



Genetic variability studies for yield and agronomic traits in chickpea (*Cicer arietinum* L.) reference set

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ABSTRACT

The improvement in chickpea productivity depends upon the magnitude of genetic variability available in the breeding material. Thus, the present investigation was carried out with chickpea reference set (280 genotypes) to study variability present for yield and agronomic traits, viz., days to first flowering, days to 50% flowering, days to first podding, days to maturity, plant height, number of pods per plant, 100 seed weight, seed yield, and harvest index. The germplasm was evaluated in an alpha lattice design with three replications at the Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India, during rabi 2022-23 and 2023-24. For nine characters GCV, PCV, heritability, and genetic advance as a per cent of the mean were analysed to understand the magnitude of genetic variability in reference set. High values of PCV and GCV were observed for 100SW, NPP, SY, and HI. High heritability and genetic advance were observed for the traits DFF, DFPE, PH, 100SW, NPP, and HI highlighting their responsiveness to selection and their contribution to yield improvement in breeding programs. This study underscores the potential of genetic variability as a foundation for enhancing yield-related traits in chickpea. Traits with moderate heritability, such as seed yield, suggest that yield improvement may benefit from indirect selection through associated stable traits with higher heritability. A combination of traits with high heritability coupled with high genetic advance can be used as a selection index for the improvement of chickpea productivity.

Key words: Chickpea, Heritability, Genetic advance and Seed yield

Chickpea (*Cicer arietinum* L.) is a self-pollinated annual legume with a genome size of approximately 738 Mb (Varshney *et al.*, 2013). It is a rabi season crop, primarily cultivated by marginal farmers in arid and semi-arid regions, and plays a significant role in global food security, particularly in Asia and Africa, by providing a valuable source of dietary protein. Additionally, chickpea contributes to sustainable agriculture through biological nitrogen fixation, thereby enhancing soil fertility. It originated in Southeastern Turkey and has since spread to India, Ethiopia, and other regions (Mohsenzadeh, 2024). Currently, India is the world's leading producer, accounting for over 70% of global chickpea production but far low in productivity form the other nations.

The self-pollinating nature of chickpea, coupled with a lack of sufficient genetic variation among existing cultivars, makes it vulnerable to a range

of environmental stresses and pests, thereby limiting production potential (Parameshwarappa *et al.*, 2011 and Gaur *et al.*, 2012). Centuries of domestication, intensive selection, and modern breeding practices have inadvertently reduced genetic variability, making chickpea a genetically depauperate flora (Roorkiwal *et al.*, 2013). This narrow genetic base among adapted genotypes limits the potential for increasing chickpea production and yield. To address this challenge, identifying novel sources of genetic variation in economically important traits is crucial. A comprehensive understanding of genetic variability within germplasm is essential for effective selection and breeding strategies to enhance chickpea grain yield.

Understanding genetic variability is a cornerstone of chickpea breeding programs aimed at improving grain yield. Genetic variation, often

quantified using coefficients of variation, reflects the potential for genetic improvement in specific traits. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) provide a comparative measure for genetic diversity and the impact of environmental factors on trait expression (Tadesse *et al.*, 2016). Heritability, which estimates the proportion of phenotypic variation attributable to genetic factors, combined with genetic advance, enables precise prediction of selection response. By partitioning total phenotypic variance into genetic and environmental components, breeders can develop more effective strategies to capitalize on genetic potential. These statistical parameters are particularly important for quantitative traits like yield components, which are susceptible to environmental influences. Thus, a diverse germplasm set explored from various geographic regions of the world was analysed for variability and heritability for yield and yield contributing traits.

MATERIAL AND METHODS

The experimental material comprised of 280 chickpea genotypes was sourced from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. These genotypes were evaluated over two consecutive rabi seasons (2022-23 and 2023-24) at the Regional Agricultural Research Station, Nandyal, Andhra Pradesh, India. The site of the experiment represents typical chickpea growing tract in Scarce Rainfall Zone of Andhra Pradesh. The experimental design employed was an alpha lattice design with three replications. Each genotype was sown in a single row of 3-meter-long, maintaining a row-to-row distance of 30 cm and a plant-to-plant distance of 10 cm. Standard agronomic practices were followed to ensure optimal crop growth and development.

