Correlation Studies and Diversity Analysis in Chickpea (*Cicer arietinum* L.) Cultivars for Seed Yield and Associated Traits

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ABSTRACT

The present investigation was carried out at Agriculture Research Sub-station, Sumerpur. In the study six popular cultivars of chickpea were under consideration. The correlation study elucidated that seed yield has positive and highly significant correlation with number of primary branches per plant (0.96) and number of pods per plant (0.97) while none of the characters showed negative correlation with seed yield. Similarly, days to 50 % flowering showed positive and significant correlation with days to maturity (0.86) and plant height (0.82). The diversity among the varieties were studied using K-means and ward's method. Through both the methods it was observed that CSJ-515, GNG-2144 and GNG-1958 were clustered into one cluster (cluster I), RSG-974 and RSG-959 were clustered into another cluster (cluster-III) and GNG-2171 remained alone (cluster-II). This showed that both the clustering methods are in agreement with each other. In terms of yield cultivar CSJ-515 reported highest mean seed yield per plot (2.65) followed by GNG-2144 (2.41).

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an important *rabi* season pulse crop of India. It occupies a significant place in cropping systems of Rajasthan and western Rajasthan in particular. Being a rich source of protein, chickpea have major role in arid parts of Rajasthan for supplementing balanced human diets. Amongst all the pulse crops chickpea occupies first place in terms of production and area in India. Rajasthan, MP, Maharashtra, Gujarat, Telangana, Haryana, are the major states producing chickpea in India. Rajasthan holds third place amongst all the chickpea producing states and contributes nearly 21.00 lakh ha area for producing chickpea (DPD, GoI, Bhopal 2020-21). The developing countries share more than 95% of the area, production and consumption of chickpea. It is grown mainly in South East Asian countries with significant cultural, religious and nutritional value (Ahmad *et al.* 2012). Productivity of chickpea is less in India as compared to other countries due to its cultivation on marginal lands in our country. Low or lack of genetic variability is the root cause for the limited progress achieved in enhancing productivity of chickpea.

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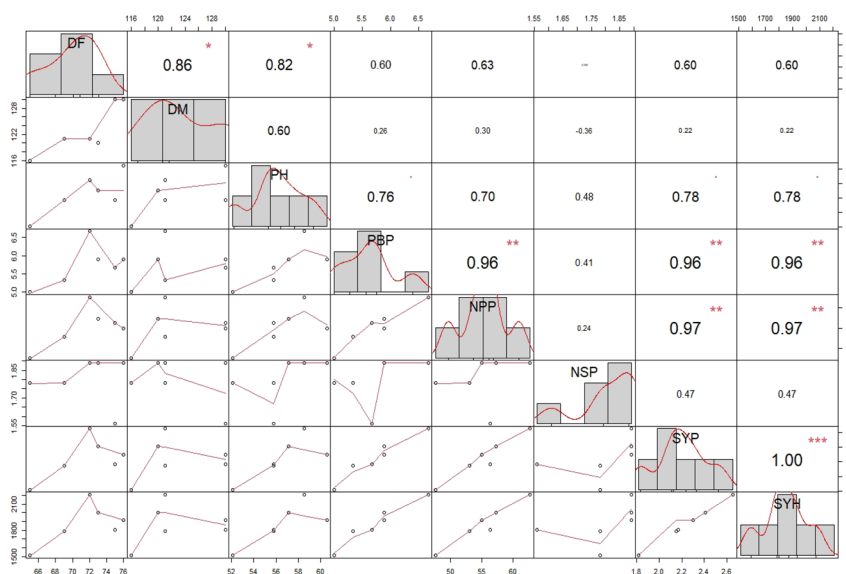ARSS-Sumerpur, Agriculture University, Jodhpur 306126, Rajasthan, India

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Graph 1. Depicting correlation among different traits.

Genetic variation among traits is important for breeding and selecting desirable types. On the other hand, an analysis of correlation between seed yield and yield components is essential in determining selection criteria.

Genetic diversity is the basis for survival of plants in nature and for crop improvement. Genetic divergence among the plants plays a vital role in cultivar improvement due to more variability in segregating generations, which can be exploited for improvement (Nimbalkar *et al.* 2017).

