"GENETIC DIVERSITY IN CHICKPEA (*Cicer arietinum* L.)"

by

Mr. Parsudkar Praful Kisan
(Reg. No. K-018/053)

DIVISION OF AGRICULTURAL BOTANY

RAJARSHEE CHHATRAPATI SHAHU MAHARAJ
COLLEGE OF AGRICULTURE, KOLHAPUR-416 004

MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI - 413 722, DIST-AHMEDNAGAR
MAHARASHTRA STATE (INDIA)

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A Thesis submitted to the
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413 722, DIST- AHMEDNAGAR,
MAHARASHTRA, INDIA

In partial fulfillment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)

DIVISION OF AGRICULTURAL BOTANY

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APPROVED BY

Dr. M. S. Kamble
(Chairman and Research Guide)

Dr. N.S. Kute
(Committee Member)

Dr. P. N. Gajbhiye
(Committee Member)

Prof. V. R. Bavadekar
(Committee Member)

DIVISION OF AGRICULTURAL BOTANY

RAJARSHEE CHHATRAPATI SHAHU MAHARAJ
COLLEGE OF AGRICULTURE, KOLHAPUR-416 004
MAHATMA PHULE KRISHI VIDYAPEETH
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2021

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
thereof has not been submitted
by me or other person to any
other University or Institute
for a Degree or
Diploma

Place: Kolhapur

Date: / /2021 (P. K. Parsudkar)

Dr. M.S. Kamble
Chairman and Research Guide
Asst. Prof. of Agril. Botany,
Rajarshee Chhatrapati Shahu Maharaj
College of Agriculture, Kolhapur.

CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC DIVERSITY IN CHICKPEA (*Cicer arietinum* L.)"**, submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfilment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **Mr. PARSUDKAR PRAFUL KISAN** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been duly acknowledged.

Place: Kolhapur (M. S. Kamble)

Date: / /2021 Research Guide

Dr. A.G. Bhoite
Head of Section,
Division of Agricultural Botany,
Rajarshee Chhatrapati Shahu Maharaj
College of Agriculture, Kolhapur.

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Place: Kolhapur

Date: / /2021 (A.G. Bhoite)

Dr. U.B. Hole
Associate Dean,
Rajarshee Chhatrapati Shahu Maharaj
College of Agriculture, Kolhapur.

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Place: Kolhapur

Date: / /2021 (U.B. Hole)

ABSTRACT

"GENETIC DIVERSITY IN CHICKPEA (*Cicer arietinum* L.)"

By

PARSUDKAR PRAFUL KISAN

A candidate for the degree of

MASTER OF SCIENCE (AGRICULTURE)

In

GENETICS AND PLANT BREEDING

2021

Research Guide: Dr. M. S. Kamble

Department: Agricultural Botany

The present investigation entitled, "Genetic Diversity in Chickpea (*Cicer arietinum* L.)" was conducted at Post Graduate Research Farm, Rajarshee Chhatrapati Shahu Maharaj College of Agriculture, Kolhapur during *kharif,* 2020-21. The experiment was conducted with the objectives to estimate genetic diversity. The thirty genotypes of chickpea were sown in a randomized block design with three replications.

High genotypic coefficients of variation (GCV) coupled with high heritability and high genetic advance were observed for pods per plant, and plant height in indicated that the preponderance of additive gene action and such characters could be improved through selection. High heritability coupled with high genetic advance as per cent of mean was recorded for the characters pods per plant indicated that, most likely the high estimates of heritability is due to additive gene effects and selection may be effective for these characters.

Days to 50 per cent flowering, days to maturity, primary branches per plant, plant spread and pods per plant showed highly significant positive correlation among themselves indicating that simultaneous selection for these characters would result in improvement of high yielding chickpea genotypes.

Among the 10 characters studied, days to maturity (0.5451) recorded highest positive direct effect on seed yield per plant followed by protein content (0.4812), primary branches per plant (0.4693) seeds per pod (0.2598) and 100 seed weight (0.1944). The characters secondary branches per plant (0.1344) exhibited relatively low magnitude of positive direct effects on seed yield. The characters *viz.,* plant height (-0.3534), days to 50 per cent flowering (-0.1926) and pods per plant (-0.0148) showed negative direct effects.

In the present investigation, D^2 values between all possible pairs of 30 genotypes ranged from 19.09 to 38.39. The maximum intra-cluster distance was found in Cluster III (4.45) followed by Cluster II (4.13) suggesting that genotypes included in the clusters might have genetically different architecture and might have originated from different genetic pool. The maximum inter-cluster distance was observed between Cluster III and Cluster VI (6.20), followed by Cluster II and VII (6.00), Cluster III and VII (5.71), Cluster III and V (5.62), Cluster IV and V (5.60) and Cluster V and VII (5.51) indicating that these clusters are more heterogeneous. This also suggests that the genetic architecture of the genotypes in one cluster differ entirely from those included in the other cluster and crossing between these clusters would create high amount of genetic diversity.

Variance of cluster means revealed that number of pods per plant (32.18 %) contributed showed maximum contribution to divergence, followed by primary branches per plant (24.83 %) and seed yield per plant (18.62 %). While, other characters like days to 50 per cent flowering (6.21 %), days to maturity (4.60 %), number of secondary branches per plant (4.37 %), 100 seed weight (3.91 %), protein content (3.91 %) and plant height (1.38 %) were magnitudinaly low. Seeds per pod (0.00 %) show 0 % contribution to diversity

High heritability for secondary branches per plant followed by 100 seed weight, primary branches per plant, protein content and seeds per pod with low genetic advance indicating that the characters are controlled by non-additive gene action i.e., dominance deviation or epistasis, and hence heterosis breeding will be effective for improvement of these characters.

On the contrary, high heritability and moderate genetic advance as percent of mean was observed for plant height, days to maturity, seed yield per plant, days to 50 per cent flowering indicating the influence of both additive and non-additive gene effects in the control of these characters. Hence, simple direct selection may not be effective to improve these traits. These traits could also be improved by using recurrent selection method.

PARSUDKAR P. K **1 to 61**

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is known by lots of names in various countries like Gram, Bengal gram, Chana. Chickpea is a very important *rabi* season legume having extensive geographical area. Chickpea is diploid species having chromosome number 2n=16. Chickpea is the third most important pulse crop in the world after peas and beans. Chickpea also plays an important role to improve soil fertility by fixing nitrogen with the help of root nodules (Anabessa *et al.,* 2006). Chickpea is native of South-Eastern Turkey and Syria.

Chickpea is considerably contained good amount of proteins and carbohydrates, which together constitute eighteen per cent of the dry seed mass. The starch content of chickpea was found to vary from 41 per cent to 50.01 per cent. The crude protein ranges from 12.30 to 31.40 per cent. Chickpea has 6 per cent fat is important in vegetarian diets of resource-poor consumers. Chickpea contains nutritionally important minerals, notably calcium, niacin and iron content is good. The protein quality of chickpea is better than other pulses. In India chickpea production in 2019-20 was 11078.50 tonnes, Madhya Pradesh was the leading with a production of 2729.14 tonnes followed by Maharashtra with chickpea production of 2239.36 tonnes (Directorate of Economics and Statistics, 2020).

Pulses are very important food crop of the world because it provides a best source of vegetable dietary protein. Pulses provide source of rich protein for those people who prefer vegetable against animal proteins in their diet for cultural or religious reasons. Pulse grain protein nutritionally complements the protein in cereal grains. Pulses contain 20-25 per cent protein on dry seed basis, which is almost 2.5 to 3.0 times of the value normally found in cereals.

Crop improvement program or study depends on the genetic variability present in the population. The improvements in yield components primarily depend on the nature and heritable portion of variation. Selection based on a single character may not always be effective and it is very cumbersome process for a breeder to consider a large number of characters simultaneously in selection program. The genetic variability in crop is very importance for any breeding study due to this reasons plant breeders have emphasized to estimate of germplasm for the improvement of crop yield and also for utilization in further breeding programmes. Evaluation of plant genetic resources is a pre-requisite for future breeding work. In addition to genetic variation, heritability of economically important traits is essential for effective breeding programme and selection of specific traits.

The ultimate product of a genotype at specific environment is phenotype. Sometime, due to decrease in the correlation between the genotypic and phenotypic interaction genotype may fail to stick out best phenotypic expression. It is frequently noticed that variation found in the yielding capacity of varieties even within single season, when these are planted in different dates. For that reason it is important to identify or develop stable genotypes to different environmental conditions.

The D^2 statistics is an important tool which gives the estimation of genetically divergent parents for their exploitation in hybridization programme as hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. Murty, B. R. and Arunachalam (1966) stated that multivariate analysis with "Mahalanobis D^2statistics" it is a very powerful tool for the clustering pattern to establish the relationship between genetic and geographic divergence and to estimate the role of different quantitative characters towards the maximum divergence.

Robinson *et al.* (1949) concluded that heritability of the character the mainly related to breeder since it indicates the possibility and extent to which improvement is possible by selection. It is seen that heritability together with genetic advance will bring out the genetic gain expected from selection (Johnson *et al*. 1955a).

Keeping the view of all the above given aspects, the current study was carried out in 30 chickpea genotypes with the following objectives.

1. To study genetic diversity.
2. To find out the per cent contribution of characters towards genetic divergence.
3. Grouping of the genotypes into different clusters.
4. Identification of the parents for hybridization programme to develop high yielding chickpea.

2. REVIEW OF LITERATURE

The experiment aimed at evaluation of the statistical parameters genetic variability, correlation coefficient, path analysis and genetic diversity in 30 treatments of chickpea. Hence, the literature pertaining to variability parameter such as genotypic coefficient of variation, phenotypic coefficient of variation, heritability (b. s.), genetic advance, in chickpea reviewed in this chapter under the headings given below.

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation and path analysis

2.4 Genetic divergence

2.1 Genetic variability:

Since, many of quantitative characters which are of economic value are highly influenced by all environmental conditions; the process of breeding in population is primarily conditioned by nature of genotypic and non-genotypic variation in the different plant characters.

Ali *et al.* (2010) studied twenty genotypes and three standard varieties of chickpea and for *per se* and parameters of variability, heritability (broad sense), genetic advance as per cent of mean and interrelationships for various parameters. Correlation coefficient studies gives the idea for pods per plant, secondary branches per plant, seeds per pod and 100-seed weight were positive and highly significant.

Parameshwarappa *et al.* (2010) carried out an investigation on chickpea germplasm lines representing minicore collection obtained from ICRISAT, Patancheru (AP) for assessing genetic variability under three environments. Considerably high variability was observed for productivity related character in E_3 (irrigated 2005–06). Moderately high heritability (b.s) and high genetic advance (GA) were observed for many productivity related traits under E_3. The higher GCV and PCV but heritability was remained same as that under E_2.

Johnson *et al.* (2015) found coefficient of variation (G.C.V.) was high for the traits seed yield plant^{-1}, biological yield plant per plant, seed volume, 100-seed weight, hydration capacity seed^{-1}, swelling index and hydration index in E_1, E_2, E_3 and E_4. GCV for seed yield was high which imparts good scope for yield improvement can be done through direct selection in chickpea. High heritability with high genetic advance was seen in character 100-seed weight.

Astereki *et al.* (2015) studied genetic diversity of 24 chickpea genotypes and estimating the genetic parameters like phenotypic and genotypic variance, phenotypic and genotypic coefficient of variation and heritability, during two seasons of 2012-2013 and 2013-2014. Analysis of variance shows that there were high significant genotypic differences for seed yield, days to maturity, flowering period, harvest index, pods per plant. Seed yield ranges from 168.3 kg ha^{-1} (L13) to 618.52 kg ha^{-1} (L10) in the first year and 248.86 kg ha^{-1} (L22) to 945.66 kg ha^{-1} (L2) in the second year.

Kashid *et al.* (2015) investigated two cultivars of chickpea (BDN 9-3 & PG-5) were practiced for mutagenic treatment of EMS and SA to examine the effect on seed coat colour characters and 100-seed weight. Mixed trend of negative and positive shift in average values was observed in both the cultivars in mutagenic treatments for the 100-seed weight and pods per plant in M_2 and M_3 generations. In this study Anthoseed mutants were observed which characterized by development of anthocyanin in the testa of seeds. They took slightly low days to gain maturity as compared with control in both BDN9-3 and PG-5. The heritability estimates for number of pods bearing branches, seed yield per plant, 100-seed weight and pods per plant were higher in M_3 than in M_2 generation in the two varieties of chickpea. High heritability in yield trait has been found to useful plant breeder's view point.

Kumar *et al.* (2016) conducted study for evaluation of correlation for quantitative traits in gram, (*Cicer arietinum* L.) during the crop season 2003 to 2004 under rainfed condition. They revealed that the late days taken to mature (151) were recorded in BG 1107 and Pusa 1063, whereas three genotypes (BG 2002, Pusa 209 and Pusa 1090) took minimum days (136) to mature. There was a great variation in genotypes that number of primary branches ranges from 9.37 to 15.33. Number of pods plant^{-1} varied from 45.53 to 68 and BG 1105 exhibited maximum number of pods (68). The variation present in trait 100-seed weight ranged from 17.05 g to 32.31 g. The high seed yield plant^{-1} was recorded for genotype BG 2002 (12.68 g), Pusa 362 (12.73g) and showed minimum seed yield (7.83 g).

Mandal *et al.* (2017) evaluated seven chickpea (*Cicer arietinum* L.) genotypes including some cultivars were considered (Collection Id of the seven genotypes are TZCP-2, TZCP-3, TZCP-4, TZCP-5, TZCP-6 and TZCP-7). All quantitative traits were collected for assessing the diversity and to find key characters in chickpea cultivars. The statistical analysis was carried out all the quantitative character (*viz.* plant height, test weight, branches per plant, pod per plant, seeds per pod, days to maturity, seed width, days to flowering and grain yield). Analysis of variance divulged significant difference in the treatments for 10 characters.

Attri *et al.* (2018) investigate 40 genotypes in F_4 derived F_5 lines consisting of eight parents: ICC-4958, ICCV- 10, JAKI-9218, JG-11, JG-130, JG-16, ICCV-97105, ICCV-00108 during *rabi* 2012-2013 and 2013-14. Primary branches, plant height, 100-seed weight, pod per plant, seed yield, had direct and positive effect. Root length, relative water content, partitioning coefficient to root, stem, and leaves seen positive significant correlation.

Johnson *et al.* (2018) found that. Values of GCV & PCV were recorded for secondary pod plant$^{-1,}$ branches plant^{-1}, hydration index, hydration capacity seed^{-1}, seed yield plant^{-1}, biological yield, primary branches plant^{-1} in all environment E_1, E_2 and E_3. High estimate of heritability (b.s.) and high genetic advance were seen for the trait's primary branches plant^{-1}, plant height^{-1}, secondary branches plant^{-1}, pods plant^{-1}, 100-seed weight, seed yield plant^{-1},

biological yield plant^{-1} all three environments E_1, E_2 and E_3 indicated the influence of additive genetic variance.

Manikanteswara *et al.* (2018) evaluated 21 chickpea genotypes and the experiment was carried out in RBD with three replications, during *rabi* 2017 maximum genotypic coefficient variance and phenotypic coefficients of variance were seen for seed yield per plant.

