GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS IN CHICKPEA (Cicer arietinum L.)

by

Mr. DESHMUKH NIRANJAN NAVANATH
Reg. No. 018/044

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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APPROVED BY

Dr. C.B. Salunke
(Chairman and Research Guide)

Prof. L.B. Mhase
(Co-Chairman)

Dr. R.S. Wagh
(Committee Member)

Dr. C.A. Nimbalkar
(Committee Member)

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MAHARASHTRA, (INDIA)
2020

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 a Degree or
Diploma

Place: MPKV, Rahuri (N.N. DESHMUKH)
Date: / / 2021

Dr. C.B. Salunke
Associate Professor,
Department of Agril. Botany,
Mahatma Phule Krishi Vidyapeeth,
Rahuri-413722, Dist. Ahmednagar,
Maharashtra (INDIA)

CERTIFICATE

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

Place : MPKV, Rahuri (Dr. C.B. Salunke)
Date : / /2021 Research Guide

Dr. A.S. Jadhav
Head,
Department of Agricultural Botany,
Mahatma Phule Krishi Vidyapeeth,
Rahuri - 413 722, Dist. Ahmednagar,
Maharashtra, (INDIA)

CERTIFICATE

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Place : MPKV, Rahuri
Date : / /2021

(A.S. Jadhav)

Dr. P.N. Rasal
Associate Dean,
Post Graduate Institute,
Mahatma Phule Krishi Vidyapeeth,
Rahuri - 413 722, Dist. Ahmednagar,
Maharashtra, (INDIA)

CERTIFICATE

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Place : MPKV, Rahuri

(P.N. Rasal)

Date : / /2021

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Place : MPKV, Rahuri *(N.N. Deshmukh)*

Date : / /2021

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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
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 AND PATH COEFFICIENT ANALYSIS IN CHICKPEA (*Cicer arietinum* L.)”

By

Mr. DESHMUKH NIRANJAN NAVANATH

A candidate for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

2020

Research Guide	**: Dr. C.B. Salunke**
Department	**: Agricultural Botany**
Major discipline	**: Genetics and Plant Breeding**

The investigation on “Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)” was conducted on 50 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.

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

Number of pods per plant exhibited highest range of variability followed by plant height, 100 seed weight, days to maturity, seed yield per plant, number of secondary branches per plant and number of primary branches per plant. The variability was lowest for number of seeds per pod

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 primary branches 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 plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight, seed yield per plant suggesting that the selection of these traits would be effective for the desired improvement.

The significant positive correlation was observed between seed yield per plant with number of primary branches per plant, 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 number of seed per pod at genotypic level and days to 50% flowering shows negative correlation with seed yields per plant.

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

The D^2 statistics showed that there was adequate diversity among the genotypes. On the basis of D^2 values 50 genotypes studied were grouped into eight clusters. On the basis of inter cluster distance and cluster means the genotypes *viz.*, NBeG-857, DC-17-1115, DBGV-217, GBM-2, Phule G-1107-275, RVSSG-68, Phule Vikram and RG-2016-134 were identified for their use in hybridization programme.

Pages 1 to 68

1. INTRODUCTION

Pulses occupy unique position in Indian agriculture because of their characteristics maintaining and restoring soil fertility, besides high nutritive value. Pulses have a significant role in farming systems as a substitute for fallow in cereal rotations, where it contributes to the sustainability of production and reduces the need for nitrogen fertilization through fixing atmospheric nitrogen.

Pulses are important constituents of the Indian diet and supply a major part of the protein requirement. Among the pulses, chickpea is important *Rabi* crop of India. Like other pulse crops chickpea has multiple function in the traditional farming systems of many developing countries. Nearly 90 % of the crop is cultivated under rainfed condition on receding soil moisture and on marginal lands. Chickpea provides high quality protein, particularly for vegetarians. It is also used as a feed for livestock.

Chickpea (*Cicer arietinum* L.) is traditionally grown in many parts of the world since ancient time, both in Asia and Europe. It is an annual, self-pollinated, diploid (2n=16) grain legume crop grown in a wide range of environments including the Mediterranean, South and West Asia, North America, and North and East Africa. It belongs to genus *Cicer* and tribe *Cicerae* Alef and family Leguminosae. Chickpea is known to have nine annual and 35 perennial species (Van der Maesen *et al.*, 2007). Based on seed protein electrophoresis, Ladizinsky and Adler (1976) considered *Cicer reticulatum* the wild progenitor of cultivated chickpea and South-Eastern Turkey as the center of origin for the crop.

In India the area under pulses was 28.63 million ha, production was 23.22 million tones and productivity 811 kg/ha during 2018-19. In Maharashtra area under pulses was 35.08 lakh ha, production was 20.75 lakh tonnes and productivity 591 kg per ha. India is the largest producer of chickpea in the world sharing 65.2% of area and 65.4% of production. In India area under chickpea was 9.67 million ha, production was 10.09 million tones and productivity 1043 kg/ha (2018-19). Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Gujarat, Andhra Pradesh and Karnataka are the major chickpea producing states sharing over 95 % area. (Anonymous, 2018-19). In Maharashtra, the area under chickpea was 23.83 lakh ha, production was 19.60 lakh tones and productivity was 825 kg/ha during the year 2019-20 (Anonymous, 2019-20).

Chickpea seed contain on average 22% protein, 4.5% fat, 63% crude fibre, 2.7% ash and 358 calories (Miao *et al.*, 2009). Being fairly tolerant to soil moisture stress, it occupy important position in different cropping system. Chickpea (*Cicer arietinum* L.) is mainly divided into two types *Desi* and *Kabuli*. *Desi* type is characterized by small, coloured seeds, angular shape with high percentage of fibre and *Kabuli* type (an allusion to origin in the Afghani capital, Kabul, before it reached India) characterized by large, ram-head-shaped, coloured seeds with low percentage of fibre. In general Kabuli type chickpea have higher protein content than *Desi* types but they are low yielder. The main constituent of is globulin. Chickpea is low in sodium and fat, high in protein. They are excellent source of both soluble and insoluble fibre, complex carbohydrates, vitamins (especially B vitamins) and minerals (especially potassium, phosphorus, calcium, magnesium, copper, iron and zinc). It is rich in nutritionally important unsaturated fatty acids such as linoleic and oleic acids. These fatty acids are beneficial in the prevention of coronary and cardiovascular diseases. It may also lower blood cholesterol levels due to their high content of soluble fibre and vegetable protein. It reduces blood lipids, which may help to reduce some serious complications of diabetes (Yadav *et al.*, 2007). It is mostly used in the form of *dhal*. About 75% of the total production is consumed as a dhal in India. The whole grains are also eaten raw or boiled and roasted. Chickpea has got special importance in the form of dhal (flour or parched). In other aspect, dhal obtained after milling either from chickpea or form red gram, forms a major part of regular diet of vegetarian. Chickpea flour is cheap source for the preparation of different forms of Indian confectionary; tender leaves are used as vegetable. Kabuli chickpea is used for the purpose of roasted *chana* ‘chhole’ as a best pulse for curry preparation. The husk and broken bits of dried chickpea are used as cattle feed. An acrid liquid from the glandular hairs is collected by spreading a cloth over the crop at night, which absorbs the exudation with the dew: it contains malic and oxalic acid and is used medicinally and as vinegar. Due to its high protein content, health benefits and various domestic uses there is wide scope for production of chickpea and develop small scale industries.

Therefore, very wide cultivation of chickpea hence the information about the nature and magnitude of genetic divergence is essential and there is need to critically analyze the formulation of yield in diverse materials of chickpea. This in turn helps in establishing the selection strategy and identification of diverse parents which upon hybridization lead to a wide spectrum of gene combination.

Association of one or more characters influenced by large number of genes is elaborated statistically by estimating correlation coefficients. Genotypic correlation coefficient provides a measure of genotypic conjugation between characters. While the method of partitioning the correlation coefficient into direct and indirect effects by path analysis suggested by Wright (1921) provides useful information on the relative merit of the trait in the selection criteria. Genetic diversity among the parents, which is heritable is a prerequisite for any successful breeding programme. The proper choice of parents in the breeding programme is of paramount importance. Genetic divergence among the parents plays a vital role in cultivar improvement because, crosses involving genetically diverse parents is likely to produce high heterotic effects and also more variability in segregating generations, which can be exploited for the improvement. Generally, plant breeders select the parents on the basis of phenotypic divergence, but for effective breeding, the knowledge of genetic diversity among the parents with respect to the characters which are to be improved is must.

The Mahalanobis (1936) D^2 statistic is powerful tool for quantifying the divergence between two populations. Many studies based on this technique also indicated that geographical diversity is not necessarily related to genetic diversity. It, thus, gives better idea about the magnitude of divergence and is independent of size of sample and provides the basis for selection of parental lines for future breeding programme. The present investigation on chickpea was, therefore, undertaken to study the genetic divergence and path analysis in fifty genotypes with the following objectives.

1. To study the nature and extent of variability in chickpea.
2. To study the association, direct and indirect effects of different characters on seed yield of chickpea.
3. To measure genetic divergence between different genotypes and group them cluster.

2. REVIEW OF LITERATURE

The literature pertaining to the present investigation entitled “Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)” has been reviewed under 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) first presented the method to separate out the genotypic effects based on phenotype and environmental factors. He expressed the genotypic variability in terms of genotypic coefficient of variation.

Burton (1952) suggested the use of heritability estimates with genotypic coefficients of variation to give precise estimates of genetic advance. Johnson *et al.* (1955) have suggested that in a selection programme heritability values as well as estimates of genetic advance are more useful then heritability alone. According to Hanson *et al.* (1956) heritability and genetic advance are the two complementary concepts. The heritability values may be used to estimate the expected genetic advance through selection. The heritability enables the plant breeder to base his selection on phenotypic performance for improvement of character.

Dumbre *et al.* (1984) studied the genetic variability in sixteen cultivars of chickpea for nine quantitative characters and reported highest range of variability for pods per plant (10.4 - 95.8) followed by days to maturity (87.0 - 125.0) and lowest for seeds per pod (1.0-1.4)

Sharma (1990) reported highest range of variability for pods/plant followed by harvest index, secondary branches per plant, days to maturity, days to flowering, while lowest for seeds/pod and protein content. Coefficient of genetic variation was highest for secondary branches followed by pods/plant 100 seed weight and primary branches. However, these were moderate for seeds/pod. Plant height and harvest index and low for protein content and days to flowering and maturity. High heritability with moderate genetic advance was observed for 100 seed weigh and number of secondary branches/plant.

Gupta and Krishna (1995) studied the variability and heritability estimates of seed yield and quality traits *viz.*, seed size and protein content in 29 varieties of Bengal gram (*Cicer arietinum* L.). They reported that, variability range was broader for seed size (21.53 to 30.23 g), protein content (16.99 to 22.55 %) and seed yield per plant (13.44 to 17.46). Protein content exhibited high heritability estimates (60 %) whereas seed size and seed yield showed low estimates of heritability of 42 and 39 per cent, respectively.

Mathur and Mathur (1996) studied genotypic and phenotypic coefficient of variation, heritability and expected genetic advance for grain yield and its contributing characters in 34 varieties of chickpea. The highest value of genotypic and phenotypic coefficients were obtained in thousand grain weight. High heritability estimates were obtained for all the fairly good value of genetic advance as percentage of mean along with high heritability and therefore these characters may be considered reliable for selection in chickpea.

Rao and Kumar (2000) studied the forty short duration *desi* chickpea genotypes obtained through single, double and multiple crosses involving genetically diverse parents. Maximum variation was observed for biological yield followed by seed yield, low variability was observed for days to maturity followed by days to 50 per cent flowering.

Sable *et al.* (2000) studied 30 genotypes of chickpea and investigated that values of G.C.V. ranged from 6.37 per cent for protein content to 33.98 per cent for seed yield per plant. The characters *viz.,* seed yield per plant, 100 seed weight and biological yield per plant exhibited high estimates of G.C.V. indicating high degree of variation due to genetic factors. The characters *viz.,* seed yield per plant, 100 seed weight and biological yield per plant exhibited high estimates of genetic advance accompanied with high estimates of heritability.

Gumber *et al.* (2002) studied 30 genotypes of chickpea and observed highest heritability in pods per plant (78.0 %) followed by secondary branches (71.50 %) and 100 seed weight (69.4 %). The estimate of phenotypic coefficient of variation (PCV) was highest for seed yield (38.64 %) and seed per pod (13.33 %).

Muhammad *et al.* (2002) studied Heritability and relationship of quantitative traits in 36 genotypes of chickpea. Low heritability percentage coupled with low and moderate genetic advance, observed for primary and secondary branches respectively, indicated that these traits were greatly influenced by environment. The genotypic association of primary branches with grain yield was negative. The genotypic correlation of secondary branches with grain yield was positive. A positive and non-significant relationship between primary branches and pods per plant was obtained. The relationship between number of pods and biological yield was positive and highly significant; both of these traits had significant and positive correlation with grain yield. They suggested that plant height, number of pods per plant and biological yield may be given more importance while making selection for higher yield potential in chickpea.

Saleem *et al.* (2002) studied heritability in twenty elite lines of chickpea. High genotypic and phenotypic coefficients of variability were observed for days taken to flowering, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight, seed yield per plant and protein content. 100-seed weight, days taken to flowering and protein content were characterized by high broad sense heritability estimates, which indicated the presence of a considerable proportion of total variability due to genetic causes.

Jeena *et al.* (2005) studied variability and correlation coefficients in 80 genetically diverse chickpea genotypes. High amount of genetic variability was expressed by pods per plant, 100-seed weight, biological yield per plant and seed yield per plant. These characters also exhibited high predicated genetic advance with high heritability. Seed yield was significantly and positively correlated with plant height, length of pod, secondary branches per plant, pods per plant, 100 seed weight, biological yield per plant and harvest index.

