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**RESEARCH PAPER**

# Genetic studies to identify climate resilient chickpea (*Cicer arietinum* L.) genotypes

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**Abstract:** The present investigation on deciphering the genetic variability in chickpea with the aim to isolate early genotypes with high productivity was carried out during *Rabi* 2020-21at College of Agriculture, Vijayapur. Seventy five genotypes inclusive of checks were evaluated under augmented design. Analysis of variation showed significant variation for most of the traits under consideration including phenological, seed and productivity traits. Estimates of GCV and PCV were high for number of primary branches, number of pods per plant, hundred seed weight and seed yield. Correlation studies showed positive and significant association of seed yield with number of pods per plant, plant height and hundred seed weight inferring scope of yield improvement through direct selection for these traits. Further, genetic diversity analysis, based on $D^2$ values, resulted into eight clusters with Cluster I being largest (47 genotypes) while five clusters (II, V, VI, VII and VIII) were solitary and highest inter cluster distance of 5095.17 was recorded between Cluster II and VIII. Cluster means were used for ranking the clusters and Cluster II was top ranked with score of 37 followed by Cluster VII (40). Principal component analysis revealed that about 80 per cent of the variability was contributed through phenological traits *viz*., flowering, podding and maturity. The promising genotypes for high productivity coupled with early maturity are need of the hour to enhance the chickpea production under changing climatic conditions. In the present study, several such potential early maturing genotypes with high productivity were isolated. The identified genotypes will be evaluated further and the best genotypes will be selected for advanced yield evaluation trials.

**Key words:** Chickpea, Cluster distance, Correlation, $D^2$ statistics, Diversity

## Introduction

Pulses are the prime group of crops and a wonderful boon of nature to the mankind, as they have deep root system, mobilize insoluble soil nutrients, restore soil fertility and bring qualitative changes in soil physical properties. Globally among the major pulse crops, chickpea (*Cicer arietinum* L.) accounts for 40 per cent of the production and it remains the largest produced pulse crop. Chickpea is the only cultivated species under the genus '*Cicer*'with 2n=2x=16 chromosomes and relatively small genome size of 738.09Mbp (Varshney *et al.,*2013). It belongs to the family *Fabaceae*, included in its subfamily *Papilionaceae*. The genus includes 43 species, among them, 9 are annual and 33 are perennial while one is unclassified. It is an important cool season grain legume with indeterminate growth habit and largely cultivated throughout tropical and sub-tropical regions of the world (Gaur *et al*., 2012) including Central-West Asia, Southern Europe, Ethiopia, North Africa and Australia.

Genetic variability is of utmost importance in breeding not only for yield improvement but also for conferring resistance to pest and disease and improved grain quality. In view of narrowing down of the genetic diversity due to several reasons including modernisation of crop impropvement, it is time to explore new sources of variation that might be used in plant breeding programmes. The genetic variability opens up the scope for selection based on the inheritance and heritability of the traits. Such studies also help in making wise decision regarding to attempt for creating new variability either through hybridization or through mutation. Diversity among the parents is a pre-requisite for ensuring the chance of improved segregate selection for various characters (Dwevedi and Gaibriyal, 2009). Assessment of the extent of genetic diversity is yet another important aspect of plant breeding based on which the parents for hybridization programme intended to improve target traits can be efficiently chosen. It also helps in the conservation of genetic resources.

Off late, climate change is posing several challenges to agriculture as a whole and specifically to the crops which are majorly grown as rainfed, due to seasonal changes, erratic and unevenly distribution of rains. This necessitates identifying the genotypes which can combat the threats posed by climate change through several means like early maturity, drought tolerance, tolerance to biotic stresses, and adaptation to the seasonal changes and so on. To identify such genotypes, it is required to study the genetic variability in the population so as to make a well informed decision of selection and evaluation. If appreciable amount of variability for the desired traits exists in the population, it opens up the opportunities for selection of superior genotypes. Although the cultivated area of chickpea in India is vast, the productivity of legumes in general and chickpea in particular have remained stagnant over the years (Merga and Haji, 2019). Therefore the information about the nature and magnitude of genetic divergence is essential, this in turn helps in identification of diverse parents. Plant breeders can use the diversity of plant genetic resources to create new and better cultivars with desirable features.