Sharifi *et al.* (2018) estimated genetic diversity of 25 chickpea treatments, the principal components (PCs) explained 69.6% variation. Factor analysis showed that three factors accounted 69.79% of the total variability. Three first factors accounted for 34.6%, 21.8% and 14.1% of total variability, respectively.

Kumar *et al.* (2019a) estimated genetic variability for yield & its component traits, path analysis and genetic correlation in forty-five treatments of chickpea (*Cicer arietinum* L.) High genetic advance gives idea that additive genes govern by these traits and selection will be rewarding for improvement of these traits. Correlation analysis shows that trait grain yield was significant and positive association with pods per plants. While it shows significant negative correlation with trait days to maturity. Path analysis suggested that pods per plant, days to 50% flowering had high direct and positive effect on trait grain yield.

Pithiya and Javia (2019) carried an experiment and examine the genetic variability and selection of mechanical harvestable population from thirty-two F_3 populations of chickpea (*Cicer arietinum* L.) during *rabi* 2017-18 in RBD with three replications. Analysis of variance revelled significant difference for all ten-character studied indicating presence of genetic. However, narrow differences observed between the GCV and PCV in certain cases indicate that these traits were less influenced by the environment.

Heidari *et al.* (2020) evaluated sixteen advanced durum wheat breeding lines under rain-fed and supplementary irrigation on seventeen agro-morphological characters to examine genetic value of yield and yield-related traits. Most traits revealed the highest coefficients of variation (CV). Results seen that high phenotypic variance (PCV) of traits were generally high as compared to genotypic coefficients of variance (GCV). Obtained heritability (b. s.) with high genetic advance for several traits indicates that heritability (b. s.) because of additive gene effects and selection can be effective in early generations for these traits.

Tsehaye *et al.* (2020) found the success of breeding totally depends on the genetic variability present in the genotype, how the current study was designed to evaluate the variability, heritability, genetic advance and interrelation of different characters of 100 chickpea treatments using triple lattice design at Takusa, North Gondar, Ethiopia. The studied genotypes were high significant for studied traits plant, hundred seed weight etc.

Zerfu *et al.* (2021) evaluated twelve varieties of chickpea collected from Sirinka Agriculture Research Center were studied at with the objectives evaluating the variability of chickpea varieties for trait grain yield and related characters determination of relation among

yield components and identify traits that used mainly to explain variation among desi chickpea varieties. Analyses of variance the mean square because of accession were high significant for the characters studied such as biological yield, grain yield and plant height. The range for PCV was 3.96% days to maturity to 30.1 per cent for biological yield. As to the GCV it ranged from 1.24 per cent for days of maturity to 28.153 % for biological yield.

2.2 Heritability and genetic advance

Zalia *et al.* (2010) conducted field experiment with 17 chickpea genotypes at the Ilam Agricultural and Natural Resources Research Center in the 2004 growing season. Genetic parameters including genotypic environmental variances and phenotypic variances; genotypic coefficients of variation; heritability (bs), genetic advances, path coefficients and correlation coefficients were estimated and cluster analysis was evaluated. Heritability values were high for days to 50% flowering (98.21%), plant height (58.78%), days to 50% maturity (98.54%), secondary branches (45.72%), seeds per plant (35.41%).

Khan *et al.* (2013) evaluated 20 (*Cicer arietinum* L.) genotypes of chickpea for genetic heritability (b s) recorded on seeds per pod, pods per plant, primary branches plant^{-1}, secondary branches plant^{-1}, seed yield plant^{-1} and 100-seed weight. Analysis of variance seen significant ($P<0.01$) variation among all the genotypes studied. Heritability estimates were highest for primary branches plant^{-1} (0.83), 100-seed weight (0.83), seed yield plant^{-1} (0.76) pods per plant (0.89) and secondary branches plant^{-1} (0.76). Genetic advance was high for pods per plant (40.15), seed yield plant^{-1} (38.25%), secondary branches plant^{-1} (30.25%) and primary branches plant^{-1} (36.65%). Grain yield plant^{-1} exhibited highly significant.

Hasan *et al.* (2017) carried out an experiment to estimate the genetic variability, genetic advance, heritability, path coefficient, correlation coefficient and construct the selection method in the material. Thirteen yield and its components of eight treatments of chickpea have been considered. The highest phenotypic coefficient of variation was observed for NPd/P followed by NS/P and PWH. The highest GCV with high PCV were found for NS/P and NPd/P. PBFF and NPBMF gave the highest expected genetic gain. Since these two traits exhibited high genetic gain in the combination of selection showed positive correlation with SW/P both at both levels hence considered as primary yield component.

Adhikari *et al.* (2018) conducted study during summer 2015 at Regional Agriculture Research Station, Dipayal, Doti, Nepal to estimate the genotypic and phenotypic variability, genetic advance, heritability, and correlation on seed yield and yield associated traits using 26 advance genotypes of lowland irrigated rice showed the significant difference for trait days to 50% flowering, plant height, maturity, seed yield and thousand seed weight. High heritability was estimated for the days to 50% flowering (0.78), maturity (0.69), thousand grain weight (0.46) and plant height (0.43) shows that these characters are in the genetic control.

Kishor *et al.* (2018) conducted field study with forty chickpea genotypes during *rabi* season of 2015-16 at field. The characters such as days to 50 per cent flowering, 100-seed weight, days to maturity, plant height, seeds per plant, pod per plant, primary branches per plant showed least differences in GCV and PCV estimates. The estimates of heritability (bs) for some of trait were low to high. High estimates were observed for seeds per plant (96.92).

Swetha and Lavanya (2019) conducted an experiment to estimate variability, heritability, genetic advance and correlation Maximum GCV were recorded for seed yield per plant. High heritability (b s) and high genetic advance was registered for pods per plant and biological yield. High genetic advance as per cent of mean observed for pods per plant and biological yield. Seed yield per plant seen significant and positive association at genotypic and phenotypic levels with harvest index and pods per plant. Heritability and correlation coefficient analysis indicated that these characters used for the selection of grain yielding chickpea genotypes to improve yield of chickpea.

2.3 Correlation and path analysis

Yocel *et al.* (2008) conducted study to estimate variability parameter, heritability (bs), and correlation between yield and components in 14 kabuli chickpea (*Cicer arietinum* L.). Direct and indirect effects of path analysis of yield character on grain yield per plant were estimated. Genotypic coefficient of variance was the high for 100-seed weight and seed per plant. Heritability (broad sense) ranges from 5.46 per cent (days to flowering) to 50.56 per cent (seed number per plant). Heritabilities for 100-seed weight, seed number and full pods were higher than the other characters.

Tripathi *et al.* (2012) evaluated eighty-six chickpea (*Cicer arietinum* L.) genotypes included 43 Kabuli (*Cicer kabulium*) type and 41 Desi (*Cicer arieatinun*) type for their morphological cooking quality and physicochemical traits. Found that significant differences among all the genotypes for days to maturity (85–121 d), days to 50 per cent flowering (33–80 d), seeds per plant (15–84), pods per plant (12–65).

Tadesse (2016) conducted an experiment during 2007/8-2009/10 to determine relationships in yield and its components using path analysis and correlations in desi chickpea grown under rainfed conditions. The path analysis based on seed yield as a dependent variable shown that biomass had the greatest direct effect on grain yield (0.0145), plant height and stand count at harvest. Both path and correlation analyses indicate that plant height, biomass and stand count at harvest were the major contributors to seed yield.

Kumar *et al.* (2017) evaluated genetic variability parameter, path analysis and correlation for grain yield and component trait in twenty-nine chickpea treatments sown under heat stress environment was analysed. Environmental temperature (≥35°C) during its reproductive stage which creates an unfavourable heat stress condition and affects seed yield. The analysis of

variance showed that significant divergences among the characters for all traits indicating presence of variability in the treatments for various characters.

Tiwari *et al.* (2016) were studied thirty-eight chickpea varieties to find out genetic variability parameter and path analysis for grain yield and contributing traits. Both genotypic variances and phenotypic variance were high and significant for the character with little higher phenotypic coefficient of variation. The low differences between the phenotypic and genotypic coefficients of variation indicate low environmental influences on the characters. High heritability (b s) with high genetic advance was obtained with pods per plant, seeds per pod and grain yield per plant.

Singh *et al.* (2018) study was conducted to determine heritability, variability and correlations between yield and contributing trait in 15 chickpea (*Cicer arietinum* L.). Path effect (direct and indirect) of yield contributing characters on trait seed yield per plant was evaluated. GCV was the highest for 100-seed weight followed by seed per plant. Heritability (b. s) ranges from 5.38 per cent (days to flowering) to 51.65 per cent (seed per plant). Heritability for seed number, full pods and 100-seed weight were higher than the other characters.

Kumar *et al.* (2019b) carried out an experiment at field experimentation centre of the Genetics to study genetic variability, path analysis and correlation in fifty germplasm of chickpea 2017-18. The high phenotypic coefficient of variance and genotypic coefficient of variance were noticed for biological 100-seed weight, yield per plant and primary branches per plant. High heritability (b s) was recorded by 100-seed weight, biological yield per plant, pods per plant, grain yield per plant and primary branches per plant.

Mohan and Thiyagarajan (2019) conducted study to evaluate 50 chickpea germplasm to understand the magnitude of variability parameter, heritability (b s), genetic advance and the association of various yield characters and their path effect i.e., direct and indirect effect on yield of chickpea based on agro-morphological traits. These traits included three vegetative traits (primary branches, plant height and secondary branches) one flowering trait (days to 50 % flowering) seven yield related traits.

Sharma *et al.* (2019) carried out an investigation in *rabi* 2016-17 at five different locations (Raipur, Bhatapara, Bemetera, Kabirdham and Korea) in Chhattisgarh to study the genetic variability parameter, character relation and coheritability for yield characters such as days to maturity, plant height, 100-seed weight (g), pods per plant and seed yield (kg/ha). Results revealed that the genotypic variation was marginally lower than the corresponding phenotypic coefficient of variation indicating the effect of environment in the expression of the trait under study.

2.4 Genetic divergence

Jain *et al.* (1981) found that the grouping of treatments from different eco-geographical areas in the same cluster confirmed that there is no parallelism in geographical area and genetic

diversity. The pattern of clustering was influenced by environment and while making general statement on this aspect, the experimental conditions should be taken into consideration. To make worthwhile improvement in chickpea, flowering period in that order, should be taken into account. The clustering pattern of genotypes has revealed that type Desi (*Cicer arieatinun*) and Kabuli (*Cicer kabulium*) types are different from each other. Hence, crossing between these two types gives more desirable segregants.

Kumar *et al.* (1998) assessed the divergence among the 17 genotypes, 5 each developed through mutation breeding and intra and inter-specific hybridization with two standard checks in chickpea, Mahalanobis' D^2 statistics was applied. All the 17 treatments were grouped into five clusters. Clusters III, I and II had 4, 5 and 6 genotypes, respectively. On the contrary, the clusters V and IV had monogenotypic each.

Durga *et al.* (2005) evaluated genetic diversity in chickpea with 132 genotypes revealed significant differences in all the treatments for yield and contributing trait. All 132 genotypes were grouped into nine clusters. Cluster I was the largest comprising of 20 genotypes followed by clusters VI and cluster V with 15 and 16 genotypes, respectively. Maximum Intra-cluster distance was observed in cluster VI cluster IV (1.79). High inter-cluster distance was found between clusters I and VIII (5.114). Crossing the genotypes between the cluster VII and I may lead to high diversity in the segregating populations and development of high yielding chickpea varieties.

Talebi (2008) evaluated the genetic relationships of 28 chickpea accessions from diverse origin using AFLP markers. On average, 13 polymorphic bands per primer were observed in AFLP analysis. The average polymorphic information content (PIC) was 0.71 and ranging from 0.49 to 0.93. The low and the high PIC value were found for primer P-GAG/M-GC and P-AT/M-GC, respectively. The average GD, based on first values among the 21 accessions was 0.42, ranging from 0.61 to 0.16.

Frenkel *et al.* (2009) estimated genetic divergence between *D. rabiei* isolates sampled from wild *Cicer judaicum* and domesticated *Cicer arietinum* and the potential role of temperature adaptation in this divergence. Neutral genetic markers showed strong differentiation between pathogen samples from the two hosts. Isolates from domesticated chickpea demonstrated increased adaptation to high temperatures when grown in vitro compared with isolates the wild host. The distribution of temperature responses among progeny from crosses of isolates from *C. judaicum* with isolates from *C. arietinum* was continuous suggesting polygenic control of this trait. In vivo inoculations of host plants suggested that pathogenic fitness of the native isolates was higher than hybrid progeny. The results indicate that there is a potential for adjustment to high temperatures; however, the chances for formation of hybrids capable of parasitizing both hosts over a broad temperature range are low.

Akhtar *et al.* (2011) evaluated 20 genotypes of chickpea collected from various sources with one check (Pb-2000). Highly significant differences existed among all the genotypes tested for all the character. Genotype BRC-61 observed high seed yield of 2394 kg ha^{-1} and check variety Bunjab-2000 yielded only 2064 kg ha^{-1}. Genotype BRC-61 was the early in maturity and had high 100-seed weight seen significant positive genotypic correlations were between plant height, pods per plant, and 100-seed weight. Heritability (b s) ranges from 89.54 (grain yield) to 99.00 per cent (100-seed weight).

Naghavi *et al.* (2012) estimated the genetic diversity of chickpea treatments from Iran, a total of 307 landraces from 4 regions including: northern areas (29 from Ardebil, 3 from Qazvin and 5 from Mazanderan provinces), temperate (16 from Kermanshah, 2 from Semnan, 54 from Khorasan and 20 from Kerman provinces), semi-arid (28 from Ghom and 56 from Isfahan provinces) and cold areas (15 from West Azarbayjan, 52 from Tehran and 27 from East Azarbayjan provinces) were analysed using 16 microsatellite loci. Genetic diversity in the northern area (He = 0.76), even with a limited available landrace (37) compared with the other three regions (84–94) might confirm the northern Persia as part of the chickpea centre of origin. The neighbour-joining tree showed a low relationship between molecular divergence and the geographical grouping of chickpea.

Sewak *et al.* (2012) evaluated genetic diversity among 495 genotypes of chickpea collected from different ecological zones of India was evaluated for several quantitative and qualitative traits. These treatments were grown in the augmented design with 3 checks 'BG-256', 'K-850' and 'L-550' after every fifteenth row. High variability was observed for both quantitative and qualitative traits. The diversity analysis indicated high genetic variation for yield per plant in the present study. Hence direct selection based on seed yield and contributing traits practiced to select better genotypes, which utilized for development of superior high yielding chickpea varieties.

Diapari *et al.* (2014) to examine the variability and to identify SNP alleles associated with seed iron, zinc and niacin concentrations was conducted using 94 diverse accessions of chickpea. The results indicated that there is substantial variability present in chickpea germplasm for iron, zinc and niacin concentrations.

Malik *et al.* (2014) estimated genetic diversity of 113 chickpea genotypes cluster analysis. High variation was seen for biological yield, maturity, days to flowering, pods $plant^{-1}$, plant height and harvest index. Some characters also showed positive significant correlation with yield. The treatments were grouped Tochers cluster analysis. Genotypes with early flowering and maturity were gathered in cluster I while cluster II showed dominant contribution for seed yield $plant^{-1}$, pods $plant^{-1}$ and harvest index. The grouping of treatments would be of practical value to breeders in identification of the genotype with desirable trait for utilization in breeding program for genetic improvement.

