“Genetic Divergence Studies in CHICKPEA (*Cicer arietinum* L.)’’

BY

SHAIKH ALTAF BABUBHAI

2018A12MB

SECTION OF AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

COLLEGE OF AGRICULTURE, BADNAPUR, DIST. JALNA

VASANTRAO NAIK MARATHWADA KRISHI VIDYAPEETH,

PARBHANI 431 402 (M.S.), INDIA

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"Genetic Divergence Studies in CHICKPEA (*Cicer arietinum* L.)''

DISSERTATION

Submitted to the

Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani

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(GENETICS AND PLANT BREEDING)

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2020

CANDIDATE'S DECLARATION

I hereby declare that this dissertation
Or part there of has not been
Previously submitted by me
For a degree of any
University or
Institute

Place: BADNAPUR

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Date: / / 2020

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CERTIFICATE - I

This is to certify that the dissertation entitled **"Genetic Divergence Studies in Chickpea [*Cicer arietinum* L.]"** submitted by Shri. **SHAIKH ALTAF BABUBHAI Reg. No. 2018A12MB** to the College of Agriculture, Badnapur in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** is record of original and bonafide research work carried out by her under my guidance and supervision. It is of sufficiently high standard to warrant its presentation for the award of the said degree.

I also certify that the dissertation or part there of has not been previously submitted for a degree of any university. The assistance and help rendered during the course of investigation and sources of literature have been duly acknowledged.

Place: BADNAPUR
Date: 8 / 12/2020

(D. K. Patil)
Research Guide and Chairman
Advisory Commitee

CERTIFICATE – II

This is to certify that the dissertation entitled **"Genetic Divergence Studies in Chickpea [*Cicer arietinum* L.]"** submitted by Shri. **SHAIKH ALTAF BABUBHAI Reg No. 2018A12MB** to the College of Agriculture, Badnapur in partial fulfillment of the requirement for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** has been approved by the student's advisory committee after viva-voce examination in collaboration with the external examiner.

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Place: Badnapur
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(Shaikh A. B.)
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Abbreviations

%	-	Per cent
/	-	Per
C.D.	-	Critical differences
Cm	-	Centimeter
d. f.	-	Degree of freedom
e.g.	-	Exampli gratia (For example)
et al.	-	Et alia (and others)
etc.	-	Et cetra
Fig.	-	Figure
Ha	-	Hectare
i.e.	-	That is
J.	-	Journal
Kg	-	Kilogram
M	-	Million
M / ha	-	Million per hectare
m2	-	Square meter
MS	-	Mean square
MSe	-	Error mean squares
MT	-	Metric Tonnes
q/ha	-	Quintals per hectare
Sci.	-	Science
SE	-	Standard Error
SE(d)	-	Standard error of difference
SE(m) ±	-	Stanadard error of mean
Sr. No.	-	Serial number
Unpub.	-	Unpublished
Viz.,	-	Videlicet (namely)
Vs	-	Versus
σ	-	Standard deviation
Σ	-	Summation

CHAPTER -I

INTRODUCTION

Chickpea (*Cicer arietinum* L.) belongs to the genus Cicer, family-leguminaceae. Chickpea is the self pollinated pulse crop having chromosome number 2n=14. Among the pulses, chickpea is important *Rabi* crop of India. It occupies the first position among the pulses grown in the country with maximum acreage and production in the world. In grain legumes, protein are an important seed component and are responsible for their relevant nutritional socio-economic importance. The chickpea seed is a good source of proteins and carbohydrate, which together constitute 80 % of the total dry weight of seed.

As per the World Health Organization (WHO) standard per capita per day availability of the pulses should be 80 g and according to the Indian Council of Medical Research (ICMR) is recommended 70 gram per day per capita, while at national level it is only 36 gram. Pulses are important source of protein in our country in vegetarian diet. The protein content of the pulses is two to three times more than that of cereals grains. Besides high protein content, pulses are also rich source of certain essential amino acids, which are lacking or very less in cereals. On the other hand, some of the sulphur containing essential amino acids i.e. metheonine, which lack in pulses are abundantly present in the cereals.

Chickpea seeds contain on an average of 23% protein, 64% total carbohydrates (47% starch, 6% soluble sugar), 5% fat, 6% crude fiber and 2% ash. It is also reported to contain high amount mineral content: phosphorus(P) (340mg/100g), calcium(Ca) (190mg/100g), magnesium(Mg) (140mg/100g), iron(F e) (7mg/100gm), zinc(Zn) (3mg/100gm) (Jukanti *et al*. 2012).

Chickpea are a nutrient-rich food, providing rich content (20% or higher of the Daily Value, DV) of protein, folate dietary fiber and certain dietary minerals, such as iron and phosphorus in a 100 gram reference amount. Vitamin B_6, thiamin, magnesium, and zinc contents are moderate, providing 10–16% of the Daily Value

(DV). Compared to reference levels established by the UN Food and Agriculture Organization and World Health Organization(WHO), proteins in cooked and germinated chickpeas are rich in essential amino acids such as lysine, isoleucine, tr yptophan, and total aromatic amino acids. A 100 gram serving of cooked chickpeas provides 164 kilocalories (690 kJ). Cooked chickpea are 60 percent water, 9 percent protein, 27 percent carbohydrates, and 3 percent fat 75 percent of the fat content is unsaturated fatty acids for which linoleic acid comprises percent of total fat (WHO).

The productivity of pulse crop continue to be very low as these crops are generally grown in rainfed area under poor management condition and face various abiotic and biotic stresses. Nutrient hungry and thirsty soil, inadequate seed replacement, socio-economic factors, in some cases high pest attack, unfavorable weather, non availability of quality seeds, poor post harvest handling and inadequate market support are some of the other constraints in realizing the potential of available technology. Beside of these factors, pulse crop have witnessed several technological milestones, which have helped not only to grain ground in new niches and in non – traditional cropping system but also made impressive productivity gains in their area of adaptation.

Pulses occupy unique position in Indian Agriculture because of their characteristics of maintaining and restoring soil fertility, besides high nutritive value. Pulses restore soil fertility through biological nitrogen fixation with the help of symbiotic bacteria *Rhizobium* in roots. Hence it fixes the high amount of nitrogen through environment. Among the pulses, chickpea is important *Rabi* crop of India. It occupies the first position among the pulses grown in the country with maximum average acreage and production.

India, a major pulse producing country, accounts roughly 33% of the total world production. Pulses are grown both during *Kharif* and *Rabi* seasons. Among the pulse, the chickpea is a important *Rabi* pulse crop of the India. Among all pulses chickpea contributes 36% area and 46% production in year 2017-2018. During 2017-2018 estimated area and production of chickpea in Maharashtra state

is 18.92 lakh ha and 17.61 lakh tons respectively. In Maharashtra, the highest chickpea was grown on 19.29 lakh ha with the highest production of 19.41 lakh tones during 2016-17. The productivity was highest during 2016-2017 (1006kg/ha).

In India percentage of area is increased upto 10.82% during year 2017-18 as compared to previous year while percentage of area decreased by 4.28% in Maharashtra. Maharashtra is having 14.57% contribution in the area with 13.51% production share in the nation. Madhya Pradesh state is having the highest area of 35.91 lakh ha, production 45.89 lakh tons and productivity 1279 kg/ha during the year 2017-2018. During 2017-18, the area in Maharashtra was 20 lakh ha with production of 17.59 lakh tons and productivity is 882 kg/ha. (Anonymous 2017).

In year 2018-19, Maharashtra was having 13.13 lakh ha area with production of 9.86 lakh tons productivity and 752 kg/ha is while Marathwada region is having 4.87 (36.21%) lakh ha area under chickpea, 2.88 (34.94%) tons production and 630 kg/ha productivity. In India chickpea is exported to countries like Algeria, Saudi Arab and Sri Lanka, Pakistan, Arab EMTS, gulf contries and however it is imported from Tanzania, USA Australia, Russia, and Canada. (Annonymous, 2018-19).

In year 2019-20, India was having 106 lakh ha area with production of 111 lakh tons with productivity1056 kg/ha while Maharashtra was having area 20.38 lakh ha with the production of 17.29 lakh tones and having productivity 848.55 kg/ha. Maharashtra occupying area about 19.22%, production 15.57%. Marathwada having 10.59 lakh ha area with the production of 7.96 lakh tones with the productivity of 760.54 kg/ha. (Annonymous, 2019-20).

Availability of sufficient genetic variability or diversity is very important in a crop improvement programme. For any successful breeding programme, amount of genetic variability present in the experimental material is a basic requirement for crop improvement. Therefore, it is essential for a plant breeder to measure the variability with the help of parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance.

Breeding new plant type is possible in wide spectrum of variability through various breeding methods. High amount of genetic diversity in genotype having high adoptability and when crossed high heterosis was observed in mostly. Recombination depends upon their recombination pattern and diverse genetic variability.

In plants, genetic diversity estimates the potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production altimately. The knowledge of genetic diversity helps in identification of gene stock, tagging of germplasm, and establishment of core collections (Upadhyaya *et al*. 2007). If the parents have diverse background selected for hybridization the more are the chances of improving the characters under consideration (Chowdhury *et al*. 2002).

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 particular characters which are to be improved is essential. Plant genetic resources or gene pool are the basis for global food security. They contain diversity of genetic material in traditional varieties, modern cultivars, currently cultivated varieties and crop wild relatives.

Mahalanobis's (1936) reported that D^2 statistics is a powerful tool for estimating the divergence between two populations. Many studies based on D^2 technique also indicated that geographical isolation is not necessarily related to genetic diversity. It thus gives better idea about the magnitude of genetic divergence and is independent of size of sample and provides the basis for selection of parental lines for further breeding programme for improving particular character.

Genetic variation for traits is important in breeding programmes for selecting desirable genotypes from population. On the other hand, an analysis of the correlation between seed yield and yield components is essential for determining selection criteria of a particular character. Path coefficient analysis may useful to determine the direct effect of traits and their indirect effects on other traits.

In plant breeding, correlation coefficient analysis measures the mutual relationship between various variables and determines the component characters on which selection can be based for genetic improvement in yield. Correlation coefficient is a statistical measure which is used to find out the degree (strength) and direction of relationship between two or more variables. The genotypic and phenotypic paths are commonly estimated to determine yield contributing characters which are mostly useful for plant breeders and geneticists in selection of elite genotypes from diverse genetic population for further improvement.

Genetic diversity among parents, which is heritable, is a pre-requisite for any successful breeding programme. The proper choice of the parents in the breeding programme is very importance in further study. Generally plant breeder selects the parents on the basis of phenotypic divergence, but for effective breeding, the knowledge of genetic diversity amongst the parents with respect to the characters which are to be improved is essential. The association of one or more characters influenced by a large number of genes is elaborated statistically by correlation coefficients. Genotypic correlation coefficient provides a measure of genotypes conjugation between characters. The method of partitioning the correlation into direct and indirect effects by path coefficients analysis was suggested Wright (1921). It provides useful information on the relative merits and demerits of the traits in the selection criteria.

In applied plant breeding, success of the programme may be depends on its genetic variability of different selection method is known. The correlation and path analysis provide information on genetic association of yield and different yield contributing characters, which in turn are useful in developing breeding strategies.

Keeping the above points, the present investigation was carried out with the following objectives:-

Objectives:

1) To study the genetic diversity in chickpea.
2) To study correlation and path analysis in chickpea.

CHAPTER-II

REVIEW OF LITERATURE

A comprehensive review of literature is an essential part of any scientific investigation. Review of literature is always necessary to compare the present findings with the previous studies undertaken by the research workers.

The literature pertaining to the present investigation on "Genetic Divergence Studies in Chickpea (*Cicer arientinum* L.)" has been reviewed under the following headings:

2.1 Genetic diversity

2.2 Correlation and path analysis.

2.1 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. It measures a generalized distance between any pairs of groups and classified the breeding material into useful groups. The genetic distance has a definite role in an efficient choice of parents for hybridization. Selection of parents based on the extent of genetic divergence has been successfully utilized by different workers in various crops. Genetic divergence is the genetic differences as observed between individuals and genetic stocks in respect to individual trait or array of traits. The inherent variations are called as genetic variations and produce genetic diversity and geographical diversity drastically.

Mahalanobis (1936) employed D^2 statistic in detailed study of anthropometric data of Uttar Pradesh classifying in 23 groups and into 3 major clusters that was Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising IX groups, the Artisan (A-cluster) in the middle consisting of IV groups and the Trival (T-cluster) at the 40 bottom consisting of X groups.

2.1.1 Genetic diversity in chickpea

Sivakumar and Muthiah (2000) studied genetic divergence among 126 chickpea genotypes consisting of 119 *desi* type and 7 *kabuli* genotype. The genotypes were grouped into seven clusters. Maximum intercluster distance was observed in the cluster IV and VII and the minimum between IV and V. The intracluster distance varied from 0 to 2.99. The maximum intracluster distance was in cluster I with 108 genotypes. The cluster III included *Kabuli* type quite diverse from *desi* types and this was again confirmed in the canonical root square analysis. *Kabuli* types possess genetic qualities as higher 100 seed weight more number of primary branches and upright compact habit. On the contrary *desi* types can contribute characters like more number of seeds per pod, pods per plant and drought resistance which were lacking in *Kabuli* types chickpeas.

Nimbalkar and Harer (2001) grouped 40 genotypes into sixteen clusters. D^2 values between all possible pair of 40 genotypes ranged from 12.62 to 3979.93. Out of sixteen clusters, ten were monogenotypic. Cluster II was the largest comprising of twelve genotypes followed by cluster I and IV containing nine and three genotypes, respectively. The genotypes of cluster XVI and cluster III were more divergent than others. Variance of cluster means indicated pods per plant followed by plant height and 100 seed weight (gram) were the main traits contributing to the genetic divergence in chickpea .

Gumber *et al.* (2002) studied thirty genotypes of chickpea and observed the highest heritability in pods per plant followed by secondary branches and 100 seed weight. The estimate of phenotypic coefficient of variation (PCV) was highest for grain yield and number of seeds per pod.

Kumar *et al*. (2002) studied 26 diverse chickpea genotypes for characters in randomized experiment. Significant variation for all traits was obtained. Phenotypic variability coefficients were higher than respective genotypic variability coefficients, indicating presence of environmental components. Pods per plant exhibited highest genetic advance under selection coupled with high variability and heritability.

Noor *et al.* (2003) reported phenotypic and genotypic variances, heritability in broad sense, genetic advance; correlation and path coefficient analysis for yield and yield components in thirty genotypes of chickpea under rainfed conditions. Medium to high genetic advance was observed for days to maturity, number of secondary branches, days to flowering, and 100 seed weight, whereas for other characters, low to medium heritability was observed along with low to high genetic advance. Improvement of these character through direct selection could be limited from germplasm used in the present study. It was concluded that to improve seed yield emphasis should be given on development of chickpea cultivar with higher seed weight and biological yield.

Jeena *et al*. (2005) recorded the observations on Eighty chickpea genotypes from different areas and diversity was recorded for 18 characters. The data was subjected to diversity analysis. Based on D^2 values Eighty genotypes were grouped into 11 clusters. The highest numbers of genotypes were observed in cluster I followed by cluster II.

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

Muhammad *et al.* (2008) experimented on chickpea and 20 elite chickpea lines were studied for variability for traits like number of days to flowering, number of days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height and seed yield per plant(gram). Varietal differences between the genotype were significant ($P<0.01$).

Dwevedi *et al.* (2009) conducted investigation among the 25 genotypes of chickpea to study the nature and magnitude of genetic variance using Mahalanobis's D^2 statistic. The data were recorded on 10 important quantitative traits from the genotypes raised in RBD having three replications. The twenty five chickpea genotypes were grouped into 6 clusters. Three characters *viz.,* 100 seed

weight, harvest index and number of pods per plant contributed maximum towards manifestation of genetic divergence. Number of pods per plant had maximum phen otypic and genotypic coefficient of variation, followed by biological yield per plant and 100 seed weight. They are recorded that the cluster I shows largest cluster with 8 genotypes. Highest inter cluster distance was observed between cluster III and cluster VI, followed by cluster I and cluster VI.

Alwawi *et al.* (2010) studied genotype - environment interaction and genetic parameters for days to maturity, seed yield per plant, protein content in chickpea. The results show that the heritability for protein content which indicated the presence of a considerable proportion of total variability due to genetic causes. A high genetic advance achieved for seed yield per plant. The environmental variance was very low for days to maturity and protein content. The differences between genotypic and phenotypic coefficient of variability was very small.

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

Sharma *et al.* (2010) estimated the twenty eight chickpea genotypes including check which revealed the presence of variability with high heritability for most of the yield and its components.

Akhtar *et al. (*2011) recorded genetic variability, heritability and interrelation ships for grain yield and its components in twenty advance genotypes of chickpea collected from various areas along with one check variety PB-2000. Significant and positive correlations were found between yield and number of pods per plant, 100-

seed weight and plant height. Heritability for 100-seed weight and number of pods per plant be the greatest compared to other traits. PCV for days taken to flowering, days taken to maturity, plant height and seed yield were higher than GCV.

Devendrappa *et al.* (2011) estimated that days to physiological maturity and seed yield per plant contributed maximum to the total diversity. Maximum inter-cluster distance was recorded between cluster VIII and cluster X followed by cluster IX and X provided maximum diversity between them.

Khan *et al*. (2011) recorded 47 genotypes of chickpea to study the nature and magnitude of genetic divergence. Highly significant differences were recorded between genotypes for days to 50% flowering, 100 seed weight, days to maturity, biological yield per plant and grain yield per plant. seed yield per plant had maximum phenotypic and genotypic coefficient of variation, followed by biological yield per plant.

Gaikwad *et al.* (2012) studied 40 different genotypes of chickpea (*Cicer arietinum* L.) obtained from the different areas and the analysis of variance for all the characters with all the genotypes show highly significant differences for all the characters except number of seeds per pod indicating the presence of considerable amount of genetic variation between the genotypes including in the study. The genotypic and phenotypic variances were higher for all the characters. The highest amount of genotypic coefficient of variation (GCV) was exhibited by seed yield per plant, number of pods per plant and 100-seed weight and number of secondary branches per plant.

Jadhav *et al.* (2012) estimated that days to maturity exhibited highest range of variability followed by number of pods per plant, number of seeds per pod, days to 50% flowering, 100 seed weight, harvest index, seed yield per plant, plant height and number of secondary branches per plant. Similar values for GCV and PCV was recorded for 100 seed weight, harvest index, seed yield per plant, number of seeds per pod, number of pods per plant, days to maturity, days to 50% flowering indicating these characters least affected by environment. High heritability with high genetic advance was observed for seed yield per plant, secondary branches per

plant, 100 seed weight and number of seeds per pod due to additive genetic effect.

Sewak *et al.* (2012) found that wide range of variability for both qualitative and quantitative traits. The diversity index indicated ample genetic variation for seed yield per plant in the present set of material. A direct selection criteria based on seed yield and component traits may be practiced to select better genotypes, which could be utilized for development of superior high yielding varieties.

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

Syed *et al.* (2012) studied genetic diversity of twenty seven chickpea genotypes through Mahalanobis D^2 and principal component analysis. The genotypes under study fall into 5 clusters. The cluster II contained the highest number of genotypes (eleven) and cluster I contained the lowest. Cluster I produced the highest mean value for number of pods per plant. The inter cluster distances was 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 andV.

Zeeshan *et al.* (2012) observed genotypic variability, heritability and correlati on of twenty chickpea genotypes for yield and its related traits under rainfed situations. High heritability for plant height and 100 seed weight coupled with high genetic advance revealed that additive gene effects were important in determining these traits. High heritability with low genetic advance for days to maturity indicated influence of dominant and epistatic genes.

Gul *et al.* (2013) studied twenty chickpea genotypes in which broad sense heritability estimates were highest for primary branches per plant, pods per plant,

100 seed weight, seed yield per plant and secondary branches per plant. Genetic advance were higher for seed yield per plant, pods per plant, primary branches per plant and secondary branches per plant.

Jain and Indapurker (2013) evaluated the nature and magnitude of genetic diversity using Mahalanobis D^2 statistics on the 30 genotypes of chickpea and these were grouped into 6 clusters. The cluster I shows largest cluster with 8 genotypes. The cluster VI was identified for pods per plant and seed yield per plant. Highest inter cluster distance was observed between cluster IV and cluster V, followed by cluster V and cluster VI.

Jeevani *et al.* (2013) evaluated the magnitude of genetic variability, heritability and genetic advance and genetic divergence using 105 diverse genotypes of chickpea. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the eleven traits. High heritability coupled with high genotypic coefficient of variation and high genetic advance as per cent of mean were observed for seed yield per plant, number of pods per plant biological yield per plant, harvest index and 100-seed weight which showed that response to selection would be very high for these yield contrubiting components.

