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**Rajmohan Sharma**  
Department of Genetics &  
Plant Breeding, JNKVV,  
College of Agriculture,  
Ganjbasoda, Madhya Pradesh,  
India

**Abhishek Baghel**  
Department of Genetics &  
Plant Breeding, JNKVV,  
College of Agriculture,  
Ganjbasoda, Madhya Pradesh,  
India

**Mujahida Sayyed**  
Department of Maths and  
Statistics, JNKVV, College of  
Agriculture, Ganjbasoda,  
Madhya Pradesh, India

**Rajkishor Bhatnagar**  
Department of Soil Science and  
Agriculture Chemistry,  
JNKVV, College of  
Agriculture, Ganjbasoda,  
Madhya Pradesh, India

**Corresponding Author:**  
**Rajmohan Sharma**  
Department of Genetics &  
Plant Breeding, JNKVV,  
College of Agriculture,  
Ganjbasoda, Madhya Pradesh,  
India

## Analysis of genetic parameters of Chickpea (*Cicer arietinum* L.) genotypes under Vindhya plateau of Madhya Pradesh

**Rajmohan Sharma, Abhishek Baghel, Mujahida Sayyed and Rajkishor Bhatnagar**

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### Abstract

In the present study, 30 chickpea genotypes were assessed for various genetic parameters. Observations were recorded on phenological traits, including days to flower initiation and days to maturity, as well as nine quantitative traits: plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). The analysis of variance for all the characters revealed significant differences among the genotypes. This indicates the presence of a substantial amount of genetic variability among the genotypes under study.

**Keywords:** Assessed, analysis, presence

### Introduction

Chickpea (*Cicer arietinum* L.) is an important legume crop belonging to the family Leguminosae (Fabaceae). Globally, its cultivation spans 13.71 million hectares, with a production of 14.24 million metric tons and a productivity of 1038.4 kg/ha (FAO, 2019). In India, chickpea is grown over 10.17 million hectares, yielding a total production of 1.35 million metric tons and a productivity of 1116 kg/ha. As the largest producer worldwide, India contributes significantly to the annual global production of 162.25 million metric tons from an area of 149.66 million hectares, with a productivity of 1252 kg/ha (Anonymous, 2019-20).

Madhya Pradesh takes the lead in chickpea cultivation, contributing an area of 1.92 million hectares, a production of 2.48 million metric tons, and a productivity of 1288 kg/ha. Despite breeding efforts that have improved chickpea yield, ensuring stable production remains a major concern for widespread adoption by farmers. Susceptibility to various biotic and abiotic stresses, including fungal diseases (such as Vascular wilt), pests (like pod borer), and drought or cold stress, poses significant challenges. *Fusarium* wilt, caused by *Fusarium oxysporum* f. sp. *ciceris* (Foc), is a prevalent soil-borne fungus affecting chickpeas globally. The Gram pod borer, *Helicoverpa armigera* (Lepidoptera: Noctuidae), stands out as the primary pest, causing substantial yield losses ranging from 26.0% to 40.1% (Sarwar, 2013) [4]. Developing crop cultivars resistant to pod borer is considered a cost-effective and eco-friendly approach, holding great promise for *Helicoverpa* management.

Assessing genetic variability, heritability, and genetic advance percentage of mean provides valuable insights into the potential genetic gains through selection. A critical analysis of these parameters for various economically important traits is a prerequisite for plant breeders involved in crop improvement programs. With this objective, the present experiment was conducted to study genetic parameters in different chickpea genotypes under vindhya plateau region of Madhya Pradesh.

### Materials and Methods

The present investigation was conducted during the rabi season of 2020 at the Instructional Farm of the College of Agriculture, Ganjbasoda, situated in the Vidisha district of Madhya Pradesh, falling within the Malwa and Vindhyan Plateau agro-climatic zone.

The experimental materials for the study included 30 genotypes of chickpea (*Cicer arietinum* L.), selected based on different genetic and geographical origins.

Ganjbasoda's climate, located in Vidisha, is characterized by hot summers and overall dry conditions, except during the southwest monsoon season. The district typically receives 1135.5 mm of normal rainfall, with the maximum occurring during the southwest monsoon period. Approximately 91.4% of the annual rainfall is received during the monsoon season, while only 8.6% occurs from October to May. The experimental material was sown in three replications using a randomized block design during the *rabi* season of 2020. The plot size was 3.0 x 2.25 m, and a spacing of 22.5 x 7.5 cm was maintained. Observations were recorded for various traits, including days to 50% flowering, days to first pod initiation, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, height of the first fruiting node (cm), stem thickness (mm), number of effective pods per plant, 100-seed weight (g), biological yield (g), harvest index (%), and seed yield per plant (g). Data were recorded for five randomly selected plants from each replication.

### Results and Discussion

The analysis of variance was calculated for ten quantitative traits of chickpea. Significant differences among the genotypes were observed for all the characters, indicating the presence of a considerable amount of genetic variability among the studied genotypes. Table 1 presents the mean sum of squares values for the ten characters. The mean sum of squares due to genotypes was significant for all the ten characters, suggesting a substantial level of genetic variability among the studied genotypes. This implies a potential for selecting promising lines from the current gene pool for yield and its components, likely due to the diverse sources of materials considered.

In any crop improvement program, a detailed study of genetic variability is crucial. This involves estimating the mean, genotypic and phenotypic coefficients of variation. Table 2

provides estimates of variances, coefficients of variation, heritability, and genetic advance percentage of mean for all thirteen characters studied.