## Material and methods

The genetic material for the present study consisted of seventy five chickpea genotypes including Multiparent

Advanced Generation Intercross (MAGIC) derived lines, advanced breeding lines and released varieties as checks. The experiment was conducted during *Rabi* 2020-21 in I block of Regional Agricultural Research Station (RARS) in Vijayapur campus of University of Agricultural Sciences, Dharwad, situated in northern dry zone (Zone-3) of Karnataka between 16°46'N latitude and 75°45'E longitude with an altitude of 595 meters above mean sea level (MSL). The experiment was laid out in augmented block design having four blocks with five checks repeated in each block with plot size of 1.2 square meters. Observations on morphological, phenological and productivity traits were recorded on five randomly selected plants from each genotype *viz.,* days to initiation of first flower, days to 50 per cent flowering, initiation of first pod, days to 50 per cent podding, days to maturity, number of primary branches per plant, number of secondary branches, plant height (cm), number of pods per plant, number of seeds per pod, hundred seed weight (g) and seed yield per plant (g). The data were analysed using "R" platform. Along with analysis of variance, correlation coefficient and genetic divergence, using Mahalanobis (1936) D$^2$statistics, were estimated. Further, clustering of the genotypes was done according to Tocher's method as described by Rao (1952).

## Results and discussion

The analysis of variance showed significant difference for most of the traits considered in the study, including important phenological traits, like days to 50 per cent flowering, days to first pod initiation, days to maturity, number of primary branches per plant and number of secondary branches per plant and seed traits *viz.* number of pods per plant, hundred seed weight and seed yield per plant (Table 1).

As analysis of variance indicated presence of significant variability for quantitative characters studied, the variability in the genetic material was considered for further analysis. Range and mean with other descriptive statistics and details on genetic parameters *viz*., phenotypic and genotypic coefficient of variation, heritability estimates and predicted genetic advance as per cent of mean for the traits were determined (Table2).

The days for initiation of first flower ranged between 28 and 54 days with a mean of 37.76 days. The trait exhibited GCV (9.79%) and PCV (14.87%) with moderate heritability (43.29 %) and moderate genetic advance of 13.28 per cent. Days to 50 per cent flowering showed a mean of 46.87 days ranging between 37 and 72 days. The trait exhibited moderate GCV (15.15%) and PCV (15.59%) while GA and high heritability (94.43%) coupled with moderate GA (14.24%). Days to first pod initiation showed a wide range from 36 to 68 days with a mean of 48.64 days. GCV, PCV, GA were observed to be moderate with 10.20 per cent, 12.87 per cent and 8.11 per cent respectively, whereas the trait exhibited high heritability of 62.76 per cent and moderate genetic advance of 16.66 per cent. Days to 50 per cent pod setting showed a range between 46 and 81 days with a mean of 56.19 days. Estimates of GCV (8.96%), PCV (12.21%), GA (7.61) and GAM (13.55) were recorded to be moderate for the trait and with moderate heritability (53.80%). Days to maturity ranged

Table 1. Analysis of variance of quantitative traits in chickpea genotypes

| Source | df | DFF | DFPF | DFP | DFPS | DM | PH | NPB | NSB | NPPP | NSPP | HSW | SYPP | YQHA |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Block (Eliminating Treatments) | 3 | 30.72 ns | 7.20 ns | 35.80 ns | 39.53 ns | 2.98 ns | 0.19 ns | 0.05 ns | 0.15ns | 0.45 ns | 0.002ns | 0.63ns | 0.54 ns | 5.96 ns |
| Treatment (Ignoring Blocks) | 74 | 33.18ns | 57.35$^{**}$ | 42.66$^{*}$ | 47.02ns | 48.50$^{**}$ | 10.74$^{**}$ | 2.80$^{**}$ | 1.10$^{**}$ | 277.05$^{**}$ | 0.03$^{**}$ | 38.15$^{**}$ | 6.05$^{**}$ | 67.23$^{**}$ |
| Treatment: Check | 4 | 63.05$^{*}$ | 136.18$^{**}$ | 96.43$^{**}$ | 55.87ns | 90.17$^{**}$ | 11.12$^{**}$ | 5.69$^{**}$ | 2.14$^{**}$ | 5.58$^{*}$ | 0.002ns | 17.27$^{**}$ | 12.75$^{**}$ | 141.63$^{**}$ |
| Treatment: Test | 69 | 31.53ns | 53.40$^{**}$ | 39.19$^{*}$ | 47.06ns | 39.18$^{**}$ | 10.62$^{**}$ | 1.91$^{**}$ | 0.91$^{**}$ | 145.55$^{**}$ | 0.03$^{**}$ | 34.96$^{**}$ | 5.44$^{**}$ | 60.43$^{**}$ |
| Treatment: Test and Test vs. Check | 70 | 26.25ns | 45.20$^{**}$ | 32.53ns | 39.16ns | 40.54$^{**}$ | 9.89$^{**}$ | 2.57$^{**}$ | 0.79$^{**}$ | 291.89$^{**}$ | 0.03$^{**}$ | 34.67 | 5.13$^{**}$ | 56.97$^{**}$ |
| Treatment: Test vs. Check | 1 | 27.16ns | 14.90$^{*}$ | 67.67ns | 8.92ns | 524.58$^{**}$ | 17.88$^{**}$ | 52.55$^{**}$ | 9.59$^{**}$ | 10436.42$^{**}$ | 0.01ns | 342.19$^{**}$ | 21.46$^{**}$ | 238.46$^{**}$ |
| Error | 12 | 17.88 | 2.97 | 14.59 | 21.74 | 3.28 | 0.27 | 0.15 | 0.09 | 1.25 | 0.002 | 3.19 | 0.37 | 4.11 |