Padmavati *et al.* (2013) tested thirty genotypes of chickpea in which wider genetic divergence with high heritability and high genetic advance has percent of mean was recorded for number of biological yield per plant, primary branches per plant and seed yield per plant.

Aarif *et al.* (2014) observed 22 genotypes of *kabuli* chickpea genotypes to assess variability, heritability, genetic advance, correlation and path analysis between yield and yield components. Among the different yield attributing traits, 100-seed weight had the highest magnitude of GCV, whereas- PCV was found to be high for 100-seed weight followed by seed yield per plant and secondary branches per plant. The correlation analysis showed that seed yield per plant showed a significant positive association with primary branches per plant, pods per plant, secondary branches per plant, biological yield per plant and harvest index;

and significant negative correlation with days to maturity at genotypic level. Path analysis for grain yield and its components showed that direct selection for biological yield per plant, harvest index, pods per plant and secondary branches per plant would likely to be effective in increasing seed yield in chickpea.

Chopdar (2016) evaluated twenty genotypes of chickpea with 3 replications and found that genotypic coefficient of variation (GCV) was high for seed yield per plant and 100 seed weight. 100 seed weight recorded highest heritability of followed by days to 50% flowering, seed yield per plant, days to maturity , biomass per plant, number of pods per plant and harvest index. It was showed that phenotypic selection would be more effective for improvement of seed yield per plant and 100 seed weight.

Alka Dev *et al*. (2017) studied 60 genotypes of chickpea in which the relative magnitude of difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low for number of pods per plant, number of seeds per pod, 100 seed weight, number of nodules per plant and days to 50% flowering indicating that these characters were less influenced by the environments. The estimates of broad sense heritability were highest for pod length, 100 seed weight, number of nodules per plant, days to 50% flowering and days tomaturity.

Ambilwade *et al*. (2018) estimated genetic divergence in chickpea germplam. The variation among genotypes were highly significant for plant height, number of primary branches per plant, days to 50% flowering, days to maturity, number of secondary branches per plant, pods per plant, number of seeds per pod and harvest index.

Kishor *et al*. (2018) studied genetic variability, heritability and genetic advance analysis in chickpea. Analysis of variance(ANOVA) showed highly significant differences among all twelve traits for days to 50% flowering, plant height, number of primary branches per plant, number of seeds per pod, harvest index, days to maturity, 100 seed weight and seed yield per plant indicating the presence of considerable variability among the all characters.

Peyman Sharifi *et al*. (2018) revealed that the extent of genetic diversity of 25 chickpea genotypes in an experiment carried out based on randomized complete block design with four replications at Brojerd Agricultural Research Station during two seasons of 2012-13 and 2013-14. The first three principal components explained 69.69% variation. 4 groups of characters were distinguished in regard to first and second principal components. Factor analysis indicated that three main factors accounted 69.69% of the total variability. Three first factors accounted for 33.69%, 20.82% and 15.19% of total variability.

Prince Raj *et al*. (2018) revealed that of variance were highly significant differences among the forty genotypes for all the characters studied indicating that significant amount of genetic variability present in the material. The cluster I had maximum elven genotypes followed by cluster VI, 08 genotypes, cluster III, 07 genotypes and IV having five genotypes, while cluster II and V had four genotypes, respectively. The cluster VII having one genotype. The intra cluster D^2 value ranged from 0.00 to 25.16 while, inter-cluster D^2 value ranged from 30.73 to 204.05. The maximum intra cluster distance was exhibited by cluster V followed by cluster I and cluster IV. The maximum inter-cluster distance was observed between cluster II and VII, followed by cluster II and V and cluster III and V.

Thakur *et al*. (2018) evaluated hundred genotypes in randomized complete block design with two replications showed highly significant differences among the genotype for all the characters studied *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total pods per plant, total number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and harvest index (%) indicating there by the wide range of genetic variability and scope of selection for these characters.

Renuka Shivwanshi and Anita Babbar (2018) assessed 434 germplasm lines of chickpea for thirteen quantitative characters. Genotypes were grouped into 14 clusters. Clusters II and cluster XIV and cluster XII and cluster XIV, had maximum inter cluster distance. The characters viz.,effective pods per plant followed by biological yield per plant, plant height and 100-seed weight were main contribution

to total diversity.

Warkad *et al.* (2018) recorded the data for ten characters to study genetic variability, heritability and genetic diversity. Analysis of variance among thirty five genotypes show highly significant difference. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was recorded for economical yield followed by biological yield and number of pods per plant. High heritability observed with high genetic advance were recorded for economical yield suggesting greater role of non-additive gene action in their heritance.

Aswathi P. V. *et al*. (2019) an conducted experiment to assess the genetic variability for quantitative and qualitative traits in 52 chickpea genotypes. The significant variation was observed for all the characters. High phenotypic and genotypic coefficient of variation was observed for plant yield followed by hundred seed weight, number of pods per plant, number of seeds per plant, number of secondary branches and first pod height.

Janghel D.K. *et al*. (2019) characterized the elite chickpea genotypes morphologically and classified them as per the guidelines for the conduct of DUS test of chickpea by the PPV&FRA, 2007, GOI. Among 13 DUS traits recorded; 7 traits were found tri-morphic, 4 traits di-morphic and 2 traits polymorphic among sixtee chickpea genotypes indicated the existence of remarkable amount of genetic variability that have great potential to assign distinctive morphological profiles which could be used for varietal identification and further characterization.

Nadiya *et al*.(2019) reported that indigenous chickpea accessions were only from three governorates viz. the highest of seven accessions seed accessions were diverse with respect to all seed characters studied, i.e. seed length (cm) and width (cm), 100-seed weight (gram) and seed color. Seed length varied from 0.645 cm to 1.210 and seed width ranged from 0.505 cm to 1.005 cm. 100 seed weight were found to vary from 12.6 to 67.9 gram. Chickpea accessions were classified into 5 groups with scores from 1 to 5 on the basis of simple 1 to complexity 5 of seed coat color pattern.

Ponnuru Akhil *et al*. (2019) studied 51 genotypes of chickpea including 1 check, these genotypes were obtained from Indian Institute of Pulses Research, Kanpur, U.P. The experiment was conducted during *Rabi*, 2018-19 at Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj in randomize block design (RBD) having 3 replications. The data was estimated on fifteen characters to study genetic diversity using Mahalanobis D^2 Statistics. Based on D^2 values, 51 genotypes were grouped into eight clusters. The cluster V consisted of maximum 18 genotypes, followed by Cluster VIII and cluster II, which had 11 and 9 genotypes, respectively.

Sneha Priya *et al*. (2019) in his divergence studies in 18 Extra-Large Seeded Kabuli genotypes done through Sequential agglomerative hierarchal nested cluster analysis of NTSYS-PC software indicated presence of considerable variability among the lines studied. Seed yield formed the primary divergent character for cluster formation and sub-grouping within a cluster followed the seed weight pattern. The clustering pattern grouped the genotypes into two major clusters and the ELSK genotypes PG4303 and KAK 2 of cluster 1 were most divergent to that of AP2 of cluster 2.

Shedge *et al*. (2019) reported that the genotypes under study fall into seven clusters. The cluster III was with the highest number of genotypes (11) followed by cluster II (10), clusters V (09), cluster VI (06) and IV and VII had one genotype. The maximum inter cluster distance (D =309.50) was observed between cluster VII and cluster V, while the minimum inter cluster distance (D = 41.46) was observed between clusters IV and II. Considering all the traits, it was suggested that the genotypes in clusters VII and cluster V are suitable for further breeding programme having most divergent.

2.2 Correlation coefficient

In the improvement of any crop, the knowledge of the association of one or more characters associated with yield is useful in selecting the individual. Such

association between plant characters is statistically elaborate by correlation coefficients, the correlation between the dependent and independent characters and the direct and indirect effects of the independent characters are completely separate parameters. Sometimes, the correlation between two characters may be highly positive but the direct effect of the independent characters on the dependent one may be negative. Therefore more correlation cannot be serve the purpose of selection in crop improvement programme.

Hence, the method of partitioning correlation coefficients into direct and indirect effects of the independent characters on the dependent characters i.e. path coefficient analysis was detailed by Wright.

Dewey and Lu (1959) gave the detailed procedure for path analysis of replicated trials which was most reliable technique in eliminating the environmental variance.

2.1.2 Correlation coefficient analysis in chickpea

Guler *et al.* (2001) examined five chickpea (*Cicer arientinum* L.) lines for relationship between the yield and yield components. In the present studied characteristics, significant positive relationship was found between the number of seeds per pod the number of pods per plant and seed yield. Significant negative relationships were determined between the number of pods per plant and 100 seed weight; between the number of seed yield per unit area and 100 seed weight. The total correlation coefficients of seed yield per plant and seed yield per unit area were 0.773 (77.3%) and 0.488 (48.8%) respectively. The total determining coefficient related to 100 seed weight was 0.896 (89.6%) in the same model.

Raval and Dobariyal (2003) evaluated genetic variability, interrelationships and path coefficients for thirteen components in a set of fifty genotypes of chickpea. The seed yield was positively and significantly correlated with biological yield per plant, number of pods per plant, 100 seed weight, harvest index, number of secondary branches per plant and plant spread both at genotypic and phenotypic levels, while correlation of seed yield with days to 50 % flowering, days to maturity and number of seeds per pod was negative and significant.

Arshad *et al.* (2004) reported that grain yield had positive and significant correlation with pods per plant, plant height, 100-seed weight and biological yield. High direct effects were contributed by biological yield and harvest index and the later had negative association with grain yield.

Renukadevi and Subbalakshami (2006) recorded numbers of branches and pods per plant had positive direct effects on the seed yield. Very low magnitude of residual effects indicates that the 11 characters had significant effects on the variability in grain yield.

Vaghela *et al.* (2009) evaluated correlation analysis which revealed that the magnitude of genotypic correlation coefficients (GCV) was higher as compared to their corresponding phenotypic correlation coefficients (PCV) for most of the characters. Seed yield per plant exhibited significant and positive correlation with harvest index, number of seeds per pod, biological yield, number of pods per plant, number of primary branches per plant and 100 seed weight at genotypic as well as phenotypic level.

Ali *et al.* (2010) studied the estimation of correlation for quantitative traits in chickpea and the studies showed that biomass per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod and 100 seed weight were positive and significant at genotypic level but positive and highly significant at phenotypic level whereas number of days taken to flowering, number of primary branches per plant, days taken to maturity, secondary branches per plant were positively correlated with the grain yield per plant at genotypic and phenotypic levels. Plant height was negative and non-significantly correlated with grain yield per plant at both genotypic and phenotypic levels.

Gohil and Patel (2010) studied twenty two genetically diverse genotypes of chickpea. The genotypic correlation coefficient were higher than corresponding phenotypic ones for most of the character combinations. Pods per plant and seeds per pod had a positive association with seed yield. 100 seed weight and harvest index had a significant positive association with seed yield. The maximum direct contribution to seed yield was observed from biological yield per plant and days to

maturity respectively.

Yucel and Anlarsal (2010) studied selection criteria by using correlation and path coefficient analysis in 22 genotypes of chickpea (*Cicer arietinum*L.) under Mediterranean conditions. In investigated characters, positive and significant relationships were found statistically among seed yield and harvest index and seed number.

Gaikwad and Monpara (2011) evaluated forty different genotype of chickpea obtained from the different locations were evaluated and correlation studies revealed that seed yield per plant exhibited highly significant positive association with number of pods per plant, 100 seed weight and secondary branches per plant at both the genotypic level and phenotypic level.

Zali *et al*. (2011) reported that association between genetic parameter and traits in chickpea genotypes with 17 chickpea genotypes. Number of seeds per plant and 100 seed weight had a positive direct effect on seed yield. Number of seeds per plant, number of secondary branches, 100 seed weight, number of pods per plant, number of primary branches and plant height also had positive and highly significant phenotypic correlations with seed yield.

Babbar *et al*.(2012) determined the seed yield per plant showed high significa nt positive correlation with total number of pods per plant, biological yield, total number of seeds per plant, plant height and 100 seed weight, whereas significant negative correlation with days to 50% flowering and damaged pod percentage.

Jha *et al.* (2012) reported highly significant and positive genotypic association between plant height, primary branches per plant and pods per plant and days to maturity, days to maturity and pods per plant, seeds per pod and days to 50% flowering, days to maturity and seed yield per plant and similarly 100 seed weight and grain yield per plant were found. Highly significant and negative genotypic correlation between primary branches per plant and plant height; primary branches per plant and pods per plant; seeds per pod and 100 seed weight; 100 seed

weight and days to 50% flowering were observed.

Kumar *et al.* (2012) reported that 100 seed weight followed by seed yield per plant and plant height shows high phenotypic genotypic and coefficient of variation.

Prakash (2013) reported that secondary branches per plant having significantly positive correlation with pods per plant seeds per pod and primary branches per plant. Days to 50% flowering with seeds per pod, days to maturity with plant height, seeds per pod with pods per plant and primary branches per plant and pods per plant with primary branches also showed significantly positive correlation. 100 seed weight had significant and negative correlation with seeds per pod.

Parhe *et al.* (2014) studied that correlation between yield components and their direct and indirect influences on seed yield of Chickpea. Seed yield was significantly correlated with characters, *viz.*,number of primary branches per plant, plant height, number of secondary branches per plant, 100 seed weight and number of pods per plant.

Samad *et al.* (2014) reported that the correlation, path coefficients and selection index in 8 irradiated chickpea lines for 11 quantitative characters to design the selection strategy towards yield. Genotypic correlation coefficients was higher than the phenotypic correlation coefficients. Seed weight per plant was positively correlated with number of primary branches at maximum flower, days to maximum flower , number of secondary branches at maximum flower, plant weight after fully dry, pod weight per plant and number of seeds per pod both at phenotypic and genotypic levels.

Ingle (2015) estimated genetic diversity analysis for yield and yield contributing traits in chickpea. Assessment of genetic divergence in existing and within germplasm groups for yield and its components to obtain superior recombinants which will help in understanding pattern of variability was performed utilizing the 60 genotypes and two standard checks of chickpea with two replications. In present study he found that number of seed per pod and 100-seed weight found to have a positive direct effect on seed yield. Number of seed per pod,

100- weight, number of pods per plant, number of secondary branches, number of primary branches and plant height also exhibited positive and highly significant phenotypic correlations with seed yield.

Nyende *et al.* (2015) found that the first 4 principal components explained significant proportion of the total variations which accounted for 77.04 percent. The first principal component was positively correlated with plant spread, plant height, number of primary and secondary branches per plant, days to flowering, days to maturity, pods per plant, pod length; biomass and seed yield. The presence of substantial genetic variations, positive and highly significant correlated characters can be exploited in breeding programmes for improvement of chickpea in the geographical region.

Chopdar *et al.* (2016) studied twenty genotypes of chickpea with three replications. He reported that seed yield per plant found to have highly significant positive correlation with primary branches per plant, number of pods per plant, harvest index, number of seeds per pod, biomass per plant and 100 seed weight respectively. The expression of yield depends upon a number of yield contributing character. The selection practiced for one character may bring change in the other related character.

Bhanu *et al.* (2017) reported positive significant relationship between seed yield number of secondary branches and number of primary branches and number of pods per plant. This results showed that any positive increase in such traits will improve the seed yield of chickpea crop. Since secondary branches plant seems to be an important yield component in present study this character shows positive correlation with seed yield plant, number of pods plant and number of primary branches. This showed that number of secondary branches would increase seed yield plant, number of pods plant and number of primary branches but with negative effect on hundred seed weight.

Shanmugam and Thiyaghajan *et al*. (2019) analysis of variance revealed significant variation existed for most of the traits. High genotypic coefficient of variation and phenotypic coefficient of variation was found for hundred seed

weight and plant height recorded high heritability with high genetic advance. Traits such as number of secondary branches, 100 seed weight, protein content, number of seeds per plant, biological yield per plant and harvest index exhibited significant positive correlation with seed yield per plant, where biological yield per plant followed by harvest index have positive and greater direct effects on single plant yield.

Shara (2019) estimated relationships among yield and some yield components using correlation and path coefficient analysis in chickpea growing under rainfed condition. The character seed yield showes positive and highly significant correlation with most characters including number of branches per plant, deep of roots, number of pods per plant, number of seeds per pod, plant height, 100 seed weight, dry mater weight, pod weight per plant, protein percentage and biological weight. Characters dry matter weight per plant recorded the highest positive direct effect on seed yield reached, while the maximum positive indirect effect on seed yield recorded by weight of pods per plant via dry matter weight per plant with.

Shedge *et al*. (2019) in his studies showed that the traits *viz.* harvest index, number of pods per plant, number of primary branches per plant, number of secondary branches per plant, days to 50% flowering, plant height, days to maturity, number of seeds per pod estimate positive and highly significant genotypic correlation with seed yield. This exibite that the contineous improvement of these characters through selection. Path coefficient analysis indicate that the characters *viz.* plant height and number of primary branches per plant exhibited negative direct effect on seed yield per plant.

2.1 Path coefficient analysis

The concept of path coefficient was formulated by Wright in 1921. The correlation coefficient is a resultant of all paths connecting two variables, so the direct influence of a variable can be measured along with a given path by standard deviation remaining in the effect after all other possible paths of influence are eliminated, while the variation of the causes back of the given path is kept as great

as ever regardless of their relations to other variables which have been made constant. Li (1956) focused on its importance and emphasized that practical implication of the method is greatly facilitated by formulation of a causal diagram.

2.1.1 Path analysis in chickpea

Muhammad *et al.* (2004) carried out correlation and path coefficient for yield and its components in chickpea and their direct effect on seed yield was exhibited by biological yield, harvest index, although the latter had a negative association with seed yield. Most of the yield components had high indirect contribution on seed yield through biological yield.

Talebi *et al.* (2007) studied correlation and path analysis of yield and yield components of chickpea under dryland condition. Thirty six genotypes were tested during the year 2005-06 for their yield performance. Harvest index have the greatest direct effect on seed yield. Also, its indirect effects on seed yield more positive through number of seeds per pod and biomass, but negative and low through days to maturity, plant height, number of pods per plant, 100 seed weight and number of primary branches. The selection for high seed yield should be based on biomass and harvest index.

Thakur and Sirohi (2009) estimated path analysis in chickpea and revealed highly positive and direct influence of biological yield per plant with seed yield per plant, harvest index and pods per plant in individuals as well as combined over seasons. Hence, selection of high biological yield and harvest index would lead to high seed yield and selection for pods per plant, primary branches per plant and plant height would facilited for high biological yield and seed yield.

Ozveren *et al.* (2010) assessed an experiment to determine selection criteria by using correlation and path coefficient analysis in twenty two genotypes of chickpea under Mediterranean region. The path coefficients analysis based on seed yield, as a dependent variable, revealed that harvest index had the greatest direct effect on seed yield with the ratio of 56.04%. Both correlation and path analysis indicated that harvest index was the major direct contributor to seed yield.

Gaikwad and Monpara (2011) studied 40 different genotype of chickpea obtained from the different locations were evaluated and path coefficient analysis indicated the highest and positive direct effect was recorded by number of pods per plant and 100 seed weight. Positive but low direct effect was exhibited by the days to 50% flowering, number of seeds per pod, number of primary branches per plant, protein content and reaction to insect pest. Based on these findings, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and days to 50 percent flowering and plant height were important traits which contributed toward higher seed yield.

Zali and sabaghpour (2011) reported that number of seeds per pod and 100-seed weight have a positive direct effect on seed yield. Stepwise regression analysis indicated that number of seeds per pod and 100-seed weight contribute 96% of total yield variation. It can be concluded that seed yield in chickpea can be improved by selecting an ideotype having greater number of secondary and primary branches, as well as higher number of pods per plant, 100-seed weight and number of seeds per pod.

Kumar *et al.* (2012) studied the genetic variation, character association and path analysis in early segregating population in chickpea. Path analysis indicated that plant height, days to 50% flowering and number of pods per plant had high direct effect on seed yield at both genotypic levels and phenotypic levels.

Mushtaq *et al.*(2012) investigated the variability parameters and path coefficient analysis in 20 elite chickpea genotypes including three standard checks. Investigations regarding path coefficient showed that days to flowering had maximum direct influence on seed yield per plant followed by total weight of plant, 100 grains weight, primary branches and plant height.

Jivani *et al.* (2013) was used 105 diverse genotype of chickpea to estimated correlation and path analysis for grain yield and observed seed yield per plant have maximum direct effect with harvest index followed by number of pods per plant biological yield per plant, and 100 seed weight.

Muhammad *et al.* (2013) assessed that the seed yield was positively correlation with all attributes under study. Investigation regarding path coefficient reviled that days to 50% flowering and maximum direct influence on seed yield per plant followed by 100 seed weight, total weight of plant, primary branches and plant height.

Puri *et al*. (2013) estimated path coefficient analysis of various characters towards 100 seed weight observed that the maximum positive direct effect on 100 seed weight was exhibited by biological yield and days to 50% flowering.