Aggarwal *et al.* (2015) conducted study to analyse the genetic diversity estimates between 124 chickpea genotypes using sequence-tagged microsatellite (STMS) markers. Percentage of polymorphic loci using POPGENE analysis was 50.99, 58.83 and 96.74 for susceptible, resistant and miscellaneous genotypes, respectively. Genetic diversity analysis in terms of Shannon's index and Nei's gene diversity for resistant, susceptible and miscellaneous cultivars show higher values for miscellaneous cultivars indicating more variability in these cultivars.

Tilahun *et al.* (2015) conducted study with objective to assess genotypic variability, heritability and correlation of 17 kabuli-type genotypes yield character under rainfed. The experiments were conducted with four replications including 17 diverse genotypes of chickpea. Significant genetic differences between treatments for all traits were found which suggested scope of genotypes selection with desirable trait. High heritability for 100-seed weight and pod per plant. Evaluation of correlation coefficients found that plant biomass, pods per plant, harvest index and plant height were positive correlation with grain yield. The characters which shown high heritability and genetic advance were controlled by additive genes which give the chance for their improvement through selection.

Thudi *et al.* (2016) analysed, the re-sequencing data for 29 varieties available from an earlier study was also included. Copy number variations and presence absence variations identified in study to drive phenotypic variations for trait improvement. Our study also reports enhanced diversity in kabuli and desi varieties as result of recent chickpea breeding. The present study will aid the explicit efforts to breed for adaptation to local in the context of anticipated climate changes.

Ahmad and Talebi (2017) found that results of variance analysis and descriptive statistics for morphological traits indicated that the treatments differed significantly for all studied characteristics. Number of polymorphic bands varied from 6 to 9 with an average of 7.14 bands per primer. PIC values range from 0.26 (SCoT22) to 0.45 (SCoT15), Cluster analysis Based on SCoT-PCR markers grouped 35 chickpea genotypes into three major clusters. Results showed a weak relationship between morphological divergence and molecular diversity pattern. Overall, we found relatively high genetic diversity in examined chickpea genotypes using morphological and SCoT molecular markers.

Aarif *et al.* (2017) estimated genetic diversity using Mahalanobis D^2 statistics was studied in 22 treatments of kabuli chickpea (*Cicer kabulium* L.) for seed yield, its components and seed quality character. The 22 genotypes were form three clusters based on D^2 analysis. The cluster III and I were largest which consist of 9 treatments each and cluster II had 4 treatments. The highest inter-cluster distance was seen in cluster III and II, cluster II and II whereas, cluster III and I with minimum distance. The high intra-cluster distance was found in cluster III cluster

II and in cluster I found minimum intra-cluster distances. The genotypes HK-06-163 and KAK-2 of cluster I having high seed yield per plant should be included in hybridization programme.

Adnan *et al.* (2017) evaluated three parental and two F_3 populations (NDC-4-20-4, ICC-19181, NDC-5-S10, ICC-19181 x NDC-4-20-4, ICC-19181 x NDC-5-S-10) were evaluated for variability and interrelationship at Malakandher research farm, The University of Agriculture Peshawar during chickpea growing season 2011-12. Analysis of variance revealed promising differences ($P \leq 0.01$) among populations for pods plant^{-1}, secondary branches plant^{-1}, seed yield plant^{-1}, days to flowering and days to maturity. Furthermore, significant differences were shown for primary branches plant^{-1}, plant height and seed yield kg ha^{-1}. F3 population of C1 revealed maximum values for pod plant^{-1}, secondary branches plant^{-1} (14.88), seed yield plant^{-1} (19.65 g), biological yield plant^{-1} (36.92g) and harvest index (52.78 g). Whereas, population of C_2 showed high value for primary branches plant^{-1} (5.00) and days to flowering (141.34). On the other hand, ICC-19181 showed minimum values for days to flowering (132), plant height (32.91 cm) and seed yield plant^{-1} (14.14 g).

Ambilwade *et al.* (2018) undertook the investigation with thirty-five genotypes of chickpea, (including one check) during *Rabi* 2017-18 at Field observed for ten characters to study genetic variability parameters, heritability (b. s) and genetic diversity. Analysis of variance among 35 genotypes showed highly significant difference. Thirty-five genotypes were grouped into six heterogeneous clusters. Among these clusters Cluster VI has maximum number of genotypes.

Thakur *et al.* (2018) conducted study on 100 promising chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D^2 Statistics. Based on D^2 values, grouping of 100 genotypes into twelve clusters. The cluster I included of maximum 49 genotypes, Cluster VII, cluster III and cluster IX, which had 12, 16 and 12 genotypes, respectively. The highest intra cluster distance was seen in clusters IX (7.66) followed by cluster VII (6.52), VIII (6.65), cluster I (5.46) and clusters III (6.13). Inter-cluster values range from 2.65 to 14.85.

Akhil *et al.* (2019) investigate 51 genotypes of chickpea including one check; these genotypes were obtained from ICAR (IIPR). Based on D^2 values, 51 treatments grouped into 8 clusters. The cluster V consisted of high 18 genotypes, Cluster II and cluster VIII, which had 9 and 11 genotypes, respectively. Intra cluster values varied from 9.73 to 44.94. The high intra cluster distance was found in cluster II (44.54) followed by cluster IV (42.59), V (42.64), cluster VIII (39.36) and cluster VII (37.25). Inter-cluster values range from 31.78 to 75.10.

Farahani *et al.* (2019) studied 186 chickpea genotypes including advanced "Kabuli (*Cicer kabulim*)" breeding lines and Iranian landrace "Desi (*Cicer arieatinum*)" chickpea genotypes, were genotyped using DArTseq-Based single nucleotide polymorphism (SNP) markers. Out of 3339 SNPs, 1152 markers with known chromosomal position were selected for genome diversity analysis. Linkage disequilibrium (LD) was extensive and LD decays in chickpea germplasm was

relatively low. High genetic diversity and low kinship value between pairs of genotypes suggest the presence of a high genetic diversity in the studied chickpea genotypes. This experiment also demonstrates the efficiency of DArTseq-based SNP genotyping for large-scale genome analysis in chickpea. The genotypic markers provided in this experiment are useful for various association mapping studies when combined with phenotypic traits, such as seed yield, abiotic and biotic stresses and therefore may be efficiently used in breeding programs to improve chickpea.

Jida and Alemu (2019) evaluated nineteen elite varieties of chickpea in Ethiopia were used to and three replications were used. These nineteen treatments of chickpea were estimated for the traits of plant height, hundred seed weight, biological yield, days to 50 per cent flowering, grain yield, primary branches, secondary branches, seeds per plant, pods per plant and days to 90 per cent maturity. Genetic variations were evident among released chickpea cultivars as confirmed by high phenotypic and genotypic variations for quantitative and qualitative characters. Analysis of variance shown significant differences in the treatments for all the character except days of 50 per cent flowering and grain yield.

Sachdeva *et al.* (2019) investigated genetic diversity among 40 chickpea (*Cicer arietinum* L.) genotypes using 125 microsatellite (SSR, simple sequence repeat) markers. Twenty-five polymorphic markers with average genetic diversity and PIC (Polymorphic Information Content) value of 0.489 and 0.437, respectively, generated a total of 90 alleles. High PIC and gene diversity (HE) values indicated good variability amongst the chickpea genotypes. Sequential Agglomerative Hierarchical Non-overlapping (SAHN) grouping revealed two main clusters with 29 treatments in clusters I and 11 treatments in cluster II. The clusters analysis does not follow geographical diversity rather it was in agreement for genetic diversity with respect to seed type and parentage per pedigree. Grouping clearly delineated the diverse kabuli and desi genotypes. Molecular variance analysis also indicated 97 per cent variation within the populations and 3 per cent variation among the populations.

Tamvar *et al.* (2019) conducted field experiment during *rabi* 2018 for study of genetic diversity in 61 different genotypes of chickpea using D^2 statistics (Mahalanobis 1936). The 60 genotypes of chickpea were grouped into five clusters suggest the wide genetic diversity among them. The cluster pattern of the treatments was independent of their geographical distribution. Among different twelve traits studied protein content, seed yield per plant, flowering contributed in genetic divergence. Based on inter-cluster distance clusters III and IV followed by IV and V, and II and IV had maximum inter-cluster distance.

Dar *et al.* (2020) conducted genetic diversity study in 38 chickpea (*Cicer arietinum* L.) genotypes. total seven clusters have been formed and range of D^2 values is from 301.68 to 8477.61, cluster II includes maximum 12 genotypes after that cluster I having 9 genotypes, cluster IV having 6 genotypes, cluster and having 4 genotypes, cluster having 2 genotypes and

cluster VII with 1 genotype. The minimum inter-cluster distance (949.33) possessed by clusters I and II. After comprehending the intra cluster divergence found that cluster IV has highest intra cluster distance (647.07) then cluster I (449.16). Since cluster VII includes only one genotype which indicates that there is no intra-cluster divergence. Total nine character have been evaluated, plant height registered higher divergence (49.15%) then pods plant^{-1} (36.22%), days to 50% flowering (4.23%) and days to maturity (2.8%), secondary branches plant^{-1} (3.34%), seed yield plant^{-1} (1.38%) and primary branches plant^{-1} (1.24%). The 100-seed weight (1.22%) and seeds pod^{-1} (1.12%) possesses less divergence.

Mohibullah *et al.* (2020) carried out study during 2017-2018 for earliness, phonological and yield related genetic parameters in desi (*Cicer arietinum* L). genotypes at Agriculture Research Institute, D. I. Khan, Pakistan. Sixteen chickpea genotypes including 14 accessions along with 2 check varieties (Bittle-2016 and Bhakkar -2011) were grown and evaluated. High variation was noted in the chickpea germplasm in days to germination, seeds per pod, 1st branches plant^{-1}, secondary branches plant^{-1}, hundred grain weight, grain yield plant^{-1} and plant height.

Tsehaye and Fikre (2020) conducted study in 100 promising chickpea (*Cicer arietinum* L.) genotypes. The intra- cluster distance values were ranged from 5.4 (cluster IV) to 76.8 (cluster VIII). The high inter-cluster distance was seen between genotypes of cluster VIII and clusters I (873.5) cluster II and cluster I (827.4), cluster V and clusters I (749.3), cluster I and clustesr III (481.4), cluster I and cluster VII (423.7).

3. MATERIALS AND METHODS

The present investigation "Genetic Diversity in Chickpea (*Cicer arietinum* L.)*"* was conducted at Post Graduate Research Farm, Rajarshi Chhatrapati Shahu Maharaj College of Agriculture, Kolhapur, during *rabi* 2020-2021. The details of the material used and procedures followed during the course of this investigation are given below.

3.1 Materials:

For the present study 30 genotypes of chickpea originating from different geographic regions and showing phenotypic variability for different agronomic and yield characters were used from the germplasm maintained by Pulses Improvement Project, MPKV, Rahuri.

3.2 Methods

3.2.1 Raising of Seedling:

The 30 genotypes of chickpea were sown in a randomized block design with three row of each entry and three replications, 2-3 grains were dibbled per hill to ensure better crop stand and a single seedling was kept per hill after thinning of seedlings. Each genotype was sown in three rows with (Net:- 4.8 m x 0.90 m) plots area with two border row (Gross:- 5 m x 0.90 m), 1 m spacing between plots and blocks, respectively using 30 cm row to row and 10 cm spacing between plants.

3.2.2 Sowing date: - 16th Dec 2020.

3.2.3 Cultural Practices:

All recommended agronomic practices were carried out as and when required. Dose of fertilizer applied to chickpea was 25 kg N, 50 kg P_2O_5 and 00 kg K_2O ha^{-1} as basal dose during land preparation.

3.3 Observations Recorded:

The observations on following 10 quantitative characters were recorded on five randomly selected plants from each plot in each replication. These plants were tagged before flowering. The characters studied and techniques adapted to record observations are given below.

3.3.1 Morphological Traits

3.3.1.1 Days to 50 per cent flowering:

The date at which 50 per cent of all the plants in a plot had at least one open flower (then calculated to days to 50 per cent flowering) each plot was recorded.

3.3.1.2 Days to maturity:

The total number of days taken by each entry from sowing to the date on which more than 90 per cent of plants showed drying up confirmed by hardness of seed to bite were taken as days to maturity.

3.3.1.3 Plant height (cm):

Mean of 5 plants per plot measured from the base of the plant to the tallest tip of each plant.

Table 3.1 List of genotypes

Sr. No.	Accession No	Trial	Identity	Source
1.	**C-19153**	**IVT(D)**	Phule G- 171105	MPKV, Rahuri
2.	**C-19155**	**IVT(D)**	NBeG- 698	MPKV, Rahuri
3.	**C-19159**	**IVT(D)**	GCP 101	MPKV, Rahuri
4.	**C-19171**	**IVT(D)**	H-12-22	MPKV, Rahuri
5.	**C-19183**	**IVT(D)**	BG-4011	MPKV, Rahuri
6.	**C-19187**	**IVT(D)**	PG-227	MPKV, Rahuri
7.	**C-19188**	**IVT(D)**	BAUG-106	MPKV, Rahuri
8.	**C-19190**	**IVT(D)**	ADBG-487	MPKV, Rahuri
9.	**C-19193**	**IVT(D)**	RVSSG-79	MPKV, Rahuri
10.	**C-19202**	**IVT(D)**	IPCD -2016-44	MPKV, Rahuri
11.	**C-19293**	**IVT(DR)**	Phule G- 1107-5	MPKV, Rahuri
12.	**C-19298**	**IVT(DR)**	GJG-1721	MPKV, Rahuri
13.	**C-19304**	**IVT(DR)**	NBeG-1632	MPKV, Rahuri
14.	**C-19308**	**IVT(DR)**	RSGD-1068	MPKV, Rahuri
15.	**C-19309**	**IVT(DR)**	DBGC- 4	MPKV, Rahuri
16.	**C-19312**	**IVT(DR)**	GJG- 1712	MPKV, Rahuri
17.	**C-19318**	**IVT(DR)**	C 19318	MPKV, Rahuri
18.	**C-19319**	**IVT(DR)**	Phule G- 1201-20	MPKV, Rahuri
19.	**C-19321**	**IVT(DR)**	NBeG- 857	MPKV, Rahuri
20.	**C-19326**	**IVT(DR)**	IPCB- 2016-222	MPKV, Rahuri
21.	**C-19482**	**DTIL**	IPC- (L4-25)	MPKV, Rahuri
22.	**C-19483**	**DTIL**	RSG-888 (ch)	MPKV, Rahuri
23.	**C-19486**	**DTIL**	NC-2	MPKV, Rahuri
24.	**C-19490**	**DTIL**	Pusa -362 (ch)	MPKV, Rahuri
25.	**C-19492**	**DTIL**	BGM-10220	MPKV, Rahuri
26.	**Vijay**	**--**	**(Check)**	MPKV, Rahuri
27.	**Vishal**	**--**	**(Check)**	MPKV, Rahuri
28.	**Digvijay**	**--**	**(Check)**	MPKV, Rahuri
29.	**Phule Vikrant**	**--**	**(Check)**	MPKV, Rahuri
30.	**Phule Vikram**	**--**	**(Check)**	MPKV, Rahuri

3.3.1.4 Number of primary branches per plant:

Branches arising from main stem were considered as basal or primary branches which were counted and recorded at the time of harvest.