Ali *et al.* (2008) studied twenty elite chickpea lines for variability and correlation for five traits. Varietal differences among the genotypes were significant ($P<0.01$). Phenotypic and genotypic variances were higher for plant height (33.29 and 32.45) and seed yield per plant (13.47 and 13.11). Broad sense heritability estimates were the highest for plant height (97.4) and seed yield per plant (97.3). Genetic advance was higher for seed yield per plant (27.42) and plant height (14.51). High heritability for both the traits coupled with high genetic advance revealed that additive genetic effects were important for these characters. Positive genotypic correlation was detected between seed yield and number of primary branches per plant (0.76), while at phenotypic association was highly significant (0.63).

Borate *et al.* (2010) studied population parameters such as range, mean, phenotypic and genotypic variances, PCV and GCV, heritability and genetic advance for 13 agronomic characters in a set of 30 chickpea genotypes. Range of variability was appreciable for days to first flowering, secondary branches, plant height, dry matter and grain yield. Values of genotypic and phenotypic variances were highest for number of pods, while lowest for number of seeds per pod. PCV showed higher values than GCV for all characters. High heritability coupled with high genetic advance was observed for grain yield. Plant height, dry matter, days to first flowering and days to maturity indicated high additive gene effects.

Sharma and Saini (2010) evaluated 28 chickpea genotype including check, which revealed the presence of sufficient variability with high heritability for most of the yield components. Correlation and path analysis indicated that the number of pods/plant and branches /plant could be useful as selection indices for development of high yielding genotype of chickpea.

Dar *et al.* (2012) carried out studies under field condition to estimate genetic variability and interrelationship among various yield components in thirty diverse germplasm lines of chickpea. High heritability with moderate to high genetic advance was recorded for 100 seed weight, seeds per plant and seed yield per plant. The high PCV and GCV were recorded in 100 seed weight followed by number of pods per plant, seed yield, plant height and days to 50% flowering.

Farshadfar *et al.* (2013) studied some agro-morphological traits and estimated genetic variability parameters in 20 genotypes of chickpea. Analysis of variance showed significant differences between the genotypes for all studied traits. Genotypic and phenotypic coefficients of variations were high for seed yield (SY), number of seed per plant (NSPL) and number of pod per plant (NPPL). Heritability estimates were high for hundred seed weight (HSW) and seed yield (SY). High genetic gain was observed for SY and HSW.

Gul *et al.* (2013) evaluated twenty chickpea genotypes for genetic potential, heritability, genetic advance and traits association of yield contributing characters. Broad sense heritability estimates were highest for 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). Genetic advance was higher 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) investigated variability parameters and path coefficient analysis in twenty elite chickpea genotypes including three standards. Heritability estimates were maximum days for taken to flowering, days taken to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100-grains weight and grain yield per plant while other characters exhibited moderate heritability.

Neelu Kumari *et al.* (2013) assessed genetic variability among 32 advanced breeding lines of chickpea for grain yield and early duration in a randomized block design. Highest genotypic coefficient of variance (GCV) was studied in seed yield per plant. Heritability in broad sense ranged from 55 per cent for total yield followed by 53 per cent for days to 50 per cent flowering. High expected genetic advance coupled with high heritability estimate was obtained for plant height, number of secondary branches per plant, number of pods per plant and seed yield per plant. It suggested the dominant role of additive gene effects in expression of these traits. Seed yield per plant has positive and significant association with biological yield, harvest index and test weight.

Astereki *et al.* (2015) studied genetic diversity of 25 chickpea genotypes, for estimating genotypic and phenotypic coefficient of variance and heritability, a field experiment was arranged in a RCBD with four replications during two seasons. Analysis of variance indicated that there were significant genotypic differences for seed yield, number of days to flowering, number of days to maturity, flowering period, canopy height, number of pods per plant, biological yield and harvest index. Seed yield ranged from 168.3 kg per ha (L13) to 618.52 kg per ha (L10) in the first year and 248.86 kg per ha (L22) to 945.66 kg per ha (L2) in the second year. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for seed yield, days to flowering, flowering period, canopy height, number of pods per plant, biological yield and harvest index, indicated the influence of environment upon these traits. Heritability of canopy height, days to flowering and days to maturity greater than the heritability of the other traits.

Dan Singh *et al.* (2016) studies on genetic variability, character association and path-coefficient analysis were conducted on 40 chickpea genotypes. Analysis of variance revealed considerable variability among the genotypes for all the characters. A high genotypic and phenotypic coefficient of variation was observed for seed yield/plant followed by number of pods/plant, 100 seed weight and number of secondary branches/plant. The highest heritability (b.s.) was observed for 100 seed weight (99.20%) followed by seed yield/plant (95.00%), number of pods/plant (94.7%), days to 50 per cent flowering (87.30%) and number of secondary branches (83.3%). Seed yield/plant was exhibited highest genetic advance as per cent of mean (78.68) followed by number of pods/plant (51.99) and 100 seed weight (50.96).

Tiwari *et al.* (2016) thirty eight chickpea varieties were studied to find out genetic variability, genetic association and path coefficient analysis for grain yield and its attributing characters. Both genotypic and phenotypic variances were highly significant for all the traits with little higher phenotypic coefficient of variation. High heritability coupled with high genetic advance were obtained with harvest index, seeds per pod, total number of pods per plant, seed yield per plant, days to maturity. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Harvest index, 100-seed weight, seeds per pod, number of effective pods per plant, total number of pods per plant, number of primary branches per plant per plant and plant height were the most important characters, which possessed positive association with seed yield per plant.

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 number of pods per plant, number of seed per pod, 100 seed weight, number of nodules per plant and days to 50% flowering indicating that these characters were less influenced by the environment. The estimate of heritability in 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) conducted experiment on forty chickpea genotypes, raised in randomized block design with three replication. The observations were recorded on days to 50% flowering, days to maturity, plant height, lower branch height, number of primary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, biological yield per plant, 100-seed weight, harvest index and seed yield per plant from five competitive plants selected randomly from in each replication for collecting the information on existing genetic variability, heritability, expected genetic advance. The analysis of variance revealed highly significant differences among genotypes for all the characters study. Number of pods per plant followed by biological yield per plant, number of seeds per plant, seed yield per plant, number of primary branches par plant, 100-seed weight had high phenotypic and genotypic coefficient of variation. The characters viz., days to 50% flowering, days to maturity, 100 seed weight, plant height, number of seeds per plant, lower branch height, number of pod per plant, biological yield per plant, seed yield per plant, number of primary branches per plant showed least differences among GCV and PCV estimates high estimates were observed for number of seeds per plant (96.90%) followed by number of pods per plant, 100 seed weight, days to 50% flowering, plant height, days to maturity, seed yield per plant, number of primary branches per plan. number of pods per plant, biological yield per plant, number of seeds per plant, seed yield per plant and number of primary branches per plant have high values of heritability coupled with high genetic advance as per cent of mean.

Shanmugam Mohan and Kalaimagal Thiyagarajan (2019) The present study was conducted to evaluate 50 chickpea germplasm accession to understand the magnitude of variability, heritability genetic advance and the association of various yield components and their direct and indirect influence on yield of chickpea on twelve agro-morphological traits. This traits included three vegetative traits (plant height, number of primary branches, number of secondary branches), one flowering trait (days to 50% flowering), seven yield related trait (days to maturity, number of pods per plant, number of seed per pod biological yield per plant, harvest index, 100 seed weight and seed yield per plant). Anova revealed significant variation for most of the traits. High genotypic coefficient of variation and phenotypic coefficient of variation was found for 100 seed weight and plant height recorded high heritability coupled with high genetic advance. Traits such as number of secondary branches, number of seed per plant, 100 seed weight, biological yield per plant and harvest index exhibited significant positive correlation with seed yield per plant whereas, biological yield per plant followed by harvest index had positive and greater direct effects on single plant yield.

2.2 Correlation and Path Analysis

In the improvement of any crop, the knowledge of association of one or more of these characters associated with yield is useful in selecting the individual with high yield on the basis of their phenotypic values. Such association between plant characters is statistically elaborated by correlation coefficients. But the correlation between the dependent and independent character and the direct and indirect effects of the independent character on the dependent character are completely separate things. Sometime the correlation between two characters may be highly positive but the direct effect of the independent characters on the dependent characters may be negative Hence, merely correlation cannot serve the purpose of selection in crop improvement programme.

Therefore, the method of partitioning the direct and indirect effects of the independent character on the dependent character i.e. path coefficient analysis was detailed by Wright (1921). Li (1954) emphasized great use of this technique in genetics and plant breeding. Further, Dewey and Lu (1959) gave the detail procedure for path analysis of replicated trials which was quite different technique in eliminating the environmental variances.

Paliwal *et al.* (1987) found that 100 seed weight had the highest positive direct effect on yield, followed by pods/plant seeds/pod and days to 95% maturity. The seed yield per plant was positively correlated with plant height, days to 95% maturity and days to 50% flowering, pods per plant and seeds per pod were recommended as selection criteria to improve the yield.

Varghese *et al.* (1993) observed significant positive correlation of seed yield with pod weight (0.99), biological yield (0.95), pods per plant (0.64) and 100 seed weight (0.53) and significant negative correlation with harvest index (-0.73). Path analysis indicated high positive direct effects of pod weight (1.20), shelling percentage (0.22), biological yield (0.07). Pods per plant and 100 seed weight are considered as important yield components in selection for better genotypes in chickpea.

Tripathi *et al.* (1995) conducted path coefficient analysis for 8 characters and yield components in 40 diverse varieties of *Cicer arietinum*. They reported that seed yield/plant was highly associated with pods/plant, primary branches and 100 seed weight.

Ozdemir (1996) studied the relationship between seed yield and 9 yield components in 38 genotype of chickpea grown during 1992-93 at Cukurova University, Adana (Turkey), correlation and path analysis showed that seed yield/plant, secondary branches/plant and number of seed /plant were the most important yield components with significant direct and indirect effects. Number of pods/plant had a significant direct and indirect effect. Number of pods/plant had a significant positive correlation with seed yield, it had a negative direct effect on seed yield. Its indirect effect was positive via seed number.

Chand and Singh (1997) studied correlation and path analysis in 49 chickpea genotypes and reported that, grain yield showed positive and significant correlation with seeds per plant, pods per plant and biological yield. The correlation of seeds per plant with plant height, pods per plant and seeds per pod were also positive and significant. The 100 seed weight showed negative significant correlation with seeds per plant, pods per plant, and seeds per pod, harvest index, biological yield and plant height. The positive association was also observed for seeds per pod with days to flowering, plant height with seeds per pod and grain yield. Number of pods and seeds per plant appear to be the most important yield contributing characters in chickpea.

Saleem and Ali (1999) studied path coefficient analysis of seed yield and quantitative traits in chickpea. A set of twelve elite chickpea lines including one standard were evaluated for grain yield and other related characters for path coefficient analysis in a triplicate randomized complete block design. Seed yield was positively correlated with all attributes except days taken to flowering. Number of seeds per plant had maximum positive direct effect on yield. Number of pods per plant and plant height had maximum negative direct effects on seed yield. The study revealed that selection may be done with optimistic compromise between number of seeds per pod, number of secondary branches per plant, number of seeds per plant, number of pods per plant and plant height.

Guler *et al.* (2001) examined five chickpea lines for relationships between the yield and yield components. The positive and significant relationships were found statistically between the number of seeds per pod and the number of pods per plant, between the number of seeds per plant and the number of pods per plant and the number of seeds per pod, between seed yield per plant and the number of pods per plant, the number of seeds per pod, the number of seeds per plant; between the number of seeds per pod and seed yield per unit area; between the number of seeds per plant and seed yield per unit area. Negative and significant relationships were determined statistically between the number of pods per plant and 100 seed weight, between the number of seeds per pod and 100 seed weight, between the number of seeds per plant and 100 seed weight, between seed yield per unit area and 100 seed weight. The total determining coefficient related to 100 seed weight was 0.896 (89.6%) in the same model.

Jeena and Arora (2002) studied 40 genotypes for yield and its component traits. Correlation among all the characters computed and subjected to path analysis. Biological yield exhibited highest positive correlation with seed yield coupled with highest positive direct effect on it. Biological yield, pods per plant, 100 seed weight and first pod forming node found to be the major yield contributor traits from selection point of view.

Kumar *et al.* (2002) studied eight quantitative traits in a randomized experiment consisting of 24 chickpea genotypes. Results of correlation analysis revealed that seed yield was positively associated with harvest index, pods per plant, biological yield and secondary branches per plant while negatively correlated with plant height. Among the yield components pods per plant positively associated with secondary branches per plant and biological yield per plant, while negatively related to 100-seed weight.

Raval and Dobriya (2003) studied genetic variability, interrelationship and path coefficients for 13 yield components in set of 52 genotypes of chickpea. The seed yield was positively and significantly correlated with biological yield/plant , 100 seed weight , number of pods/plant, harvest index, number of secondary branches /plant, while correlation of seed yield with days to 50% flowering, days to maturity and number of seed/pod was negative and significant.

Muhammad *et al.* (2004) studied variability, heritability, genetic advance, correlation coefficient and path coefficient for yield and its components in 24 advance lines of chickpea. High heritability with low genetic advance of days to flowering, days to maturity and 100 seed weight indicated the influence of dominant and epispastics genes for these traits. High heritability of secondary branches and biological yield coupled with high genetic advance revealed that additive gene effects are important in determining these characters. Grain yield had positive and significant correlation with plant height, pods per plant, 100 seed weight and biological yield. High direct effects were contributed by biological yield and harvest index although the later had negative association with grain yield.

Yucel *et al.* (2006) studied 15 *kabuli* genotypes. Direct and indirect effect of yield components on seed yield per plant were investigated. Genotypic variance was the highest for 1000 seed weight followed by seed number per plant. Positive and significant (PL < 0.05) relationship were determined between seed yield per plant and plant height, first pod height, secondary branch, total pod and number of full pods and seeds per plant. This research suggests that seed and full pod numbers can be good selection criteria for improving seed yield per plant in *Kabuli* winter Chickpea.

Singh (2007) analysed 45 five diverse genotype of chickpea. The genotypic correlation were, higher than the corresponding phenotypic ones. Seed yield had highly significant positive correlation with biological yield/plant, pods/plant, secondary branches/plant. Biological yield/plant and pods/plant had highly significant correlation with seed yield and its direct effect was very strong. Pods per plant, 100 seed mass and secondary branches/plant were indirect contributory components.