Hasan and Deb (2014) studied that the direct and indirect effects and selection index in 8 genotypes of chickpea reported that number of seeds per pod had maximum positive direct effect on seed yield followed by days to first flower and plant height at first flower at genotypic level while at phenotypic level, plant height at maximum flowers have the highest positive direct effect on yield followed by plant weight at harvest and number of pods per plant. These results confirmed that the characters had maximum contribution in determining seed yield. Seed yield have correlation with traits, *viz.*, secondary branches per plant, plant height, number of primary branches per plant, number of 100 seed weight and number of pods per plant.

Parhe *et al.*(2014) studied correlation between yield components and their direct and indirect effect on seed yield of Chickpea. Path coefficient analysis revealed that number of pods per plant, 100 seed weight and number of secondary branches per plant had the highest positive direct effects on seed yield. Improvement of the grain yield can be immensely efficient via number of primary branches per plant, 100 seed weight, number of pods per plant and number of secondary branches per plant on the basis of selection.

Samad *et al.* (2014) recorded the correlation, path coefficients and selection index in 8 irradiated chickpea lines for 11 quantitative characters to design the selection towards the higher yield. Genotypic correlation coefficients was higher than the phenotypic correlation coefficients. Seed weight per plant was positively correlated with days to maximum number flower, number of primary branches at

maximum flower, number of secondary branches at maximum flower , plant weight after fully dry, pod weight per plant and number of seeds per pod both at genotypic level and phenotypic level.

Chopdar (2016) studied that positive direct effect on grain yield per plant was exhibited by primary branches per plant, day to maturity, harvest index and protein content. Among these all characters, harvest index showes the highest positive direct effect on seed yield. Harvest index also having positive indirect effect on grain yield per plant through number of seeds per pod followed by biomass per plant and number of primary branches per plant. This completely showed that while selecting for high grain yield, emphasis should be given on those characters which showed high direct positive effect with positive correlation with seed yield.

Sohaib *et a*l. (2016) studied harvest index and number of seeds per pod have the significant and positive association with seed yield. The path analysis was done by using seed yield as dependent variable, that maximum positive direct toward seed yield was by number of pods per plant with 52.87% ratio. Correlation coupled with path coefficient analysis revealed that number of pods per plant had a direct effect with seed yield.

Alkadev *et a*l. (2017) estimated that days to 50% flowering, harvest index, number of seeds per pod and number of pods per plant showed high and positive direct effect on grain yield per plant. All these traits turned out to be the major component of seed yield. Positive moderate direct effect was observed for number of primary branches per plant whereas, negative effect was observed for days to maturity in estimation.

Bhanu *et a*l. (2017) studied the direct and indirect analysis clearly showed that days to maturity had indirect negative effect on yield plant through plant height ,days to maturity and number of seeds pod. The positive indirect effect of plant height on yield plant was through days to flowering, seeds per pod and secondary branches but have negative indirect effect on yield plant through days to maturity and harvest index(%). High indirect effects of harvest index, plant height and number of secondary branches through pods plant on seed yield indicate that the

selection of genotypes having more number of pods plant will be effective for breeding.

Thakur *et a*l. (2018) reported that highest positive direct effect to seed yield per plant was recorded by harvest index followed by primary branches per plant, plant height, biological yield, pods per plant, days to 50% flowering. Whereas, negative direct effects on grain yield per plant was observed due to 100 seed weight and days to maturity.

Singh *et a*l. (2018) studied path coefficient analysis on the seed yield per plant, as a dependent variable, showed that all of the other traits, excluding days to flowering, first pod height and total pod number, revealed high positive direct effects. Number of seeds and full pods showed the highest direct influence. Therefore, this research showed that seed and full pod numbers can be good selection criteria for improving seed yield per plant in chickpea(*Cicer arietinum* L.).

Manasa *et al*. (2019) evaluated 30 kabuli chickpea genotypes in a RBD with three replications. Traits association analysis revealed that number of secondary branches per plant, number of pods per plant shoot biomass per plant and harvest index showed highly significant and positive correlation with seed yield per plant. Path analysis also revealed that among correlated traits, harvest index and shoot biomass have high direct effect on grain yield per plant. therefore, selection would be more effective through harvest index and shoot biomass to improve seed yield.

CHAPTER-III

MATERIALS AND METHODS

The present investigation entitled, "Genetic Divergence Studies in Chickpea **(***Cicer arietinum* L.)" was conducted at Agricultural Research Station, Badnapur, during *Rabi* season of 2019-20. The details of the materials used, methods adopted and statistical analysis followed during investigations are described below.

3.1 Materials

Experimental material comprising 40 germplasm lines with wider variability for different characters were studied including 4 checks (2 from ICRISAT and 2 from ARS Badnapur) at ARS Badnapur. Out of 40 genotypes 36 with 2 checks from ICRISAT, Hyderabad, and 2 checks from ARS, Badnapur. The list of genotypes is given in Table 1.

3.2 Experimental design

Thirty six genotypes of chickpea along with four standard checks *viz.* Akash (BDNG-797), Digvijay, NBeG-47, JG-16 were evaluated in randomized block design with two replications during *Rabi* season of 2019-20. Each genotype was sown in four rows of 4 m length with spacing of 30 cm between rows 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, 50 kg P_2O_5 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 is given after sowing.

Table 1. List of fourty genotypes of chickpea

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	ICCV181601	21	ICCV181101
2.	ICCV181602	22	ICCV181102
3.	ICCV181603	23	ICCV181103
4.	ICCV181604	24	ICCV181104
5.	ICCV181605	25	ICCV181105

6.	ICCV181606	26	ICCV181106
7.	ICCV181607	27	ICCV181107
8.	ICCV181608	28	ICCV181108
9.	ICCV181609	29	ICCV181109
10.	ICCV181610	30	ICCV181110
11.	ICCV181611	31	ICCV181111
12.	ICCV181612	32	ICCV181112
13.	ICCV181613	33	ICCV181113
14.	ICCV181664	34	ICCV181114
15	ICCV181667	35	ICCV181115
16	ICCV181668	36	ICCV181116
17	ICCV181673	37	ICCV181117
18	ICCV181674	38	ICCV181118
19	NBe G 47 (Ch)	39	JG 16 (Ch)
20	BDNG 797 (Ch)	40	DIGVIJAY(Ch)

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

3.4 Experimental details:

1) Design : RBD
2) No. of replications : Two
3) Treatments : 40(36 germplasm lines +4 checks)
4) Plot size : One row of 4 meter length
5) Spacing : 30 x 10 cm
6) Fertilizer dose : 25:50:00NPK (kg/ha)
7) Season : *Rabi*
8) Locations : Agricultural Research Station, Badnapur

3.5 Observations recorded

Five competitive plants per genotype were selected at a random for recording observations on following characters in each replication and average for each was worked out for statistical analysis.

1. Initial plant stand

The number of initial plant stand counted after 11-12 days after sowing and after germination in each plot and average number of Initial plant stand was calculate.

2. Days to 50% flowering

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

3. Days to maturity

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

4. Plant height (cm)

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

5. Number of primary branches per plant

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

6. Number of secondary branches per plant

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

7. Number of pods per plant

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

8. Number of seeds per pod

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

9. 100 seed weight (gram)

It was recorded by weighing randomly selected 100 seeds.

10. Seed yield per plant (gram)

The seed weight is obtained as a mean of five observational plants represent seed yield per plant.

11. Harvest index (%)

The harvest index was counted by the five randomly selected plants from the plot. it is in percentage estimated in percentage.

$$\text{Harvest index (\%)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.6 Statistical analysis

3.6.1 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).

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

Where,

$_i$ = 1, 2… ...G
$_j$ = 1, 2… .....R
Y_{ij} = Observation on i^{th}genotype in j^{th} replication
μ = General mean
G_i = Effect of i^{th}genotype
R_j = Effect of j^{th}replication
E_{ij} = Random error associated with Y_{ij} observation

ANOVA Table:

Source	Degree of Freedom	Mean of sum	expected Mean sum of squares
Replication	r-1	RMS	$б^2_e + {}_g б^2_r$
Treatment	g-1	GMS	$б^2_e + {}_r б^2_g$
Error	(r-1)(g-1)	EMS	$б^2_e$

Where,

r = Number of replications
g = Number of genotypes
$б^2_r$ = Variance due to replications
$б^2_g$ = Variance due to genotypes and
$б^2_e$ = Variance due to error

The genotype mean square (GMS) was tested against error mean square (EMS) by 'F' test for $n_1 = (g-1)$ and $n_2 = (r-1)(g-1)$ degrees of freedom, where, g = number of genotypes and r = number of replications. 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. × S.E.m

b. Estimation of mean and range

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

$$\overline{X} = \frac{1}{n} \sum_{i=1}^{n} X_i$$

Where,

$\overline{X}$ = Mean of character

$\sum X_i$ = Total of all the observations for character

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 using the respective mean squares from variance table (Johnson *et al.* 1955) as below.

Environmental variance (σ^2_e) = EMS

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

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficient of variation

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

i) Genotypic coefficient of variation (GCV)

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

Where,

σ^2_g = Genotypic variance and,

$\overline{X}$ = Mean of character

ii) Phenotypic coefficient of variation (PCV)

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

Where,

σ^2_p = Phenotypic variance and,

$\overline{X}$ = Mean of character

GCV and PCV estimates were classified as Low : < 10 per cent, Medium: 10 to 20 per cent and High: > 20 per cent.

e. Estimation of heritability (b.s.)

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

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} 100$$

Where,

h^2 = Heritability

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

f. Genetic advance (G.A.)

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

i) Genetic advance (G.A.)

$$G.A. = k \times \frac{\sigma^2_g}{\sigma^2_p} \times \sqrt{\sigma^2_p}$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

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

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

Where,

G.A. = Genetic advance

$\overline{X}$ = Character mean

GA (As percentage of mean) was classified as

Low : 10 per cent

Medium : 10 to 20 per cent s

High : > 20 per cent

3.4.2 Genetic divergence

D^2 analysis

The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1928, 1936) as described by Rao (1952). Analysis of variance for the individual character was worked out as per randomized block design analysis to test the significances of differences among the genotypes.The characters exhibited significant differences so all were used for further analysis of D^2 statistics. The analysis of covariance for character pair based on plant average was carried out (Cochran and Cox, 1957).

a. Wilk's criteria

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

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

Where,

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

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

The significance of Wilk's criteria (Λ) was tested by χ^2 as,

χ^2_{pq} = V = -m.log$_e$ (Λ)

Where,

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

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

p = Number of significant characters

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

K = Number of genotypes

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

The generalized distance between any two populations is defined as:

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

Where,

λij = Reciprocal matrix to the common dispersion matrix

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

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

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

$D^2 = \Sigma\Sigma$ Sij$\sigma i\sigma j$

Where,

Sij, σi, σj are the sample estimates of λij, σi and σj respectively, since this formula for computation requires 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, D^2 was calculated. Thus total 80(79)/2 = 3160 number of D^2 values were worked out.

d. Determination of population constellation

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

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

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

e. Average intra-cluster distances

The intra cluster distances were calculated as,

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

Where,

ΣDi^2 = Sum of distances between all possible combinations

n = Number of genotypes included in a cluster

f. Average inter-cluster distances

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

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

Where,

ni = Number of genotypes in cluster ‘i'

nj = Number of genotypes in cluster ‘j’

g. Cluster diagram

The intra and inter-cluster distances (D values) were obtained by taking square root of average D^2 values of respective groups.

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

3.6.3 Correlations

Analysis of covariance was carried out by taking two characters at a time. The genotypic co-variance was calculated as per Johnson *et al.* (1955) as below:

Source	Degree of Freedom	Sum of squares	Mean sum of squares	Expectation of mean sum of squares
Replications	(r-1)	RP	RMP	$COVe_{1.2+ g}COVr_{1.2}$
Genotypes	(g-1)	GP	GMP	$COVe_{1.2 + r}COV_{g1.2}$
Error	(r-1) (g-1)	EP	EMP	$COVe_{1.2}$

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

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

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

Where,

GMP = Genotypic mean sum of product

EMP = Error mean sum of product

r = Replication

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

The phenotypic correlation coefficient (r_p) was calculated as:

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

Where,

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

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

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

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

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

Where,

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

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

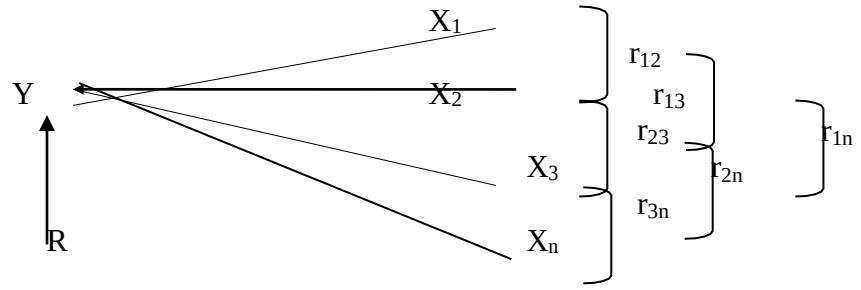
σ^2_{g1}, σ^2_{g} = Genotypic variance of character 1 and 2 respectively.

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

3.6.4 Path coefficient analysis

To establish a cause and effect relationship the first step used was 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 path analysis is to prepare path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X_1, X_2, X_3 and these component showed following type of association with each other.



In path diagram the yield is the result of X_1, X_2, X_3.....Xn and some other undefined factors designated by R. The double arrow lines indicated mutual association as measured by correlation coefficient. The single arrow represents direct influence as measured by path coefficient P_{ij}.

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

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

Where,

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

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

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

Matrix A Matrix B

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

Where,

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

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

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

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

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

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

Where,

i = 1 to 9

j = 1 to 9

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

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were diagrammatically presented. The residual factor i.e. variation in yield unaccounted for by these associations was calculated with the following formula:

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

Where,

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

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

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

CHAPTER - IV

RESULTS

The present investigation was undertaken with 40 germplasm lines of chickpea (*Cicer arietinum* L.) including four checks *Viz*, Digvijay, Akash, NBeG 47 and JG16. The objective of experiment was to study genetic diversity, correlation and path analysis for various traits in chickpea.

Eleven characters studied were subjected to analysis for various quantitative characters have been presented under the following major heading

1. Analysis of variance

2. Mean performance

3. Genetic diversity

4. Correlation

5. Path analysis

Analysis of variance

The variation among genotypes were highly significant for day to 50 % flowering, day to maturity, plant height, number of primary branches per plant, number of secondary branches per plants, number of pods per plant, number of seeds per pod, 100 seed weight, harvest index and seed yield per plant and non significant for initial plant stand (Table 4.1).

Table 4.1 Analysis of variance for ten quantitative characters in chickpea.

Sources of Variation	d. f.	Mean sum of squares										
		Initial plant stand	Days to 50 % Flowering	Days to maturity	Plant height	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight	Seed yield / plant	Harvest Index
Replications	1	10.78	4.51	16.20	1.12	0.00	16.56	258.40	0.0080	8.67	28.92	13.04
Genotypes	39	5.25	42.29**	37.50**	78.73**	2.25**	24.29**	1491.9**	0.20**	83.92**	103.7**	216.25**
Error	39	3.10	1.30	7.45	6.02	0.072	2.38	77.35	0.015	1.31	12.52	3.81

* -Significant at 5 % level of significance
**- Significant at 1 % level of significance

Table 4.2. Mean performance for eleven quantitative characters in fourty genotypes of chickpea

Sr No.	Name of genotype	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight (gm)	Seed yield / plant (gm)	Harvest index
1.	ICCV181667	28.50	72.00	129.50	65.50	4.30	13.25	123.40	1.90	16.00	28.00	34.03
2.	ICCV181605	27.75	74.00	128.50	52.30	3.45	14.95	96.31	1.40	23.55	21.98	22.97
3.	ICCV181608	25.75	72.00	129.50	57.00	3.20	10.50	109.60	1.30	22.52	26.78	47.07
4.	ICCV181673	29.12	72.50	124.00	65.85	5.60	15.15	113.90	1.00	16.43	18.03	42.14
5.	ICCV181611	29.50	74.00	130.50	69.50	4.40	18.20	118.40	1.70	24.32	34.55	52.83
6.	ICCV181603	28.87	70.50	128.00	68.10	5.00	18.65	74.85	1.00	24.25	21.49	52.25
7.	ICCV181118	29.75	64.00	126.00	55.95	3.30	12.55	146.80	1.70	18.88	22.47	30.90
8.	ICCV181602	27.00	61.50	121.50	60.10	4.55	20.90	103.00	1.75	26.52	27.73	40.99
9.	ICCV181606	26.50	70.00	126.00	60.10	2.20	13.30	74.10	1.45	23.35	19.33	48.69
10.	ICCV181612	26.50	65.00	130.00	70.95	3.60	16.05	109.90	1.00	16.12	19.63	48.48
11.	ICCV181604	27.75	74.50	124.00	52.95	1.35	17.70	102.75	1.00	15.44	18.81	39.99
12.	ICCV181610	25.50	75.00	128.50	53.05	3.45	17.10	88.40	1.00	19.60	20.36	52.30

Table 4.2. contd…….

Sr No.	Name of genotype	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branches / plant	No. of Secondary branches / plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight (gm)	Seed yield / plant (gm)	Harvest index
13	ICCV181664	26.50	74.50	129.50	64.75	2.95	14.70	70.05	1.30	23.03	18.26	52.29
14.	ICCV181607	28.87	72.00	132.00	58.55	2.80	16.95	69.30	1.55	28.26	20.44	52.98
15.	ICCV181609	25.50	72.00	132.00	61.45	1.70	13.60	59.50	1.65	20.96	19.36	51.12
16.	ICCV181113	27.50	67.00	123.00	47.90	3.20	14.60	92.60	1.70	19.07	27.42	65.24
17.	ICCV181613	25.50	74.50	127.50	58.45	2.90	18.50	90.85	1.00	18.67	16.16	42.42
18.	ICCV181601	29.00	73.50	126.00	59.28	2.25	16.30	65.10	1.00	25.17	19.75	48.22
19.	ICCV181668	27.25	73.00	123.50	58.70	1.00	7.20	76.75	1.30	34.87	26.90	43.47
20.	ICCV181674	27.50	63.50	130.00	62.50	2.95	11.95	68.90	1.00	31.95	25.90	46.59
21.	ICCV181108	23.50	70.00	133.50	63.65	2.00	13.40	96.55	1.90	33.46	27.27	55.91
22.	ICCV181114	25.37	61.00	122.00	57.00	3.05	12.45	110.25	1.00	35.84	37.39	57.36
23.	ICCV181111	27.50	62.50	129.00	53.75	2.75	15.55	110.50	1.00	26.76	24.12	48.93

Table 4.2. contd…….

Sr No.	Name of genotype	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height (gm)	No. of Primary branches / plant	No. of Secondary branches / Plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight (gm)	Seed yield / plant (gm)	Harvest index
24.	ICCV181116	26.00	69.00	129.50	55.75	3.60	18.50	130.00	1.60	18.16	22.34	27.78
25.	ICCV181102	27.00	69.50	128.50	62.97	1.80	12.95	110.25	1.00	29.33	27.86	37.10
26.	ICCV181115	27.50	64.00	126.00	46.70	2.05	10.10	52.25	1.00	45.28	23.43	73.78
27	ICCV181109	27.50	67.00	124.00	61.25	3.20	21.80	105.20	1.50	24.69	29.41	33.53
28	ICCV181103	27.50	68.00	118.00	59.20	2.60	15.00	90.00	1.50	24.11	25.81	52.51
29	ICCV181112	28.00	62.50	117.00	58.30	3.25	16.50	91.10	1.00	16.97	18.88	64.87
30	ICCV181107	26.50	70.50	120.50	61.60	2.90	24.50	90.35	1.25	26.78	31.85	43.67
31	ICCV181106	27.00	74.50	129.50	63.15	3.70	23.20	144.20	1.25	22.33	42.20	44.57
32	ICCV181117	28.87	63.50	132.00	43.60	1.90	12.75	143.10	1.15	26.70	30.47	36.11
33	ICCV181110	28.50	62.50	128.50	59.65	2.45	16.45	101.70	1.00	28.93	28.31	43.35
34	ICCV181105	24.75	75.00	135.50	62.00	2.25	15.75	101.70	1.75	29.39	30.68	38.55
35	ICCV181101	23.50	65.00	122.00	68.96	3.80	20.20	133.30	1.35	37.12	40.60	52.62

Table 4.2. contd…….