3.3.1.5 Number of secondary branches per plant:

Fruiting branches arising from primary branches were recorded as secondary branches at the time of harvest.

3.3.1.6 Number of pods per plant:

The total number of pods was counted from five randomly selected plants at physiological maturity and average was worked out at harvest.

3.3.1.7 Number of seeds per pod:

The observation was recorded by taking the seeds of randomly selected five pods from a plant and the average of five plants was estimated.

3.3.1.8 Seed yield/plant (g):

Seeds of all the five selected plants in each plot were weighed and average yield per plant was recorded.

3.3.1.9 100- seeds weight (g):

Weight of one hundred randomly selected filled grains was recorded in gram for each genotype in each replication.

3.3.1.10 Protein content (%):

Protein content of each genotype is estimated and average of three replications is determined as protein percentage.

The chemical analysis of protein was done by standard biochemical procedure. Seed sample from selected plant were grinded in a grinder and 0.2 g of grinded sample was analysed in laboratory for protein content. Percent crude protein of the chickpea sample was estimated by determining total nitrogen content of seed by adopting Micro-Kjeldhal distillation method and percent protein was calculated by using formula

Protein (%) = Nitrogen % x 6.25

The percent protein in seeds was calculated by multiplying percent nitrogen in sample by 6.25 representing the common factor for material used.

3.3 Statistical Analysis:

The data collected for each character on individual plant basis for five randomly selected plants were analysed first by randomized block design (Panse and Sukhatme, 1967) to test the significance of differences among the genotypes. The analysis for divergence was done by following Mahalanobis (1936) D^2 stastistic. The path coefficient analysis was carried by the procedure suggested by Dewey and Lu (1959). The variability parameters were measured by the formula suggested by Johnson *et al.* (1955b).

3.4.1 Analysis of variance (ANOVA):

The analysis of variance was done as suggested by Panse and Sukhatme (1985) in following form.

Source of variation	DF	MSS	Expected mean square
Replication	(r-1)	RMS	σ2e + t σ2r
Treatment	(t-1)	TMS	σ2e + r σ2r
Error	(r-1) (t-1)	EMS	σ2e
Total	(rt-1)		

Where,

r = Number of replications,

t = Number of treatments,

e = Error.

3.4.2 Estimation of mean and range:

The mean values for each character were worked out by the following formula:

$$X = \frac{1}{N} \sum_{i=1}^{n} Xi$$

Where,

X = Mean of character

Xi = Sum total of characters

N = Number of observations

The difference between the highest and the lowest values, from mean of each character were recorded as range.

3.4.3 Estimation of standard error of mean, standard error of difference and critical difference:

i. The S.E. of mean difference was calculated as

$$\text{S.E. of mean (SEm)} = \sqrt{\frac{\sigma^2 e}{r}}$$

ii. The standard error of difference between two means was

Calculated as:

S.E. of difference [SE (d)] = SEm x $\sqrt{2}$

iii. The critical difference between any two means was

Calculated as,

C.D. = SE (d) x "t" at error d.f.

3.4.4 Estimation of components of variation:

The phenotypic and genotypic variance was calculated by utilizing the respective means square values from the variance Table (Johnson *et al*., 1955a).

I. Environmental variance (σ^2 e) =MSe

II. Genotypic variance (σ^2 g) = (MSt –MSe) / r

III. Phenotypic variance (σ^2p) = σ^2g +σ^2

Where,

MSt = Treatment mean sum of square

MSe = Error mean sum of square

r = Number of replications

3.4.5 Estimation of coefficient of variation:

The genotypic and phenotypic coefficient of variation was calculated by the formulae as suggested by Burton and Devane (1953).

i) Phenotypic coefficient of variation (PCV)

$$PCV = \sqrt{\sigma^2 p} / x \times 100$$

Where,

σ2p = Phenotypic variance and,

$\bar{X}$ = General mean of character

ii) Genotypic coefficient of variation (GCV)

$$GCV = \sqrt{\sigma^2 g} / \bar{x} \times 100$$

Where,

σ^2g = Genotypic variance and,

$\bar{\bar{x}}$ = General mean of character.

3.4.6 Estimation of heritability percentage (h^2 b.s):

Heritability percentage in broad sense was estimated as per the formula given by Burton (1952).

h^2 (b.s) = (Vg / Vp) ×100 or h^2 (b.s) = ($\sigma^2 g / \sigma^2$ p)×100

Where,

h^2 (b.s) = Heritability in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Robinson (1966).

Low heritability = 5-10 percent.

Moderate heritability = 10-30 percent.

High heritability = 30-60 percent.

3.4.7 Estimation of genetic advance:

Genetic advance was calculated by the formula given by Johnson *et al*. (1955a).

$GA = K \times (\sigma^2 g / \sigma^2 p) \times \sigma p$ or $GA = K \times h^2 \times \sigma p$

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

σp = phenotypic standard deviation

h^2 (b.s) = heritability broad sense

$\bar{X}$ = Mean of the character

The range of genetic advance as per cent of mean was classified by Johnson *et al*. (1955a)

Less than 10 per cent : Low

10 - 20 per cent : Moderate

More than 20 per cent: High

3.4.8 Mahalanobis generalized distance:

The generalized distance between two population is defined by Mahalanobis (1936) as

$D^2 = \Sigma\Sigma \lambda i.j.\ di.\ dj$

Where,

$\lambda i.j$ = reciprocal matrix to the common dispersion matrix.

di = difference between the mean values of two Populations for ith character.

d j = difference between the mean values of two populations for jth character.

Estimation of D^2 values from the above formula is very complicated in the present study, since it requires the inversion of a tenth order determinant and then the evaluation 55 of 10 (10+1)/2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variables reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977).

The coefficients for the transformation were obtained by dividing the first row of reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.9 Determination of group constellation:

Tochers method as described by Rao, 1952 was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not a well-defined term. The only criteria appears to be that any two groups belonging to same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. A simple device suggested by K. D. Tocher described by Rao (1952) is to start with the two closely associated groups and find a third group which has the smaller D^2 from the two. Similarly the

fourth is chosen to have the smaller D^2value from the first three and so on. If at any stage the average D^2 of group from those already listed appears to be high. Then this group does not fit in the former groups and is therefore, taken outside the former cluster. The group of first cluster is then omitted and rests are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to inclusion of an additional group.

3.4.10 Average intra and enter cluster D^2 and D values:

3.4.10.1 Average intra cluster D^2 :

The intra-cluster distances were calculated as

$$D^2 = \Sigma Di^2 / n$$

Where,

Di is sum of distances between all possible combinations (n) of the population included in a cluster.

3.4.10.2 Average inter cluster D^2:

The procedure followed for calculating the inter-cluster distance was first to measure the distance between cluster I and II, between I and III and between I and IV and so on. Likewise, the clusters were taken one by one and the distance from other clusters were calculated. The average inter-cluster distance was then calculated as:

$$D^2 = \frac{\Sigma \text{ distance between the population of cluster I and j}}{ni.nj}$$

Where,

ni = number of population in cluster i

nj = number of population in cluster j

3.4.10.3 Average intra and inter cluster distance (D):

$$D = \sqrt{D^2}$$

3.4.10.4 Cluster means:

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

3.4.10.5 Contribution of individual characters towards divergence:

In all the combinations each character was ranked on the basis of di = Yji − Ykj The first rank was given to highest mean difference. The percentage contribution was calculated on the basis of number of times a character appeared first in the rank in all combinations (Singh and Chaudhary, 1977).

3.4.10.6 Cluster diagram:

In D^2 analysis a line diagram is constructed with the help of D^2 or D values, which known as cluster diagram.

3.4.10.7 Genetic diversity as an index for desirable Parents for hybridization:

The possible limits to the parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyay (1984). They advised to delineate the divergence among parents into 4 divergence classes to take into account the variable magnitude of variation in parental divergence; the mean (M) and standard deviation (S) of values of divergence were calculated. The divergence classes were defined as follows,

DC_1=D> or = M+S

DC_2=D< (M+S) and > or = M

DC_3=D> or = (M-S) and < M

DC_4 =D< (M-S)

4. RESULTS AND DISCUSSION

The present investigation on "Genetic Diversity in Chickpea (*Cicer arietinum* L.)" was undertaken to know the genetic diversity of thirty genotypes for ten quantitative traits in *rabi,* 2020-21.

The results obtained in present investigation are discussed in this chapter.

4.1 Analysis of variance:

The analysis of variance of ten characters is presented in Table 4.1. It revealed that there was highly significant difference among the genotypes for all the characters under study. It indicated that appreciable amount of diversity among genotypes.

Table 4.1 Analysis of variance for 10 different characters in chickpea

Sr. No.	Characters	Mean sum of square		
		Replication (2)	Treatments (29)	Error (58)
1.	Days to 50 % flowering	2.4111	90.73**	2.2272
2.	Days to maturity	0.8444	183.72**	4.5226
3.	Plant height	7.6168	224.22**	8.2518
4.	Primary branches per plant	0.0786	8.97**	0.0696
5.	Secondary branches per plant	0.2472	58.14**	1.0242
6.	Pods per plant	0.0380	1646.85**	9.6153
7.	Seeds per pod	0.0063	0.107**	0.0125
8.	100-seed weight	0.5666	45.32**	1.2878
9.	Protein content	0.1045	5.00**	0.4573
10.	Seed yield per plant	0.3600	118.28**	1.6457

****indicate significant at 1 per cent level, values in parenthesis indicate degrees of freedom.**

4.2 Mean performance of genotypes:

Significant differences were revealed among all the thirty genotypes for all the yield components. The mean values of the genotypes for different characters studied are given in Table 4.2, while the estimates of range are given in Table 4.3.

4.2.1 Days to 50 per cent flowering:

Days to 50 per cent flowering ranged from 41 to 65.33 days with a mean flowering of 51.09 days. Among all the genotypes, H-12-22 (41.00) flowered early, whereas ADBG-487

(75.33) flowered very lately. Fourteen genotypes were earlier in flowering when compared to the mean flowering of the genotypes. GJG-1721 followed by BAUG-106 (43.67), NBeG- 857 (45.00) and Phule Vikram (45.67).

4.2.2 Days to maturity:

The mean values among the genotypes ranged from 84 to 120 days with a mean maturity of 99.28 days. The genotype H-12-22 (84.00) matured early while, Pusa -362 (Ch) (120.00) was found to be very late in maturity. Sixteen genotypes were found earlier in maturity when compared to mean maturity of genotypes. Genotype Phule-G-171105 (86.00) matured early followed by Phule Vikram (86.67), PG-227 (87.33) and BAUG-106 (91.33).

4.2.3 Plant height (cm):

The mean values of genotypes for plant height ranged from 26.19 to 65.93 cm with a general mean height of 43.48 cm. Among all the genotypes Phule G- 1201-20 was the shortest (26.19 cm) followed by Digvijay (28.01 cm) and C 19318 (61.33 cm), whereas, RVSSG-79 (65.93 cm) was the tallest. Eighteen genotypes were found dwarf in height as compared to their general mean height.

4.2.4 Primary branches per plant (No.):

Number of primary branches per plant ranged from 1.93 (ADBG-487) to 8.27 (BGM-10220) with mean 4.23. Ten genotypes recorded higher number of primary branches as compared to the mean performance. Genotype GCP 101 (7.33) produced maximum number of primary branches followed by RVSSG-79 (7.13), Digvijay (6.60), IPCB- 2016-222 (6.53) and BG-4011 (6.27).

4.2.5 Secondary branches per plant (No.):

Number of secondary branches per plant was minimum in genotype Pusa -362 (ch) (6.00),while maximum in case of IPCD -2016-44 (26.00) with mean 15.62. Sixteen genotypes recorded higher number of secondary branches per plant as compared to the mean performance. Phule Vikrant (23.00) was followed by GCP 101 (20.13), Phule G- 1201-20 (19.73) and C 19318 (19.50).

4.2.6 Pods per plant (No.):

Fourteen genotypes recorded higher values for number of pods per plant than the population mean 68.25. The genotype IPCD -2016-44 (124.00) recorded maximum numberof pods per plant followed by Phule Vikrant (113.49), GCP 101 (112.87), GJG-1721 (102.27) and Vijay (92.53). The genotype ADBG-487 (42.13) recorded minimum number of pods per plant.

4.2.7 Seeds per pod (No.):

Fourteen genotypes showed significantly superior number of seeds per pod when compared with population mean of 1.55. The variation for number of seeds per pod ranged from 1.00 to 1.80. The genotypes Phule G- 171105, BG-4011 and RVSSG-79 showed the

highest number of seeds per pod followed by Phule G- 1201-20 (1.73) and IPC- (L4-25), RSG-888 (ch), Phule Vikrant and H-12-22, respectively. Genotypes IPCD -2016-44, PG-227 and NBeG-1632 showed least number of seeds per pod.

4.2.8 100-seed weight (g):

The population mean for 100 seed weight was 24.22 g. The character 100-seed weight was varied between 17.27 g and 32.01 g. The genotype BG-4011 (32.01 g) recorded highest 100- seed weight followed by genotype Phule G- 1201-20 (30.55 g), NBeG-1632 (30.53 g), IPCB- 2016-222 (30.10 g) and BAUG-106 (28.14 g). Seventeen genotypes out of fifty-six showed higher 100-seed weight than population mean. The genotype GCP 101 showed lowest 100-seed weight (17.28 g).

4.2.9 Protein content (%):

The variation for protein content ranged between 20.13 to 25.46 per cent with mean of 22.93. The lowest protein content was recorded in case of Pusa -362 (Ch) while maximum in case of Phule Vikram followed by Phule Vikrant (25.37), IPC- (L4-25) (25.01), Phule G-1201-20 (24.96) and GJG-1721 (24.48), respectively. Fourteen genotypes recorded higher protein content than mean.

4.2.10 Seed yield per plant (g):

The seed yield per plant in the genotypes ranged from 3.96 to 30.58 g. The genotype Phule G- 1201-20 recorded the highest seed yield whereas PG-227 recorded the lowest seed yield per plant with mean seed yield 14.41 g. Fourteen genotypes recorded higher yield than the general mean. The highest seed yield per plant after Phule G- 1201-20 was recorded by IPCB- 2016-222 (28.90 g) followed by BG-4011 (23.68 g), ADBG-487 (22.43 g) and Phule Vikrant (21.01 g)

The genotype H-12-22 exhibited desirable *per se* performance for days to 50 per cent flowering and days to maturity. The genotype BGM-10220 recorded highest *per se* performance for number of primary branches per plant, while the genotype Phule Vikrant recorded highest *per se* performance for number of secondary branches per plant. The genotype Phule G- 1201-20 exhibited highest *per se* performance for plant height, the genotype IPCD -2016-44 recorded maximum number of pods per plant, while genotypes Phule G- 171105, BG-4011 and RVSSG-79 recorded highest number of seeds per pod. The genotype Phule G- 1201-20 exhibited highest *per se* performance for characters seed yield per plant. The genotype BG-4011 exhibited highest *per se* performance for 100-seed weight and protein content.