ns $P > 0.05$; $^{*}P <= 0.05$; $^{**}P <= 0.01$

| | | | |
|---|---|---|---|
| DFF: Days to first flowering | DFPF: Days to 50per cent flowering | DFP: Days to first podding | DFPS: Days to 50 per cent pod setting |
| DM: Days to maturity | PH: Plant Height per Plant | NPB: Number of primary branches | NSB: Number of secondary branches |
| NPPP: Number of pods per plant | NSPP: Number of seeds per pod | HSW: Hundred seed weightS | YPP: Seed yield per plant |

Table 2. Genetic parameters for the twelve traits studied

| Trait | Mean | Min. | Max. | GCV (%) | PCV (%) | $h^2$(BS) | GA (%) | GAM (%) |
|---|---|---|---|---|---|---|---|---|
| Days to first flowering | 37.76 | 28.35 | 53.55 | 9.79 | 14.87 | 43.29 | 5.01 | 13.28 |
| Days to 50 per cent flowering | 46.87 | 37.35 | 72.35 | 15.15 | 15.59 | 94.43 | 14.24 | 30.37 |
| Days to first podding | 48.64 | 35.50 | 68.30 | 10.20 | 12.87 | 62.76 | 8.11 | 16.66 |
| Days to 50 per cent pod setting | 56.19 | 46.10 | 80.90 | 8.96 | 12.21 | 53.80 | 7.61 | 13.55 |
| Days to maturity | 93.13 | 80.15 | 104.50 | 6.43 | 6.72 | 91.64 | 11.83 | 12.71 |
| Plant height | 34.27 | 27.66 | 43.66 | 9.39 | 9.51 | 97.48 | 6.55 | 19.12 |
| Number of primary branches | 5.24 | 2.31 | 8.55 | 25.33 | 26.36 | 92.35 | 2.63 | 50.21 |
| Number of secondary branches | 9.54 | 7.84 | 12.44 | 9.54 | 10.02 | 90.67 | 1.79 | 18.74 |
| Number of pods per plant | 39.49 | 14.61 | 64.94 | 30.42 | 30.55 | 99.14 | 24.68 | 62.49 |
| Number of seeds per pod | 1.03 | 0.97 | 2.01 | 15.75 | 16.34 | 92.90 | 0.32 | 31.31 |
| Hundred seed weight | 25.93 | 12.67 | 41.28 | 21.73 | 22.80 | 90.88 | 11.08 | 42.74 |
| Seed yield per plant | 7.75 | 1.62 | 12.59 | 29.04 | 30.08 | 93.19 | 4.48 | 57.83 |