Sr No.	Name of genotype	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of Primary branchs / plant	No. of Secondary branches / Plant	No. of pods/ plant	No. of seeds/ pod	100 seed weight (gm)	Seed yield / plant (gm)	Harvest index
36	ICCV181104	28.87	63.00	119.50	67.22	4.50	24.50	91.65	1.00	24.69	21.33	36.40
37	Akash (ch)	30.25	65.50	129.50	52.05	3.75	14.20	78.30	1.70	21.95	32.53	39.15
38	NBeG 47 (ch)	25.37	72.50	131.00	66.20	1.00	13.00	80.45	1.00	28.77	20.05	59.51
39	JG-16 (ch)	25.37	73.50	126.00	55.45	1.75	18.75	130.95	1.00	19.96	27.52	51.40
40	Digvijay (ch)	26.50	72.50	122.00	54.30	2.05	20.05	149.00	1.80	23.51	48.54	54.51
	Mean	27.13	69.16	126.82	59.39	2.96	16.04	100.78	1.31	24.84	26.10	46.66
	CV %	4.49	1.65	2.15	4.13	9.10	9.63	8.72	9.46	4.61	13.56	4.18
	SE +/-	1.24	0.80	1.93	1.73	0.19	1.09	6.21	0.08	0.81	2.50	1.38
	CD 5%	3.56	2.31	5.52	4.96	0.54	3.12	17.79	0.25	2.31	7.15	3.95

A) Mean performance and the range of variability

The mean values of the genotypes for different characters studied are given in Table 4.2, while the estimates of range of variability are given in table 4.3

1) Initial plant stand

The variation in initial plant stand ranged between 23.50 for ICCV 181108 to 30.25 for check Akash. Mean value for this character was 27.13. the maximum initial plant stand is observed in check Akash (30.25).

2) Days to 50 per cent flowering

The variation in days to 50 per cent flowering ranged between 61.00 to 75.00 days. Genotype ICCV 181114 flowered in 61.00 days while highest days (75.00) were taken by ICCV 181105 and ICCV 181610. Mean value for traits to days 50% flowering was 69.16 days. The value of checks for days to 50% flowering is Aakash 65.50 days, NBeG 47 72.50 days, JG16 73.50 days and Digvijay 72.50 days. The genotype ICCV 181105 recorded highest number of days to 50% flowering i.e.75 days followed by ICCV 181610 75 days and ICCV 181106, ICCV 1811613 74.50 days.

3) Days to maturity

The variation in days to maturity ranged between 117.00 to 135.50 days. Genotype ICCV 181112 matured in least number of days (117) while ICCV 181105 matured very late (135.50 days). Mean value for this character was 126.82 days. The checks Akash, NBeG 47, JG-16 and Digvijay recorded 129.50, 131, 126 and 122 days respectively. The genotype ICCV 181112 recorded highest days to maturity of 135.50 days followed by ICCV 181105 135.50 days and ICCV 181108 133.50 days.

4) Plant height (cm)

The variation in plant height ranged between 43.60 to 70.95 cm. The plant height was maximum in case of ICCV 181612 (70.95 cm) while it was minimum in case of ICCV 181117 (43.60 cm). Mean value for this character was 59.39 days. The checks *viz.* Akash, NBeG 47, JG-16 and Digvijay had recorded 52.05, 58.45, 55.45 and 54.30 plant height (cm) respectively. While the genotype

ICCV 181612 recorded highest plant height 70.95 (cm) followed by ICCV 181611 69.50 (cm) and ICCV 181101 68.96 (cm) respectively.

5) Number of primary branches per plant

Number of primary branches per plant ranged from 1.00 (ICCV 181668 and check NBeG 47) to 5.60 (ICCV 181673). Mean value for this character was 2.96. The checks *viz.* Akash, NBeG 47, JG-16 and Digvijay had recorded 3.75, 1.00, 1.75 and 2.05 number of primary branches per plant, respectively. The genotype ICCV 181673 recorded highest number of primary branches per plant i.e. 5.60 followed by ICCV 18161613 5.00 and ICCV 181602 4.50.

6) Number of secondary branches per plant

Numbers of secondary branches per plant were minimum in case of ICCV181668 (7.20), while maximum in case of ICCV 181107 and ICCV 181104 (24.50) and mean value for this character was 16.04. Nineteen genotypes were found to have more number of secondary branches per plant than mean value. The checks *viz.* Akash, NBeG 47, JG 16 and Digvijay had recorded 14.20, 13.00, 18.75 and 20.05 number of secondary branches per plant, respectively. The genotype ICCV 181107 recorded highest number of secondary branches per plant i.e. 24.50 followed by ICCV 181105 24.50 and ICCV 181106 23.20.

7) Number of pods per plant

Number of pods per plant ranged from 52.25 to 149.00. The genotype ICCV 181115 recorded lowest, while Digvijay had maximum number of pods per plant. Twenty genotypes were with more number of pods per plant than the mean performance. Mean value for this character was 100.78. The checks *viz.* Akash, NBeG 47, JG-16 and Digvijay had recorded 78.30, 80.45, 130.95 and 149.00 number of pods per plant, respectively.

8) Number of seeds per pod

The lowest number of seeds per pod recorded was 1.00 while maximum seeds per pod were 1.90 (ICCV 181667&ICCV 181108) and the general mean value for this character was 1.31. The checks Akash, NBeG 47, JG-16 and Digvijay recorded number of seeds per pod i.e. 1.70, 1, 1 and 1.80 respectively. Genotype ICCV 181667 (1.90) and ICCV 181108 (1.90) were found superior than all four checks.

9) 100 seed weight (g)

The variation for 100 seed weight ranged between 15.44 g to 45.28 g. Genotype ICCV 181604 (15.44 g) was lowest while ICCV 181115 (45.28 g) with highest 100 seed weight and mean value for this character was 24.84 g. sixteen genotypes were with more 100 seed weight than the mean performance. The checks Akash, NBeG 47, JG16 and Digvijay had 21.95, 28.77, 19.96 and 23.51 g 100 seed weight respectively. The genotypes ICCV 181668, ICCV 181674, ICCV 181108, ICCV 181102, ICCV 181110, ICCV 181105, ICCV 181101, ICCV 181114 and ICCV 18115 were found superior than all four checks. The genotype ICCV 181115 recorded highest 100 seed weight i.e. 45.28 (gm) followed by ICCV 181101 37.12 (gm) and ICCV 181114 35.84 (gm) respectively.

10) Seed yield per plant (g)

The variation for seed yield per plant was ranged between 16.16 g and 48.54 g. The genotype ICCV 181613 had minimum seed yield per plant (16.16 gm) while Digvijay produced maximum seed yield per plant (48.54gm) and mean value for this character was 26.10 g. The checks Akash, NBeG 47, JG16 and Digvijay recorded 32.53 (gm), 20.05 (gm), 27.52 (gm) and 48.54 respectively.

11) Harvest Index (%)

The variation for harvest index ranged between 22.97% to 73.78%. The genotype ICCV 181605 showed lowest harvest index (22.97 %) while ICCV 181115 recorded highest harvest index (73.78%). Mean value for this character was 46.66%. The checks Akash, NBeG 47, JG16 and Digvijay had 39.15%, 59.51%, 51.40% and 54.51 harvest index respectively. The genotype ICCV 181115 recorded highest highest harvest index of 73.78(%) followed by ICCV 181113 65.24(%) and ICCV 18112 64.87(%).

B) Genetic variability

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (b.s.) and genetic advance as per cent of mean for the different characters studied are presented in table 4.3.

The magnitude of genotypic variance was highest for number of pods per plant (707.27) followed by Harvest index (106.21), Seed yield per plant (45.60), 100 seed weight (41.30) and Plant height (36.35). The phenotypic variance, ranged between 0.10 to 784.63. The pods per plant recorded highest phenotypic variance (784.63) followed by Harvest index (110.03), Seed yield per plant (58.13).

Table 4.3. Estimates of variability parameters for Eleven quantitative characters in chickpea

Sr. No.	Name of the characters	Range	σ^2g	σ^2p	GCV (%)	PCV (%)	h^2 (b.s.) (%)	G.A. % (5%)	G.A. % (1%)	G.A. as % of mean (5%)	G.A. as % of mean (1%)
1.	Initial plant stand	23.50-30.25	1.074	4.17	3.81	7.53	25.70	1.082	1.386	3.98	5.10
2.	Days to 50 % flowering	61.00-75.00	20.49	21.80	6.54	6.75	94.00	9.041	11.58	13.07	16.75
3.	Days to maturity	117.00-135.00	15.02	22.47	3.056	3.73	66.80	6.527	8.36	5.14	6.59
4.	Plant height	43.60-70.95	36.35	42.38	10.15	10.96	85.80	11.50	14.74	19.36	24.82
5.	Number of primary branches per plant	1.00-5.60	1.08	1.16	35.22	36.38	93.70	2.081	2.66	70.24	90.02
6.	Number of secondary branches per plant	7.20-24.50	13.55	15.93	22.94	24.88	85.00	6.99	8.96	43.58	55.85
7.	Number of pods per Plant	52.25-149.00	707.27	784.63	26.38	27.79	90.10	52.01	66.65	51.61	66.14
8.	Number of seeds per pod	1.00-1.90	0.094	0.10	23.33	25.18	85.90	0.585	0.74	44.54	57.08
9.	100 seed weight	15.44-45.28	41.30	42.61	25.86	26.27	96.90	13.03	16.70	52.46	67.23
10.	Harvest index	22.97-73.78	106.21	110.03	22.08	22.47	96.50	20.85	26.73	44.69	57.28
11.	Seed yield per plant	16.16-48.54	45.60	58.13	25.87	29.21	78.40	12.32	15.79	47.20	60.50

C) Genotypic and phenotypic coefficients of variation

Genotypic coefficient of variation (GCV) was highest for number of primary branches per plant (35.22%) followed by number of pods per plant (26.38%), seed yield per plant (25.87%) and 100 seed weight (25.86). Phenotypic coefficient of variation (PCV) was highest for number of primary branches per plant (36.38%) followed by number of pods per plant (27.79), seed yield per plant (29.21) and 100 seed weight (26.27).

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

D) Heritability, genetic advance and genetic advance as percent of mean

Maximum heritability was observed for 100 seed weight (96.90%) followed by Harvest index (96.50%), days to 50 % flowering (94.00%), number of primary branches per plant (93.70%), number of pods per plant (90.10%), number of seeds per pod (85.90 %), plant height (85.80%) number of secondary branches per plant (85.00%), seed yield per plant (78.40%), days to maturity (66.80%) and initial plant stand (25.70%).

The estimates of genetic advance ranged from 0.58% to 52.01% at 5% level of significance and 0.74% - 66.65% at 1% level of significance with the highest estimate in case of number of pods per plant (52.01%) and (66.65%), harvest index (20.85%) and (26.73 %), 100 seed weight (13.03%) and (16.70 %), seed yield per plant (12.32%) and (15.79%), plant height (11.50%)and (14.74%), days to 50 % flowering (9.04%) and (11.58 %), number of primary branches per plant (6.99 %) and (8.96 %), days to maturity (6.52%) and (8.36%), number of primary branches per plant (2.08%) and (2.66%), initial plant stand (1.08%) and (1.38%) and number of seeds per pod (0.58%) and (0.74 %) at 5% and 1% level of significance, respectively.

The estimates of genetic advance as percent of mean ranged from 3.98% to 70.24 % at 5 % level of significance and 5.10 % to 90.02 % at 1 % level of significance with the highest estimate in case of number of primary branches per plant (70.24%) and (90.02 %) followed by 100 seed weight (52.46%) and (67.23 %), number of pods per plant (51.61 %) and (66.14 %), seed yield per plant (47.20 %) and (60.50%), harvest index (44.69 %) and (57.28 %), of seeds per pod (44.54 %) and (57.08 %), number of secondary branches per plant (43.58 %) and (55.85%

) plant height (19.36 %) and (24.82 %), days to 50 % flowering (13.07 %) and (16.75 %), days to maturity (5.14%) and (6.59%) and initial plant stand (3.98%) and (5.10%) at 5% and 1% level of significance, respectively.

E) Genetic divergence

1) Mahalanobis's generalized distance (D^2)

Wilk's criterion showed significant differences between the genotypes for the pooled effect of the eleven characters studied. Hence, further analysis was done to calculate D^2 values for all the possible pairs of comparison among fourty genotypes. The calculated D^2 values ranged from 104.47 to 498.13.

Based upon the observations of eleven characters, the Mahalanobis's D^2 statistics was computed for all possible pairs of fourty genotypes in order to assess the genetic diversity present among the genotypes under study.

2) Clustering pattern of the genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values studied, are presented in Table 4.4.

These fourty genotypes were grouped into ten clusters. The cluster I was with the highest number of genotypes (22) followed by cluster IV (07), clusters VII (04). cluster II, III, V, VI, VIII, IX and X had one genotype.

3) Intra and inter cluster divergence

The average intra and inter cluster D^2 and D values are presented in Table 4.5 and Table 4.6.

The intra cluster distance (D^2) range from 104.47 to 183.14. The maximum inter cluster distance (D^2=498.13) was observed between cluster IX and cluster VIII, followed by cluster VII and II (D = 467.98), cluster VIII and cluster IV (D = 467.16), cluster VII and cluster IV (D = 424.41). The minimum inter cluster distance (D = 139.19) was between clusters II and I.

At inter cluster level, cluster IX and VII had the highest value which was followed by cluster VII and II.

Table. 4.4. Composition of fourty chickpea genotypes into different clusters by Tocher's method.

Cluster No.	No. of genotypes	Genotypes included in the cluster
I	22	ICCV181111, ICCV181110, ICCV181102, ICCV181674, ICCV181103, ICCV181608, ICCV181606, ICCV181109, ICCV181106, ICCV181107, ICCV181105, ICCV181607, ICCV181601, ICCV181611, ICCV181610, ICCV181613, ICCV181664, ICCV181609, ICCV181612, JG16, ICCV181603, ICCV181113.
II	1	ICCV181604.
III	1	ICCV181104
IV	7	ICCV181116, ICCV18118, ICCV181602, ICCV181605, ICCV181667, Akash (ch),ICCV 181673.
V	1	ICCV181668.
VI	1	ICCV18112
VII	4	ICCV181101, ICCV181114, ICCV181108, ICCV181115.
VIII	1	NBeG47(ch)
IX	1	ICCV181117
X	1	Digvijay(ch)

Fig. 1 Diagram showing formation of clusters by Tocher method

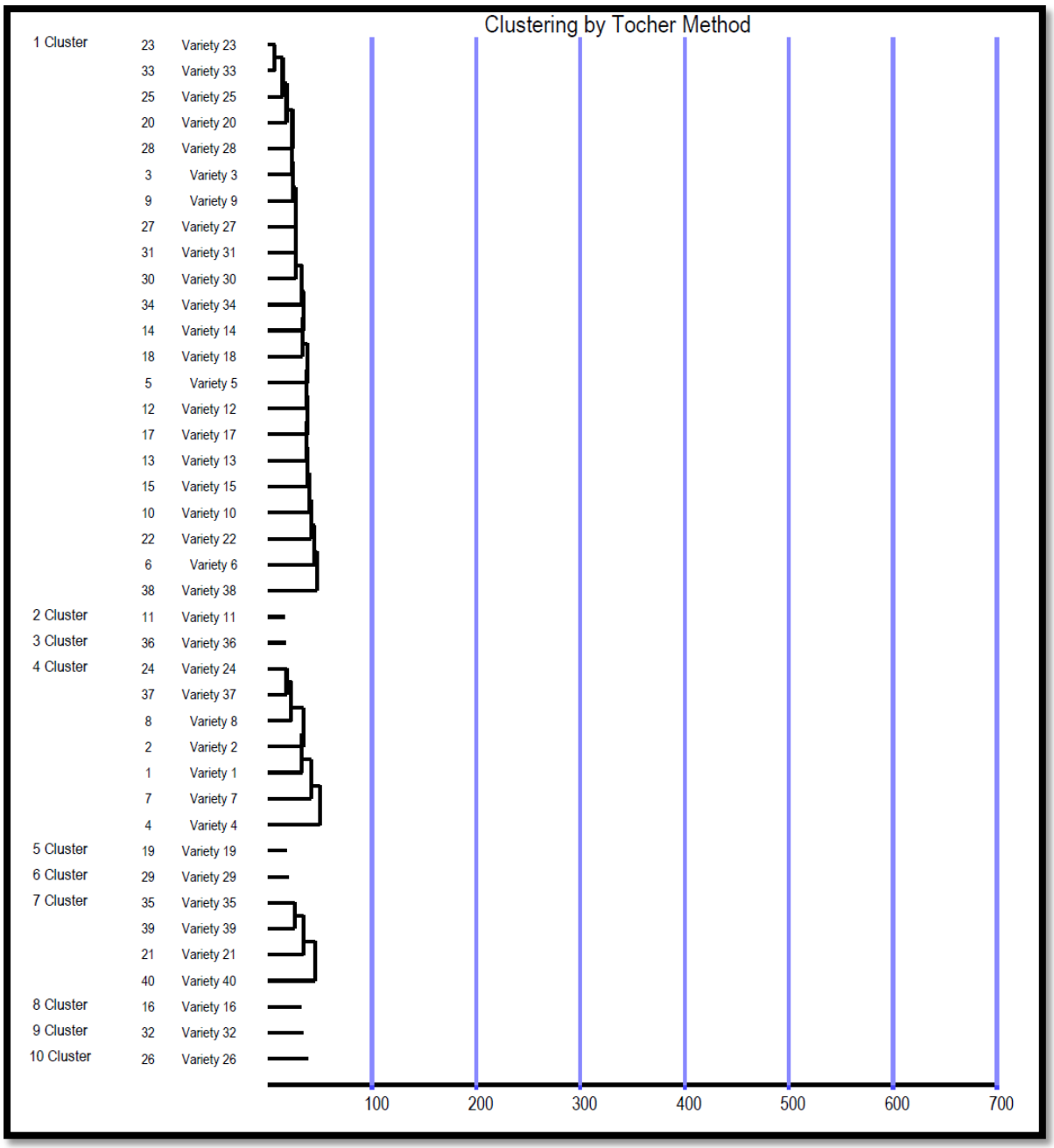


Table. 4.5. Average intra and inter cluster D^2 values in chickpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	104.47	139.19	152.71	201.97	185.52	170.71	264.99	165.71	315.65	221.91
II		0.00	193.08	243.12	295.48	161.72	467.98	207.89	364.64	232.80
III			0.00	139.63	354.74	164.07	355.71	364.64	302.76	313.80
IV				125.10	318.50	300.77	424.41	467.16	259.66	328.15
V					0.00	415.94	177.66	174.31	252.28	238.95
VI						0.00	361.19	243.54	411.17	251.29
VII							138.19	241.09	279.93	225.40
VIII								0.00	498.13	248.18
IX									0.00	183.14
X										0.00

Table 4.6 Average intra and inter cluster D values in chickpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	10.22	11.79	12.35	14.21	13.60	13.06	16.27	12.87	17.76	14.89
II		0.00	13.89	15.59	17.18	12.71	21.63	14.41	19.19	15.25
III			0.00	11.81	18.83	12.80	18.86	19.09	17.40	17.71
IV				11.18	17.84	17.34	20.60	21.61	16.11	18.11
V					0.00	20.39	3.65	13.20	15.88	15.45
VI						0.00	19.00	15.60	20.27	15.85
VII							11.75	15.52	16.73	15.01
VIII								0.00	22.31	15.75
IX									0.00	13.53
X										0.00

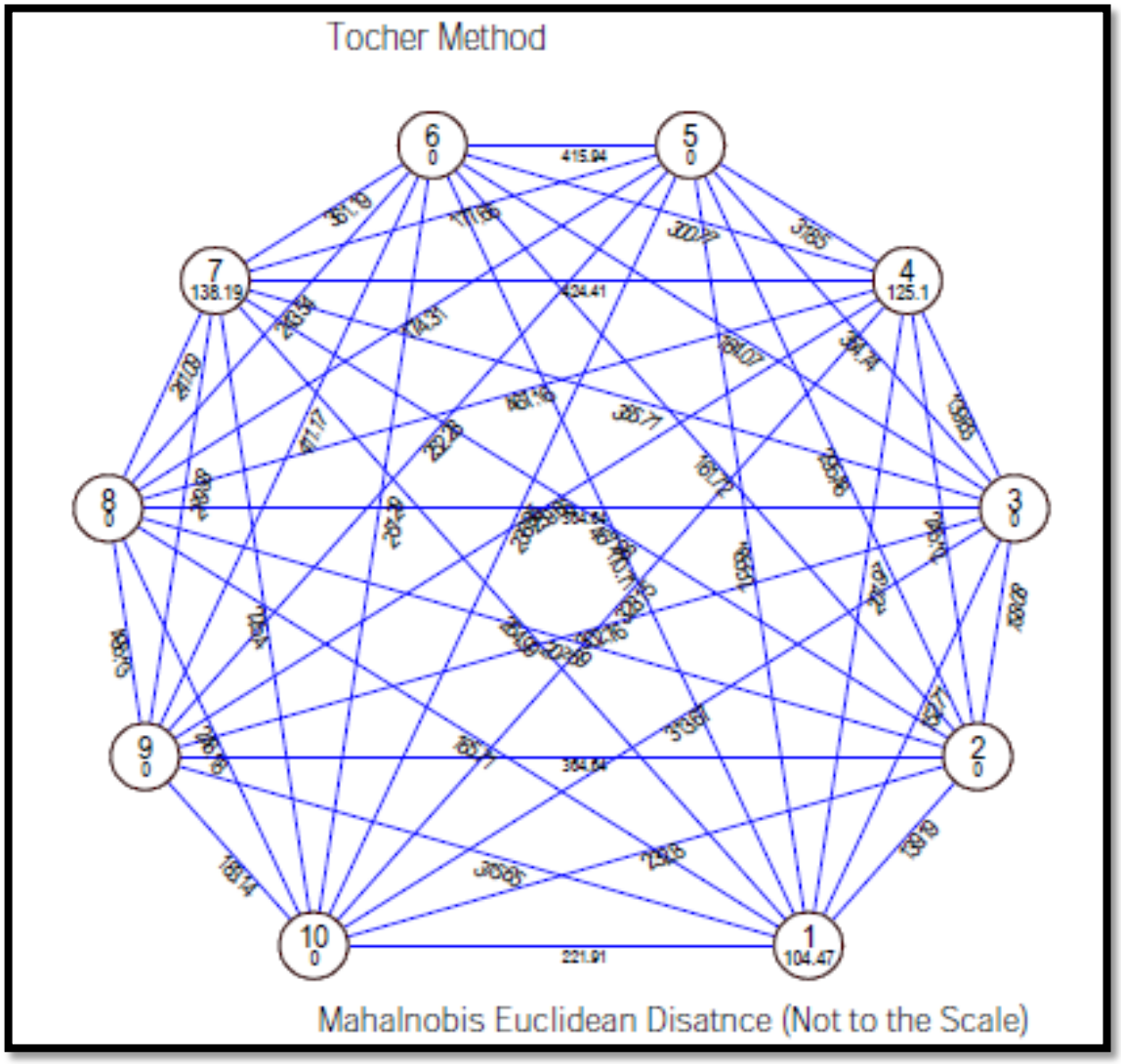


Fig.2 Diagram showing the cluster distance

4.4 Cluster means for different characters

The cluster mean for the eleven characters are presented in Table 4.7. A considerable inter cluster variation was observed among the cluster means for the characters studied *viz,* initial plant stand, 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, seed yield per plant, 100 seed weight and harvest index.