Zena *et al.* (2008) studied path coefficient analysis for enhancing yield of chickpea 36 traits of chickpea were tested in RBD for total 12 quantitative characters including yield. Path coefficient analysis was carried out to determine the effect of various production factors on the yield. Biological yield had shown highest direct effect on the seed yield which was followed by test weight, yield index, initial flowering period, maturity period, secondary branches/plant and seeds/pod, respectively while 50% flowerings period has shown negative direct effect on the yield of gram.

Ali *et al.* (2009) studied twenty chickpea genotypes for evaluation of selection criteria in chickpea using correlation coefficients and path analysis. The genotypes demonstrated highly significant differences ($P<0.01$) for all the traits studied. The results of correlation analysis revealed that grain yield per plant had significant genotypic and highly significant phenotypic relationship with primary branches, pods/plant, seeds/plant, seeds/pod and total biological yield. The path analysis confirmed that biological yield followed by number of seeds per pod, 100-grain weight, had the maximum positive direct influence on grain yield/plant.

Thakur and Sirohi (2009) studied correlation and path coefficient analysis in 53 chickpea genotypes. Correlation studies indicated that seed yield/plant exhibited stable positive association with biological yield/plant, pods/plant, primary branches /plant, plant height and harvest index at genotypic and phenotypic levels in individually as well as combined over seasons. Path analysis revealed high positive and direct influence of biological yield/plant with seed yield/plant followed by harvest index and pods/plant in individual as well as combined over seasons.

Kobraee *et al.* (2010) carried out investigation of correlation analysis and relationships between grain yield and quantitative traits in 3 chickpea cultivars and 3 sowing date. A 3 x 3 factorial experiment in RCBD format with 3 replications was conducted. The results showed that both sowing date and cultivar had significant effect on grain yield and yield components.

Early planting chickpea produced the highest plant height, distance of first pod from the earth surface, number of sub branches, number of pods /plant, number of seeds/plant, 100 seed weight, grain yield, biological yield and harvest index. There was significant difference between cultivars for grain yield. Results showed that number of seeds/plant, number of pods/plant, plant height and biological yield had the highest positive correlation with grain yield. The number of seeds per plant had high and positive direct effects on seed yield.

Yucel *et al.* (2010) determined selection criteria by using correlation and path coefficient analysis in 22 genotypes of chickpea under Mediterranean conditions. In investigated characters, positive and significant relationships were found statistically among seed yield and harvest index and seed number. The path coefficients analysis based on seed yield, as a dependent variable, revealed that harvest index had the greatest direct effect on seed yield (0.4206) with the ratio of 56.04 per cent. Both correlation and path analyses indicated that harvest index was the major direct contributor to seed yield.

Bibani *et al.* (2011) studied the relationship between grain yield and the other characteristics with two cultivars of chickpea. The experiment was a factorial completely randomized design with 2 factors. At harvest time, height of plant, filled and unfilled pods/plant, number of seeds/plant, plant dry weight and yield were measured. Result showed the yield had highly positive correlation with filled pod/plant ($r=0.96$) ($p<0.01$). In Arman and Hashem cultivar, yield had highly correlation with seed number/plant ($r=0.95$) ($p<0.01$) negative. Dependence of seed yield to highest was a great with deterioration 14 days; and the correlation coefficient between filled the pod number and height after 7 days deterioration was significantly ($p<0.01$) negative ($r=-0.95$) ($p<0.01$) but it was of greater magnitude in 14 days deterioration ($r=0.79$) ($p<0.01$).

Padmavathi *et al.* (2013) studied the extent of genetic variability, correlation and path analysis for yield and yield contributing characters in thirty genotypes of *kabuli* chickpea. Wider genetic variability with high heritability and high genetic advance as per cent of mean was recorded for number of primary branches/ plant, biological yield/plant and seed yield/plant. Correlation studies revealed that seed yield was significantly and positively correlated with plant height, number of primary branches/plant, number of secondary branches/plant, number of pods per/plant, 100-seed weight, harvest index and biological yield/plant. Path coefficient analysis indicated that biological yield/plant, number of pods/ plant and harvest index had high positive direct effect on seed yield signifying the importance of these traits in improvement of seed yield.

Chopdar (2016) showed that positive direct effect on seed yield per plant was exhibited by day to maturity, primary branches per plant, harvest index and protein content. Among these traits, harvest index exhibited highest positive direct effect on seed yield. Harvest index also exhibited positive indirect effect on seed yield per plant followed by biomass per plant and number of primary branches per plant. This showed that while selecting for high yield, emphasis should be given on those character which show high direct positive effect with positive correlation with seed yield.

Bhanu *et al.* (2017) fifty three germplasm of chickpea were undertaken to determine relationships among yield and some yield components using direct (variability, heritability, and genetic advance) and indirect selection parameters (correlation and path coefficient analysis). The present investigation was carried out at the Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during the rabi season of 2011-12. Significant genetic variations were observed among the genotypes for days to flower, days to maturity, plant height, number of branches plant^{-1}, number of pods plant^{-1}, 100-seed weight and seed yield plant^{-1}. Correlation studies revealed that seed yield was positively and significantly correlated with number of primary branches, number of secondary branches and number of pods plant^{-1}. The path coefficient analysis based on seed yield, as a dependent variable, showed that pods plant^{-1} had the greatest direct effect on seed yield (0.81) followed by number of secondary branches. Both correlation and path analysis indicated that pods plant^{-1} and number of secondary branches were the major direct contributors to seed yield.

Astereki *et al.* (2017) studied the correlation coefficients and path analysis between seed yield, morphological traits and yield components. Twenty five chickpea genotypes, including advanced lines and commercial varieties. The field experiment was arranged in RCBD with four replications. The correlation coefficients indicated that there were significant and positive correlations between seed yield and number of pods per plant and harvest index in two years. Path analysis indicated that days to flowering, days to maturity, canopy height and width, number of pods per plant and flowering period directly and indirectly affected seed yield. Therefore, this study suggested that chickpea improvement program could be based on these traits, especially number of pods/plant and canopy height, according to positive direct effect on seed yield over two years, as selection criteria.

Singh *et al.* (2017) forty genotypes along with three check varieties of chickpea (*Cicer arietinum* L.) were assessed to work out the association of different seed yield traits, direct and indirect effects of their various attributes on seed yield. Seed yield/plant showed significant and positive correlation with pods/plant, seed yield/plant showed highly significant and negative correlation with days to 50% flowering and non significant correlation with other characters. The characters showing significant positive correlation among yield and important characters would be highly effective and efficient in improving respective traits. Path analysis identified pods per plant and seedling length as important component having high order of direct effect to secondary branches/plant and vigour index as important components having high order of indirect effect on seed yield/plant. The characters identified above as important direct and indirect yield components merit due consideration in formulating selection strategy in chickpea for selection of high yielding varieties.

Manilkanteswara *et al.* (2019) the experimental material comprised of 21 chickpea genotypes and the experiment was laid out in Randomised Complete Block Design with three replications, during *rabi,* 2017 Maximum GCV and PCV were recorded for seed yield per plant and harvest index. High genetic advance as per cent of mean recorded for seed yield per plant. Seed yield per plant showed high positive significant correlation with harvest index and pods per plant at phenotypic and genotypic levels. Biological yield and Harvest index exhibited high direct positive effect on seed yield per plant at phenotypic and genotypic levels. Genotypes C138, C108, C201 and C1021 of chickpea were found to be superior for seed yield per plant.

2.3 Genetic Diversity

2.3.1 Concept of Genetic Diversity

The concept of D^2 statistic for measuring the divergence between two populations was introduced by Mahalanobis (1936). It gives a result based on the magnitude of divergence and is independent of size of the sample.

Mahalanobis *et al.* (1949) employed D^2 statistic in detailed study of anthropometric data of Uttar Pradesh classifying in 23 groups and into three major clusters i.e. Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising nine groups, the Artisan (A-cluster) in the middle consisting of four groups and the Trival (T-cluster) at the bottom consisting of ten groups.

Murthy and Arunachalam (1966) stated that, a change in breeding structure could bring about a substantial change in character association and the pattern of distribution of genetic variability, geographical distribution and genetic diversity could not be directly related in many of the crops examined the by them. Genetic drift and selection in different environment many cause greater diversity than geographic diversity.

2.3.2 Genetic Divergence in Chickpea

Jain *et al.* (1981) measured genetic divergence by Mahalanobis' D^2 statistic in 32 genotypes of chickpea originating from 13 different countries of Asia, Africa, Europe and North America. The grouping of genotypes from different eco geographical areas in the same cluster confirmed that there is no parallelism between genetic diversity and geographical distribution. The pattern of clustering was highly influenced by environment and while making general statement on this aspect, the experimental conditions should be taken into consideration. To make worthwhile improvement in chickpea, 100 seed weight, pods per plant, flowering period and harvest index, in that order, should be taken into account. The clustering pattern of genotypes has revealed that *Desi* and *Kabuli* types are different from each other. Hence, crossing among these two types may provide more desirable segregants.

Shrivastava and Gupta (1982) grouped 49 genotypes into 9 clusters. Such cluster included the genotypes of different eco geographical regions. They also observed maximum genetic diversity for number of pods per plant followed by days to flowering, biological yield, harvest index and seed size.

Dasgupta *et al.* (1987) performed assessment of genetic diversity in chickpea by Mahalanobis D^2 statistic which revealed that 100 seed weight was the most important character, which contributed maximum towards divergence. The 22 varieties studied were grouped into five clusters and observed that the cluster of *desi* type was distinct from that of *kabuli* type and genetic divergence was not necessarily associated with geographical diversity.

Mian and Bahl (1989) had done multivariate analysis to find out genetic divergence among 28 chickpea populations comprising 7 parents and 21 hybrids from all possible crosses among the parents. The D^2 values ranged from 2.20 to 147.71, indicating sufficient divergence in the populations for different characters. The 28 chickpea populations were grouped into 13 clusters. Parental genotypes originating from the same geographical region also did not show any affinity among themselves in the formation of clusters, thus, showing lack of correspondence between geographical and genetic diversity. Study of relationship between divergence of the parents and heterosis in the hybrids revealed that the parents separated by D^2 values of medium magnitude generally showed higher heterosis for different characters.

Mishra and Rao (1990) grouped 117 genotype into 13 cluster. The maximum of 93 genotypes were found in cluster-1. Eleven clusters had only one genotype each. They further observed that, metroglyph analysis did not show similar type of clustering pattern as in D^2 analysis, but canonical analysis showed similar type of clustering.

Narendra Kumar (1997) studied multivariate analysis of divergence among 60 entries of chickpea for seven developmental characters led to their grouping into five clusters. Grouping of entries in different clusters was not related to their geographic origin. The inter cluster D^2 values ranged from 8.0 to 38.2. Based on the mean performance, genetic distance and clustering pattern; hybridization involving parents from cluster II and V may give higher yielding varieties.

Arun Kumar *et al.* (1998) studied the genetic divergence among the 17 chickpea genotypes, 5 each developed through mutation breeding and intra and interspecific hybridization and two standard checks in chickpea. The genotypes were grouped into 5 clusters. Cluster II, I and III had 6, 5 and 4 genotypes, respectively and cluster IV and V had only one genotype each. The genotypes falling in cluster III had the maximum divergence which were closely followed by those of clusters II and I. The maximum and minimum divergence was revealed between clusters II and V and between III and V, respectively. In general, the cluster II and V exhibited high and low mean values, respectively for most of the characters. It has been suggested that for varietal improvement the hybridization among the genotypes of divergent clusters should be done rather than depending on those genotypes of the cluster having maximum divergence.

Raj and Khare (1999) grouped 21 chickpea genotypes into 6 clusters. Highest inter-cluster distance was observed between clusters IV and V. Hundred seed weight was associated with higher seed yield/plant and had the largest contribution towards total divergence. Selection of diverse parents on the basis of seed size seemed to be effective.

Sivakumar and Muthiah (2001) reported that clusters IV and VII exhibited highest divergence while the lowest was between clusters IV and V. The highest inter cluster distance was in cluster I with 108 genotypes.

Nimbalkar and Harer (2001) grouped 40 genotypes into 16 clusters. D^2 values between all possible pair of 40 genotypes ranged 12.62 -3979.93. Out of 16 clusters, 10 were mono genotypic, cluster II was the largest comprising of 12 genotypes followed by clusters I and IV containing 9 and 3 genotypes respectively. The genotypes of cluster XVI and cluster III were maximum divergent. Variance of cluster means indicated pods per plant followed by plant height and 100 seed weight were the main trait contributing to the genetic divergence.

Kashyap and Rastogi (2003) studied genetic divergence by D^2 techniques for seed yield and it's components in 60 chickpea germplasm accessions. The analysis of variance revealed significant differences among the genotypes for each character under study. The genotypes were grouped into 6 clusters and maximum intra- cluster distance was observed in cluster I, comprising 14 genotypes, cluster III and VI were identified as genetically divergent. Considering the cluster means and cluster distances the genotypes IG-327, IG-326, IG-323, IG-311, IG-314 of cluster V, ICCV-89243, ICCV-91020, ICCV-91024, ICCV-91007, IG-313 of cluster VI, ICCV-91004, ICCV-91003, ICCV-89228, ICCV-91012 ICCV-89224 of cluster I were the most promising genotypes. They may be utilized in future breeding programme to obtain high heterotic effect or to develop desirable recombinants.

Dasgupta and Singh (2003) reported that intercluster distance highest between clusters V and VIII and lowest between clusters II and III. High genetic diversity was observed among the genotypes based on cluster mean distance.

Jeena *et al.* (2005) recorded observations on 80 chickpea genotypes collected from different geographical areas for eighteen characters. Based on D^2 values 80 genotypes were grouped into eleven clusters. The highest numbers of genotypes were included in cluster I (60) followed by cluster IX (7). No definite relationship was observed between genetic diversity and geographical distribution. Based on inter-cluster distances, crossing between BGM-419 and KPG33 are expected to produce a broad spectrum of variability in segregating generations to isolate transgressive segregants for yield and its components.