between from 80 and 104 days with a mean of 93.13 days. Estimates of GCV (6.43%) and PCV (6.72%) were low. High heritability of 91.64 per cent with moderate GA (11.83%) was recorded. Mean plant height of the genotypes was 34.27 cm with a minimum being 27.66 and maximum of 43.66cm. Low GCV (9.39%) and PCV (9.51) were recorded for the trait. The heritability was found to be high (97.48%) whereas low GA of 6.55 per cent was noticed. Several researchers, including Ojha *et al*., (2010), found high phenotypic and genotypic coefficients of variation for 100 seed weight, followed by pods per plant, with low estimates of coefficients of variation for days to maturity and days to 50 per cent flowering. High GCV and PCV for 100 seed weight, seed yield, and plant height were also found in another study by Kumar *et al*. (2012), showing a large genetic basis and genetic variability for these characteristics in chickpea. The findings of the current study indicate the appreciable extent of genetic variability and scope for improving desirable and targeted phenological characteristics. Wide range for days to maturity, an important trait to be considered while breeding for the genotypes resilient to climate change specially to suit into delayed or late sown windows, existing in the genetic material used might be effectively utilized through appropriate breeding strategies to achieve significant genetic gain. The genotypes which can mature early without significant compromise on yield are in fact need of the hour. Significant genetic variability was recorded for days to flowering, days to maturity, plant height, pods per plant, biological yield and harvest index by Malik *et al*. (2014).

Number of primary branches varied between 2.31 and 8.55 with an average of 5.24. The trait exhibited high GCV and PCV of 25.33 per cent and 26.36 per cent respectively. High heritability of 92.35 per cent with low GA of 2.63 per cent was recorded. The mean number of secondary branches was 9.54 with a minimum of 7.84 and maximum 12.44. Low GCV (9.54%) and moderate PCV (10.02%) were observed for the trait along with high heritability (90.67%) and low GA (1.79%). Wide range of 14.61 to 64.94 was recorded for number of pods per plant with an average of 39.49. It exhibited high genotypic (30.42%) and phenotypic (30.55%) coefficient of variances. High heritability of 99.14 per cent coupled with high GA (24.68%) was evident for the trait. Seeds per pod varied from 0.97 to 2.01 with a mean of 1.03. Moderate GCV (15.75%) and PCV (16.34%) with high heritability (92.90%) and low GA (0.32%) were recorded. A wide range of 12.67 g to 41.28 g was observed for hundred seed weight with a mean of 25.93 g. Both GCV (21.73%), PCV (22.80%) estimates and heritability (90.88%) were found to be high while moderate genetic advance of 11.08 per cent was noticed. A significant variability for seed yield per plant was observed with a wide range of 1.62 g to 12.59 g with average yield per plant of 7.75 g. Further, the trait exhibited high GCV of 29.04 per cent and high PCV of 30.08 per cent, high heritability of 93.19 per cent coupled with low GA of 4.48 per cent.

The $D^2$ analysis was carried out using all the traits of the study and generalized distance ($D^2$) was calculated for each pair of genotypes in all possible combinations. The method suggested by Tocher (Rao, 1952) was employed to group the genotypes into different clusters. In present study 75 genotypes were grouped into eight clusters (Table 3). It is also important to decipher the information on the trait contributing to the diversity. The data on per cent contribution of various characters under study to the diversity showed maximum contribution by number of pods per plant (16.69%) followed by seed yield per plant (14.7%), 100 seed weight (8.47%), fifty per cent flowering (7.78%), days to maturity (6.52%), fifty per cent podding (5.12%), initiation of first flower (3.90%), initiation of first pod (3.46%), plant height (1.55%), secondary branches (1.32%), primary branches (1.09%) and seeds per pod (0.19%). Similar studies on genetic diversity wherein clustering of the genotypes was done and useful information on genotypes and superior clusters was reported by Jakhar *et al.* (2016).

Among the eight clusters formed, intra cluster distance was found to be zero in clusters II V VI VII and VIII as the clusters were solitary in nature. Maximum distance among the genotypes within the same clusters (Intra cluster) was recorded in Cluster IV (566.39) followed by Cluster I (463.32). The inter cluster distance varied from 185.77 to 5095.17 and maximum inter cluster distance of 5095.17 was found between Cluster II and VIII whereas, lowest inter cluster distance was noticed between Cluster V and VI (185.77) as presented in Table 4.

