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

by

Mr. Gulwane Vaibhav Parmeshwar
(Reg. No. 019/039)

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

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY

POST GRADUATE INSTITUTE,
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RAHURI - 413 722, DIST. AHMEDNAGAR,
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2021

CANDIDATE'S DECLARATION

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

Place : MPKV, Rahuri
Dated : / /2021 (V.P. Gulwane)

Dr. G.N. Deore
Associate Professor and Officer Incharge
Agriculture Research Station, Savalivihir
Tal. Rahata, Dist. Ahmednagar,
Maharashtra (INDIA)

CERTIFICATE

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

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

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LIST OF ABBREVIATIONS

% : Per cent
/ : Per
∑ : Summation of
б^{2} : Variance
b.s. : Broadsence
cm : Centimeters
C.D. : Critical difference
Cov. : Covariance
C.V. : Coefficient of variation
D.F. : Degrees of freedom
EC : Exotic collection
EMP : Error Mean Sum of Product
et al. : *et allia* (And other)
Fig. : Figure
g : Grams
GA : Genetic advance
GAM : Genetic advance as per cent of mean
GCV : Genotypic coefficient of variation
GMP : Genotypic mean sum of products
h^{2} : Heritability
i.e. : *id est* (that is)
IC : Indigenous collection
kg : Kilogram (s)
M.S.S. : Mean sum of squares
m : Meters
No. : Numbers
PCV : Phenotypic coefficient of variation
R.B.D. : Randomized Block Design
r : Correlation coefficient
S.E. : Standard Error
S.S. : Sum of Squares
Via. : By way of, by means of
Viz. : Videlicet (Namely)
Vs. : Versus

ABSTRACT

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

By

Mr. GULWANE VAIBHAV PARMESHWAR

A candidate for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

2021

Research Guide	**: Dr. G.N. Deore**
Department	**: Agricultural Botany**
Major discipline	**: Genetics and Plant Breeding**

The investigation on "Genetic diversity studies in chickpea (*Cicer arietinum* L.)" was conducted on 44 genotypes of chickpea to know the variability, interrelationship among yield and its components, their direct and indirect effects on seed yield and genetic divergence of various chickpea genotypes for traits under study.

Observations were recorded for days to 50 per cent flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant.

A wide range of variability was observed for almost all the characters except number of seeds per pod. The character number of pods per plant showed highest range of variability followed by 100 seed weight, plant height, days to 50 per cent flowering, seed yield per plant showed considerable amount of variability. The variability was lowest for number of seeds per pod and number of secondary branches per plant.

Genotypic and phenotypic coefficients of variation were highest for 100 seed weight followed by seed yield per plant, number of pods per plant, number of secondary branches per plant and plant height. High heritability coupled with high genetic advance as percent of mean was observed for the 100 seed weight, number of seeds per plant, number of pods per plant, number of secondary branches per plant, plant height, seed yield per plant suggesting that the selection of these traits would be effective for the desired improvement.

Abstract contd…. **Mr. Vaibhav P. Gulwane**

The significant positive correlation was observed between seed yield per plant with plant height, number of secondary branches per plant, number of pods per plant and 100 seed weight. While, seed yield per plant exhibited significant negative correlation with days to 50 per cent flowering and days to maturity both at phenotypic and genotypic level.

Path coefficient analysis revealed that 100 seed weight had highest direct effect on seed yield per plant followed by number of pods per plant, number of seeds per pod, number of secondary branches per plant, plant height. Whilst, days to 50 per cent flowering and days to maturity showed negative direct effect.

The D^2 statistics showed that there was adequate diversity among the genotypes. On the basis of D^2 values 44 genotypes were grouped into eleven clusters. On the basis of inter cluster distance and cluster means the genotypes *viz.*, BG-4010, Phule Vikram, NDG 18-9, RVSSG-79, GNG-2462, RKG 19-1, BAUG-106 and BRC 9-14 were identified for their use in hybridization programme for further improvement of programme of chickpea through selection of desired transgressive segregants for traits of interest.

Pages 1 to 74

1. INTRODUCTION

Pulses production in India is distinguished by crop variety and regional uniqueness based on adaptation to existing agro-climatic conditions. This category of crops generally makes better use of limited soil moisture and nutrients than cereals. Pulses play an important function in agricultural systems as a fallow replacement in cereal rotations, where it helps to production sustainability and lowers the requirement for nitrogen fertilizer by fixing atmospheric nitrogen. Chickpea is crucial *rabi* crop in India, and it is one among the pulses.

Chickpea (*Cicer arietinum* L.) is traditionally grown in many parts of the world since ancient time, both in Asia and Europe. Chickpea (*Cicer arietinum* L.) is an annual, cleistogamous, self-pollinated having cleistogamous flowers and diploid (2n=16) grain legume crop grown in a diverse environments. Chickpea is reported to have 9 annual and 35 perennial species (Van der Maesen *et al.,* 2007) in the globe. Ladizinsky and Adler (1976) recognized *Cicer reticulatum* to be the wild progenitor of cultivated chickpea, and South Eastern Turkey is the center of origin of crop, relying on seed protein electrophoresis.

Chickpea is prominent *Rabi* crop in India and it is one among the pulses. Almost 90 per cent of the crop is cultivated on receding soil moisture under rainfed condition and on marginal lands. In India, the area under chickpea was 10.17 million ha, with yield of around 11.35 million tons and an all-time high productivity of 1116 kg/ha (Anonymous, 2019-20). In India, Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Tamilnadu and Telangana are major chickpea producing states contributing more than 88 *per cent* to the total chickpea production. Madhya Pradesh is single largest producer in the country accounting above than 40 *per cent* of total yield while Rajasthan, Maharashtra, Uttar Pradesh and Karnataka each contribute roughly 18, 14, 7 and 6 *per cent.* Maharashtra grows total pulses on about 43.87 lakh ha area producing 40.27 lakh ton with 918 kg/ha productivity in the year 2019-20. (Anonymous, 2019-20). The chickpea area in Maharashtra was about 23.21 lakh hectare with production 25.97 lakh tons and the productivity 1118 kg/ha (Anonymous, 2019-20).

Pulses are vital part of diet of Indian and provide a significant amount of the protein requirement. Chickpea offers good quality protein source, especially for vegetarians. It is also utilized as a livestock feed. Like other pulse crops chickpea serves a variety of functions in the traditional farming systems across several developing nations.

Chickpea seed contains on average 22 per cent protein, 4.5 per cent fat, 63 per cent carbohydrates, 1-5 per cent crude fibre, 2.7 per cent ash and 358 calories (Miao *et al.*, 2009). As tolerant to soil moisture stress, it occupy important position in different cropping system. Desi and Kabuli are two types of chickpea crop. The Desi type has small, coloured seeds with an angular form and a high per centage of fibre, whereas the Kabuli type has large, ram-head-shaped, coloured seeds with less per centage of fibre. Kabuli type chickpea have higher protein content than Desi types, although they produce less. The main constituent of is globulin. Chickpea is rich in protein and low in sodium and fat. They are high in soluble and insoluble fibre, complex carbohydrates, vitamins (particularly B vitamins) and minerals (primarily potassium, phosphorus, calcium, magnesium, copper, iron and zinc). It is high in unsaturated fatty acids like linoleic and oleic acids, which are essential for our health. These fatty acids are also helpful to lessen vulnerability of coronary and cardiovascular diseases. Due to high amount of soluble fibre and vegetable protein, it also helps to reduce blood cholesterol levels. It lowers blood lipids, which may assist to prevent certain severe diabetic complications (Yadav *et al.*, 2007). Chickpea is most frequently used as dhal. In India, consumption of dhal accounts for around 75 *per cent* of overall production. Whole grains may be eaten raw or cooked and roasted. Chickpea has a unique place (flour or parched) in the form of dhal. In other words, dhal produced after milling either from red gram or chickpea, is an significant component of daily diet vegetarian. Chickpea flour is a low-cost ingredient in a variety of Indian confections and tender leaves of chickpea are eaten as vegetable. As a great pulse for curry preparation, Kabuli chickpea is used to make roasted chana "chhole." Cattle feed is made out of the husk and broken pieces of dried chickpeas. Spreading cloth over the crops at night absorbs the exudation with dew, giving an acrid liquid that contain malic and oxalic acid and which is used as vinegar and as medicinally. Chickpea production and small-scale enterprises based on it have a lot of potential because of its high protein content, health advantages and numerous household uses.

Because the cultivation of chickpea is so wide, not only knowledge of the nature and magnitude of genetic divergence but also the critical analysis of yield formulation in various chickpea materials are important. This, in turn, aids in the development of selection strategy and the recognition of diverse parents which, when hybridized, result in a broad range of gene combinations.

Statistical analysis of one or more characteristics affected by a large number of genes is determined by calculating correlation coefficients. The genotypic correlation coefficient is a measure for character genotypic conjugation. While, Wright (1921) proposed division of the correlation to direct and indirect effects by using path coefficient analysis as this approach offers valuable cognition on the relative merit of attributes in the selection criterion. Any effective breeding programme requires high level of genetic diversity among the parents which is heritable in nature. In a breeding programme, proper parent selection is crucial. Because crosses involving genetically different parents are anticipated to generate significant heterotic effects as well as greater diversity in segregating generations, which may be exploited for improvement. Genetic divergence among the parents plays a vital role into cultivar development. Plant breeders often choose parents based on phenotypic divergence, but knowledge of genetic diversity among the parents in the form of the desirable characters is required for successful breeding.

The D^2 statistic, developed by Mahalanobis in 1936, is a useful tool for calculating population divergence. Many studies were using this method, also shown that the geographical diversity is not always linked to genetic diversity. As a result, it offers a better understanding about the degree of divergence. It is independent of sample size as well as a foundation for selecting parental lines for forthcoming breeding programme. The current research was carried out in order to evaluate the genetic diversity in forty three chickpea genotypes along with one check, considering the following objectives.

1. To study the direct and indirect effect of different yield contributing characters on seed yield of chickpea.
2. To group various genotypes into various cluster.

2. REVIEW OF LITERATURE

A thorough examination of the literature is an essential component of every scientific investigation because it allows the researcher to compare the current findings to prior investigations.

The literature relevant to the present research entitled "Genetic diversity studies in chickpea (*Cicer arietinum* L.)" has been evaluated within the following headings:

2.1 Variability and Genetic Parameters
2.2 Correlation and Path Analysis
2.3 Genetic Diversity

2.1 Variability and Genetic Parameters

Fisher (1930) initially provided the approach to distinct out the genotypic effect depending on phenotypic an environmental variable. He expressed the genotypic variability in terms of genotypic coefficient of variation.

Burton (1952) proposed the combination of heritability estimates with genotypic coefficients of variation to provide accurate estimates of the genetic advance.

Johnson *et al.* (1955) reported, heritability values combined with estimates of genetic advance are more helpful in a selection programme than just heritability.

Dumbre *et al.* (1984) assessed the genetic variability of sixteen chickpea cultivars for nine quantitative characteristics, observed that pods per plant (10.4 -95.8) had the greatest range of variability, followed by days to maturity (87.0 - 125.0 days), while seeds per pod had the lowest (1.0 - 1.4).

Jivani and Yadavendra (1988) reported, high heritability parameters for the seed yield related characters in 42 genetically diverse genotypes of chickpea and noticed that, both coefficient of variation were high for the pods per plant and pods per plant, 100 seed weight, plant height, days to flowering, days to maturity, and harvest index, as well as high heritability for pods per plant, 100 seed weight and harvest index.

Samal and Jagdev (1989) found high PCV as well as GCV for seed weight and seed yield. Moderately high PCV and GCV for plant height and days to flowering, indicating the modest effect of environment on these traits. For seed weight and yield, high heritability was detected in conjunction with high genetic advance, which might be attributed to the strong additive effect and selection pressure may most likely be applied to these characters for yield enhancement.

Sharma *et al.* (1990) found that pods per plant had the largest range of variability, along with secondary branches, harvest index, days to maturity as well as days to flowering. Seeds per pod and protein content had the lowest range of variability. Secondary branches had the largest coefficient of genetic variation, followed by the pods and seed per plant, 100 seed weight, and primary branches. These were average for seed per pod, plant height and harvest index, but poor for protein content, days to flowering and days to maturity. For 100 seed weight and number of secondary branches per plant, there was high heritability with moderate genetic advance.

Jahagirdar *et al.* (1994) found significant GCV too PCV for the number of pods per plant, as well as relatively high genetic variability for the number of days to 50 per cent flowering, plant height and the number of primary branches per plant. For the 100 seed weight, days to 50 per cent flowering, number of secondary branches per plant, and number of pods per plant, substantial heritability and genetic advance were detected.

Gupta and Krishna (1995) assessed the variability then heritability of seed yield and quality parameters such as seed size in addition protein content in 29 chickpea (*Cicer arietinum* L.). They found that the variability range for seed size (21.53 - 30.23 g) was wider than for protein content (16.99 - 22.55 per cent) and seed yield (13.44 - 17.46 g plant^{-1}). Protein content had a high heritability estimate of 60 per cent, but seed size and seed yield each had low heritability values 42 and 39 per cent.

Mathur and Mathur (1996) studied the genotypic and phenotypic coefficients of variation, heritability and expected genetic advance for seed yield and its contributing traits in 34 chickpea varieties. The greatest genotypic and phenotypic coefficient values were found in 100 seed weight. High heritability values estimated for all of the rather good values of genetic advance as a percentage of mean and so these traits may be regarded trustworthy for selection in chickpea.

Rao and Kumar (2000) evaluated forty short duration desi chickpea genotypes derived from single, double and triple crosses with genetically heterogeneous parents. Maximum variability was reported in biological yield, followed by seed yield with minimal variability found in days to maturity then days to 50 per cent flowering.

Gumber *et al.* (2002) examined 30 chickpea genotypes and found the highest heritability in the pods per plant (78.00 %), secondary branches (71.50%) and 100 seed weight (69.40%). Seed yield (38.64%) and seed per pod (13.33%) had the maximum estimates of the phenotypic coefficient of variation (PCV).

Saleem *et al.* (2002) assessed chickpea heritability in 20 elite lines. High genotypic and phenotypic coefficients of variability were found for seven characters namely, days to flowering, number of secondary branches, number of pods, number of seed per pod, 100 seed weight, seed yield per plant and protein content. High broad sense heritability estimates were found for 100 seed weight, days to flowering and protein content, indicating that genetic factors accounted for a significant part of overall variation.

Jeena *et al.* (2005) analysed 80 genetically different chickpea genotypes for the variability and correlation coefficients. High degree of genetic variability was indicated by pods per plant, 100 seed weight, biological yield and seed yield per plant. These traits also showed high expected genetic advance along the high heritability.

