

**“ASSESSMENT OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES
AGAINST *FUSARIUM* WILT”**

by

Mr. Prasenjit Paul

(Reg. No.017 /050)



DEPARTMENT OF AGRICULTURAL BOTANY

**POST GRADUATE INSTITUTE
MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI – 413 722, DIST. AHMEDNAGAR
MAHARASHTRA, INDIA.**

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A Thesis submitted to the
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MAHARASHTRA, INDIA.**

In partial fulfilment of the requirements for the degree
of

**MASTER OF SCIENCE (AGRICULTURE)
in
AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)**



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2019

CANDIDATE'S DECLARATION

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

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This is to certify that the thesis entitled. “**ASSESSMENT OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES AGAINST *FUSARIUM WILT* ”** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE) in AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the result of a piece of bonafide research work carried out by **Mr. PRASENJIT PAUL** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

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

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LIST OF ABBREVIATIONS AND SYMBOLS

%	: Per cent
/	: Per
Σ	: Summation of
σ^2	: Variance
b.s.	: Broad sense
cm	: Centimeter(s)
C.D.	: Critical difference
Cov.	: Covariance
C.V.	: Coefficient of variation
D.F.	: Degrees of freedom
EC	: Exotic collection
EMP	: Error Mean Sum of Product
<i>et al.</i>	: <i>et allia</i> (And other)
Fig.	: Figure
g	: Gram(s)
GA	: Genetic advance
GAM	: Genetic advance as per cent of mean
GMP	: Genotypic mean sum of products
h^2	: Heritability
i.e.	: <i>id est</i> (that is)
IC	: Indigenous collection
kg	: Kilogram (s)
M.S.S.	: Mean sum of squares
m	: Meter(s)
No.	: Number(s)

PCV : Phenotypic coefficient of variation

R.B.D. : Randomized Block Design

r : Corrélation coefficient

S.E. : Standard Error

S.S. : Sum of Squares

Via. : By way of, by means of

Viz. : Videlicet (Namely)

Vs. : Versus

JG-62 : Jabalpur Gram-62

ABSTRACT

“ASSESSMENT OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES AGAINST *FUSARIUM* WILT ”

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MAHATMA PHULE KRISHI VIDYAPEETH,
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2019

Research Guide	: Dr. S.S. Patil
Department	: Agricultural Botany

The investigation on “Assessment of chickpea (*Cicer arietinum* L.) genotypes against *Fusarium* wilt” was conducted on thirty three genotypes of chickpea including three checks Digvijay, Vijay and Vishal with objectives- viz., to identify the resistant genotypes against *Fusarium* wilt, to study the correlation between yield and yield contributing characters in chickpea.

Observations were recorded for days to 50 per cent flowering, days to maturity, plant height (cm), plant spread (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and wilt incidence (%).

Number of pods per plant exhibited highest range of variability followed by plant height, seed yield per plant, plant spread, days to 50% flowering and 100 seed weight shows considerable amount of variability. The lowest variability was observed for number of seeds per pod.

Genotypic and phenotypic coefficients of variation were highest for seed yield per plant followed by number of pods per plant, number of secondary branches per plant, number of primary branches per plant and 100 seed weight. The estimates of genotypic as well as

phenotypic coefficient of variation were highest for number of pods per plant, and genotypic coefficient of variation were lowest in number of seeds per pod as well as phenotypic coefficient of variation lowest in days to 50 per cent flowering. Maximum heritability was observed for number of pods per plant followed by 100 seed weight and plant height. The highest genetic advance as percent of mean was observed for number of pods per plant followed by seed yield per plant and number of secondary branches per plant. This suggest that desired improvement of these traits like number of pods per plant followed by seed yield per plant and number of secondary branches per plant would be effective by simple selection.

The significant positive correlation was reported between seed yield per plant with number of pods per plant at both genotypic and phenotypic level and plant height, number of secondary branches per plant and plant spread at phenotypic level. It was observed that genotypic correlation coefficient were higher than corresponding phenotypic ones for most of the characters. The non significant positive correlation was reported between seed yield per plant and days to maturity, number of primary branches per plant, number of seeds per pod and 100 seed weight. However days to 50 per cent flowering, showed non-significant negative correlation with seed yield per plant at genotypic as well as phenotypic level.

Path coefficient analysis revealed that number of pods per plant had highest direct effect (0.95) on seed yield per plant with positive and significant followed by number of primary branches per plant, number of secondary branches per plant and plant height are mainly responsible for positive association of these characters with seed yield per plant. The direct effect of days to 50 per cent flowering is positive and its association with seed yield per plant was negative. The direct effect of days to maturity, plant spread, number of seeds per pod and 100 seed weight were negative however, their association with seed yield per plant was positive, indicating that they played their role via indirect effects.

The D^2 statistics showed that there was adequate diversity among the genotypes with D^2 values ranging from 16.96 to 1445.65. On the basis of D^2 values 33 genotypes studied were grouped into seven clusters. On the basis of inter cluster distance and cluster means the genotypes viz., BDNG 2017-49, Digvijay and Vishal were identified for their use in hybridization programme.

Out of thirty three genotypes seventeen genotypes viz. Phule G 15109, Phule G 0819-43, Phule G 16101, Phule G 1022-3, Phule G 1010-4, Phule G 1022-10-6, Phule G 171112, BDNG 2017-44, BDNG 2017-06, BDNG 2016-2, AKG 1301, AKG 1402, Phule G 171103, Phule G 171113, Digvijay, Vijay and Vishal exhibited resistant reaction for *Fusarium* wilt. Therefore, these seventeen genotypes can be used in resistant breeding programme as a source of resistance parents for developing resistant cultivar.

1 . INTRODUCTION

Chickpea (*Cicer arietinum* L.) has been cultivated since the Roman era who named it Erebinthos. In India, chickpea was known during the Aryan age and was called Chanaka. Chickpea is the third most important grain legume cool season food crop in Mediterranean countries and other parts of the world. It occupies a prime position among the pulses in India. The crop is known to be photo-thermo-sensitive and its maturity ranges from 80 to 180 days depending on genotype, soil moisture and time of sowing, latitude and altitude. Lower temperatures, shorter photoperiods and optimal soil moisture, individually or in combinations, help in extending growth period, while higher temperatures, longer photoperiods and moisture stress conditions are known to shorten all developmental phases thereby reducing the crop duration (Summerfield *et al.*, 1990). This crop is important for sustainable agriculture as they boost the soil health and soil fertility through biological nitrogen fixation. In Maharashtra this crop is called harbhara, in other Northern part it's called chana.

Chickpea is an annual, small, herbaceous self-pollinated, diploid ($2n=16$) grain legume crop which branches from the base attaining a height of about 2 feet or more. The plant is mostly covered with glandular or non-glandular hairs but some genotypes do not possess hair. This crop is grown in a wide range of environments including the Mediterranean, South and West Asia, North America and North and East Africa. Because of having deep-root system this crop can sustain drought condition. It belongs to order Fables, family Fabaceae, genus Cicer. Chickpea is known to have nine annual and thirty five perennial species (Van der Maesen *et al.*, 2007) based on seed protein electrophoresis. Ladizinsky and Adler (1976) considered *Cicer reticulatum* the wild progenitor of cultivated chickpea and South-Eastern Turkey as the centre of origin for the crop. Based on seed size and colours cultivated chickpea is mainly divided into two types (Cubero 1975).

- 1) Microsperma (Desi type): Desi type is characterized by small, coloured seeds (colour varies from cream, black, brown, yellow to green), angular shape with high percentage of fibre and contribute to around 80% in total production. There are 2-3 ovules per pod But on an average 1- 2 seeds per pod are produced. The plants are short with small leaflets and purplish flowers with anthocyanin and it grown in the semi-arid tropics.
- 2) Macrosperma (Kabuli type): It is characterized by large, ram head-shaped, cream coloured seeds with low percentage of fiber. The plants are medium to tall in height, with large leaflets and white flowers and no anthocyanin. Kabuli type is mostly grown temperate regions and contributes to around 20% in total production. Kabuli chickpea is used for the purpose of roasted chana.

Chickpea contains 22 per cent protein, 63 per cent carbohydrates, 4.5 per cent fat, 8.0 per cent crude fibre and 27 cent ash (Miao *et al* 2009). Chickpea is low in per sodium and fat, high in protein content. They are excellent source of both soluble and insoluble fibre, complex carbohydrates, vitamins and minerals. It is rich in nutritionally important unsaturated fatty acids such as linoleic and oleic acids.

Chickpea crop has got special importance in Indian diet because it can be consumed in a various ways. Chickpea split seeds are used in the form of dal, parched, fried, roasted and boiled as snack food, sweet and condiments. The seeds are ground to flour known as besan and used in preparing various dishes like pakora, laddu etc. The tender leaves of chickpea are used as fresh green vegetables, while dry plant parts above ground are used as cattle feed. Exudation from leaves called “amb” contains oxalic and malice acids which possess medicinal value and used for intestinal disorders, stomach aches, blood purification etc. The germinated seeds are prophylactic against scurvy disease.

India is the largest producer of chickpea in the world sharing 65.2 per cent of area and 5.4 per cent of production. In India the area under chickpea was 10.20 million ha, production was 9.38 million tons and productivity was 919 kg/ha during 2016-17. Madhya Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Karnataka and Uttar Pradesh are the major chickpea producing states sharing over 95 per cent area (Anonymous, 2017). In Maharashtra, the area under chickpea was 19.29 lakh ha, production was 19.41 lakh tons and productivity was 1006 kg/ha during the year 2016-17 (Anonymous, 2017).

In spite of having a large growing area in India the productivity is less as compared to countries like Italy, Turkey, Iran, etc. The bottlenecks factors are such as rainfed crop, diseases and insect pest problem. The exploration of genetically superior accessions is the key source for development of new variety and potential breeding material for the future and to meet the demand of better yielding chickpea cultivars in India. This in turn helpful in establishing the selection strategy and identification of diverse parent which depend upon hybridization lead to a wide spectrum of gene combination.

In present context, for the development of new variety we need to have deep knowledge of genetic diversity and also about different diseases and pest. So that it will be possible to develop different variety according to need.

Wilt of chickpea caused by soil born fungus *Fusarium oxysporum* f.sp. *ciceri* is an important disease of this crop and causes heavy yield losses in most of the growing pockets. Different cultivars show disease symptoms at different growth stages and influenced the yield loss with different degree of severity. It is typical vascular disease causing xylem browning or

blackening. In India four races of *Fusarium* pathogen are present which causes the wilt diseases in chickpea. Due to prolonged nature of survival of the pathogen, cultural control such as crop rotation is not feasible and chemical control is costly. The only and the most economic control measure of chickpea wilt is the use of durable and stable resistance lines or cultivar.

Chickpea wilt is the most destructive disease in India and also first reported from India in 1918 . This disease has been reported from 33 countries of the world causing 10-15 per cent yield losses annually depending upon the environment condition . Sometimes under favorable conditions, there is a total loss of crop and yield . The pathogen can infect at all stages of plant growth with more incidences in flowering and pod filling stage. The wilt appeared in field within three to four week after sowing, if the variety is susceptible . Pathogen is seed and soil borne, saprophytic fungus optional in absence of its host, and it can survive on plant debris in soil for 6 years .

Evaluation of chickpea material in *Fusarium* wilt sick plot for the source of resistance against *Fusarium oxysporum* f.sp.*ciceri* has been a regular feature of most chickpea breeding programmes in India. To assist plant breeders to develop disease resistant material, techniques have been worked out and standardized at ICRISAT to screen germplasm. At ICRISAT, it was found that early wilting causes more loss than late wilting and the seeds harvested from late wilted plants were less heavy and dull than that from healthy plants (Haware & Nene, 1980).

The multivariate analysis by means of D^2 statistic (Mahalanobis, 1936) and path analysis are powerful tools for qualifying the degree of divergence at genotype level in respect of several traits considered together. By this analysis we can measure divergence among the various genotypes and we can also know the direct and indirect effect of various plant characters on yield. Thereafter selecting diverse genotype we can screen them for resistance against *Fusarium* wilt to identify resistant lines That's why in present investigation programme two trials was conducted first one for diversity analysis and second one for screening against *Fusarium* wilt. Screening of 33 genotypes was conducted in wilt sick plot at Pulses Improvement Project, M.P.K.V. Rahuri.

The present investigation was undertaken in chickpea with the following objectives

- 1) To identify the resistance genotypes against *Fusarium* wilt in chickpea. .
- 2) To study the correlation between yield and yield contributing characters in chickpea.

2. 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 entitled “Assessment of chickpea (*Cicer arietinum* L.) genotypes against *Fusarium* wilt” has been reviewed under the following different aspects :

2.1 Variability and genetic parameters

2.2 Correlation and Path analysis

2.3 D² Analysis or Genetic diversity analysis

2.4 Screening of chickpea for wilt resistance

2.1 Variability and Genetic Parameters

Fisher (1930) first presented the method to separate out the genotypic effects based on phenotype and environmental factors. He expressed the genotypic variability in terms of genotypic coefficient of variation.

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

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

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

Bakhsh *et al.* (1996) studied the variability in 15 chickpea genotypes of diverse origin for seed size, starch content and starch composition. They observed highly significant differences for seed weight which ranged from 191 to 496 mg, relatively small differences occurred for total starch, which made up 38-45 per cent of dry seed weight. The values for amylose and amylopectin percentage of starch were 32-42 and 58-68 per cent, respectively. Within genotype variation for starch content and amylose percentage was insignificant.

Mathur and Mathur (1996) studied genotypic and phenotypic coefficient of variation, heritability and expected genetic advance for grain yield and its contributing characters in 34 varieties of chickpea. The highest values of genotypic and phenotypic coefficients were obtained in 1000 grain weight. High heritability estimates were obtained for all the characters under study. 1000 grain weight and grain yield per plant had fairly good value of genetic advance as percentage of mean along with high heritability and therefore these characters may be considered reliable for selection in chickpea.

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

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

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

Muhammad *et al.* (2002) studied heritability and relationship of quantitative traits in 36 genotypes of chickpea. Low heritability percentage coupled with low and moderate genetic advance, observed for primary and secondary branches respectively, indicated that these traits were greatly influenced by environment. The genotypic association of primary branches with grain yield was negative. The genotypic correlation of secondary branches with grain yield was positive. A positive and non-significant relationship between primary branches and pods per plant was obtained. The relationship between number of pods and biological yield was positive

and highly significant; both of these traits had significant and positive correlation with grain yield. They suggested that plant height, number of pods per plant and biological yield may be given more importance while making selection for higher yield potential in chickpea.

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

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

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

Farshadfar and Farshadfar (2008) evaluated chickpea landraces and lines for genetic variability and path analysis. Among the morphological characters, numbers of branches, pod numbers with CV: 41.77 and 37.25% had higher variation, respectively while leaflet with CV: 10.49% had minimum variation. Path analysis revealed that the pod numbers with 0.745, seed numbers with 0.386, 100 seed weight 0.268 and single seed with 0.267 had highest direct effect on yield.

Borate *et al.* (2010) studied for population parameters such as range, mean, phenotypic and genotypic variances, PCV and GCV, heritability and genetic advance for 13 agronomic characters in a set of 30 chickpea genotypes. Range of variability was appreciable for days to first flowering, secondary branches, plant height, dry matter and grain yield. Values of genotypic

and phenotypic variances were highest for number of pods, while lowest for number of seeds per pod. PCV showed higher values than GCV for all characters. High heritability coupled with high genetic advance was observed for grain yield. Plant height, dry matter, days to first flowering and days to maturity indicated high additive gene effects.

Akhtar *et al.* (2011) estimated genetic variability, heritability and interrelationships for seed yield and its components in 20 advance genotypes in chickpea. Significant and positive correlations were found between yield and 100-seed weight, number of pods per plant and plant height. Broad sense heritability ranged from 89.61 (seed yield) to 99.99% (100 seed weight). Heritability's for 100-seed weight and number of pods per plant were the greatest compared to other traits. Phenotypic coefficient of variation (PCV) for days taken to flowering, days taken to maturity, plant height and seed yield were higher than genotypic coefficient of variations (GCV), which means that the expression of these traits is more influenced by environmental effects. They reported that the grain yield could be improved by using the 100 seed weight and number of pods per plant in chickpea.

Zali *et al.* (2011) studied 17 chickpea genotypes and determined the association between genetic parameters and traits. Heritability values were greater for number of days to maturity (98.43%), number of days to 50 per cent flowering (98.19%), plant height (58.87%), number of secondary branches (45.81%), number of primary branches (42.03%) and number of seeds per plant (35.42%), indicating that these traits were controlled mainly by additive genes and that selection of such traits may be effective for improving 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 had positive and highly significant phenotypic correlations with seed yield. Stepwise regression analysis indicated that number of seeds per plant and 100-seed weight explained 96 per cent of total yield variation. Hence 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, number of seeds per plant and 100 seed weight.

Ali and Ahsan (2012) evaluated twenty elite genotypes and three standard varieties of chickpea for means and components of variability, heritability, genetic advance and interrelationships for various parameters. Correlation studies showed that genotypic and phenotypic correlations of grain yield per plant with number of secondary branches per plant, total plant weight, number of pods per plant and number of grains per plant was positive and highly significant. Genotypic correlation of grain yield per plant with plant height was positive and significant. Genotypic and phenotypic correlations of grain yield per plant with number of days taken to maturity were negative and highly significant.

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

Gul *et al.* (2013) evaluated twenty chickpea genotypes for genetic potential, heritability, genetic advance and traits association of yield contributing characters. Broad sense heritability estimates were highest for pods per plant (0.88), primary branches per plant (0.83), 100-seed weight (0.82), seed yield per plant (0.75) and secondary branches per plant (0.77). Genetic advance was higher for pods per plant (40.14), seed yield per plant (38.24%), primary branches per plant (36.64%) and secondary branches per plant (30.25%). Seed yield per plant showed highly significant genetic as well as phenotypic correlation with pods per plant, number of primary branches per plant, secondary branches per plant and 100 seed weight in positive direction. Hence, pods per plant, number of primary branches per plant, number of secondary branches per plant and 100 seed weight would be the appropriate selection criteria for better seed yield in chickpea.

Mushtaq *et al.* (2013) investigated for variability parameters and path coefficient analysis in twenty elite chickpea genotypes including three standards. Heritability estimates was maximum for days taken to flowering, days taken to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100-grains weight and grain yield per plant while other characters exhibited moderate heritability. Seed yield was positively correlated with all attributes under study. Investigations regarding path coefficient showed that days taken 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 b.) assessed the magnitude of genetic variability, heritability and genetic advance and genetic diversity 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 (GCV) and high genetic advance as per cent of mean (GA%) were observed for seed yield per plant, biological yield per plant, harvest index, number of pods per plant and 100-seed weight which indicated that response to selection would be very high for these yield components. Three traits viz., seed yield per plant, 100-seed weight and number of pods per plant contributed more than 63% of towards total genetic divergence.

