**Genetic Diversity Analysis in Chickpea (*Cicer arietinum* L.) Genotypes in South-Eastern Rajasthan, India**

**Abstract**

A field experiment was conducted during *Rabi* 2019-20 to study genetic diversity in forty chickpea genotypes. The grouping of chickpea genotypes into eight clusters suggested the presence of wide genetic diversity among them. The Cluster III was the largest including 10 genotypes followed by cluster IV (9 genotypes), cluster II (7 genotypes), cluster VI (6 genotypes), cluster V (4 genotypes), cluster VI (2 genotypes) while clusters I and VIII had one genotype each. The maximum inter cluster distance was observed between cluster V and cluster VIII, followed by cluster I and VIII, cluster VI and cluster VIII, cluster I and cluster II indicating wide diversity among genotypes in these clusters that could be well exploited in chickpea hybridization programme for improving seed yield. The present investigation revealed that the clusters I and VII are most diverse to each other, therefore, the genotypes constituted in these clusters may be used as parents for further hybridization programme. The present study revealed that the maximum contribution towards divergence was made by seed yield per plant (18.07 %), biological yield (15.5 %), number of pods per plant (13.26 %), number of branches per plant (10.61 %) and number of seeds per pod (8.16 %)**.** Therefore, these characters should be given importance during selection for high yielding chickpea genotypes and varieties.

**Keywords:** Chickpea, diversity analysis, cluster, D2 statistics, cluster distance

**Introduction**

“Chickpea (*Cicer arietinum* L*.*) also called *chana* (Hindi) and gram or Bengal gram (English) belongs to genus *Cicer,* tribe *Cicereae,* family Fabaceae (Leguminosae) and sub family Papilionaceae” [1]. “It is diploid in nature with chromosome number 2n=16. The origin of the crop is considered to be Western Asia from where it spread in India and other parts of the world” [2]. “Chickpea is a legume plant that grows in subtropical and temperate regions. It is grown in more than 44 countries representing all the continents under eight geographically diverse agro-climatic conditions. India is one of the major pulses growing country of the world. Over 60 per cent of pulses produced in India are grown during the *Rabi* season” [3].

“The total world acreage under pulses is about 93.18 million hectares with production of 89.82 million tons and productivity of 964 kg/ ha. India ranked first in area and production with 31% and 28% share respectively, to world area and production. In India, chickpea is cultivated in 9.90 million hectares area with a production of 10.7 million tons and at a highest productivity level of 1086 kg/ha. As usual, MP has contributed a significant 28 and 34%, respectively to the total chickpea area and production in the country, thereby ranking first both in area and production followed by Maharashtra (20 % and 18%), Rajasthan (19% and 18%), Karnataka (10% and 6 %), Uttar Pradesh (4.65% and 4.61%), and other remaining states.In Rajasthan, it is cultivated in 18.59 Lakh/ha area, with the production of 19.72 Lakh tons and productivity 1061kg/ha” [4].

“The knowledge of genetic diversity is a useful tool in gene-bank management and breeding experiments like tagging of germplasm, identification and elimination of duplicates in the gene stock and establishment of core collections. Genetic diversity is the base for survival of plants in nature and for crop improvement. Genetic divergence among the parents play a vital role in cultivar improvement due to availability of sufficient genetic variability in segregating generations, which can be exploited for improvement” [5]. The present study aims to find out the genetic diversity among forty chickpea genotypes for selection and development of high yielding genotypes and varieties.

**Materials and methods**

The experimental material consisted of forty chickpea genotypes sown in randomized block design with three replications during *Rabi* 2019-20 at Agricultural Research Station, Ummedganj, Kota, Rajasthan. Each genotype was accommodated in four rows plot of 4.0 m length with a spacing of 30×10 cm. The genotypes were randomly allotted to each plot in each replication. All the recommended agronomic package of practices was followed timely for successful raising of crop. The observations were recorded on five randomly selected plants per replication for eleven traits *viz.*, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100 seed weight, protein content and seed yield per plant except days to 50% flowering and maturity which were recorded on plot basis. The D2analysis was done according to [6]. The clustering of genotypes was done by Tochers' method, as described by [7]. The intra and inter cluster distances were computed as suggested by [8]. The grouping of genotypes into various clusters was done and average intra and inter cluster distance was estimated.

**Results and Discussion**

**Genetic divergence analysis**

Based on the estimates of genetic divergence, all the forty chickpea genotypes were grouped into 8 different clusters (Table-1). Generalized distance was estimated through Mahalanobis’ D2 – statistic. Among the eight clusters, cluster III was the largest including 10 genotypes followed by cluster IV with 9 genotypes, cluster II with 7 genotypes, cluster VII with 6 genotypes, cluster V with 4 genotypes, cluster VI with 2 genotypes and cluster I and VIII each with one genotype each. These results indicated that some homology existed between closely situated clusters. Therefore, crossing the genotypes from different clusters would unfold more genetic variability for exploiting it in future breeding programme. Similar results were also reported by [9] and [10].