The cluster mean for initial plant stand varied from 24.97 (cluster VII) and 28.88 (cluster III&IX). The cluster mean for days to 50 per cent flowering varied from 62.50 (VI) to 74.50 (II). The cluster mean for days to maturity ranged between 117.00 (VI) to 132.00 days (IX). The highest cluster mean for plant height was 67.23 cm, which was observed in cluster (III) and lowest for (cluster IX) 43.60. The cluster mean for the number of primary branches per plant ranged from 1.00 (cluster V&VIII) to 4.50 (cluster III). The cluster mean for secondary branches per plant ranged between 7.20 (cluster V) and 24.50 (cluster III).

The cluster mean for number of pods per plant was maximum in cluster X (185.00) and it was minimum in cluster V (76.75). The cluster mean for number of seeds per pod was maximum in cluster X (1.80) and it was minimum in cluster II, III, VI, VIII (1.00).The cluster mean for 100 seed weight was minimum in cluster II (15.45) and it was maximum in cluster VII (37.93). The cluster mean for seed yield per plant ranged between (18.82) cluster II and (48.54) cluster X. The cluster mean for harvest index was maximum in cluster VI (64.88) % and minimum in case of cluster IV (34.00 %).

Table 4.7 Cluster means of different characters to genetic diversity in chick pea.

Clusters	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height	No. of pri. Branches/plant	No. of sec. branches/plant	Number of pods per plant	Number of seeds per pod	100 seed weight	Seed yield per plant	Harvest Index
I	27.03	70.30	127.82	60.48	2.91	16.56	94.38	1.27	24.07	25.33	47.92
II	27.75	74.50	124.00	52.96	1.35	17.70	102.75	1.00	15.45	18.82	39.99
III	28.88	63.00	119.50	67.23	4.50	24.50	91.65	1.00	24.69	21.33	36.40
IV	28.34	68.36	126.93	58.21	4.08	15.64	113.11	1.58	20.22	24.73	34.00
V	27.25	73.00	123.50	58.70	1.00	7.20	76.75	1.30	34.87	26.90	43.47
VI	28.00	62.50	117.00	58.30	3.25	16.50	91.10	1.00	16.98	18.89	64.88
VII	24.97	65.00	125.88	59.08	2.73	14.04	98.09	1.31	37.93	32.17	59.92
VII	25.38	72.50	131.00	66.20	1.00	13.00	80.45	1.00	28.78	20.05	59.52
IX	28.88	63.50	132.00	43.60	1.90	12.75	143.10	1.15	26.70	30.47	36.11
X	26.50	72.50	122.00	54.30	2.05	20.05	185.00	1.80	23.52	48.54	54.51

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 eleven characters studied, towards total divergence is presented in Table 4.8.

It was observed that, 100 seed weight (30.64 %) contributed highest for divergence. It was followed by harvest index (25.26 %), number of pods per plant(16.03%), number of primary branches per plant (8.85 %), days to 50% flowering (6.92%), seed yield per plant (4.74%), number of secondary branches per plant (3.72%), number of seeds per pod (2.18%), plant height (1.54 %), and days to maturity (0.13%).

Table 4.8. Per cent contribution of different characters to genetic diversity in chickpea

Sr. No.	Characters	No. of times appearing Ist in ranking	% contribution
1.	Initial plant stand	0	0
2.	Days to 50 % flowering	54	6.92%
3.	Days to maturity	1	0.13%
4.	Plant height	12	1.54%
5.	Number of primary branches per Plant	69	8.85%
6.	Number of secondary branches per Plant	29	3.72%
7.	Number of pods per plant	125	16.03%
8.	Number of seeds per pod	17	2.18%
9.	100 seed weight	239	30.64%
10.	Seed yield per plant	37	4.74%
11.	Harvest Index	197	25.26%
	Total	780	100%

F) Correlation studies

The genotypic and phenotypic correlations for yield and its component characters studied are presented in Table 4.9, 4.10 and Fig. 3 and 4. The only significant correlations either in positive or negative directions are described in this chapter. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients.

1) Association of seed yield with its components

Seed yield per plant had positive significant correlation with number of pods per plant (p=0.6197; g=0.6068), number of seed per pod (p=0.6197;g=0.3489), 100 seed weight (p=0.2979;g=0.3619), secondary branches per plant (p=0.2839; g=0.9968), harvest index (p=0.0371;g=0.0337) and number of primary branches per plant (p=0.0479;g=-0.0119).

2) Interrelationship of yield components

2.1) Initial plant stand

Initial plant stand showed significant and positive association with number of primary branches per plant (p=0.2741; g=0.5456).

2.2) Days to 50 per cent flowering

Days to 50 per cent flowering showed significant and positive association at both phenotypic and genotypic level with days to maturity (p=0.2952; g=5.7945), plant height (p=0.1272; g=0.8789), number of seeds per pod (p=0.1224; g=1.8154) and number of secondary branches (p=0.0471; g=0.0609).

2.3) Days to maturity

The characters *viz.* days to 50% flowering (p=0.2952; g=5.7945), number of seed per pod (p=0.1647; g=0.1913), plant height (p=0.0480; g=0.0643) and 100 seed weight (p=0.0169; g=0.0609) had significant and positive association with days to maturity at both phenotypic and genotypic level respectively. While it had the significant and negative association with number of secondary branches per plant (p=-0.2471; g=-0.4221).

2.4) Plant height

The character plant height had positively significant correlation with number of primary branches per plant (p=0.3489; g=0.3489), number of secondary branches per plant (p=0.2651; g=0.3084) and days to maturity (p=0.0480; g=0.0643), at both phenotypic and genotypic level respectively.

2.5) Number of primary branches with other characters

The number of primary branches per plant showed significant positive correlation at both phenotypic and genotypic level with number of secondary branches per plant (p=0.4017; g=0.3880), plant height (p=0.3489;g=0.3489), number of pods per plant (p=0.1612;g=0.1353) and initial plant stand (p=0.2741;g=0.5456). While it had the significant and negative relation with 100 seed weight (p=-0.3128; g=-0.2024) and 100 seed weight (p=-0.3128; g=-0.3211).

2.6) Number of secondary branches per plant

The number of secondary branches per plant showed significant positive correlation with number of primary branches per plant (p=0.4017; g=0.3880), number of pods per plant (p=0.3010; g=0.2704), seed yield per plant (p=0.2839;g=0.1784) both at phenotypic and genotypic level.

2.7) Number of pods per plant

The number of pods per plant showed highly significant positive correlation with seed yield per plant (p=0.6197;g=0.6068), number of secondary branches per plant (p=0.3010; g=0.2704) number of seed per pod(p=0.2115;g=0.2407) and both at phenotypic and genotypic levels while significant and negative correlation with 100 seed weight (p=-0.2565; g=-0.2465) at phenotypic and genotypic level.

2.8) Number of seeds per pod

The number of seeds per pod showed highly significant positive correlation with seed yield per plant (p=0.6197;g=0.3489) and number of pods per plant (p=0.2115;g=0.2407) and number of primary branches per plant (p=0.0860;g=0.1073) both at genotypic and phenotypic level.

2.9) 100 seed weight

100 seed weight showed significant positive correlation with harvest index (p=0.3322; g=0.3452), seed yield per plant (p=0.2979;g=0.3619) and negatively correlated with number of primary branches per plant (p=-0.3128; g=-0.3211) both at phenotypic and genotypic level.

2.10) Harvest index

Harvest index had significant positive correlation with harvest index (p=0.3322;g=0.3452) both at phenotypic and genotypic level. While significant and negative correlation with number of pods per plant (p=-0.3016;g=-0.3242).

Table 4.9. Estimation of phenotypic (above diagonal) correlation coefficients in chickpea.

Characters	Initial plant stand	Days to 50 % flowering	Days to maturiy	Plant height	Number of primary branches / plant	Number of secondary branches / plant	Number of pods / plant	Number of seeds / pod	100 seed weight	Harvest Index	Seed yield /plant
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
Initial plant stand	**1.0000**	-0.1518	-0.1192	-0.1080	0.2741 *	-0.0552	-0.0439	-0.0705	-0.2007	-0.1955	-0.1535
Days to 50 % flowering		**1.0000**	0.2952 **	0.1272	-0.1635	0.0471	-0.0265	0.1224	-0.2940 **	-0.0930	-0.0888
Days to maturity			**1.0000**	0.0480	-0.1408	-0.2471 *	-0.0422	0.1647	0.0169	-0.1576	-0.0505
Plant height				**1.0000**	0.3489 **	0.2651 *	-0.0380	-0.0023	-0.0404	-0.0395	-0.0108
No. of primary branches / plant					**1.0000**	0.4017 ***	0.1612	0.0860	-0.3128 **	-0.1992	0.0479
No. of secondary branches / plant						**1.0000**	0.3010 **	0.0063	-0.2531 *	-0.1741	0.2839
Number of pods per plant							**1.0000**	0.2115	-0.2565 *	-0.3016 **	0.6197
Number of seeds per pod								**1.0000**	-0.0887	-0.1682	0.6197
100 seed weight									**1.0000**	0.3322 **	0.2979
Harvest index										**1.0000**	0.0371
Seed yield /plant											**1.000**

***** Significant at 5 % level of probability or level of significance,

****** Significant at 1 % level of probability or level of significance

Fig. 3 Diagram showing the phenotypic correlation in yield and its component characters of Chickpea

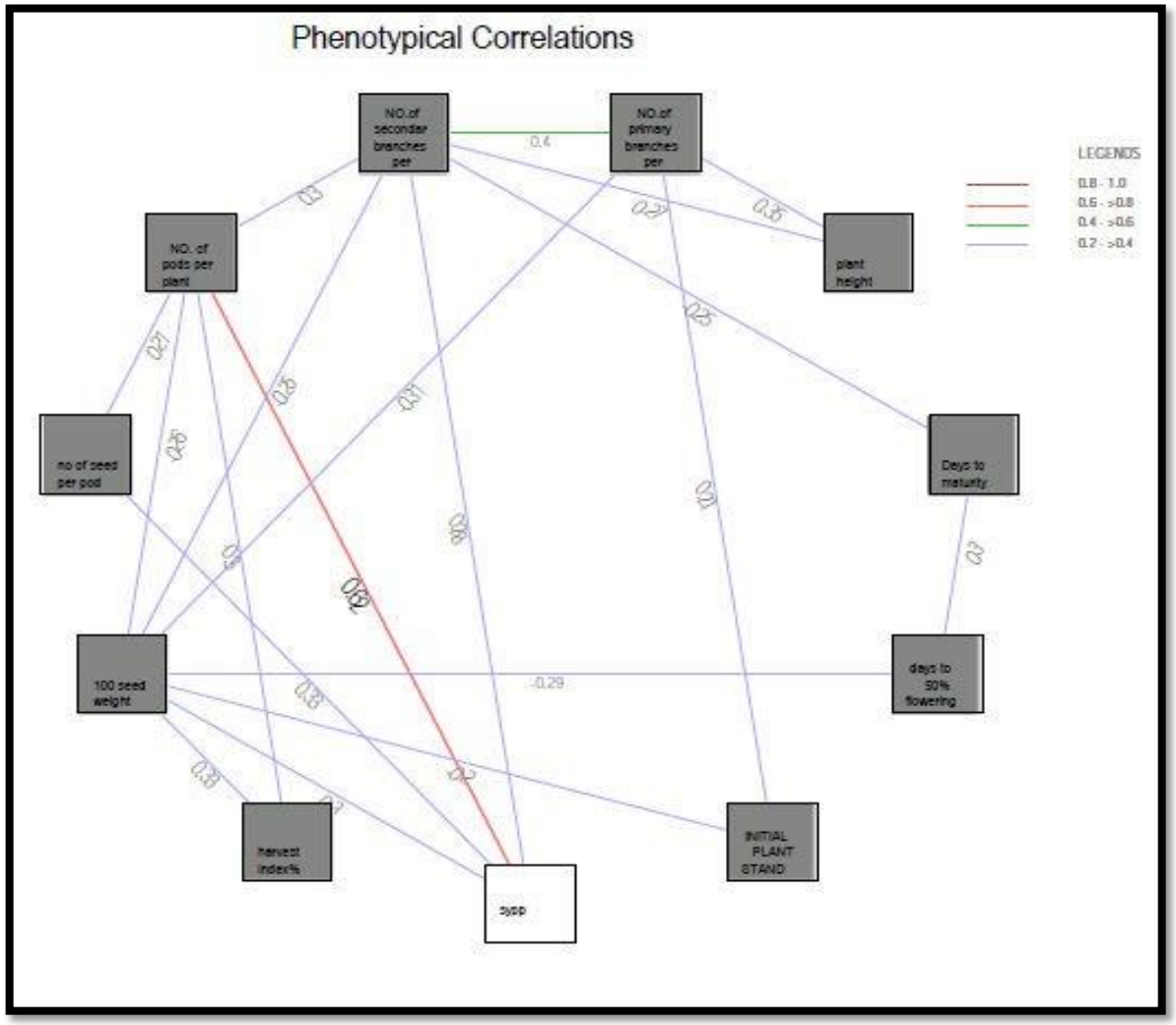


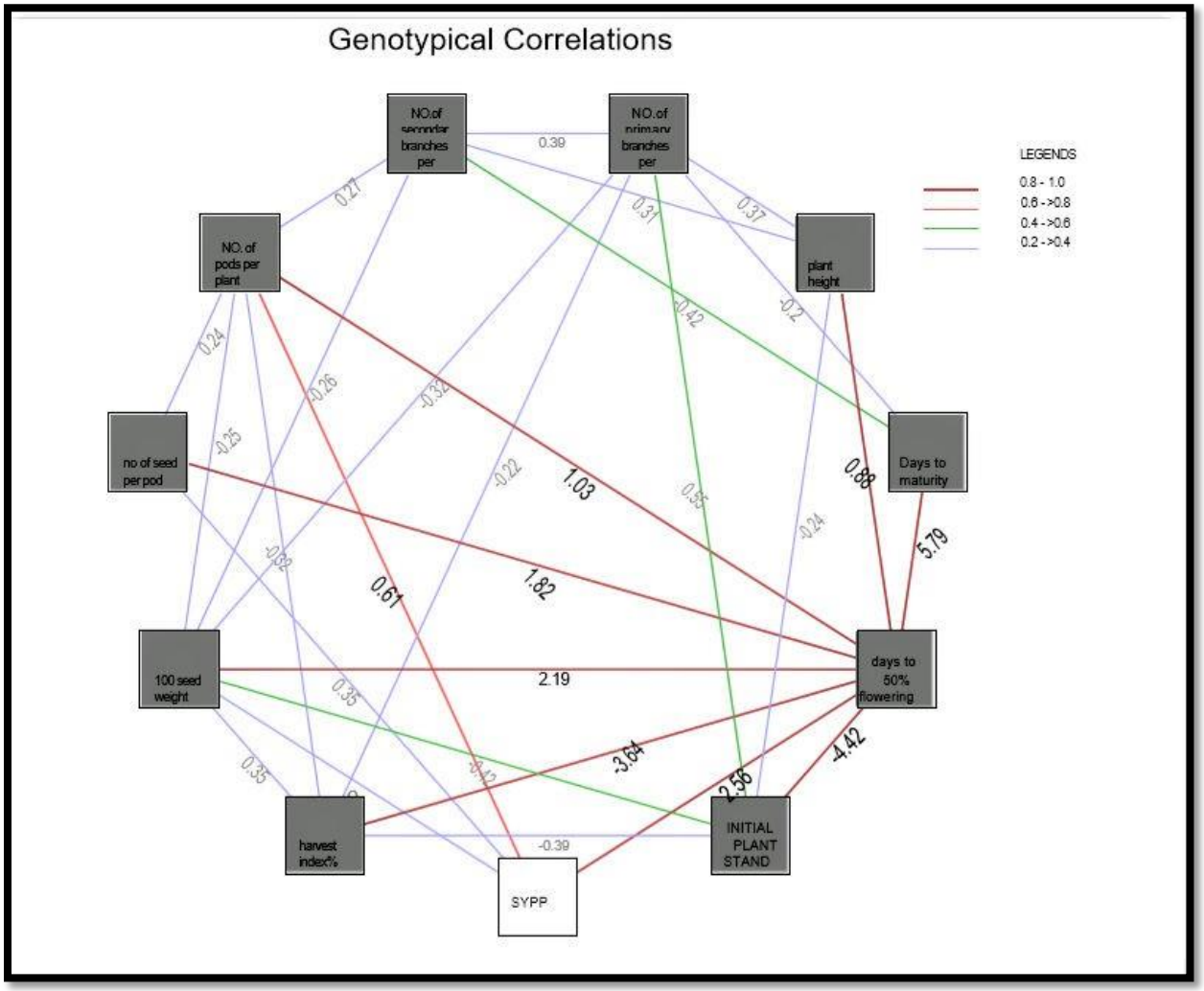
Table 4.10. Estimation of Genotypical (above diagonal) correlation coefficients in chickpea.

Characters	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height	Number of primary branches / plant	Number of secondary branches / plant	Number of pods / plant	Number of seeds / pod	100 seed weight	Harvest Index	Seed yield /plant
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
Initial plant stand	**1.0000**	-4.4232	-0.1271	-0.2382	0.5456	0.1222	-0.1064	0.0179	-0.4170	-0.3923	-0.1743
Days to 50 % flowering		**1.0000**	5.7945	0.8789	-0.1985	0.0609	1.0339	1.8154	2.1927	-3.6410	2.5584
Days to maturity			**1.0000**	0.0643	-0.2024	-0.4221	-0.1317	0.1913	0.0609	-0.1821	-0.1804
Plant height				**1.0000**	0.3489	0.3084	-0.0703	-0.0072	-0.0433	-0.0265	-0.0379
No. of primary branches / plant					**1.0000**	0.3880	0.1353	0.1073	-0.3211	-0.2193	-0.0119
No. of secondary branches / plant						**1.0000**	0.2704	-0.0130	-0.2626	-0.1761	0.1784
Number of pods per plant							**1.0000**	0.2407	-0.2465	-0.3242	0.6068
Number of seeds per pod								**1.0000**	-0.0951	-0.1882	0.3489
100 seed weight									**1.0000**	0.3452	0.3619
Harvest index										**1.0000**	0.0337
Seed yield per plant											**1.000**

***** Significant at 5 % level of probability or level of significance,

******Significant at 1 % level of probability or level of significance

Fig. 4 Diagram showing the genotypic correlation in yield and its component character of Chickpea



G) Phenotypic and Genotypic path coefficient analysis

To find out the direct and indirect contribution from each of the character towards seed yield per plant, path coefficient analysis was carried out. The phenotypic and genotypic correlation coefficients being more important are only partitioned to direct and indirect effects which are presented in Table 4.11 and 4.12.