Ali *et al.* (2008) evaluated variability and correlation for five characters in the twenty elite chickpea lines. Varietal variations among genotypes were considerable (P (P<0.01). Phenotypic and genotypic variances were maximum for plant height (33.29 and 32.45) and seed yield per plant (13.47 and 13.11). Broad sense heritability estimates were the maximum for plant height (97.4%) and seed yield per plant (97.3%). Genetic advance was significantly high for seed yield per plant (27.42) and plant height (14.51). Significant heritability for both the characters coupled with high genetic advance proved that additive genetic effects were crucial for both the characters. Positive genotypic correlation was observed between seed yield and number of primary branches per plant (0.76), while at phenotypic association was extremely significant (0.63).

Sharma and Saini (2010) assessed 28 chickpea genotypes containing check which demonstrated the presence of adequate variability with maximum heritability for majority of the yield components. Number of pods per plant and branches per plant could be useful as selection indices for generation of high yielding genotype of chickpea, as it was suggested by correlation and path analysis estimates.

Zali *et al.* (2011) analyzed 17 chickpea genotypes and found the correlation between genetic factors and characters. These traits were controlled by additive genes and selection of such traits possibly will be effective for enhancing the seed yield, as it were observed that the heritability was greater for the traits such as days to maturity (98.43%), days to 50 per cent flowering (98.19%), number of secondary branches (45.81%), number of primary branches (42.03%) and number of seed per plant (35.42%).

Zeeshan *et al.* (2012) evaluated genotypic variability, heritability and association of 20 chickpea genotypes for yield and its associated characters under rainfed condition. They observed substantial heritability for plant height and 100 seed weight paired with high genetic advances showed that additive gene effects were significant in influencing these characters. High heritability with little genetic advance for days to maturity showed effect of dominant and epistatic genes.

Gul *et al.* (2013) assessed genetic potential, heritability, genetic advance and phenotypic correlation of yield contributing characters of the twenty chickpea genotypes. Highest broad sense heritability estimates had for the pods per plant (0.88), Primary branches per plant (0.83), 100 seed weight (0.82), seed yield per plant (0.75) and secondary branches per plant (0.77). The genetic advance was greater for pods per plant (40.14%), seed yield per plant (38.24%), primary branches per plant (36.64%) and secondary branches per plant (30.25%).

Mushtaq *et al.* (2013) looked at path coefficient analysis and variability factors in twenty elite chickpea genotypes, with three checks. Days to flowering, days to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100 seed weight and yield of grain all had maximum heritability estimates, while, other characters had moderate heritability.

Neelu Kumari *et al.* (2013) evaluated genetic diversity among 32 advanced breeding lines of chickpea for grain yield per plant with the highest genotypic coefficient of variation (GCV) was assessed. The range for broad sense heritability varied from 53 per cent (days to 50 per cent flowering) to 55 per cent (total yield). Plant height, number of pods per plant, secondary branches per plant, and seed yield per plant all had high expected genetic advance and heritability. It indicated that additive gene effects play the most important role in the traits improvement. Yield of grain had a positive and substantial relationship with biological yield, harvest index and test weight.

Astereki *et al.* (2015) analysed 25 chickpea genotypes for genetic diversity and heritability and estimated GCV and PCV for the same. During two seasons, the field experiment was set up in RCBD with four replications. Seed yield, days to flowering, days to maturity, flowering period, number of pods per plant, canopy height, harvest index and biological yield all displayed significant genotypic variations as per analysis of variance. For seed yield, days to flowering, canopy height, number of pods per plant, biological yield and harvest index, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV), indicating the impact of environment on these attributes. Days to flowering, canopy height and days to maturity had a higher heritability than the other attributes.

Tiwari *et al.* (2016) examined genetic variability, genetic association and path coefficient analysis for grain yield and its contributing parameters in 38 chickpea varieties. For all the parameters, both genotypic as well as phenotypic variations were very significant, with the phenotypic coefficient of variation being somewhat greater. Seed per pod, harvest index, seed yield per plant, number of pods per plant and days to maturity all demonstrated significant heritability and genetic advance. They found that, in majority of the characters, genotypic correlation coefficients were greater than phenotypic correlation coefficients. The most significant characters that had a positive relationship with seed yield per plant were 100 seed weight, harvest index, seed per pod, number of effective pods per plant, number of primary branches per plant, and plant height.

Alka Dev *et al.* (2017) studied 60 genotypes of chickpea in which the relative magnitude of difference between phenotypic coefficient of variation and genotypic coefficient of variation was low for the number of seed per pod, number of pods per plant, 100 seed weight, number of nodules per plant along with days to 50 % flowering showed that these traits were less influenced by the environment. The estimate of heritability of broad sense were highest for pod length, number of nodules per plant, 100 seed weight, days to 50 % flowering, and days to maturity.

Kishor *et al.* (2018) evaluated forty chickpea genotypes that were grown into the randomized block design having three replications. For all the traits studied, the analysis of variance showed very significant difference between the genotypes. The phenotypic as well as genotypic coefficients of variation for biological yield, number of pods, number of seed per plant, 100 seed weight and yield of seed per plant were all high. Days to maturity, days to 50 per cent flowering, 100 seed weight, plant height, seed yield per plant, number of seeds per plant along with biological yield per plant showed the least differences between GCV and PCV estimates. The heritability of the biological yield per plant, number of pods per plant, seed yield per plant, number of seed per plant and primary branches per plant is high, as is the genetic advance as a per cent of mean.

Shanmugam and Kalaimagal (2019) conducted a study to evaluate 50 chickpea germplasm accessions to know the extent of variability, heritability, genetic advance, and the association of various components of yield and their direct and indirect influence on chickpea yield on twelve agro-morphological traits. Anova showed that there was significant variation for the majority of the characters. For 100 seed weight and plant height, high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed, indicates high heritability along high genetic advance.

Anusha *et al.* (2020) assessed 25 chickpea genotypes to study the genetic variability parameters for yield as well as quality characters of chickpea and observed highly significant differences among genotypes for all eleven traits studied, namely plant height, number of branches per plant, days to 50 per cent flowering, days to maturity, number of pods, harvest index, 100 seed weight, iron content and seed yield per plant. The genetic variability parameters revealed moderate to high estimates of phenotypic coefficient of variation and genotypic coefficient of variation. High heritability in general and high genetic advance as a per cent of mean for the traits such as, plant height, number of pods per plant, 100 seed weight, seed yield per plant, and iron content, indicating that these characters had wide range of variability. Heritability in these traits was attributed to additive gene effects and selection may be beneficial. This will assist the breeders for direct selection of plants on the basis of phenotypic expression.

2.2 Correlation and Path Analysis

Knowledge of the correlation of one or more of these characters associated with yield is supportive in choosing individuals with high yield based on their phenotypic values in crop improvement. Correlation coefficients quantitatively elaborate such associations between plant characters. However, the relationship amid the dependent and independent characters, as well as the direct and indirect impacts of the independent character on the dependent character, are entirely distinct. The correlation between two characters may be very positive at times, while the direct impact of the independent characters on the dependent characters can be detrimental at other times. As a result, a weak association cannot be used to choose crops in a plant crop improvement programme.

Therefore, the technique of dividing the direct and indirect effects of the independent character on the dependent character, nothing but the path coefficient analysis was described by Wright (1921). Li (1954) highlighted the importance of this method in genetics and plant breeding. Dewey and Lu (1959) also provided a detailed procedure for path analysis of replicated trials, which was somewhat different strategy in removing the environmental variances.

Paliwal *et al.* (1987) observed that the 100 seed weight exhibited the greatest direct positive impact on yield, along with pods per plant, seed per pod and days to 95 per cent maturity. Seed yield per plant was showed positive association with plant height, days to 95 per cent maturity, days to 50 per cent flowering. Pods per plant and seed per pod were advised as selection criteria to increase yield.

Jivani and Yadavendra (1988) analyzed correlation and path analysis in 42 genotypes of chickpeas. Genotypes sown on three different dates yielded (r = 0.3). It was proposed that branches and pods per plant, 100 seed weight, and harvest index selection might be utilized to create indirect significant positively associated with branches per plant (r = 0.2), pods per plant (r = 0.4), 100 seed weight (r = 0.3), and the harvest index selection for increasing seed yield.

Arora and Kumar (1994) assessed 40 chickpea genotypes in order to compute correlation and path analysis and estimated that seed yield per plant exhibited a significant and positive relationship with biological yield per plant, pods per plant, plant height, 100 seed weight and plant spread. As per path coefficient studies, biological yield, pods per plant, harvest index and 100 seed weight had the greatest direct impact on seed yield.

Kumar *et al.* (2002) observed while, evaluating 24 chickpea genotypes for eight quantitative characters with randomized design. Correlation study showed that seed yield was positively linked to harvest index, pods per plant, biological yield, and secondary branches per plant while being negatively related to plant height. Pods per plant were positively correlated to secondary branches per plant along biological yield per plant but negatively related to 100 seed weight.

Muhammad *et al.* (2004) observed that, the grain yield had a positive and significant correlation to 100 seed weight, pods per plant, plant height, and biological yield. The harvest index and biological yield showed significant direct impact, while the latter exhibited a negative relationship with grain yield.

Jeena *et al.* (2005) assessed 80 chickpea genotypes from different genetic lineages in view to compute the correlation coefficients. Plant height, pod length, pods per plant, 100 seed weight, secondary branches per plant, biological yield per plant and harvest index were all significantly also positively associated with seed yield.

Yucel *et al.* (2006) evaluated 15 different kabuli genotypes. The impact of yield components on seed yield per plant was studied both directly and indirectly. The greatest genetic variation was found in 100 seed weight, followed by seed number per plant. The association between seed yield per plant and plant height, first pod height, secondary branches per plant, total pod and number of full pods and seed per plant was positive and significant. According to the findings of this study, seed and full pod numbers might be used as selection criteria to improve seed yield per plant in winter Kabuli chickpea.

Singh (2007) examined 45 diverse genotypes of chickpea. The genotypic association was greater than the corresponding phenotypic one. The biological yield per plant, pods per plant, secondary branches per plant all showed that a highly significant positive association with the seed yield. Indirect contributing components were pods per plant, 100 seed weight and secondary branches per plant.

Zena *et al.* (2008) used path coefficient analysis to evaluate the impact of different production variables on the yield. Biological yield had the greatest direct impact on seed yield, followed by yield index, initial flowering period, test weight, secondary branches per plant, maturity period, and seed per pod, in that order, whereas 50 per cent flowering period exhibited a negative direct effect on the gram yield.

Sharma and Saini (2010) examined 28 chickpea genotypes, including a check. The correlation and path analysis studies revealed that the branches per plant and the number of branches per plant might be helpful as selection indicators for the creation of high yielding chickpea genotypes.

Padmavathi *et al.* (2013) studied the correlation and path analysis for yield and yield contributing characters in thirty genotypes of Kabuli chickpea. Correlation studies reported that number of primary branches per plant, plant height, number of pods per plant, 100 seed weight, secondary branches per plant, harvest index and biological yield per plant were all substantially and positively associated with seed yield. Path coefficient study reported that, the harvest index, number of pods per plant and biological yield per plant all had a significant positive direct impact on seed yield, indicating the significance of these parameters in seed yield improvement.

Mehta *et al.* (2015) conducted experiment comprised 21 genotypes (including local and national checks) and was grown in 3 replications. Days to maturity, plant height, and primary branches per plant each one had positive significant relationships with seed yield per plant under standard sown circumstances that were altered in rainfed regions. These are some intriguing findings. The morphological data clearly show the genetic variety of the material under investigation. The information collected will be utilized to determine the approach of chickpea improvement for dry environments.

Samayuktha *et al.* (2015) used correlation, path analysis and cluster analysis to assess the selection criteria in 48 chickpea germplasm accessions based on 14 morphological characters. ANOVA showed that majority of the traits had substantial genotypic variation. Plant width (0.346), number of pods per plant (0.788), seeds per pod (0.055), seeds per plant (0.675) and 100 seed weight (0.477) all had strong positive association with single plant yield, whereas days to 50 per cent flowering (-0.418) and days to maturity (-0.331) had a significant negative relationship. Correlation analysis of component traits showed a significant negative relationship amid 100 seed weight and seeds per plant (-0.360). According to path analysis, the number of pods per plant (0.860) and 100 seed weight (0.589) had the strong positive direct impact on single plant yield.

Chopdar *et al.* (2016) determined that days to maturity, primary branches per plant, harvest index and protein content all had a positive direct impact on seed yield per plant. Among these parameters, harvest index had the greatest direct positive impact on seed yield. The harvest index had a positive indirect impact upon seed yield per plant, biomass per plant and the number of primary branches per plant. Hence, while selecting for high yield, attention must be placed on those traits that have a strong direct beneficial impact and a positive relationship with seed yield.

Banik *et al.* (2017) experimented sixty chickpea genotypes at the Pulses Improvement Project, Mahatma Phule Krishi Vidhyapeeth, Rahuri, Maharashtra, India. The experiment was carried out in two replications on sixty chickpea genotypes using randomized block design. Correlation studies reported a strong negative correlation among seed yield per plant and 50 per cent flowering and number of seed per plant, as well as a significant positive association among plant height and seed yield per plant, number of secondary branches per plant, 100 seed weight, plant spread and number of primary branches per plant. Path coefficient findings shows that the number of pods per plant had the greatest direct impact on seed yield, along with plant height, 100 seed weight and days to maturity, with the exception of seeds per pod and days to 50 per cent flowering, which had a negative effect on seed yield.

Kumar *et al.* (2019) analysed the volume of genetic variability for yield and its component characters, genetic association and path coefficient analysis in 45 chickpea genotypes (*Cicer arietinum* L.). The correlation study indicated that grain yield had a substantial and positive relationship with the number of pods per plant, whereas it had a significant as well as negative relationship with days to maturity. The number of pods per plant, plant height and days to 50 per cent flowering had the greatest direct positive impact on grain yield, according to path analysis. This research has clearly shown the need of providing equal weightage to 100 seed weight and pods per plant in order to improve chickpea production.

Ajay Kumar *et al.* (2020) conducted experiment with sixty varieties of chickpea to check the correlation along the path co-efficient of there lines in different environment. The results showed that, with the exception of plant height, seed yield per plant was positively related with all of the component characters. The seed yield correlation coefficient was very significant with secondary branches and biological yield correlated significantly with primary branches, pods per plant, seed per pod, and harvest index. Path coefficient analysis of pooled data revealed that biological yield, harvest index, secondary branches, and days to flowering were significant characteristics that might be considered to select for improvement of seed yield in chickpea.

2.3 Genetic Diversity

2.3.1 Concept of genetic diversity

Mahalanobis (1936) proposed the D^2 statistic for evaluating population divergence among the two populations. It provides a result depending on the amount of divergence and is unaffected by sample size.