Kumari *et al.* (2013) assessed genetic variability among 32 advanced breeding lines of chickpea for grain yield and early duration in a randomized block design. Highest genotypic

coefficient of variance (GCV) was studied in seed yield per plant. Heritability in broad sense ranged from 55 per cent for total yield followed by 53 per cent for days to 50 per cent flowering. High expected genetic advance coupled with high heritability estimate was obtained for plant height, number of secondary branches per plant, number of pods per plant and seed yield per plant. It suggested the dominant role of additive gene effects in expression of these traits. Grain yield per plant had positive and significant association with biological yield, harvest index, test weight was also estimated.

Mohamed *et al.* (2015) assessed genetic variability and yield stability in chickpea cultivars. Eight chickpea cultivars (Shendi, Jabel Marra, Wad Hamid, Atmor, Hwata, Burgeig, Salwa and Matama) were evaluated for genetic variability, yield stability and contribution of yield attributes to seed yield. Field experiments were carried out for four seasons in RBD with six replications. Most of the studied traits recorded highly significant difference ($P < 0.01$) due to cultivars, seasons and their interaction. High heritability and low level of differences among phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for studied traits indicated that cultivars influenced more in the expression of these traits. Based on the stability analysis for seed yield; the top yielding cultivars Burgeig and Hwata were adapted to favourable conditions. Both cultivars were late in flowering and maturity and had high number of seeds plant⁻¹, biomass and harvest index. The cultivar Atmor with an intermediate seed yield was the most stable cultivar across seasons. The cultivar Salwa is optional due to its relatively high yield and large seed size. Combining farmer preferred traits such as high and stable yield, large seed size, plant type and maturity into new cultivars will remain the main objective of the chickpea breeding program in Sudan.

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

Arora *et al.* (2018) studied fifty genotypes of kabuli chickpea for assessment of genetic variability. All genotypes exhibited wide range of variability for all the characters. Maximum variability was recorded for number of pods per plant and minimum for number of days to maturity. There were close agreement between GCV and PCV for number of days to flowering,

number of days to maturity and 100-seed weight. Highest heritability was observed for 100 seed weight. Genetic advance as per cent of mean was maximum for number of pods per plant. High heritability coupled with high genetic advance was observed in case of number of pods per plant. Thus, it may be concluded that a great amount of variability existed in the present material.

Kishor *et al.* (2018) investigated forty chickpea genotypes to find out genetic variability, genetic association and path coefficient analysis for grain yield and its attributing characters. The analysis of variance revealed highly significant differences among genotypes for all the characters studied. Number of pods per plant followed by biological yield per plant, number of seeds per plant, seed yield per plant, number of primary branches per plant, 100 seed weight had high phenotypic and genotypic coefficient of variation. The characters viz., days to 50 per cent flowering, days to maturity, 100 seed weight, plant height, number of seeds per plant, lower branch height, number of pod per plant, biological yield per plant, seed yield per plant, number of primary branches per plant showed least differences among GCV and PCV. Estimates of high heritability were observed for number of seeds per plant (96.90%) followed by number of pods per plant, 100 seed weight, days to 50 per cent flowering, plant height, days to maturity, seed yield per plant, number of primary branches per plant. number of pods per plant, biological yield per plant, number of seeds per plant, seed yield per plant and number of primary branches per plant have high values of heritability coupled with high genetic advance as per cent of mean.

2.2 Correlation and Path Analysis

In chickpea breeding programme, the knowledge of association of one or more of these characters associated with yield is useful in selecting the individual with high yield on the basis of their phenotypic values. Such association between plant characters is statistically elaborated by correlation coefficients. But the correlation between the dependent and independent character and the direct and indirect effects of the independent character on the dependent character are completely separate things. Sometime the correlation between two characters may be highly positive but the direct effect of the independent characters on the dependent characters may be negative. Hence, mere correlation cannot serve the purpose of selection in crop improvement programme. In a complex situation, selection for an optimum advance should be based on judiciously computed index. Therefore, the method of partitioning the direct and indirect effects of the independent character on the dependent character i.e. path coefficient analysis was detailed by Wright (1921). Li (1954) emphasized great use of this technique in genetics arid plant breeding. Further, Dewey and Lu (1959) gave the detail procedure for path analysis of replicated trials which was quite different technique in eliminating the environmental variances.

Dasgupta *et al.* (1992) studied for yield correlation with 9 yield components in 28 chickpea genotypes and reported that, seed yield was significantly and positively correlated with pods per plant, seeds per plant, 100 seed weight and seeds per pod but not to days to maturity. The correlation between pods per plant and seeds per plant was also significant and positive. Path coefficient analysis indicated that pods per plant, seeds per plant, 100 seed weight and seeds per pod registered highly positive direct effects on yield.

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

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

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

Jeena and Arora (2002 b.) studied 40 genotypes for yield and its component traits. Correlation among all the characters computed and subjected to path analysis. Biological yield exhibited highest positive correlation with seed yield coupled with highest positive direct effect

on it. Biological yield, pods per plant, 100 seed weight and first pod forming node found to be the major yield contributor traits from selection point of view.

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

Saleem *et al.* (2002 b.) studied interrelationships and path analysis of yield attributes in a set of 20 chickpea elite genotypes. Seed yield per plant was positively and significantly correlated with days to flowering, total weight of plant, number of pods per plant and 100-seed weight both at the genotypic and phenotypic levels. The correlation of number of secondary branches per plant with seed yield was negative and significant. Number of pods per plant had maximum positive direct effect on seed yield. They concluded that number of pods per plant and 100-seed weight could be used as selection criteria to improve the yield.

Noor *et al.* (2003) studied that phenotypic and genotypic variances, heritability in broad sense (h^2), G.A., correlation and path analysis for yield and yield components in 30 genotypes of chickpea under rainfed conditions. Medium to high G.A. for days to flowering, maturity, secondary branches and 100 seed weight, while low to medium heritability observed with low G.A. for other characters. Improvement of these traits through direct selection was suggested. Days to flowering, maturity and low seed weight exhibited high heritability coupled with high G.A. hence crop improvement through these traits is possible by simple selection. It was concluded that to improve grain yield emphasis should be given on development of chickpea with higher seed weight and biological yield. Both correlation and path analysis indicated that pods per plant and 100 seed weight were potent contribution to grain yield through direct effects.

Arora *et al.* (2003) studied eighty chickpea genotypes for eighteen traits including seed yield per plant. The correlation study revealed that primary branches per plant expressed the highest significant positive relationship with seed yield per plant followed by biological yield per plant, pods per plant, 100-seed weight, plant height, canopy spread, seeds per plant, secondary branches per plant and harvest index. Biological yield per plant had the highest positive direct effect on seed yield per plant followed by harvest index, pods per plant, 100 seed weight and seeds per pod.

Muhammad *et al.* (2004) studied in chickpea for variability, heritability, genetic advance, correlation coefficient and path coefficient for yield and its components in 24 advance

lines. High heritability with low genetic advance of days to flowering, days to maturity and 100 seed weight indicated the influence of dominant and epistatic genes for these traits. High heritability of secondary branches and biological yield coupled with high genetic advance revealed that additive gene effects are important in determining these characters. Grain yield had positive and significant correlation with plant height, pods per plant, 100 seed weight and biological yield. High direct effects were contributed by biological yield and harvest index although the latter had negative association with grain yield.

Yucel *et al.* (2006) studied 15 kabuli genotypes. Direct and indirect effect of yield components on seed yield per plant was investigated. Genotypic variance was the highest for 100 seed weight followed by number of seeds per plant. Positive and significant ($P < 0.05$) relationships were determined between seed yield per plant and plant height, first pod height, secondary branch, total pod and number of full pods and seeds per plant. This research suggests that seed and full pod numbers can be good selection criteria for improving seed yield per plant in kabuli winter chickpea.

Renukadevi and Subbalaxmi (2006) worked out correlations and path coefficient analysis for eleven characters including seed yield in fifty chickpea genotypes. Plant height, number of primary branches, number of pods per plant, 100 seed weight, biological yield per plant and harvest index had positive and significant correlation with seed yield. The positive direct effect on seed yield was revealed by plant height, number of primary branches per plant, number of pods per plant, biological yield per plant, harvest index, days to maturity and soluble protein content. The magnitude of residual effect was very low which indicated that the studied eleven characters contributed most of the portions of the variability in the seed yield.

Talebi *et al.* (2007) studied correlation and path analysis of yield and yield components of 36 chickpea genotypes under dry land condition. Positive and significant relationships were found statistically between 100 seed weight and plant height, between number of secondary branches and plant height, between days to heading and days to maturity, between days to maturity and number of primary and secondary branches, between seed yield and number of pods per plant and number of seeds per pod, between seed yield and biomass and harvest index were determined significantly. Negative and significant relationships were determined statistically between number of pods per plant and 100 seed weight, between seeds per pod and number of secondary branches. Harvest Index had the greatest direct effect on seed yield ($PC = 0.901$). Also, its indirect effect on seed yield was more positive through plant height, number of pods per plant, number of seeds per pod and biomass, but negative and low through days to heading and maturity, 100 seed weight and number of primary branches. The selection for high seed yield should be based on biomass and harvest index.

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

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

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

Vaghela *et al.* (2009) studied correlation coefficient and path coefficient for yield and its components in chickpea genotypes. The magnitude of genotypic correlation coefficients was higher as compared to their corresponding phenotypic correlation coefficients for most of the characters. Seed yield per plant exhibited significant and positive correlation with biological yield, number of pods per plant, harvest index, number of seeds per pod, number of primary branches per plant and 100 seed weight at genotypic as well as phenotypic levels. Path coefficient analysis indicated the highest positive direct effect of biological yield per plant followed by harvest index towards seed yield. The biological yields per plant and harvest index were found to be the most valuable traits for formulating selection criterion to improve seed yield in chickpea.

Gohil and Patel (2010) evaluated twenty-two genetically diverse genotypes of chickpea under rainfed condition to understand the contribution of various characters to the yield. The genotypic correlation coefficients were higher than corresponding phenotypic ones for most of the character combinations. 100 seed weight and harvest index had a significant positive

association with seed yield. Pods per plant and seed per pod had a positive association with seed yield. The maximum direct positive and negative contribution to seed yield was observed from biological yield per plant and days to maturity, respectively. The harvest index, 100 seed weight, pods per plant and earliness were most important characters which can be used to improve yield in chickpea under rain fed area.

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

Ali *et al.* (2011) estimated correlation for quantitative traits in chickpea (*Cicer arietinum*). Correlation studies showed that biomass per plant, number of pods per plant, number of secondary branches 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 days taken to maturity, primary branches per plant, 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 level.

Zali *et al.* (2011) determined the association between genetic parameters and traits in 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 correlation with seed yield. Stepwise regression analysis indicated that number of seeds per plant and 100 seed weight explained 96 per cent of total yield variation. Hence, 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, number of seeds per plant and 100 seed weight.

Kumar *et al.* (2012) studied the genetic variability, character association and path analysis in early segregating population in chickpea. 100 seed weight followed by harvest index, pods per plant and seed yield per plant exhibited high estimates of heritability (broad sense) as well as genetic advance. Correlation coefficient analysis revealed that seed yield per plant exhibited significant and positive correlation with harvest index, 100 seed weight and number of pods per plant at both phenotypic and genotypic levels. Direct selection for 100 seed weight and

number of pods could be helpful in the improvement of chickpea breeding. 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 phenotypic and genotypic levels.

Mehmet and Babagil (2013) studied in chickpea cultivars across three locations and three years to find out the correlation and path coefficients between seed yield and plant height, number of main branches, first pod height, pod number per plant, seed number per plant and 100 kernel weight of four chickpea cultivars. Seed yield positively and significantly correlated with all characters except 100 kernel weight. Positive direct effects of plant height and pod number per plant had significant correlation with seed yield suggested that these yield components may be good selection criteria to improve chickpea cultivars.

Jivani *et al.* (2013 a.) estimated correlation and path coefficient analysis for seed yield per plant and its ten component characters in a set of 105 diverse genotypes of chickpea. The seed yield per plant had significant and positive correlation with number of pods per plant, biological yield per plant and harvest index at both genotypic and phenotypic levels. Among the component traits, biological yield per plant had significant and positive association with plant height, number of pods per plant and 100-seed weight. Path coefficient analysis revealed that the maximum positive direct effect was observed for harvest index followed by biological yield per plant, number of pods per plant, and 100-seed weight towards seed yield and these were considered to be the most promising traits for selection for higher seed yield in chickpea.

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

Parhe *et al.* (2014 b.) evaluated chickpea lines for studying correlation among yield components and their direct and indirect influences on grain yield. Path coefficient analysis revealed that 100 seed weight, number of pods plant⁻¹ and number of secondary branches plant⁻¹ had the highest positive direct effects on grain yield. Improvement of the grain yield can be immensely efficient via 100 seed weight, number of pods plant⁻¹, number of primary branches plant⁻¹ and number of secondary branches plant⁻¹ based selection.

Barde (2015) studied in 83 chickpea genotypes; the path coefficient analysis revealed that number of pods per plant had highest direct effect (0.79) on seed yield per plant followed by 100 seed weight and number of primary branches per plant and number of seeds per plant.

Muhammad *et al.* (2016) studied in 20 genotypes of chickpea for estimation of genetic variability and interrelation of various yield component traits by using path analysis and correlation analysis. It was found that, harvest index and number of seeds per plant had a significant and positive association with seed yield. The path analysis was done by using seed yield as dependent variable, revealed that maximum positive direct effect toward seed yield was exerted by number of pods per plant (0.4451) with 52.87% ratio. Correlation coupled with path coefficient analysis revealed that number of pods per plant had a direct relationship with seed yield. This research suggests that for improvement of seed yield the selection upon number of pods per plant will provide favourable results in chickpea.

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

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

Singh *et al.* (2018) study was conducted to determine heritability, variability, and correlations between yield and yield components in 15 chickpea (*Cicer arietinum* L.) genotypes

for 2 years. Direct and indirect effects of yield components on seed yield per plant were investigated. Heritability for seed number, 100 seed weight, and number of full pods were greater than those for the other traits. Positive and significant ($P < 0.05$) relationships were determined between seed yield per plant and plant height, first pod height, secondary branch, total pods, and number of full pods and seeds per plant. The path coefficient analysis based on seed yield per plant, as a dependent variable, revealed that all of the other traits, except days to flowering, first pod height, and total pod number, exhibited high positive direct effects. Number of seeds and full pods showed the highest direct influence with 47.49% and 44.73%, respectively. Therefore, this research suggests that number of seeds and full pod numbers can be good selection criteria for improving seed yield per plant in chickpea.

2.3 D² Analysis or Genetic Diversity Analysis

2.3.1 Concept of Genetic Diversity

The approach for assessing variability involves the study of genetic diversity present within a population. Two important biometrical techniques, viz., D² statistic and metroglyph analysis, are commonly used for this purpose. In my research work I had used D² Statistic for measuring the genetic diversity. A brief description of these techniques is described below.

2.3.2 D² Statistic

The variability present among different genotypes of a species is known as genetic diversity. A population of an organism when contains a large gene pool that is, if the genetic blueprints of individuals in the population vary significantly the group has a greater chance of surviving and flourishing than a population with limited genetic variability.

One of the potent techniques for measuring the divergence between two populations is the concept of D² statistic proposed 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 two pairs of groups and classifies 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 or genetic stocks with respect to individual trait or array of traits. The inherent variations are called as genetic variations and produce genetic diversity.

Mahalanobis *et al.* (1949) employed D² statistical analysis in detailed study of anthropometric data of Uttar Pradesh classifying in 23 groups and into three major clusters i.e. Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising nine groups, the Artisan

(A-cluster) in the middle consisting of four groups and the Trivial (T-cluster) at the bottom consisting of ten groups.

2.3.3 Genetic Divergence in Chickpea

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

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

Adhikari and Pandey (1983) measured genetic divergence by Mahalanobis's D^2 and principal component analysis in 36 varieties obtained from ten major chickpea growing states of India. The varieties were grouped into 9 different clusters. The cluster of desi group was quite diverse from kabuli ones. Further independent classification by principal component analysis confirmed the classification derived by D^2 analysis.

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

Mian and Bahl (1989) had done multivariate analysis to find out genetic divergence among 28 chickpea populations comprising 7 parents and 21 hybrids from all possible crosses among the parents. The D^2 values ranged from 2.20 to 147.71, indicating sufficient divergence in the populations for different characters. The 28 chickpea populations and 21 hybrids were grouped into 13 clusters. Parental genotypes originating from the same geographical region also

did not show any affinity among themselves in the formation of clusters, thus, showing lack of correspondence between geographical and genetic diversity. Study of relationship between divergence of the parents and heterosis in the hybrids revealed that the parents separated by D^2 values of medium magnitude generally showed higher heterosis for different characters.

Samal and Jagdev (1989) studied genetic diversity in 23 cultivars of chickpea. They obtained six clusters on the basis of D^2 analysis with seven yield components.

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

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

Sirohi *et al.* (1999) noted a wide range of genetic divergence in 25 genotypes of chickpea for six yield related traits. These strains were grouped into 7 clusters. The cultivars within a cluster showed smaller D^2 values than those belonging to two different clusters. 100-seed weight and seed yield per plant were mainly responsible for genetic divergence. Based on inter cluster distances, crossing of cluster IV genotypes with V, VI and VII was suggested to get maximum heterotic effect in F_1 and a broad spectrum of variability in the segregating generations to isolate superior individuals for yield and its components.

Khan (1999) studied for genetic divergence among 36 geographically diverse chickpea genotypes by using D^2 statistic. The genotypes were grouped into eight clusters on the basis of yield and yield components. It was concluded that hybridization among the genotypes from cluster I and II may result in high yielding varieties.

Nimbalkar and Harer (2001) grouped 40 genotypes into 16 clusters. D^2 values between all possible pair of 40 genotypes ranged 12.62-3979.93. Out of 16 clusters, 10 were

monogenotypic, cluster II was the largest comprising of 12 genotypes followed by cluster I and IV containing 9 and 3 genotype respectively. The genotypes of cluster XVI and cluster III were maximum divergent. Variance of cluster means indicated pods per plant followed by plant height and 100 seed weight were the main trait contributing to the genetic divergence.

Jeena and Arora (2002 a.) measured genetic diversity among forty genotypes of chickpea by Mahalanobis D^2 technique for 18 quantitative traits. These genotypes grouped into 12 diverse clusters. Genotypes from U.P. distributed in most of the clusters showed greater diversity among them. Maximum intra-cluster distance was recorded for cluster IV, while highest inter-cluster distance was observed between cluster VIII and XII.