The cluster means of 12 characters and overall score across all the clusters are presented in the Table 5. Based on the scores of individual trait means across clusters, Cluster II found to be top ranked with score of 37 and Cluster VII was ranked second

Table 3. Grouping of chickpea genotypes based on $D^2$ analysis

| Cluster number | Number of genotypes | Name of genotypes |
|---|---|---|
| I | 47 | BGD 9132, BGD 9130, ICCV 04502, ICCV 93954, ICC 14672, ICC 5853, ICC 16340, ICCV 92944, ICRISAT 3155, ICCV 05107, S3-3, PUSA 261, ICC 11680, ICC 9023, ICC 14350, L.C – 1, ICC 10301, ICC 5988, DG 5033, ICC 03112, ICC 96029, M – 113, M – 27, M – 97, M – 70, M – 71, M – 112, M – 50, M – 111, M – 103, M – 65, ICC 4958, ICCV 2, ICC 5912, ICC 16641, DIBG 205, DIBG 207, DIBG 208, GJG 0205, ICCV 191151, ICCV 191153, ICCV 191155, ICCV 191156, ICCV 191157, ICCV 191158, ICCV 191159, ICCV 191259. |
| II | 1 | BGD 223-1 |
| III | 13 | BGD 9123, BGD 7050, BGD 7047, JG-11(C), BGD 111-1 (C), JAKI 9218 (C), ANNIGERI 1 (C), BGD 7041, BGD 7057, BGD 103, M-84, ICCV 191160, ICCV 191161. |
| IV | 10 | ICC 12346, BGD 212, ICC 92809, ICCV 191154, ICC 10910, BGD 121, ICC 5003, ICC 12288, ICCV 191152, JG 16 |
| V | 1 | DIBG 203 |
| VI | 1 | GL 12003 |
| VII | 1 | ICCV 96029(C) |
| VIII | 1 | ICC 5402 |

Table 4. Intra and inter cluster distances of the eight clusters of chickpea genotypes

| | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII |
|---|---|---|---|---|---|---|---|---|
| Cluster I | 463.32 | 685.53 | 1239.65 | 1293.87 | 694.49 | 851.51 | 1202.43 | 3333.77 |
| Cluster II | | 0.00 | 1815.97 | 1939.23 | 612.82 | 999.11 | 1579.46 | 5095.17 |
| Cluster III | | | 380.92 | 1960.99 | 2320.19 | 2683.37 | 928.82 | 3210.79 |
| Cluster IV | | | | 566.39 | 1124.13 | 1329.78 | 2831.69 | 1270.50 |
| Cluster V | | | | | 0.00 | 185.77 | 1830.80 | 3273.26 |
| Cluster VI | | | | | | 0.00 | 2113.73 | 3374.27 |
| Cluster VII | | | | | | | 0.00 | 4631.35 |
| Cluster VIII | | | | | | | | 0.00 |

Bold values indicate intra cluster $D^2$ values

with a score of 40 while third rank was shared by Cluster I and III with same score values (44). Fourth, fifth, sixth and last rank among the clusters was designated to Cluster VI, V, IV and VIII with scores 49, 59, 66 and 81 respectively. Cluster means for initiation of first flower ranged from 32.00 days (Cluster II, VII and VIII) to 45.10 days (Cluster IV). Cluster VI (89 days) showed minimum, whereas Clusters IV and VIII showed maximum (101 days) cluster means for days to maturity. Cluster mean for fifty per cent flowering was minimum in Cluster II (37.00 days) and maximum in Cluster VII (72 days). Cluster II was found to have high yielding genotypes (31.51 q/ha) followed by Cluster III and I with 29.78q and 27.07q respectively. The genotypes superior for yield and other yield attributing traits including plant height (36.00 cm), primary branches (4.40), pods per plant (34.40), seeds per pod (1.00) and yield per plant (31.15) were observed to be grouped in Cluster I, whereas genotypes with short plant height (31.00 cm), primary branches (5.60), pods per plant (30.80), seeds per pod (1.00) and yield per plant (5.65 q/ha) were grouped in Cluster VIII. Cluster II and VIII contained bold and small seeded genotypes with mean 100 seed weight of 41.59 g and 12.98 g respectively.

The correlation studies aid in identifying the trait associations which in turn assist to formulate selection criteria to accomplish desired improvement in target traits. Most commonly, yield improvement is the prime objective of any breeding programme, hence, knowing the correlation among related traits, with magnitude and direction, influencing productivity is very important. In the present study, both phenotypic (using original data) and genotypic (using adjusted means) correlations were computed among all the traits and is presented in Table 6. The findings on character association are in consistent with those of Thakur and Sirohi (2009), who found a positive and stable relationship between seed yield per plant, biological yield per plant, pods per plant, primary branches per plant, plant height, and harvest index at genotypic and phenotypic levels, both individually and across seasons. Similarly, grain yield was found to have a highly significant and positive relationship with biological yield, secondary branches, and number of pods per plant by Malik *et al.* (2010), with secondary branches positively correlated with number of pods per plant and grain yield per plant and negatively associated with 100 grain weight. A strong positive correlation of grain yield per plant with biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod, and 100 seed weight was observed in another study by Ali *et al.* (2011).