Sandhu *et al.* (2006) assessed 90 genotypes of chickpea in 3 environments using Mahalanobis D^2 statistic. The genotypes were grouped into ten clusters, which were more genetically divergent than the others. Common genotypes were sorted out within a cluster for combination of environments and pooled data over environments.

Durga *et al.* (2005) studied genetic diversity in chickpea with 132 genotypes. The genotypes were grouped into nine clusters. Cluster I was the largest, comprising of 20 genotypes, followed by clusters V and VII with 16 and 15 genotypes, respectively. Maximum intra - cluster distance was observed in cluster VI followed by cluster IV, cluster I and cluster IX. Maximum inter cluster distance was noticed between clusters I and VIII. Crossing the genotypes between the clusters I and VIII may lead to maximum diversity in the segregating populations and development of high yielding

Tomar *et al.* (2011) grown 45 genotypes of chickpea (*Cicer arietinum* L.) in twelve environments and subsequently in order to select potential parents for hybridization. Based on D2 values, 45 genotypes were grouped into eight clusters. Cluster V consisted of 8 genotypes followed by cluster VIII and VI, which had 7 and 6 genotypes, respectively. Maximum intra-cluster distance (2.89) was observed in cluster VIII, followed by cluster VI (2.58), cluster IV

(2.34) and cluster I (2.33). Maximum inter-cluster distance was noticed between cluster IV and VIII (6.38). They suggested that crossing between genotypes from the cluster IV and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

Singh *et al.* (2012) carried out an investigation among the 64 genotypes of chickpea that included 60 interspecific derivatives, their parents and two standard checks, to study the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. Highest inter-cluster distance was recorded between cluster VI and IX while highest intra cluster distance was found among the genotypes of cluster VIII. Characters like biological yield per plot, seed yield per plot and days to 50 per cent flowering contributed maximum towards the genetic diversity.

Syed *et al.* (2012) measured genetic diversity among 27 chickpea genotypes through Mahalanobis D^2 and Principal Component Analysis. The genotypes under study fall into five clusters. The cluster II contained the highest number of genotypes (11) and Cluster I contained the lowest. Cluster I produced the highest mean value for number of pods per plant. The inter cluster distances were much higher than the intra cluster distances. Cluster V exhibited the highest intra cluster distance while the lowest distance was observed in cluster I. The highest inter cluster distance was observed between cluster I and II while the lowest was between cluster III and V. Considering all the characters, it was suggested that the genotypes BD6549, BD6603 and BD6548 could use as parents for future breeding programmes to develop high yielding varieties of chickpea.

Jain and Indapurker (2013) studied the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics on the thirty genotypes of chickpea and these were grouped into six clusters. The cluster I shows largest cluster with eight genotypes. Highest inter cluster distance was observed between cluster IV and cluster V, followed by cluster V and VI. The cluster VI was identified for pods per plant and seed yield per plant.

Parhe *et al.* (2014) an experiment with fifty one genotypes of Chickpea carried out to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics, in randomized block design with two replications. The data for eight important quantitative traits recorded from the genotypes raised. The fifty one Chickpea genotypes were grouped into five clusters. Cluster I was largest with forty genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster I and V, followed by cluster II and V suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters *viz.* 100 seed weight, No. of pods per plant and Days to 50% flowering were contributed maximum in manifestation of genetic diversity. Seed yield plant^{-1} had maximum Phenotypic and Genotypic Coefficient of Variation (PCV and GCV), followed by 100 seed weight. High magnitude of heritability (broad sense) was recorded for 100 seed weight. High heritability coupled with high genetic advance was observed for number of pod per plant, 100 seed weight, Days to 50% flowering and Plant height suggesting genetic progress through selection. The genotypes IC-270936, IC-487323, IC-350889, Vishal, Digvijay, IC-442831, IC-268927, IC-327656, IC-299779, EC-490044 and IC-269004 were identified as genetically diverse parents who could be used for future use.

Suneeta Pandey (2016) conducted experiment in 100 promising chickpea genotypes sown under late planting using Mahalanobis's D^2 Statistics. Further the diversity is also confirmed by using SSR molecular markers. Based on D^2 values, 100 genotypes were grouped into sixteen clusters. The cluster I consisted of maximum 29 genotypes, followed by Cluster II, cluster V and cluster VI, which had 26, 13 and 12 genotypes, respectively. Maximum intra-cluster distance (164.10) was observed in cluster V, followed by cluster VI (150.23), cluster III (123.98) and cluster II (102.52). However, maximum inter cluster distance was noticed 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).

Gediya *et al.* (2018) studied genetic diversity among 58 genotypes of chickpea, which were grouped into sixteen clusters. In general, intra-cluster distances were lower than inter-cluster distances, indicating that genotypes included within a cluster tended to diverse less from each other. Maximum genetic divergence was observed between cluster IX and XVI, followed by Cluster IX and XIV, while closest proximity was noticed between cluster III and VIII. The characters *viz.,* seed yield per plant, 100 seed weight, seeds per plant and pods per plant contributed much to the total genetic divergence. Hence, selection for divergent parents based on these characters would be useful for developing potential hybrids and increasing scope of isolating desirable recombinants in segregating generation in chickpea. On the basis of cluster mean values, cluster XII was superior for seed yield per plant and harvest index; cluster XV for pods per plant, seeds per plant and first pod height and cluster X for 100 seed weight. For early flowering and maturing, cluster XIV was found superior, while cluster VII was best for protein content. The genotypes belonging to the clusters separated by high genetic distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants.

Agrawal *et al.* (2018) conducted experiment to study the existing genetic diversity in thirty six *Desi* chickpea genotypes under normal sown condition. All the genotypes were grouped into seven clusters as per ward minimum variance method revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and yield attributing traits. The cluster II containing the maximum of 13 genotypes followed by 9 genotypes in cluster I, 5 genotypes in cluster III, 3 genotypes each in cluster IV and V, 2 genotypes in cluster in cluster VI and mono-genotypes in cluster. The intra-cluster D2 value ranged from 0.00 to 421.27 while, inter-cluster D value ranged from 402.80 to 3912.66. The highest intra-cluster distance was exhibited by cluster I (421.27) followed by cluster VI (316.27) and III (315.69). The highest inter cluster distance was observed between cluster II and VII (3912.66) followed by cluster II and VII (3831.40), cluster III and VI (2804.51) and cluster IV and VII. The genotypes of cluster VII showed the highest mean values for grain yield per plant, harvest index, biological yield per plant, primary and secondary branches per plant, plant height and days to maturity, while cluster VI showed the highest mean for grain yield per plot, total number of pods per plant, effective pods per plant and days to 50% flowering.

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 were grouped into twelve clusters. The cluster I consisted of maximum 49 genotypes, followed by Cluster III, cluster VII and cluster IX, which had 16, 12 and 12 genotypes, respectively. The maximum intra cluster distance was found in cluster IX (7.72) followed by cluster VIII (6.65), VII (6.52), cluster III (6.14) and cluster I (5.46). Inter cluster values varied from 2.75 to 14.95. However, maximum 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). whereas, days to 50 % flowering (22.89 %) followed by 100 seed weight (21.29 %), total number of seeds per plant (14.16 %) and plant height (13.80 %) contributed maximum 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.

Ambilwade *et al.* (2018) The present investigation was undertaken with thirty five genotypes of chickpea, (including one check) during *Rabi* 2017-18 in a randomized block design with three replications at Field Experimentation Center of Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology & Sciences

Allahabad. The data was recorded for ten characters to study genetic variability, heritability and genetic diversity. Analysis of variance among 35 genotypes showed highly significant difference. High estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for economical yield followed by biological yield and number of pods per plant. High heritability coupled with high genetic advance was recorded for economical yield suggesting greater role of non-additive gene action in their heritance. Mahalnobis's D^2 analysis revealed considerable amount of diversity in the material. Thirty five genotypes were grouped into six heterogeneous clusters. Among these clusters Cluster VI has maximum number of genotypes. On the basis of mean performance of the genotypes, IC-275323 was recorded high yield among 35 genotypes under study. Characters such as economical yield, biological yield should be given top priority for effective selection. The present investigation revealed that the cluster II and cluster V are most diverse to each other, and the genotypes constituted in these clusters may be used as a parent for further hybridization programme.

3. MATERIAL AND METHODS

The experiment entitled, “Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)” was conducted at Post Graduate Institute Research Farm, M.P.K.V., Rahuri, during *Rabi* season of 2019-2020. The details of material used, methods adopted and statistical analysis followed during the investigations are described below.

3.1 Material

The experimental material used for the study consisted of 50 genotypes which were obtained from the Principle Scientist Pulses Improvement Project, M.P.K.V., Rahuri. The list of genotypes is given in Table 1.

Table 1. List of fifty genotypes of chickpea

Sr. No.	Genotype	Sr. No.	Genotype
1	IVT (MH) RKGM 18-6	2	IVT (DI) BRC-6
3	IVT (MH) PG-2018	4	IVT (DI) NBeG-798
5	IVT (DI) JG 2018-52	6	IVT (MH) GBM-2
7	IVT (DI) ICCV -171105	8	IVT (DR) RVSSG -74
9	Phule-G 17115	10	IVT (DR) DBGV-2018
11	Phule-G-16109	12	IVT (MH) IPC 14-120
13	IVT (DI) RLBG-3	14	IVT (MH) RKGM 18-5
15	IVT (DI) RVSSG-68	16	IVT (MH) CB-4002
17	IVT (DR) H 15-11	18	IVT (DI) NBeG-857
19	IVT (DR) PBC-507	20	IVT (DR) RKG 18-4
21	IVT (DR) RVSIG-18-593	22	IVT (DI) NBeG-857
23	IVT (DR) JG-16	24	IVT (DI) IG 2018-51
25	IVT (DI) DBGV-221	26	IVT (DI) GNG-2434
27	IVT (DI) GIG-1610	28	IVT (DI) RG 2016-134
29	IVT (DI) RVSSG -475	30	IVT (DI) DC 17-1115
31	Phule G -1012-15	32	IVT (DR) GJG -1603
33	IVT (DR) PBC 546-18	34	IVT (DI) RVSSG -69
35	IVT (DI) CSJ -1065	36	IVT (DR) CSJ -1070
37	IVT (DR) BG-4004	38	IVT (DR) RVSIG -18-370
39	IVT (DI) IPC -1439	40	IVT (DI) DBGV-217
41	Phule G -1107-275	42	IVT (DI) RKG-1322
43.	IVT (DI) RKG -18-1	44	IVT (DR) GJG -1611
45	IVT (MH) GL-16056	46	Phule vikram
47	Digvijay	48	Phule vikrant
49	Vishal	50	Vijay

3.2 Experimental Design

During *Rabi* 2019-2020, 50 genotypes of chickpea were evaluated in a Randomized Block Design (RBD) with two replications. Each genotype was sown in single row of 3 m length with spacing 45 cm between row and 10 cm within rows.

3.3 Cultural Practices

The land selected for the experiment was medium black which was brought to fine tilth. The fertilizer @ 25 kg N/ha in the form of urea and 50 kg P/ha in the form of single super phosphate were applied as a basal dose at the time of sowing. In order to facilitate easy and better germination, a light irrigation was given after sowing.

The operations like thinning, weeding, hoeing and plant protection measures were carried out regularly to ensure satisfactory crop growth.

3.4 Observations Recorded

Five plants per genotypes were selected at random for recording observations on following characters except days to 50% flowering and days to maturity, in each Replications and averages were calculated.

3.4.1 Days to 50% Flowering

Number of days from sowing to the date when 50 per cent plants in each plot initiated flowering was recorded and the average number of days for 50 per cent flowering was calculated.

3.4.2 Days to Maturity

Number of days taken from the date of sowing to the physiological maturity of crop was recorded as days to maturity.

3.4.3 Plant Height (cm)

Plant height was recorded at the time of harvesting by measuring the height of a plant from ground level to the top of the main axis.

3.4.4 Number of Primary Branches/Plant

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

3.4.5 Number of Secondary Branches/Plant

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

3.4.6 Number of Pods Per Plant

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

3.4.7 Number of Seeds Per Pod

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

3.4.8 100-Seed Weight (g)

It was recorded by weighing randomly selected 100 seeds.

3.4.9 Seed Yield Per Plant (g)

The weight of seeds obtained as a mean of five observational plants represented the yield of seed per plant.

3.5 Statistical Methodology

3.5.1 Assessment of Variability

a. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1967).

Yij = μ + Gi + Rj + Eij

Where,

i = 1, 2…....g
j = 1, 2……..r
μ = General mean
Gi = Effect of i^{th} genotype
Rj = Effect of j^{th} replication
Eij = Random error associated with Yij observation

ANOVA Table

Sources	d.f.	m.s.	expected m.s.
Replications	r-1	RMS	б2e + gб2r
Treatments	g-1	GMS	б2e + rб2g
Error	(r-1)(g-1)	EMS	б2e

Where,

r = Number of replications
g = Number of genotypes
б2r = Variance due to replications
б2g = Variance due to genotypes
б2e = 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:

$$\bar{X} = \frac{1}{N} \left(\sum_{i=1}^{n} X_i\right)$$

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 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):

$$\text{GCV} = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

Where,

σ2g = Genotypic variance, and

X = Mean of Character

Phenotypic coefficient of variation (PCV) :

$$PCV = \frac{\sqrt{\sigma^2 P}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance, and

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

e. Estimation of heritability (b.s.)

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

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma 2g$ = Genotypic variance

$\sigma 2p$ = Phenotypic variance

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

Low Heritability = < 30 %

Medium Heritability = 30.1 to 60 %

High Heritability = > 60 %

f. Genetic advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated by the formula cited by Allard (1960).

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

Where,

$\sigma 2g$ = Genotypic variance

$\sigma 2p$ = Phenotypic variance

k = Selection differential (at 5 % selection intensity the value of k =2.06)

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

$$GAM = \frac{G.\ A.}{\bar{X}} \times 100$$

Where,

G.A. = Genetic advance

$\bar{X}$ = Character mean

Low : 10 %

Medium : 10.1 to 20 %

High : > 20 %

3.5.2 Correlations

Analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic co-variances were then calculated as per the formulae given by Johnson *et al.* (1955) as below.