Kashyap and Rastogi (2003) studied genetic divergence by D^2 techniques for seed yield and its components in 60 chickpea germplasm accessions. The analysis of variance revealed significant differences among the genotypes for each character under study. The genotypes were grouped into 6 clusters and maximum intra-cluster distance was observed in cluster I, comprising 14 genotypes, cluster III and VI were identified as genetically divergent. Considering the cluster means and cluster distances the genotypes IG-327, IG-326, IG-323, IG-311, IG-314 of cluster V, ICCV-89243, ICCV-91020, ICCV-91024, ICCV-91007 IG-313 of cluster VI, ICCV-91004, ICCV-91003, ICCV-89228, ICCV-91012 ICCV-89294 of cluster I were the most promising genotypes. They may be utilized in future breeding programme to obtain high heterotic effect or to develop desirable recombinants.

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

Singh *et al.* (2006) studied cluster analysis among 204 genotypes of chickpea excluding checks for nine quantitative traits revealed considerable genetic diversity in the material. Ten clusters for nine characters were obtained. Cluster II was consist of maximum 38 genotypes followed by cluster X which consisted of 35 genotypes, whereas cluster I consisted of two genotypes. The maximum inter cluster distance was recorded between cluster I and IX followed by cluster I and IV, I and VI. Hence genotypes belonging to these clusters can be used as parents for hybridization programme for the development of high yielding chickpea genotypes.

Sikarvar *et al.* (2006) assessed that genetic diversity among 204 genotypes of chickpea excluding checks for nine quantitative traits. Ten clusters for nine characters were obtained. Cluster III consisted of maximum 38 genotypes followed by cluster X which consisted of 35 genotypes whereas, cluster I consisted of two genotypes (as cluster I showed the maximum intra cluster distances with other clusters hence both genotypes) the maximum inter cluster distance was recorded between clusters I and IX followed by clusters I and V and I and VI. Hence genotypes belonging to these clusters can be used as parents for hybridization programme for the development of high yielding chickpea genotypes.

Verma *et al.* (2008) divided 108 genotypes into four different groups of cultivars on the basis of seed size viz., i) desi- medium seeded, ii) desi-bold seeded, iii) kabuli-bold seeded and iv) kabuli-extra bold seeded. All the diverse genotypes were planted in a randomized block design with three replications.

Dwevedi and Gaibryal (2009) studied the nature and magnitude of genetic divergence using Mahalanobis's D^2 statistics among the 25 genotypes of chickpea. The data were recorded on ten important quantitative traits from the genotypes. 25 genotypes were grouped into six clusters. The cluster I shows largest cluster with cluster I and VI. There characters viz. harvest Index, 100 seed weight and number of pods per plant contributed maximum in manifestation of genetic diversity.

Sidramappa *et al.* (2010) studied 126 RILs derived from a cross ICCV-2 x JG 62 along with six checks were evaluated to study the genetic divergence. Mahalanobis's D^2 statistical analysis was used for assessing the genetic divergence among the RIL's involving phenological and yield component traits. The 126 genotypes formed 15 clusters and out of which eight clusters were solitary suggesting the very diverse nature of eight RIL's from rest of the genotypes. The two solitary clusters VIII and X showed their distinctiveness from the other groups as reflected by generally higher magnitude of 04, inter cluster distance values of these two clusters with other clusters and were characterized by mean high pod number, seed yield and ideal duration of productivity phase. The pods per plant contributed maximum (76.58%) among all the characters studied.

Jadhav *et al.* (2011) evaluated eighty seven genotypes along with four checks viz., BDN-9-3, BDNG- 797, G-12 and Annegiri for eleven yield and yield contributing characters. Analysis of variance showed significant differences for all characters except number of primary branches per plant and number of seeds per pod. All the 91 genotypes were grouped into 7 clusters. The first cluster was largest with 80 genotypes. On the basis of D^2 estimates and mean performance of yield and other traits, genotypes viz., G-95, G-63, G-79 B-32, BCP-17, L-111 and L-313 can be fairly utilized in hybridization programme for further improvement.

Tomar *et al.* (2011) had grown forty-five genotypes of chickpea in twelve environments in order to select potential parents for hybridization. Based on D^2 values, 45 genotypes were grouped into eight clusters. Cluster V consisted of 8 genotypes followed by cluster VIII and VI, which had 7 and 6 genotypes, respectively. Maximum intra-cluster distance (2.89) was observed in cluster VIII, followed by cluster VI (2.58), cluster IV (2.34) and cluster I (2.33). Maximum inter-cluster distance was noticed between cluster IV and VIII (6.38). They suggested that crossing between genotypes from the cluster IV and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

Ahmad *et al.* (2012) studied the genetic diversity of 70 accessions from Pakistan and USA using morphological traits and seed protein. Based on four morphological traits, the average coefficient of variation was calculated as 56.8 per cent with significant correlation among yield traits. The cluster analysis based on protein data revealed 50 per cent genetic diversity among accessions.

Sewak *et al.* (2012) assessed genetic diversity among 495 accessions of chickpea collected from different agro-ecological zones of India for several qualitative and quantitative traits. These accessions were grown in the augmented design with 3 intermittent checks “BG 256”, “K 850” and “L 550” after every fifteenth row. Wide range of variability was observed for both qualitative and quantitative traits. The number of primary branches, 100 seed weight (g) and days to maturity showed moderate to high heritability and genetic advance. This suggests that the selection based on these traits would be useful in improving the grain yield. The diversity index indicated ample genetic variation for seed yield per plant in the present set of materials. Therefore, a direct selection 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) studied the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics in 64 genotypes of chickpea that included 60 interspecific derivatives, their parents and two standard checks on 11 morphological traits. The 64 genotypes were grouped into 9 clusters. Cluster II was the largest with 14 genotypes. Highest inter-cluster distance was recorded between cluster VI and IX, while highest intra cluster distance was found among the genotypes of cluster VIII. Characters like biological yield per plot, seed yield per plot and days to 50 per cent flowering contributed maximum towards the genetic diversity. The genotypes GL29009, GL29012, GL29013, GL29017, GL29019, GL29034, GL29042, GL29046, GL29069, GL29072 and GL29078 were identified as genetically diverse parents who can be used for future crop improvement programme.

Syed *et al.* (2012) measured genetic diversity among 27 chickpea genotypes through Mahalanobis D^2 and Principal Component Analysis. The genotypes under study fall into five

clusters. The cluster II contained the highest number of genotypes (11) and cluster I contained the lowest. Cluster I produced the highest mean value for number of pods per plant. The inter cluster distances were much higher than the intra cluster distances. Cluster V exhibited the highest intra cluster distance, while the lowest distance was observed in cluster I. The highest inter cluster distance was observed between cluster I and II, while the lowest was between cluster III and V. Considering all the characters, it was suggested that the genotypes BD6549, BD6603 and BD6548 could use as parents for future breeding programmes to develop high yielding varieties of chickpea.

Pandey *et al.* (2013) evaluated twenty two chickpea genotypes were evaluated during Rabi seasons of 2007-08 and 2008-09 to explore the possibility of introducing chickpea crop into the cropping system of the mid-altitudes of Meghalaya. All the test chickpea genotypes could be grouped into five distinct clusters. An analysis of the percentage contribution of individual characters towards genetic diversity revealed that days to flowering, 100-seed weight and number of pods/plant were the major characters contributing to genetic diversity in chickpea. Based on the results it may be concluded that chickpea can be successfully grown in Meghalaya and chickpea improvement can be undertaken in the mid hill conditions of north eastern hill region of India.

Parashi *et al.* (2013) grouped sixty chickpea genotypes into 13 clusters. The cluster I was the largest cluster with 33 genotypes. Highest inter-cluster distance was observed between cluster VII and cluster XIII ($D^2 = 194.04$) followed by cluster XI and III ($D^2 = 156.50$), cluster VI and XIII ($D^2 = 130.64$), cluster IV and XI ($D^2 = 119.46$). Three characters viz. yield per plant (34.29%), stomatal conductance (27.97%), number of pods per plant (16.33%), contributed maximum genetic diversity. The genotypes Virat, Digvijay, Rajas, IC-269643, IC-268978, IC-269257 and Vijay were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

Nawab *et al.* (2013) studied in twenty chickpea genotypes for patterns of morphological diversity and character association through multivariate approach. Three principal components were deduced (Eigen value > 1) which contributed to a total variability of 62.83% among the genotype. PC-I contributed 34.78% to total variation. Factor loadings revealed that all the characters contributed positively to PC-I except days to flowering and plant height. Days to flowering exerted maximum negative load on the factor I while the highest positive contribution to the PC-I was endorsed by number of pods per plant, seeds per plant, biological yield, and grain yield per plant. Secondary branches, plant height, seeds per plant, 100 seed weight and biological yield had positive weight on PC-II where secondary branches followed by plant height showed the maximum contribution. Days to maturity, primary branches, plant height, seeds/pod

and 100-seed weight exerted positive factor loadings on PC-III among which the highest weight was contributed by plant height followed by number of primary branches. Cluster I and II comprised of seven lines each. This study suggested scope for selection for grain yield and its components.

Devendrappa *et al.* (2013) measured genetic diversity among 121 genotypes of chickpea using Mahalanobis D^2 statistics. Based on D^2 values, 121 genotypes were grouped into 16 clusters of which cluster I was largest with 27 genotypes. Days to physiological maturity (45.46%) and seed yield per plant (42.79%) contributed maximum to the total divergence. Maximum intra cluster distance was observed for Cluster IV (49.12) which indicated that twenty one genotypes in cluster IV were most divergent. Maximum inter cluster distance was observed between Cluster VIII and X (89.46) followed by Cluster IX and X (89.4), suggesting maximum diversity between them. Three genotypes from cluster VIII (ICC6816, ICC 12492, and ICC 13461) could be utilized as parents in further breeding programme with the desirable genotypes belonging to cluster X.

Malik *et al.* (2014) studied genetic diversity analysis of morpho-genetic traits in 113 desi chickpea genotypes was studied through descriptive, principal component and cluster analysis. High variances were observed for days to flowering, maturity, plant height, pods plant⁻¹, biological yield and harvest index. These traits also showed positive significant correlation with yield which was confirmed through principal component analysis.

Parhe *et al.* (2014 a.) studied chickpea genotypes to investigate the nature and magnitude of genetic divergence using Mahalanobis's D^2 statistics. The fifty one Chickpea genotypes were grouped into five clusters. Cluster I was largest with forty genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster I and V, followed by cluster II and V suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters *viz.*, 100 seed weight, number of pods per plant and days to 50% flowering contributed maximum in manifestation of genetic diversity.

Johnson *et al.* (2015) studied 112 genotypes (85 germplasm accession, 12 improved varieties and 15 advance breeding lines) to know the nature and magnitude of genetic divergence using Mahalanobis's D^2 statistics, correlation using Miller and path analysis by Dewey and Lu. 112 genotypes of chickpea were grouped in eight clusters. The highest inter cluster distance was observed clusters IV and VII (6.296) followed by I and VII (5.867), IV and V (5.681), I and IV (5.658). The highest intra-cluster distance was observed cluster V (2.328). Hence, genotypes belonging to this cluster *viz.*, ICC 251834, ICC 275466, ICC 269530, Indira Chana-1, ICC

269563, RG 2011-01, RG 2011-03 and JG 11 can be utilized as parents in future chickpea improvement programmes.

Kushwaha *et al.* (2017) studied eighty-four genotypes of chickpea to know the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics. The data were recorded on ten important traits from the genotypes grown in randomized block design having three replications. All the 84 genotypes were classified into 8 clusters. The inter-cluster distances were greater than intra-cluster distances this indicates that a considerable amount of genetic variability was present in the study material. Inter cluster D^2 values ranged from 22.935 to 6.589. Maximum inter cluster distance was between cluster V & cluster VIII (22.935), while minimum inter cluster distance (6.589) was observed between cluster II & cluster IV indicating presence of diversity in these clusters. The cluster V showed maximum intra cluster D^2 value (5.645). Cluster VIII which consists of 8 genotypes showed maximum mean value for number of pods per plant and seed yield per plant may be of importance for yield characters. diverse clusters namely, V and VIII consists of diverse parents hold good promise for potential hybrids for desirable characters and thereby creating greater possibilities of obtaining early type high yielders.

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

Agrawal *et al.* (2018) conducted an experiment to study the existing genetic diversity in thirty six Desi chickpea genotypes under normal sown condition. All the genotypes were grouped into seven clusters as per ward minimum variance method revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and yield attributing traits. The cluster II containing the maximum of 13 genotypes followed by 9 genotypes in cluster I, 5 genotypes in cluster III, 3 genotypes each in cluster IV and V, 2

genotypes in cluster VI and mono-genotypes in cluster VII. The intra-cluster D^2 value ranged from 0.00 to 421.27 while, inter-cluster D value ranged from 402.80 to 3912.66. The highest intra-cluster distance was exhibited by cluster I (421.27) followed by cluster VI (316.27) and III (315.69). The highest inter cluster distance was observed between cluster II and VII (3912.66) followed by cluster II and VII (3831.40), cluster III and VI (2804.51) and cluster IV and VII. The genotypes of cluster VII showed the highest mean values for grain yield per plant, harvest index, biological yield per plant, primary and secondary branches per plant, plant height and days to maturity, while cluster VI showed the highest mean for grain yield per plot, total number of pods per plant, effective pods per plant and days to 50% flowering.

Saha *et al.* (2018) studied 70 elite lines of desi chickpea from diverse sources sown in RCBD in seed breeding farm, JNKVV, Jabalpur (2016-17). Maximum per cent contribution towards the divergence observed for total number of pods per plant followed by height of first fruiting node, harvest index and biological yield. These characters were responsible for expressing maximum diversity between the clusters should be considered prime during selection. On the basis of D^2 values 70 elite lines were grouped into 11 clusters, the maximum lines were grouped in cluster I (24 lines) followed by cluster II and VII (11 lines), IV (10 lines), III (8 lines) and cluster V, VI, VIII, IX, X and XI had only one line in each. Cluster VII was the most diversified, having highest Intra-cluster distance followed by cluster VI, III, II and I, whereas cluster V, VI, VIII, IX, X, XI were mono-genotypic. The inter cluster divergence was observed maximum between genotypes of cluster VII and VIII followed by cluster V and VIII, cluster VI and X, cluster VI and VIII, cluster V and X. Cluster VI showed maximum mean value for 100 seed weight, biological yield plant⁻¹ had high mean value in cluster VIII, harvest index were recorded maximum in cluster V, seed yield plant⁻¹ showed maximum value in cluster VI. Divergence elite lines *viz.*, SAGL 152210, ICCX-090021-P19, IPC 2012-31, JG 14, JG 2016-141611, NBeG 873, Phule G 0805-17-5, JAKI 9218 grouped in different clusters, intercrossed for inducing variability in the respective characters and their rationale improvement for increasing seed yield in chickpea.

2.4 Screening of Chickpea for Wilt Resistance

Haware *et al.* (1992) studied 13500 chickpea (*Cicer arietinum* L.) germplasm accessions for resistance to race 1 of *Fusarium oxysporum* f.sp. *ciceri* at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. One hundred and sixty accessions were found resistant through field and pot screening.

Halila and Strange (1997) screened 1915 kabuli chickpea lines against resistance to *Fusarium* wilt. Out of 1915 lines complete resistance was found in 110 lines and this result was

confirmed by a laboratory screening method. Principal components analysis showed that > 80% of the variation of the resistant lines was explained by hundred seed weight and days to maturity.

Muhammad *et al.* (2001) screened chickpea germplasm against *Fusarium* wilt. Out of 31 lines evaluated only three lines 99109, 99112 and 99115 were found to be highly resistant; two lines 1040/99 and 99104 were moderate resistant and other exhibited susceptible to highly susceptible reaction.

Chaudhry *et al.* (2006) evaluated 414 germplasm against *Fusarium* wilt in a wilt sick plot developed at Pulses Research Institute, Faisalabad. Six lines (02007, 02024, 02065, 02095, 03009, and 03020) of Pulses Research Institute, Faisalabad and four of AZRI, Bhakkar (981(007, ICCV97038, ICCV37 and 2KCC005) were found resistant. Similarly six lines originated from ICARDA and six lines of BARI, Chakwal were found intermediate resistant to chickpea wilt, whereas Karak-98, Balkassar-2000 susceptible and CM-98, Punjab-91 and Noor-91 highly susceptible to *Fusarium* wilt.

Bakhsh *et al.* (2007) studied one hundred and fifty eight genotypes of recent origin chickpea were evaluated under artificial disease condition in an augmented design with single replication to identify genetic sources of resistance against wilt disease. At seedling stage, 107 genotypes exhibited resistant response, 29 were tolerant and 22 were susceptible. Three genotypes, F98-75C, F98-181C and F98-193C were consistently resistant at both stages. Three genotypes (CM32/91 X PAIDAR 91, F98-166C, and F98-28C) were resistant at seedling stage and tolerant at reproductive stage whereas single genotype (ICC 11514 X ICC422x C44) was consistently tolerant. These genotypes may be exploited in breeding programs to pyramid resistant genes.

Chaudhry *et al.* (2007) studied one hundred and ninety six chickpea germplasm lines/cultivars were screened for resistance to wilt disease caused by *Fusarium oxysporum* f.sp. *ciceri* in a wilt sick plot. Lines 03001, 03006, 03009, 03012, 03016, 03020 and 03045 obtained from Pluses Research Institute, Faisalabad, found to be resistant, while 03024, 03026, 03037, 03041, 03046, 03050, Pb 2000 and Pardar-91 were moderately resistant. Flip 97-17C, Flip 01-38C, Flip 02-39C, Flip 02-40C, Flip 03-36C, Flip 03-45C, Flip 03-53C and Flip 03-141 from ICARDA, Syria were resistant. Out of 39 test lines 92 A-186 and 93 A-086 from Arid Zone Research Institute were also resistant, with 93 A-304 to be moderately resistant. From Barani Agri. Research Institute Chakwal only one line 2 KCC-101 was found to be resistant.

Muhammad *et al.* (2010) screened for 321 genotypes against *Fusarium* wilt of chickpea. At seedling stage disease incidence varied from 0 to 29.3% whereas, at reproductive stage ranged from 0 to 57%. At seedling stage 173 genotypes were resistant, 54 were tolerant and 94

were susceptible, whereas at reproductive stage, 102 genotypes were resistant, 36 were tolerant and 183 were susceptible. Eighty two genotypes showed steady resistance at both stages. These genotypes may be exploited for the development of resistant cultivars against wilt.