Principal component analysis (PCA) is a preferred standard tool in modern data analysis because, it is a simple, non-parametric method for extracting relevant information from ambiguous data sets. PCA helps to interpret the results of

Table 5. Cluster means for different traits

| Clusters | | | | | | Characters | | | | | | | Productivity traits | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | DFF | DFPF | DFP | DFPS | DM | PH | NPB | NSB | NPPP | NSPP | HSW | SYPP | YQHA | Score | Rank |
| 1 | 35.60(3) | 43.85(4) | 46.38(4) | 53.34(4) | 90.00(2) | 34.24(4) | 5.05(5) | 9.39(4) | 36.73(3) | 1.04(1) | 26.69(4) | 8.12(3) | 27.07(3) | 44 | III |
| 2 | 32.00(1) | 37.00(1) | 39.00(2) | 48.00(1) | 98.00(6) | 36.00(2) | 4.40(7) | 8.60(7) | 34.40(4) | 1.00(2) | 41.59(1) | 9.45(1) | 31.51(1) | 37 | I |
| 3 | 40.37(4) | 49.00(5) | 52.10(5) | 59.37(5) | 97.63(5) | 34.51(3) | 6.09(2) | 10.40(1) | 61.78(2) | 1.00(2) | 23.11(6) | 8.93(2) | 29.78(2) | 44 | III |
| 4 | 45.10(6) | 57.40(6) | 55.90(6) | 65.80(6) | 101.00(7) | 33.70(5) | 5.14(4) | 9.22(5) | 26.20(6) | 1.00(2) | 25.45(5) | 5.92(4) | 19.73(4) | 66 | VI |
| 5 | 44.00(5) | 42.00(3) | 44.00(3) | 50.00(3) | 96.00(4) | 33.60(6) | 4.60(6) | 8.80(6) | 22.60(7) | 1.00(2) | 32.36(2) | 4.31(6) | 14.36(6) | 59 | V |
| 6 | 35.00(2) | 42.00(3) | 44.00(3) | 50.00(3) | 89.00(1) | 43.60(1) | 4.20(8) | 10.40(1) | 19.80(8) | 1.00(2) | 27.66(3) | 3.80(7) | 12.67(7) | 49 | IV |
| 7 | 32.00(1) | 38.00(2) | 38.25(1) | 49.75(2) | 91.00(3) | 31.53(7) | 6.41(1) | 9.52(3) | 62.55(1) | 1.00(2) | 21.13(7) | 4.87(5) | 16.22(5) | 40 | II |
| 8 | 32.00(1) | 72.00(7) | 67.00(7) | 81.00(7) | 101.00(7) | 31.00(8) | 5.60(3) | 9.80(2) | 30.80(5) | 1.00(2) | 12.98(8) | 1.70(8) | 5.65(8) | 81 | VII |

Values in bracket indicates scores

DFF: Days to first flowering DFPF: Days to 50 per cent flowering DFP: Days to first podding DFPS: Days to 50 per cent pod setting
DM: Days to maturityPH: Plant Height NPB: Number of primary branches NSB: Number of secondary branches NPPP: Number of pods per plantNSPP: Number of seeds per pod HSW: Hundred seed weight SYPP: Seed yield per plant YQHA: Yield in quintal per hectare

