotypes. 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 percent 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 percent of mean was shown by harvest index (17.80%), while the low estimates of genetic advance (<10%) for days to maturity (6.96%).

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 high estimates of 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 percent 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 percent 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 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]).
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 78.21 cm (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 = 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>
<thead>
<tr>
<th>Characters</th>
<th>Range</th>
<th>Mean</th>
<th>Coefficient of Variation (%)</th>
<th>Heritability in broad sense (%)</th>
<th>Genetic advance</th>
<th>Genetic advance in percent of mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to 50% flowering</td>
<td>58 – 83</td>
<td>67.9</td>
<td>10.407</td>
<td>95.4</td>
<td>14.215</td>
<td>20.938</td>
</tr>
<tr>
<td>Days to maturity</td>
<td>125 – 142</td>
<td>133.6</td>
<td>3.602</td>
<td>88.0</td>
<td>9.305</td>
<td>6.963</td>
</tr>
<tr>
<td>Primary branches per plant</td>
<td>1.40 – 2.87</td>
<td>1.976</td>
<td>13.144</td>
<td>64.10</td>
<td>0.428</td>
<td>21.673</td>
</tr>
<tr>
<td>Secondary branches per plant</td>
<td>4.40 – 11.42</td>
<td>7.674</td>
<td>19.571</td>
<td>82.70</td>
<td>2.814</td>
<td>36.668</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>39.5 – 89.7</td>
<td>65</td>
<td>22.687</td>
<td>95.90</td>
<td>29.762</td>
<td>45.767</td>
</tr>
<tr>
<td>Pods per plant</td>
<td>33.33-79.67</td>
<td>53.32</td>
<td>21.95</td>
<td>91.10</td>
<td>23.015</td>
<td>43.16</td>
</tr>
<tr>
<td>Seeds per pod</td>
<td>1.00 – 2.27</td>
<td>1.602</td>
<td>17.917</td>
<td>71.70</td>
<td>0.501</td>
<td>31.249</td>
</tr>
<tr>
<td>100 seed weight (g)</td>
<td>12.19-30.89</td>
<td>21.004</td>
<td>24.453</td>
<td>96.70</td>
<td>10.405</td>
<td>49.539</td>
</tr>
<tr>
<td>Biological yield per plant</td>
<td>19.72-93.12</td>
<td>47.458</td>
<td>38.299</td>
<td>97.60</td>
<td>36.988</td>
<td>77.938</td>
</tr>
<tr>
<td>Harvest Index (%)</td>
<td>29.37-43.03</td>
<td>37.661</td>
<td>9.918</td>
<td>75.90</td>
<td>6.704</td>
<td>17.801</td>
</tr>
<tr>
<td>Seed yield per plant (g)</td>
<td>6.20-40.02</td>
<td>18.243</td>
<td>44.738</td>
<td>97.60</td>
<td>16.613</td>
<td>91.066</td>
</tr>
</tbody>
</table>
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, Bidhanchana 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.

References