Therefore, it can be concluded that genotypes H-12-22, BGM-10220, Phule Vikrant, Phule G- 1201-20, IPCD -2016-44, Phule G- 171105, BG-4011, RVSSG-79, Phule G- 1201-20 and BG-4011 were the best genotypes having desired per se performance for yield components and can be used as potential parents in future crop improvement programme.

Table 4.2 Mean performance of 30 genotypes of chickpea evaluated for grain yield and components

Sr. No.	Name of genotype	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Primary branches per plant (No.)	Secondary branches per plant (No.)	Pods per plant (No.)	Seeds per pod (No.)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
		1	2	3	4	5	6	7	8	9	10
1.	Phule G- 171105	49.00	86.00	38.87	3.53	15.30	47.20	1.80	27.15	22.27	15.13
2.	NBeG- 698	45.67	96.33	52.31	3.20	14.27	75.40	1.47	24.87	24.22	11.11
3.	GCP 101	67.00	109.67	41.70	7.33	20.13	112.87	1.47	17.28	23.07	20.41
4.	H-12-22	41.00	84.00	40.46	4.40	16.07	55.93	1.67	20.97	22.40	10.77
5.	BG-4011	52.67	97.00	34.41	6.27	18.47	76.53	1.73	32.01	20.94	23.68
6.	PG-227	50.00	87.33	50.07	4.20	9.80	25.60	1.27	25.39	22.28	3.96
7.	BAUG-106	43.67	91.33	47.79	3.13	12.93	49.00	1.53	28.14	22.93	7.61
8.	ADBG-487	75.33	118.33	39.69	1.93	15.93	42.13	1.53	26.67	22.92	22.43
9.	RVSSG-79	51.67	101.67	65.93	7.13	13.27	53.60	1.73	24.71	24.04	15.64
10.	IPCD -2016-44	45.33	96.33	39.14	2.73	26.00	124.00	1.00	18.34	23.03	10.27
11.	Phule G- 1107-5	52.67	102.67	47.56	2.67	16.87	68.60	1.27	24.00	23.32	13.97
12.	GJG-1721	43.00	93.00	40.09	2.73	13.27	102.27	1.67	18.90	24.48	9.81
13.	NBeG-1632	47.67	104.00	40.06	3.27	16.73	55.93	1.33	30.53	21.81	11.55
14.	RSGD-1068	45.33	95.33	35.37	3.13	9.79	48.73	1.40	21.94	22.33	9.03
15.	DBGC- 4	54.67	104.33	35.92	3.73	15.20	64.40	1.40	23.85	24.04	12.47
16.	GJG- 1712	54.33	101.00	47.28	3.13	13.13	72.33	1.67	26.33	21.79	14.97
17.	C 19318	61.33	98.00	33.71	2.47	19.50	33.53	1.67	24.73	22.22	9.23
18.	Phule G- 1201-20	52.67	96.33	26.19	5.27	19.73	81.60	1.73	30.55	24.96	30.59
19.	NBeG- 857	45.00	100.33	47.74	3.53	19.20	87.67	1.67	26.29	23.25	10.91
20.	IPCB- 2016-222	57.67	110.00	40.15	6.53	18.73	63.11	1.67	30.10	22.27	28.90

Table continued….

Sr. No.	Name of genotype	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Primary branches per plant (No.)	Secondary branches per plant (No.)	Pods per plant (No.)	Seeds per pod (No.)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**
21	IPC- (L4-25)	53.33	98.67	50.77	2.67	10.87	46.80	1.73	27.19	25.01	11.27
22	RSG-888 (ch)	50.67	102.67	42.65	2.87	17.87	77.50	1.73	24.87	22.23	15.51
23	NC-2	47.67	103.00	37.42	2.73	7.53	44.87	1.33	20.99	21.93	13.00
24	Pusa -362 (ch)	56.00	120.00	59.67	2.93	6.00	63.67	1.53	21.19	20.13	6.67
25	BGM-10220	50.00	96.67	42.70	8.27	14.40	47.33	1.40	25.27	22.23	17.53
26	Vijay	72.67	111.33	50.08	6.07	17.80	92.53	1.47	19.81	22.86	13.60
27	Vishal	65.33	98.00	37.05	2.53	18.83	73.20	1.67	24.73	22.22	6.19
28	Digvijay	55.33	99.33	28.01	6.60	16.33	92.33	1.40	22.66	23.09	14.11
29	Phule Vikrant	55.67	97.00	55.47	5.22	23.00	113.49	1.73	18.88	25.37	21.01
30	Phule Vikram	45.67	86.67	53.04	2.73	11.53	75.43	1.53	20.28	25.47	17.94
	Mean	**51.09**	**99.28**	**43.48**	**4.23**	**15.62**	**68.25**	**1.55**	**24.22**	**22.93**	**14.41**
	C.V. (%)	**2.92**	**2.14**	**6.61**	**6.23**	**6.48**	**4.54**	**7.24**	**4.69**	**2.95**	**8.90**
	S.E.+/-	**0.86**	**1.23**	**1.66**	**0.15**	**0.58**	**1.79**	**0.06**	**0.66**	**0.39**	**0.74**
	C.D. at 5%	**2.44**	**3.48**	**4.69**	**0.43**	**1.65**	**5.07**	**0.18**	**1.85**	**1.11**	**2.10**

4.3. Parameters of Genetic variability:

The parameters of genetic variability *viz*., range of variability, GCV, PCV, heritability (bs), genetic advance, genetic advance as per cent of mean are summarized in Table 4.3. The important findings are presented as below.

The estimates of genetic parameters *viz.,* phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense, genetic advance and genetic advance as per cent of mean were computed for ten characters under two sowings.

The genotypic coefficient of variation measures the magnitude of genetic variability present in the crop. Since, it reflects the heritable portion of variability. It is considered to be more useful than phenotypic coefficient of variation. Moreover, the difference between phenotypic and genotypic coefficients of variation indicates the operation of sowing factors. Information on heritability along with genetic advance will be helpful in formulating selection criteria.

Heritability and genetic advance are regarded as important selection parameters. Burton (1952) suggested that genetic variation along with heritability estimates would give a better idea about the efficiency of selection. Heritability is a good index of the transmission of hereditary values from parent to their offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

Heritability estimates are generally influenced by the type of genetic material, sample size, method of sampling, conduct of experiment, method of calculation and effect of linkage, therefore, their scope in terms of prediction is restricted. Thus, heritability values coupled with genetic advance would be more reliable and useful in predicting the genetic gain under selection than heritability estimates alone.

The results on genetic parameters obtained in the present study are discussed here under two different sowings.

4.3.1. Coefficients of variation:

It is observed that the estimates for genotypic coefficients of variation (G.C.V.) were lower than the phenotypic coefficients of variation (P.C.V.) for all the characters, indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors. Similar findings were reported by Saki *et al*. (2009), Sewak *et al.* (2012), Kumar *et al.* (2016), Manikanteswara *et al*. (2018).

The trait protein content exhibited the lowest G.C.V. (5.37). Whereas, the seed yield per plant had the highest G.C.V. (43.28). It was followed by primary branches per plant (40.69), pods per plant (34.23), secondary branches per plant (27.94), plant height (19.52), 100-seed weight (15.82) and number of seeds per pod (11.48). The trait protein content exhibited the lowest P.C.V. (5.63). Whereas, the seed yield per plant had the highest P.C.V. (43.58). It was followed by primary branches per plant (40.85), pods per plant (34.33),

secondary branches per plant (28.19), plant height (19.89), 100-seed weight (16.05) and number of seeds per pod (12.21).

The estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) in the present study were highest for seed yield per plant followed by primary branches per plant, pods per plant, secondary branches per plant, plant height, 100-seed weight and number of seeds per pod indicating good scope for their improvement through selection. Also, these genotypes exhibited much variation among themselves with respect to these characters. Similar findings were also reported by Saki *et al*. (2009), Kumar *et al.* (2019a), Babbar *et al.* (2011), Manikanteswara *et al*. (2018) and *Balasaheb et al. (2018)* for pods per plant.

4.3.2 Heritability:

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicators of heritable portion of the variation (Burton, 1952). The broad sense heritability includes the contribution of additive gene effects, allelic interactions due to dominance and non-allelic due to epistasis.

The heritability (b.s.) estimate varied between 88.3 per cent (number of seeds per pod) to 99.4 per cent (number of pods per plant). High estimates of heritability were observed for almost all the attributes. High estimate of heritability was observed for number of pods per plant (99.4 %), followed by primary branches per plant (99.2 %), seed yield per plant (98.6 %), days to 50 per cent flowering (97.5 %), days to maturity (97.5 %), 100-seed weight (97.2 %), plant height (96.3 %) and protein content (90.9 %). Lowest estimate of heritability was observed for seeds per pod (88.3 %).

Saki *et al*. (2009) observed high heritability values for number of days to maturity, number of days to 50 per cent flowering, plant height, number of secondary branches and number of primary branches. Kumar *et al*. (2016) recorded similar results for plant height, protein content. Manikanteswara *et al*. (2018) noticed high heritability for number of pods per plant, seed yield per plant, plant height and 100-seed weight.

4.3.3 Genetic advance:

The character number of pods per plant (47.98) exhibited highest magnitude of genetic advance. Plant height (17.15), days to maturity (15.72), seed yield per plant (12.76) and days to 50 per cent flowering (11.05) shown moderate genetic advance. Lowest estimates of genetic advance observed for secondary branches per plant (8.91) followed 100-seed weight (7.78), primary branches per plant (3.54), protein content (2.42) and seeds per pod (0.34). Upadhyay *et al*. (2019) reported similar result for the pods per plant.

In the present investigation, number of pods per plant and days to maturity exhibited high estimates of heritability (b.s.) accompanied with high genetic advance, indicating that these traits could be predominantly governed by additive gene action and selection of these traits could be more effective for desired genetic improvement. Similar findings were reported

by Kumar *et al.* (2019b) observed high heritability coupled with high genetic advance, indicating presence of additive gene action for governing inheritance of characters for number of pods per plant. Manikanteswara *et al*. (2018) observed high heritability coupled with high genetic advance were obtained with number of pods per plant, seed yield per plant and 100 seed weight. Kumar *et al.* (2017) noticed high heritability withhigh genetic advance as percentage of mean for number of pods per plant.

High heritability for secondary branches per plant followed by 100 seed weight, primary branches per plant, protein content and seeds per pod with low genetic advance indicating that the characters are controlled by non-additive gene action *i.e*., dominance deviation or epistasis, and hence heterosis breeding will be effective for improvement of these characters.

On the contrary, high heritability and moderate genetic advance as percent of mean was observed for plant height, days to maturity, seed yield per plant, days to 50 per cent flowering indicating the influence of both additive and non-additive gene effects in the control of these characters. Hence, simple direct selection may not be effective to improve these traits. These traits could also be improved by using recurrent selection method. Similar results were found by Babbar *et al.* (2011).

4.3.4 Genetic advance as per cent of mean:

High value of genetic advance as per cent of mean was observed for seed yield per plant (88.52) followed by number of primary branches per plant (83.50), number of pods per plant (70.30), number of secondary branches per plant (57.05), plant height (39.46), and 100-seed weight (32.13) protein content (10.55) recorded lowest value of genetic advance as per cent of mean followed by days to maturity (15.84) days to 50 per cent flowering (21.63) and number of seeds per pod (22.21). Similar findings were also reported by Balasaheb *et al*. (2018) for pods per plant.

4.4 Correlation:

The genotypic correlation coefficients provide an estimate of an inherent association between genes controlling any two characters *i.e*., when two characters are invariably and linearly associated. The genetic mechanism causing such association may be due to pleiotropy or complete linkage between the two characters. Hence, genotypic correlation is of greater significance and canbe effectively utilized in formulating an effective selection scheme. It may also help to identify the characters those prove to be of little or no importance in the selection programme.

The genotypic correlations between yield and yield contributing ten characters studied are presented in Table 4.4. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients. Similar findings were reported by Manikanteswara *et al*. (2018), Babbar *et al.* (2011) and Tilahun *et al*. (2015).

4.4.1 Association between seed yield and its component:

The seed yield per plant recorded highly significant positive correlation with number of primary branches per plant (0.4887), number of secondary branches per plant (0.4118), number of seeds per pod (0.3715), days to 50 per cent flowering (0.3252), 100-seed weight (0.3086) also the seed yield per plant recorded significant positive correlation with days to maturity (0.2455) and protein content (0.2375) at genotypic level. While the seed yield per plant recorded highly significant negative correlation with plant height (-0.2845).

Similar results were reported for highly significant and positive correlation with seed yield by Babbar *et al.* (2011) for pods per plant and 100 seed weight; Ali *et al*. (2010) for primary branches, pods per plant and seeds per pod; Upadhyay *et al.* (2019) for number of pods per plant, seeds per pod and 100-seed weight.

4.4.2 Inter-relationship between yield components:

The correlation between yield components at genotypic level are presented below. Days to 50 per cent flowering was high significantly and positively correlated with days to maturity (0.6114) followed by number of primary branches per plant (0.2189) and 100 seed weight (0.2174). It was non-significantly and positively correlated with number of secondary branches per plant (0.1856) and number of pods per plant (0.0313). Whereas, days to 50 per cent flowering showed negative correlation with protein content (-0.1305) and plant height (-0.0770).

Days to maturity was non-significantly and positively correlated with 100 seed weight (0.1244), plant height (0.0718) and number of pods per plant (0.0001). Whereas, days to maturity showed significantly negative correlation with protein content (-0.3435). It was also non-significantly and negatively correlated with number of secondary branches per plant (-0.0473), number of seeds per pod (-0.0159) and number of primary branches per plant (-0.0106).

Plant height was positively correlated with number of seeds per pod (0.1366) and protein content (0.1815). Whereas, plant height showed significantly negative correlation with number of secondary branches per plant (-0.3117). It was also non-significantly and negatively correlated with 100-seed weight (-0.1913), number of pods per plant (-0.1137) and number of primary branches per plant (-0.0650). Adhikari *et al.* (2018) found that plant height is negatively correlated with grain yield per plant; Tilahun *et al.* (2015) and Manikanteswara *et al*. (2018) reported similar results for plant height.

Number of primary branches per plant was significantly and positively correlated with number of secondary branches per plant (0.2953). It was non-significantly and positively correlated with number of number of seeds per pod (0.1884) and number of pods per plant (0.0624). Whereas, number of primary branches per plant showed negative correlation with protein content (-0.0711) and 100 seed weight (-0.0468)

Table 4.3 Estimates of variability parameters for 10 different characters.

Sr. No.	Name of the Character	Range	Mean	G.C.V. (%)	P.C.V. (%)	Heritability (h^2) (bs) %	Genetic advance (at 5% K)	GA as % of mean (at 5% K)
1.	Days to 50 % flowering	41-65.33	**51.09**	10.63	10.77	97.5	11.05	21.63
2.	Days to maturity	84-120	**99.28**	7.79	7.88	97.5	15.72	15.84
3.	Plant height	26.19-65.93	**43.48**	19.52	19.89	96.3	17.15	39.46
4.	Primary branches per plant	2.66-7.33	**4.23**	40.69	40.85	99.2	3.54	83.50
5.	Secondary branches per plant	6-26	**15.62**	27.94	28.19	98.2	8.91	57.05
6.	Pods per plant	25.6-124	**68.25**	34.23	34.33	99.4	47.98	70.30
7.	Seeds per pod	1.0-1.8	**1.55**	11.48	12.21	88.3	0.34	22.21
8.	100-seed weight	17.27-32.01	**24.22**	15.82	16.05	97.2	7.78	32.13
9.	Protein content	20.13-25.46	**22.93**	5.37	5.63	90.9	2.42	10.55
10.	Seed yield per plant	3.96-30.58	**14.41**	43.28	43.58	98.6	12.76	88.52

Where, K = 2.06

Number of secondary branches per plant was significantly and positively correlated with number of pods per plant (0.6313), plant spread (0.3069) and plant height (0.2189). Whereas, number of secondary branches per plant showed positive and non-significant correlation with protein content (0.1704), number of seeds per pod (0.0490), and 100-seed weight (-0.0252).