Mahalanobis *et al.* (1949) used D^2 statistic to classify anthropometric data from Uttar Pradesh into 23 groups and three major clusters; Brahmin (B-cluster) at the top of the Hindu social hierarchy with nine groups, Artisan (A-cluster) in the middle with four groups and Trivial (T-cluster) at the bottom with ten groups.

Allard (1961) used three separate degrees of genetic diversity to explain the relationship in between genetic diversity and consistency of performance in various environments. He came to the conclusion that genetic diversity and productivity were totally linked and that numerous variables influenced the productivity of mixed populations.

Murthy and Arunachalam (1966) asserted that a change in breeding structure might result in a significant change in character association and the pattern of distribution of genetic variability, geographical distribution and genetic diversity in many of the crops evaluated by them. Diversity reported due to the genetic drift and selection in various environments may be greater than the geographic diversity.

2.3.2 Genetic divergence in chickpea

Narendra Kumar (1997) conducted a multivariate study of divergence among 60 chickpea accessions for seven developmental characters, which resulted in their classification into five groups. The clustering of items into various clusters had nothing to do with their geographical origin. The D values across clusters varied from 8.0 to 38.2. Based on mean performance, genetic distance and clustering pattern; hybridization between parents from cluster II and V may result in better yielding cultivars.

Arun Kumar *et al.* (1998) assessed the genetic divergence among 17 chickpea genotypes, 5 of which were produced *via* mutation breeding, intra and inter specific hybridization, and two chickpea standard checks. The genotypes were divided into five groups. Cluster II, I and III each contained six, five and four genotypes, whereas clusters IV and V each had just one genotype. Cluster III genotypes showed the most divergence, closely along with cluster II and I. The greatest and least divergence was found between clusters II and V and between cluster III and V, also they had high and low mean values for the majority of the characters, respectively. It has been proposed that hybridization amongst the genotypes of divergent clusters should be used for varietal improvement rather than relying on genotypes of the cluster with the greatest divergence.

Sivakumar and Muthiah (2001) reported that clusters IV and VII exhibited highest divergence even though the lowest was between clusters IV and V. Cluster I had the greatest inter-cluster distance, with 108 genotypes.

Nimbalkar and Harer (2001) clustered 40 genotypes into 16 groups. D^2 values between all probable pair of 40 genotypes varied from 12.62 to 3979.93. Out of the 16 clusters, 10 remained mono genotypic, with cluster II having the most genotypes (12), along with cluster I and IV having 9 and 3 genotypes, respectively. Cluster XVI and cluster III genotypes were the most divergent. The major characters leading to genetic divergence was the variation of cluster means, which showed pods per plant, along the 100 seed weight and plant height.

Kashyap and Rastogi (2003) examined the genetic divergence in 60 chickpea germplasm accessions using D^2 methods for yield as well as its component traits. For each attribute under consideration, the analysis of variance showed substantial variations between genotypes. The genotypes were divided into six clusters, with cluster I (14 genotypes) having the greatest intra-cluster distance. Cluster III and IV were found as genetically dissimilar. Taking cluster means and cluster distances into account, the genotypes IG-327, IG-323, IG-326, IG-311, IG-314 of cluster V, ICCV-910201, ICCV-89243, ICCV-91007, ICCV-91024, IG-313 of the cluster VI, ICCV-91003, ICCV-91004, ICCV-89228, ICCV-89224, ICCV- 91012 of the cluster I were they, may be used in future breeding programmes to achieve a strong heterotic impact or to create desired recombinants.

Durga *et al.* (2005) examined the genetic diversity of chickpea using 132 genotypes. The genotypes were separated into nine groups. Cluster I had the most genotypes (20), followed by clusters V and VII, which had 16 and 15 genotypes, respectively. Cluster VI has the greatest intra-cluster distance, followed by Cluster IV, Cluster I, and Cluster IX. The greatest inter-cluster distance had been observed between clusters I and VIII. Crossing genotypes between clusters I and VIII might results in maximal variability in segregating populations and the creation of high yielding variety.

Sandhu *et al.* (2006) used the Mahalanobis D^2 statistic to evaluate 90 chickpea genotypes in three environments. The genotypes were divided into 10 groups, each with a higher genetic divergence than the one others. Common genotypes were identified within a cluster for each combination of environments and data was pooled across environments.

Dwevedi and Gaibryal (2009) used Mahalanobis D^2 statistics to assess the nature and degree of genetic divergence among 25 genotypes of chickpea. The genotypes data on 10 key quantitative characteristics were collected. Six clusters were formed by grouping 25 genotypes. Cluster I is the biggest cluster, which includes clusters I and VI. There were three characters that contributed most to the expression of genetic diversity: harvest index, 100 seed weight, and pods per plant.

Tomar *et al.* (2011) grew forty five genotypes of chickpea in twelve environments and the selected prospective parents for hybridization. Forty five genotypes were divided into eight groups based on D^2 values. Cluster V contained eight genotypes, followed by clusters VIII and VI, which had seven and six genotypes, respectively. Cluster VIII has the greatest intra-cluster distance (2.89), followed by cluster VI (2.58), cluster IV (2.34) and cluster I (2.33). Cluster IV and VIII had the greatest inter-cluster distance (6.38). They hypothesized that crossing genotypes from clusters IV and VIII would result in maximal variety in segregating populations and the creation of high yielding cultivars.

Singh *et al.* (2012) used Mahalanobis D^2 statistics to identify the nature and degree of genetic divergence among 64 genotypes of chickpea, which comprised 60 interspecific derivatives, their parents, and two standard checks. Cluster VI and IX had the greatest inter-cluster distance, whereas cluster VIII genotypes had the greatest intra-cluster distance. Characters such as biological yield per plot, seed yield per plot, and days to 50 per cent flowering contributed the most to genetic diversity.

Jain and Indapurker (2013) applied Mahalanobis D^2 Statistics to assess the nature and degree of genetic divergence in thirty chickpea genotypes, which were divided into six groups. The biggest cluster, having eight genotypes, is shown in Cluster I. Cluster

IV and V had the greatest inter-cluster distance, along with Cluster V and VI. For the pods per plant and seed yield per plant, cluster VI was found.

Parashi *et al.* (2013) classified sixty chickpea genotypes into 13 groups. Cluster I had the most genotypes, 33 in total. Cluster VII and Cluster XIII had the greatest inter-cluster distance (D^2 = 194.04), along with Cluster XI and XIII (D^2 = 156.50), Cluster VI and XIII (D^2 = 130.64), and Cluster IV and XI (D^2 = 119.46). Maximum genetic diversity was provided by three characters: yield per plant (34.29 %), stomatal conductance (27.97 %), and number of pods (16.33 %). Virat, Digvijay, Rajas, IC-268978, IC-269643, IC-269257 and Vijay were recognized as genetically diverse parents.

Malik *et al.* (2014) used descriptive, principal component, and cluster analysis for the genetic diversity of 113 desi chickpea genotypes. Days to flowering and maturity showed significant variations. Plant height, biological yield, pods per plant, and harvest index are all factors to consider. These characters also had a strong positive association with yield, which was verified by principal component analysis. Four main components accounted for 71.99 per cent of the overall variance, according to principal component analysis (PCA). Chickpea seed yield, pods per plant, secondary branches, biological yield, and plant height all had a positive relationship with the first component (PC1). Days to flowering, days to maturity, and 100 seed weight all correlated positively with the second component (PC2). Using cluster analysis, the genotypes were divided into four groups. Cluster I included genotypes with early flowering and maturity, while Cluster II contributed significantly to grain yield per plant, harvest index, and pods per plant. The genotype grouping would be useful to chickpea breeders in identifying the genotype with the required characteristic for use in breeding programmes for genetic improvement.

Parhe *et al.* (2014) conducted an experiment with fifty one genotypes of chickpea to assess the nature and degree of genetic divergence using Mahalanobis D^2 statistics in a randomized block design with two replications. The 51 chickpea genotypes were divided into five groups. Cluster I had the most genotypes (forty), followed by Cluster II (eight). The greatest inter-cluster distance was found between clusters I and V, followed by clusters II and V, indicating that the genetic architecture of genotypes in one cluster differs completely from those in other clusters. The three characters, namely 100 seed weight, pods per plant and days to 50 per cent flowering all contributed substantially to the manifestation of genetic diversity.

Pandey (2016) utilised Mahalanobis D^2 statistics to perform an experiment on 100 potential chickpea genotypes planted late. SSR molecular markers are also used to validate the diversity. D^2 values were used to divide 100 genotypes into the sixteen clusters. Cluster I had the most genotypes (29), along with Cluster II, Cluster V, and Cluster VI, which contained (26), (13), and (12) genotypes, respectively. Cluster V has the greatest intra-cluster distance (164.10), followed by Cluster VI (150.23), Cluster III (123.98), and Cluster II (102.52). Nevertheless, the greatest inter-cluster distance was seen between cluster IX and cluster XV (853.43), followed by cluster X and cluster XV (749.13) and cluster VII and cluster XV (742.58).

Aarif *et al.* (2017) studied genetic diversity using Mahalanobis's D^2 statistics in 22 genotypes of kabuli chickpea (*Cicer arietinum* L.) for seed yield, its components and seed quality traits. Based on D^2 analysis, the 22 genotypes were divided into three groups. Clusters I and III were the biggest, with 9 genotypes each, while Cluster II contained 4 genotypes. Cluster II and III had the greatest inter-cluster distance, followed by Cluster I and II, while Cluster I and III had the smallest distance. Cluster II had the greatest intra-cluster distance, along with Cluster III and Cluster I, which had the smallest intra-cluster distances. Cluster I contained genotypes KAK-2 and HK-06-163 with high seed yield per plant may be included in the hybridization programme. Cluster II genotypes, namely RVSSG-11, RVSSG-12, Phule G-09311 and Phule G-09316, used as parents in future breeding programs.

Ambilwade *et al.* (2018) carried out the study of thirty five chickpea genotypes in a randomized block design with three replications. Mahalanobis D^2 analysis utilised to assess the extent of genetic diversity and it was reported that the substantial amount of diversity exists in the material. Thirty five genotypes were grouped into six heterogeneous clusters. Among these clusters Cluster VI has the greatest number of genotypes. Based on the mean performance of the genotypes, IC-275323 was recorded high yield among 35 genotypes under study. They also observed that the cluster II and cluster V are most diverse to each other and the genotypes constituted in these clusters might be used as a parent for further hybridization programme.

Gediya *et al.* (2018) assessed genetic diversity in 58 chickpea genotypes, which were divided into sixteen clusters. In general, intra-cluster distances were smaller than inter-cluster distances, suggesting that genotypes within a cluster diverged less from one another. Cluster IX and XVI had the most genetic difference, followed by Cluster IX and XIV, while Cluster III and VIII had the closest proximity. The traits seeds per plant, 100 seed weight, seed yield per plant and pods per plant all contributed significantly to the overall genetic divergence. As a result, selection for divergent parents on based of these traits would be beneficial for developing potential hybrids and expanding the scope of isolating acceptable recombinants in segregating generation of chickpea.

Geethanjali *et al.* (2018) studied genetic diversity among 30 chickpea genotypes was assessed for quality and yield attributing and traits at Regional Agricultural Research Station, Nandyal during *rabi* 2016-17 under both rainfed and irrigated conditions individually. The genotypes grew in randomized block design (RBD) with three replications each. Genetic diversity study grouped 30 chickpea genotypes into five different clusters under both the tested environments. 100 seed weight, followed by cooking time for soaked seeds contributed highest towards diversity under rainfed and irrigated conditions. Inter cluster average D^2 values stretched between 9.32 and 21.96 under rain fed condition, although it was comparatively lower and ranged between 3.77 and 15.76 under irrigated condition. Cluster II under rainfed and cluster V under irrigated were identified to be the most divergent clusters.

Thakur *et al.* (2018) genetic diversity study was conducted in 100 promising chickpea (*Cicer arietinum* L.) genotypes using Mahalanobis D^2 Statistics. Based on D^2 values, 100 genotypes had clustered into twelve clusters. The cluster I consisted of maximum 49 genotypes, followed by the Cluster III, cluster VII and cluster IX, which had 16, 12 and 12 genotypes, respectively. The greater intra cluster distance was found in cluster IX (7.72) followed by the cluster VIII (6.65), VII (6.52), cluster III (6.14) and cluster I (5.46). The range for inter cluster value were from 2.75 14.95. Though, highest inter cluster distance was noticed between cluster VII and cluster X (14.95), followed by cluster XI and cluster XII (14.08), cluster VI and cluster XI (13.43) and cluster II and cluster XI (13.22). Although, days to 50 per cent flowering (22.89 %) followed by 100 seed weight (21.29 %), number of seed per plant (14.16 %) and plant height (13.80 %) contributed most towards diversity. Based on inter cluster distances and *per se* performance PG 0749, BCG 79, ICC 5003, ICC 1058, HK 06-171 and PKV KABULI 4 were identified for inclusion in hybridization programme for realizing desirable transgressive segregates.

Ponnuru *et al.* (2019) conducted the experiment which consists of 51 genotypes of chickpea in RBD having three replications and including one check. The data was recorded on 15 characters to study genetic divergence by utilising Mahalanobis D^2 statistics. On such basis of D^2 values, 51 genotypes were clustered into eight clusters. The cluster V consisted of maximum 18 genotypes, followed by Cluster VIII and cluster II, which had 11 and 9 genotypes, respectively. Intra cluster values varied from 9.93 to 44.84. The greatest intra-cluster distance was found in cluster II (44.84) followed by cluster IV (42.49), V (42.44), cluster VIII (39.26) and cluster VII (37.15). Inter cluster values varied from 31.09 to 75.10. Nevertheless, the most inter cluster distance was noticed between cluster II and cluster VII (75.10), followed by the cluster V and cluster VII (70.13), cluster VI and cluster VII (68.83), cluster III and cluster VII (63.11) and cluster II and cluster IV (62.35).

Brindaban *et al.* (2020) conducted experiment with 20 genotypes for genetic diversity. Study revealed high variability of most of the economically important traits. The diversity analysis revealed grouping of 20 chickpea genotypes in five clusters. The cluster I consisted of maximum 13 genotypes. The inter- and intra-cluster distances revealed highest intra-cluster diversity in cluster I (13.81) followed by cluster III (9.84). Cluster IV and V had the greatest inter-cluster distance (306.92), followed by Cluster I and V (252.98), and Cluster II and V (142.78). The greatest contribution to genetic variation was found by 100 seed weight (45.26%), followed by plant height (11.05%), biomass yield per plant (8.95%), and grain yield per plant (7.89%), suggesting higher diversity in the population for these parameters.