Data were recorded on nine yield and agronomic traits *viz.*, Days to first flowering (DFF), Days to 50% flowering (DFPF), Days to first podding (DFP), Days to maturity (DM), Plant height (cm) (PH), Number of pods per plant (NPP), 100 seed weight (g) (SW), Seed yield (g) (SY) and Harvest index (%) (HI). For the traits DFF, DFPF, DFP, DM and 100SW data were recorded from the date of sowing on total plant basis in each accession in each replication, separately. Field data pertaining to the remaining traits were recorded on five randomly selected plants from each accession.

Pooled mean values of each trait across both seasons were used for statistical analysis. Genotypic and phenotypic coefficients of variation were estimated using the method described by Sivasubramanian and Madhavamenon (1973) and categorized as low (0-10%), medium (10-20%), and high (>20%) according to Burton (1952). Broad-sense heritability (h^2_b) was estimated for each trait using Lush (1940) method and classified as low (<30%), medium (30-60%), and high (>60%) according to Johnson *et al.* (1955). Genetic advance as a percentage of the mean (GAM) was calculated using the method proposed by Johnson *et al.* (1955) and categorized as low (0-10%), medium (11-20%), and high (>20%).

RESULTS AND DISCUSSION

To enhance chickpea productivity, understanding genetic variability is crucial for the informed breeding strategies. Key genetic parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) assess the extent to which genetic and environmental factors influence trait expression. High heritability combined with substantial genetic advance as a percentage of the mean (GAM) indicates the traits are primarily controlled by genetic factors and maximize the response to selection. These parameters collectively guide breeders in identifying traits that can reliably contribute to yield improvement and disease resistance, laying the groundwork for effective breeding programs focused on sustainable chickpea production.

The critical examination of 280 chickpea germplasm lines for nine yield and agronomic traits exhibited varying degrees of variability, heritability, genetic advance and favourable mean performance providing insights into their potential for selection (Table 1 and Figure 1).

High values of variability (PCV and GCV) with greater estimates of PCV were observed for 100SW, NPP, SY, and HI. This indicates that both genetic and environmental factors significantly influence these traits (Bharadwaj *et al.*, 2011). While genetic factors play a major role, environmental conditions also have a substantial impact. Despite this influence, the high genetic variability offers promising potential for improvement through selective breeding. To maximize the benefits of genetic potential, efforts

Table 1. Mean, range, variability, heritability and genetic advance as per cent of mean for yield and agronomic traits in 280 chickpea germplasm accessions

Traits	Mean	Range		GCV (%)	PCV (%)	h ² (%)	GAM (%)
		Maximum	Minimum				
DFE	54	36	70	11.45	12.8	80.01	21.06
DFPF	59	42	78	11.24	12.57	79.88	20.65
DFP	62	43	78	10.08	11.31	79.37	18.46
DM	101	82	117	8.06	8.29	94.62	16.12
PH	43	29	66	13.32	14.37	85.93	25.39
100SW	20.6	11.2	47.9	36.52	37.07	97.07	73.98
NPP	25	3	60	21.81	27.26	64.02	35.88
SY	5.7	1	12.2	23.59	37.56	39.45	30.46
HI	33	5	68	34.09	42.96	62.97	55.62