The character number of pods per plant was significantly and positively correlated with protein content (0.3557), harvest index (-0.3332) and number of seeds per pod (-0.4826). It was significantly and negatively correlated with 100 seed weight (-0.3560). Whereas, the character number of pods per plant was negatively correlated with number of seeds per pod (-0.0639).

The character number of seeds per pod was significantly and positively correlated with 100-seed weight (0.3570). Whereas, it showed positively correlation with protein content (0.0848). Mohan *et al*. (2019) found similar results for protein content.

The trait 100 seed weight was non-significantly and negatively correlated with protein content (-0.1224).

On the basis of results, it is concluded that the wide range of variation in the characters is the basis of selection in a breeding programme. The study of correlations provides the inter relationships among the quantitative traits which is useful in the choice of breeding method for crop improvement. The genetic correlation coefficient provides close measure of association between characters, which is useful in overall crop improvement.

Yield is a complex character and the result of interaction between various yield components. The success of any breeding programme depends on the efficiency of selection. Thus, ithelps a breeder in selection of characters for future breeding programme.

In the present study, various quantitative characters were studied and their relation with yield as well as among themselves was examined using correlation analysis. Number of days to 50 per cent flowering, number of days to maturity, number of primary branches per plant, plant spread and number of pods per plant showed highly significant positive correlation among themselves indicating that simultaneous selection for these characters would result in improvement of high yielding chickpea genotypes.

4.5 Path analysis:

Path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficients into direct and indirect effects. In the present investigation, path analysis was worked out by following Dewey and Lu (1959) to estimate the magnitude and direction of direct and indirect effects of various yield and yield contributing characters. Correlation coefficients along with path effects provide more reliable information, which can be effectively used in various crop improvement programme. If the correlation between a causal factor and direct effect is more or less of equal magnitude, indicating the true and

perfect relationship between the traits and direct selection through these traits will be rewarding. However,if the correlation coefficient is positive and the direct effect is negative or negligible, the indirect causal factors are to be considered in simultaneous selection. Thus, path analysis provides the information about characters and their relative importance.

The direct and indirect contributions of each character towards seed yield per plant are presented in Table 4.5 The magnitude of genotypic correlation coefficient is important and considered for path analysis.

4.5.1 Direct effect:

Among the 10 characters studied, days to maturity (0.5451) recorded highest positive direct effect on seed yield per plant followed by protein content (0.4812), number of primary branches per plant (0.4693), number of seeds per pod (0.2598) and 100-seed weight (0.1944). The characters number of secondary branches per plant (0.1344) exhibited relatively low magnitude of positive direct effects on seed yield. The characters *viz*., plant height (-0.3534), days to 50 per cent flowering (-0.1926) and number of pods per plant (-0.0148) showed negative direct effects.

The characters *viz.,* days to maturity, number of primary branches per plant, number of seeds per pod and 100-seed weight recorded high and positive direct effect on seed yield per plant and correlationof these characters with seed yield was positively significant except days to maturity, indicating true and perfect relationship between yield and these characters, suggesting direct selection basedon these characters would help in selecting the high yielding genotypes in chickpea. Zali *et al.* (2010) studied positive direct effect on seed yield per plant was exhibited by days to 50 per cent flowering, number of pods per plant and plant height.

The characters *viz*., days to 50 per cent flowering and number of pods per plant showed negative direct effects however, they were significantly and positively correlated with seed yield per plant except indicating that they played their role *via* indirect effects. Singh *et al*. (2018) reported negative direct effect of days to 50 per cent flowering with pods per plant. Manikanteswara *et al*. (2018) found that, days to 50 per cent flowering, plant height and number of pods per plant showed negative direct effects.

Days to maturity exhibited high magnitudinal direct effect and also showed significantly positive correlation with seed yield per plant, indicating true and perfect relationship between these traits. However, number of primary branches exhibited high magnitudinal direct effectand significant association with seed yield per plant suggesting that under these circumstances restricted simultaneous model should be followed.

The residual effect determines how best the causal factors account for the variability of the dependent factor, the seed yield, in this case. In present study, residual effect was low (0.5254) indicating that characters studied consider sufficient for the variability in seed yield of chickpea.

Based on findings of the present investigations, the most desirable plant type should possess higher number of pods per plant, number of seeds per pod, number of primary branches per plant and number of secondary branches per plant and 100 seed weight.

4.5.2 Indirect effect:

Looking to the indirect effect of various characters, it was observed that the traits numberof primary branches per plant, number of secondary branches per plant, number of pods per plant,plant height, number of pods per plant, number of seeds per pod and 100 seed weight exhibited highly significant and positive correlation with seed yield per plant which was mainly due to indirect effects of number of pods per plant and number of seeds per pod. While, the character plant height had highly significant and negative correlation with seed yield per plant.

Days to 50 per cent flowering had significant and positive correlation with seed yield per plant (0.3252), through its positive indirect effect *via*, days to maturity followed by number of primary branches per plant, number of seeds per pod, 100-seed weight, plant height and number of secondary branches per plant but negative indirect effect through protein content, and pods per plant. Mohan *et al.* (2019) found similar results for days to 50 per cent flowering.

Days to maturity had significant and positive correlation with seed yield per plant (0.2455), through its positive indirect effect *via*, 100 seed weight but showed negative indirect effect through protein content followed by days to 50 per cent flowering, plant height, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod.

Plant height exhibited significant and negative correlation with seed yield per plant (-0.2845), through its positive indirect effect via, days to 50 per cent flowering followed by, protein content, days to maturity, number of seeds per pod and number of pods per plant but showed negative indirect effect mainly through number of secondary branches per plant followed by 100-seed weight and number of primary branches per plant.

Number of primary branches per plant had significant and positive correlation with seed yield per plant (0.4887), through its positive indirect effect via, number of seeds per pod followed by number of secondary branches per plant and plant height but showed negative indirect effect through days to 50 per cent flowering followed by protein content, days to maturity, 100-seed weight and pods per plant.

Number of secondary branches per plant exhibited significant and positive correlation with seed yield per plant (0.4118), through its positive indirect effect *via*, number of primary branches per plant followed by plant height, protein content, number of seeds per pod and 100 seed weight but showed negative indirect effect through days to 50 per cent flowering followed by days to maturity and pods per plant.

Table 4.4 Genotypic correlation coefficients of 9 characters of 30 genotypes of chickpea on seed yield

Name of the Character	Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	100-seed weight	Protein content	Seed yield perplant
Days to 50 % flowering	**1.0000**	0.6114**	-0.0770	0.2189*	0.1856	0.0313	0.1949	0.2174*	-0.1305	0.3252**
Days to maturity		**1.0000**	0.0718	-0.0106	-0.0473	0.0001	-0.0159	0.1244	-0.3435**	0.2455*
Plant height			**1.0000**	-0.0650	-0.3117**	-0.1137	0.1366	-0.1913	0.1815	-0.2845**
Primary branches per plant				**1.0000**	0.2953**	0.0624	0.1884	-0.0468	-0.0711	0.4887**
Secondary branches per plant					**1.0000**	0.6313**	0.0490	0.0252	0.1704	0.4118**
Pods per plant						**1.0000**	-0.0639	-0.3560**	0.3557**	0.2187*
Seeds per pod							**1.0000**	0.3570**	0.0848	0.3715**
100-seed weight								**1.0000**	-0.1224	0.3086**
Protein content									**1.0000**	0.2375*

***, ** Significant at 5 and 1 per cent level respectively.**

Number of pods per plant exhibited significant and positive correlation with seed yield per plant (0.4118), through its positive indirect effect via, protein content followed by number of secondary branches per plant, plant height, Primary branches and days to maturity but showed negative indirect effect through 100-seed weight followed by number of seeds per pod and days to 50 per cent flowering.

Number of seeds per pod exhibited significant and positive correlation with seed yield per plant (0.3482), through its positive indirect effect *via*, number of primary branches per plant followed by 100 seed weight, protein content, number of secondary branches per plant and number of pods per plant, but showed negative indirect effect through plant height followed by days to 50 per cent flowering and days to maturity.

100 seed weight exhibited significant and positive correlation with seed yield per plant (0.3086), through its positive indirect effect via, number of seeds per pod followed by days to maturity, plant height, number of pods per plant and number of secondary branches per plant. But showed negative indirect effect through protein content followed by days to 50 per cent flowering and number of primary branches per plant.

Protein content exhibited significant and positive correlation with seed yield per plant (0.2375), showed positive indirect effect mainly through days to 50 per cent flowering followed by number of secondary branches per plant and number of seeds per pod but showed negative indirect effect through days to maturity followed by plant height, number of primary branches per plant, 100 seed weight and pods per plant.

4.6 Genetic divergence:

Genetic divergence which is due to genetic factors is the basis for heritable improvement. Therefore, the plant breeders have always been fascinated by great amount of diversity in crop plants. The precise information about the genetic divergence therefore, is crucial for productive breeding programme. Genetically diverse parents are known to produce highly heterotic effects and consequently give desirable recombinants in breeding material. Multivariate analysis (D^2 statistic)is a measure that appraises the genetic diversity quantitatively among a set of genotypes given by Mahalanobis (1936). The 30 genotypes under study were therefore, assessed for genetic diversity based on 10 characters.

4.6.1 Genetic diversity based on a set of twelve characters:

The estimates of D^2 values corresponding to the pair of comparison between these genotypes ranged from 14.64 to 38.39 (Table No. 4.7). This clearly indicated that the presence of adequate diversity among the genotypes studied. Nimbalkar and Harer (2001), Thakur *et al*. (2018) also reported wide genetic diversity in chickpea germplasm.

4.6.2 Cluster formation:

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for selecting parents for hybridization programme. The theoretical concept

Table 4.5 Direct (diagonal) and indirect (above and below diagonal) effects of different characters towards grain yield at genotypic level in chickpea.

Name of the Character	Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	100-seed weight	Protein content	Seed yield per plant (g)
Days to 50 % flowering	**-0.1926**	0.3333	0.0272	0.1027	0.0249	-0.0005	0.0507	0.0423	-0.0628	0.3252
Days to maturity	-0.1178	**0.5451**	-0.0254	-0.005	-0.0064	0.0002	-0.0041	0.0242	-0.1653	0.2455
Plant height	0.0148	0.0391	**-0.3534**	-0.0305	-0.0419	0.0017	0.0355	-0.0372	0.0873	-0.2845
Primary branches per plant	-0.0422	-0.0058	0.023	**0.4693**	0.0397	-0.0009	0.049	-0.0091	-0.0342	0.4887
Secondary branches per plant	-0.0357	-0.0258	0.1101	0.1386	**0.1344**	-0.0094	0.0127	0.0049	0.082	0.4118
Pods per plant	-0.006	0.0002	0.0402	0.0293	0.0848	**-0.0148**	-0.0166	-0.0692	0.1712	0.2187
Seeds per pod	-0.0376	-0.0087	-0.0483	0.0884	0.0066	0.0009	**0.2598**	0.0694	0.0408	0.3715
100-seed weight	-0.0419	0.0678	0.0676	-0.022	0.0034	0.0053	0.0928	**0.1944**	-0.0589	0.3086
Protein content	0.0251	-0.1872	-0.0641	-0.0334	0.0229	-0.0053	0.022	-0.0238	**0.4812**	0.2375

R=0.5254

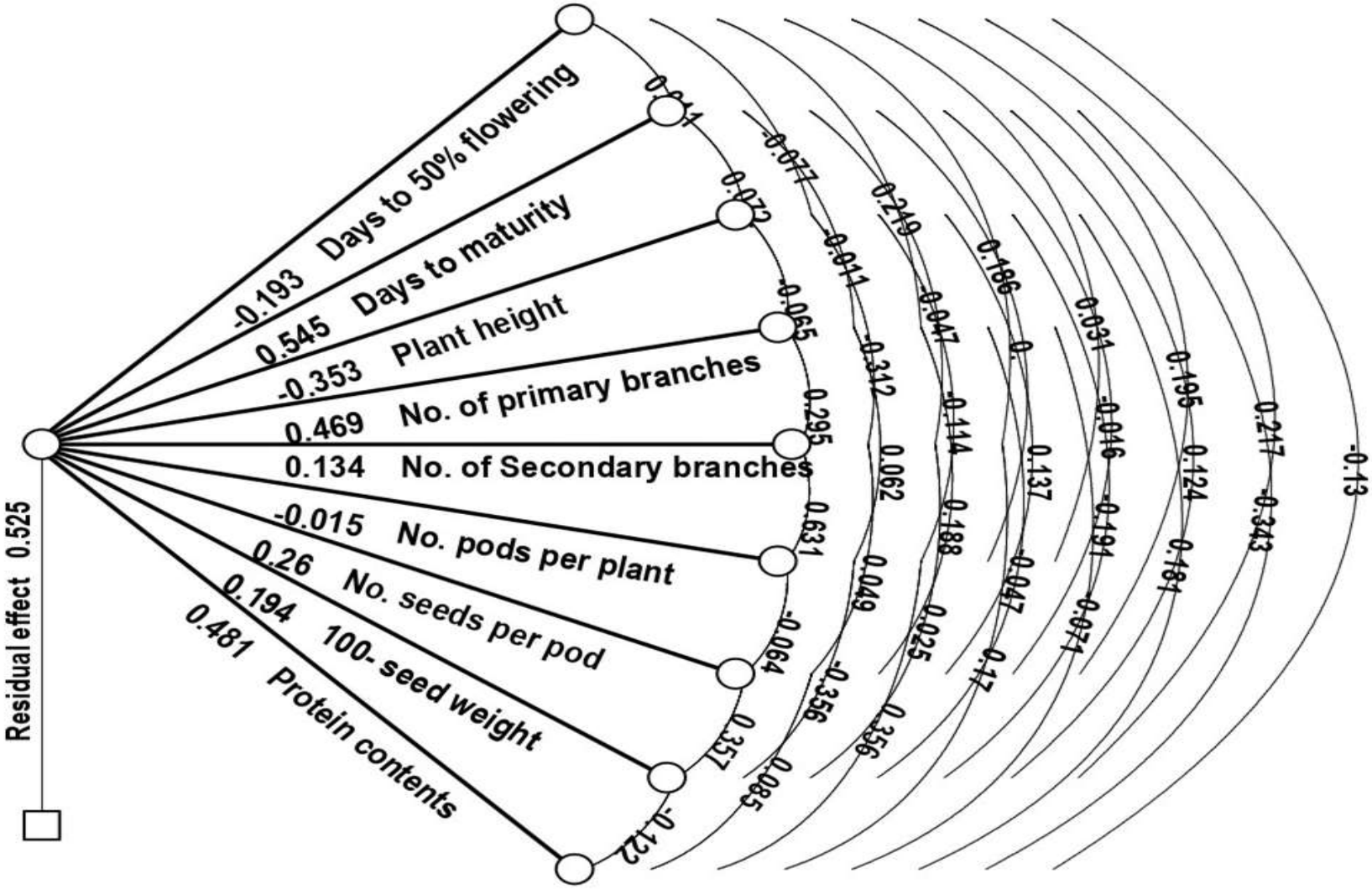


Fig. 1. Genotypical path diagram for seed yield per plant.