Table 6. Phenotypic/ Genotypic correlation among traits

| | DFF | DPFF | DFP | DPPS | DM | PH | NPB | NSB | NPPP | NSPP | HSW | SYPP | YQHA |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | 1.000 | 0.758 | 0.827 | 0.795 | 0.499 | 0.16 | 0.224 | 0.055 | -0.019 | 0.026 | -0.324 | -0.195 | -0.195 |
| DPFF | 0.695$^{**}$ | 1.000 | 0.847 | 0.891 | 0.666 | 0.048 | 0.249 | 0.158 | -0.027 | -0.024 | -0.332 | -0.209 | -0.209 |
| DFP | 0.860$^{**}$ | 0.825$^{**}$ | 1.000 | 0.87 | 0.527 | 0.156 | 0.208 | 0.152 | 0.002 | 0.031 | -0.319 | -0.077 | -0.077 |
| DPPS | 0.777$^{**}$ | 0.866$^{**}$ | 0.859$^{**}$ | 1.000 | 0.567 | 0.009 | 0.224 | 0.136 | 0.001 | -0.041 | -0.391 | -0.234 | -0.234 |
| DM | 0.458$^{**}$ | 0.603$^{**}$ | 0.511$^{**}$ | 0.558$^{**}$ | 1.000 | 0.072 | 0.192 | 0.039 | 0.138 | -0.084 | -0.041 | -0.068 | -0.068 |
| PH | 0.226$^{*}$ | 0.097 | 0.235$^{*}$ | 0.123 | -0.001 | 1.000 | 0.015 | 0.099 | -0.086 | 0.319 | 0.185 | 0.158 | 0.158 |
| NPB | 0.164 | 0.246$^{*}$ | 0.171 | 0.199 | 0.274$^{**}$ | -0.043 | 1.000 | 0.407 | 0.285 | -0.182 | -0.259 | 0.027 | 0.027 |
| NSB | 0.148 | 0.226$^{*}$ | 0.232$^{*}$ | 0.269$^{*}$ | 0.1400 | 0.091 | 0.469$^{**}$ | 1.000 | 0.338 | -0.188 | -0.259 | 0.066 | 0.066 |
| NPPP | -0.040 | -0.033 | -0.047 | -0.003 | 0.298$^{**}$ | -0.135 | 0.456$^{**}$ | 0.416$^{**}$ | 1.000 | -0.190 | -0.220 | 0.452 | 0.452 |
| NSPP | -0.001 | 0.000 | 0.030 | -0.018 | -0.083 | 0.323$^{**}$ | -0.157 | -0.108 | -0.175 | 1.000 | 0.146 | -0.078 | -0.078 |
| HSW | -0.245$^{*}$ | -0.252$^{*}$ | -0.215$^{*}$ | -0.293$^{**}$ | - 0.119 | 0.221$^{*}$ | -0.349$^{**}$ | -0.295$^{**}$ | 0.337$^{**}$ | 0.147 | 1.000 | 0.332 | 0.332 |
| SYPP | -0.009 | -0.090 | 0.065 | -0.050 | -0.043 | 0.244$^{*}$ | -0.016 | 0.045 | 0.238$^{*}$ | -0.049 | 1.000$^{**}$ | 1.000 | 1.000? |
| YQHA | -0.009 | -0.090 | 0.065 | -0.050 | -0.043 | 0.244$^{*}$ | -0.016 | 0.045 | 0.238$^{*}$ | -0.049 | 0.356$^{**}$ | 1.000$^{**}$ | 1.000 |

(above diagonal-genotypic / below diagonal - phenotypic )

DFF: Days to first flowering DFPF: Days to 50 per cent flowering DFP: Days to first podding DFPS: Days to 50 per cent pod setting
DM: Days to maturityPH: Plant Height NPB: Number of primary branches NSB: Number of secondary branches NPPP: Number of pods per plantNSPP: Number of seeds per pod HSW: Hundred seed weight SYPP: Seed yield per plant YQHA: Yield in quintal per hectare

Table 7. Eigen values, variance (%) and cumulative (%) values of chickpea genotypes

| Traits | Component | Eigen value | Variance (%) | Cumulative (%) |
|---|---|---|---|---|
| Days to first flowering | PC1 | 4.473 | 34.40 | 3.441 |
| Days to 50 per cent flowering | PC2 | 2.518 | 53.78 | 1.937 |
| Days to first podding | PC3 | 1.740 | 67.17 | 1.338 |
| Days to 50 per cent pod setting | PC4 | 1.183 | 76.27 | 9.100 |
| Days to maturity | PC5 | 7.553 | 82.08 | 5.809 |
| Plant height | PC6 | 6.745 | 87.26 | 5.188 |
| Number of primary branches | PC7 | 5.667 | 91.62 | 4.359 |
| Number of secondary branches | PC8 | 5.068 | 95.52 | 3.898 |
| Number of pods per plant | PC9 | 2.352 | 97.33 | 1.809 |
| Number of seeds per pod | PC10 | 1.862 | 98.76 | 1.432 |
| 100 seed weight | PC11 | 8.366 | 99.40 | 6.435 |
| Seed yield per plant | PC12 | 7.689 | 100.00 | 5.914 |

Extraction Method: Principal Component Analysis.