Manasa *et al.* (2020) estimated the genetic divergence among 30 genotypes using Mahalanobis D^2 statistic for 19 traits and assessing for the diversity among Kabuli chickpea was done which suggested for the crosses among the genotypes *viz*., ICCV 171314, Vihar, NBeG 1010, ICCV 171313, Phule G 0517 from cluster IV with high cluster means for the number of pods per plant, number of seeds per plant and seed yield per plant. NBeG 805 genotype from cluster VI with superior cluster means for

SCMR, primary branches per plant, 100 seed volume and cooking time for soaked seeds can be used.

Vishnu *et al.* (2020) studied genetic diversity amongst 30 chickpea genotypes and that was assessed for yield attributing and traits related to the mechanical harvesting during a *rabi* 2016–17 under both the rainfed and the irrigated conditions as separate experiments. The genotypes were cultivated in three replications using randomized block design (RBD). They grouped 30 chickpea genotypes into five different clusters under both the tested environments. Days to 50 per cent flowering, followed by days to maturity and 100 seed weight contributed greatest towards diversity under the rainfed and the irrigated conditions. Inter cluster average D^2 values stretched between 7.42 and 20.11 under the rainfed condition, while it was slightly higher and ranged from 8.64 to 28 under the irrigated condition. The greatest divergent clusters were IV and V under both the situations.

3. MATERIAL AND METHODS

During the *Rabi* season of 2019-2020, the experiment named “Genetic diversity studies in chickpea (*Cicer arietinum* L.)” was completed at the Pulses Improvement Project, M.P.K.V., Rahuri. The materials utilized, methods employed and statistical analysis used throughout the studies are explained in detail as below.

3.1 Material

The studys experimental material included 44 genotypes acquired from the Principal Scientist, Pulses Improvement Project, M.P.K.V., Rahuri. Table 1 contains a list of genotypes.

Table 1. List of genotypes of chickpea

Sr. No.	Genotype	Source
1	NDG 18-9	Faizabad
2.	PG 237	Pantnagar
3.	Phule G 171105	Rahuri
4.	GNG2462	Sriganganagar
5.	NBeG 698	Nandyal
6.	GCP 101	Junagadh
7.	RSGD-1071	Durgapur
8.	RLBG-6	Jhansi
9.	DC 18-1107	Dholi
10.	RKG 19-2	Kota
11.	DC 18-1104	Dholi
12.	H12-22	Hisar
13.	BUC-1	Banda
14.	GJG 1708	Junagadh
15.	GL 17020	Ludhiana
16.	IPC 2016-107	IIPR, Kanpur
17.	AKG 1506	Akola
18.	H13-36	Hisar
19.	BDNG 2017-44	Badnapur
20.	Phule G 0405	Rahuri
21.	BG 4011	IARI, New Delhi
22.	BDNG 2017-49	Badnapur

Table 1 contd…

Sr. No.	Genotype	Source
23.	IPC 2015-12	IIPR, Kanpur
24.	BG 4010	IARI, New Delhi
25.	PG 227	Pantnagar
26.	BAUG 106	Ranchi
27.	GNG-2477	Sriganganagar
28.	ADBG-487	Adilabad
29.	RVSSG-79	Sehore
30.	GL 16063	Ludhiana
31.	RSGD-1057	Durgapur
32.	JG 315	Jabalpur
33.	GJG 1707	Junagadh
34.	JG 2019-155-118	Jabalpur
35.	DBGC-1	CER, Patna
36.	IPCD 2016-44	IIPR, Darwad
37.	JG 16	Jabalpur
38.	Phule G 171103	Rahuri
39.	NDG 18-2	Faizabad
40.	RVSSG-81	Sehore
41.	RKG 19-1	Kota
42.	BRC 9-14	Dholi
43.	NBeG 690	Nandyal
44.	Phule Vikram (Check)	Rahuri

3.2 Experimental Design

During *Rabi* 2019-2020, 44 chickpea genotypes were assessed using a Randomized Block Design (RBD) with three replications. Each genotype was grown in a single row of 4 m length, with 30 cm between rows and 10 cm between rows.

3.3 Cultural Practices

The land used for the experiment was medium black with a fine tilth. At the time of sowing, a fertilizer dosage of 25 : 50 : 30 NPK kg/ha was given as a basal dose. After sowing, a light irrigation was used to help with easier and better germination.

To maintain optimal crop growth, activities such as thinning, weeding, hoeing, and plant protection measures were carried out on a regular basis.

3.4 Observations Recorded

Five plants per genotype were picked at random for recording observations on the following characters, with the exception of days to 50 per cent flowering and days to maturity, in each replication, and average out.

3.4.1 Days to 50 per cent Flowering

The number of days between sowing and the day when 50 per cent of plants in each genotype initiated flowering was recorded on plant basis and the average number of days for 50 per cent flowering was estimated.

3.4.2 Days to Maturity

Days to maturity were recorded as the number of days from the date of sowing to the 80% physiological maturity of the plants of grown genotype on plot basis.

3.4.3 Plant Height (cm)

Plant height was measured at harvest time by measuring the height of a plant from the crushed level to the top of the main axis.

3.4.4 Number of Secondary Branches per Plant

At the time of harvest, fruiting branches emerging from primary branches were recorded as secondary branches.

3.4.5 Number of Pods per Plant

At maturity, the total number of pods was totalled from five randomly selected plants, and the average was calculated.

3.4.6 Number of Seeds per Pod

This parameter was recorded by five randomly taking the pods from the selected plants and the average out.

3.4.7 100 Seed Weight (g)

It was estimated by weighing 100 seeds selected at random.

3.4.8 Seed Yield per Plant (g)

The yield of seed per plant in gram was projected by the weight of seeds collected as a mean of five randomly selected plants.

3.5 Statistical Methodology

3.5.1 Assessment of Variability

a. Analysis of variance

The data collected on discrete characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1995).

$Yij = \mu + G_i + R_j + E_{ij}$

Where,

$i = 1, 2 \ldots\ldots g$

$j = 1, 2 \ldots\ldots r$

Y_{ij} = observation on i^{th} genotype in j^{th} replication

μ = General mean

G_i = Effect of i^{th} genotype

R_j = Effect of j^{th} replication

E_{ij} = Random error associated with Yij observation

ANOVA Table

Sources	d.f.	m.s.	expected m.s.
Replications	r-1	RMS	$\sigma^2 e + g\sigma^2 r$
Treatments	g-1	GMS	$\sigma^2 e + r\,\sigma^2 g$
Error	(r-1) (g-1)	EMS	$\sigma^2 e$

Where,

r = Number of replications

g = Number of genotypes

$\sigma^2 r$ = Variance due to replications

$\sigma^2 g$ = Variance due to genotypes

$\sigma^2 e$ = Variance due to error

The genotype mean square (GMS) was tested against error

Mean square (EMS) by F test for n1= (g-1) and n2 = (r-1) (g-1) degrees of freedom. The characters showing significant differences were subjected to further analysis.

Estimation of S.E. and C.D.

S.E. of mean (S.Em) = $\sqrt{\sigma^2 e / r}$

C.D. = t at error d.f. x S.E.m $\sqrt{2}$

b. Estimation of mean and range

The mean values for each character were worked out by dividing the total by corresponding number of observations.

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

Where,

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

Xi = Total of all the observations for the character and,

N = Number of observations

The lowest and highest values juxta posed such of mean of each character represented the range.

c. Estimation of components of variation

The phenotypic and genotypic variances were calculated by using the respective mean squares from the variance ANOVA table (Johnson *et al.,* 1955) as below.

Environmental Variance ($\sigma^2 e$) = EMS

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{GMS - EMS}}{r}$$

Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where,

GMS = Genotypic Mean sum of Squares

EMS = Error Mean sum of Squares

r = Number of replication

d. Estimation of coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated by using the following formulae given by Burton (1952).

i. Genotypic Coefficient of Variation (GCV)

$$GCV\ (\%) = \frac{\sigma^2{}_g}{\bar{X}} \times 100$$

Where,

$\sigma^2{}_g$ = Genotypic variance and,

$\overline{X}$ = Mean of character

ii. Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \frac{\sigma^2{}_p}{\bar{X}} \times 100$$

Where,

$\sigma^2{}_p$ = Phenotypic variance and,

$\overline{X}$ = Mean of character

The high, medium and low GCV and PCV estimates were classified as:

Low	: 10 per cent
Medium	: 10 to 20 per cent
High	: > 20 per cent

e. Estimation of heritability (b.s.)

Heritability in broad sense was estimated as suggested by Hanson *et al.* (1956).

$$h^2\ (b.s.) = \frac{\sigma^2{}_g}{\sigma^2{}_p} \text{ x } 100$$

Where,

h^2 = Heritability

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

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

Low heritability	= < 30 %
Moderate heritability	= 30.1 to 60 %
High heritability	= > 60 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was estimated using the formula given by Allard (1960).

i. Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma^2_{\ g}}{\sigma^2_{\ p}} \times \sqrt{\sigma^2_{\ p}}$$

Where,

$\sigma^2_{\ g}$ = Genotypic variance

$\sigma^2_{\ p}$ = Phenotypic variance

k = Selection differential (at 5 % selection = 2.06)

$\sqrt{\sigma^2_{\ p}}$ = Phenotypic standard deviation

ii. G.A. as percentage of means (GAM)

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where,

G. A. = Genetic advance

$\overline{X}$ = Character mean

GA (As percentage of mean) was categorised as

Low	: 10 per cent
Medium	: 10 to 20 per cent
High	: > 20 per cent

3.5.2 Correlation

Analysis of covariance was determined by taking two characters at a time. The genotypic co-variance was estimated according to Johnson *et al.,* (1955) as below:

Sources	d.f.	Sum of product	Mean sum of product	Expectation of mean sum of product
Replications	(r-1)	RP	RMP	$COVe_{1.2}+ {}_{g}COVr_{1.2}$
Genotypes	(g-1)	GP	GMP	$COVe_{1.2} + {}_{r}COV_{g1.2}$
Error	(r-1) (g-1)	EP	EMP	$COVe_{1.2}$

Environmental covariance ($COV.\ e_{1.2}$) = EMP

$$\text{Genotypic covariance } (COV.\ g_{1.2}) = \frac{GMP - EMP}{r}$$

Phenotypic covariance ($COV.\ p_{1.2}$) = ($COV.\ g_{1.2}$) + ($COV.\ e_{1.2}$)

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

Appropriate variances and co-variances were utilised for estimating phenotypic and genotypic correlation coefficients (Johnson *et al.,* 1955).

The phenotypic correlation coefficient (r_p) was calculated as:

$$r_{p1.2} = \frac{COV._{p1.2}}{\sqrt{(\sigma^2_{p1}).(\sigma^2_{p2})}}$$

Where,

$r_{p1.2}$ = Phenotypic correlation coefficient between character 1 and 2.

$COV._{p1.2}$ = Phenotypic covariance between character 1 and 2.

σ^2_{p1}, σ^2_{p2} = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to formula given by Fisher and Yates (1943). The genotypic correlation coefficient (rg) was calculated as:

$$r_{g1.2} = \frac{COV._{g1.2}}{\sqrt{(\sigma^2_{g1}).(\sigma^2_{g2})}}$$

Where,

$r_{g1.2}$ = Genotypic correlation coefficient between character 1 and 2

$COV._{g1.2}$ = Genotypic covariance between character 1 and 2

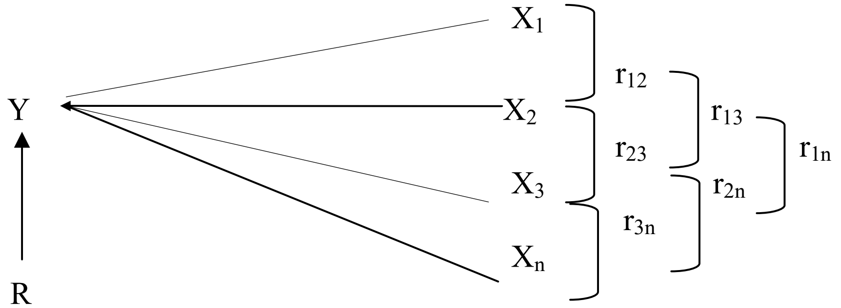
σ^2_{g1}, σ^2_{g2} = Genotypic variance of character 1 and 2 respectively.

The significance of correlation coefficients was tested from the statistical table of correlation coefficient at 1 and 5 per cent level of significance (Snedcor and Cochran, 1967).

3.5.3 Path coefficient analysis

The initial stage in establishing a cause and effect association was to divide the genotypic and phenotypic correlation coefficients into direct and indirect effects using path analysis, as proposed by Dewey and Lu (1959) and developed by Wright (1921).

The second step in path analysis is to prepare path diagram based on cause and effect relationship. In the current research, path diagram was created by using yield as the effect i.e. function of different components such as X_1, X_2, X_3 and these component demonstrated the following kind of association with the each other.



The yield in a path diagram is the outcome of X_1, X_2, X_3 ……..Xn and some additional unknown elements denoted by R. Mutual relationship was shown by the dual arrow lines, as assessed by the correlation coefficient. The single arrow indicates direct impact as determined by the path coefficient P_{ij}.

Path coefficients were calculated by solving a set of simultaneous equations of Dewey and Lu (1959) type.

$$r_{ny} = P_{ny} + r_{n2} P_{2y} + r_{n3} P_{3y} + \ldots\ldots\ldots\ldots\ldots$$

Where,

r_{ny} = represents the correlation between one component and yield

P_{ny} = represents path coefficient between that character and yield

r_{n2} = represents correlation between that character and each of the other components in turn.

Matrix A Matrix B C

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{pmatrix} = \begin{pmatrix} r_{11} & r_{12} & r_{13} \ldots\ldots\ldots\ldots r_{1n} \\ r_{21} & r_{22} & r_{23} \ldots\ldots\ldots\ldots r_{2n} \\ r_{n1} & r_{n2} & r_{n3} \ldots\ldots\ldots\ldots 1 \end{pmatrix} \begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{ny} \end{pmatrix}$$

Where,

r_{12} = r_{21} and so on

r_{1y} = Correlation between one component character and seed yield

The B matrix was inverted $[B]^{-1}$ and path coefficients (Pij) were obtained as,

i.e. $Pij = (B)^{-1}.A$

The indirect effects of a one character through other characters were derived by multiplying of direct paths and specific correlation between these characters individually.