ANOVA Table:

Sources	**d.f.**	**Sum of product**	**Mean sum of product**	**Expectation of mean sum of product**
Replications	(r-1)	RP	RMP	COVe1.2+ gCOVr1.2
Genotypes	(g-1)	GP	GMP	COVe1.2 + rCOVg1.2
Error	(r-1) (g-1)	EP	EMP	COVe1.2

Environmental covariance (COV. e1. 2) = EMP

$$\text{Genotypic covariance (COV. g1. 2)} = \frac{\text{GMP - EMP}}{r}$$

Phenotypic covariance (COV. p1. 2) = (COV. g1. 2 + COV. e1. 2) Appropriate variances and co-variances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al.*, 1955).

i. The phenotypic correlation coefficient (rp) was calculated as:

$$rp1.2 = \frac{\text{COV. p1. 2}}{\sqrt{(\sigma^2 p1).\ (\sigma^2 p2)}}$$

Where,

rp1. 2 = Phenotypic correlation coefficient between character 1 and 2

COV. p1. 2 = Phenotypic covariance between character 1 and 2

σ2p1, σ2p2 = Phenotypic variance of character 1 and 2 respectively.

The significance of the phenotypic correlation coefficient was tested by referring to Fisher and Yates (1943).

ii. The genotypic correlation (rg) coefficient was calculated as:

$$rg1.2 = \frac{\text{COV. g1. 2}}{\sqrt{(\sigma^2 g1).\ (\sigma^2 g2)}}$$

Where,

rg1. 2 = Genotypic correlation coefficient between character 1 and 2

COV. g1. 2 = Genotypic covariance between character 1 and 2

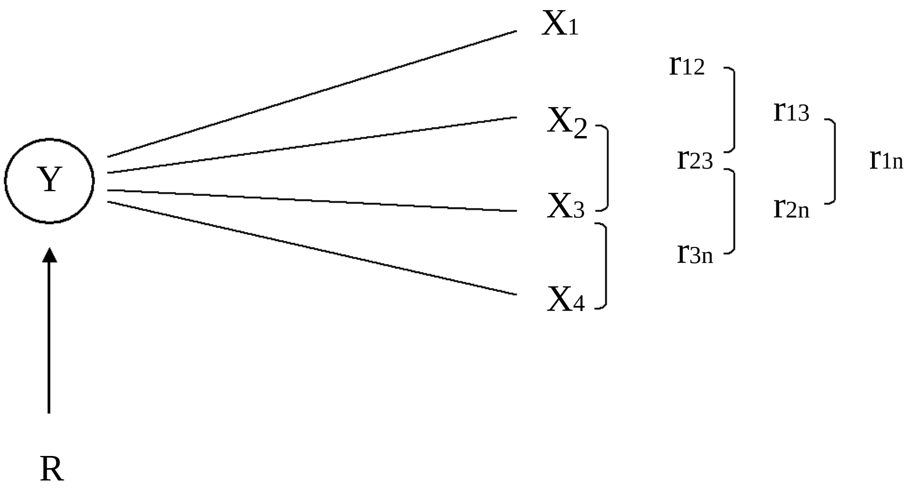
σ2g1, σ2g2 = Genotypic variances of character 1 and 2, respectively.

The significance of correlation was tested by ‘t’ test.

3.5.3 Path coefficient analysis

To establish a cause and effect relationship, the first step was used to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in the path analysis is to prepare the path diagram based on cause and effect relationships. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X1, X2, X3 …. Xn and these components showed following type of association with each other.



In path diagram, the yield is the result of X1, X2, X3… Xn and some other undefined factors designated by R. The double arrowed lines indicated mutual association as measured by linear correlation coefficients and the single arrowed line resent direct influence as measured by path coefficient Pij.

Path coefficients were obtained by solving a set of simultaneous equations of the form as per Dewey and Lu (1959).

Rny = rn1.P1y + rn2.P2y + rn3.P3y +…. + Pny

Where,

Rny = Represents the correlation between one component and yield

Pny = Represents path coefficient between that character and yield

Rn2 = Represents correlation between that character and each of the other components in turn

$$\begin{array}{ccc} \text{Matrix A} & \text{Matrix B} & \text{C} \\ \begin{pmatrix} R1y \\ \\ R2y \\ \\ Rny \end{pmatrix} & = r21 \begin{pmatrix} r11 & r12 & r13 \ldots\ldots\ldots\ldots r1n \\ \\ & r22 & r23 \ldots\ldots\ldots\ldots r2n \\ \\ rn1 & rn2 & rn3 \ldots\ldots\ldots\ldots rnn \end{pmatrix} & \begin{pmatrix} P1y \\ \\ P2y \\ P3 \\ y \end{pmatrix} \end{array}$$

Where,

r12 = r21 and so on

r1y = Correlation between one component character and seed yield

The ‘B’ matrix was inverted [B]-1 and path coefficients (Pij) were obtained as,

C = (B)-1.A

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

The indirect effects of a particular character through other characters were obtained by multiplication of direct paths and particular Correlation coefficient between the characters separately.

Indirect effects = rij x Pij

Where,

i = 1 to 9

j = 1 to 9

Pij = P1y. P2y ………. Pny

Path coefficients (Pij), correlation coefficients (rij) and residual factor (R) were diagrammatically presented. The residual factor, i.e. variation in yield unaccounted for by these associations was calculated from the following formula,

Residual factor (R) = (1 – R2)

Where,

R^2 = P1y. r1y + P2y. r2y + P3y. r3y +………… Pny. rny

P1y, P2y, …….. Pny = Path values

r1y, r2y … rny = Correlation coefficients

3.5.4 Genetic diversity

D^2 analysis

The analysis of divergence was carried out by D^2 statistics of Mahalanobis’ (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D., to test significance of differences among the genotypes.

The characters exhibiting significant differences were only used for further analysis of D2 statistic. The analysis of co-variance for the character pairs, based on plot averages was carried out (Cochran and Cox, 1957).

a. Wilk's criteria

After testing for differences between the population for nine characters, a simultaneous test of significance of difference in the mean values of a number of correlated variables with regard to the pooled effect of the nine characters considered together was carried out using Wilk's criteria 'Λ' (Wilk, 1932) which was estimated using the relationship that :

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

Where,

| E | = Determinant of the experimental error sum of squares and sum of products matrix

|E + V| = Determinant of experimental error sum of squares and sum of products, plus the population sum of squares and product matrix.

Significance of Wilk's criteria (Λ) was estimated by X_2 as, X_2 pq = V = - m log Λ

Where,

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

n = N1 + …… + NK-1

= Total number of observations - 1

P = Number of significant characters

Q = K -1 (d. f. of varieties)

K = Number of varieties/genotypes

Calculated X_2 values were tested against X_2 able value at pq degrees of freedom.

b. Mahalanobis' generalized distance (D^2)

The generalized distance between any two populations is defined as:

$\Delta 2 \quad = \sum \sum \lambda ij.\ \delta i.\ \delta j$

Where,

λij = Reciprocal matrix to the common dispersion matrix

δi = Difference between the mean values of the two populations for the ith character

δj = Transpose δi

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

$D_2 = \sum \sum \delta ij.\ di.\ dj$

Where,

δij, di and dj are the sample estimate of δij, δi and δj.

Since this formula for computation requires the inversion of tenth order determinant and then evaluation of 10 (10+1) terms, whose sum is D^2.

c. Computation of D^2 values

For each combination among 50 genotypes D^2 values were calculated. Thus, total 50 (49)/2 = 1275 numbers of D^2 values were worked out.

d. Determination of population constellations

No rules can be laid down for finding the clusters because cluster is not a well-defined term. The only criterion appears to be that any two genotypes belonging to the same cluster should be at least, on an average show a smaller D^2 value than those belonging to two different clusters.

A simple device or method suggested by Tocher (Rao, 1952) for cluster formation is to start with two closely related groups and find the third group which had the smaller average D^2 from the first two. Similarly, the fourth group is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further for the cluster formation, if at any stage, the average D^2 value of a group appears to be high than those already listed, then this group does not fit in that former group and is to be taken outside of that cluster.

The genotypes included in the first cluster are then omitted and the rests are treated similarly to form next cluster.

e. Average intra-cluster distance

The intra-cluster distances were calculated as:

$\Sigma Di^2 / n$

Where,

ΣDi^2 = Sum of distance between all possible combinations (n) genotypes included in a cluster

n = number of genotypes included in a cluster

f. Average inter-cluster distances

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

$\Sigma Di^2 / (ni.\ nj)$

Where,

ΣDi^2 = Sum of distance between all possible combinations of genotypes included in both clusters

ni = Number of genotypes in cluster i and

nj = Number of genotypes in cluster j

The intra and inter cluster distances (D) values were obtained by taking square root of average D_2 values of the respective groups.

g. Cluster diagram

With the help of D^2 values between the clusters, a diagram showing the relationships between different populations was drawn.

4. EXPERIMENTAL RESULTS

The results obtained of the present investigation entitled “Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)” are presented in this chapter under different subheadings.

4.1 Genetic Variability and Heritability

The analysis of variance revealed significant genotypic differences for all the characters (Table 2).

Table 2. Analysis of variance for nine different character in chickpea.

Sr. No.	Characters	Mean sum of squares		
		Replication (d.f.1)	Genotype (d.f.49)	Error (d.f.49)
1.	Days to 50 per cent flowering	1.210	28.081**	1.373
2.	Days to maturity	4.410	49.716**	20.573
3.	Plant height	3.572	96.398**	6.290
4.	Number of primary branches per plant	0.577	0.293**	0.064
5.	Number of secondary branches per plant	0.036	6.271**	1.236
6.	Number of pods per plant	28.944	134.777**	24.546
7.	Number of seed per pod	0.004	0.024**	0.002
8.	100 seed weight	6.110	52.423**	3.192
9.	Seed yield per plant	2.825	33.588**	6.575

*** indicate significant at 5 and 1 per cent level, respectively
Note: Figures in the parenthesis indicates the degrees of freedom

4.1.1 Mean performance and the range of variability

The mean values of the genotypes for different characters studied are given in Table 3.

4.1.1.1 Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 47.50 and 61.50 days. Genotype GJG-1611 exhibited significantly least days (47.50) followed by GJG-1603 (48) while significantly highest days (61.50) were shown by three genotype that is GNG-2434, IPC 14-39 and GL-16056. General mean for days to 50 per cent flowering was 54.93 days. Out of fifty genotype twenty genotype found earlier than general mean.

4.1.1.2 Days to maturity

The general mean for this character was 99.79. The variation in days to maturity ranged between 78.00 and 109.00 days. Genotype PBC-507 matured in significantly least number of days (78.00) followed by GJG-1611(91.50). Twenty one genotypes out of fifty showed significantly early maturity than general mean (99.79), while IPC 14-39 matured very late (109.00 days).

Table 3. Mean Performance of fifty chickpea genotypes studied for nine characters

Sr. No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	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	RKGM 18-6	55.00	103.50	47.20	2.30	10.90	50.90	1.21	18.26	17.25
2	BRC-6	55.00	100.50	92.20	2.40	12.70	58.10	1.14	17.67	16.36
3	PG-2018	55.50	100.00	40.50	2.50	10.20	60.40	1.21	24.29	19.38
4	NBeG-798	57.50	102.00	47.65	2.10	10.60	57.50	1.24	24.44	17.85
5	JG 2018-52	58.00	102.50	46.50	2.30	10.40	37.40	1.33	24.76	14.29
6	GBM-2	51.50	106.00	56.20	2.50	11.10	60.70	1.20	32.91	30.17
7	ICCV -171105	56.50	101.00	53.10	1.90	9.70	36.80	1.20	23.78	13.72
8	IPCS-15-116	58.00	98.00	58.40	2.20	11.10	60.10	1.00	17.01	24.41
9	RVSSG -74	56.50	93.00	57.20	2.40	13.10	60.80	1.00	17.57	22.51
10	Phule-G 17115	56.50	100.00	48.30	2.60	11.00	56.90	1.06	21.59	28.80
11	DBGV-2018	50.50	99.00	53.30	3.00	9.70	55.20	1.12	29.91	23.44
12	Phule-G-16109	57.50	99.00	49.40	2.20	9.70	53.20	1.00	24.62	26.37
13	IPC 14-120	59.50	103.00	56.70	2.20	11.30	53.60	1.16	19.81	18.95
14	RLBG-3	51.50	100.00	63.10	2.40	12.40	51.20	1.13	30.60	23.41
15	RKGM 18-5	59.50	95.00	67.65	1.90	8.90	46.90	1.00	15.36	17.84
16	RVSSG-68	59.50	101.00	41.10	1.90	9.20	41.90	1.42	30.65	18.90
17	CB-4002	56.00	97.00	51.10	2.30	10.30	44.30	1.23	33.21	18.91
18	H 15-11	59.00	99.00	60.10	2.40	10.50	51.90	1.09	24.36	21.90
19	PBC-507	52.50	78.00	56.70	2.40	11.80	49.80	1.17	22.54	20.25
20	RKG 18-4	54.00	96.50	48.60	2.30	12.10	60.50	1.00	23.92	26.36
21	RVSIG-18-593	59.00	105.50	50.30	2.20	12.00	35.10	1.19	32.73	23.71
22	NBeG-857	55.00	99.50	53.70	2.90	13.60	49.10	1.00	20.37	21.88
23	JG-16	51.50	95.00	47.40	3.30	13.50	56.20	1.00	28.98	26.03
24	JG 2018-51	50.50	94.50	44.80	2.30	13.70	50.60	1.00	15.15	20.24
25	DBGV-221	57.50	97.00	51.80	2.70	13.00	54.30	1.19	26.37	27.26
26	GNG-2434	61.50	107.00	54.80	2.40	9.10	44.80	1.33	16.92	17.37
27	GJG-1610	48.50	97.00	53.20	2.00	11.30	49.20	1.08	24.56	16.21