Phenotypic and genotypic path diagrams are given in figure 5.

1. Direct effect:

Among all the components, number of pods per plant (p=0.6197), exhibited the highest direct effect on seed yield followed by number seeds per pod (p=0.3274), 100 seed weight (p=0.2979), number of secondary branches per plant (p=0.2839), primary branches (p=0.0479) and harvest index (p=0.0371) while plant height (p=-0.0108), days to maturity (p=-0.0505), days to 50% flowering (p=-0.0888) recorded negative direct effect at phenotypic level.

At genotypic level days to 50% flowering (g=2.5584) exhibited the highest positive direct effect on seed yield followed by number of pods per plant (g=0.6068), 100 seed weight (g=0.3619), number of seeds per pod (g=0.3489) and harvest index (g=0.0337) while number of primary branches per plant (g=-0.0119), plant height (g=-0.0379), initial plant stand (g=-0.1743), secondary branches per plant (g=-0.1784) and days to maturity (g=-0.1801) negative direct effect by genotypic level.

2. Indirect effect

1. Initial plant stand

Initial plant stand had significant negative phenotypic and genotypic correlation (p=-0.1535; g=-01743) with seed yield per plant. and negative indirect effect through number of pods per plant (p=-0.0021; g=-0.0129), number of secondary branches (p=-0.0026 g=0.0662) seeds per pod (p=-0.0033; g=0.0022), plant height (p=-0.0051; g=-0.0289), days to maturity (p=-0.0056; g=-0.0154), days to 50% flowering (g=-00071; g=-0.5366), harvest index (p=-0.0092; g=-0.0476), 100 seed weight (p=-0.0094; g=-0.0506).

2. Days to 50% flowering

Days to 50% flowering had significant negative phenotypic and positive genotypic correlation (p=-0.0888; g=2.5584) with seed yield per plant. It exhibited positive indirect effects through days to maturity (p=0.237), plant height (p=0.102), number of seeds per pod (p=0.0098), number of secondary branches (p=0.0038). positive indirect effect through harvest index (g=0.1050), initial plant stand (g=0.1275) and primary branches per plant (g=0.0057) at genotypic level. Negative indirect effect through pods per plant (p=-0.0021; g=-0.0298), harvest index (p=-0.0075), initial plant stand (p=-0.0122), primary branches per plant (p=-0.0131) followed by 100 seed weight (p=-0.0236; g=-0.0632) at both phenotypic and genotypic level. Thus these indirect causal factors are to be considered during selection process for improving seed yield per plant.

3. Days to maturity

Days to maturity had negative direct phenotypic and genotypic correlation (p=-0.0505; g=-0.1804) with seed yield per plant. It exhibited positive indirect effects through days to 50% flowering (p=0.008; g=0.4951), number of seed per pod (p=0.0005; g=0.0163), plant height (p=0.0001; g=0.0055), and negative indirect effect through number of pods per plant (p=-0.0001; g=-0.0113), initial plant stand (p=-0.0003; g=-0.0109), harvest index (p=-0.0004; g=-0.01561), number of primary branches per plant (p=-0.0004; g=-0.0173) followed by number of secondary branches per plant (p=-0.0007; g=-0.0361), at both phenotypic and genotypic level in the decreasing order of their magnitude.

4. Plant height

Number of primary branches per plant showed negative direct phenotypic and genotypic correlation (p=-0.0108; g=0.-0.0379) with seed yield per plant. It has positive indirect effect *via* initial plant stand (p=0.0040), 100 seed weight (p=0.0015), number of seeds per pod (p=0.0001) at phenotypic level and harvest index (p=0.00015; g=0.0015) at both phenotypic and genotypic level. also show positive indirect effect through days to 50% flowering (g=0.0494), number of primary branches per plant (g=0.0210), days to maturity (g=0.0036), number of secondary branches

(g=0.0173) at genotypic level. Negative indirect effect through days to 50% flowering (p=-0.0047), days to maturity (p=-0.0018), number of secondary branches (p=-0.0099) at both phenotypic level in the decreasing order of their magnitude. number of pods per plant (g=-0.0039), 100 seed weight (g=-0.0024) Followed by initial plant stand (g=-0.0134) at genotypic level of magnitude.

5. Number of primary branches per plant

Number of primary branches per plant had positive phenotypic correlation (p=0.0479) and negative genotypic correlation (g=-0.0119) with seed yield per plant. It showed positive indirect effects at both phenotypic and genotypic level through plant height (p=0.0132; g=0.123). Number of secondary branches per plant (p=0.0152), initial plant stand (p=0.0104), number of pods per plant (p=0.0061), number of seeds per pod (p=0.003) shows the positive indirect correlation at phenotypic level. 100 seed weight (g=0.0195), harvest index (g=0.013), days to 50% flowering (g=0.0120) positive indirect effect by genotypic correlation. It showed negative indirect effects at phenotypic level through days to maturity (p=-0.0053), days to 50% flowering (p=-0.0062), harvest index (p=-0.0076), 100 seed weight (p=-0.0119).

6. Number of secondary branches per plant

Number of secondary branches per plant had positive phenotypic correlation (p=0.2839) and Negative genotypic correlation (g=-0.1781) with seed yield per plant. It showed positive indirect effects through number of primary branches per plant (p=0.0955; g=0.0798), number of pods per plant (p=0.0716; g=0.0556), plant height (p=0.0630; g=0.0635), days to 50 % flowering (p=0.0112; g=0.0125), number of seeds per pod (p=0.0015). It showed negative indirect effect through initial plant stand (-0.0131; g=-0.0252), harvest index (p=-0.0414; g=-0.30362) days to maturity (p=-0.0588; g=-0.0869), and 100 seed weight (p=-0.0602; g=0.1827) at phenotypic level and genotypic level.

7. Number of pods per plant

Number of pods per plant had positive phenotypic and genotypic correlation (p=0.6197; g=0.6068) with seed yield per plant. It displayed positive indirect effect through number of secondary branches per plant (p=0.2055; g=0.2004), number of seeds per pod (p=0.1444; g=1784), number of primary branches per plant (p=0.1101; g=0.1002) at phenotypic level and genotypic level. It showed negative indirect effect through plant height cm (p=-0.0259; g=-0.0521), days to maturity (p=-0.0288; g=-0.0976), initial plant stand (p=-0.0300; g=-0.0788), 100 seed weight (p=-0.1771; g=-0.1827) and harvest index (p=-0.2059; g=-0.2402). Days to 50% flowering (p=-0.0181) show negative indirect effect at phenotypic level.

8. Number of seeds per pod

Number of seeds per pod had positive phenotypic and genotypic correlation (p=0.3274; g=0.3489) with seed yield per plant. Number of pods per plant (p=0.0524; g=0.0706), days to maturity (p=0.0408; g=0.0562), days to 50% flowering (p=0.0303; g=0.5328), number of primary branches per plant (p=0.0213; g=0.0315) number of secondary branches per plant (p=0.0016) showed positive indirect effect at both phenotypic and genotypic level. Days to maturity (g=0.0562) show positive indirect effect on genotypic level. Plant height (p=-0.0006; g=-0.0021), initial plant stand (p=-0.0175), 100 seed weight (p=-0.0220; g=-0.0279) and harvest index (p=-0.0417; g=0.0552) it show negative indirect effect at phenotypic level and genotypic level.

9. 100 seed weight

100 seed weight had positive phenotypic and genotypic correlation (p=0.2979; g=0.0.3619) with seed yield per plant. It showed positive indirect effect through harvest index (p=0.1801; g=0.2393), days to maturity (p=0.0092; g=0.0422), at both phenotypic and genotypic level. And days to 50% flowering (g=1.5198) and show positive indirect level on genotypic level. Plant height (p=-0.0219; g=-0.0300), number of seeds per pod (p=-0.0481; g=-0.0659),initial plant stand (p=-0.1088; g=-0.2890) number of secondary branches per plant (p=-0.1373; g=-0.1820), number of pods per

plant (p=-0.1391; g=-0.1709) showed negative indirect effect through both at phenotypic and genotypic level.

10. Harvest index

Harvest index had positive phenotypic and genotypic correlation (p=0.0371; g=0.0337) with seed yield per plant. It exhibited positive indirect effect through 100 seed weight (p=0.0562; g=0.0250) at phenotypic and genotypic level. Plant height (p=-0.0067; g=-0.0019), days to 50% flowering (p=-0.0157; g=-0.2638), days to maturity (p=-0.0267; g=-0.0132), number of seeds per pod (p=-0.0284; g=-0.0136), number of secondary branches per plant (p=-0.0294; g=-0.0128), initial plant stand (p=-0.0331;g=-0.0284), number of primary branches per plant (p=-0.0337; g=-0.0159) and number of pods per plant (p=-0.0510; g= -0.0235) show indirect negative effect at both phenotypic and genotypic level.

Table. 4.11 Direct and indirect effect of yield and its component characters on grain yield at phenotypic level.

Sr. No.	Characters	Initial plant stand	Days to 50 % 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	Harvest index	Total phenotypic correlation with seed yield / plant
1.	Initial plant stand	**0.0470**	-0.0071	-0.0056	-0.0051	0.0129	-0.0026	-0.0021	-0.0033	-0.0094	-0.0092	-0.1535
2.	Days to 50 % flowering	-0.0122	**0.0802**	0.0237	0.0102	-0.0131	0.0038	-0.0021	0.0098	-0.0236	-0.0075	-0.0888
3.	Days to maturity	-0.0003	0.0008	**0.0028**	0.0001	-0.0004	-0.0007	-0.0001	0.0005	0.0000	-0.0004	-0.0505
4.	Plant height	0.0040	-0.0047	-0.0018	**-0.0372**	-0.0130	-0.0099	0.0014	0.0001	0.0015	0.0015	-0.0108
5.	No. of primary branches per plant	0.0104	-0.0062	-0.0053	0.0132	**0.0379**	0.0152	0.0061	0.0033	-0.0119	-0.0076	0.0479
6.	No. of secondary branches per plant	-0.0131	0.0112	-0.0588	0.0630	0.0955	**0.2377**	0.0716	0.0015	-0.0602	-0.0414	0.2839
7.	Number of pods per plant	-0.0300	-0.0181	-0.0288	-0.0259	0.1101	0.2055	**0.6826**	0.1444	-0.1751	-0.2059	0.6197
8.	Number of seeds per pod	-0.0175	0.0303	0.0408	-0.0006	0.0213	0.0016	0.0524	**0.2478**	-0.0220	-0.0417	0.3274
9.	100 seed weight	-0.1088	-0.1594	0.0092	-0.0219	-0.1696	-0.1373	-0.1391	-0.0481	**0.5423**	0.1801	0.2979
10	Harvest index	-0.0331	-0.0157	-0.0267	-0.0067	-0.0337	-0.0294	-0.0510	-0.0284	0.0562	**0.1691**	0.0371

Residual effect = 0.5233, Underlined figures indicate direct effect.

*, ** indicates significant at 5 and 1 % level of significant respectively.

Fig. 5 Diagram showing the phenotypic path correlation of yield and its component characters of Chickpea.

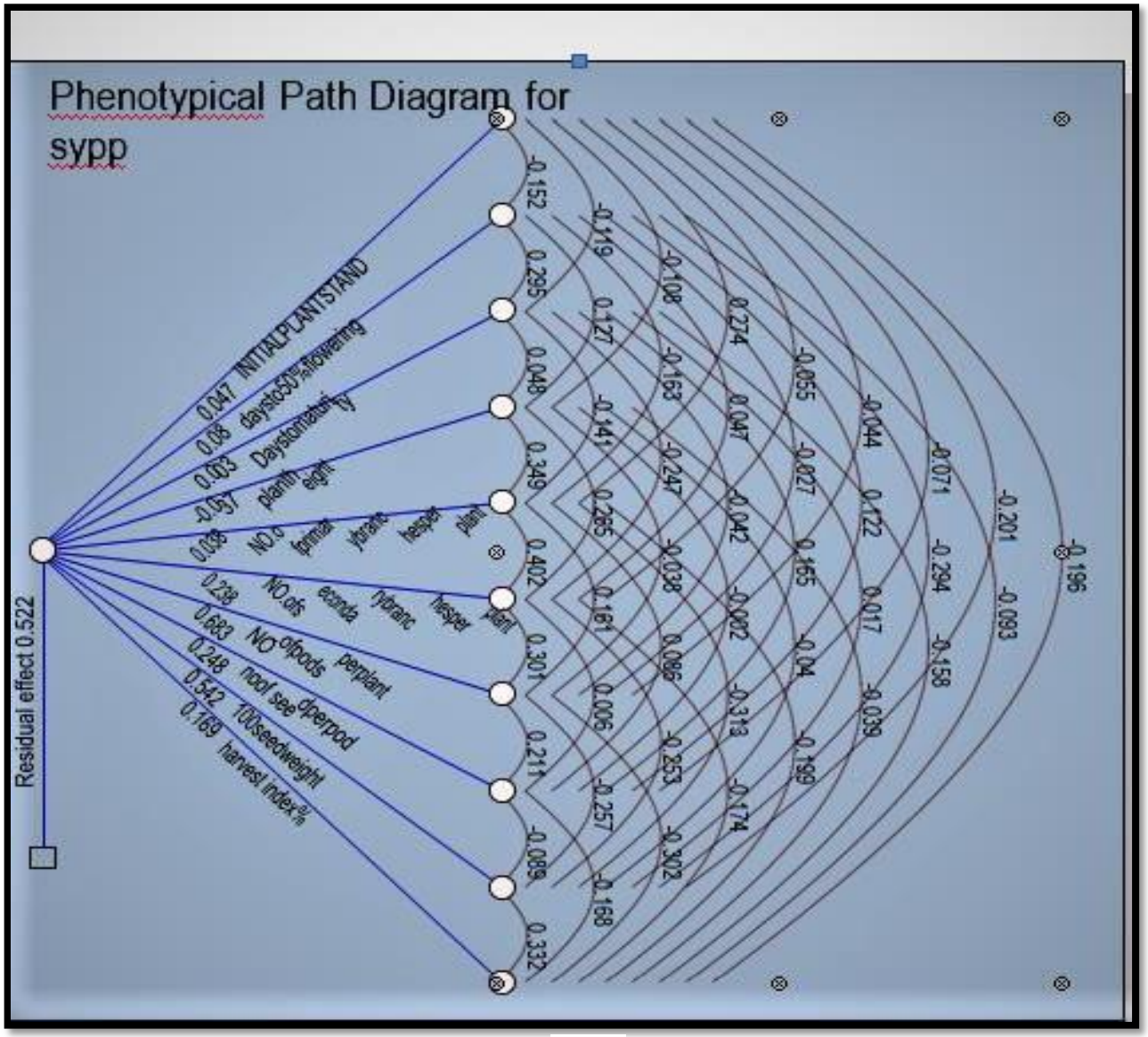


Table. 4.12 Direct and indirect effect of yield and its component characters on grain yield at genotypic level.

Sr. No.	Characters	Initial plant stand	Days to 50 % flowering	Days to maturity	Plant height	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	No. of seeds per pod	100 seed weight	Harvest index	seed yield / plant
1.	Initial plant stand	**0.1213**	-0.5366	-0.0154	-0.0289	0.0662	0.0148	-0.0129	0.0022	-0.0506	-0.0476	-0.1743
2.	Days to 50 % flowering	0.1275	**-0.0288**	-0.1671	-0.0253	0.0057	-0.0018	-0.0298	-0.0523	-0.0632	0.1050	2.5584
3.	Days to maturity	-0.0109	0.4951	**0.0854**	0.0055	-0.0173	-0.0361	-0.0113	0.0163	0.0052	-0.0156	-0.1804
4.	Plant height	-0.0134	0.0494	0.0036	**0.0562**	0.0210	0.0173	-0.0039	-0.0004	-0.0024	-0.0015	-0.0379
5.	No. of primary Branches plant	-0.0331	0.0120	0.0123	-0.0227	**-0.0606**	-0.0235	-0.0082	-0.0065	0.0195	0.0133	-0.0119
6.	No. of sec. branches / plant	-0.0252	0.0125	-0.0869	0.0635	0.0798	**0.2058**	0.0556	-0.0027	-0.0540	-0.0362	-0.1784
7.	No. of pods per plant	-0.0788	0.7661	-0.0976	-0.0521	0.1002	0.2004	**0.7410**	0.1784	-0.1827	-0.2402	0.6068
8.	No. of seeds per pod	0.0052	0.5328	0.0562	-0.0021	0.0315	-0.0038	0.0706	**0.2935**	-0.0279	-0.0552	0.3489
9.	100 seed weight	-0.2890	1.5198	0.0422	-0.0300	-0.2226	-0.1820	-0.1709	-0.0659	**0.6931**	0.2393	0.3619
10.	Harvest index	-0.0284	-0.2638	-0.0132	-0.0019	-0.0159	-0.0128	-0.0235	-0.0136	0.0250	**0.0725**	0.0337

DISCUSSION

CHAPTER - V

The genetic improvement in any crop species is inevitable and continuous process to meet the future challenges. The strengths of available germplasm has to be evaluated to identify potential genotypes which can be exploited for evolving desirable varieties to meet future demands which ultimately leads to food and nutritional security of the country and world. Success of any breeding programme mostly depends upon the knowledge of genetic variability present in a given crop species for the characters under improvement. Yield was a complex character and dependent on a number of component characters which are quantitatively inherited in a particular manner. As such, before organizing any breeding programme it is necessary to have thorough knowledge on variability or divergence present in the available genetic material and the extent of association existing between the yield and yield components. Any successful hybridization programme, the diversity of parents is of most importance (Murthy and Arunachalam,1966), hence the crosses between the parents with maximum genetic divergence are likely to yield desirable recombinants in the progenies and hence useful for further improvement . But it is a difficult task for any plant breeder to select the most suitable and genetically divergent parents, unless he is provided with necessary information about the genetic diversity and genetic variability present in the available germplasm.

In the present studies, forty germplasms of chickpea obtained from ARS, Badnapur and International Crop Research Institute for Semi Arid Tropics, Hyderabad including four checks were evaluated for genetic diversity and correlation and path analysis, to study the associations between component characters and to estimate direct and indirect effect of the component characters on seed yield.

The results obtained on these aspects are presented in chapter IV and are discussed in this chapter under appropriate headings.

MEAN PERFORMANCE

On the basis of mean performance in initial plant stand maximum in check variety Akash and days to 50% flowering genotype ICCV 181114 found early and in days to maturity in the genotype ICCV 181112 observed early maturing. The plant height is also important parameter which affects yield performance of a species and is observed highest in ICCV 181612. ICCV 181673 showed maximum number of primary branches and the highest number of secondary branches was found in ICCV 181107& ICCV181104. Highest number of pods per plant was observed in check variety Digvijay. Genotypes ICCV 181667 & ICCV 181108 showed highest number of seeds per pod. ICCV 181115 showed highest 100 seed weight and yield per plant found maximum in check variety Digvijay.

GENETIC PARAMETERS

Variability

The knowledge of the amount of variability present for important economic character and its efficient management in population or germplasm determines the success of any breeding programme work. Knowledge of the nature and degree of genetic variability in the population is of immense value for planning efficient breeding programme to improve the yield potential of the genotypes. The coefficient of variations serves as measure of the range of variability present for the different characters. But, the extent of heritable variation can not be estimated genotypic coefficient of variation individually. The heritable estimates along with genotypic coefficients of variation (GCV) would provide a better knowledge of amount of genetic advance to be expected by phenotypic selection (Burton, 1952). The present day breeding activities do involve hybridization, mutation and other techniques to generate variability. Many technique was involved to study the variability. This will almost help in identifying donors which are excelling in one or few yield contributing traits and such genotypes can be effectively used in combination breeding for further yield improvement. The genetic gain in conjunction with heritability estimates should form the criteria for selection based on phenotypic performance (Johansson *et al*.1955).

In the present study, the estimates of phenotypic coefficient of variation (PCV) for all the characters were higher than the estimates of genotypic coefficient of variation (GCV), which may be due to the interaction of genotypes with environment.

Range of variability

The characters number of pods per plant, harvest index, seed yield per plant, 100 seed weight (gram) and plant height(cm) shows highest range of variability. The character secondary branches per plant showed considerable amount of variability. Such variability present for quantitative traits in the present study could profitably be utilized for crop improvement in chickpea. The variability was lowest for number of seeds per pod. Similar results were obtained by Jeena *et al.* (2005), Dwevedi and Gaibriyal (2009), Borate *et al.* (2010), Sharma *et al.* (2010) and Thakur *et al.* (2018).