Indirect effects = $r_{ij} \times p_{iy}$

Where,

i = 1 to 9

j = 1 to 9

P_{iy} = $P_{1y}, P_{2y}, \ldots\ldots\ldots\ldots\ldots\ldots, P_{ny}$

The path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were shown diagrammatically. The residual factor or variation in yield not accounted for by these relationships, was determined by using the following formula:

Residual factor (R) = $(1 - R^2)$

Where,

$R^2 = P_{1y}\, r_{1y} + P_{2y}\, r_{2y} + \ldots\ldots\ldots\ldots\ldots + P_{ny}\, r_{ny}$

$P_{1y}, P_{2y}, \ldots\ldots\ldots\ldots, P_{ny}$ = Direct path values

r_{1y}, r_{2y}, r_{ny} = Correlation coefficient

3.5.4 Genetic diversity

D^2 analysis

The D^2 statistics introduced by Mahalanobis (1936) and detailed by Rao (1952) were used to analyse divergence. To test the significance of variations across genotypes, the analysis of variance for the individual character investigated was undertaken using randomized block design analysis. Because all of the characters differed in a significant way, they were all utilized for additional D^2 statistical analysis. The covariance analysis for character pair based on plant average was estimated (Cochran and Cox, 1957).

a. Wilks criteria

Following the testing differences among populations for eight characters, a simultaneous test of significance of difference between the mean value of number of correlated variables with regard to pooled effect of seven characters considered together was performed using Wilks criteria Λ (Wilks, 1932), which was estimated using the relationship.

$$\Lambda = \frac{|E|}{|E+V|}$$

Where,

$|E|$ = The determinant of experimental error sum of squares and sum of products matrix

$|E+V|$ = The determinant of experimental error sum of squares and sum of products plus population sum of squares and product matrix

The significance of Wilks criteria (Λ) was tested by χ^2 as,

$$\chi^2_{pq} = V = -m.\log_e (\Lambda)$$

Where,

$$m = n - \frac{(p+q+1)}{2}$$

n = $N_1 + \ldots\ldots\ldots + N_{k-1}$ (Total number of observations-1)

p = Number of significant characters

q = k-1 (Number of genotypes -1)

K = Number of genotypes

b. Mahalanobis's generalized distance (D^2)

The generalized distance between any two populations is defined as:

$$D^2 = \Sigma\Sigma\ \lambda ij\ \delta i\ \delta j$$

Where,

λij = Reciprocal matrix to the common dispersion matrix

δi = Difference between mean value of the two populations for the i^{th} character

δj = Difference between mean value of the two populations for the j^{th} character.

This quantity is estimated by D^2 statistic (Mujumdar and Rao, 1958) as:

$$D^2 = \Sigma\Sigma\ S_{ij}\ \delta_i\ \delta_j$$

Where,

Sij, δi, δj are sample estimates of λij, δi and δj respectively, since this formula for computation needs inversion of tenth order determinant and then evaluation of 10 (10+1) terms, the total of which is D^2.

c. Computation D^2 values

For each combination, D^2 was calculated. Thus total 946 D^2 values [(44)(43)/2] were worked out.

d. Determination of population constellation

There are no criteria for locating clusters since the word "cluster" is not clearly defined. The sole criterion seems to be that any two groups belonging to the same cluster should, on average, have a lower D^2 value than those belonging to two different clusters.

Tocher (Rao, 1952) proposed a simplistic technique for cluster formation: start with two closely linked groups and identify a third group with a lower average D^2 value than the first two. Similarly, the fourth group is selected to have lower average D^2 values than the previous three groups, and so on. If, at any point after cluster creation, the average D^2 value of the group seems to be higher than those previously mentioned, then this group does not fit in that format group.

The genotypes in the first cluster are then removed and the remaining genotypes are handled identically to create next cluster.

e. Average intra-cluster distances

The intra cluster distances were calculated as,

$$\frac{\Sigma\ D_i^2}{n}$$

Where,

$\Sigma\ D_i^2$ = Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

f. Average inter-cluster distances

To calculate inter-cluster distances, first measure the distance between cluster-I and cluster-II, then between cluster-I and cluster-III, then between cluster-I and cluster-IV, and so on. Similarly, the clusters were collected one at a time, and the distances between them were computed. They estimated the average inter-cluster distances as follows

$$\frac{\Sigma Di^2}{(ni.nj)}$$

Where,

ni = Number of genotypes in cluster i

nj = Number of genotypes in cluster j

g. Cluster diagram

A diagram showing the association between different populations was created using D values between clusters.

h. Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). In all the combinations, each character was ranked on the basis of di = yi j – yi k values. Where, di = mean deviation, yi j = mean value of the j^{th} genotype for the i^{th} character and yi k = mean value of the k^{th} genotype for the i^{th} character. Rank I is given to the highest mean difference and rank P is given to the lowest mean difference Where, P is the total number of characters. Finally, the number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

4. RESULTS AND DISCUSSION

4.A. Results

The present study, entitled "Genetic diversity studies in chickpea (*Cicer arietinum* L.)" was conducted to know about the genetic diversity of forty four diverse chickpea genotypes in *rabi,* 2019-20. This chapter presents the results collected on numerous parameters under several subheadings.

4.1 Genetic Variability and Heritability

The analysis of variance showed that all eight characters had substantial genotypic differences (Table 2). For all the characters, the mean sum of squares due to treatments was significant, suggesting that genotypes varied substantially.

Table 2. Analysis of variance for eight different characters in chickpea

Sr. No.	**Characters**	**Mean sum of squares**	
		Genotype (d.f.43)	**Error (d.f.86)**
1.	Days to 50 per cent flowering	54.555**	1.002
2.	Days to maturity	27.026**	1.490
3.	Plant height	121.304**	12.488
4.	Number of secondary branches per plant	16.672**	1.697
5.	Number of pods per plant	326.014**	32.474
6.	Number of seed per pod	0.042**	0.002
7.	100 seed weight	101.469**	1.492
8.	Seed yield per plant	35.699**	4.405

* , ** indicate significant at 5 and 1 per cent level, respectively

Note: Figures in the parenthesis represents the degrees of freedom

4.1.1 Mean performance and the range of variability

The mean values of the genotypes for different characters evaluated are reported in Table 3.

4.1.1.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed variation, which were ranged from 43.00 and 63.00 days. The average number of days it took to reach 50 per cent flowering was 52.25. Twenty nine genotypes were identified earlier than the general mean, whereas fifteen genotypes were found late. The genotype RVSSG-79 took the less days (43.00), followed by BAUG-106 (44.00). RSGD-1071 had the highest number of days (63.00). RVSSG-79 (43.00 days) and BAUG-106 (44.00 days) genotypes were found to be substantially earlier than the check Phule Vikram (47.00 days).

4.1.1.2 Days to maturity

The general mean for this character was recorded 98.40 days. The days to maturity varied from 92.00 to 105.00 days. Twenty six genotypes out of forty four showed early maturity than general mean (98.40), while GL-16063 matured very late (105.00 days). However, seven genotypes were significantly earlier than the check Phule Vikram (98.00 days).

4.1.1.3 Plant height (cm)

The average height of the plants was 45.21 cm. There were seventeen genotypes that were taller than the average. The stature of the plants varied from 34.90 to 58.00 cm. None of the genotype was significantly taller than the check Phule Vikram (58.00 cm). However, the genotypes RKG 19-2 (34.90) and BRC 9-14 (36.90 cm) were dwarf among all the genotypes.

4.1.1.4 Number of secondary branches per plant

Twenty genotypes surpassed the mean performance (11.58) in respect of secondary branches. Number of secondary branches per plant ranged from 8.20 to 19.60. The three genotypes *viz.,* H 12-22 (17.60), BG-4010 (16.30) and RKG 19-1 (19.60) has considerably a greater number of secondary branches per plant than the check Phule Vikram (12.50). The genotypes *viz.*, Phule G-171105 and RSGD-1071 (8.20) both exhibited lowest branches followed by Phule G-71103 (8.50) among all the genotypes.

4.1.1.5 Number of pods per plant

Number of pods per plant ranged from 23.80 to 70.00. Seventeen genotypes recorded higher values for number of pods per plant than the mean performance (45.92). Genotype JG 2019-155-118 (23.80) recorded lowest followed by RSGD-1071 (29.10). This characters mean performance was 45.92. The ten genotypes produced substantially more pods per plant than the check Phule Vikram (45.70).

Table 3. Mean Performance of forty four chickpea genotypes studied for eight characters

Sr. No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of secondary branches per plant	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
1	NDG 18-9	52.00	98.00	45.00	12.70	42.80	1.03	32.14	14.87
2	PG-237	50.00	94.00	41.00	13.70	43.00	1.11	25.00	13.40
3	Phule G-171105	51.00	98.00	43.00	8.20	34.20	1.00	33.10	11.76
4	GNG 2462	58.00	101.00	43.60	9.30	64.20	1.11	28.42	20.30
5	NBeG 698	51.00	102.00	53.70	12.10	45.50	1.00	35.46	17.46
6	GCP -01	52.00	97.00	39.30	10.30	35.20	1.31	20.41	10.23
7	RSGD-1071	63.00	102.00	41.70	8.20	29.10	1.11	12.53	6.34
8	RLBG-6	50.00	95.00	55.80	10.80	44.60	1.12	29.76	15.73
9	DC 18-1107	50.00	97.00	50.80	12.20	42.20	1.20	30.52	16.67
10	RKG 19-2	49.00	97.00	34.90	13.50	55.50	1.00	16.22	13.90
11	DC 18-1104	53.00	98.00	56.90	9.30	49.70	1.30	22.13	14.94
12	H12-22	53.00	98.00	45.70	17.60	46.80	1.20	16.27	10.40
13	BUC-1	51.00	99.00	51.80	10.10	43.80	1.10	27.91	14.51
14	GJG-1708	50.00	98.00	43.60	11.00	41.00	1.00	28.00	12.52
15	GL 17020	50.00	97.00	54.40	11.20	50.10	1.11	25.26	16.21
16	IPC 2016-107	53.00	98.00	46.20	9.10	40.30	1.00	23.53	11.32
17	AKG 1506	49.00	97.00	42.10	10.50	55.00	1.00	24.81	15.70
18	H13-36	62.00	103.00	44.90	8.80	37.00	1.00	19.87	8.35
19	BDNG 2017-44	50.00	98.00	42.90	12.40	55.60	1.30	24.71	19.64
20	Phule G 0405	50.00	99.00	41.70	10.20	36.80	1.00	23.48	10.30
21	BG -4011	58.00	102.00	39.00	11.80	44.30	1.10	24.73	12.61
22	BDNG 2017-49	50.00	100.00	37.40	13.20	48.10	1.20	21.78	13.97
23	IPC 2015-12	61.00	100.00	50.80	13.20	69.20	1.11	17.62	13.80
24	BG -4010	54.00	97.00	46.60	16.30	70.00	1.12	24.61	21.60
25	PG -227	51.00	95.00	40.70	13.50	43.10	1.11	24.96	15.81
26	BAUG -106	44.00	102.00	46.80	13.30	60.00	1.15	20.72	16.17

Table 3 contd…

Sr. No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of secondary branches per plant	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
27	GNG -2477	54.00	101.00	38.80	10.30	47.80	1.40	18.00	11.11
28	ADBG -487	52.00	98.00	42.20	12.00	60.10	1.13	30.00	19.60
29	RVSSG-79	43.00	97.00	37.10	9.00	37.50	1.40	35.31	18.30
30	GL -16063	62.00	105.00	41.30	10.50	48.20	1.11	17.84	11.61
31	RSGD-1057	55.00	102.00	45.10	12.50	41.50	1.51	18.62	12.67
32	JG-315	51.00	93.00	40.10	10.30	36.00	1.20	21.75	10.40
33	GJG -1707	52.00	99.00	38.00	11.00	39.40	1.10	22.51	11.71
34	JG 2019-155-118	51.00	98.00	56.90	9.80	23.80	1.00	37.76	10.50
35	DBGC-1	52.00	99.00	41.00	11.70	52.50	1.00	25.62	15.38
36	IPCD 2016-44	50.00	99.00	52.40	10.30	39.40	1.12	22.41	11.23
37	JG-16	51.00	94.00	41.30	13.30	66.00	1.14	18.57	12.90
38	Phule G 171103	46.00	92.00	40.10	8.50	36.20	1.13	31.11	13.70
39	NDG 18-2	54.00	103.00	49.10	11.30	36.30	1.11	23.33	11.90
40	RVSSG-81	55.00	103.00	41.90	10.60	42.50	1.11	25.56	13.70
41	RKG 19-1	52.00	92.00	52.00	19.60	43.40	1.26	30.92	22.90
42	BRC 9-14	52.00	96.00	36.90	13.60	58.80	1.10	18.38	14.10
43	NBeG 690	55.00	98.00	56.80	10.00	38.60	1.05	32.91	15.56
44	Phule Vikram	47.00	98.00	58.00	12.50	45.70	1.13	20.96	15.30
	Mean	**52.25**	**98.40**	**45.21**	**11.58**	**45.92**	**1.13**	**24.67**	**14.11**
	C.V.	1.92	1.24	7.81	11.25	12.53	4.41	4.95	14.87
	S.E.	0.58	0.70	2.04	0.75	3.30	0.03	0.71	1.21
	C.D. 5%	1.63	1.98	5.74	2.11	9.29	0.08	1.98	3.41

4.1.1.6 Number of seeds per pod

This characters mean performance was 1.13. Number of seeds per pod was least in case of Phule G-171105, NBeG 698, RKG 19-2, GJG-1708, IPC 2016-107, AKG-1506, H-13-36, Phule G-0405, JG 2019-155-118 and DBGC-1 (1.00) among all the genotypes. Thirteen genotypes recorded for maximum number of seeds per pod than the mean performance. The seven genotypes produced significantly maximum number of seeds per pod than the check Phule Vikram (1.13).

4.1.1.7 100 seed weight (g)

The mean performance of this character was 24.67 g. The variation for 100 seed weight ranged between 12.53 g to 37.76 g. Twenty two genotypes recorded higher 100 seed weight than the mean performance. While, the genotypes *viz.*, RSGD-1071 (12.53 g) showed lowest 100 seed weight followed by RKG 19-2 (16.22 g) and H 12-22 (16.27 g) among all the genotypes. However, twenty six genotypes showed significantly higher 100 seed weight than the check Phule Vikram (20.96 g).

4.1.1.8 Seed yield per plant (g)

This characters average performance was 14.11 g. The variation for seed yield per plant varied between 6.34 g and 22.90 g. The genotype RSGD-1071 had the lowest seed yield per plant (6.34 g), along with H 13-36 (8.35 g) and GCP-101 (10.23 g). Nineteen genotypes outperformed the mean performance (14.11 g) in terms of seed yield per plant. While, five gave considerably greater seed yield per plant over the check Phule Vikram (15.30 g).

4.1.2 Genotypic and Phenotypic Coefficients of Variation

Estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were classified as proposed by Sivasubramanian and Madhavamenon (1973) and are specified in Table 4.