The purpose of this study was to estimate the genotypic variability, correlations and genetic diversi-ty among some important traits for assessing selection criteria for improving yield in chickpea.

MATERIALS AND METHODS

The experimental material involved six popular culti-vars of chickpea (CSJ-515, GNG-2144, GNG-2171, GNG-1958, RSG-974 and RSG-959) which were sown during *rabi* 2021-22 in a Randomized Block Design at experimental farm of agriculture research sub-station, Sumerpur. Observations were recorded on following parameters Table 1.

In order to determine the relationships between examined traits and seed yield per plot, correlation co-efficients were calculated using R-program. Similarly, genetic diversity amongst cultivars was estimated by Mahalanobis D^2 statistics (1936) and the genotypes were grouped into different clusters according to Ward's and K-means methods.

Table 1. Observations recorded.

Sl. No.	Observed parameters	Abbreviation
1	Days to 50% flowering	DF
2	Days to maturity	DM
3	Plant height (cm)	PH
4	Number of primary branches per plant	PBP
5	Number of pods per plant	NPP
6	Number of seeds per pod	NSP
7	Seed yield per plot/ hectare (kg)	SYP/SYH

Table 2. Clustering pattern of cultivars.

Cluster	Cultivars
I	CSJ-515, GNG-2144, GNG-1958
II	RSG-974, RSG-959
III	GNG-2171
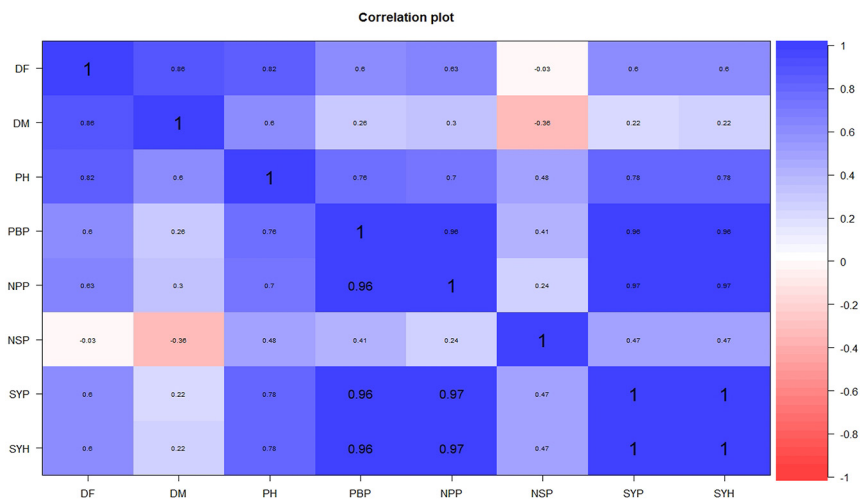
**Graph 2.** Correlation plot depicting correlation of different traits.

## RESULTS AND DISCUSSION

Correlation studies

The seed yield per plot exhibited highly significant and positive correlation with number of primary branches per plant (0.96) and number of pods per plant (0.97) indicating that any positive increase in such traits will enhance the seed yield per plot (Graphs 1–2). Results on similar lines were reported by Kanaka *et al.* (2007), Jivani *et al.* (2013), Aarif *et al.* (2014), Chopdar *et al.* (2017), Nitesh *et al.*

(2018) and Singh *et al.* (2022). Days to 50% flowering showed significant and positive correlation with days to maturity (0.86) and plant height (0.82) indicating that selecting earlier flowering cultivars will lead to timely maturity and availability of crop produce to farmers on time, saving time and space for those farmers who are looking for a crop in *zaid* season. These results were in accordance with Prakash (2013).