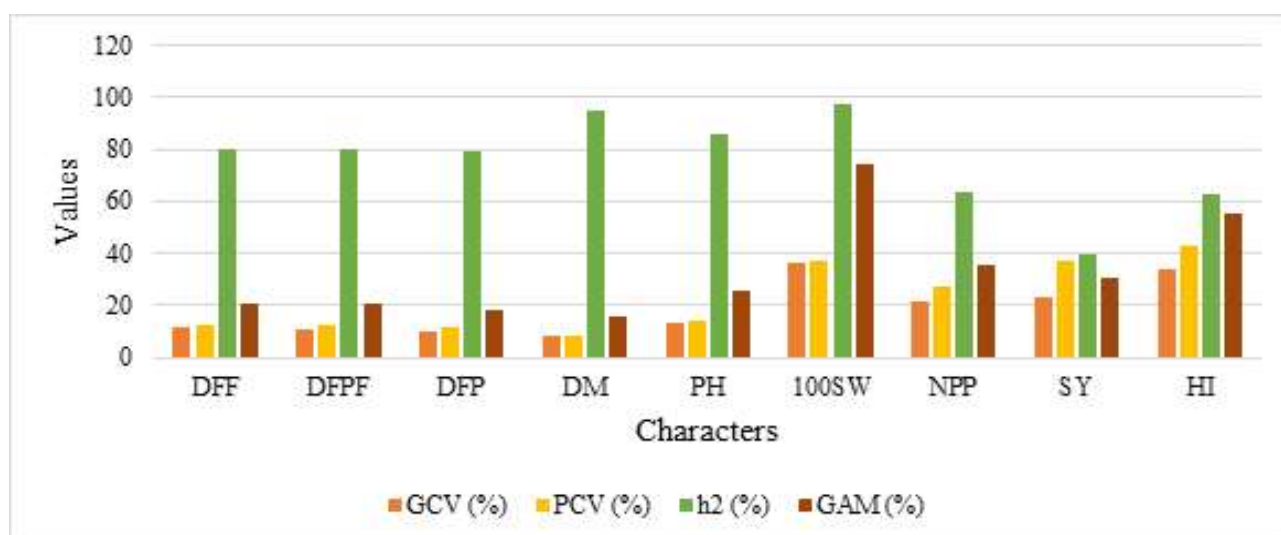


Figure 1. Pattern of GCV, PCV, Heritability and Genetic advance as per cent of mean (GAM) for yield and agronomic traits in chickpea reference set

should be directed towards stabilizing environmental conditions. By selecting superior genotypes, breeders can make significant strides in enhancing these traits. Moderate values of PCV and GCV were observed for DFE, DFPF, DFP, and PH. While PCV values were slightly higher than GCV values and the difference was minimal, suggesting a limited influence of the environment. Therefore, selection based on phenotypic observations is likely to be effective for most of these characters. Low PCV and GCV values were observed for DM, suggesting that the trait is relatively stable with minimal influence from both genetic and environmental factors. The limited variability may indicate that the trait has either reached a selection

plateau or recessive to the limiting environment. These findings are in agreement with Yadav *et al.* (2015), Jayalakshmi *et al.* (2019), Jayalakshmi *et al.* (2022), Balpande *et al.* (2022), Karthikeyan *et al.* (2022), Mihoariya *et al.* (2023), Ningwal *et al.* (2023), and Itana *et al.* (2024).

High heritability estimates were observed for all agronomic traits, indicating that the variation in these traits is attributed to genetic differences among individuals. However, seed yield exhibited moderate heritability, suggested that both genetic and environmental factors play roles in influencing this trait. Moderate genetic advance was reported for DFP and DM, indicating a reasonable response to selection

for these traits. High genetic advance as a percentage of the mean was observed for DFF, DFPP, 100SW, NPP, SY and HI, suggesting that these traits are highly responsive to selection. Significant genetic gains can be achieved through simple selection for these traits. Velpula and Gaibriyal (2022) and Ningwal *et al.* (2023) also reported similar results in chickpea.

The traits, DFF, DFPP, PH, 100SW, NPP and HI reported high heritability and high GAM. This combination indicated that maximum genetic gain can be made through selective breeding as these traits may be governed by additive gene action. The traits, DFP and DM, reported high heritability and moderate GAM, indicated that these traits are largely controlled by genetic factors but shows a moderate response to selection. Whereas, SY reported moderate heritability and high GAM, indicated that the trait is influenced by both genetic and environmental factors, yet it shows high response to selection. However, the high response to selection may be due to specific environmental conditions or management practices amplifying the genetic response, making direct selection challenging. Previous studies by Balpande *et al.* (2022), Karthikeyan *et al.* (2022) and Ningwal *et al.* (2023) are aligned with the above results in chickpea.

CONCLUSION

This study highlights the potential of genetic variability to enhance yield-related traits in chickpea. For most traits, phenotypic coefficient of variation (PCV) was larger than genotypic coefficient of variation (GCV) indicating significant environmental influence on trait expression. High heritability and high genetic advance was noted for key traits (DFF, DFPP, PH, 100SW, NPP and HI), indicating their genetic stability and responsiveness to selection, making them ideal targets for breeding programs. Traits with moderate heritability, such as SY, may benefit from indirect selection through associated stable traits with higher heritability. The substantial genetic advance in these key traits affirms the feasibility of improving yield, a critical factor for sustainable chickpea production, especially in regions with limited rainfall. This research provides a foundation for developing chickpea cultivars with stable yields, contributing to long-term sustainability in chickpea production systems.

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