Kumar *et al.* (2013) studied 100 chickpea genotypes for resistance to pod borer and *Fusarium* wilt in Karnataka, India. Out of 100 genotypes 44 showed resistant reaction, 11 MR, 22 tolerant, 15 moderately susceptible and 8 susceptible to *Fusarium* wilt. Among the 100 genotypes 14 genotypes recorded resistance to both *Fusarium* wilt and pod borer damage. Such genotypes can be used for further improvement.

Shah *et al.* (2015) screened fifty four chickpea advanced lines for sources of resistance against blight and wilt. The results of early wilt showed 19 genotypes as highly resistant and 15 as resistant. The genotypes 1(0070-09, BK1(17106, CH 65/02 and BKO4A013 were highly susceptible to wilt during early pathogen infection at seedling stage while the genotypes K0063-09, BKK17106 & BKO4A013 were susceptible during late season. Resistance sources identified could be exploited directly and also may be transferred through hybridization to high yielding disease susceptible genotypes.

Kumar *et al.* (2015) screened one hundred one genotypes for resistant sources in chickpea accessions against *Fusarium* wilt. It was observed that 57 lines were resistant, 28 were tolerant while 16 were susceptible to the wilt disease at seedling stage. Whereas, 31 genotypes were resistant, 26 were tolerant and 44 were susceptible at reproductive stage. On an average basis 56.44% disease resistance was recorded at early stage and 30.69% at reproductive stage, whereas 15.84% disease incidence was observed at seedling stage and 43.56% at reproductive stage. The disease incidence of tolerant genotypes was screened at seedling stage of 27.72% and 25.74% at reproductive stage.

3 . MATERIAL AND METHODS

The present field experiment entitled “Assessment of chickpea genotypes against *Fusarium* wilt” was carried out in 33 chickpea genotypes including three checks viz., Digvijay, Vijay and Vishal for studying genetic diversity and assessing this germplasm resistance against *Fusarium* wilt. The germplasm material was obtained from Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri. The first experiment was conducted in plot having normal soil and second experiment was conducted on wilt sick plot, at Pulses Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri, during rabi season of 2018-19. The account of the key materials used, methods adopted and statistical analysis followed, during the investigations, are described below.

3.1 Experimental Material Used

3.1.1 For Diversity Analysis :

The experimental material used for the study of genetic diversity consisted of 33 genotypes including three checks (Digvijay, Vijay and Vishal) are listed in Table No.1.

3.1.2 For *Fusarium* Wilt Screening :

The experimental material used for the study of screening of *Fusarium* wilt consisted of 33 genotypes including three checks (Digvijay, Vijay and Vishal) along with *Fusarium* wilt susceptible check JG-62.

3.2 Experimental Details:

a) For diversity analysis

i) Number of genotypes	:	33 (Including check viz., Digvijay, Vijay and Vishal)
ii) Season	:	Rabi 2017-2018
iii) Experimental design	:	Randomized Block Design
iv) Number of Replications	:	Two
v) Plot size	:	Single row of 4 m length
vi) Spacing	:	30 cm x 10 cm

vii) Fertilizer Dose : 25:50:30 NPK (kg/ha)

b) For recording of wilt incidence

i) Number of genotypes : 33 (Including check viz., Digvijay, Vijay and Vishal), susceptible check JG-62

ii) Season : Rabi 2018-2019

iii) Experimental design : Randomized Block Design

iv) Number of Replications : Two

v) Plot size : Single row of 4 m length

vi) Spacing : 30 cm x 10 cm

vii) Fertilizer Dose : 25:50:30 NPK (kg/ha)

3.3. Experimental Design

a) For diversity analysis

Thirty three genotypes along with three check viz., Digvijay, Vijay and Vishal evaluated in a Randomized Block Design (RBD) with two replications during Rabi 2017-2018. Each genotype was sown in single row of 4 m length with spacing 30 cm between row and 10 cm within row.

b) For recording of wilt incidence

Thirty three genotypes along with *Fusarium* wilt susceptible check were planted in artificial epiphytotic created wilt sick plot at Pulses Improvement Project, M.P.K.V, Rahuri. Sowing was done on 17th Nov 2018. Each genotype was planted on a 4 m row length and row to row and plant-to-plant distances were maintained at 30 cm and 10 cm respectively. A highly wilt susceptible check i.e., JG-62, was planted after every two test entries.

3.4 Observations Recorded

Ten plants per genotype were selected randomly for recording observations on following characters in each replication and averages were calculated.

3.4.1 Days to 50% Flowering

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

Table No. 1. List of thirty three genotypes of chickpea .

Sr.no	Genotype	Sr.no.	Genotype
1	Phule G 15109	2	Phule G 0819-43
3	Phule G 16101	4	Phule G 1022-3
5	Phule G 1010-4	6	Phule G 16115
7	Phule G 1022-10-6	8	Phule G 171112
9	Phule G 1115-13-6	10	BDNG 2017-44
11	BDNG 2017-49	12	BDNG 2017-21
13	BDNG 2017-23	14	BDNG 2015-1
15	BDNG 2017-06	16	BDNG 2016-2
17	BDNG 21-1	18	AKG 1506
19	AKG 1401	20	AKG 1303
21	AKG 1301	22	AKG 1402
23	Phule G 16312	24	Phule G 0739
25	BDNG 2018-1	26	Phule G 171101
27	Phule G 171103	28	Phule G 171104
29	Phule G 171105	30	Phule G 171113
31	Digvijay	32	Vishal
33	Vijay		

3.4.2 Days to Maturity

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

3.4.3 Plant Height (cm)

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

3.4.4 Plant Spread (cm)

Plant spread was recorded at the time of harvesting by measuring maximum spread of plant.

3.4.5 Number of Primary Branches per Plant

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

3.4.6 Number of Secondary Branches per Plant

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

3.4.7 Number of Pods per Plant

The total numbers of pods were counted from six plants at maturity and the average was worked out.

3.4.8 Number of Seeds per Pod

This observation was recorded by taking the seeds of randomly selected six pods from observation plants and the average was estimated.

3.4.9 100 Seed Weight (g)

It was recorded by weighing randomly selected 100 seeds.

3.4.10 Seed Yield per Plant (g)

The weight of seeds obtained as a mean of six observational plants represented the yield of seed yield per plant, which was recorded in gram.

3.4.11 Wilt Incidence as Percentage

The observation was recorded on germination percentages of all genotypes. The disease data were recorded at 15, 30, 45, 60 days after sowing.

3.5 Statistical Methodology

3.5.1 Assessment of Variability

a. Analysis of variance

The analysis of variance is the procedure of splitting the overall variation into different components (sources). Each component is attributed to an identifiable cause or source of variation. For this analysis data collected from first year trial on individual characters were subjected to the method of analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1985)

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

Where,

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

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

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:

Sources	d.f.	M.S.S	Expected M.S.S
Replications	$r-1$	RMS	$\sigma_e^2 + \sigma_r^2$
Genotypes	$g-1$	GMS	$\sigma_e^2 + \sigma_g^2$
Error	$(r-1)(g-1)$	EMS	σ_e^2

Where,

r = Number of replications

g = Number of genotypes

σ_r^2 = Variance due to replications

σ_g^2 = Variance due to genotypes and

σ_e^2 = 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. The characters showing significant differences were subjected to further analysis.

a. Estimation of S.E. and C.D.

S.E. of mean (S.E.m) = $\sqrt{\sigma_e^2/r}$

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

b. Estimation of mean and range

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

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

Where,

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

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

N = Number of observations

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

c. Estimation of components of variation

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

Environmental variance (σ_e^2) = EMS

Genotypic variance (σ_g^2) = $\frac{GMS-E}{r}$

Phenotypic variance (σ_p^2) = $\sigma_e^2 + \sigma_g^2$

Where,

GMS = Genotypic mean sum of squares

EMS= Error mean sum of squares

r =Number of replications

d. Estimation of coefficients of variation

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

i) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

σ_g^2 = Genotypic variance, and

$\bar{x}$ = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where,

σ_p^2 = Phenotypic variance ,and

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

e. Estimation of heritability (b.s.)

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

$$h^2 \text{ (b.s.)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h^2 = Heritability

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

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

Low Heritability = < 30%

Medium Heritability = 30.1 to 60%

High Heritability = > 60%

f. Genetic advance (G.A.)

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

$$i) \quad G.A. = K \times \sqrt{\sigma_p^2} \times \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

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

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

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

Where,

G.A. = Genetic advance

X = Character mean

GA (As percentage of mean) were classified as

Low : 10 per cent

Medium : 10.1 to 20 per cent

High : > 20 per cent

3.5.2 Correlation

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

ANOVA Table :

Sources	d.f	Sum of product	Mean Sum of product	Expectation of Sum of product
Replications	(r-1)	RP	RMP	COV. $e_{1.2}$ + g COV. $e_{1.2}$
Genotypes	(g-1)	GP	GMP	COV. $e_{1.2}$ + r COV. $e_{1.2}$
Error	(r-1)(g-1)	EP	EMP	COV. $e_{1.2}$

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

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

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).

i) 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).

ii) The genotypic correlation coefficient (r_g) was calculated as:

$$r_{g1.2} = \frac{COV.p1.2}{\sqrt{(\sigma^2_{g1}).(\sigma^2_{g2})}}$$

Where,

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

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

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

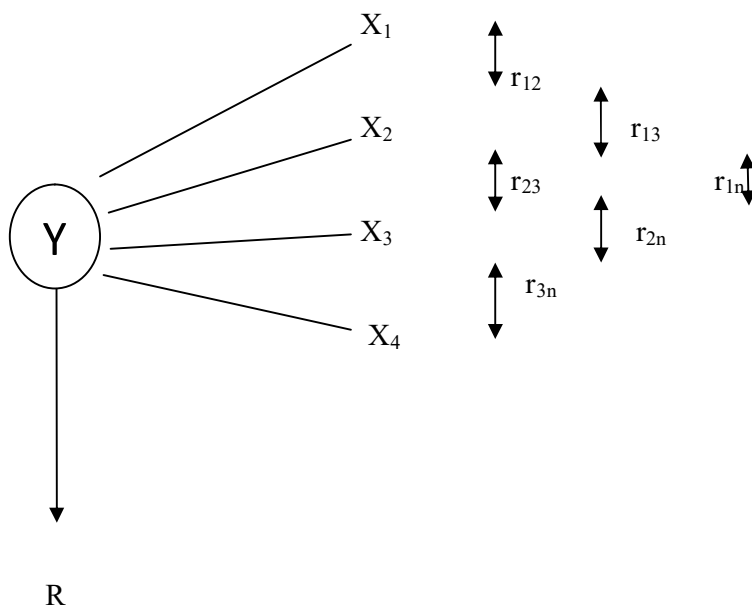
The significance of correlation was tested from the statistical table of correlation at 1 and 5 percent level of significance (Snedcor and Cochran, 1967)

3.5.3 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 $X_1, X_2, X_3, \dots, X_n$ 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).

$$R_{ny} = r_{n1} \cdot P_{1y} + r_{n2} \cdot P_{2y} + r_{n3} \cdot P_{3y} + \dots + P_{ny}$$

Where,

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

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

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

Matrix A

Matrix B

C

$$\begin{pmatrix} R_{1y} \\ R_{2y} \\ R_{ny} \end{pmatrix} = \begin{pmatrix} r_{11} & r_{12} & r_{13} & \dots & r_{1n} \\ r_{21} & r_{22} & r_{23} & \dots & r_{2n} \\ r_{n1} & r_{n2} & r_{n3} & \dots & r_{nn} \end{pmatrix} \begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \end{pmatrix}$$

Where,

 $r_{12} = r_{21}$ and so on r_{1y} = Correlation between one component character and seed yieldThe 'B' matrix was inverted $[B]^{-1}$ and path coefficients (P_{ij}) were obtained as,

$$C = (B)^{-1}.A$$

$$\text{i.e. } P_{ij} = (B)^{-1}.A$$

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

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

Where,

$$I = 1 \text{ to } 9$$

$$j = 1 \text{ to } 9$$

$$P_{ij} = P_{1y}, P_{2y}, \dots, P_{ny}$$

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:

$$\text{Residual factor (R)} = (1 - R^2)$$

Where,

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

$$P_{1y}, P_{2y}, \dots, P_{ny} = \text{Path values}$$

$$r_{1y}, r_{2y}, \dots, r_{ny} = \text{Correlation coefficient}$$

3.5.4. Genetic Diversity

D² analysis

The analysis of divergence was carried out by D² statistics of Mahalanobis's (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D., to test significance of differences among the genotypes. The characters exhibiting 61 significant differences were only used for further analysis of D² statistic. The analysis of co-variance for the character pairs, based on plot averages was carried out (Cochran and Cox, 1957)

a. Wilk's criteria

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

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

Where,

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

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

Significance of Wilk's criteria (Λ) was estimated by X² as,

$$X^2_{pq} = V = -m \log (\Lambda)$$

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

Where,

$$n = N_1 + \dots + N_{K-1}$$

m = Total number of observations - 1

P = Number of significant characters

q = k - 1 (d.f. of varieties)

k = Number of varieties/genotypes

Calculated X² values were tested against X² table value at pq degrees of freedom.

b. Mahalanobis' generalized distance (D²)

The generalized distance between any two populations is defined as :

$$\Delta^2 = \sum \sum \lambda_{ij} \cdot \delta_i \cdot \delta_j$$

Where,

λ_{ij} = Reciprocal matrix to the common dispersion matrix

δ_i = Difference between the mean values of the two populations for the i^{th} character

δ_j = Transpose δ_i

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

$$D^2 = \sum \sum \delta_{ij} \cdot d_i \cdot d_j$$

Where,

δ_{ij} , d_i and d_j are the sample estimate of λ_{ij} , δ_i and δ_j .

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

c. Computation of D^2 values

For each combination among 30 genotypes D^2 values were calculated. Thus, total $33 \times 32 / 2 = 528$ numbers of D^2 values were worked out.

d. Determination of population constellations

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

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

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

e. Average intra-cluster distance

The intra-cluster distances were calculated as

$$D^2 = \sum D_i^2 / n$$

Where,

$\sum D_i^2$ = Sum of distance between all possible combinations (n) of genotypes included in a cluster.

n = number of genotypes included in a cluster

f. Average inter-cluster distances

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

$$\Sigma D_i^2 / (n_i \cdot n_j)$$

Where,

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

n_i = Number of genotypes in cluster i and

n_j = Number of genotypes in cluster j

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

g. Cluster diagram

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

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

h. Wilt incidence percentage

Wilt incidence recorded as percentage. The wilt incidence of each entry was calculated by the following formula :

$$\text{Wilt incidence} = \frac{\text{no of plants wilted}}{\text{Total no.of plants}}$$

The level of resistance and susceptibility of each test entry was determined by using nine point scales. The disease rating scale were put in Table NO. 2, according to this rating scale thirty three chickpea genotypes along with four check were grouped into resistant , moderately resistant, susceptible and highly susceptible category.

Table No. 2. Disease rating scale

Asy	0%	Asymptomatic
R	0.0 to 10%	Resistant
MR	10.1 to 20%	Moderately Resistant
S	20.1 to 40%	Susceptible
HS	Above 40%	Highly Susceptible

4. EXPERIMENTAL RESULTS AND DISCUSSION

The experimental results were obtained from the investigation entitled - “Assessment of chickpea (*Cicer arietinum* L.) genotypes against *Fusarium* wilt” based on different parameter with a view to select the most diverse parents having wilt resistance are presented in this chapter under different sub headings.

4.1 Genetic Variability and Heritability

The analysis of variance revealed highly significant genotypic differences for all the ten characters studied, indicated the presence of wide variability in the existing material selected for present investigation (Table 3).

Table No. 3. Analysis of variance for ten different characters in chickpea

Sr. No.	Name of characters	Mean Sum of Squares		
		Replications (d.f. 1)	Genotypes (d.f. 32)	Error (d.f. 32)
1	Days to 50 per cent Flowering	0.9696	15.852**	1.094
2	Days to maturity	2.560	84.230**	1.654
3	Number of primary branches plant ⁻¹	0.064	0.438**	0.183
4	Number of secondary branches plant ⁻¹	0.432	5.932**	0.574
5	Plant height (cm)	0.409	48.856**	0.938
6	Plant spread (cm)	0.316	14.915**	1.882
7	Number of pods plant ⁻¹	4.592*	83.133**	0.810
8	Number of seeds pod ⁻¹	0.001	0.011**	0.004
9	100 seed weight (gm)	0.170	18.398**	0.230
10	Seed yield plant ⁻¹ (g)	6.097*	50.484**	1.230

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

Note: Figure in the parenthesis indicates the degrees of freedom.