100 seed weight (23.40 %) had the greatest genotypic coefficient variation (GCV), along with seed yield per plant (22.88 %), number of pods per plant (21.65 %) and number of secondary branches per plant (19.30 %). Although, days to maturity (2.97 %) and days to 50 per cent flowering (8.09 %) had low GCV.

Seed yield per plant (24.44 %), 100 seed weight (23.57 %), number of pods per plant (22.82 %) and number of secondary branches per plant (20.36 %) all had high PCV estimations. However, plant height (14.05 %), number of seeds per pod (10.52 %), days to 50 per cent flowering (8.17 %) and days to maturity (3.05 %) all had low PCV.

The phenotypic coefficient of variation was often higher than the genotypic coefficient of variation. Seed yield per plant (1.56) had the greatest magnitudinal difference between GCV and PCV, along with number of pods per plant (1.17), number of secondary branches per plant (1.06) and plant height (0.74). While, days to maturity (0.08) and days to 50 per cent flowering (0.08) had the smallest variation between GCV and PCV.

4.1.3 Heritability and Genetic Advance

Estimates of heritability in broad sense are portrayed in Table 4. The heritability (b.s.) estimate varied between 100 seed weight (98.50 %) and seed yield per plant (87.70 %). Heritability estimates (>60%) were found to be high for nearly all of the characters examined. The maximum estimates of heritability exhibited in 100 seed weight (98.50 %) afterwards days to 50 per cent flowering (98.20 %), days to maturity (94.50 %), number of seeds per pod (94.10 %), number of pods per plant (90.00 %), number of secondary branches per plant (89.80 %), plant height (89.70 %) and seed yield per plant (87.70 %).

The range of genetic advance (GA) observed from 0.23 to 19.32. The highest estimate of GA recorded for number of pods per plant (19.32), followed by 100 seed weight (11.80), plant height (11.75), days to 50 per cent flowering (8.62) and seed yield per plant (6.30).

4.1.4 Genetic Advance as per cent of Mean

As proposed by Johnson *et al.* (1955), the range of genetic advance as per cent of mean is categorized. High estimates of genetic advance as per cent of mean recorded for the 100 seed weight (47.85 %), along with seed yield per plant (44.13 %), number of pods per plant (42.30 %), number of secondary branches per plant (37.68 %). Although, days to maturity (5.94 %) had the lowest performance in genetic advance as per cent of mean.

Table 4. **Estimates of variability parameters for seed yield and its contributing characters in forty four chickpea genotypes**

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	Heritability (h^2) (b.s.) (%)	Genetic Advance	Genetic Advance % of Mean
1	Days to 50 per cent flowering	52.25	43.00-63.00	8.09	8.17	98.20	8.62	16.51
2	Days to maturity	98.40	92.00-105.00	2.97	3.05	94.50	5.84	5.94
3	Plant height (cm)	45.21	34.90-58.00	13.31	14.05	89.70	11.75	25.96
4	Number of secondary branches/plant	11.58	8.20-19.60	19.30	20.36	89.80	4.36	37.68
5	Number of pods/plant	45.92	23.80-70.00	21.65	22.82	90.00	19.32	42.30
6	Number of seeds/pod	1.13	1.00-1.51	10.21	10.52	94.10	0.23	20.40
7	100 seed weight (g)	24.67	12.53-37.76	23.40	23.57	98.50	11.80	47.85
8	Seed yield /plant (g)	14.11	6.34-22.90	22.88	24.44	87.70	6.30	44.13

4.2 Correlation Studies

The genotypic and phenotypic correlation coefficients between seed yield and its components were calculated. Table 5 shows the genotypic (rg) and phenotypic (rp) correlations for the eight characters evaluated. In general, genotypic correlation coefficients were greater than the phenotypic correlations.

In present study the result on genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient for most of the characters indicated strong association between these characters and they are useful in yield improvement.

4.2.1 Association of Seed Yield with its Components

Seed yield per plant had significant positive correlation with the plant height (r_g = 0.228, r_p = 0.216), number of secondary branches per plant (r_g = 0.413, r_p = 0.447), number of pods per plant (r_g = 0.528, r_p = 0.555) and 100 seed weight (r_g = 0.471, r_p = 0.468) as it has been observed from the Table 5. Non-significant positive correlation was found between seed yield per plant with number of seeds per pod (r_g = 0.130, r_p = 0.151). Nevertheless, seed yield per plant had negative and significant correlation with days to 50 per cent flowering (r_g = -0.344, r_p = -0.324) and days to maturity (r_g = -0.335, r_p = -0.288) at both genotypic and phenotypic levels.

4.2.2 Interrelationship of Yield Components

4.2.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited significant positive correlations with days to maturity (r_g = 0.571, r_p = 0.552) while, it had significant and negative correlation with 100 seed weight (r_g = -0.389, r_p = -0.385), seed yield per plant (r_g = -0.344, r_p = -0.324). At a both genotypic and phenotypic levels, it also had non-significant positive correlation with the number of pods per plant and non-significant negative correlation with height of plant, number of secondary branches per plant, number of seed per pod.

4.2.2.2 Days to maturity

Days to maturity exhibited substantial positive correlation with days to 50 per cent flowering (r_g = 0.571, r_p = 0.552), but it showed significant negative association

Table 5. **Estimates of phenotypic (above diagonal) and genotypic correlation coefficients (below diagonal) among seed yield and yield contributing characters in forty four chickpea genotypes**

Sr. No.	Name of character	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of secondary branches/ plant	Number of pods / plant	Number of seed / pod	100 seed weight (g)	Seed yield/ plant (g)
1.	Days to 50 per cent flowering	**1.000**	0.552**	-0.010	-0.101	0.042	-0.106	-0.385**	-0.324**
2.	Days to maturity	0.571**	**1.000**	-0.017	-0.280**	-0.001	-0.049	-0.258**	-0.288**
3.	Plant height (cm)	-0.013	-0.010	**1.000**	0.054	-0.093	-0.095	0.331**	0.216*
4.	Number of secondary branches/ plant	-0.108	-0.310**	0.049	**1.000**	0.471**	0.152	-0.152	0.447**
5.	Number of pods/plant	0.050	-0.021	-0.106	0.450**	**1.000**	0.055	-0.268**	0.555**
6.	Number of seeds/pod	-0.112	-0.052	-0.115	0.140	0.040	**1.000**	-0.200*	0.151
7.	100 seed weight (g)	-0.389**	-0.271**	0.345**	-0.189**	-0.310**	-0.214*	**1.000**	0.468**
8.	Seed yield /plant (g)	-0.344**	-0.335**	0.228*	0.413**	0.528**	0.130	0.471**	**1.000**

*and ** significant at P= 5 and P = 1 level of significance, respectively through number of secondary branches per plant (r_g = -0.310, r_p = -0.280), 100 seed weight (r_g = -0.271, r_p = -0.258), seed yield per plant (r_g = -0.335, r_p = -0.288) and it also had non significant negative correlation with rest of all characters *viz.* plant height, number of pods per plant, number of seeds per pod.

4.2.2.3 Plant height

Plant height recorded significant positive association with 100 seed weight (r_g =0.345, r_p =0.331), seed yield per plant (r_g = 0.228, r_p = 0.216) both at genotypic and phenotypic levels. Other characters are non-significant such as number of secondary branches per plant (positively), it also had non-significant negative correlation with days to 50 per cent flowering, days to maturity, number of pods per plant and number of seed per pod at genotypic as well as phenotypic level.

4.2.2.4 Number of secondary branches per plant

The number of secondary branches per plant had positive and significant correlation with number of pods per plant (r_g =0.450, r_p =0.471) and seed yield per plant (r_g = 0.413, r_p = 0.447). It also showed significant negative correlation with days to maturity (r_g = -0.310, r_p = -0.280) at both the genotypic and phenotypic levels, with the exception of 100 seed weight (r_g = -0.189, r_p = -0.152), which showed a significant negative correlation at the genotypic and non-significant negative correlation at phenotypic levels. It also had non-significant, positive correlation with plant height and the number of seed per pod, as well as a negative correlation with days to 50 per cent flowering.

4.2.2.5 Number of pods per plant

The number of pods per plant had significantly positive correlation with the number of secondary branches per plant (rg = 0.450, rp = 0.471) and seed yield per plant (r_g = 0.528, r_p = 0.555) at both genotypic and phenotypic level. However, it showed a significantly inverse (negative) relation with 100 seed weight (r_g = -0.310, r_p = -0.268). Among rest of all the characters days to 50 per cent flowering, number of seed per pod and days to maturity, plant height showed non-significant positive and negative association respectively.

4.2.2.6 Number of seed per pod

The number of seed per pod had significant negative association with 100 seed weight (r_g = -0.214, r_p = -0.200). However, it showed non-significant positive correlation with the number of secondary branches per plant, number of pods per plant and seed yield per plant, as well as a non-significant negative association with days to 50 per cent flowering, days to maturity and plant height not only, at genotypic but also phenotypic levels.

4.2.2.7 100 seed weight

It exhibited significant positive correlation with the plant height (r_g = 0.345, r_p = 0.331), seed yield per plant (r_g = 0.471, r_p = 0.468). Whilst, it showed significant negative association with days to 50 per cent flowering (r_g = -0.389, r_p = -0.385), a days to maturity (r_g = -0.271, r_p = -0.258), number of pods per plant (r_g = -0.310, r_p = -0.268), number of seed per pod (r_g = -0.214, r_p = -0.200) at both genotypic and phenotypic levels with excepting the number of secondary branches per plant (r_g = -0.189, r_p = -0.152) as it had significant negative association at genotypic and non-significant negative correlation at phenotypic levels.

4.3 Path Coefficient Analysis

Correlation coefficient values do not reveal the real association pattern of the independent variables with the dependent one. This alone is not adequate to interpret the cause and effect relationships among the traits and ultimately with seed yield. So, in order to achieve a clear picture of inter-relationship of various component characters with the seed yield per plant, direct and indirect impacts were estimated at the genotypic level using path coefficient analysis. Seed yield, a polygenic trait is influenced by various components directly as well as indirectly *via* other traits, which create a complex situation before a breeder for making selection. As a result, path coefficient analysis may offer a more realistic information of the inter-relationship, as it considers both direct and indirect effects of the variables by partitioning the correlation coefficient into direct and indirect effects were presented in Table 6.

4.3.1 Days to 50 per cent flowering

Days to 50 per cent flowering had negative direct effect (-0.0276) and a negative indirect effect nearly through all the characters except number of pods per plant (0.033), resulting in a negative and significant association with seed yield (-0.344).

4.3.2 Day to maturity

Days to maturity exhibited direct negative effect on the seed yield (-0.035). It also had negative indirect effects *via* nearly all the characters and thus leading to negative correlation with seed yield (-0.335).

Table 6. Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on seed yield in forty four chickpea genotype

Sr. No.	Name of character	Days to 50 per cent flowering	Days to Maturity	Plant height (cm)	Number of secondary branches/ plant	Number of pods / plant	Number of seed / pod	100 seed weight (g)	Genotypic correlation with Seed yield/ plant (g)
1.	Days to 50 % flowering	**-0.0276**	-0.020	-0.001	-0.022	0.033	-0.026	-0.281	-0.344**
2.	Days to maturity	-0.016	**-0.035**	-0.001	-0.063	-0014	-0.012	-0.196	-0.335**
3.	Plant height (cm)	0.0004	-0.0003	**0.065**	0.010	-0.070	-0.027	0.249	0.228*
4.	Number of secondary branches/ plant	0.003	0.011	0.003	**0.202**	0.297	0.033	-0.136	0.413**
5.	Number of pods/plant	-0.001	0.001	-0.007	0.091	**0.660**	0.001	-0.224	0.528**
6.	Number of seeds/pod	0.003	0.002	-0.008	0.028	0.026	**0.232**	-0.154	0.130
7.	100 seed weight (g)	0.011	0.009	0.023	-0.038	-0.205	-0.050	**0.721**	0.471**

Residual effect (R) = 0.403, Underlined figures indicated direct effect

4.3.3 Plant height

The plant height had direct positive impact (0.065) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.0004), number of secondary branches per plant (0.010), 100 seed weight (0.249). Thus, resulting to overall genotypic correlation with seed yield was significant and positive (0.228).

4.3.4 Number of secondary branches per plant

The number of secondary branches per plant, exhibited positive direct effect (0.202) on the seed yield. Except for 100 seed weight (-0.136), it had a positive indirect effect on all the traits. All in all, it had positive and highly significant correlation with seed yield per plant (0.413).

4.3.5 Number of pods per plant

It exhibited a highly significant and positive correlation with seed yield (0.528). It showed positive direct effect (0.660) on seed yield and indirect positive effect on the number of secondary branches per plant (0.091). It also had the indirect negative effect for the days to 50 per cent flowering, plant height and 100 seed weight.

4.3.6 Number of seed per pod

The number of seed per pod had a direct positive effect (0.232) on seed yield. It had positive indirect effect *via* nearly all the characters with the exception of plant height (-0.008), 100 seed weight (-0.154), resulting in positive correlation with the seed yield (0.130).

4.3.7 100 seed weight

Among the all characters studied, 100 seed weight had high and positive direct effect on seed yield (0.721). Except for the number of secondary branches per plant (-0.038), number of pods per plant (-0.205) and number of seed per pod (-0.050), it had a positive indirect influence on all the traits evaluated. It had a highly substantial and positive association with seed yield (0.471).

4.4 Genetic Divergence

Improvement of seed yield or any further characters is often accomplished through involvement of genetically diverse parents in breeding programme. For identifying such parents for crossing, multivariate analysis by means of Mahalanobis D^2 statistics has been used in several crops. It is powerful technique for quantifying the degree of genetic diversity among the genotypes and relating clustering pattern to geographic region.

4.4.1 Mahalanobis's generalised distance (D^2)

Wilks criterion revealed substantial variations across genotypes for the pooled effect of eight evaluated characters. Due to of that, additional analysis was done to calculate D^2 values. The D^2 were obtained for all available pairs of comparison between 44 genotypes including 1 check. The Mahalanobis D^2 statistics were computed for all possible pairs of 44 genotypes including 1 check based on the observations of eight traits, in order to assess the genetic diversity existed between the genotypes.

The estimated D^2 value ranged from 6.39 to 1050.90, the lowest values being between the pair of genotypes PG-237 and PG-227 and the highest between genotype RVSSG-79 and IPC 2015-12.

The Mahalanobis D^2 statistics were computed for all possible pairs of 44 genotypes based on the observations of eight traits, in order to assess the genetic diversity existed between the genotypes under the evaluation.

The mean values of forty four genotypes $[(X_1) - (X_2)]$ were transformed into standardized uncorrelated mean values $[(Y_1) - (Y_2)]$. The D^2 values were computed for all possible combination that is 44 (44-1)/2 = 946 pairs of genotypes.