**Table 1. Distribution of different chickpea genotypes in to clusters based on D2 statistics**

|  |  |  |
| --- | --- | --- |
| **Cluster No.** | **No. of genotypes** | **Genotypes included** |
| I | 1 | RKG 12-297 |
| II | 7 | RKG 13-75, RKG 13-205, RKG 12-172, RKG 2019-15, C –1218, C–1256, ICCV 16115 |
| III | 10 | RKG 13-380, RKG 18-1, RKG 13-112, RKG 13-190, RKG 2019-15, C–1062, RKGD 17-7, ICCV 16114, GNG 1958 (C), GNG 469 (C)  |
| IV | 9 | RKG 13-515, C–1060, C–1082, C-1213-1, C-1201, C– 1016, GCP 101 (C), JG 16 (C), PC 1 (C) |
| V | 4 | RKG 13-515-1, RKG 13-136, RKG 13-180, ICCV 16111 |
| VI | 2 | RKG 13–55, PA 083 (5679) |
| VII | 6 | RKG 13-125, PA 083 (5005), RKG 2019-29, ICCV 16118, CSJ 515 (C), GNG 1581 (C) |
| VIII | 1 | RKG 13-205 |

**Intra and inter cluster distances**

The intercluster distances were greater than intracluster distances, revealing that considerable amount of genetic diversity existed among the genotypes. Intercluster distance is the main criterion for selection of diverse genotypes for crop improvement programme using D2 analysis. Genotypes belonging to the clusters with maximum intercluster distance were genetically more divergent and hybridization between genotypes of divergent clusters is likely to produce wide spectrum of genetic variability with desirable segregates.

“The intra and inter cluster distances D2 between all possible pairs of eight clusters were computed and presented in Table-2. The inter cluster distance (D) ranged from 4.469 to 33.014. The maximum inter cluster distance (D=33.014) was observed between cluster V and cluster VIII, followed by cluster I and VIII (D=32.503), cluster VI and cluster VIII (D=24.385), cluster I and cluster II (D=23.501) indicating wide diversity among genotypes in these clusters that could be well utilized in chickpea hybridization programme for improving seed yield. The minimum inter cluster distance (D = 4.469) was between III and VII which, indicated that the genotypes of these cluster are genetically less diverse and were almost with more or less same genetic makeup and may have followed the same evolutionary progress during the development of genotypes of these clusters. Similar results were obtained by” [11].

At intra cluster level, the intra cluster distance ranged from 0.00 to 15.526 (Table-2), cluster-II had the highest value (D=15.526) which was followed by cluster-VII (D=15.399) revealing the inclusion of diverse genotypes in these clusters. The lowest intra cluster value was recorded for cluster I (D = 0.00) and VIII (D = 0.00) as there was only one genotype in both of these clusters.

The utility of D2 analysis is enhanced by its application to estimate the relative contribution of various characters to genetic divergence. The contribution of each character towards total genetic diversity is presented in table-3. The present study revealed that the characters seed yield per plant (18.07 %), biological yield per plant (15.05 %), number of pods per plant (13.26 %), number of branches per plant (10.61 %), number of seeds per pod (8.16 %) contributed largely towards genetic divergence followed by 100-seed weight (7.79 %), plant height (7.40 %), protein content (6.64 %), harvest index (6.47 %), days to 50 % flowering (4.56 %) and days to maturity (1.94 %). Therefore, selection for such traits may be given more emphasis during hybridization programme to generate greater variability so as to provide immense scope for yield improvement through selection. Similar results were also reported by [12] and [13]. Later, [14] also reported that the traits like number of pods per plant, biological yield and harvest index should be used in selection programme for crop improvement.

**Table. 2. Average Intra and inter cluster distance (D2) values**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster | I | II | III | IV | V | VI | VII | VIII |
| I | **0.000** | 23.501 | 22.614 | 20.806 | 15.891 | 13.593 | 21.151 | 32.503 |
| II |  | **15.526** | 8.750 | 7.355 | 21.742 | 14.825 | 9.010 | 14.950 |
| III |  |  | **11.957** | 9.175 | 16.751 | 15.406 | 4.469 | 21.264 |
| IV |  |  |  | **10.832** | 19.902 | 13.805 | 9.621 | 17.792 |
| V |  |  |  |  | **10.126** | 15.038 | 17.925 | 33.014 |
| VI |  |  |  |  |  | **4.925** | 14.781 | 24.385 |
| VII |  |  |  |  |  |  | **15.399** | 20.567 |
| VIII |  |  |  |  |  |  |  | **0.000** |