Table No. 4. Mean performance of thirty three chickpea genotypes for ten characters

Sr. No.	Genotype	Days to 50 per cent Flowering	Days to maturity	Number of primary branches plant⁻¹	Number of secondary branches plant⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods plant⁻¹	Number of seeds pod⁻¹	100 seed weight (g)	Seed yield plant⁻¹ (g)
1	Phule G 15109	43.50	112.50	2.17	9.08	32.50	14.17	18.16	1.06	26.41	17.98
2	Phule G 0819-43	47.50	105.00	2.00	7.66	34.41	11.50	16.50	1.02	24.91	16.95
3	Phule G 16101	45.00	96.50	2.83	8.00	27.50	13.50	19.17	1.22	21.58	20.91
4	Phule G 1022-3	48.50	104.00	3.17	8.66	38.45	14.50	29.17	1.22	26.91	22.91
5	Phule G 1010-4	49.50	108.50	3.83	10.66	34.16	13.67	17.16	1.17	25.75	17.91
6	Phule G 16115	51.00	97.50	2.50	9.95	35.66	22.00	18.16	1.22	21.50	18.00
7	Phule G 1022-10-6	45.50	99.50	3.17	9.58	32.00	18.83	37.33	1.22	21.50	32.00
8	Phule G 171112	48.00	92.00	2.17	11.66	38.00	16.83	21.50	1.06	28.50	22.95
9	Phule G 1115-13-6	42.50	105.00	2.50	9.16	37.33	17.00	42.00	1.11	19.91	35.41
10	BDNG 2017-44	44.50	110.00	2.00	8.41	34.83	14.83	31.50	1.22	27.17	27.41
11	BDNG 2017-49	43.50	98.50	2.50	11.67	28.50	16.33	21.58	1.16	19.41	19.91

12	BDNG 2017-21	50.00	105.00	2.50	7.66	35.41	15.50	25.50	1.11	27.17	25.16
13	BDNG 2017-23	46.50	106.50	3.17	9.75	36.50	14.83	31.00	1.22	27.48	26.91
14	BDNG 2015-1	50.00	107.50	2.50	10.16	35.50	18.83	30.33	1.06	25.38	26.58
15	BDNG 2017-06	47.50	109.50	2.50	11.41	34.00	18.16	36.00	1.06	26.41	27.41
16	BDNG 2016-2	45.50	103.50	2.83	8.00	34.00	12.65	17.50	1.06	28.15	18.65
17	BDNG 21-1	43.50	96.50	3.67	6.91	30.67	9.85	22.33	1.22	21.58	23.00
18	AKG 1506	47.50	109.50	3.17	10.00	31.67	13.83	23.41	1.06	21.30	25.33
19	AKG 1401	44.00	105.50	2.17	13.00	32.50	13.17	28.67	1.06	24.83	30.08
20	AKG 1303	48.00	103.50	2.50	9.00	39.00	13.80	28.48	1.21	24.08	30.50
21	AKG 1301	49.50	119.50	3.50	13.00	39.66	15.16	30.00	1.28	25.60	31.33
22	AKG 1402	45.00	97.50	2.83	10.00	34.48	14.33	28.00	1.11	27.91	28.58
23	Phule G 16312	46.50	110.50	3.17	11.83	41.83	19.50	36.91	1.06	29.41	31.41
24	Phule G 0739	43.50	105.50	2.50	10.00	38.00	19.33	32.16	1.19	28.33	32.08
25	BDNG 2018-1	44.00	94.50	2.33	8.25	32.00	13.17	26.50	1.06	23.41	27.50
26	Phule G 171101	46.00	101.50	2.83	13.16	32.98	18.68	32.83	1.11	27.38	31.67
27	Phule G 171103	49.00	96.50	2.83	8.00	34.00	14.00	28.91	1.06	28.91	29.91

28	Phule G 171104	41.50	95.50	3.00	12.33	36.00	18.33	30.00	1.17	28.17	30.41
29	Phule G 171105	46.00	105.50	3.17	8.83	36.00	12.67	22.33	1.17	26.41	21.41
30	Phule G 171113	43.50	96.50	2.83	8.00	39.16	14.50	25.88	1.05	27.38	23.91
31	Digvijay (Check)	51.50	112.50	2.80	11.30	52.33	17.20	33.41	1.11	24.58	30.58
32	Vishal (Check)	52.00	112.50	2.25	9.33	48.33	18.58	25.41	1.05	28.91	26.33
33	vijay (Check)	49.50	109.50	2.25	8.83	40.08	17.91	26.16	1.05	19.00	24.33
34	Mean	46.63	104.04	2.72	9.79	35.98	15.66	27.08	1.12	25.31	25.92
35	S.E.	0.73	0.90	0.30	0.53	0.68	0.97	0.63	0.04	0.33	0.78
36	C.D.at 5%	2.13	2.61	0.87	1.54	1.97	2.79	1.83	0.14	0.97	2.25
37	C.D. 1%	2.86	3.52	1.17	2.07	2.65	3.75	2.46	0.19	1.31	3.03
38	C.V.	2.24	1.23	15.68	7.74	2.69	8.75	3.32	6.22	1.89	4.28

Mean performance and the range of variability

The genotypes mean values for different characters studied are presented in Table 4.

4.1.1 Days to 50 per cent Flowering

The variation in days to 50 per cent flowering ranged between 41.50 and 52 days. Genotype Phule G 171104 took significantly least 41.50 days while significantly highest 52 days were taken by Vishal. The mean value for days to 50 per cent flowering was 46.63 days and fifteen genotypes had days for 50 per cent flowering higher than mean value (46.63).

4.1.2 Days to Maturity

The variation in days to maturity ranged between 92 and 119.50 days. Genotype Phule G 171112 matured in significantly least numbers of (92) days while AKG 1301 matured very late (119.50) days. The mean number of days for maturity was 104.04 days and seventeen genotypes had days to maturity higher than mean value (104.04).

4.1.3 Number of Primary Branches per Plant

Number of primary branches per plant ranged from 2 to 3.83. Genotype Phule G 0819-43 recorded lowest, while Phule G 1010-4 had maximum number of primary branches per plant. Fifteen genotypes recorded higher number of primary branches than the mean value (2.72).

4.1.4 Number of Secondary Branches per Plant

Number of secondary branches per plant ranged from 6.91 to 13.16. Genotype BDNG 21-1 recorded lowest, while Phule G 171101 had maximum number of secondary branches per plant. Fifteen genotypes were recorded having more number of secondary branches than the mean (9.79).

4.1.5 Plant Height (cm)

The variation for plant height ranged between 27.50 cm to 52.33 cm. Genotype Phule G 16101 recorded lowest, while the genotype Digvijay highest plant height . Fourteen genotypes were found taller when compared to mean (35.98 cm).

4.1.6 Plant Spread (cm)

The variation for plant spread ranged between 9.85 cm to 22.00 cm. Genotype BDNG 21-1 had minimum while Phule G 16115 had maximum plant spread and the mean value for plant spread was 15.66 cm. Fourteen genotypes recorded higher plant spread than mean value.

4.1.7 Number of Pods per Plant

Number of pods per plant ranged from 16.50 to 42.00. Genotype Phule G 0819-43 recorded lowest while Phule G 1115-13-6 had maximum number of pods per plant. The mean for this character was 27.08. Seventeen genotypes recorded highly significant number of pods per plant.

4.1.8 Number of Seeds per Pod

Number of seeds per pod ranged from 1.02 to 1.28. Number of seeds per pod was lowest in case of Phule G 0819-43 while maximum number of seeds per pod recorded in AKG 1301. The general mean for this character was 1.12. Fourteen number of genotype recorded highly significant number of seeds per pod.

4.1.9 100 Seed Weight (g)

The variation in 100 seed weight ranged between 19.00 g to 28.91 g. Genotype Vijay was with lowest while Vishal with highest 100 seed weight and the mean for this character was 25.31 g. Twenty genotypes recorded highly significant 100 seed weight.

4.1.10 Seed Yield per Plant (g)

The variation for seed yield per plant ranged between 16.95 g and 35.41 g. The genotype Phule G 0819-43 recorded minimum seed yield per plant (16.95 g), while Phule G 115-13-6 recorded maximum seed yield per plant (35.41 g). Out of thirtythree genotypes, eighteen genotypes recorded higher seed yield per plant than the mean (25.92 g) .

4.1.2. Estimates of Components of Variation

The estimates of GCV, PCV, heritability (b. s.) and genetic advance as per cent of mean for the different characters studied are presented in Table 5.

4.1.3. Genotypic and Phenotypic Coefficients of Variation

Genotypic coefficient of variation (GCV) was highest for number of pods per plant (23.68 %) followed by seed yield per plant (19.14%), number of secondary branches per plant (16.71%), plant spread plant (16.29%), plant height (13.60%). The maximum phenotypic coefficient of variation was recorded for number of pods per plant (23.91%) followed by number of primary branches per plant (20.42%) , seed yield per plant (19.61%), plant spread (18.49%) and number of secondary branches per plant (18.41%).

4.1.4 Heritability and Genetic Advance

Maximum heritability was observed for number of pods per plant (98.10%) followed by 100 seed weight (97.50%), plant height (96.20%), days to maturity (96.10%), seed yield per plant (95.20%). High heritability (>60%) was observed for eight characters. The estimates of genetic advance ranged from 0.07 to 13.08 with the highest estimate in case of number of pods per plant. The highest genetic advance as per cent of mean was observed for number of pods per plant (48.31%) followed by seed yield per plant (38.48%), number of secondary branches per plant (31.23%).

Table No. 5. Estimates of variability parameters for ten different characters in chickpea.

Sr. No.	Characters	Mean	Range	GCV %	PCV %	h² % (b.s)	GA	GA as % mean
1	Days to 50 per cent flowering	46.63	41.50-52.00	5.82	6.24	87.10	5.22	11.19
2	Days to maturity	104.04	92-119.50	6.17	6.29	96.10	12.97	12.47
3	Number of primary branches plant ⁻¹	2.72	2.00-3.83	13.08	20.42	41.00	0.47	17.27
4	Number of secondary branches plant ⁻¹	9.79	6.91-12.99	16.71	18.41	82.30	3.05	31.23
5	Plant height (cm)	35.98	27.49-52.33	13.60	13.86	96.20	9.89	27.49
6	Plant spread (cm)	15.66	9.85-21.99	16.29	18.49	77.60	4.63	29.56
7	Number of pods plant ⁻¹	27.08	16.49-42	23.68	23.91	98.10	13.08	48.31
8	Number of seeds pod ⁻¹	1.12	1.01-1.27	5.00	7.98	39.20	0.07	6.45
9	100 seed weight (g)	25.31	19.00-28.91	11.90	12.05	97.50	6.13	24.22
10	Seed yield plant ⁻¹ (g)	25.92	16.95-35.41	19.14	19.61	95.20	9.97	38.48

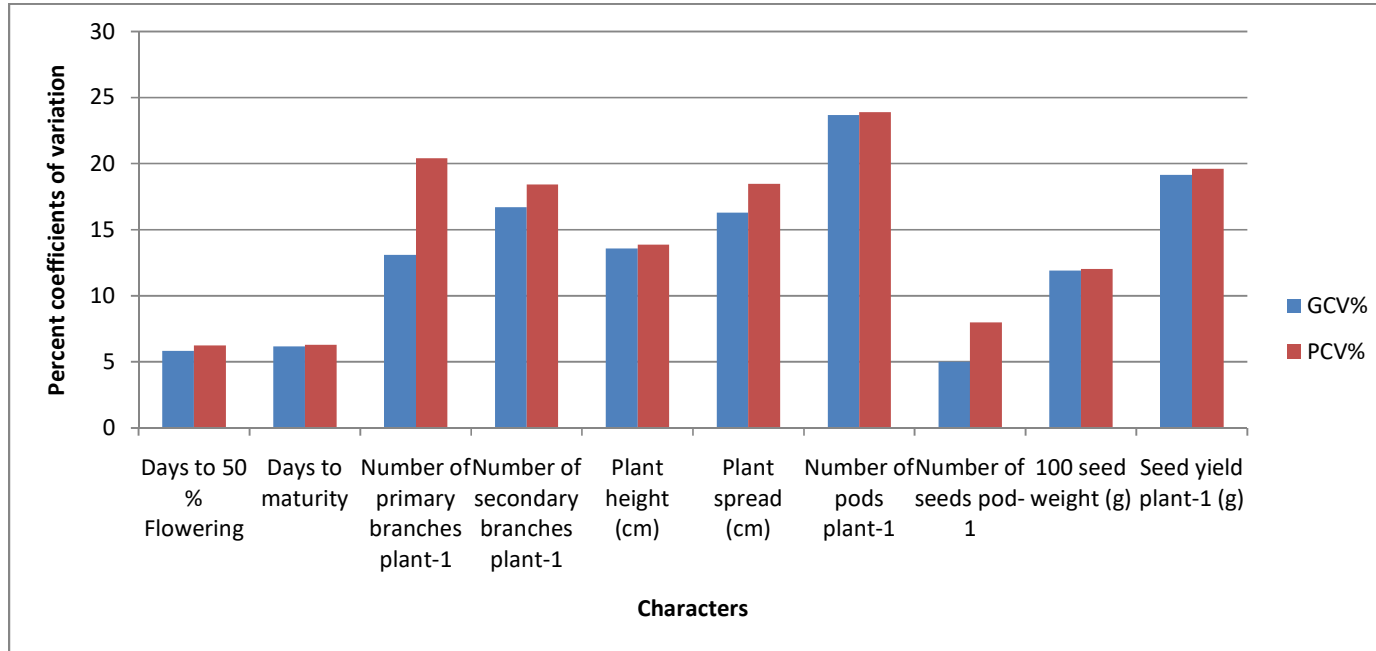


Fig.1. Graphical comparison of GCV and PCV for ten characters studied in chickpea

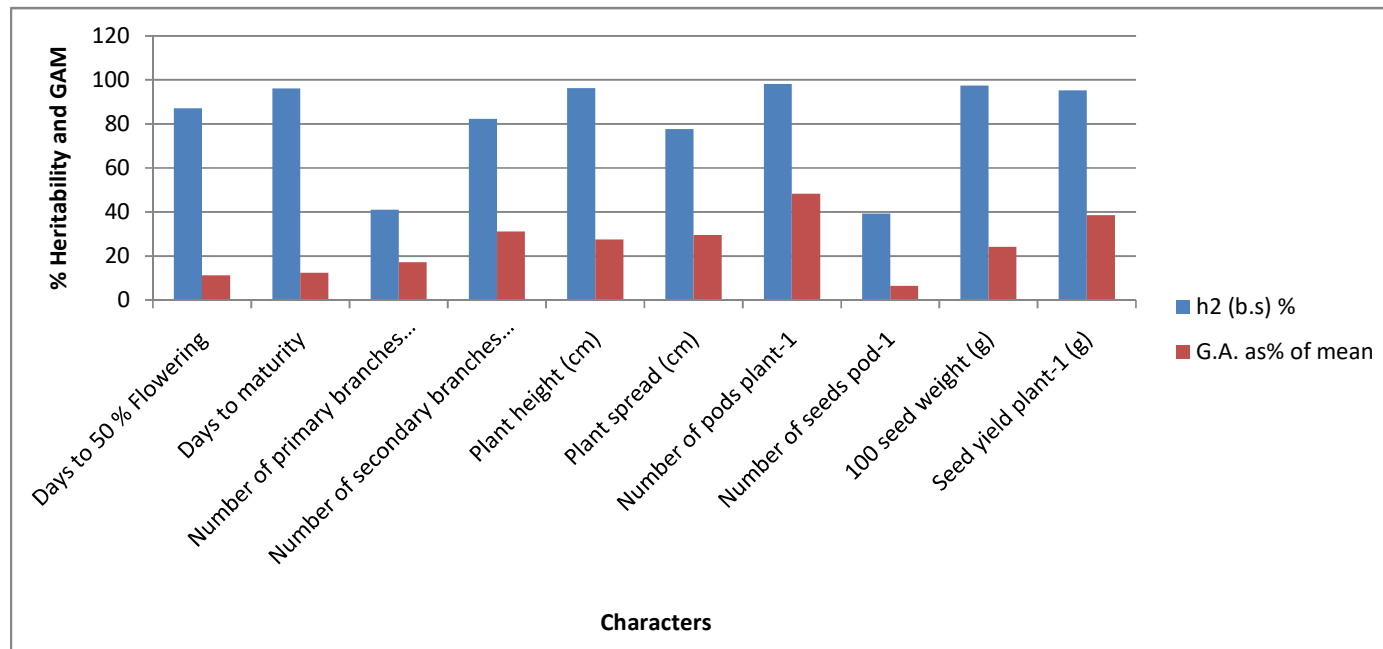


Fig.2. Graphical comparison of heritability and genetic advance as percent of mean for ten characters studied in chickpea

4.2 Correlation Studies

For ten different characters in chickpea the genotypic and phenotypic correlations were studied and presented in Table 6. The significant correlations either in positive or negative direction are described in this chapter. In general genotypic correlation coefficients were higher than their corresponding phenotypic correlations.

4.2.1 Association of Seed Yield with its Components

It is revealed from Table 6 that seed yield per plant shows significant positive correlation with number of secondary branch per plant ($r_g=0.3888, r_p=0.3770$), plant height ($r_g=0.3050, r_p=0.3156$) and plant spread ($r_g=0.3644, r_p=0.3465$) at phenotypic level only. It also shows significant positive correlation with number of pods per plant ($r_g=0.9097, r_p=0.9017$) at both genotypic and phenotypic level only. It shows non significant positive correlation with number of seeds per pod ($r_g=0.1017, r_p=0.0903$), days to maturity ($r_g=0.1332, r_p=0.1194$), number of primary branches per plant ($r_g=0.1078, r_p=0.0030$) and 100 seed weight ($r_g=0.1193, r_p=0.1343$) at both level. It also shows non significant negative correlation with days to 50 per cent flowering ($r_g=-0.1250, r_p=-0.1403$) at both level.

4.2.2. Interrelationship of Yield Components

4.2.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering showed significant positive correlations with days to maturity ($r_g=0.4122, r_p=0.3798$), plant height ($r_g=0.5564, r_p=0.4945$) at phenotypic level and non significant positive correlation with genotypic level. It is non-significant negative correlation with number of seeds per pod ($r_g=-0.0752, r_p=-0.0739$), number of pods per plant ($r_g=-0.1168, r_p=-0.1204$) at both genotypic and phenotypic level, and seed yield ($r_g=-0.1250, r_p=0.1403$) at genotypic level only. It is non-significantly positively correlated with number of secondary branches per plant ($r_g=0.0669, r_p=0.0028$), number of primary branches per plant ($r_g=0.0150, r_p=0.0291$), number of pods per plant ($r_g=-0.1168, r_p=-0.1204$), plant spread ($r_g=0.3224, r_p=0.2080$), and 100 seed weight ($r_g=0.0895, r_p=0.0706$) at both genotypic and phenotypic level.

4.2.2.2 Days to maturity

Days to maturity non-significantly positively correlated with primary branches per plant ($r_g=0.0364, r_p=0.0290$), number of secondary branches per plant ($r_g=0.2349, r_p=0.2135$), plant spread ($r_g=0.1113, r_p=0.1017$), number of pods per plant ($r_g=0.2059, r_p=0.1964$), 100 seed weight ($r_g=0.0907, r_p=0.0838$) and also with seed yield ($r_g=0.1332, r_p=0.1194$) at both genotypic and phenotypic level. It is non-significantly negatively correlated with number of seeds per pod ($r_g=-0.0355, r_p=-0.0026$) at both genotypic and phenotypic level. It is significantly positive correlated with plant height with ($r_g=0.4642, r_p=0.4420$) at phenotypic level and non significantly correlated at genotypic level.

4.2.2.3 Number of primary branches per plant

The number of primary branches per plant positively significant with number of seeds per pod ($r_g=0.9881, r_p=0.1855$) at genotypic level only. It shows non significantly positively correlation with number of pods per plant ($r_g=0.1021, r_p=0.0025$) and seed yield per plant ($r_g=0.1078, r_p=0.0030$) at both genotypic and pgenotypic level. It is non significantly negatively correlated with plant height ($r_g=-0.0004, r_p=-0.1046$), plant spread ($r_g=-0.1423, r_p=-0.2139$) at both genotypic and phenotypic level and 100 seed weight ($r_g=0.0769, r_p=-0.0267$) and number of secondary branches per plant ($r_g=0.3072, r_p=-0.0333$) at phenotypic level only.

4.2.2.4 Number of secondary branches per plant

The number of secondary branches per plant showed significant positive correlation at plant spread ($r_g=0.4767, r_p=0.4871$), number of pods per plant ($r_g=0.3308, r_p=0.3344$), seed yield per plant ($r_g=0.3888, r_p=0.3770$) at phenotypic level only, it also had non significant positive correlation with plant height ($r_g=0.1311, r_p=0.1815$) and 100 seed weight ($r_g=0.1193, r_p=0.1535$) at both level, it has non significant negative correlation with and number of seeds per pod ($r_g=-0.0996, r_p=0.0983$) at genotypic level and non significant positive at phenotypic level.