4.4.2 Clustering pattern of the genotypes

The clustering pattern generated based on the magnitude of D^2 was formed and shown in Table 7, as well as clustering using Tochers method, as described by Rao (1952). The 44 genotypes including 1 check were grouped into eleven clusters. Table 7 shows that cluster I contained the most number of genotypes (21), followed by cluster VII (6), cluster II (5), cluster VI (4) and cluster IV (2) genotypes. The clusters III, V, VIII, IX, X and XI were solitary since they had only one genotype.

Table 7. Grouping of forty four genotypes of chickpea into different clusters based on D^2 values

Cluster No.	Number of genotypes	Name of Genotypes
I	21	PG-237, PG-227, JG-315, GJG-1707, Phule G-0405, IPC 2016-107, DBGC-1, AKG-1506, GL-17020, IPCD 2016-44, GJ-1708, BUC-1, BDNG 2017-44, ADBG-487, RVSSG-81, NDG 18-2, BDNG 2017-49, GCP-101, DC 18-1104, DC 18-1107, RLBG-6
II	5	JG-16, BRC 9-14, RKG 19-2, BG-4010, Phule Vikram
III	1	BG-4011
IV	2	GNG-2477, RSGD-1057
V	1	NDG 18-9
VI	4	RSGD-1071, GL-16063, H-13-36, IPC 2015-12
VII	6	Phule G-171105, NBeG-698, NBeG-690, JG 2019-155-118, Phule G-171103, RVSSG-79
VIII	1	BAUG-106
IX	1	GNG-2462
X	1	RKG 19-1
XI	1	H-12-22

4.4.3 Intra and inter-cluster divergence

Table 8 displays the average intra and inter cluster D values. The inter cluster distance (D) ranged between 8.75 to 28.40. The clusters VII and XI had the greatest inter cluster distance (D=28.40), followed by cluster VI and VII (26.63) and cluster IV and VII (24.01). Cluster III and IX had the shortest inter cluster distance (D=8.75). An analysis of intra cluster divergence amongst the eleven clusters revealed that, cluster VII reported highest intra cluster distance (D=10.99), followed by cluster II (8.18). There was no intra cluster divergence since clusters III, V, VIII, IX, X and XI were solitary. The reciprocal connection of the clusters is depicted diagrammatically in Fig. 4.

Table 8. Average intra (bold) and inter cluster D balues for eleven clusters in forty four chickpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**7.51**	11.85	9.60	13.13	10.33	16.16	15.51	13.15	11.42	12.36	16.41
II		**8.18**	13.66	12.11	18.20	14.31	23.49	10.41	16.34	16.72	10.85
III			**0.00**	12.20	10.86	11.01	17.52	17.01	8.75	14.22	15.76
IV				**4.41**	19.42	12.68	24.01	12.97	16.56	18.80	11.20
V					**0.00**	20.78	9.45	19.63	11.51	11.23	22.57
VI						**7.76**	26.63	18.85	15.24	21.20	13.65
VII							**10.99**	23.56	16.23	16.29	28.40
VIII								**0.00**	19.42	19.98	13.59
IX									**0.00**	16.40	21.92
X										**0.00**	19.48
XI											**0.00**

Diagonal : Intra cluster and above diagonal inter cluster D values

4.4.4 Cluster means for different characters

Table 9 shows the cluster mean for the eight characters. Most of the characters exhibit a broad range of variation.

4.4.4.1 Days to 50 per cent flowering

Cluster means for this character varied from 44.00 (cluster VII) to 62.00 (cluster VI). Cluster VIII (44.00) had the earliest days to 50 per cent flowering, along with cluster VII (49.50), cluster II (50.60), cluster I (51.14) and cluster V (52.00), cluster X (52.00), while, genotypes in cluster VI (62.00), cluster III (58.00), cluster IX (58.00), cluster IV (54.50) and cluster XI (53.00) was late to 50 per cent flowering.

4.4.4.2 Days to maturity

The cluster means for this character varied from 92.00 (cluster X) to 102.50 (cluster VI). The genotypes in cluster X (92.00) was earliest for days to maturity along with cluster II (96.27), cluster VII (97.50), cluster I (97.91), cluster V and cluster XI (98.00). While, the genotypes in cluster VI (102.50), along with cluster III (102.00) and cluster VIII (102.00), cluster IV (101.50) and cluster IX (101.00) matured late.

4.4.4.3 Plant height (cm)

Cluster means for such a character were ranged between 39.00 (cluster III) and 53.45 (cluster X). The maximum cluster mean for this character was detected in cluster X (53.45) followed by cluster VII (47.92), cluster VIII (46.78), while the lowest cluster mean recorded in cluster III (39.00) followed by cluster IV (41.94), cluster IX (43.55).

4.4.4.4 Number of secondary branches per plant

The cluster means for this character varied from 9.30 (cluster IX) to 19.60 (cluster X). Cluster X had the highest cluster mean for this character (19.60), followed by cluster XI (17.60) and cluster II (13.84. Although, cluster IX had the lowest number of secondary branches per plant (9.30), along with cluster VII (9.60) and cluster VI (10.18).

4.4.4.5 Number of pods per plant

The range of the cluster means for this character were observed from 35.96 (cluster VII) to 64.22 (cluster IX). The greatest number of pods per plant observed in cluster IX (64.22), followed by cluster VIII (60.00) and cluster II (59.18). While, least number of pods per plant observed in cluster VII (35.96), followed by cluster V (42.78) and cluster X (43.45).

4.4.4.6 Number of seed per pod

Cluster IV had the highest cluster mean (1.46), followed by cluster X (1.26) and cluster XI (1.20). The cluster II (1.01) had the lowest cluster mean, followed by cluster V (1.03) and cluster VI (1.08). Cluster means for this character were ranged between cluster II (1.01) and cluster IV (1.46).

4.4.4.7 100 seed weight (g)

The range of the cluster mean for this character were observed from 16.27 (cluster XI) to 34.27 (cluster VII). The maximum cluster mean detected in cluster VII (34.27) followed by cluster V (32.14) and cluster X (30.92). Whereas, minimum 100 seed weight recorded in cluster XI (16.27) followed by cluster VI (16.97) and cluster IV (18.31).

Table 9. Mean values of the eleven clusters for eight characters in forty four chickpea genotypes

Cluster No.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of secondary branches per plant	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
I	51.14	97.91	45.20	11.18	43.95	1.13	24.93	14.04
II	50.60	96.27	43.79	13.84	59.18	1.01	19.75	15.56
III	58.00	102.00	39.00	11.80	44.33	1.10	24.73	12.61
IV	54.50	101.50	41.94	11.40	44.65	1.46	18.31	11.89
V	52.00	98.00	45.00	12.70	42.78	1.03	32.14	14.87
VI	62.00	102.50	44.67	10.18	45.89	1.08	16.97	10.03
VII	49.50	97.50	47.92	9.60	35.96	1.09	34.27	14.55
VIII	44.00	102.00	46.78	13.33	60.00	1.15	20.72	16.17
IX	58.00	101.00	43.55	9.30	64.22	1.11	28.42	20.30
X	52.00	92.00	53.45	19.60	43.45	1.26	30.92	22.90
XI	53.00	98.00	45.74	17.60	47.33	1.20	16.27	10.40
Population mean	**53.16**	**98.97**	**45.19**	**12.78**	**48.34**	**1.15**	**24.31**	**14.85**

4.4.4.8 Seed yield per plant (g)

The range of cluster means for this such s character were varied between cluster VI (10.03 to cluster X (22.90). The greatest seed yield per plant observed in cluster X (22.90), followed by cluster IX (20.30) and cluster VIII (16.17). The cluster VI (10.03) recorded least seed yield per plant, along juxta a by cluster XI (10.40) and cluster IV (10.89).

Based on inter-cluster distance, cluster mean and *per se* performance, the genotypes *viz*., BG-4010, Phule Vikram, NDG 18-9, RVSSG-79, GNG-2462, RKG 19-1, BAUG-106 and BRC 9-14 are suggested to utilize for future breeding programme.

4.4.5 Per cent contribution of different characters to genetic diversity

The utility of D^2 analysis was improved by its use to assess the relative contribution of the different plant characters to genetic divergence. The per cent contribution of eight characters examined was provided in Table 10. It was found that 100 seed weight (57.93 %) and days to 50 % flowering (18.92 %) contributed highest for divergence, along with number of seeds per pod (7.93 %). Seed yield per plant (0.63 %), number of secondary branches per plant (2.96 %), number of pods per plant (3.28 %), plant height (4.02 %) and days to maturity (4.33 %) were contributed least for genetic divergence.

Table 10. Per cent Contribution of different characters

Sr. No.	Character	No of times appearing first in ranking	Contribution (%)
1	Days to 50 % flowering	179	18.92
2	Days to maturity	41	4.33
3	Plant height (cm)	38	4.02
4	Number of secondary branches/plant	28	2.96
5	Number of pods/plant	31	3.28
6	Number of seeds/pod	75	7.93
7	100 seed weight (g)	548	57.93
8	Seed yield /plant (g)	6	0.63
	Total		100

4.B. Discussion

The success of plant breeding relies on selection of superior genotypes, which ultimately depends on understanding of variability and genetic diversity of germplasm. Plant breeding deals with maintenance and use of genetic diversity. Hence, evaluation of genetic variability, study of the character association and genetic diversity in the available germplasm is of great importance to design a selection strategy and to recognize the superior, genetically diverse genotypes to be utilised as parents in future hybridization programme. It is, thus essential to identify and use this diversity systematically for future genetic enhancement of biological population.

Likewise, assessment of the degree and association of direction between various yield contributing characters, particularly yield, is helpful in selecting desirable genotypes based on their phenotypic values. In this direction simple correlation coefficients are of limited utility. So, it is imperative to know the cause and effect relationship between yield and its component characters through the correlation and path analysis studies.

The genetic divergence enables the evaluation of parents actual without crossing and grouping of parent material into clusters in a significant pattern. The D^2 statistics suggested by Mahalanobis (1936) and clustering by Rao (1952) helps to select the diverse genotypes for hybridization programme.

In this study, the degree of genetic variability in 44 different genotypes of chickpea was assessed. These genotypes were obtained from the Pulses Improvement Project, M.P.K.V., Rahuri. Correlation and path analysis were also used to study the relationship between component characters and the direct and indirect path coefficients of the component characters on yield, as well as to examine genetic divergence. The findings on these areas are presented in this chapter under the proper headings. The current studys findings in 44 genotypes are presented under the following sub headings.

4.5 Variability and genetic parameters
4.6 Correlation studies
4.7 Path analysis
4.8 Genetic divergence

4.5 Variability and Genetic Parameters

The existence of genetic variability is expedient to the evolutionary survival of a species. Yield enhancement in any crop may be achieved *via* plant breeding, but the essential variability for selection must be present in the crops genetic material. As a result, before embarking on any crop improvement programme, a plant breeder must survey and evaluate the variability for a given agronomic or yield component character. Which can be estimated using variance, coefficient of variation (GCV, PCV), heritability and genetic advance as per cent of mean.

4.5.1 Range of Variability

Except for the number of seed per pod, there was a large range of variability found for nearly all of the characters. The pods number of per plant had the greatest range of variability, along with 100 seed weight plant height, days to 50 per cent flowering, seed yield per plant and days to maturity. The least variable parameter were the number of secondary branches per plant. Malik *et al.,* (2014) found similar findings, reported significant variability for the number of pods per plant, secondary branches per plant and seed yield. Sharma et al., (1990) found the most variability in number of pods per plant, along with secondary branches per plant, harvest index, days to maturity and days to flowering, also the least variability in seed per pod. Rao and Kumar (2000) observed maximum variation in biological yield, with minimal variability observed in days to maturity and days to 50 per cent flowering.

4.5.2 Genotypic and Phenotypic Coefficient of Variation

Genetic variability is the foundation for every heritable improvement in the crop plant. The estimations of GCV and PCV for the characters examined revealed minimal difference, the latter being somewhat higher than the former, thus suggesting that the variability present in these attributes was not just attributable to genetic factors but also related to environmental variables.

The character 100 seed weight and seed yield per plant showed highest estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) signifying excellent scope for their enhancement *via* selection. The phenotypic coefficients of variation (PCV) were highest for the character 100 seed weight and seed yield per plant. This was in the conformity with the results, Astereki *et al.* (2015) studied genetic diversity of 25 chickpea genotypes, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for seed yield, days to flowering, canopy height, number of pods per plant, Kishor *et al.* (2018) recorded lowest GCV and PCV for the days to maturity and days to 50 per cent flowering, as well as high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was found for 100 seed weight.

The magnitudinal difference between the genotypic coefficient of variation and the phenotypic coefficient of variation was greatest for seed yield per plant (1.56), along with number of pods per plant (1.17), number of secondary branches per plant (1.06) and plant height (0.74) indicating that environment played significant role in expression of these characters. While, the lowest difference between GCV and PCV was found for days to maturity, days to 50 per cent flowering (0.08), followed by 100 seed weight (0.17) and number of seeds per pod (0.31), indicting that environment plays a minor role in the phenotypic expression of these characters and that selection can be based solely on the phenotype.

4.5.3 Heritability (b.s) and Genetic Advance

The genotypic coefficient of variation does not alone reflect the portion of net heritable variation. On the other hand, the heritability estimates are better predictors of the heritable component of the variation. Heritability in broad sense encompasses the contribution of additive gene effects, allelic interactions due to dominance and non-allelic interactions due to epistasis. In the current study, the highest estimates of heritability were found in 100 seed weight (98.50 %), along with days to 50 per cent flowering (98.20 %), days to maturity (94.50 %), number of seed per pod (94.10 %), number of pods per plant (90.00 %), number of secondary branches per plant (89.80 %), plant height (89.70 %) and seed yield per plant (87.70 %). These findings are confirmed by Mathur and Mathur (1996), Ali *et al.* (2008) found that broad sense heritability estimates for plant height (97.4) and seed yield per plant (97.3) were the highest. Mushtaq *et al.* (2013) observed that heritability estimates for pods per plant, days to maturity, days to flowering, total weight of plant, secondary branches per plant, plant height, 100 seed weight and seed yield per plant were the maximum.

Plant height, number of secondary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant all had significant heritability and genetic advance as a per cent of mean in the current study. The genetic advance as a per cent of mean had range from 5.94 to 47.85. High estimations of genetic advance as per cent of mean recorded for 100 seed weight (47.85 %), followed by seed yield per plant (44.13

%), number of pods per plant (42.30%), number of secondary branches per plant (37.68 %). Days to maturity (5.94 %) had the lowest performance in terms of genetic advance as a per cent of mean. This finding was supported by Ali *et al.,* (2008), who found that genetic advance was higher for seed yield per plant (27.42), Neelu kumari *et al.,* (2013) found that high expected genetic advance combined with a high heritability estimate was obtained for, plant height, number of secondary branches per plant, number of pods per plant and seed yield per plant. Accompanied by significant genetic advance as a per cent of mean, suggesting that these characters might be heavily influenced by the additive gene action and that selection of these traits might be more successful for desired genetic enhancement.