Table 4.6 Distribution of 30 genotypes into different clusters

Cluster no.	No. of genotypes included	Genotypes
I	17	Vijay, C 19318, H-12-22, Phule G- 171105, BAUG-106 NBeG-1632, RSGD-1068, DBGC- 4, GJG- 1712, Phule G- 1107-5, RSG-888 (ch), NBeG- 698, NBeG- 857, IPC-(L4-25), NC-2, Phule Vikram, PG-227
II	5	BG-4011, Phule G-1201-20, IPCB- 2016-222, BGM-10220, Digvijay
III	4	GCP 101, Phule Vikrant, GJG-1721, IPCD-2016-44
IV	1	Vishal
V	1	RVSSG-79
VI	1	ADBG-487
VII	1	Pusa-362(ch)

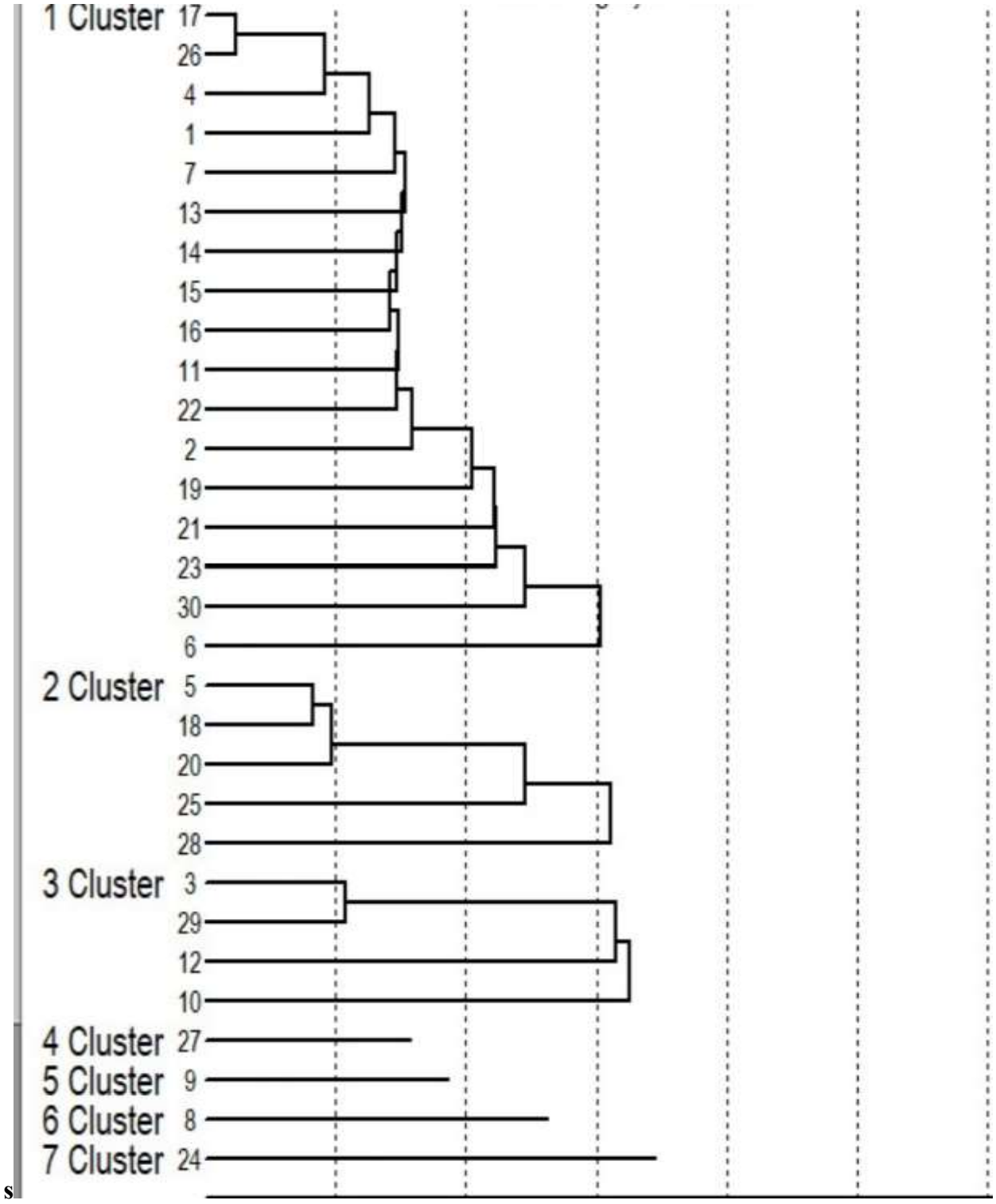


Fig.2 Dendrogram: Cluster formation of genotype

Table 4.7 Average intra and inter cluster D^2 and D values of 7 clusters formed from 30 chickpea genotypes.

Clusters	I	II	III	IV	V	VI	VII
I	**14.64 (3.83)**	22.71 (4.77)	26.66 (5.16)	19.09 (4.37)	22.96 (4.79)	21.61 (4.65)	23.25 (4.82)
II		**17.07 (4.13)**	29.43 (5.43)	29.45 (5.43)	21.51 (4.64)	28.10 (5.30)	36.01 (6.00)
III			**19.80 (4.45)**	27.05 (5.20)	31.54 (5.62)	38.39 (6.20)	32.63 (5.71)
IV				**0.00**	31.31 (5.60)	22.99 (4.79)	21.64 (4.65)
V					**0.00**	30.04 (5.48)	30.38 (5.51)
VI						**0.00**	25.44 (5.04)
VII							**0.00**

Figures in parenthesis indicate D value

behind such grouping is that the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to different clusters (Rao, 1952) and thus crossing between the genotypes belonging to the same clusters will not give desired results, so that the parents selected for crossing should be from different clusters. Greater the divergence between the two clusters, wider is the genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.,* 1965). Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean for the characters also need due consideration in the crop improvement programme.

The cluster formation was done by following Tocher's method, as described by Rao (1952). All the 30 genotypes under investigation were grouped into seven clusters. Cluster I with 17 genotypes emerged as the largest cluster followed by Cluster II with 5 genotypes and Cluster III with 4 genotypes. The Cluster IV, V, VI and VII were monogenotypic containing only one genotype. The distributions of 30 genotypes into different clusters are presented in Table 4.6. Similar results found by Kumar *et al.* (1998) On the basis of divergence, 17 genotypes under investigation have been grouped into 5 clusters. Nimbalkar and Harer (2001)

grouped 40 chickpea genotypes into 16 clusters. Out of that, 10 were solitary.

4.6.3 Intra and inter cluster distance:

Intra and inter cluster D^2 and D values were worked out using D^2 values from divergence analysis are presented in Table 4.7.

The maximum intra-cluster distance was found in Cluster III (4.45) followed by Cluster II (4.13) suggesting that genotypes included in the clusters might have genetically different architecture and might have originated from different genetic pool. However, the lowest intra-cluster distance was observed in Cluster I (3.83), indicating that the strains of this cluster resemble on another genetically and appeared to have evolved from common gene pool. The monogenotypic Clusters IV, V, VI and VII showed intra-cluster value 0.00.

The maximum inter-cluster distance was observed between Cluster III and Cluster VI (6.20) followed by Cluster II and VII (6.00), Cluster III and VII (5.71), Cluster III and V (5.62), Cluster IV and V (5.60) and Cluster V and VII (5.51) indicating that these clusters are more heterogeneous. This also suggests that the genetic architecture of the genotypes in one cluster differ entirely from those included in the other cluster. These results are also in conformity with Thakur *et al*. (2018).

The minimum inter-cluster distance was observed between Cluster I and Cluster IV (4.37) indicating proximity with each other, followed by Cluster II and Cluster V (4.64), Cluster I and Cluster VI (4.65), Cluster IV and Cluster VII (4.65), Cluster I and Cluster II (4.77), Cluster IV and Cluster VI (4.79) and Cluster I and Cluster V (4.79). The lower D^2 values between these clusters indicating the proximity with each other.

Cluster I was more distant from the Cluster III (5.16) followed by Cluster VII (4.82), Cluster V (4.79), Cluster II (4.77), Cluster VI (4.65), and Cluster IV (4.37). While, Cluster II showed the highest inter cluster distance from Cluster VII (6.00) followed by Cluster IV (5.44), Cluster III (5.43), Cluster VI (5.30) and Cluster V (4.64).

Cluster III showed the maximum distance from Cluster VI (6.20) followed by Cluster VII (5.71), Cluster V (5.62), and Cluster IV (5.20). Cluster IV showed the maximum distance from Cluster V (5.60) followed by Cluster VI (4.79) and Cluster VII (4.65). Cluster V showed the maximum distance from Cluster VII (5.51) followed by Cluster VI (5.48). The cluster VI has distance from cluster VII (5.04).

Critical examination of Table 4.7 indicated that the genotypes originating in different geographical area could form one cluster, while different genotypes evolved in the same area could be grouped into different clusters. Thus, clustering pattern of the genotypes in the present study revealed that the genetic diversity was not always related to geographical diversity. Mahalanobis (1936) revealed from clustering pattern of the genotypes that genetic diversity was not always related to geographical diversity confirming the present findings.

4.7 Cluster mean:

Cluster mean for 10 characters studied and presented in Table 4.8. It revealed wide range of variation for most of the characters.

4.7.1 Days to 50 per cent flowering (No.):

The genotypes in Cluster I (48.84) were earliest for days to 50 per cent flowering followed by Cluster III (50.25), Cluster V (51.67) and Cluster II (53.67), whereas genotypes in Cluster IV (65.33), Cluster VI (60.00) and Cluster VII (56.00) were late for days to 50 per cent flowering. Similar results found by Kumar *et al.* (1998); Balasaheb *et al.* (2018).

4.7.2 Days to maturity (No.):

Cluster means for this character were ranged between 96.94 and 120.00 days. The highest cluster mean for this character was recorded in Cluster VII (120) followed by Cluster VI (118.33), whereas the lowest cluster mean was observed in Cluster I (96.94) followed by Cluster I V(98.00) and Cluster IV (98.25). Similar results were also found by Kumar *et al*. (1998).

4.7.3 Plant height (cm):

Cluster V (65.93) showed maximum plant height followed by Cluster VII (59.67) and Cluster I (44.36). While, minimum plant height recorded in Cluster II (34.29), Cluster IV (37.05) and Cluster VI (39.69) similar results found by Kumar *et al.* (1998) and Balasaheb *et al*. (2018).

4.7.4 Primary branches per plant (No.):

Cluster means for this character were ranged between 2.53 and 7.13. The highest cluster mean for this character was recorded in Cluster V (7.13) followed by Cluster II (6.59) and Cluster III (4.51), whereas the lowest cluster mean was observed in Cluster IV

4.7.5 Secondary branches per plant (No.):

Cluster means for this character were ranged from 6.00 to 20.60. The highest cluster means for this character was recorded in Cluster III (20.60) followed by Cluster IV (18.38), Cluster II (17.53) and Cluster VI (15.93), whereas the lowest cluster mean was observed in Cluster VII (6.00) followed by Cluster V (13.27) and Cluster I (14.38). Similar results were also found by Balasaheb *et al.* (2018).

4.7.6 Pods per plant (No.):

The highest cluster mean for number of pods per plant was recorded by Cluster III (113.16) followed by Cluster IV (73.20), Cluster II (72.18) and Cluster VII (63.67). The Cluster VI (42.13) recorded lowest cluster mean followed by Cluster V (53.60) and cluster I (58.91).

4.7.7 Seeds per pod (No.):

Cluster means for number of seeds per pod were ranged from 1.47 to 1.73. The highest

cluster mean for this character was recorded in Cluster V (1.73) followed by Cluster IV (1.67) and Cluster II (1.59), whereas the lowest cluster mean was observed in Cluster III (1.47), Cluster VI (1.53), Cluster VII (1.53) and Cluster I (1.54).

4.7.8 100-seed weight (g):

The highest cluster means for 100-seed weight was recorded by Cluster II (27.32) followedby Cluster IV (26.73) and Cluster VI (26.67). The lowest cluster mean was recorded by Cluster III (18.85) followed by Cluster VII (21.19) and Cluster I (24.43). Similar results were also reported by Kumar *et al.* (1998) and Balasaheb *et al*. (2018).

4.7.9 Protein content (%):

The highest cluster mean was recorded for Cluster V (24.04) followed by Cluster III (23.99) and Cluster VI (22.92). The least cluster mean was observed for Cluster VII (20.13) followed by Cluster VI (22.70).

4.7.10 Seed yield per plant (g):

Cluster VII (6.67) exhibited minimum seed yield per plant. Whereas, maximum seed yieldper plant recorded in Cluster II (22.96) followed by Cluster VI (22.43), Cluster V (15.64) and Cluster III (15.38).

4.8 Per cent contribution of 12 characters for divergence:

The per cent contribution of 10 characters studied towards total divergence is presented in Table 4.9. It was observed that number of pods per plant contributed highest (32.18 %) for divergence, followed by number of primary branches per plant (24.83 %), seed yield per plant (18.62 %), indicating that these characters were considerably responsible for total divergence in the material under study. Dar *et. al* (2020) reported that the character number of pods per plant contributed maximum in manifestation of genetic diversity. Akhil *et. al*. (2019) reported that characters, seed yield per plant are highest contributor towards divergence.

The contribution of other characters like days to 50 per cent flowering (6.21 %), days to maturity (4.60 %), number of secondary branches per plant (4.37 %), 100-seed weight (3.91 %), protein content (3.91 %), plant height (1.38 %) and number of seeds per pod (0.00 %), were magnitudinally low. Thus, some discrepancies in the characters contributing to divergence were observed in the present investigation and results of previous workers. Such discrepancies in the results might be due to thedifferent sets of material and also due to the role of environmental variability which was in contrast with results of Dar *et al.* (2020) and Nimbalkar and Harer (2001). The characters number of seeds per pod showed no contribution towards divergence.

4.4 Genetic divergence and selection of potent parents:

The success of crop improvement programme involves selection of the best parents having high potential for the economically important characters. Among the different

approaches of selecting parents, selection based on diversity has its own significance as diversity is the basic need of crop improvement.

In the present study, studies on diversity among different genotypes yielded valuable information, which could be useful in suggesting potent parents for crossing. The possible limits of parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyay (1984).

The cluster combinations were classified into four divergence classes (Table 4.10) as follows

On the basis of the above results, initially choice of the parents should be made from the cluster combinations falling in the divergence classes DC1, DC2 and DC3. However, while choosing among the genotypes of a cluster, the *per se* performance of genotypes for different traits such as seed yield per plant, number of secondary branches per plant, pods per plant, 100-seed weight, etc. should be taken into account, so that desirable segregates would be obtained after hybridization.