Genotypic and phenotypic coefficient of variation

The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) for all the characters studied showed little difference. The magnitude of PCV was higher than GCV for all the characters indicating that the apparent variation is not only due to genotypes but also due to environment. Selection for such traits sometimes may be misleading. The estimates of genotypic as well as phenotypic coefficient of variation in the present study were highest for number of primary branches per plant followed by number of pods per plant, seed yield per plant and 100 seed weight. Number of seed per pod, secondary branches per plant, harvest index showed medium genotypic and phenotypic coefficient of variation. For days to maturity, Initial plant stand, days to 50% flowering and plant height both the genotypic and phenotypic coefficient of variation was lowest. Earlier workers, Gumber *et al.* (2002) repoported highest values of phenotypic coefficient of variation (PCV) for seed yield per plant. Borate *et al.* (2010) reported values of phenotypic and genotypic variance were highest for number of pods per plant. Dwevedi and Gaibriyal (2009) reported highest values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the trait 100 seed weight and number of pods per plant. Aarif *et al.* (2014) reported that 100 seed weight had the highest magnitude of coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Jadhav

et al. (2012) reported similar values for genotypic coefficient of variation and phenotypic coefficient of variation for 100 seed weight, harvest index, seed yield per plant. Kumar *et al.* (2012) reported high estimates of genotypic coefficient of variation and phenotypic coefficient of variation for 100 seed weight, seed yield per plant and plant height. Chopdar (2016) reported highest values of genotypic coefficient of variation for seed yield per plant. Alka dev *et al.* (2017) reported low phenotypic coefficient of variation and genotypic coefficient of variation for days to 50 % flowering. Thakur *et al*. (2018) reported significant difference among all characters like number of pods per plant, number of primary branches per plant, 100 seed weight and harvest index.

Heritability and Genetic advance

Genotypic coefficient of variation (GCV) alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicator of heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects and allelic interaction due to dominance and allelic due to epistasis. Burton (1952) suggested that the genetic coefficient of variation(GCV) and heritability estimates together give better idea about the amount of genetic advance(GA) expected through selection. Johnson *et al.* (1955) estimated that in a selection programme, heritability values as well as estimates together gives better idea about the genetic advance expected through selection. The progress of any breeding programme is conditioned by the magnitude and the nature of genotypic and non-genotypic variation in the various characters since, most of the economic characters (e.g., yield) are complex in inheritance and are greatly influenced by various environmental conditions or factors. The study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. The heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype appearance.

In the present investigation the range of broad sense heritability was from 25.70% in initial plant stand to 96.90 % in 100 seed weight. Maximum heritability was observed for 100 seed weight (96.90%) followed by Harvest index

(96.50%), days to 50 % flowering (94.00%), %), number of primary branches per plant (93.70%), number of pods per plant (90.10%), number of seeds per pod (85.90 %), plant height (85.80%) number of secondary branches per plant (85.00%), seed yield per plant (78.40%), days to maturity (66.80%) and initial plant stand (25.70%). The broad sense heritability is referred to the genetic portion of the phenotypic variability. The character having maximum broad sense heritability, there is a scope for selection for that character. Zeeshan *et al.* (2012) found high heritability for 100 seed weight and plant height.The highest genetic advance was noticed for the character highest estimate in case of number of primary branches per plant (70.24%) and (90.02 %) followed by 100 seed weight (52.46%) and (67.23 %), number of pods per plant (51.61 %) and (66.14 %), seed yield per plant (47.20 %) and (60.50%), harvest index (44.69 %) and (57.28 %), of seeds per pod (44.54 %) and (57.08 %), number of secondary branches per plant (43.58 %) and (55.85%) plant height (19.36 %) and (24.82 %), days to 50 % flowering (13.07 %) and (16.75 %), days to maturity (5.14%) and (6.59%) and initial plant stand (3.98%) and (5.10%) at 5% and 1% level of significance, respectively. indicating that these traits are under control of additive gene action and potential possibilities exist for the improvement of these characters through simple selection. These finding are supported by similar noting of Padmawati *et al*. (2013) for number of primary branches per plant, Kumar *et al,* (2002) for number of pods per plant. Akhtar *et al.* (2011) for number of pods per plant and 100 seed weight, Jadhav *et al.* (2012) for 100 seed weight, Gul *et al.* (2013) for number of pods per plant, Suyog *et al.* (2018) seed yield per plant.

The characters *viz.* number of primary branches per plant, number of pods per plant seed yield and harvest index showed high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). High heritability was found in 100 seed weight, harvest index and days to 50% flowering where high genetic advance was found in number of primary branches per plant followed by 100 seed weight, number of pods per plant and seed yield per plant by percent of mean.

Thus considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as per cent of mean, it can be

pointed out that, the characters like 100 seed weight, number of primary branches per plant, seed yield per plant, number of pods per plant, harvest index, days to 50% flowering ,number of secondary branches per plant, number of primary branches per plant and number of seeds per pod are the most important characters in chickpea improvement.

Genetic divergence

Genetic divergence, which is due to genetic factors, is the basis for heritable improvement. The plant breeders have always therefore, been fascinated by great amount of diversity in crop plants as could serve as raw material for any breeding programme. The precise information about the genetic divergence is therefore, important for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants in the breeding material. Multivariate analysis as shown by Mahalanobis (1936) D^2 statistics is a measure that appraises the genetic variability quantitatively among a set of genotypes. Genetic divergence analysis therefore, was attempted to identify the suitable lines among fourty genotypes of chickpea.

Diversity

The estimates of D^2 values ranged from 104.47 to 498.13 which indicates the presence of adequate diversity between genotypes studied. Sivakumar and Muthiah (2000), Kumar et al. (2002), Jeena et al. (2005), Sandhu et al. (2006), Dwevedi and Gaibriyal (2009), Gaikwad et al. (2012), and Ambilwade et al. (2018), Ponnuru Akhil et al. (2019) also reported wide genetic diversity in chickpea germplasm.

Cluster formation

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for hybridization programme. The theoretical concept behind such grouping is that, the genotypes grouped into the same cluster are less diverse from each other than those belonging to the different clusters and will not give expected desired heterotic response and segregants in further generations.

Therefor breeding programme should be designed in such a way that, the parents are selected from different clusters with wider in genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.*, 1965). hence, while selecting the parents by considering the genetic diversity, their performance and cluster mean for the characters also need due consideration in the crop improvement programme.

In the present investigation fourty genotypes were grouped into ten clusters. The cluster I was with the highest number of genotypes (22) followed by cluster IV (07), clusters VII (04). Cluster II, III, V, VI, VIII, IX and X had one genotype Nimbalkar and Harer (2001) reported ten solitary clusters.

The intra cluster distance (D^2) range from 104.47 to 183.14. The maximum inter cluster distance (D^2=498.13) was observed between cluster IX and cluster VIII, followed by cluster VII and II (D = 467.98), cluster VIII and cluster IV (D = 467.16), cluster VII and cluster IV (D = 424.41). The minimum inter cluster distance (D = 139.19) was between clusters II and I.

At inter cluster level, cluster IX and VII had the highest value which was followed by cluster VII and II. At inter cluster level, cluster IX and VII had the highest value which was followed by cluster VII and II. The cluster means for different characters showed considerable difference among the clusters for all the characters.

The cluster mean for initial plant stand varied from 24.97 (cluster IV) and 28.88 (cluster III&IX). The cluster mean for days to 50 per cent flowering varied from 62.50 (VI) to 74.50 (II). The cluster mean for days to maturity ranged between 117.00 (VI) to 132.00 days (IX). The highest cluster mean for plant height was 67.23 cm, which was observed in cluster (III) and lowest for (cluster IX) 43.60. The cluster mean for the number of primary branches per plant ranged from 1.00 (cluster VIII) to 4.50 (cluster III). The cluster mean for secondary branches per plant ranged between 7.20 (cluster V) and 24.50 (cluster III).

The cluster mean for number of pods per plant was maximum in cluster X (149.00) and it was minimum in cluster V (76.75). The cluster mean for number of seeds per pod was maximum in cluster X (1.80) and it was minimum in cluster II, III, VI, VIII (1.00).The cluster mean for 100 seed weight was minimum in cluster II

(15.45) and it was maximum in cluster VII (37.93). The cluster mean for seed yield per plant ranged between (18.82) cluster II and (48.54) cluster X. The cluster mean for harvest index was maximum in cluster VI (64.88) % and minimum in case of cluster IV (34.00 %).

It was found that the characters *viz.*, 100 seed weight, harvest index, number of pods per plant were the major contributors towards divergence. The performance of genotypes and the characters with the maximum contribution towards divergence should be considered for improvement of chickpea.

The maximum contribution towards divergence was observed by Renuka *et al.* (2018) in pods per plant, harvest index and 100 seed weight. Dwevedi and Gaibriyal (2009) observed that highest contribution was exhibited by harvest index, 100 seed weight and number of pods per plant. Singh *et al.* (2012) reported maximum contribution by days to 50% flowering. Devendrappa *et al*. (2011) for days to maturity

CHARACTER ASSOCIATION

Correlation studies

Correlated characters are of interest for three chief reasons, firstly in connection with the genetic cause of correlation through the linkage and pleiotropic action of genes, secondly in connection with the change brought about by selections. It is important to understand, how the improvement of one character will cause simultaneous changes in other characters and thirdly in connection with natural selection (Falconer, 1960).

In the present study, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients, in general, indicating that though there exist an intrinsic association between the characters studied, with least influence of environment in determining these associations (Johanson *et al.*1955).

The characters *viz.* number of pods per plant, number of seeds per pods, 100 seed weight, number of secondary branches per plant, harvest index and number of primary branches per plant recorded highly positive significant with seed yield. In other words, an increase in the magnitude of these characters would lead to an increase in the magnitude of grain yield.

Earlier studies too have indicated such positive significant correlation for number of pods per plant by Guler *et al*. (2001). Arshad *et al*. (2004) found that seed yield had positive and significant correlation with number of pods per plant, plant height, and 100 seed weight. Vaghela *et al*. (2009) found that seed yield per plant have significant and positive correlation with number of pods per plant, number of primary branches per plant, harvest index, and 100 seed weight at genotypic as well as phenotypic levels.

Gohil and Patel (2010) reported that 100 seed weight, harvest index, number of pods per plant and number of seeds per pod has positive significant relationship with seed yield per plant. Yucel and Anlarsel (2010) found significant and positive relationships among seed yield and harvest index. Akhtar *et al.* (2011) observed that seed yield per plant had significant and positive correlation with 100 seed weight, number of pods per plant and plant height. Babbar *et al.* (2012) reported that seed yield per plant showed high significant and positive correlation with number of seeds per pod, number of pods per plant, plant height and 100 seed weight. Bhanu *et al.* (2017) found positive significant relationship between seed yield, and number of pods per plant, number of secondary branches.

Shedge *et al.* (2019) found positive significant relationship between harvest index, number of pods per plant, number of secondary branches per plant, number of primary branches per plant and number of seeds per pod. Shara *et al.* (2019) observed that seed yield per plant had significant and positive correlation with number of secondary branches, 100 seed weight, number of pods per plant. Shanmugam *et al.* (2019) reported that seed yield per plant showed high significant positive correlation with number of seeds per pod, number of secondary branches per plant,100 seed weight and harvest index.

From the foregoing discussion on character associations, it is evident that characters *viz.*, number of pods per plant, number of seeds per pods,100 seed weight, number of secondary branches per plant, harvest index, number of primary branches per plant displayed positive correlation with seed yield per plant at both genotypic and phenotypic levels. Hence, these characters could be given due emphasis in formulating selection criterion for improvement of seed yield in chickpea.

Path coefficient analysis

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation into the measures of direct and indirect effects. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated coefficient need to be split into direct and indirect effects by using path coefficient analysis since, many characters affect a given trait. Thus, the correlation and path coefficient in combination can give a better insight into cause and effect relationship between different pairs of characters. As guideline for interpretation of path analysis results, the following key points may be kept in view as suggested by Singh and Chaudhary (1977).

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective. If the correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on that character.

The characters number of pods per plant, number of seeds per pods,100 seed weight, number of secondary branches per plant, number of primary branches per plant, harvest index and 50% flowering on seed yield in decreasing order of magnitude revealing that these were major yield contributing traits in chickpea.

Similar results were reported by Talebi *et al.* (2007) for number of seeds per pod, number of pods per plant and harvest index. Thakur and Sirohi (2009) reported highest positive direct effect of harvest index and number of pods per plant on grain yield. Harvest index showed positive direct effect on seed yield as reported by Ozveren and Anlarsal (2010), Yucel and Anlarsel (2010) and Chopdar (2016). Number of pods per plant had also directly effect on grain yield as reported by Gaikwad and Monpara (2011). Zali *et al.* (2011) recorded number of secondary branches per plant height have positive direct effect on grain yield. Kumar *et al.* (2012) reported highest positive direct effect of number of pods per plant on seed yield. Jeevani *et al.* (2013) and Muhammad *et al.* (2013) reported positive direct effect of number of pods per plant, harvest index on

seed yield. Hasan and Deb (2014) and Parhe *et al.* (2014) reported number of secondary branches per plant, 100 seed weight, number of pods per plant had positive direct effect on grain yield. Harvest index showed positive direct effect on seed yield studied by Sohaib *et al.* (2016). Alka Dev *et al.* (2017) reported number of pods per plant and harvest index had positive direct effect on seed yield. Similarly Thakur *et al.* (2018) showed harvest index and number of pods per plant had positive direct effect on seed yield per plant.

Singh *et al.* (2018) reported that days to flowering, and total pod number, exhibited high positive direct effects on seed yield. Shara *et al*.(2019) showed number of branches per plant, number of seeds per pod, harvest index and number of pods per plant had positive direct effect on seed yield per plant. Mansa *et al.* (2019) Character association analysis revealed that number of secondary branches per plant, number of pods per plant, and harvest index showed highly significant and positive correlation with seed yield per plant.

From the above discussion, it is evident that harvest index, number of pods per plant, 100 seed weight, number of secondary branches per plant, primary branches per plant and days to 50% flowering showed positive direct effect on seed yield.

CHAPTER – VI

SUMMARY AND CONCLUSION

The present investigation entitled, "Genetic divergence studies in chickpea (*Cicer arietinum* L.)" was conducted during *Rabi* season of 2019-20 to study the nature and extent of genetic variability present among the genotypes for quantitative characters in chickpea and grouping genotypes into various clusters.

Fourty genotypes of chickpea were evaluated in a randomized block design with two replications. Eleven characters were studied *viz.,* Initial plant stand, 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 seeds per pod, 100 seed weight (gram), harvest index (%) and seed yield per plant (gram).

The treatment differences in ANOVA were found statistically significant for most of the characters. The magnitude of genotypic and phenotypic coefficient of variation also indicated the presence of good amount of variability in the experimental materials. In the present study, high estimates of genotypic and phenotypic coefficient of variation were observed for number of primary branches per plant followed by number of pods per plant, seed yield per plant and 100 seed weight.

Variability and genetic parameters

The highest broad sense heritability was observed for 100 seed weight followed by Harvest index, days to 50 % flowering, number of primary branches per plant, number of pods per plant, number of seeds per pod, plant height, number of secondary branches per plant, seed yield per plant, days to maturity and initial plant stand. The highest genetic advance as percent of mean was noticed for the character number of primary branches per plant followed by 100 seed weight, number of pods per plant and seed yield per plant by percent of mean. The remaining characters recorded low genetic advance as percent of mean.

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 ten clusters with varying number of genotypes in the clusters. The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance D^2 value 498.13 which indicates the presence of adequate diversity between genotypes studied.

Cluster formation

The aim of cluster formation and measuring inter and intra cluster divergence is to provide the basis for selecting parents for hybridization programme. Crossing between the genotypes belonging to the same clusters will not give desired improvement in any character hence; the parents selected for crossing should be from different clusters. Greater the divergence between the two clusters, more is the genetic diversity in the genotypes. The crosses involving the parents with large divergence have also been reported to exhibit decrease in heterosis. Therefore, while selecting the parents by considering the genetic diversity, their performance and cluster mean for the characters also need due consideration in the crop improvement programme. In the present investigation, the cluster means for the ten characters studied are presented in Table 4.7.

The cluster mean for initial plant stand varied from 24.97 (cluster IV) and 28.88 (cluster III&IX). The cluster mean for days to 50 per cent flowering varied from 62.50 (VI) to 74.50 (II). The cluster mean for days to maturity ranged between 117.00 (VI) to 132.00 days (IX). The highest cluster mean for plant height was 67.23 cm, which was observed in cluster (III) and lowest for (cluster IX) 43.60. The cluster mean for the number of primary branches per plant ranged from 1.00 (cluster VIII) to 4.50 (cluster III). The cluster mean for secondary branches per plant ranged between 7.20 (cluster V) and 24.50 (cluster III).

The cluster mean for number of pods per plant was maximum in cluster X (149.00) and it was minimum in cluster V (76.75). The cluster mean for number of seeds per pod was maximum in cluster X (1.80) and it was minimum in cluster II, III, VI, VIII (1.00).The cluster mean for 100 seed weight was minimum in cluster II

(15.45) and it was maximum in cluster VII (37.93). The cluster mean for seed yield per plant ranged between (18.82) cluster II and (48.54) cluster X. The cluster mean for harvest index was maximum in cluster VI (64.88) % and minimum in case of cluster IV (34.00 %).

Correlation

Correlation studies at both genotypic and phenotypic levels were made to resolve the direction and magnitude of association among characters. It indicates that strong inherent association between various character studied and genotypic expression of correlation was comparatively less influenced by the environmental condition. The traits *viz.* number of pods per plant, number of seeds per pods,100 seed weight, number of secondary branches per plant, harvest index, number of primary branches per plant also exhibited positive and highly significant genotypic correlations with seed yield. This indicates the simultaneous improvement of these characters through selection.

Path coefficient analysis

Path coefficient analysis indicated that the characters *viz.*, harvest index, number of pods per plant, 100 seed weight, number of secondary branches per plant, primary branches per plant and days to 50% flowering showed positive direct effect on seed yield. Hence, the selection of genotypes based on these characters as selection criterion would be helpful in improving the seed yield potential of chickpea.

CONCLUSION

On the basis of finding generated from the present investigation, following conclusions can be drawn, which may be considered for improvement in chickpea crop in future breeding programmes.

The wide range of genetic variability observed for most of the characters as evidenced by significant variances due to genotypes suggesting that, it could be helpful in isolation of better germplasm line. The phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients (GCV) of variation which suggest the role of environment in governing these traits. Similarly, the magnitude of GCV and PCV was observed high for the characters *viz.*, number of primary branches per plant followed by number of pods per plant, seed yield per plant

and 100 seed weight. It indicates that selection of desired germplasm for these traits may be worthwhile for improving seed yield in future breeding programme.

The characters *viz.*, number of primary branches per plant showed high GCV and PCV, high heritability and high genetic advance as percent of mean. Number of pods per plant show high GCV and PCV, high heritability and high genetic advance as percent of mean. seed yield per plant showed high GCV and PCV, moderate heritability and genetic advance as percent of mean.

LITERATURE CITED

Aarif, M.; Rastogi, N.K.; Johnson, P.L. and Chandrakar, P.K. 2014**.** Genetic Analysis of seed yield and its attributing traits in *Kabuli* chickpea (*Cicer arietinum* L.). *J.Food Leg.*, **27**(1): 24-27.

Abhishek Kumar, G., Suresh Babu and RupaLavnya, G. (2012). Character association and path analysis in early segregating population in chickpea (*Cicer arietinum* L.) *Legume Res.;* **35**(4): 337-340.

Aher, B.M.; Desai, A.; Pithia, M. S. and Rao, K.2014**.** Genetic variability of yield and it'scontributing characters in kabuli chickpea (*Cicer arietinum* L.). *Trends in biosciences,* **7**(23): 4025-4032.

Akhtar L. H., Parvez Muhammad A. and Muhammad N. 2011. Genetic divergence and inter- relation studies in chickpea (*Cicer arietinum* L.). *Pak. J. Agri. Sci.* **48**(1),35-39.

AlkaDev 2017. Genetic variability studies in *Desi*chickpea (*Cicer arientinum L.*) Genotypes IJCM *App. Sci.* 2017 **6**(4): 20-25.

Allard, R. W. 1961. Relationship between genetic diversity and consistency performan ce in different environments. *Crop Sci*., **1**(2): 127-133.

Ali, M.A., Nawab, N.N., Abbas, A. Zulkiffal, M. and Sajjad, M. 2009. Evaluation of selection criteria in (*Cicer arietinum* L.) using correlation coefficients and path analysis. *Australian J. Crop Sci.*, **3**(2): 65-70.

Ali Q., Ahsan M., Farooq J. and Saleem M. 2010.Genetic variability and trait association in chickpea (*Cicer arietinum* L.). *Electron J. Plant Breed.,***1**(3): 328-333.