4.2.2.5 Plant height

Plant height showed highly significant positive association with plant spread ($r_g=0.3710, r_p=0.3633$), number of pods plant ($r_g=0.3097, r_p=0.3204$), seed yield per plant ($r_g=0.3050, r_p=0.3156$) and 100 seed weight ($r_g=0.3084, r_p=0.3219$) at phenotypic level only. It also showed non significant negative relation with number of seeds per pod ($r_g=-0.2173, r_p=-0.0640$) at both level.

4.2.2.6 Plant spread

Plant spread showed positive significant correlation with seed yield per plant ($r_g=0.3644, r_p=0.3465$) and number of pods per plant ($r_g=0.4677, r_p=0.4436$) at phenotypic level only. It shows non significant positive correlation with 100 seed weight ($r_g=0.0256, r_p=0.0503$) at both level. It also showed non significant negative correlation with number of seeds per pod ($r_g=-0.0565, r_p=0.0510$) at genotypic level.

4.2.2.7 Number of pods per plant

The number of pods per plant showed significant positive correlation with seed yield per plant ($r_g=0.9097, r_p=0.9017$) at both genotypic and phenotypic level. It shows non significant positive correlation with number of seeds per pod ($r_g=0.1059, r_p=0.0838$) and 100 seed weight ($r_g=0.0784, r_p=0.0901$) at both level.

4.2.2.8 Number of seeds per pod

Number of seeds per pod showed non significant positive correlation with seed yield per plant ($r_g=0.1017, r_p=0.0903$) at both genotypic and phenotypic level. It shows negative non-significant correlation with 100 seed weight ($r_g=-0.2790, r_p=-0.1344$) at both level.

4.2.2.9 100 seed weight

100 seed weight shows non significant positive correlation with seed yield per plant ($r_g=0.1193, r_p=0.1343$) at both genotypic and phenotypic level.

4.3. Genotypic Path Coefficient Analysis

To find out the direct and indirect contribution from each of the characters towards seed yield per plant, path coefficient analysis was carried out. The genotypic correlation coefficients being more important were only partitioned into direct and indirect effects which are presented in Table 7.

4.3.1 Seed Yield vs. Days to 50 per cent Flowering

Days to 50 per cent flowering showed positive direct effect (0.0277) and it had negative indirect effects through days to maturity (-0.0511), plant spread (-0.0467), number of pods per plant (-0.1111), number of seeds per pod (0.0102) and 100 seed weight (-0.0022), whereas it had positive indirect effect number of primary branches per plant (0.0018), number of secondary branches per plant (0.0076) thus results into non-significant negative correlation with seed yield per plant (-0.1250).

4.3.2 Seed Yield vs. Days to Maturity

Days to maturity showed negative direct effect (-0.1239). The indirect effects of it were negative through plant spread (-0.0161), 100 seed weight (-0.0023) whereas it had positive indirect effect days to 50 per cent flowering (0.0114), number of primary branches per plant (0.0045), number of secondary branches per plant (0.0266), plant height (0.0324), number of seeds per pod (0.1958), number of seeds per pod (0.0048). Thus leads to positive correlation with seed yield per plant (0.1332).

4.3.3 Seed Yield vs. Number of Primary Branches per Plant

The primary branches per plant showed positive direct effect (0.1225). The indirect effects of it were negative through days to maturity (-0.0045), number of seeds per pod (-0.1611) and 100 seed weight (-0.0019). It had indirect positive effect through days to 50 per cent flowering (0.0004), number of primary branches per plant (0.1225), number of secondary branches per plant (0.0348), plant spread (0.0206), number of pods per plant (0.0971). Thus leads to positive correlation with seed yield per plant (0.1078).

Table No. 6. Genotypic (above diagonal) and Phenotypic (below diagonal) correlation coefficients in chickpea .

Characters	Days to 50 per cent flowering	Days to maturity	Number of primary branches plant¹	Number of secondary branches plant⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods plant⁻¹	Number of seeds Pod⁻¹	100 seed weight (g)	Seed yield plant⁻¹ (g)
Days to 50% flowering	1.0000	0.4122	0.0150	0.0669	0.5564	0.3224	-0.1168	-0.0752	0.0895	-0.1250
Days to maturity	0.3798 **	1.0000	0.0364	0.2349	0.4642	0.1113	0.2059	-0.0355	0.0907	0.1332
Number of primary branches plant ¹	0.0291	0.0290	1.0000	0.3072	-0.0004	-0.1423	0.1021	0.9881**	0.0769	0.1078
Number of secondary branches plant ⁻¹	0.0028	0.2135	-0.0333	1.0000	0.1311	0.4767	0.3308	-0.0996	0.1193	0.3888
Plant height (cm)	0.4945 **	0.4420	-0.1046	0.1815	1.0000	0.3710	0.3097	-0.2173	0.3084	0.3050
Plant spread (cm)	0.2080	0.1017	-0.2139	0.4871 **	0.3633 **	1.0000	0.4677	-0.0565	0.0256	0.3644
Number of pods plant ⁻¹	-0.1204	0.1964	0.0025	0.3344 **	0.3204 **	0.4436 **	1.0000	0.1059	0.0784	0.9097**
Number of seeds Pod ⁻¹	-0.0739	-0.0026	0.1855	0.0983	-0.0640	0.0510	0.0838	1.0000	-0.2790	0.1017
100 seed weight (g)	0.0706	0.0838	-0.0267	0.1535	0.3219 **	0.0503	0.0901	-0.1344	1.0000	0.1193
Seed yield plant ⁻¹	-0.1403	0.1194	0.0030	0.3770**	0.3156*	0.3465**	0.9017**	0.0903	0.1343	1.0000

4.3.4 Seed Yield vs. Number of Secondary Branches per Plant

It showed positive direct effect on seed yield (0.1132). It showed positive effect through days to 50 per cent flowering (0.0019), number of primary branches per plant (0.0376), plant height (0.0092), number of pods per plant (0.3146) and number of seeds per pod (0.0135). The indirect effects of it were negative through days to maturity (-0.0291), plant spread (-0.0691) and 100 seed weight (-0.0030). Thus leads to positive correlation with seed yield per plant (0.3888).

4.3.5 Seed Yield vs. Plant Height

The plant height showed positive direct effect (0.0699) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.0154), number of secondary branches per plant (0.0148), number of pods per plant (0.2945) and number of seeds per pod (0.0295). The indirect effects of it were negative through days to maturity (-0.0575), plant spread (-0.0538) and 100 seed weight (-0.0077). Thus leads to positive correlation with seed yield per plant (0.3050).

4.3.6 Seed Yield vs. Plant Spread

The plant spread showed negative direct effect (-0.1450) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.0089), number of primary branches per plant (0.0174), number of secondary branches per plant (0.0540), plant height (0.0259), number of pods per plant (0.4448) and number of seeds per pod (0.0077). The indirect effects of it were negative through days to maturity (-0.0138) and 100 seed weight (-0.0006). Thus leads to positive correlation with seed yield per plant (0.3644).

4.3.7 Seed Yield vs. Number of Pods per Plant

The number of pods per plant showed positive direct effect (0.9510) on seed yield. The indirect effects of it were positive through number of primary branches per plant (0.0125), number of secondary branches per plant (0.0375) and plant height (0.0216). The indirect effects of it were negative through days to 50 per cent flowering (-0.0032), days to maturity (-0.0255), plant spread (-0.0678), number of seeds per pod (-0.0144) and 100 seed weight (-0.0020). Thus leads to significant positive correlation with seed yield per plant (0.9097).

4.3.8 Seed Yield vs. Number of Seeds per Pod.

The number of seeds per pod showed negative direct effect (-0.1356) on seed yield. The indirect effects of it were positive through days to maturity (0.0044), number of primary branches per plant (0.1455), plant height (0.0152), plant spread (0.0082), number of pods per plant (0.1007) and 100 seed weight (0.0070). The indirect effects of it were negative through days

to 50% flowering (-0.0021), number of secondary branches per plant (-0.0113). Thus leads to positive correlation with seed yield per plant (0.1017).

4.3.9 Seed Yield vs. 100 Seed Weight

The plant height showed negative direct effect (-0.0251) on seed yield. The indirect effects of it were positive through days to 50 per cent flowering (0.0025), number of primary branches per plant (0.0094), number of secondary branches per plant (0.0135), plant height (0.0215), number of pods per plant (0.0746) and number of seeds per pod (0.0378). The indirect effects of it were negative through days to maturity (-0.0112) and plant spread (-0.0037). Thus leads to positive correlation with seed yield per plant (0.1193).

Table No. 7. Genetic direct and indirect effects of ten causal variables on seed yield in chickpea .

Sr. No.	Characters	Days to 50 per cent flowering	Days to maturity	Number of primary branches plant ¹	Number of secondary branches plant ⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods plant ⁻¹	Number of seeds Pod ⁻¹	100 seed weight (g)	Total genotypic correlation with seed yield per plant
1	Days to 50% flowering	<u>0.0277</u>	-0.0511	0.0018	0.0076	0.0389	-0.0467	-0.1111	0.0102	-0.0022	-0.1250
2	Days to maturity	0.0114	<u>-0.1239</u>	0.0045	0.0266	0.0324	-0.0161	0.1958	0.0048	-0.0023	0.1332
3	Number of primary branches plant ¹	0.0004	-0.0045	<u>0.1225</u>	0.0348	0.000	0.0206	0.0971	-0.1611	-0.0019	0.1078
4	Number of secondary branches plant ⁻¹	0.0019	-0.0291	0.0376	<u>0.1132</u>	0.0092	-0.0691	0.3146	0.0135	-0.0030	0.3888
5	Plant height (cm)	0.0154	-0.0575	0.000	0.0148	<u>0.0699</u>	-0.0538	0.2945	0.0295	-0.0077	0.3050
6	Plant spread (cm)	0.0089	-0.0138	0.0174	0.0540	0.0259	<u>-0.1450</u>	0.4448	0.0077	-0.0006	0.3644
7	Number of pods plant ⁻¹	-0.0032	-0.0255	0.0125	0.0375	0.0216	-0.0678	<u>0.9510</u>	-0.0144	-0.0020	0.9097**
8	Number of seeds Pod ⁻¹	-0.0021	0.0044	0.1455	-0.0113	0.0152	0.0082	0.1007	<u>-0.1356</u>	0.0070	0.1017
9	100 seed weight (g)	0.0025	-0.0112	0.0094	0.0135	0.0215	-0.0037	0.0746	0.0378	<u>-0.0251</u>	0.1193

4.4. Genetic Divergence

4.4.1 Mahalanobis's Generalised Distance (D^2)

Wilk's criterion showed significant differences between the genotypes for the pooled effect of ten different characters studied. Hence, further analysis was done to calculate D^2 values. The D^2 values for all the possible pairs of comparison between 33 genotypes were calculated. The calculated D^2 values ranged from 16.96 to 1445.65, the lowest value being between the pair of genotypes (Phule G 171104 and AKG 1402) and the highest between (Vishal and Phule G 1022-10-6). Based upon the observations of 10 characters, the Mahalanobis's D^2 statistics was computed for all possible pairs of 33 genotypes in order to assess the genetic diversity present among the genotypes under study.

4.4.2 Clustering Pattern of the Genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values presented in table 8. The thirty three genotypes were grouped into seven clusters. Cluster I had highest number of genotypes (18) followed by cluster II with 8 genotypes, cluster V with 2 genotypes, cluster VII with 2 genotypes, cluster III, IV and VI were solitary.

4.4.3 Intra and Inter-Cluster Divergence

The average intra and inter cluster D values are presented in Table 9. The inter cluster distance (D) from 17.73 to 37.29. The minimum inter cluster distance ($D = 17.73$) was between clusters I and IV. Highest inter cluster distance ($D = 37.29$) was found between the clusters III and VII followed by 35.02 by the clusters (V and VII), 31.38 between (II and V), 28.10 between (II and VII), 27.54 between (I and VII). An examination of intra cluster divergence among seven clusters revealed that cluster VII had maximum intra cluster distance ($D = 17.11$) followed by cluster II (15.31), cluster I (13.97). As the clusters III, IV and VI were solitary; there was no intra cluster divergence.

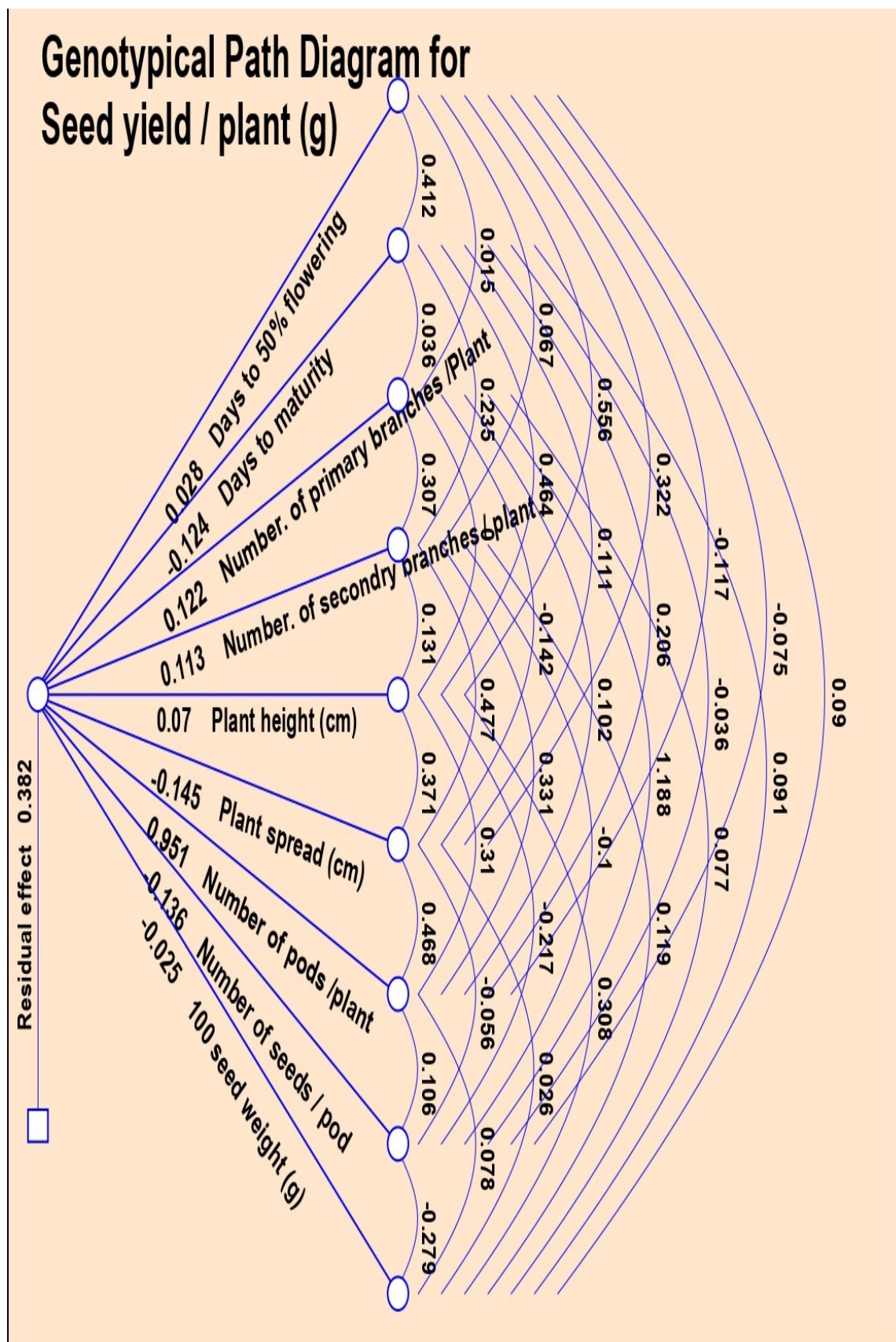


Fig.3. Genotypical Path Diagram.

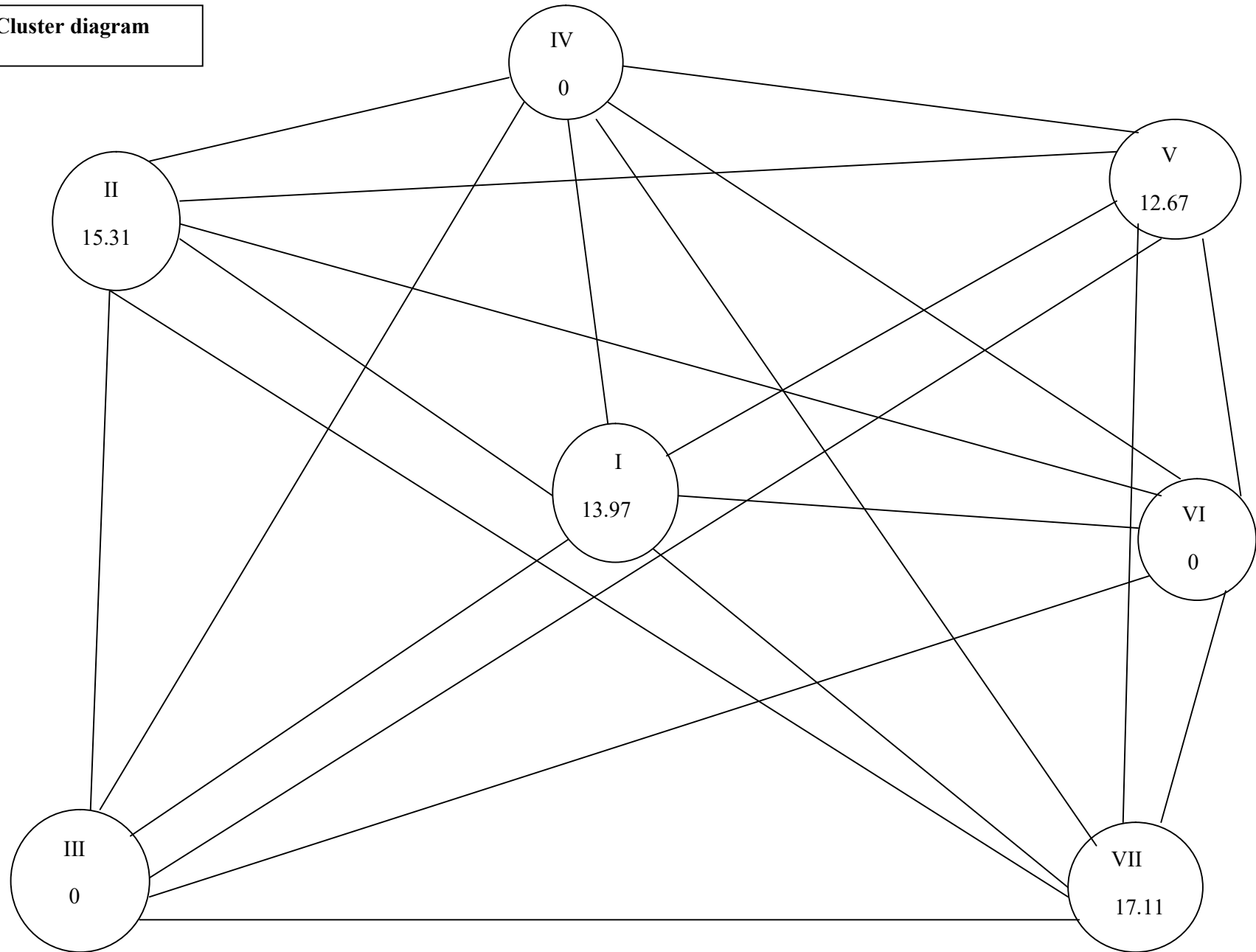
Table No. 8. Composition of thirty three chickpea genotypes including three checks into different clusters .