On the basis of divergence classes, the following genotypes are suggested for further breeding programme.

1) Pusa-362(ch)	2) Vishal	3) RVSSG-79	4) ADBG-487
5) GCP 101	6) Phule Vikrant	7) IPCD-2016-44	8) Digvijay
9) Phule Vikram	10) Vijay		

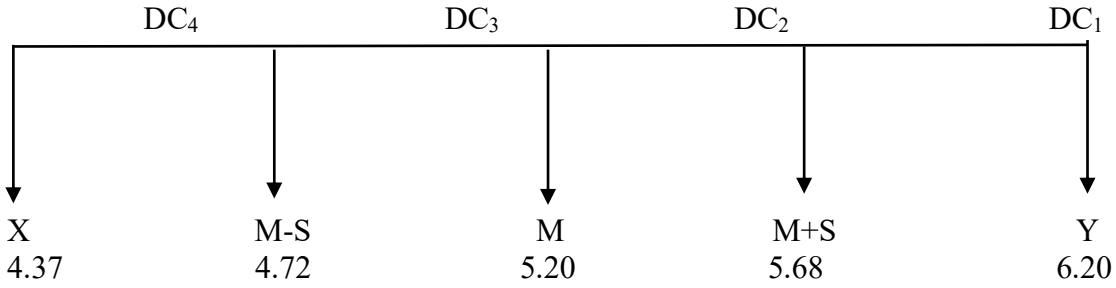
Table 4.8 Cluster means for 10 characters in chickpea.

Clusters	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Primary branches per plant (No.)	Secondary branches per plant (No.)	Pods per plant (No.)	Seeds per pod (No.)	100-seed weight (g)	Protein content (%)	Seed yield per plant (g)
I	48.84	96.94	44.36	3.58	14.38	58.91	1.54	24.43	22.90	12.06
II	53.67	99.87	34.29	6.59	17.53	72.18	1.59	27.32	22.70	22.96
III	50.25	98.25	44.10	4.51	20.60	113.16	1.47	18.85	23.99	15.38
IV	65.33	98.00	37.05	2.53	18.83	73.20	1.67	26.73	22.22	6.19
V	51.67	101.67	65.93	7.13	13.27	53.60	1.73	24.71	24.04	15.64
VI	60.00	118.33	39.69	2.69	15.93	42.13	1.53	26.67	22.92	22.43
VII	56.00	120.00	59.67	2.93	6.00	63.67	1.53	21.19	20.13	6.67

Table 4.9 Per cent contribution of various characters to divergence

Sr. No.	Characters	Times ranked 1st	Contribution (%)
1.	Days to 50 % flowering	27	6.21 %
2.	Days to maturity	20	4.60 %
3.	Plant height	6	1.38 %
4.	Primary branches per plant	108	24.83 %
5.	Secondary branches per plant	19	4.37 %
6.	Pods per plant	140	32.18 %
7.	Seeds per pod	0	0.00 %
8.	100 seed weight	17	3.91 %
9.	Protein content	17	3.91 %
10.	Seed yield per plant	81	18.62 %
	Total	431	100

Table 4.10 Distribution of different cluster combinations into 4 divergent classes based on D values between them.



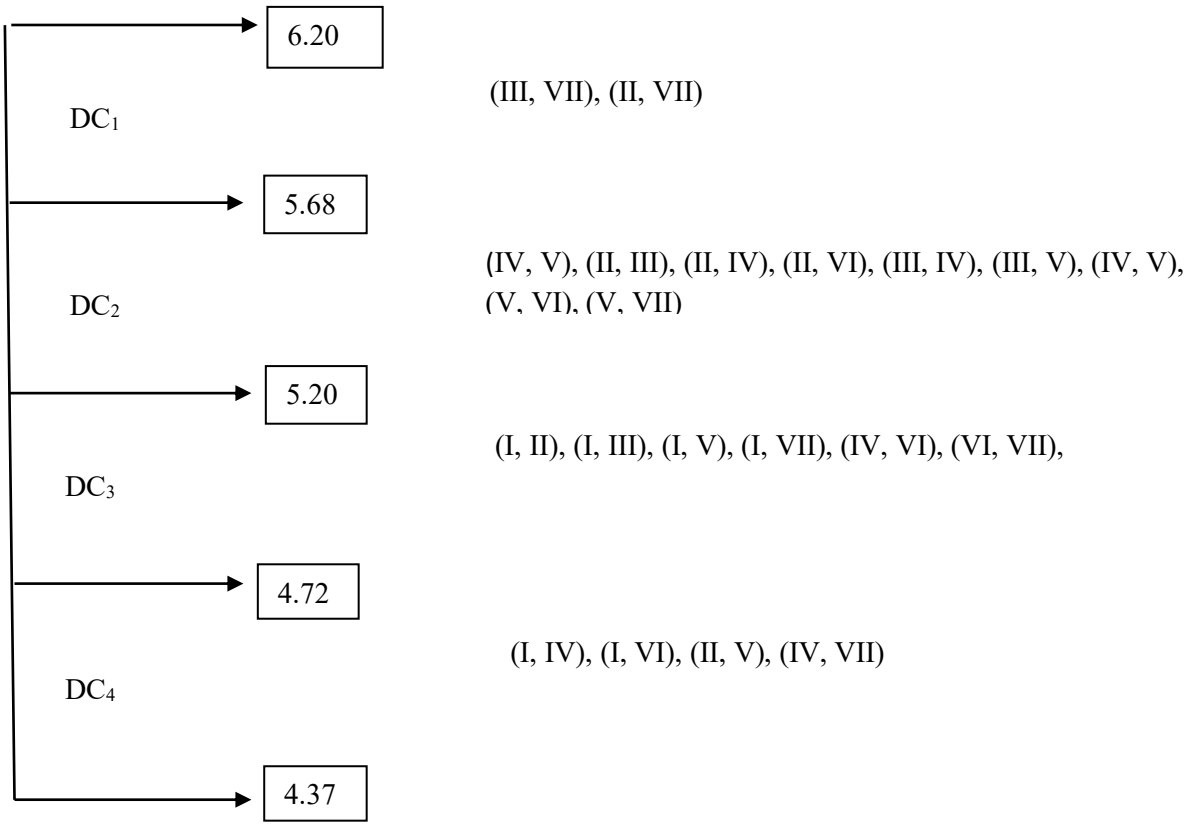


Table No. 4.20 Superior genotypes on the basis of cluster mean

Sr. No.	Source	Cluster	Genotypes
1.	Days to 50 % flowering	I, V	H-12-22, GJG-1721, RVSSG-79
2.	Days to maturity	I, IV	H-12-22, Phule G-171105, Vishal
3.	Plant height	II, IV	Phule G-1201-20, Digvijay,
4.	Primary branches per plant	V, II	RVSSG-79, BGM-10220, Digvijay
5.	Secondary branches per plant	III, IV	IPCD-2016-44, Phule Vikrant, GCP-101
6.	Pods per plant	III, IV	IPCD-2016-44, Phule Vikrant, Vishal
7.	Seeds per pod	V, IV	RVSSG-79, Vishal
8.	100 seed weight	II, IV	BG-4011, IPCB-2016-222, Vishal
9.	Protein content	V, III	GCP-101, Phule Vikrant, RVSSG-79
10.	Seed yield per plant	VI, II	Phule G-1201-20, IPCB-2016-222, ADBG-487

5. SUMMARY AND CONCLUSION

The present investigation "Genetic Diversity in Chickpea (*Cicer arietinum* L.)" was undertaken with the following objectives:

1. To study genetic diversity.
2. To find out the per cent contribution of characters towards genetic divergence.
3. Grouping of the genotypes into different clusters.
4. Identification of the parents for hybridization programme to develop high yielding chickpea.

Thirty genotypes of chickpea collected from Pulses Improvement Project, M. P. K. V. Rahuri, were used for the present investigation. The experiment was laid out in a Randomized Block Design with three replications during *rabi*, 2020-21. The 30 genotypes were evaluated for 10 yield and yield contributing characters *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondarybranches per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), protein content (%) and seed yield per plant (g).

The genotype H-12-22 exhibited desirable *per se* performance for days to 50 per cent flowering and days to maturity. The genotype BGM-10220 recorded highest *per se* performance for number of primary branches per plant, while the genotype Phule Vikrant recorded highest *per se* performance for number of secondary branches per plant. The genotype Phule G- 1201-20 exhibited highest *per se* performance for plant height, the genotype IPCD -2016-44 recorded maximum number of pods per plant, while genotypes Phule G- 171105, BG-4011 and RVSSG-79 recorded highest number of seeds per pod. The genotype Phule G- 1201-20 exhibited highest *per se* performance for characters seed yield per plant. The genotype BG-4011 exhibited highest *per se* performance for 100-seed weight and protein content.

Therefore, it can be concluded that genotypes H-12-22, BGM-10220, Phule Vikrant, Phule G- 1201-20, IPCD -2016-44, Phule G- 171105, BG-4011, RVSSG-79, Phule G- 1201-20 and BG-4011 were the best genotypes having desired *per se* performance for yield components and can be used as potential parents in future crop improvement programme.

Significant treatment mean sum of square for all the characters studied, revealed the presence of considerable amount of variability in genotypes evaluated. The magnitude of GCV and PCV were high for seed yield per plant, number of pods per plant, secondary branches per plant, plant height and 100-seed weight, indicating the presence of good amount of variability for these characters. The trait protein content exhibited the lowest G.C.V.

The heritability (b.s.) estimate varied between 88.3 per cent (Seeds per pod) to 99.4 per cent (number of pods per plant). High estimates of heritability were observed for almost all the attributes. High estimate of heritability was observed for number of pods per plant

(99.4 %), followed by primary branches per plant (99.2 %), seed yield per plant (98.6 %), days to 50 per cent flowering (97.5 %), days to maturity (97.5 %), 100-seed weight (97.2 %), plant height (96.3 %) and protein content (90.9 %). Lowest estimate of heritability was observed for seeds per pod (88.3 %).

Seed yield per plant was significantly and positively correlated with primary branches per plant, secondary branches per plant, seeds per pod, days to 50 per cent flowering, 100 seed weight also the seed yield per plant recorded significant positive correlation with days to maturity and protein content at genotypic level. While, the seed yield per plant recorded highly significant negative correlation with plant height.

In path coefficient analysis, days to maturity, protein content, primary branches per plant and seeds per pod showed maximum direct effect in the desirable direction. The association of these characters with the seed yield was also significant and positive except days to 50 per cent flowering, indicating the fact that there exists a true and perfect association between these characters. This also suggested that direct selection for these characters will help in isolating early and high yielding genotypes. However, days to 50 per cent flowering, plant height and number of pods per plant showed negative direct effects. However, these traits were significantly and positively correlated with seed yield except plant height which is significantly and positively associated with yield per plant, indicating that they played their role via indirect effects. Correlation and path analysis revealed that number of days to maturity, primary branches per plant and seeds per pod were good indicators of yield per plant in chickpea and can be used for making direct selection for yield.

In present study D^2 values between all possible pairs of 30 genotypes ranged from 19.09 to 38.39. All the genotypes under investigation were grouped into seven clusters. Cluster I with 17 genotypes emerged as the largest cluster followed by Cluster II with 5 genotypes and Cluster III with 4 genotypes. The Cluster IV, V, VI and VII were monogenotypic containing only one genotype.

The maximum intra-cluster distance was observed in the Cluster III (4.45) followed by Cluster II (4.13) and Cluster I (3.83) suggesting that genotypes included in these clusters might have genetically different architecture and might have originated from different genetic pool.

The maximum inter-cluster distance was observed between Cluster III and Cluster VI (6.20) followed by Cluster II and VII (6.00), Cluster III and VII (5.71), Cluster III and V (5.62), Cluster IV and V (5.60) and Cluster V and VII (5.51) indicating that these clusters are more heterogeneous. This also suggests that the genetic architecture of the genotypes in one cluster differ entirely from those included in the other cluster. The minimum inter-cluster distance was observed between Cluster I and IV (4.37) followed by Cluster II and Cluster V (4.64), Cluster I and Cluster VI (4.65).

In the present investigation number of pods per plant contributed highest (32.18 %) for divergence, followed by primary branches per plant (24.83 %), seed yield per plant (18.62 %). While, the contribution of character days to 50 per cent flowering (6.21 %), days to maturity (4.60 %), number of secondary branches per plant (4.37 %), 100 seed weight (3.91 %), protein content (3.91 %), plant height (1.38 %) and seeds per pod (0.00 %). The positive contribution of these yield components in genetic divergence may be considerably help in selecting genotypes for yield and other economic traits. However, the characters seeds per pod not contributed for divergence.

On the basis of divergence classes analysis, the genotypes were suggested for further breeding programme.

1) Pusa-362(ch)	2) Vishal	3) RVSSG-79	4) ADBG-487
5) GCP 101	6) Phule Vikrant	7) IPCD-2016-44	8) Digvijay
9) Phule Vikram	10) Vijay		

Conclusions

Based on present study, following conclusion have been drawn

1. Estimation of genotypic coefficients of variation (GCV) was lower than phenotypic coefficients of variation (PCV) for all the characters. The magnitude of GCV and PCV were high for seed yield per plant, primary branches per plant and pods per plant.
2. Heritability (b.s.) of all the characters in present investigation was ranging from 88.3 per cent (seeds per pod) to 99.4 per cent (number of pods per plant).
3. The genetic advance was found ranging from secondary branches per plant (8.91) to number of pods per plant (47.98).
4. All the characters were positively correlated with grain yield per plant except for the plant height.
5. All the characters were positive and direct effect on grain yield per plant except for the plant height, days to 50 per cent flowering and number of pods per plant.
6. The present investigation revealed that the cluster III and cluster VI, cluster II and cluster VII, cluster III and cluster VII are most diverse to each other, and the genotypes constituted in these clusters may be used as a parent for further hybridization programme.
7. The per cent contribution of 10 characters studied towards total divergence it was observed that number of pods per plant contributed highest (32.18 %) for divergence, followed by primary branches per plant (24.83 %), seed yield per plant (18.62 %), indicating that these characters were considerably responsible for total divergence in the material under study.

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(* - Original articles not seen)

VITAE

MR. PRAFUL KISAN PARSUDKAR

MASTER OF SCIENCE (AGRICULTURE)

GENETICS AND PLANT BREEDING

2021

Title of thesis		**:**	"GENETIC DIVERSITY IN CHICKPEA (*Cicer arietinum* L.)"
Major field		**:**	Genetics and Plant Breeding
Biographical information:			
Personal	**Date of Birth**	**:**	15th June 1997
	Place of Birth	**:**	Pandhurna (khu.) (Village), Yavatmal (Dist.)
	Father's name	**:**	Kisan Parsudkar
	Mother's name	**:**	Sunita
Educational	**Bachelor Degree Obtained**	**:**	Bachelor of Science in Agricultual
	Class	**:**	Ist class
	Name of University	**:**	Punjabrao Deshmukh Krishi Vidyapith, Akola
Address		**:**	Titvi (village), Rajurwadi (Post), Ghatanji (Taluka), Yavatmal (Dist.), Maharashtra Pin Code- 445301.
	Email-id	**:**	praful.parsudkar@gmail.com
	Contact Number	**:**	9011368550