Table 3 contd…

Sr. No.	Name of genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	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)
28	RG 2016-134	49.00	97.50	59.00	3.10	14.70	56.60	1.18	24.09	22.18
29	RVSSG -475	53.50	100.00	56.10	2.10	10.50	45.10	1.21	14.04	18.23
30	DC 17-1115	56.50	102.50	58.80	2.60	14.00	49.10	1.15	31.26	27.89
31	Phule G -1012-15	48.50	101.00	60.90	2.90	9.60	45.90	1.38	24.25	23.45
32	GJG -1603	48.00	92.00	38.50	1.90	10.40	37.70	1.33	19.34	19.05
33	PBC 546-18	52.00	100.00	53.40	2.30	14.10	47.70	1.24	26.56	23.01
34	RVSSG -69	53.50	100.50	36.30	1.70	7.80	36.00	1.13	14.70	12.14
35	CSJ -1065	56.00	101.50	50.80	2.50	13.50	55.20	1.22	28.53	29.26
36	CSJ -1070	56.00	101.00	41.70	2.40	10.30	45.10	1.11	24.04	23.90
37	BG-4004	60.00	107.00	45.20	2.50	13.00	52.70	1.02	23.71	25.80
38	RVSIG -18-370	52.50	103.00	45.85	2.70	12.40	52.30	1.00	21.46	21.17
39	IPC -1439	61.50	109.00	64.00	2.60	11.30	54.60	1.15	20.33	20.04
40	DBGV-217	56.50	99.00	48.70	2.30	12.30	61.80	1.22	32.01	28.16
41	Phule G -1107-275	50.00	100.00	42.75	1.80	12.00	75.00	1.26	24.89	24.97
42	RKG-1322	58.00	103.00	52.00	2.50	12.60	51.10	1.08	18.86	19.50
43	RKG -18-1	52.50	97.00	49.30	2.50	9.90	50.50	1.25	24.39	22.07
44	GJG -1611	47.50	91.50	43.50	1.90	10.70	44.40	1.33	23.47	19.47
45	GL-16056	61.50	108.00	41.60	2.10	12.30	50.30	1.22	15.57	20.82
46	Phule Vikram	54.50	99.00	52.60	3.60	15.30	62.90	1.28	26.82	23.59
47	Digvijay	56.50	100.50	47.00	2.90	14.20	57.00	1.29	23.35	22.03
48	Phule Vikrant	52.50	99.00	42.80	2.80	14.90	54.40	1.19	23.90	21.66
49	Vishal	56.00	105.00	48.60	2.60	13.40	60.40	1.50	25.80	24.45
50	Vijay	52.50	103.00	48.35	2.60	14.75	67.80	1.13	19.71	22.92
	Mean	**54.93**	**99.79**	**50.57**	**2.41**	**11.69**	**52.01**	**1.16**	**23.46**	**21.79**
	C.V.	2.13	4.54	4.95	10.53	9.50	9.52	3.93	7.61	11.76
	S.E.	0.82	3.20	1.77	0.18	0.78	3.50	0.03	1.26	1.81
	C.D. 5%	2.35	9.11	5.04	0.51	2.23	9.95	0.09	3.59	5.15

4.1.1.3 Plant height (cm)

The general mean for plant height was 50.57 cm. Twenty four genotypes were taller than the general mean. Plant height was ranged between 36.30 to 67.65 cm. The genotype RVSSG-69 was found to be significantly superior for plant height (36.30 cm) followed by GJG-1603 (38.50 cm). The genotype RKGM 18-5 was tallest (67.65 cm) among the all genotypes.

4.1.1.4 Number of primary branches per plant

The mean performance of this character was 2.41. Number of primary branches per plant ranged from 1.70 to 3.60. Genotype RVSSG-69 recorded lowest while Phule Vikram had maximum number of Primary branches per plant. Twenty one genotypes recorded higher number of primary branches than the mean performance (2.41).

4.1.1.5 Number of secondary branches per plant

Twenty four genotypes recorded higher number of secondary branches per plant than the mean performance (11.69). Number of secondary branches per plant ranged from 7.82 to 15.30. Among them Phule Vikram showed maximum number of secondary branches per plant (14.66) followed by Phule Vikrant (14.90), Vijay (14.75) and RG-2016-134 (14.70) than the general mean. The genotype RVSSG-69 showed lowest branches followed by RKGM-18-5 (8.90).

4.1.1.6 Number of pods per plant

Number of pods per plant ranged from 35.10 to 75.00. Twenty five genotype recorded higher values for number of pod per plant than the mean performance. Genotype RVSIG-18-593 (35.10) recorded lowest followed by RVSSG-69 (36.00), while Phule G-1107-275 (75.00) had maximum number of pods per plant followed by genotypes Vijay (67.80) and Phule vikram (62.90). The mean performance for this character was 52.01.

4.1.1.7 Number of seeds per pod

The mean performance of this character was 1.16. Number of seeds per pod ranged from 1.00 to 1.42. Number of seeds per pod was minimum in case of IPCS-15-116, RVSSG-74, Phule G-16109, RKGM 18-5, RKG-18-4, NBeG-857, JG-16, JG-2018-51, and RVSIG-18-370 while maximum number of seeds per pod recorded in RVSSG-68 (1.42) followed by Phule G 1012-15 (1.38). Twenty five genotype recorded for maximum number of seeds per pod than the mean performance.

4.1.1.8 100 seed weight (g)

The mean performance of this character was 23.46 g. The variation for 100 seed weight ranged between 14.04 g to 33.21 g. Genotype RVSSG-475 (14.04 g) showed lowest 100 seed weight followed by RVSSG-69 (14.70 g) and JG-2018-51 (15.15 g). While CB-4002 (33.21 g) exhibited highest 100 seed weight followed by GBM-2 (32.91 g) and DBGV-217 (32.01 g). Thirty genotypes recorded higher 100 seed weight than the mean performance.

4.1.1.9 Seed yield per plant (g)

The mean performance of this character was 21.79. The variation for seed yield per plant ranged between 12.14 g and 30.17 g. The genotype RVSSG-69 showed minimum seed yield per plant (12.14 g) followed by ICCV-171105 (13.72 g) and JG-2018-52 (14.29 g), while GBM-2 (30.17 g) produced maximum seed yield per plant followed by genotypes CSJ-1065 (29.26 g), Phule G-171105 (28.80 g) and was significant. Twenty seven genotypes recorded higher seed yield per plant than the mean performance (21.79 g).

4.1.3 Genotypic and Phenotypic Coefficients of Variation

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

Genotypic coefficient variation (GCV) was highest for 100 seed weight (21.14 %) followed by seed yield per plant (16.86 %), number of pods per plant (14.77 %) and number of primary branches per plant (13.98 %). The character days to maturity (3.82 %) recorded lowest GCV. The maximum phenotypic coefficient of variation (PCV) was recorded for 100 seed weight (22.47 %), followed by seed yield per plant (20.56 %) and number of primary branches per plant (17.51 %).

In general, the magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation.

4.1.4 Heritability and Genetic Advance

Estimates of heritability in broad sense are presented in Table 4. High estimates of heritability (>60%) was observed for all the studied characters except days to maturity (41.50 %). The highest estimates of heritability exhibited in days to 50 per cent flowering (90.70%) followed by 100 seed weight (88.50), plant height (87.70%), number of pods per plant (84.40 %), number of pods per plant (69.20), seed yield per plant (67.70 %), number of secondary branches per plant (67.10 %) and number of primary branches per plant (63.80 %).

The range of genetic advance observed from 0.20 to 12.95. The highest estimate of GA for plant height (12.95) followed by number pod per plant (12.72), 100 seed weight (9.61), days to 50 per cent flowering (7.16) and seed yield per plant (6.20).

4.1.5 Genetic Advance as per cent of Mean

The range of genetic advance as per cent of mean is classified as suggested by Johansson, *et al.* (1955). High estimates of genetic advance as per cent of mean observed for 100 seed weight (40.98 %), followed by seed yield per plant (28.48 %), plant height (25.61%), number of pods per plant (24.45 %). While, days to maturity (5.07 %) showed 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 fifty chickpea genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability (bs) (%)	Genetic Advance	Genetic Advance % of Mean
1	Days to 50 per cent flowering	54.93	47.50-61.50	6.65	6.98	2.13	90.70	7.16	13.05
2	Days to maturity	99.79	91.50-109.00	3.82	5.94	4.54	41.50	5.06	5.07
3	Plant height (cm)	50.57	36.30-67.65	13.27	14.16	4.95	87.70	12.95	25.61
4	Number of primary branches/plant	2.41	1.70-3.60	13.98	17.51	10.54	63.80	0.55	23.00
5	Number of secondary branches/plant	11.69	7.80-15.30	13.56	16.56	9.50	67.10	2.67	22.88
6	Number of pods/plant	52.01	35.10-75.00	14.27	17.16	9.52	69.20	12.72	24.45
7	Number of seeds/pod	1.16	1.42-1.00	9.15	9.95	3.93	84.40	0.20	17.31
8	100 seed weight (g)	23.46	14.04-33.21	21.14	22.47	7.61	88.50	9.61	40.98
9	Seed yield /plant (g)	21.79	12.14-30.17	16.86	20.56	11.76	67.30	6.20	28.48

4.2 Correlation Studies

The correlation coefficient between seed yield and its components were estimated at genotypic and phenotypic level. The genotypic (rg) and phenotypic (rp) correlations for nine characters studied are presented in Table 5. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlations.

4.2.1 Association of Seed Yield with its Components

It is revealed from Table 5 that, significant positive correlation was reported between seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of pods per plant and 100 seed weight. Non-significant positive correlation was reported between seed yield per plant with days to maturity and plant height. However, significant negative correlation was reported between seed yield per plant with number of seed per pod only at genotypic level. Non-significant negative correlation with days to 50 per cent flowering.

4.2.2 Interrelationship of Yield Components

4.2.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed significant positive correlations with days to maturity (rg =0.544, rp =0.449) and other characters are non significant.

4.2.2.2 Days to maturity

Days to maturity exhibited non significant positive association with all character except plant height with non significant negative association.

4.2.2.3 Plant height

Plant height recorded significant positive association with number of primary branches per plant (rg =0.234, rp =0.267) and other characters are non significant.

4.2.2.4 Number of primary branches per plant

Number of primary branches per plant exhibited significant positive correlations at both genotypic and phenotypic levels with plant height (rg = 0.234, rp = 0.267), number of secondary branches per plant (rg =0.665, rp =0.542), number of pods per plant (rg =0.471, rp=0.305), 100 seed weight (rg =0.321, rp =0.218) and seed yield per plant (rg =0.460, rp =0.408).

4.2.2.5 Number of secondary branches per plant

Number of secondary branches per plant showed positive and significant correlation with number of primary branches per plant (rg = 0.665, rp = 0.542), number of pods per plant (rg =0.575, rp =0.452), seed yield per plant (rg = 0.448, rp = 0.446).

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

Sr. No.	Name of character	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches/ plant	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**	0.449^{***}	0.167	-0.124	-0.101	-0.076	-0.088	-0.114	-0.049
2.	Days to maturity	0.544^{***}	**1.000**	-0.029	-0.001	0.023	0.031	0.101	0.034	0.013
3.	Plant height (cm)	0.211^{*}	-0.002	**1.0000**	0.267^{**}	0.108	0.111	-0.180	0.018	0.188
4.	Number of primary branches/plant	-0.109	0.152	0.234*	**1.000**	0.542^{***}	0.305^{**}	-0.124	0.218^{*}	0.408**
5.	Number of secondary branches/ plant	-0.158	0.033	0.022	0.665^{***}	**1.000**	0.452^{***}	-0.147	0.153	0.446**
6.	Number of pods/plant	-0.117	0.041	0.069	0.471^{***}	0.575^{***}	**1.000**	-0.222^{*}	0.073	0.496**
7.	Number of seeds/pod	-0.086	0.105	-0.192	-0.095	-0.173	-0.290^{***}	**1.000**	0.236^{*}	-0.170
8.	100 seed weight (g)	-0.119	0.067	0.033	0.321^{***}	0.208^{*}	0.061	0.270^{**}	**1.000**	0.454**
9.	Seed yield /plant (g)	-0.053	0.127	0.124	0.460**	0.448**	0.582**	-0.286**	0.560**	**1.000**

*and ** significant at P= 5 and P = 1 level of significance, respectively

4.2.2.6 Number of pods per plant

The number of pods per plant recorded significant positive correlation with number of secondary branches per plant (rg = 0.575, rp = 0.452), number of primary branches per plant (rg = 0.471, rp = 0.305), seed yield per plant (rg = 0.582, rp = 0.496). However, it exhibited negative correlation with number of seeds per pod (rg =-0.290, rp =-0.222).

4.2.2.7 Number of seed per pod

The number of seed per pod showed significant positive correlation with 100 seed weight (rg= 0.270, rp = 0.236) and its negative correlation with number of pods per plant (rg= -0.290, rp = -0.222) and seed yield per plant (rg= -0.286, rp = -0.170)

4.2.2.8 100 seed weight

It showed significant positive correlation with seed yield per plant (rg = 0.560, rp = 0.454), number of seed per pod (rg = 0.270, rp = 0.236) and number of primary branches per plant (rg = 0.321, rp = 0.218).

4.3 Path Coefficient Analysis

In order to achieve a clear picture of inter-relationship of various component traits with seed yield per plant, direct and indirect effects were calculated using path coefficient analysis at genotypic level. 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. Therefore, path coefficient analysis could provide a more realistic picture of the inter-relationship, as it considers direct as well as indirect effects of the variables by partitioning the correlation coefficient into direct and indirect effects were given in Table 6.

4.3.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed negative direct effect (-0.022) and it had negative indirect effects through number of secondary branches per plant (-0.001), number of pods per plant (-0.051), 100 seed weight (-0.073), thus leading to negative correlation with seed yield (-0.053).

4.3.2 Days to maturity

Days to maturity exhibited direct positive effect on seed yield (0.115). It had positive indirect effects through number of pods per plant (0.018), 100 seed weight (0.041) and thus leading to positive correlation with seed yield (0.127).

4.3.3 Plant height

The plant height showed positive direct effect (0.014) on seed yield. The indirect effects of it were positive through number of pods per plant (0.030), number of seed per pod (0.064), 100 seed weight (0.020). The total genotypic correlation with seed yield is positive (0.124).