Cluster No.	No. of genotypes	Genotypes included in the cluster	Origin of genotype
I.	18	AKG 1402, Phule G 171104, Phule G 171103, Phule G 0739, BDNG 2017-21, BDNG 2017-23, BDNG 2015-1, Phule G 171105, Phule G 1022-3, BDNG 2017-44, Phule G 171113, Phule G 16312, BDNG 2017-06, AKG 1303, Phule G 171101, BDNG 2018-1, BDNG 21-1, AKG 1401,	MPKV,RAHURI- Phule G 171104, Phule G 171103, Phule G 0739, Phule G 171105, Phule G 1022-3, Phule G 1022-3, Phule G 171101, Phule
II.	8	Phule G 15109, BDNG 2016-2, Phule G 0819-43, Phule G 1010-4, Phule G 171112, Phule G 16101, Phule G 16115, AKG 1506	G 15109, Phule G 0819-43, Phule G 1010-4, Phule G 171112, Phule G
III.	1	BDNG 2017-49	16101, Phule G 16115,
IV.	1	AKG 1301	Phule G 1022-10-6,
V.	2	Phule G 1022-10-6, Phule G 1115-13-6	Phule G 1115-13-6,
VI.	1	vijay	Vijay, Digvijay, Vishal ARS,BADNAPUR- BDNG 2017-21, BDNG 2017-23, BDNG 2015-1, BDNG 2017-44, BDNG 2017-06, BDNG 2018-1, BDNG 21-1, BDNG 2016-2, BDNG 2017-49 PDKV,AKOLA- AKG 1402, AKG 1303, AKG 1401, AKG 1506, AKG 1301
VII.	2	Digvijay, Vishal	

Table No. 9. Average intra and inter cluster D values of chickpea genotypes

Cluster No.	CI-I	CI-II	CI-III	CI-IV	CI-V	CI-VI	CI-VII
CI-I	13.97	19.45	24.40	17.73	23.05	25.84	27.54
CI-II		15.31	20.30	20.81	31.38	23.41	28.10
CI-III			0.00	24.75	26.09	22.39	37.29
CI-IV				0.00	23.94	19.80	22.20
CI-V					12.67	26.02	35.02
CI-VI						0.00	21.66
CI-VII							17.11

Fig.4. Cluster diagram



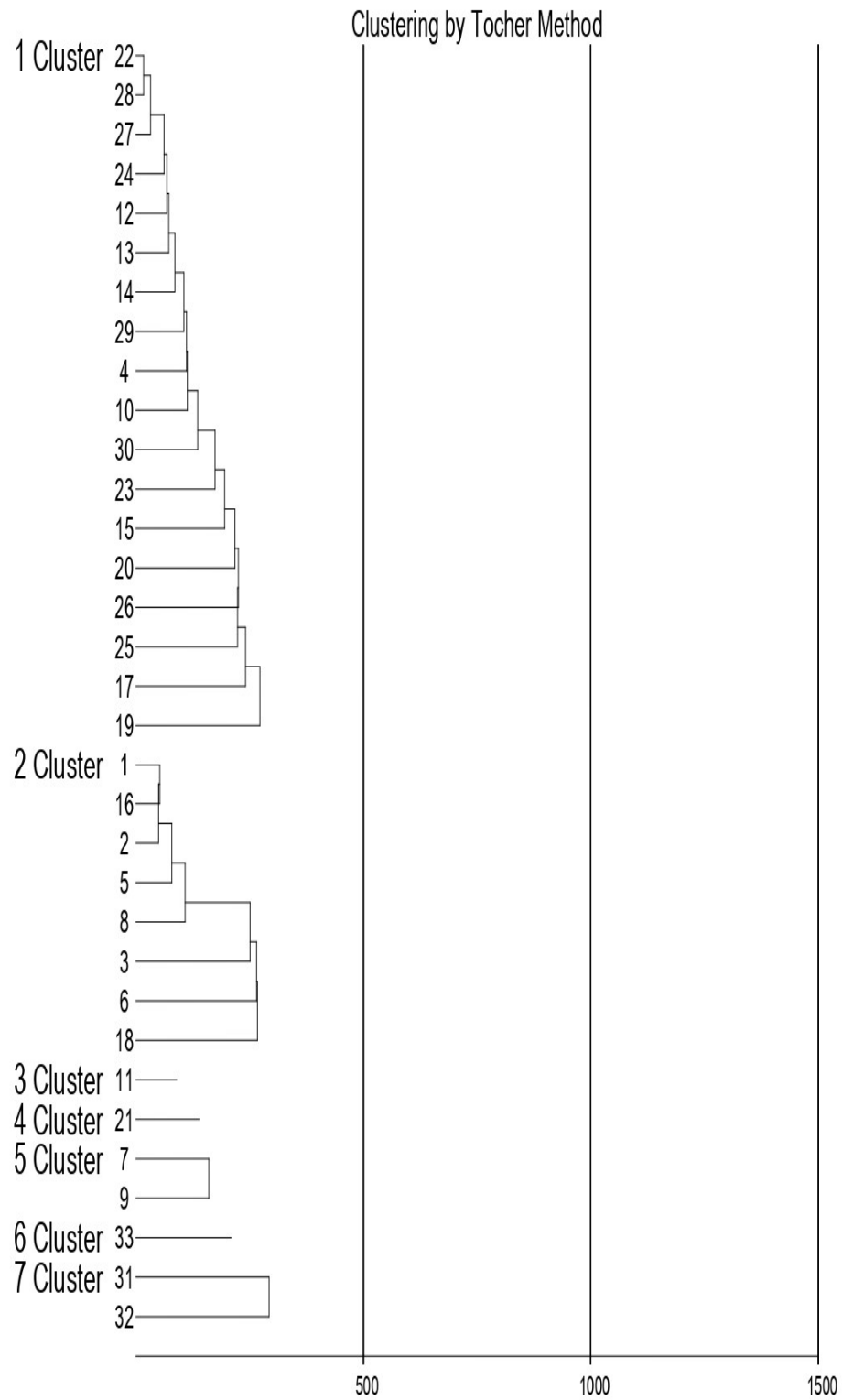


Fig.5. Dendrogram : Cluster formation of genotypes

4.4.4 Cluster Means for Different Characters

For ten different characters studied in this investigation the cluster mean were presented in Table 10. A considerable inter-cluster variation showed by plant height, number of pods per plant and days to maturity. Cluster means for plant height varied from 28.50 (III) to 50.33 (VII). The cluster mean for number of pods per plant ranged between 18.94 (II) to 39.67 (v). The cluster mean for 100 seed weight range from 19.00 (VI) to 26.75 (VII).

The cluster mean for days to 50 per cent flowering ranged between 43.50 (III) to 51.75 (VII). The cluster mean for days to maturity was maximum in cluster IV (119.50) and minimum in cluster III (98.50). The cluster mean for number of primary branches per plant was maximum in the cluster IV (3.50) and minimum in cluster VI (2.25). The cluster mean for number of secondary branches per plant were lowest in cluster VI (8.83) and maximum in cluster IV (13.00). The cluster mean values for plant spread were highest maximum in cluster V (17.92) . The cluster mean values for number of seeds per pod were less among all the characters and the highest mean value of this character was (1.28) in cluster IV, while the lowest cluster mean value (1.05) in cluster VI.

Table No. 10. Cluster means for ten different characters in chickpea.

Cluster No.	Days to 50 per cent flowering	Days to maturity	Number of primary branches plant⁻¹	Number of secondary branches plant⁻¹	Plant height (cm)	Plant spread (cm)	Number of pods plant⁻¹	Number of seeds Pod⁻¹	100 seed weight (g)	Total seed yield per plant
CI-I	45.97	102.86	2.76	9.74	35.63	15.44	29.25	1.13	26.57	27.60
CI-II	47.19	103.13	2.69	9.38	33.48	14.77	18.94	1.11	24.76	19.83
CI-III	43.50	98.50	2.50	11.67	28.50	16.33	21.58	1.16	19.41	19.91
CI-IV	49.50	119.50	3.50	13.00	39.66	15.16	30.00	1.28	25.60	31.33
CI-V	44.00	102.25	2.83	9.37	34.66	17.92	39.67	1.17	20.71	33.70
CI-VI	49.50	109.50	2.25	8.83	40.08	17.91	26.16	1.05	19.00	24.33
CI-VII	51.75	112.50	2.53	10.32	50.33	17.89	29.41	1.08	26.75	28.46

9 . Per cent contribution of different characters to genetic diversity

The utility of D^2 analysis was enhanced by its application to estimate the relative contribution of the various plant characters to genetic divergence. The per cent contribution of ten characters studied was given in Table 11. It was observed that, number of pods per plant (34.09%) contributed highest for divergence followed by 100 seed weight (24.05%), plant height (23.86%), seed yield per plant (10.61%), days to maturity (5.68%) and number of secondary branches per plant (1.33%).

Table No. 11. Per cent contribution of different characters to genetic diversity.

Sl. No.	Name of characters	Number of times appearing 1st in ranking	Contribution
1	Days to 50% flowering	2	0.38%
2	Days to maturity	30	5.68%
3	Number. of primary branches plant ⁻¹	0	0.00%
4	Number. of secondary branches plant ⁻¹	7	1.33%
5	Plant height (cm)	126	23.86%
6	Plant spread (cm)	0	0.00%
7	Number of pods plant ⁻¹	180	34.09%
8	Number of seeds pod ⁻¹	0	0.00%
9	100 seed weight (g)	127	24.05%
10	Seed yield per plant (g)	56	10.61%

4.5 Wilt Incidence

Total thirty three chickpea genotypes along with four checks were screened in wilt sick plot of Pulses Improvement Project M.P.K.V, Rahuri. The wilt susceptible check i.e., JG-62 was sown after every two test entries to ensure high disease pressure. There was a significant variation between genotypes for their disease reaction. Out of thirty three genotypes seventeen genotypes *viz.*, Phule G 15109, Phule G 0819-43, Phule G 16101, Phule G 1022-3, Phule G 1010-4, Phule G 1022-10-6, Phule G 171112, BDNG 2017-44, BDNG 2017-06, BDNG 2016-2, AKG 1301, AKG 1402, Phule G 171103, Phule G 171113, Digvijay, Vijay and Vishal exhibited resistant reaction for *Fusarium* wilt. However five genotypes *viz.*, BDNG 2017-49, BDNG 2015-1, AKG 1506, Phule G 171101 and BDNG 2018-1 found to be moderately resistant towards *Fusarium* wilt. Moreover one genotype *viz.*, BDNG 21-1 exhibited susceptible reaction, while remaining two genotypes *viz.*, BDNG 2017-23, AKG 1401 showed highly susceptible reaction for wilt pathogen. Eight genotypes *viz.*, Phule G 16115, Phule G 1115-13-6, BDNG 2017-21, AKG 1303, Phule G 16312, Phule G 0739, Phule G 171104 and Phule G 171105 shows asymptomatic respond. The check varieties Digvijay, Vijay and Vishal showed resistance reaction towards wilt disease.

Percent contribution of different characters to genetic diversity

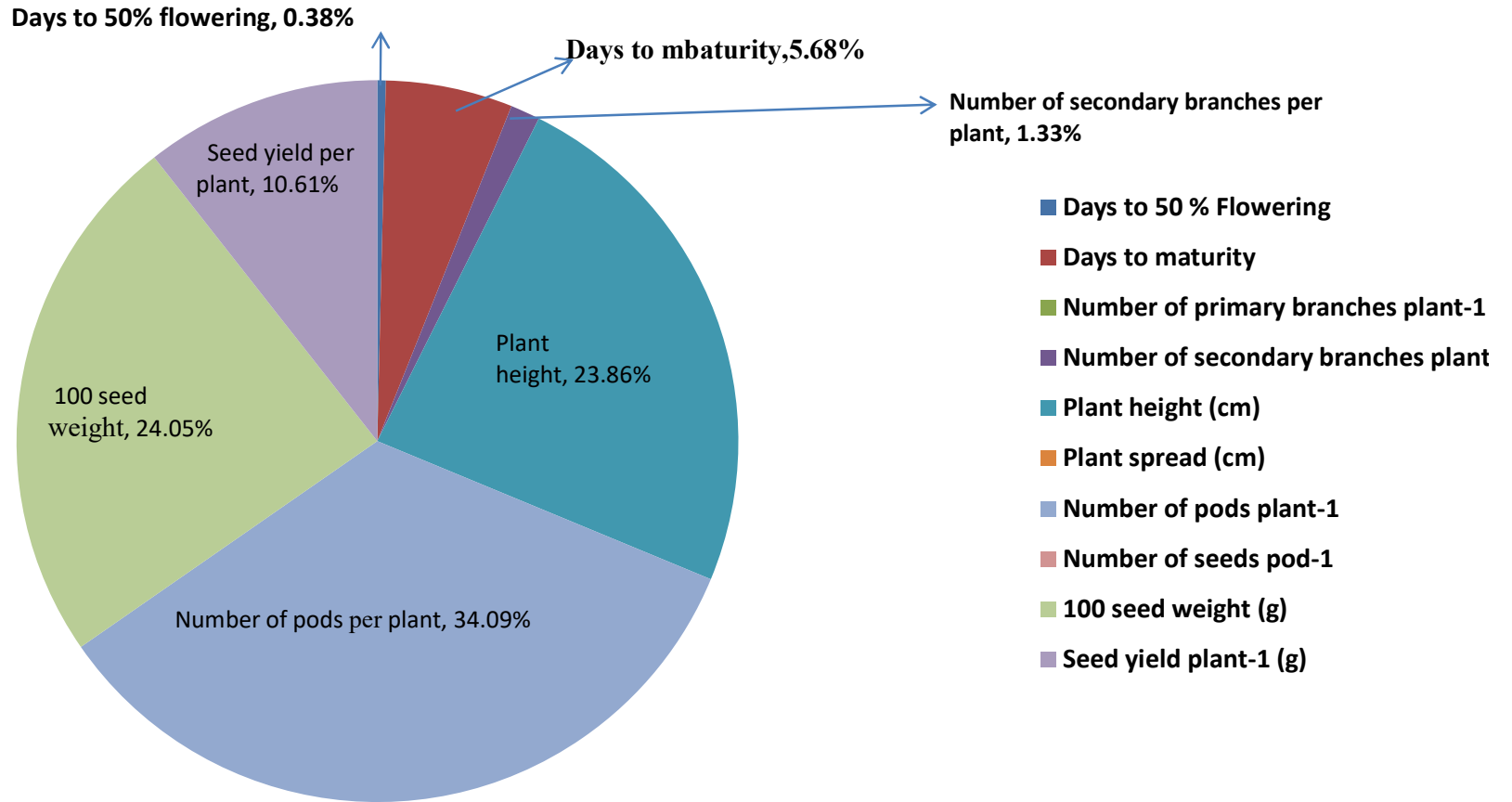


Fig.6. Percent contribution of different characters to genetic diversity

Table no. 12. Evaluation of chickpea genotypes against *Fusarium* wilt disease.

Sl. No.	Genotype	wilt incidence(%)	Disease reaction
1	Phule G 15109	1.72	R
2	Phule G 0819-43	5.00	R
3	Phule G 16101	3.33	R
4	Phule G 1022-3	3.70	R
5	Phule G 1010-4	1.56	R
6	Phule G 16115	0.00	ASY
7	Phule G 1022-10-6	1.43	R
8	Phule G 171112	9.33	R
9	Phule G 1115-13-6	0.00	ASY
10	BDNG 2017-44	5.97	R
11	BDNG 2017-49	12.18	MR
12	BDNG 2017-21	0.00	ASY
13	BDNG 2017-23	87.85	HS
14	BDNG 2015-1	14.99	MR
15	BDNG 2017-06	5.48	R
16	BDNG 2016-2	5.39	R
17	BDNG 21-1	21.96	S
18	AKG 1506	11.87	MR
19	AKG 1401	44.23	HS
20	AKG 1303	0.00	ASY
21	AKG 1301	2.70	R
22	AKG 1402	3.23	R
23	Phule G 16312	0.00	ASY
24	Phule G 0739	0.00	ASY
25	BDNG 2018-1	11	MR
26	Phule G 171101	10.60	MR
27	Phule G 171103	3.13	R
28	Phule G 171104	0.00	ASY
29	Phule G 171105	0.00	ASY
30	Phule G 171113	2.94	R
31	Digvijay	5.80	R
32	Vishal	7.14	R
33	Vijay	7.31	R



Plate 1. Over view of wilt screening plot



Plate 2. Susceptible and Resistant reaction of genotypes

4.6 DISCUSSION

Plant breeding deals with management and utilization of genetic variability. Hence, assessment of genetic variability, study of character association and genetic diversity in the available germplasm is of immense value to design a selection programme and to identify the superior, genetically diverse genotypes to be used as parents in future hybridization programme. In extreme cases, low genetic diversity may lead to complete elimination of some plant species resulting in loss of overall biological diversity. It is, therefore necessary to classify and utilize this variability systematically for genetic up gradation of biological population.

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

Among various diseases in chickpea *Fusarium* wilt is a major problem in most of the growing areas of this crop, not only in India but also countries like Pakistan, Bangladesh, and Syria etc. Hence, it is not only to select diverse parent but also to select disease resistant diverse parent which can be used in the development of resistant variety.

In this investigation correlation and path analysis were worked out to study the associations between component characters and the direct and indirect path coefficients of the component characters on yield; and to study the genetic divergence. The results obtained on genetic aspects are discussed in this chapter along with disease reaction of (*Cicer arietinum* L.) 33 accessions under appropriate headings.