Table 8. The promising early genotypes with high productivity

| Genotypes | DFF | DFPF | DFP | DFPS | DM | PH | NPPP | HSW | SYPP |
|---|---|---|---|---|---|---|---|---|---|
| M-97 | 33 | 37 | 43 | 51 | 83 | 33.4 | 43.4 | 21.4 | 10.9 |
| M-111 | 37 | 41 | 46 | 50 | 83 | 33.0 | 40.6 | 28.8 | 9.5 |
| M-71 | 33 | 37 | 44 | 51 | 88 | 33.4 | 41.0 | 23.2 | 9.8 |
| ICRISAT 3155 | 33 | 41 | 45 | 50 | 88 | 35.2 | 35.0 | 33.1 | 10.1 |
| DG 5033 | 33 | 47 | 49 | 56 | 89 | 33.8 | 37.2 | 32.6 | 12.7 |
| ICCV 191153 | 37 | 43 | 43 | 54 | 88 | 41.8 | 36.4 | 28.3 | 9.1 |
| ICCV 191159 | 35 | 44 | 44 | 50 | 88 | 35.0 | 47.6 | 32.1 | 9.5 |
| ICC 5853 | 38 | 44 | 46 | 60 | 90 | 35.0 | 40.4 | 28.4 | 9.9 |
| ICCV 93954 | 38 | 42 | 48 | 54 | 90 | 33.2 | 38.6 | 23.5 | 9.0 |
| ICC 11680 | 33 | 41 | 46 | 51 | 89 | 34.4 | 39.4 | 39.8 | 11.2 |
| JG-11 (C) | 33 | 53 | 48 | 57 | 97 | 33.0 | 64.9 | 20.1 | 6.1 |
| BGD111-1 (C) | 42 | 50 | 51 | 60 | 100 | 36.0 | 64.9 | 24.4 | 9.3 |
| JAKI 9218 (C) | 38 | 45 | 49 | 55 | 105 | 32.6 | 63.2 | 20.0 | 7.6 |
| A-1 (C) | 39 | 44 | 48 | 56 | 99 | 33.3 | 62.7 | 23.2 | 5.4 |
| ICCV 96029 (C) | 32 | 38 | 38 | 50 | 92 | 31.5 | 62.6 | 20.1 | 4.9 |

DFF: Days to first flowering
DFPF: Days to 50 per cent flowering
DFP: Days to first podding
DFPS: Days to 50 per cent pod setting
DM: Days to maturity
PH: Plant height (cm)
NPPP: Number of pods per plant
HSW: Hundred seed weight (g)
SYPP: Seed yield per plant (g)

complex data set by revealing the rarely hidden and simplified structures that often underlie it. In the present study, PCA was carried out and the results obtained on the basis of communalities revealed that the traits *viz.,* initiation of first flower (4.473), days to maturity (7.553), plant height (6.745), primary branches (5.667), secondary branches (5.068), 100 seed weight (8.366) seed yield per plant (7.689) showed considerably high variability compared to other traits. All the twelve PCs showed more than 0.5 Eigen values (Table 7). It was noticed that phenological traits put together exhibited more than 80 per cent variability (82.08) indicating the scope for selection of desired genotypes. Tesfamichael *et al.* (2015) studied 39 genotypes and discovered that the first principal component explained 57 per cent of the total variation and was linked to positive contributors such as days to 50 per cent flowering and podding, plant height, number of primary and secondary branches per plant, days to 75 per cent maturity, number of pods per plant, and biomass yield per plant. The recorded information on genetic diversity and the relationship between agronomic characteristics and seed yield may be used to develop appropriate breeding methods and conserve chickpea germplasm.

Several genotypes with earliness having maturity days ranging between 83-90 days coupled with high yielding potential have been identified (Table 8). These genotypes will further be tested for their *per se* performance and the promising ones will be selected for varietal identification and/or to use as parents in breeding for climate resilient varieties.

## Conclusion

The present study involving 75 chickpea genotypes, significant variability among the genotypes was noticed with several promising lines for high productivity and earliness. Early genotypes with high productivity *viz*., M 97, M 111, M 71, ICC 3155, DG 5033, ICCV 191153, ICCV 191159, ICC 5853, ICCV 93954 and ICC 11680 will further be evaluated and promising ones will be advanced. In the present changing climatic conditions, these genotypes may be well suited to escape from terminal drought and heat stress and thus show resilience to climate change.

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