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

Sr. No.	Name of character	Days to 50 per cent flowering	Days to Maturity	Plant height (cm)	Number of primary branches/ plant	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	**-0.022**	0.062	0.003	0.000	-0.001	-0.051	0.029	-0.073	-0.053
2.	Days to maturity	-0.012	**0.115**	0.000	0.000	0.000	0.018	-0.035	0.041	0.127
3.	Plant height (cm)	-0.005	0.000	**0.014**	0.000	0.000	0.030	0.064	0.020	0.124
4.	Number of primary branches/plant	0.002	0.018	0.003	**0.000**	0.003	0.206	0.032	0.196	0.460 **
5.	Number of secondary branches/ plant	0.004	0.004	0.000	0.000	**0.004**	0.251	0.058	0.128	0.449 **
6.	Number of pods/plant	0.003	0.005	0.001	0.000	0.003	**0.437**	0.097	0.037	0.582 **
7.	Number of seeds/pod	0.002	0.012	-0.003	0.000	-0.001	-0.127	**-0.335**	0.165	-0.286 **
8.	100 seed weight (g)	0.003	0.008	0.001	0.000	0.001	0.027	-0.090	**0.612**	0.560 **

Residual effect (R) = 0.536

4.3.4 Number of primary branches per plant

Number of primary branches per plant recorded direct positive effect on seed yield (0.000). It had positive indirect effect on all characters. It exhibited positive and highly significant correlation with seed yield per plant (0.460).

4.3.5 Number of secondary branches per plant

It showed positive indirect effect on all characters. It showed positive and highly significant correlation with seed yield per plant (0.449).

4.3.6 Number of pods per plant

Among the all characters studied, number of pods per plant showed high and positive direct effect on seed yield (0.437). It had highly significant correlation with seed yield (0.582) and positive indirect effect on number of seeds per pod (0.097). It shows the indirect positive effect through all the characters.

4.3.7 Number of seeds per pod

Number of seed per pod showed negative direct effect (-0.335) on seed yield. Its negative indirect effects on plant height (-0.003), number of secondary branches per plant (-0.001), number of pods per plant (-0.127) and thus leading to significant negative correlation with seed yield (-0.286).

4.3.8 100 seed weight

The 100 seed weight showed positive direct effect on seed yield (0.612). It showed positive indirect effects for all the characters except number of seed per pod (-0.090). Its correlation with seed yield was highly significant and positive (0.560).

4.4 Genetic Divergence

Improvement of seed yield or any other traits is normally attained 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 tool used to quantify the degree of genetic diversity between the genotypes and to relate clustering pattern with the geographic region.

4.4.1 Mahalanobis's generalised distance (D^2)

Wilk's criterion showed significant differences between the genotypes for the pooled effect of nine characters studied. Hence, further analysis was done to calculate D^2 values. The D^2 values for all the possible pairs of comparison between 50 genotypes were calculated. Based upon the observations of 9 characters, the Mahalanobis D^2 statistics was computed for all possible pairs of 50 genotypes in order to assess the genetic diversity present among the genotypes under study.

4.4.2 Clustering pattern of the genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values was made and presented in Table 7 and clustering as per Tocher method. The 50 genotypes were grouped into eight clusters. It is revealed from table 7 that cluster I had highest number of genotypes (19) followed by cluster IV (11), cluster III (9) genotypes and cluster VI (7) genotypes. The cluster II, V, VII, VIII, was solitary since they had only one genotype.

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

Cluster No.	Number of genotypes	Name of Genotypes
I	19	CSJ-1065, DBGV-217, DBGV-221, Vishal, RKG-18-1, NBeG-798, Digvijay, PG-218, RKGM-18-6, RKG-1322, CSJ-1065, NBeG-857, BRC-6, PBC-546-18, Phule G-171105, BG-4004, RKG-18-4, Phule G -16109, RVSSG-74
II	1	IPCS-15-116
III	9	GJG-1603, GJG-1611, GJG-1610, Phule Vikrant, Vijay, Phule G-1107-275, RVSIG-18-370, JG-2018-51, RVSSG-69
IV	11	IPC 14-120, H-15-11, IPC 14-39, ICCV-171105, GNG-2434, JG 2018-52, CB-4002, PBC-507, DC 17-1115, RVSIG-18-593, RVSSG-68
V	1	Phule Vikram
VI	7	GBM-2, DBGV-218, RLBG-3, RG-2016-134, Phule G-2012-15, JG-16, RVSSG-475
VII	1	GL-16056
VIII	1	RKGM-18-5

4.4.3 Intra and inter-cluster divergence

The average intra and inter cluster D^2 values are presented in Table 8. The inter cluster distance (D) range from 6.16 to 14.65. Highest inter cluster distance (D=14.65) was found between the clusters III and VIII, followed by the cluster V and VIII (14.04) and cluster VI and VIII (11.86). The minimum inter cluster distance (D=6.16) was between clusters I and VII. An examination of intra cluster divergence among the eight clusters revealed that, cluster VI had maximum intra cluster distance (D=6.59) followed by cluster IV (6.00). As the clusters II, V, VII, VIII was solitary; there was no intra cluster divergence. The mutual relationship among the clusters has been diagrammatically shown in Fig. 4.

Table 8. Average intra (bold) and inter cluster D^2 values for eight clusters in fifty chickpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**5.02**	6.48	7.24	7.31	6.83	6.89	6.16	11.15
II		**0.00**	9.59	7.63	10.25	8.35	7.08	6.45
III			**5.44**	10.97	8.99	8.11	8.61	14.65
IV				**6.00**	8.16	8.44	8.09	9.09
V					**0.00**	7.75	8.16	14.04
VI						**6.59**	9.78	11.86
VII							**0.00**	11.55
VIII								**0.00**

4.4.4 Cluster means for different characters

The cluster mean for the nine characters are presented in Table 9. A considerable inter-cluster variation was observed among the cluster means for the characters studied *viz.*, number of pods per plant, 100 seed weight and seed yield per plant. Cluster means for days to 50% flowering varied from 50.50 (III) to 61.50 (VII). The cluster mean for days to maturity ranged between 95.00 (VIII) to 108.00 (VII). The lowest cluster mean for plant height was (41.60) observed in cluster VII and highest for cluster VIII (67.65). The cluster mean for number of primary branches was ranged from (1.90) cluster VIII to cluster V (3.60). The cluster mean for secondary branches per plant ranged between 8.90 (VIII) to 15.30 (V). The cluster mean for number of pods per plant was observed maximum in cluster V (62.90) and it was observed minimum in cluster IV (45.39). The cluster mean for number of seeds per pod was observed maximum in the cluster V (1.28) and minimum (1.00) in II and VIII cluster. The cluster mean values for 100 seed weight was maximum in the cluster V (26.82) and minimum (15.36) in cluster VIII. The cluster mean for seed yield per plant ranged between 17.84 (VIII) to 24.41 (II).

Table 9. Mean values of the eight clusters for nine characters in fifty chickpea genotypes

Cluster No.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	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	55.95	100.26	49.12	2.47	12.12	54.91	1.14	23.48	23.28
II	58.00	98.00	58.40	2.20	11.10	60.10	1.00	17.02	24.41
III	50.50	97.83	42.89	2.19	11.77	51.90	1.16	20.80	19.76
IV	58.14	100.50	53.93	2.29	10.87	45.39	1.22	25.49	19.63
V	54.50	99.00	52.60	3.60	15.30	62.90	1.28	26.82	23.60
VI	50.86	99.79	56.57	2.76	11.64	52.99	1.17	26.40	23.85
VII	61.50	108.00	41.60	2.10	12.30	50.30	1.22	15.58	20.83
VIII	59.50	95.00	67.65	1.90	8.90	46.90	1.00	15.36	17.84
Population mean	**56.11**	**99.79**	**52.84**	**2.43**	**11.75**	**53.17**	**1.14**	**21.36**	**21.65**

4.4.5 Per cent contribution of different characters to genetic diversity

The utility of D^2 analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of nine characters studied was given in Table 10. It was observed that 100 seed weight (22.04%), days to 50% flowering (21.71%), contributed highest for divergence followed by plant height (15.59%), number of seed per pod (12.90%), number of secondary branches per plant (9.06%). days to maturity (1.80%), number of primary branches per plant (2.86%), number of pods per plant (5.39%) and seed yield per plant (8.65%) 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	266	21.71
2	Days to maturity	22	1.80
3	Plant height	191	15.59
4	No of primary branches	35	2.86
5	No of secondary branches	111	9.06
6	No of pod per plant	66	5.39
7	No of seeds per pod	158	12.90
8	100 seed weight	270	22.04
9	Seed yield per plant	106	8.65
	Total		100

4. B. Discussion

Success of plant breeding depends on selection of elite genotypes, which ultimately depends on knowledge of variability and genetic diversity of germplasm. Plant breeding deals with management and utilization of genetic variability. Hence, assessment of genetic variability, study of character association and genetic diversity in the available germplasm is of immense value to design a selection programme and to identify the superior, genetically diverse genotypes to be used as parents in future hybridization programme. It is, therefore necessary to classify and utilize this variability systematically for genetic up gradation of biological population.

Similarly, the assessment of the magnitude and direction of association between different yield contributing characters especially with yield is useful in selecting desired genotypes on the basis of their phenotypic values. Simple correlation coefficients in this direction are of limiting value. Hence, it is important to study the cause and effect relationship between yield and its component characters through correlation and path analysis studies.

In the present investigation, 50 diverse genotypes of chickpea collected from Pulses Improvement Project, MPKV Rahuri were evaluated to assess the amount of genetic variability. Correlation and path analysis were also worked out to study the associations between component characters and the direct and indirect path coefficients of the component characters on yield; and to study the genetic divergence. The results obtained on these aspects are discussed in this chapter under appropriate headings. The result obtained of the present investigation in 50 genotypes are discussed 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 presence of genetic variability is benificial to the evolutionary survival of a species. In any crop yield improvement can be brought about through plant breeding but necessary variability upon which selection is to be practiced must be available in the genetic material of such crop. Therefore, before going to any crop improvement programme, a plant breeder must survey and assess the variability for a given agronomic or yield component characters which can be estimated through variance, coefficient of variability (GCV, PCV), heritability and genetic advance, genetic advance as percent of mean.

4.5.1 Range of Variability

Wide range of variability was observed for almost all the characters except primary branches per plant. Number of pods per plant exhibited highest range of variability followed by plant height, 100 seed weight, days to maturity, seed yield per plant showed considerable amount of variability. The variability was lowest for number of seeds per pod, number of primary branches per plant, number of secondary branches per plant. Similar results were obtained by Sharma (1990) reported highest range of variability for pods/plant followed by harvest index, secondary branches per plant, days to maturity, days to flowering, while lowest for seeds/pod, Rao and Kumar (2000) Maximum variation was observed for biological yield followed by seed yield, low variability was observed for days to maturity followed by days to 50 per cent flowering, Gupta and Krishna (1995) studied the variability, They reported that variability range was broader for seed size than for protein content.

4.5.2 Genotypic and Phenotypic Coefficient of Variation

Genetic variability is the basis for any heritable improvement in the crop plants. The estimates of GCV and PCV for all the characters studied showed little difference the latter being slightly greater than the former, thus indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors.

The character 100 seed weight and seed yield per plant exhibited highest estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) indicating good scope for their improvement through selection. This was in the conformity with the results Dar et al (2012) the high PCV and GCV were recorded in 100 seed weight followed by number of pods per plant, seed yield, plant height and days to 50% flowering, Astereki *et al.* (2015) studied genetic diversity of 25 chickpea genotypes, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for seed yield, days to flowering, flowering period, canopy height, number of pods per plant, Kishor *et al.* (2018). Lowest GCV and PCV were recorded for days to maturity and days to 50% flowering, High genotypic coefficient of variation and phenotypic coefficient of variation was found for 100 seed weight.

4.5.3 Heritability (b.s.) and Genetic Advance

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicators of heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects, allelic interactions due to dominance and non-allelic due to epistasis. In the present investigation, the highest estimates of heritability exhibited in days to 50% flowering (90.70%) followed by 100 seed weight (88.50), plant height (87.70%), number of seeds per pod (84.40 %), number of pods per plant (69.20), seed yield per plant (67.30 %), number of secondary branches per plant (67.10 %) and number of primary branches per plant (63.80 %). These results are supported by Mathur and Mathur (1996), Ali *et al.* (2008) broad sense heritability estimates were the highest for plant height (97.4) and seed yield per plant (97.3). Genetic advance was higher for seed yield per plant (27.42) and plant height (14.51)., Borate *et al.* (2010) range of variability was appreciable for days to first flowering, secondary branches per plant, plant height, dry matter and grain yield and Mushtaq *et al.* (2013) investigated heritability estimates were maximum for days taken to flowering, days taken to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100-grains weight and grain yield per plant

In the present investigation high heritability coupled with high genetic advance as per cent of mean was observed for the plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100 seed weight, seed yield per plant. Range of genetic advance observed from 0.20 to 12.95. The highest estimate of GA for plant height (12.95) followed by number pod per plant (12.72), 100 seed weight (9.61), days to 50% flowering (7.16) and seed yield per plant (6.20). This result also supported by Ali *et al.* (2008) Genetic advance was higher for seed yield per plant (27.42) and plant height (14.51), Neelu kumari *et al.* (2013) high expected genetic advance coupled with 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 high genetic advance as per cent of mean indicating that these traits could be prominently governed by additive gene action and selection of these traits could be more effective for desired genetic improvement.

4.6 Correlation Studies

The genotypic correlation coefficients provide an estimate of an inherent association between gene controlling any two character i.e. when two characters are invariably and linearly associated, the genetic mechanism causing such association may be due to pleiotropy or complete linkage between the two character. The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown. Even similarly strong association between plant spread and number of pods per plant was noticed through the highly significant positive values of correlation coefficients. This indicates the simultaneous improvement of these characters through selection.