Similarly, number of pods per plant showed significant and positive correlation with primary branches per plant indicating that selecting lines
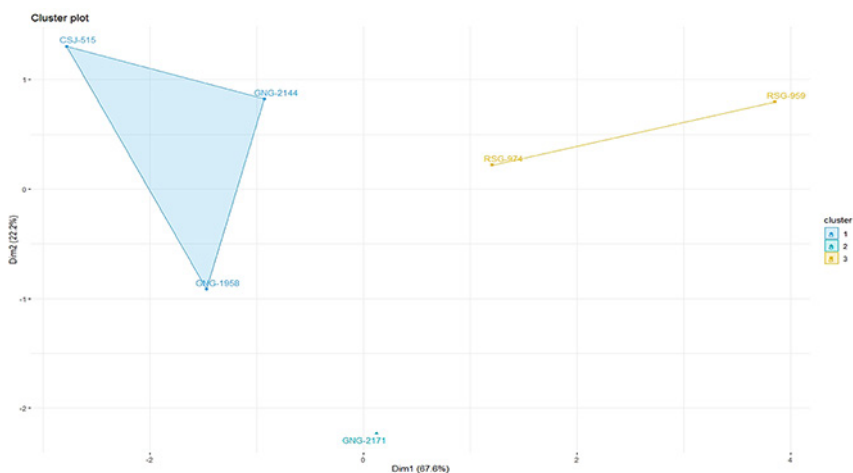
Graph 3. Depicting clustering of cultivars through K-means method.

Cluster Dendrogram
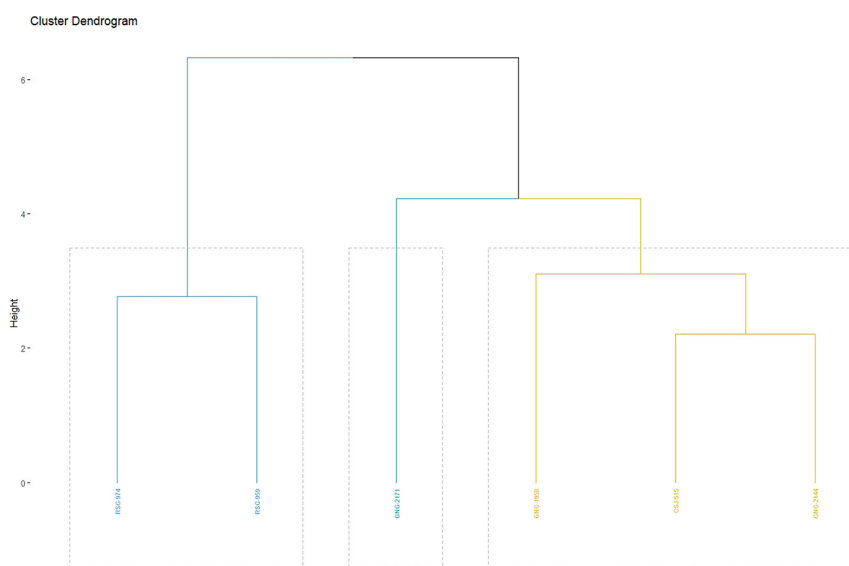
Graph 4. Depicting clustering of cultivars through Ward's method.

with higher branches will result into increased pods per plant and that will eventually leads to enhanced seed yield per plant. Similar results were reported by Nimbalkar *et al.* (2017), Thakur *et al.* (2009).

Diversity analysis

Diversity analysis among the chickpea cultivars was studied using K-means method and Ward's method of clustering. The purpose of using two different methods is to highlight discrepancy if any among the clustering pattern on utilizing different methods.

On observing clustering pattern (Table 2) through K-means method (Graph 3) cultivars CSJ-515, GNG-2144 and GNG-1958 came together in cluster-I, GNG-2171 remain sole entry in cluster-II while RSG-974 and RSG-959 were grouped in cluster-III. Clustering patterns on these lines were also reported by Tomar *et al.* (2011), Vijayakumar *et al.* (2017), Devendrappa *et al.* (2013), Balasaheb *et al.* (2018).

On analyzing all the cultivars again through Ward's method (Graph 4), as expected all the cultivars followed the same pattern of clustering indicating that both methods are in consonance with each other. Genotypes appearing in different clusters can be uti-

lized in hybridization for generating superior hybrids or for producing transgressive segregants. Similar suggestions were emphasized by Lad *et al.* (2022), Jayalakshmi *et al.* (2022).

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