Thus, based on estimates of genetic parameters such as genotypic coefficient of variation, heritability and genetic advance as a per cent of mean, selection in the characters such as 100 seed weight, seed yield per plant, number of pods per plant, plant height, number of secondary branches per plant and number of seed per pod must be done to improve chickpea yield.

4.6 Correlation Studies

Correlated characters are interesting for three reasons: first, because of the genetic cause of correlation *via* gene linkage and pleiotropic action, second, because it is important to understand how one characters improvement causes simultaneous changes in other characters, and third, because of natural selection (Falconer, 1960).

The genotypic correlation coefficients provide an estimate of an inherent association between gene 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 amid the two characters. The correlation coefficients value cannot remain constant all of the time. It varies greatly depending on the kind of material handled, the method of observation used, cultural practices followed and the environment in which the item is cultivated. The very significant positive values of correlation coefficients revealed a similar substantial relationship between number of secondary branches per plant and number of pods per plant. This implies that these characters are improving at the same time as a result of selection.

In the present research, seed yield per plant was shown to have a significant positive relationship with plant height, number of secondary branches per plant, number of pods per plant and 100 seed weight. Tiwari *et al.* (2016) backs up these findings, as they found that the most significant characters that had a positive relationship with seed yield per plant were 100 seed weight, seeds per pod, number of effective pods per plant, number of pods per plant, number of primary branches per plant and plant height. According to Kumar *et al.* (2019) correlation studies, revealed that grain yield had significant and positive association with the number of pods per plant, whereas it had a significant and negative relationship with days to maturity. Number of secondary branches per plant, number of seed per plant,100 seed weight, harvest index and biological yield were shown to have a significant positive correlation with the seed yield per plant by Shanmugam and Kalaimagal (2019). This result is consistent with previous research by Banik *et al.* (2017) and Kumar *et al.* (2019), who found a strong negative correlation between seed yield per plant and days to 50 per cent flowering and days to maturity.

4.7 Path Coefficient Analysis

Path coefficient analysis is nothing more than a standardized partial regression coefficient that divides correlation coefficients into direct and indirect effects. Aside from correlation studies, path coefficient analysis is crucial for determining how the component characters interact to affect seed yield. The correlation coefficient, in combination with path effects, offers the foundation for selecting better genotypes from a varied breeding programme. The interaction of component characters results in the seed yield.

Direct effect of any component character on seed yield gives an idea about reliability of indirect selection to be made through that character to bring about improvement in seed yield. If both correlation coefficient and the direct effect are high and positive then correlation explains its true relationship and a selection for that character will be effective. If the correlation coefficient is positive, but the direct effect is negative or negligible, in such relations the indirect causal factors are to be considered simultaneously for selection, when correlation coefficient is negative but the direct effect is positive and high in such cases direct selection for such traits should be practiced to reduce the undesirable indirect effect.

The residual effect determines how best the causal factor accounts for variability of the dependent factor, the grain yield per plant. In this case if the value of residual effect is moderate or high, it indicates that besides the characters studied there is some other attributes which contributes for yield.

In the present research, as per path analysis study it were reported that, 100 seed weight (0.721) reported maximum direct effect on seed yield per plant subsequently, number of pods per plant (0.660), number of seeds per pod (0.232), number of secondary branches per plant (0.202) and plant height (0.065) also exhibit the same. These direct impacts are primarily responsible for the positive association of these character with the seed yield per plant. The direct impact of number of pods on seed yield per plant was noted by the other workers which includes, Paliwal *et al.* (1987) found that 100 seed weight showed highest positive direct effect on yield, followed by pods per plant, seeds per plant, Jeena *et al.* (2005) observed biological yield recorded maximum positive association with seed yield combined with highest positive direct impact on it, Muhammad *et al.* (2004) and Yucel *et al.* (2006) mentioned the direct effect of other characters on the seed yield per plant.

The days to 50 per cent flowering and days to maturity had a direct negative effect on seed yield. Zena *et al.* (2008) found a similar outcome in which the 50 per cent flowering phase had a negative direct effect on gram yield. Based on the findings of the current studies, it could be upheld that the most desirable plant type in chickpea should have a higher 100 seed weight (bold seeds), a higher number of pods per plant, a higher number of seeds per plant, a higher number of secondary branches per plant and a higher plant height.

4.8 Genetic Divergence

Genetic divergence, which occurs as a result of genetic factors, is the foundation for heritable improvement. It is usually advantageous for plant breeder when there is a high level of diversity in crop plants since it may serve as a raw material for crop improvement programme to produce better ones. As a result, precise information about genetic divergence is vital and helpful for an effective breeding programme.

Higher heterotic effects are known to be produced as of by genetically diverse parents, resulting in desirable recombinants from the breeding material. Multivariate analysis, as demonstrated by Mahalanobis D^2 Statistics, is a quantitative measure of genetic diversity among a set of genotypes.

4.8.1 Diversity

The estimates of D^2 values ranged from 6.39 to 1150.90. This clearly exhibit that there is sufficient diversity among the genotypes evaluated. Gupta and Krishna (1995), Arun Kumar *et al.* (1998), Nimbalkar and Harer (2001), Sandhu *et al.* (2006), Parhe *et al.* (2014), Ambilwade *et al.* (2018), Thakur *et al.* (2018), Brindaban *et al.* (2020) all found significant genetic diversity in chickpea germplasm. The greatest D^2 value was found between IPC-2015-12 and RVSSG-79 (1150.90), while the lowest (6.39) was found between PG-237 and PG-227.

4.8.2 Cluster Formation

The objective of cluster generation and evaluating intra and inter cluster divergence is to give the information to breeder, as it foundation serve as the for parent selection for the hybridization programme, the basic idea underlying such grouping is that the genotypes clustered into the same cluster apparently are less dissimilar from each other than those belonging to separate clusters (Rao, 1952). Thus, the crossing among the genotypes belonging to the same clusters would not produce significant heterosis so that the parents chosen for crossover should be distant from separate clusters. Greater the difference among the two groups, broader is the genetic diversity in the genotypes. The crosses involving the parents with severe divergence have also been found to show reduction in heterosis (Moll *et al.,* 1965). Therefore, when choosing the parents by evaluating the genetic diversity, *per se* performance and cluster mean for the traits also require careful attention in the crop improvement programme.

In the present research, forty four genotypes were classified into eleven clusters. The biggest cluster was the cluster I consisting of 21 genotypes, cluster VII contained 6 genotypes, cluster II with 5 genotypes and cluster VI with 4 genotypes, cluster IV (2) genotypes. The cluster III, V, VIII, IX, X, XI was solitary since they had only one genotype. Cluster VII and XI had greatest cluster distance (D=28.40), followed by cluster VI also such VII (26.63) and cluster IV and VII (24.01). This suggested that in future generations, hybridization between the genotypes in these clusters will result in successful hybrids and attractive segregants. Cluster VII (D=10.99) had the highest intra cluster value, followed by cluster II (8.18), suggesting that these clusters are more diverse.

Jeena *et al.* (2005) divided 80 genotypes into 11 clusters, with a maximum of 60 genotypes clustered in cluster I. Durga *et al.* (2005) studied genetic diversity of chickpea using 132 genotypes. The genotypes were alienated into nine clusters. Cluster I was the biggest, with 20 genotypes; they also reported cluster VI has the greatest intra-cluster distance. Nimbalkar and Harer (2001) categorized 40 chickpea genotypes into 16 clusters, with 10 of them being solitary. Pandey (2016) conducted experiment in 100 genotypes and these were categorized into sixteen clusters. The cluster I consisted of maximum 29 genotypes, Brindaban *et al.* (2020) the diversity analysis revealed grouping of 20 chickpea genotypes into the five clusters. Cluster I had a maximum of 13 genotypes.

4.8.3 Relative contribution of different characters towards divergence

In the present finding, the trait 100 seed weight (57.93 %), days to 50 per cent flowering (18.92 %) and number of seed per pod (7.933 %) were contributed the most to divergence, demonstrating that these characters were significantly responsible for the total divergence in the material under study. These results are supported by Samal and Jagdev (1989), Dwevedi and Gaibryal (2009), Parhe *et al.* (2014), Gediya *et al.* (2018), Brindaban *et al.* (2020).

Other characters such as seed yield per plant (0.63 %), number of secondary branches per plant (2.96 %), number of pods per plant (3.28 %), plant height (4.02 %) and days to maturity (4.33 %) contributed the bare minimum to genetic divergence, indicating that there was little variability among genotypes for these traits. The positive contribution in the genetic divergence may be of great assistance in identifying genotypes for yield and other economic traits.

Taking into the consideration the cluster means for imperative yield components, inter-cluster distance of the different clusters that may offer desirable parents for further hybridization programme, and for enhancement in characters are listed below.

Genotypes included into the clusters,

Cluster II : BG-4010
Cluster II : Phule Vikram
Cluster V : NDG 18-9
Cluster VII : RVSSG-79
Cluster IX : GNG-2462
Cluster X : RKG 19-1
Cluster VIII : BAUG-106
Cluster II : BRC 9-14

5. SUMMARY AND CONCLUSION

The present research entitled, "Genetic diversity studies in Chickpea (*Cicer arietinum* L.)" was conducted during *rabi* season of 2019-20 to understand the direct and indirect impact of different characters on the seed yield and to analyse the extent and nature of genetic diversity and variability exist among the genotypes for quantitative and qualitative traits *viz,* days to 50 per cent flowering, days to maturity, plant height (cm), number of secondary branches per plant, number of pods per plant, 100 seed weight (g), number of seed per pod and seed yield per plant (g). The findings have been summarized and conclusion have been drawn as follow.

5.1 Variability and Genetic Parameters

Sufficient diversity among the genotypes was exhibited for the traits under study except for the seeds per pod. The most variable factor was the number of pods per plant, which was followed by 100 seed weight, plant height, days to 50 per cent flowering, and seed yield per plant. Number of seed per pod had the least fluctuation, followed by number of secondary branches per plant. The GCV and PCV estimations for all of the characters examined revealed minimal difference, with the latter somewhat higher than the former, suggesting that the variability in these characters was attributable to both genetic and environmental causes. The genotypic (GCV) and phenotypic coefficients of variation (PCV) estimations for the characters such as 100 seed weight and seed yield per plant were the greatest, suggesting that there was good scope for improvement through selection. For 100 seed weight, number of seed per pod number of secondary branches per plant, high heritability was observed along with high genetic advance as a percent of mean, representing that these traits were under the influence of additive gene action and that potential opportunities for improving these characters through simple selection were exist.

5.2 Correlation

Correlation studies at both genotypic as well as phenotypic levels were performed to assess the direction of magnitude of relationship among traits. The substantial positive relationship was found between seed yield and plant height, number of secondary branches, number of pods per plant and 100 seed weight. This suggested concurrent improvement of both characters *via* selection. Nevertheless, days to 50 per cent flowering and days to maturity exhibited negative association with seed yield per plant at both genotypic and phenotypic level indicating early genotype also produced greater grain yield. Non-significant positive association was found between seed yield per plant and number of seed per plant.

5.3 Path Coefficient Analysis

Path coefficient study showed that 100 seed weight (0.721) had greatest direct effect on the yield of seed per plant, followed by number of pods per plant (0.660), number of seeds per pod (0.232), number of secondary branches per plant (0.202) and plant height (0.065). The direct effect is primarily accountable for positive correlation of the genotype with the seed yield per plant. Therefore, attention should be placed on these traits to make selection for needed improvement for grain yield in chickpea. These traits likewise showed substantial positive relationship with seed yield per plant apart from number of seeds per pod as it exhibits non-significant positive association. Whereas, days to 50 per cent flowering and days to maturity had the, significant negative relationship through seed yield per plant suggested early genotype also produce greater yield of grain. The number of secondary branches exhibited its influence on seed yield *via* number of pods per plant and 100 seed weight signifying that indirect selection through such traits would be helpful in yield improvement.

5.4 Genetic Divergence

The D^2 values indicating that the genotypes evaluated had sufficient genetic diversity. Based on D^2 values, all genotypes were divided into eleven clusters, each with a different number of genotypes. The highest D^2 value (1150.90) was between a pair of genotypes *viz*., IPC-2015-12 and RVSSG-79 showed that highest genetic distance between these genotypes. The highest cluster distance (D=28.40) was found between the clusters VII and XI, followed by the cluster VI and VII (26.63) and cluster IV and VII (24.01). This suggested that hybridization between the genotypes in these clusters for traits of interest will result in successful hybrids and desired segregants in subsequent generations. Cluster VII had the highest intra cluster value (D=10.99), followed by cluster II (8.18), suggesting that these clusters were more heterogenous.

5.4.1 Cluster formation

The cluster means for the examined characters, namely number of pods per plant, 100 seed weight and seed yield per plant had remarkable inter-cluster variation. The cluster means for days to 50 per cent flowering ranged from 44.00 (VIII) to 62.00 (VI). The cluster mean for the days to maturity varied from 92.00 (X) to 102.50 (VI). Cluster III had the lowest cluster mean for plant height (39.00) while, cluster X had the highest (53.45). Range of cluster mean for secondary branches per plant varies from 9.30 (IX) to 19.60 (X). The range of cluster mean for number of pods per plant varied from 35.9 (VII) to 64.22 (IX). The cluster mean for number of seed per pod was observed highest in the cluster IV (1.46) and lowest (1.01) in cluster II. The greatest cluster mean for 100 seed weight was (34.27) detected into cluster VII and lowest for cluster XI (16.97).

Keeping in view that the cluster means for key yield components and inter-cluster distance of different clusters, the following parents may be utilized for yield enhancement in future breeding programme.

Table 11. Selected genotypes for future breeding programme

Sr. No.	Genotype	Selection for Characters
1.	BG-4010	Number of pods per plant, Seed yield per plant (g).
2.	Phule Vikram	Plant height (cm), 100 seed weight (g).
3.	NDG 18-9	100 seed weight (g).
4.	RVSSG-79	Days to 50% flowering, 100 seed weight (g), Seed yield per plant (g).
5.	GNG-2462	Seed yield per plant (g).
6.	RKG 19-1	Number of secondary branches per plant, Seed yield per plant (g).
7.	BAUG-106	Days to 50% flowering, Number of pods per plant.
8.	BRC 9-14	Days to 50% flowering, Number of pods per plant, Number of pods per plant.

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*** Original not seen**

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IN
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