In the present investigation, seed yield per plant exhibited significant positive correlation with number of primary branches per plant, number of secondary branches per plant, number of pods per plant and 100 seed weight. These results are supported by Tiwari *et al.* (2016) harvest index, 100-seed weight, seeds per pod, number of effective pods per plant, total number of pods per plant, number of primary branches per plant per plant and plant height were the most important characters, which possessed positive association with seed yield per plant. Shanmugam Mohan and Kalaimagal Thiyagarajan (2019) traits such as number of secondary branches, number of seed per plant, 100 seed weight, biological yield per plant and harvest index exhibited significant positive correlation with seed yield per plant. Seed yield per plant exhibited significant negative correlation with number of seeds per pod at genotypic level, this result supported by Raval and Dobriya (2003) studied correlation of seed yield with days to 50% flowering, days to maturity and number of seeds/pod was negative and significant.

4.7 Path Coefficient Analysis

Apart from correlation studies, path coefficient analysis is important to obtain information about how the component characters influence the seed yield through each other. Correlation coefficient along with path effects provides basis for selection of superior genotypes from the diverse breeding programme. Seed yield is the product of interaction of component traits.

In the present study, path coefficient analysis revealed that 100 seed weight had highest direct effect on seed yield per plant followed by number of pods per plant, days to maturity, plant height and number of secondary branches per plant. These direct effects are mainly responsible for positive association of these characters with seed yield per plant. The direct effect of number of pods per plant on seed yield per plant was reported by the other workers namely Paliwal et al (1987) found that 100 seed weight had the highest positive direct effect on yield, followed by pods/plant seeds/pod and days to 95% maturity, Jeena and Arora (2002) biological yield exhibited highest positive correlation with seed yield coupled with highest positive direct effect on it, Mohammad *et al.* (2004) and Yucel *et al.* (2006) reported the direct effect of other characters on seed yield per plant.

Days to 50% flowering and number of seed per pod had negative direct effect on seed yield. The similar result was reported earlier by Zena *et al.* (2008) 50% flowerings period has shown negative direct effect on the yield of gram. Based on findings of the present investigations it could be enforced that the most desirable plant type in chickpea should possess more 100 seed weight (bold seeds), number of pods per plant, days to maturity, plant height, number of secondary branches per plant.

4.8 Genetic Divergence

Genetic divergence, which due to genetic factors, is the basis for heritable improvement. It’s always beneficial for the plant breeder when great amount of diversity in crop plants as it could serve as raw material for crop improvement programme to produce superior one. The precise information about the genetic divergence is therefore, crucial and beneficial for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants from the breeding material. Multivariate analysis as shown by Mahalanobis (1936) D^2 statistic's, is a measure that appraises the genetic diversity quantitatively among a set of genotypes.

4.8.1 Diversity

The estimates of D^2 values ranged from 5.02 to 14.65. This clearly indicates the presence of adequate diversity between genotypes studied. Gupta and Krishna (1995), Arun Kumar *et al.* (1998), Nimbalkar and Harer (2001), Sandhu *et al.* (2006), Parhe *et al.* (2014), Agrawal *et al.* (2018), Thakur *et al.* (2018) reported wide genetic diversity in chickpea germplasm.

4.8.2 Cluster Formation

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the information to breeder basis for selecting parents for hybridization programme. The theoretical concept behind such grouping is that the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to different clusters (Rao, 1952). Thus, crossing between the genotypes belonging to the same clusters would not give high heterosis so that the parents selected for crossing should be far from different clusters. Greater the divergence between the two clusters, wider is the genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.,* 1964). Therefore, while selecting the parents by considering the genetic diversity and per se performance and cluster mean for the characters also need due consideration in the crop improvement programme.

In the present investigation fifty genotypes were grouped into eight clusters. The cluster I was the largest cluster comprising of 19 genotypes, cluster IV was 11genotypes, cluster III with 9 genotypes and cluster VI with 7 genotypes. The clusters II, V, VII and VIII were solitary. The highest statistical distance (D=14.65) was found between the clusters III and VIII, followed by the cluster V and VIII (14.04) and cluster VI and VIII (11.86). This indicated that hybridization among the genotypes between these clusters would produce successful hybrids and desirable segregants in further generations. The intra cluster value was highest in cluster VI (D=6.59) followed by cluster IV (6.00), indicating that this cluster is more heterogeneous.

Jeena *et al.* (2005) grouped 80 genotypes into 11 clusters out of which in cluster I maximum of 60 genotypes were grouped. Durga *et al.,* (2005) studied genetic diversity in chickpea with 132 genotypes. The genotypes were grouped into nine clusters Cluster I was the largest, comprising of 20 genotypes, they recorded also Maximum intra - cluster distance was observed in cluster VI. Nimbalkar and Harer (2001) grouped 40 chickpea genotypes into 16 clusters; out of that, 10 were solitary. Suneeta Pandey (2016) conducted experiment in 100 genotypes were grouped into sixteen clusters. The cluster I consisted of maximum 29 genotypes,

Among these traits 100 seed weight showed highest per cent contribution towards diversity followed by days to 50 per cent flowering, plant height, number of seed per pod, number of secondary branches per plant, seed yield per plant, number of pod per plant, number of primary branches, whereas the traits days to maturity contributed least indicating not much variability among the genotypes was present for this trait. Nimbalkar and Harer (2001) reported maximum genetic divergence for plant height and 100 seed weight. Parhe *et al.* (2014) observed 100 seed weight, number of pods per plant and days to 50% flowering were contributed maximum in manifestation of genetic diversity. Gediya *et al.* (2018) observed the characters *viz.*, seed yield per plant, 100 seed weight, seeds per plant and pods per plant contributed much to the total genetic divergence.

4.8.3 Selection of Potent Parent

The success of any crop improvement programme involves selection of best parent. Among different approaches for selection of parents, selection based on diversity has its own significance, as diversity is a basic need of crop improvement programme. Therefore, in the present investigation diversity among different genotypes was studied, which yielded valuable information that could be useful in selection of potent parent for hybridization.

Arunachalam and Bandyopadhyay (1984) advised a method to delineate parental divergence into four divergence classes (DC). To take into account the variable magnitude of variation in parental divergence, the mean (m) and standard deviation (s) values of intra and inter cluster divergence (D) classes as below

DC 1 : D ≥ (m+s)
DC 2 : D < (m+s) and ≥ m
DC 3 : D ≥ (m-s) and < m
DC 4 : D < (m-s)

Experiment by them (two in groundnut and one in rapeseed) showed that the chances for occurrence of high frequency of heterotic crosses with high values of heterosis were more, when the parents were chosen to have their divergence in the interval, m-s and m+s, compared to the crosses between parents, whose divergence fall outside this interval i.e. those fall in DC 1 and DC 4.

In the present study, an attempt was made to classify the cluster combination into four divergence classes by following the above procedure. The statistical distance (D^2) given in Table 8, represents the index of genetic diversity among the clusters. The mean of eight clusters and 4 intra-clusters (as monogenotypic cluster II, V, VII and VIII had no intra cluster distance) was 8.52 and standard deviation 2.31. The minimum (X) and maximum (Y) values among these distances were 5.02 and 14.65, respectively. Thus, the divergence classes were as presented below.

Divergence Classes

DC 4		DC 3	DC2	DC1
↓	↓	↓	↓	↓
X	m-s	m	m+s	Y
(5.02)	(6.21)	(8.52)	(10.83)	(14.65)

Table 11. Distribution of different cluster combinations into four divergence classes based on D^2 values between them. (Cluster Combinations)

- Y (14.65)

DC 1
(III, V), (I, VIII), (III, VIII), (V, VIII), (VI, VIII),
(VII, VIII)

- m+s (10.83)

DC 2
(II, III), (II, V), (II, VI), (III, V), (III, VI), (III, VII),
(IV, V), (IV, VI), (IV, VII), (IV, VIII), (V, VII),
(VI, VII)

- m (8.52)

DC 3
(I, II), (I, III), (I, IV), (I, V), (I, VI), (I, VII),
(II, IV), (II, VII), (II, VIII), (V, VI), (VI, VI)

- m-s (6.21)

DC 4
(I, I), (III, III), (IV, IV)

- X (5.02)

Grouping of cluster pairs into the divergence class (DC) are presented in Table 11. On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC 2 and DC 3. While crossing among the genotypes of a cluster, the *per se* performance of the genotypes for different trait such as early maturity, number of secondary branches, seed yield per plant, number of pods per plant, number of seed per pod and 100 seed weight etc. should be taken into account. So, that desirable transgressive segregants would be obtained after hybridization. Keeping in view all the above aspects and considering the inter-cluster distance, cluster mean and *per se* performance of genotypes and divergence class, the genotypes listed in Table 12 may be utilized in future breeding programme for creating maximum spectrum of variability for different yield contributing characters, which would help in developing superior genotypes with high yield and desired traits.

Table 12. Suggested parents for crossing programme for specific traits improvement

Sr. No.	Characters to be Improved	Cluster Combination	Possible crosses
1.	Number of secondary branches per plant	(I, IV) (IV, VI)	NBeG-857 × DC-17-1115 DC-17-1115 × RG-2016-134
2.	Number of pods per plant	(I, III) (III,VI)	Phule G-1107-275 × DBGV-217 Phule G-1107-275 × GBM-2
3.	Number of seed per pod	(IV, VI) (I, IV)	RVSSG-68 × GBM-2 DBGV-217 × RVSSG-68
4.	100 seed weight	(I, VI) (IV, VI)	DBGV-217 × GBM-2 DC-17-1115 × GBM-2
5.	Seed yield per plant	(I, VI) (IV, VI)	DBGV-217 × DC-17-1115 DC-17-1115 × GBM-2

5. SUMMARY AND CONCLUSION

The present investigation entitled, “Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)” was conducted during *rabi* season of 2019-20 to understand the direct and indirect effect of different characters on seed yield and study the nature and extent of genetic diversity and variability present among the genotypes for quantitative and qualitative characters in chickpea.

Fifty genotypes of chickpea were evaluated in a randomized block design with two replications. Nine characters were studied *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seed per pod, 100 seed weight (g) and seed yield per plant (g). The results obtained are summarized and conclusions were drawn as below.

5.1 Variability and Genetic Parameters

Sufficient variability was present among the genotypes studies for all the characters. Number of pods per plant exhibited highest range of variability followed by plant height, 100 seed weight, days to maturity and seed yield per plant showed considerable amount of variability. The variability was lowest for number of seed per pod followed by number of primary branches per plant, number of secondary branches per plant. The estimates of GCV and PCV for all the characters studied showed little difference the latter being slightly greater than the former, thus indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors. The character 100 seed weight and seed yield per plant exhibited highest estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) indicating good scope for their improvement through selection. High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of secondary branches, number pods per plant, 100 seed weight, days to 50% flowering and seed yield per plant suggesting that, these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection.

5.2 Correlation

Correlation studies at both genotypic and phenotypic levels were made to resolve the direction of magnitude of association among characters. The significant positive correlation was reported between seed yield per plant with number of primary branches per plant, number of secondary branches per plant, number of pods per plant and 100 seed weight. This indicate simultaneous improvement of these characters through selection whereas, days to 50%

flowering showed negative correlation with seed yields per plant at genotypic as well as phenotypic level indicates early genotype also produce higher grain yield.

5.3 Path Coefficient Analysis

Path coefficient analysis revealed that 100 seed weight had highest direct effect on seed yield per plant followed by number of pods per plant, days to maturity, plant height and number of secondary branches per plant. Therefore emphasis should be given on these characters while making selection for desired improvement for grain yield in chickpea. These traits also showed significant positive association with seed yield per plant. The number of secondary branches exerted its effect on seed yield through all characters suggesting that the indirect selection through such traits would be effective in yield improvement.

5.4 Genetic Divergence

The D^2 values showed adequate genetic diversity among the genotypes studied. On the basis of D^2 values all the genotypes were grouped into eight clusters with varying number of genotypes in the clusters. The maximum genetic distance (D) of 14.65 was found between the clusters III and VIII.

Cluster formation

A considerable inter-cluster variation was observed among the cluster means for the characters studied *viz.*, number of pods per plant, 100 seed weight and seed yield per plant. Cluster means for days to 50% flowering varied from 50.50 (III) to 61.50 (VII). The cluster mean for days to maturity ranged between 95.00 (VIII) to 108.00 (VII). The lowest cluster mean for plant height was (41.60) observed in cluster VII and highest for cluster VIII (67.65). The cluster mean for number of primary branches was ranged from (1.90) cluster VIII to cluster V (3.60). The cluster mean for secondary branches per plant ranged between 8.90 (VIII) to 15.30 (V). The cluster mean for number of pods per plant was observed maximum in cluster V (62.90) and it was observed minimum in cluster IV (45.39). The cluster mean for number of seed per pod was observed maximum in the cluster V (1.28) and minimum (1.00) in II and VIII cluster. The cluster mean values for 100 seed weight was maximum in the cluster V (26.82) and minimum (115.36) in cluster VIII.

Taking into account the cluster means for important yield components and inter-cluster distance the various clusters the following parents may be used in further hybridization programme, for yield improvement.

1.	NBeG-857	5.	Phule G-1107-275
2.	DC-17-1115	6.	RVSSG-68
3.	DBGV-217	7.	Phule Vikram
4.	GBM-2	8.	RG-2016-134

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7. VITAE

DESHMUKH NIRANJAN NAVANATH

MASTER OF SCIENCE (AGRICULTURE)
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Title of thesis		:	**“**Genetic Diversity and path coefficient analysis in Chickpea (*Cicer arietinum* L.)”
Major field		:	Genetics and Plant Breeding
Biographical Information		:	
Personal	**Date of Birth**	:	3 September 1996
	Place of Birth	:	A/P-Bhalawani, Tal-Pandharpur, Dist-Solapur
	Father’s Name	:	Deshmukh Navanath Murlidhar
	Mother’ Name		Deshmukh Vidya Navanath
Educational	**Bachelor Degree Obtained**	:	Loknete Mohanrao Kadam College of Agriculture, Kadegaon.
	Class	:	First class
	Name of University	:	Mahatma Phule Krishi Vidyapeeth, Rahuri
Address		:	A/P-Bhalawani, Tal-Pandharpur, Dist-Solapur
	Email- id	:	niranjandeshmukh799@gmail.com
	Contact Number	:	7350315726