**Table 3: Contribution of eleven characters under study towards total genetic divergence**

|  |  |  |
| --- | --- | --- |
| S. No. | Characters | Percent contribution towards divergence |
| 1 | Days to 50 per cent flowering | 4.56 |
| 2 | Days to maturity | 1.94 |
| 3 | Plant Height (cm) | 7.40 |
| 4 | Number of branches per plant | 10.61 |
| 5 | Number of pods per plant | 13.26 |
| 6 | Number of seeds per pod | 8.16 |
| 7 | 100-seed weight | 7.79 |
| 8 | Biological yield per plant (g) | 15.05 |
| 9 | Harvest Index (%) | 6.47 |
| 10 | Protein Content (%) | 6.64 |
| 11 | Seed yield per plant (g) | 18.07 |

**Cluster means of various characters**

The cluster means for the eleven characters presented in table 4 indicated wide range of variation for all the characters under the study. The cluster mean for days to 50 per cent flowering varied from 69.333 (I) to 76.667 days (VIII). The cluster means for days to maturity ranged between 117 (I) to 122.667 days (VIII). The highest cluster mean for plant height was 61.107cm, which was observed in cluster (III) and lowest for cluster I (48.267cm).The cluster mean for number of branches per plant ranged from 8.333 (I) to 11.700 (VI).The cluster mean for number of pods per plant was highest in cluster VIII (71.867) and it was lowest in cluster V (42.683).

The cluster mean for number of seeds per pod was highest in cluster VI (1.367) and it was lowest in cluster V (1.083). The cluster mean for 100-seed weight was highest in cluster V (24.108 g) and it was minimum in cluster I (16.700 g). The cluster mean for biological yield per plant varied from 19.467 g (I) to 34.067 g (VIII). The highest cluster mean for harvest index was 49.270 %, which was observed in cluster (I) and lowest for cluster VIII (39.815 %). The cluster mean for protein content was highest in cluster IV (24.056 %), while lowest for cluster VIII (19.400 %). The cluster mean for seed yield per plant ranged between 9.600 g (cluster I) and 15.252 g (cluster II). Similar results were shown by [15], hybridization between genotypes accounting wide genetic variance should be earnestly exploited in breeding programme for developing extreme divergent heterotic cross combinations for developing high yielding chickpea genotypes.

**CONCLUSION**

D2 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 [16]. Results of this study have clarified that maximum inter cluster distance was observed between cluster V and cluster VIII indicating wide diversity among genotypes in these clusters that could be well utilized in chickpea hybridization programme for improving seed yield. The utility of D2 analysis is enhanced by its application to estimate the relative contribution of various characters to genetic divergence shown by seed yield per plant, biological yield per plant and number of pods per plant. Concentrating on these traits in selection process will help in crop improvement programme in devising further breeding strategies and selection procedures to evolve high yielding varieties which will benefit the chickpea growing farmers.

**Table 4. Cluster mean value for eleven characters in chickpea (*Cicer arietinum* L.)**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Character** | **Days to 50% flowering**  | **Days to maturity**  | **Plant****height****(cm)**  | **Number****of branches plant-1** | **Number of pods plant-1** | **Number of seeds pod-1** | **100 -seed weight (g)** | **Biological yield plant-1****(g)** | **Harvest index (%)** | **Protein content (%)** | **Seed yield plant-1****(g)**  |
| I | 69.333 | 117.000 | 48.267 | 8.333 | 46.933 | 1.200 | 16.700 | 19.467 | 49.270 | 21.133 | 9.600 |
| II | 75.286 | 118.429 | 56.119 | 9.990 | 59.629 | 1.152 | 22.452 | 33.686 | 44.870 | 19.495 | 15.252 |
| III | 72.433 | 119.967 | 61.107 | 10.260 | 53.720 | 1.293 | 22.118 | 33.370 | 43.602 | 21.423 | 14.447 |
| IV | 71.037 | 117.556 | 54.289 | 11.356 | 57.704 | 1.311 | 20.111 | 33.559 | 44.829 | 24.056 | 15.056 |
| V | 70.417 | 117.417 | 56.708 | 9.283 | 42.683 | 1.083 | 24.108 | 24.017 | 40.164 | 22.692 | 9.650 |
| VI | 75.833 | 120.833 | 48.333 | 11.700 | 49.700 | 1.367 | 20.217 | 27.600 | 44.544 | 20.317 | 12.300 |
| VII | 72.944 | 121.556 | 61.072 | 10.544 | 54.722 | 1.311 | 19.661 | 31.211 | 45.838 | 20.822 | 14.644 |
| VIII | 76.667 | 122.667 | 53.133 | 9.133 | 71.867 | 1.333 | 18.500 | 34.067 | 39.815 | 19.400 | 13.567 |

**Disclaimer (Artificial intelligence)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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