Phenotypic and genotypic coefficients of variation were computed to assess the nature and magnitude of existing variability in the experimental material. The highest phenotypic coefficient of variation (PCV) was recorded for the number of primary branches per plant, followed by height at the first fruiting node, grain yield, number of effective pods per plant, 100-seed weight, biological yield per plant, and number of secondary branches per plant. Moderate estimates of PCV were recorded for stem thickness, harvest index, and plant height, while the least estimates were for days to 50% flowering, days to maturity, and days to first pod initiation. Similar findings were reported by Nizam *et al.* (2013)

The highest genotypic coefficient of variation (GCV) was recorded for height at the first fruiting node, followed by grain yield, number of effective pods per plant, 100-seed weight, and biological yield per plant. Moderate estimates of GCV were recorded for stem thickness, harvest index, plant height, and number of secondary branches per plant. The least estimates of GCV were for days to 50% flowering, days to maturity, days to first pod initiation, and number of primary branches per plant. Similar findings were reported by Babbar and Tiwari (2018) <sup>[1]</sup>,

The highest heritability was recorded for biological yield per plant, number of effective pods per plant, days to maturity, height at first fruiting node, plant height, days to first pod initiation, stem thickness, 100 seed weight, grain yield per plant, days to 50% flowering, number of secondary branches per plant, number of primary branches per plant harvest index. The higher genetic advance recorded for height at fruiting node followed by no of effective pods per plant, grain yield, biological yield per plant, 100 seed weight, stem thickness, secondary branches per plant, plant height.

The high heritability coupled with high genetic advance as percentage of mean was recorded for height of first fruiting node, number of effective pod per plant, grain yield per plant, biological yield per plant and 100 seed weight.

**Table 1:** Mean sum of squares Grain Yield / plant (g) and its components

| Source of variation | D.F | Days to 50% flowering | Days to first pod initiation | Days to maturity | Plant height (cm) | No. of primary branches per plant | No. of secondary branches per plant | Height of first fruiting node | Stem thickness | No. of effective pods per plant | 100 seed weight | Harvest Index (%) | Biological yield/ plant (g) | Grain Yield / plant (g) |
|---------------------|-----|-----------------------|------------------------------|------------------|-------------------|-----------------------------------|-------------------------------------|-------------------------------|----------------|---------------------------------|-----------------|-------------------|-----------------------------|-------------------------|
| Replications        | 2   | 2.40                  | 1.06                         | 12.15            | 5.25              | 1.05                              | 7.08                                | 4.050                         | 1.098          | 2.0166                          | 2.666           | 118.84            | 75.062                      | 1.727                   |
| Treatments          | 29  | 30.10*                | 40.13*                       | 160.67**         | 42.39*            | 28.15**                           | 6.24**                              | 33.01**                       | 0.459*         | 694.747*                        | 45.921*         | 65.894*           | 64.031**                    | 15.655*                 |
| Error               | 58  | 31.71                 | 1.65                         | 1.80             | 1.44              | 1.012                             | 0.86                                | 0.691                         | 0.656          | 2.223                           | 2.839           | 22.009            | 0.290                       | 1.222                   |

\*, \*\* Significant at 5% and 1% level of probability, respectively

**Table 2:** Parameters of genetic variability for grain yield and its attributing traits

| S. No. | Character                           | PCV   | GCV   | h <sup>2</sup> (bs) % | GA as % of mean |
|--------|-------------------------------------|-------|-------|-----------------------|-----------------|
| 1.     | Days to 50% flowering               | 5.92  | 5.54  | 87                    | 10.69           |
| 2.     | Days to first pod initiation        | 6.44  | 6.30  | 95                    | 12.72           |
| 3.     | Days to maturity                    | 7.71  | 7.66  | 98                    | 15.70           |
| 4.     | Plant height (cm)                   | 12.22 | 12.01 | 96                    | 24.33           |
| 5.     | No. of primary branches per plant   | 26.28 | 5.42  | 81                    | 9.93            |
| 6.     | No. of secondary branches per plant | 20.84 | 19.34 | 86                    | 36.97           |
| 7.     | Height of first fruiting node       | 26.22 | 25.94 | 97                    | 52.88           |
| 8.     | Stem thickness                      | 18.41 | 17.95 | 95                    | 36.05           |
| 9.     | No. of effective pods per plant     | 23.70 | 23.66 | 99                    | 48.68           |
| 10.    | 100 seed weight                     | 21.23 | 20.56 | 93                    | 41.03           |
| 11.    | Harvest Index (%)                   | 13.93 | 10.92 | 66                    | 18.37           |
| 12.    | Biological yield/ plant (g)         | 20.96 | 20.92 | 99                    | 42.99           |
| 13.    | Grain Yield / plant(g)              | 24.30 | 23.41 | 92                    | 46.47           |

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h<sup>2</sup> (bs) = Heritability (broad sense), GA= Genetic advance as percentage of mean 5%

### Conclusion

The analysis of variance for all the characters revealed significant differences among the genotypes, indicating the presence of a substantial amount of genetic variability in the studied genotypes. The genotype with the earliest maturity was Phule G 0-714 (102.50 days), while late maturity was registered for BGD-1063 (131.00 days). The highest magnitude of phenotypic coefficient of variation (PCV) was recorded for the number of primary branches per plant, followed by height at the first fruiting node, grain yield, number of effective pods per plant, 100-seed weight, biological yield per plant, and the number of secondary branches per plant. The higher magnitude of genotypic coefficient of variation (GCV) was recorded for height at the first fruiting node, followed by grain yield, number of effective pods per plant, 100-seed weight, and biological yield per plant.

Traits like height of first fruiting node, number of effective pod per plant, grain yield per plant, biological yield per plant and 100 seed weight showed high heritability coupled with high genetic advance as percentage of mean. These characters showed substantial contribution of additive gene action for their phenotypic expression. They can be further improved by direct selection for these characters.

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