Alwawi, H., Moulla M. and Choumane W. 2010. Genotype-environment interaction and genetic parameters in Chickpea (*Cicer arietinum* L.) landraces. *J. Agric. Sci*. **2**(1):154-161.

Ambilwade B., Magar A. S., Gadade S. B. and Suresh B.G. 2018. Genetic Diversity studies in chickpea (*Cicer arietinum* L.) germplasm. *Int. J. Curr. Microbiol. App.Sci.***7**(9):2757-2763.

Anonymous, (2017-18) Annual report of research work on pulses 2017-2018, IIPR Kanpur.

Anonymous, (2018-19) Annual report of research work on pulses 2018-2019, IIPR Kanpur.

Anonymous, (2019-20) Annual report of research work on pulses 2019-2020, IIPR Kanpur.

Arshad M., A. Bakhsh, and Ghafoor A., 2004. Path coefficient analysis in chickpea under rainfed condition. *Pak. J. Bot.* **36**: 75-81.

Aswathi P.V, K. Ganesamurthy, and P. Jayamani 2019. Genetic variability for morphological and biometrical traits in chickpea (*Cicer arietinum*L.) *Electronic Journal of Plant Breeding*, **10** (2): 699-705.

Babbar, A., Prakash V., Tiwari P. and Iquebal M. A. 2012. Genetic variability for chickpea (Cicer arietinum L.) under late sown season. Legume res. 35 (1): 1-7.

Bhanu A. N., Singh M.N., Tharu R. and Saroj S.K. 2017. Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea genotypes. *Indian J. Agric. Res.*, **51**(5): 425-430.

Borate, V.V. Dalvi, V.V. and Jahav, B.B. 2010. Estimates of genetic variability and heritability.*J. Maharashtra Agric. Univ*., **35**(1): 47-49.

Burton, G. W. 1952. Quantitative inheritance in pearl millet (*P.glaucum* L.). *Agron. J*., 501- 503.

Chowdhury M. A., Vandenberg B. and Warkentin T. 2002. Cultivar identification and genetic relationship among selected breeding lines and cultivars in chickpea (*Cicer arietinum* L.). *Euphytica,* **127**: 317-325.

Chopdar D.K., Baudhbharti, Sharma P.P., Dubey R.B., Bragendra and Meena B.L. 2016. Studies on genetic variability, character association and path analysis for yield and itscontributingtraits in chickpea (*Cicer arietinum* L.). *Agril. Res. Communiction Centre J. Legume res.* **40**(5): 824-829.

Cochran, W.G. and Cox, G.M. 1957. Experimental design. John Wiley and Sons N.Y., London. : 82-90 and 403-412.

Devendrappa, J.Viswanatha, K.P. Mallikarjun, B. P. Ambalika, D.S. and Gavisiddappa, Choudki V.M. 2011. Assessment of genetic diversity in chickpea (*Cicer arietinum* L.) *Am.-Eu. J. Sustain Agric*., **2**(3): 205-211.

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of component of Wheat grass seed production. *Agron. J*., **51**: 515-518.

Dwevedi, K.K. and Gaibriyal, L. M. 2009. Assessment of genetic diversity of cultivated Chickpea. Asian *J. of Agricultural Sciences*, **1**(1): 7-8.

Falconer, D. S. 1960. Correlated character, introduction to quantitative genetics, 312, published by Longman Group Ltd., London.

Fisher, R.A and Yates.F.1943. Statistical table for Biological Agricultural and Medical Research, 2nd ed. Oliver and Boyd Ltd.London.

Gaikwad, S.R. and Monpara, B.A. 2011. Genetic variation in F2 populations and their potential in the improvement of seed yield in chickpea (*Cicer arietinum* L.). *J. Agric. Res. Technol.* **36**(3): 527- 530.

Gaikwad A.R., Desai N.C., Langhi A.M. and Jadhav S.D. 2012. Studies on genetic variability in Chickpea (*Cicer arietinum* L.). *EM Int.* **17**(3): 585-558.

Gohil, D. P. and Patel, J.D. 2010. Character association and path analysis in chickpea (*Cicerarietinum* L.) under conserved soil moisture. *Legume Res*. **33**(4): 283-286.

Gul R., H. Khan, Bibi, M., Ain Q. U. and Imran. B. 2013. Genetic analysis and interrelationship of yield attributing traits in chickpea (*Cicer arietinum* L.). *J. Anim. & Pl. Sci***., 23**(2): 521-526.

Guler, M., Adak, M.S. and Ulukah, H. 2001. Determining relationship among yield and some yield components using path coefficient analysis in Chickpea. *European J. Agron*., **14**(2): 161-166.

Gumber, R.K., Singh, S., Rathore P. and Singh, K. 2002. Selection indices and character association in Chickpea. *Indian J. Pulses Res*., **13**(2):56-58.

Hasan M.T. and Deb A.C. 2014. Estimates of direct and indirect effects between

yield and yield Components and selection indices in chickpea (*Cicer arietinum* L.). *Tropical Res. an Int.J.* **1**(2): 65-72.

Hanson, W.D., Robinson, H.F. and Comstock, R.E. 1956. Biometrical studies of yield in segregating population Korean Lespandeza. *Agron. J.*, **48**: 268-272.

Ingle P.M. 2015 Studies on Genetic diversity analysis for yield and yield contributing traits in chickpea (*Cicer arientinum* L.). Thesis submitted to V.N.M.K.V. parbhani.

Jadhav, R.S., Mohir, M.N. and Ghodke M.K. 2012. Genetic variability in Chickpea. *Bioinfolet,* **9**(2): 199-201.

Jain, Sudhanshu and Indapurkar, Y.M. 2013. Assessment of genetic divergence in chickpea genotypes. *Trends in Biosci*. 6(1): 68-69.

Janghel, D. K., Krishan Kumar, R. Sunil and Chhabra, A. K. 2019. Genetic Diversity Analysis, Characterization and Evaluation of Elite Chickpea(*Cicer arietinum* L.) Genotypes. *Int.J.Curr.Microbiol.App.Sci.* **9**(01): 199-209.

Jeena, A.S., Arora P.P. and Arora P.P. and Upreti M.E. 2005. Divergence analysis inChickpea. *Legumes res*. **28**(2): 152-154.

Jeevni J.V., Mehta Dr., Vaddoria M.A. and Ravallata, 2013. Correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.). *Elec. J. of Plant Breeding,* **4**(2): 1167-1170.

Jha, U., Singh B.P. and Lavnya G.R. 2012. Assessment of genetic variability and correlation of important yield related traits in chickpea. *Legume Res.* **35**(4) 341-344.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Genotypic and phenotypic correlation in soybean and their implications in selection. *Agron. J.*, **47**: 477-482.

Jukanti A. K., Gaur P. M., Gowda C. L. L. and Chibbar R. N. 2012. Nutritional quality and health benefits of chickpea (*Cicer arietinum* L.). *British J. of Nutrition.* 108: s11-s26.

Khan, R., F. and Khan, H. 2011. Dissection of genetic variability and heritability estimates of Chickpea germplasm for various morphological markers and quantitative traits. *Saehad J. Agric.* **27**(1): 67- 72.

Kishor L.,Swarup I., Nehra A., Kirar G. and Jeetarwal R.C. 2018. Genetic Variability, Heritability and Genetic Advance Analysis in Chickpea (*Cicer arietinum* L.), *Int. J. Pure App. Biosci.* **6**(4): 141- 144.

Kumar, A., Babu, G. U., Lavnya, G. R. 2012. Character association and path analysis in early Segregating population in chickpea. *Legume Res.;* **35**(4):337-340.

Kumar S, Jeena A.S. and Arora P.P. 2002. Genetic variability and its importance in chickpea (*Cicer arientinum* L.) *Agric. Sci. Digest*. **22**(3): 215-216.

Mahalanobis, P.C. 1928. A statistical study at chinese head measurement. *J. of Asiatic Soc.*, **25**: 301- 377.

Mahalanobis, P.C. 1936. On generalized distance in statistics. *Proc. Nat. Ins. Sci. India*. **2**: 49-55.

Moll R.H. Quantitative Genetics Empirical Results Relevant to plant Breeding 1966.

Muhammad A., Bakhsh A. and Ghafoor A. 2004. Path coefficient analysis in Chickpea. *pak. J. Bot*., **36**(1):75-81.

Muhammad A. A., Nawab, N.N. Ghulam, R. and Muhammad, S. (2008). Estimates of variability and correlation for quantitative traits in chickpea. *J. Agri. Soc. Sci.*, **4**: 177-179.

Muhammad A.M., Muhammad M.B., and Muhammad Saleem 2013. Estimation of genetic variability and path analysis of grain yield and its components in chickpea (*Cicer arietinum* L.). *Int. J. Scientific and Engineering Research* 4, ISSN 2229-5518.

Mujumdar, D.N. and Rao, L.R. 1958. Bengal anthropometric survey. A statistical study.Somkhya.19: 201-408.

Manoj Kumar Singh, Anshuman Singh and Devi S Rhods 2018 Correlation, path analysis and genetic variability, of yield, and yield Components in chickpea (*Cicer arietinum L.*) International Journal of Fauna and Biological Studies 2018; 5(3): 131-135

Manasa B., M. Shanthi Priya, J. Jayalakshmi and P. Umamaheswari 2019. Character Association and Path Coefficient Analysis in Extra Large and Large Seeded *Kabuli* Chickpea (*Cicer arietinum* L.) *Ind. J. Pure App. Biosci.* (2019) *7*(5), 166-171.

Mushtaq, M.A., BajawM. M. and Saleem, M. 2012. Estimation of genetic variability and Path analysis of grain yield and its components in chickpea (*Cicer arietinum* L.). *Int. J. Scient. And Engi. Res.* **4**(1):01-04.

Murty B.R.,V. Arunachalam, The nature and genetic divergence in relation to breeding system in crops, *Indian Journal of Genetics And Plant Breeding*, Vol. **26** No. A (1966), pp. 188-189.

Nadiya A. Al-Saady, Saleem K. Nadaf, Ali H. Al-Lawati1 and Saleh A. Al-Hinai, 2019. Genetic Diversity of Indigenous Chickpea (*Cicer arietinum* L.) Germplasm Collection. *Global Advanced Research Journal of Agricultural Science* (ISSN: 2315-5094) Vol. **8**(4) pp. 166-174.

Nimbalkar, R.D. and Harer, P.N. 2001. Genetic diversity in chickpea. *J. Mah. Agric. Univ*., **26**(1): 106- 107.

Noor, F., Ashraf, M. and Gafoor A. 2003. Path analysis and relationship among quantitative traits in Chickpea. Pakistan *J. of biological Science*, **6**(6): 551-555.

Nyende A. B. and Rao, N.V., Ganga P. R. 2015. Assessment of interrelationship among agronomic and yield characters of chickpea. *Int. J. of Agril. And Crop Sci.* **8**(2): 128-135.

Ozveren, Y.D. and Anlarsal, A.E. 2010. Determination of selection criteria with path coefficient analysis in chickpea breeding. *Bulg. J. Agric. Sci.*, **16**: 42-48.

Padmavati, P.V., S.S. Murthy, V.S. Rao and M. LalAhamad. 2013. Correlation and path coefficient analysis in kabuli chickpea (*Cicer arietinum* L.) *Int. J. Appl. Biol. Pharma. Tech.* **4**(3): 107-110.

Panse, V.G. and Sukhatme, P.V. 1967. Statistical methods of genotypic and phenotypic variability in groundnut. *J. Maharashtra Agric. Univ*., **12**(3): 319-321.

Parhe S.D., Harer P.N. and Nagawade D.R. 2014. Investigation of genetic divergence in chickpea (*Cicerarietinum*L.) geotypes. *The Bioscan an Int. Quarterly J. of Life Sci*. **9**(2):879-882.

Peyman Sharifi , Hossein Astereki , Masoumeh Pouresmael 2018. Evaluation of variations in chickpea (Cicer arietinum L.) yield and yield components by multivariate technique. *Annals of Agrarian Science* **16** (2018) 136-142.

Ponnuru Akhil, GM Lal and Munagala Sai Kiran 2019. Genetic diversity studies in chickpea (*Cicer arietinum* L.) germplasm. *Journal of Pharmacognosy and Phytochemistry* **8**(4): 2549-2552.

Prakash, V. 2013. Component analysis for grain yield on chickpea under moisture deficit conditions. *J. Progressive Agric.;* **4**(1): 50-51.

Prince Raj, Anand Kumar, Sadia Perween, Ravi Ranjan Kumar, Satyendra,Tushar Ranjan and P. K. Singh 2018. Exploring Genetic Diversity in Chickpea (*Cicer arietinum* L.) Under Normal Sown Condition.*Current Journal of Applied Science and Technology **31**(4): 1-5, 2018.*

Puri M.K., Johansan P.I. and Sharma R.N. 2013. Study of variability, diversity and association analysis of chickpea (*Cicer arietinum* L.) germplasm under normal and late sown condition of chhattisgarh state. *Trends in Bio. Sci.* **6**(6): 723-731.

Rao, C.R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons. Inc., New York.351-364.

Raval L.J. and Dobariyal K.L. 2003. Yield components in improvement of chickpea (*Cicer arietinum* L.) *Annals of Agric. Res*. **24**(4): 789-794.

Renukadevi, P. and B. Subbalakshmi. 2006. Correlations and path coefficients analysis in chickpea. *Legume Res.* **29**(3): 201-211.

Renuka Shivwanshi and Anita Babbar 2018.Genetic divergence analysis in chickpea germplasm Legume Research-*An International Journal*.**(42)**:715-718.

Robinson, H.F. 1966. Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian J. Genet*. **26**(A): 171-187.

Samad, M. A.; Sarker, N. and Deb, A. C. 2014. Study on relationship and selection index in chickpea. *Trop. Pl. Res.*, **1**(3): 27–35.

Sandhu, J.S., Singh, P., and Sing, A. 2006. Genetic divergence in chickpea in different environments. *Tropical science*.**46**:23-30.

Sewak, S.; Iquebal, M.; Singh, N.; Solanki, R. and J. Sarika. 2012. Genetic diversity studies in chickpea (*Cicerarietinum*L.) germplasm. *J. of Food Legumes*. 25: 31-36.

Shanmugam Mohan and Kalaimagal Thiyagarajan. 2019. Genetic Variability, Correlation and Path Coefficient Analysis in Chickpea (*Cicer arietinum* L.) for Yield and its Component Traits. *Int.J.Curr.Microbiol.App.Sci.* **8**(05): 1801-1808.

Shara J. Hama 2019. Correlation and Path Coefficient Analysis for Seed Yield and Yield Components in Chickpea under Rainfed Condition. *Journal of Kerbala for Agricultural Sciences* Vol.(6), No.(1) (2019).

Sharma L.K. and Saini D.P. 2010. Variability and association studies for seed yield and yield components in chickpea (*Cicer arietinum* L.). *Res. J. Agric. Sci.* **1**(3): 209-211.

Shedge P. J., D. K. Patil and Gite V. K. 2019.(a) Study on Genetic Divergence in Desi Chickpea (*Cicer arietinum* L.). *Int.J.Curr.Microbiol.App.Sci.* **8**(07): xx-xx.

Shedge P. J., D. K. Patil and Misal M. R. 2019. (b) Assessment of Genetic Variability in Chickpea (*Cicer arietinum* L.). *Int.J.Curr.Microbiol.App.Sci.* **8**(07): xx-xx.

Singh, R. K. and Chaudhary, B. D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi. 215-218.

Singh, Rupinder Pal; Singh, Inderjit; Singh, Sarvjeet and Sandhu, J.S. 2012. Assessment of genetic diversity among interspecific derivatives in chickpea. *J. of Food Legumes*. **25(**2): 150-152.

Sivakumar, S. and Muthiah, A.R. 2000. Genetic divergence in chickpea germplasm. *Madras Agric. J*., **87**(1-3): 48-50.

Snedcor, G. W. and Cochran, W. G. 1967. Statistical methods. 6thOxford and IBH Publ. Co. Calcutta,: 172.

Sneha Priya PR, C Bharadwaj, Tapan Kumar, Suriya Sachdeva, Afroz Alam, BS Patil, Sarvjit Singh and Ashutosh Sarker 2019. Variability, divergence and SAHN grouping studies in extra-large seeded Kabuli chickpea (*Cicer arietinum* L.) genotypes. *IJCS* **7**(5): 13-16.

Sohaib S. M., Ahsan M., Mehmood Z., Abdullah M., Shakoor A. and Irfan Ahmad M., 2016. Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in chickpea (*Cicer arietinum* L.). *Academia J. of Agril. I Res*.**4**(2):082-085.

Suyog D. Warkad, Gabrial M. Lal, and Nikhil A. study on genetic diversity in chickpea *(cicerarietinum l.*) Suryawanshi 2018. germplasm. ijabr, **8** (3) 2018: 347-35.

Syed, M.A.; Islam M.R.; Hossain, M.S.; Alam, M.M. and Amin M.N. 2012. Genetic divergence in chickpea (*Cicer arietinum* L.). *Bangladesh J. Agric. Res*.; **37**(1):129-136.

Talebi, R., Faydz, F. and Jelodar, A. 2007. Correlation and path coefficient analysis of yield and yield components of Chickpea under dryland condition in west of Iran. *Asian J. of Plant Sci.*,**6** (7): 1151-1154.

Thakur N.R., Toprope V.N. and Phanindra K. S. 2018. Genetic diversity analysis in chickpea (*Cicer arietinum* L.). *Int. J. Curr. Microbiol. App. Sci.* Special issue-**6**: 904-91.

Thakur S. and Sirohi A. (2009). Correlation and path analysis in chickpea under differentseasons. *Legume Res.,* **32**(1): 1-6.

Upadhyaya H. D., Dwivedisl, Gowda C. L. L. and Singh S. 2007. Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.). Core collection for use in crop improvement. *Field Crop Res.* **100**: 320-326.

Vaghela M.D., Poshiya V.K., Savaliya V.K., Davada B.K. and Mungra K.D. 2009. Studies on character association and path analysis for seed yield and its components in chickpea (*Cicer arietinum* L.) *Legume Res.;* **32**(4); 245-249.

Wilks, S.S. 1932. Certain generalization in the analysis of variance. Biometrics.24:471-494.

Wright, S. 1921. Correlation and causation. *J. Agric. Re*., **20**: 557-565.

Yucel D.O. and Analarsal A. E. 2010. Determination of selection criteria with path coefficient analysis in chickpea (*Cicer arietinum* L.) breeding. *Bulgarian J. Agric. Sci.* **16**(1):42-48.

Zali, H., Farshadfarb E. And Sabaghpour S. H. 2011. Genetic variability and interrelationships among agronomic traits in chickpea (*Cicer arietinum* L.) genotypes. *Crop Breed. J.* **1**(2):127-132.

Zeeshan, M., W. Arshad, S. Ali, M. Owais, M. Zulkiffal and M. Hussain. 2012. Genetic Divergence and character association in chickpea (*Cicer arietinum* L.) under rainfed conditions. *Wudpecker J. Agric. Res.* **2**(1): 028-032.

THESIS ABSTRACT

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ABSTRACT

The exploration of genetically variable accession or genotypes is the key source of germplasm conservation and potential breeding material for the future use.The highly divergence group of cultivars provides an opportunity to breeders for developing superior and new varieties considering their quality traits for direct commercial utilization. Assessment of genetic diversity existing in and within germplasm groups for yield and its components to obtained superior recombinants which will helpful in understanding pattern of variation was performed utilizing the thirtysix genotypes and four standard checks of chickpea replicated twice. To study the nature and magnitude of genetic divergence using Mahalanobis (1936) D^2 statistics, phenotypic variances, coefficient of variation, heritability, genetic advance, correlation coefficient and path coefficient was estimated and cluster analysis was performed. The data was recorded on eleven morphological traits. The forty genotypes were grouped into 10 clusters. Cluster I was the largest with 22 genotypes. Highest inter cluster distance was recorded between cluster IX and cluster VII, while highest intra cluster distance was found among the genotypes of clusters IX and cluster VIII. Maximum heritability was observed for 100 seed weight (96.90%) followed by Harvest index (96.50%), days to 50 % flowering (94.00%), %), number of primary branches per plant (93.70%), number of pods per plant (90.10%), number of seeds per pod (85.90 %), plant height (85.80%) number of secondary branches per plant (85.00%), seed yield per plant (78.40%). Number of pods per plant, number of seeds per pods and 100 seed weight found to have a positive direct effect on seed yield. Harvest index, number of seeds per pod, 100 seed weight, days to 50% flowering also exhibited positive and highly significant genotypic correlations with seed yield. Character 100 seed weight contributed highest for divergence. It was followed by harvest index, Number of pods per plant, number of primary branches per plant contributed maximum towards the genetic diversity.

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