4.6.1 Genetic variability and heritability

4.6.2 Correlation studies

4.6.3 Path coefficient analysis

4.6.4 Genetic divergence

4.6.5 Wilt incidence percentage

4.6.1 Genetic Variability and Heritability

The existence of genetic variability is advantageous to the evolutionary survival of a species. Yield improvement in any crop can be brought about through plant breeding but necessary variability upon which selection is to be practiced must be

available in the genetic material. Therefore, before embarking on any crop improvement programme, a plant breeder must survey and assess the variability for a given agronomic or yield component characters which can be estimated through variance, coefficient of variability (GCV, PCV), heritability and genetic advance.

4.6.1.1 Range of variability

Wide range of variability was observed for almost all the characters except number of seeds per pod (1.02-1.28) and number of primary branches per plant (2.00-3.83). Days to maturity (92-119.50) exhibited highest range of variability followed by Number of pods per plant (16.50-42.00), plant height (27.50-52.33), seed yield per plant (16.95-35.41), plant spread (9.85-22), days to 50 per cent flowering (41.50-52), 100 seed weight (19.00-28.91) and number of secondary branches per plant (6.91-13.16). Similar results were reported by Mushtaq *et al.* (2013), Gul *et al.* (2013), Dumbre *et al.* (1984). Akhtar *et al.* (2011) reported highest range of variability for pods per plant. Borate *et al.* (2010) reported considerable range of variability for days to first flowering, secondary branches, plant height, dry matter and grain yield. Mohamed *et al.* (2015) also reported genetic variability for seed yield, days to 50 per cent flowering, days to maturity and number of seeds per plant.

4.6.1.2 Genotypic and phenotypic coefficient of variation

Genetic variability is the basis for any heritable improvement in the crop plants. The estimates of GCV and PCV for all the characters studied showed little difference the latter being slightly greater than the former, thus indicating that the variability existing in these characters was not only due to genetic factors but also due to environmental factors. The estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) in the present study were highest for 100 seed weight followed by seed yield per plant, plant spread, number of primary branches per plant showing wide variation among the genotypes with respect to these characters.

Mathur and Mathur (1996) reported high GCV and PCV in case of 1000 grain weight. Sable *et al.* (2000) reported high estimates of GCV for seed yield per plant, 100 seed weight, and biological yield per plant. Kumar *et al.* (2012) reported high estimates of GCV and PCV for 100 seed weight, seed yield per plant and plant height. GCV and PCV estimates lowest for days to maturity. This is also reported by Jeena *et al.* (2005), Zali *et al.* (2011). Mushtaq *et al.* (2013) reported highest values of GCV and PCV for 100 seed weight and lowest for days to maturity.

4.6.1.3 Heritability (b. s.) and genetic advance

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. The heritability estimates are better indicators of heritable portion of the variation. The broad sense heritability includes the contribution of additive gene effects, allelic interactions due to dominance and non-allelic due to epistasis. In the present investigation, number of pods per plant (98.10) followed by 100 seed weight (97.50), plant height (96.20), days to maturity (96.10), seed yield per plant (95.20) showed high ($> 60\%$) estimates of heritability (b. s.). Saleem *et al.* (2002 a) assessed that 100 seed weight, days taken to flowering were characterized by high (b. s.) heritability estimates, which indicated the presence of a considerable proportion of total variability due to genetic causes. Farshadfar *et al.* (2013) reported that heritability estimates were high for 100 seed weight and seed yield.

Genetic advance is measure of genetic gain under selection which depends upon main factors *viz.*, genetic variability, heritability, selection index (Allard 1960). High genetic advance was observed for number of pods per plant (13.08) followed by days to maturity (12.97), seed yield per plant (9.97) and other characters accompanied with low to moderate genetic advance. Low genetic advance was observed for number of seed per pod (0.07), number of primary branches per plant (0.47) and secondary branches per plant (3.05).

In the present investigation, number of pods per plant, days to 50 per cent, 100 seed weight, plant height showed high estimates of broad sense heritability (b. s.) accompanied by high genetic advance as per cent of mean indicating that these traits could be prominently governed by additive gene action. That's why selection of these traits could be more effective for desired genetic improvement. It is supported by similar findings of Gumber *et al.* (2002), Kumar *et al.* (2012) and Mushtaq *et al.* (2013).

High heritability accompanied with low genetic advance observed for number of secondary branches per plant (3.05), days to 50 per cent flowering (5.22) and 100 seed weight (6.13).

These results are parallel with the results of other researcher such as, Muhammad *et al.* (2002) who found that low heritability percentage coupled with low and moderate genetic advance for primary and secondary branches respectively, indicated that these traits were greatly influenced by environment. Jeena *et al.* (2005) reported pods per plant, 100 seed weight, biological yield per plant and seed yield per plant exhibited high predicted genetic advance with high heritability. Kumari *et al.* (2013) assessed that high genetic advance coupled with high heritability estimate for plant height, number of secondary branches per plant, number of pods per plant and seed yield per plant. Same results were also reported by Ali *et al.* (2008), Borate *et al.* (2010), Akhtar *et al.* (2011) and Jivani *et al.* (2013).

Thus estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as per cent of mean, selection must be done in the characters like number of pods per plant, 50 per cent flowering, 100 seed weight, the characters like number of pods per plant, Plant height, seed yield per plant, plant spread, number of secondary branches per plant and days to maturity for improving the yield in chickpea.

4.6.2 Correlation Studies

Correlation measures the degree and direction of association between two or more variables. 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 it is important to know how the improvement of one character causes simultaneous changes in other characters and thirdly in connection with natural selection (Falconer, 1960). The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown.

In the present investigation genotypic correlation coefficients were higher than their corresponding phenotypic correlations. Significant positive correlation was observed between seed yield per plant with number of pods per plant at both genotypic and phenotypic level. It also shows significant positive correlation with plant height, number of secondary branches per plant and plant spread at phenotypic level only. Highly positive and significant correlation observed for number of pods per plant ($r_g = 0.9097$, $r_p = 0.9017$). This indicates the simultaneous improvement of these characters through selection will be rewarding.

Non significant positive correlation was reported between seed yield per plant with days to maturity, 100 seed weight, number of primary branches per plant and number of seeds per pod. The characters days to 50 per cent flowering show non significantly negatively correlation with seed yield per plant. Similar results were obtained by Padmavathi *et al.* (2013).

Saleem and Ali (1999) reported seed yield was positively correlated with all attributes except days taken to 50 per cent flowering. Similar results were reported by Muhammad *et al.* (2004). Talebi *et al.* (2007) worked the results that negative and significant relationship was determined statistically between number of pods per plant and 100 seed weight.

4.6.3 Path Coefficient Analysis

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

In the present investigation, path coefficient analysis revealed that number of pods per plant had highest direct effect (0.9510) on seed yield per plant followed by number of primary branches per plant (0.1225) and number of secondary branches per plant (0.1132). These direct effects are mainly responsible for positive association of these characters with seed yield per plant. Genotypic correlation coefficients were higher than corresponding phenotypic correlations. Total genotypic correlation with seed yield per plant was positively correlated with all the characters except days to 50 per cent flowering . Indicating that increase in the value of one character will lead to decrease in second character and vice versa.

Highest direct effect of number of pods per plant on seed yield was reported by Saleem *et al.* (2002). Gohil and Patel (2010) showed that genotypic correlation coefficients were higher than corresponding phenotypic ones for most of the character combinations. 100 seed weight had a positive association with seed yield.

Barde (2015) revealed that number of pods per plant had highest direct effect on seed yield per plant. Ali *et al.* (2009) and Padmavathi *et al.* (2013) reported negative effect of days to 50 per cent flowering on seed yield. Based on findings of the present investigations it could be enforced that the most desirable plant type in chickpea should possess more number of pods per plant, plant height and higher 100 seed weight, i.e. bold seeds. Noor *et al.* (2003) reported both correlation and path analysis indicated pods per plant and 100 seed weight were potent contribution to grain yield through direct effects. Mehmet *et al.* (2013) reported positive direct effect of plant height and pods per plant had significant correlation with seed yield suggested that these yield components may be good criteria to improve chickpea cultivars. Muhammad *et al.* (2016) reported that maximum positive direct effect towards seed yield was exerted by number of pods per plant (0.4451) with 52.87% ratio.

4.6.4 Genetic Divergence

Divergence 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 it could serve as raw material for crop improvement programme. The precise information about the genetic divergence is therefore, crucial for effective breeding programme. The genetically diverse parents are known to produce higher heterotic effects and consequently give desirable recombinants from the breeding material. Multivariate analysis as shown by Mahalanobis (1936) D^2 statistics, is a measure that appraises the genetic diversity quantitatively among a set of genotypes.

4.6.4.1 Diversity

The estimates of D^2 values ranged from 16.96 to 1445.65. This clearly indicates the presence of adequate diversity between genotypes studied. Gupta and Krishna (1995), Kumar *et al.* (1998), Khan (1999), Sirohi *et al.* (1999) and Nimbalkar and Harer (2001) reported wide genetic diversity in chickpea germplasm. The highest D^2 value was between a pair of genotype viz., Vishal and Phule G 1022-10-6 (1445.65), while lowest (16.96) was between Phule G 171104 and Vijay.

4.6.4.2 Cluster formation

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

Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean for the characters also need due consideration in the crop improvement programme.

In the present investigation thirty three genotypes were grouped into seven clusters. The cluster I was the largest cluster comprising of 18 genotypes, cluster II with 8 genotypes, cluster V and VII with 2 genotypes. The clusters III, IV and VI were solitary. The highest statistical distance was found between the cluster III and VII ($D = 37.29$) followed by cluster V and VII ($D = 35.02$). This indicated that hybridization among the genotypes between these clusters would produce successful hybrids and desirable segregants in further generations. The intra cluster value was highest for cluster VII ($D=17.11$) indicating that this cluster is more heterogeneous. However the lowest intra-cluster distance was observed in cluster V, indicating that the strains of these cluster are genetically similar.

Jeena and Arora (2002 a.) grouped 40 chickpea genotypes into 12 clusters. Jeena *et al.* (2005) grouped 80 genotypes into 11 clusters out of which in cluster I maximum of 60 genotypes were grouped. Nimbalkar and Harer (2001) grouped 40 chickpea genotypes into 16 clusters. Out of that, 10 were solitary. D^2 values of between all possible pair of 40 genotypes ranged from

12.62 to 3979.93. Jeena *et al.* (2005) based on D^2 values of 80 genotypes were grouped into eleven clusters. Sidramappa *et al.* (2010) found 15 clusters out of which 8 clusters were solitary suggesting the very diverse nature of eight RIL's from rest of the genotypes. Devendrappa *et al.* (2013) reported 16 clusters of which cluster I was with largest 27 genotypes. Parhe *et al.* (2014 a.) reported 5 clusters and Johnson *et al.* (2015) reported 8 clusters and highest inter cluster distance between cluster IV and VII followed by I and VII, hence genotypes belonging to these clusters can be utilized as parents in future chickpea improvement programme.

The cluster mean revealed that clusters II, IV and VII varied considerably for most of the characters from those of other clusters. This indicates that the genotypes included in these clusters might have entirely different genetic architecture from the genotypes included in the other clusters. The cluster means revealed high variability among the clusters for the traits days to maturity, 100 seed weight, seed yield per plant, number of pods per plant, plant height. Among these traits, number of pods per plant(34.09) showed highest percent contribution towards diversity followed by 100 seed weight, plant height, seed yield per plant and days to maturity, whereas the traits days to 50 per cent flowering contributed least indicating not much variability among the genotypes was present for this trait. Samal and Jagdev (1989) reported the contribution of 100 seed weight, seed yield per plant and days to 50 per cent flowering to the total divergence. Nimbalkar and Harer (2001) reported maximum genetic divergence due to plant height and 100 seed weight.

4.6.4.3 Selection of potent parent

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

Timothy (1963) reported that genetic divergence is one of the criteria for selecting the parents for hybridization; which may produce transgressive segregants.

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

DC 1 : $D \geq (m+s)$

DC 2 : $D < (m+s)$ and $\geq m$

DC 3 : $D \geq (m-s)$ and $< m$

DC 4 : $D < (m-s)$

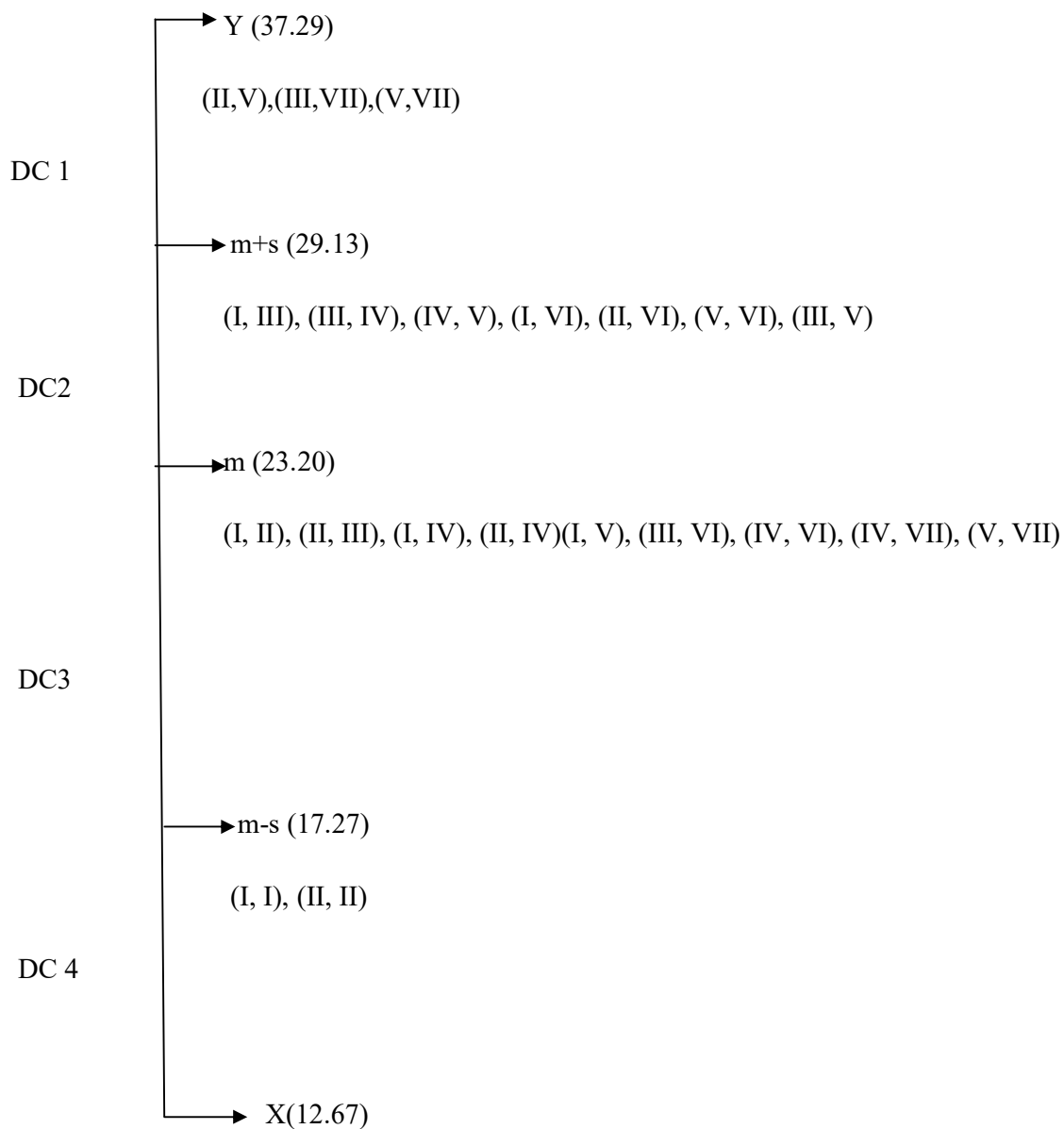
Experiment by them (two in groundnut and one in rapeseed) showed that the chances for occurrence of high frequency of heterotic crosses with high values of heterosis were more, when the parents were chosen to have their divergence in the interval, $m-s$ and $m+s$, compared to the crosses between parents,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

In the present study, an attempt was made to classify the cluster combination into four divergence classes by following the above procedure. The statistical distance (D^2) given in Fig. 7, represents the index of genetic diversity among the clusters. The mean of seven clusters and 3 intra-clusters (as monogenotypic cluster III, IV and VI had no intra cluster distance) was 23.20 and standard deviation 5.93. The minimum (X) and maximum (Y) values among these distances were 12.67 and 37.29 respectively. Thus, the divergence classes were as presented below.

Divergence Classes

DC 4		DC 3		DC 2		DC 1	
↓		↓		↓		↓	
X	$m-s$		m		$m+s$		Y
(12.67)	(17.27)		(23.20)		(29.13)		(37.29)

Fig.7. Distribution of different cluster combinations into four divergence classes based on D^2 values between them (Cluster Combinations)



Grouping of cluster pairs into the divergence class (DC) are presented in Fig 7. On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC 2 and DC 3. While crossing among the genotypes of a cluster, the *per se* performance of the genotypes for different trait such as early maturity, number of secondary branches, seed yield per plant, number of pods per plant, number of seeds per pod, 100 seed weight etc. should be taken into account. So, that desirable transgressive segregants would be obtained after hybridization.

Keeping in view all the above aspects and considering the inter-cluster distance, cluster mean and *per se* performance of genotypes and divergence class, the genotypes listed in Table 13 may be utilized in future breeding programme for creating maximum spectrum of variability for different yield contributing characters, which would help in developing superior genotypes with high yield and desired traits.

Table No. 13. Suggested parents for the crossing programme for specific traits.

Sr. No	Characters	Cluster combination	Possible crosses
1	100 seed weight (g)	(I,IV)	Phule G 171101 × AKG 1301
2	Number. of secondary branches plant ⁻¹	(IV,III)	AKG 1301×BDNG 2017-49
3	Number of pods plant ⁻¹	(V, VII)	Phule G 1115-13-6 ×Digvijay
4	Seed yield per plant	(V, VII)	Phule G 1115-13-6 ×Digvijay

4.6.5 Wilt Incidence

The disease reaction for chickpea wilt was recorded at 15, 30, 45, 60 days after sowing. The highly susceptible genotypes died in 15 days from the date of sowing followed by susceptible genotypes within 30-45 days and some lines were susceptible even after reproductive stage. In present investigation out of thirty three genotypes seventeen genotypes *viz.*, Phule G 15109, Phule G 0819-43, Phule G 16101, Phule G 1022-3, Phule G 1010-4, Phule G 1022-10-6, Phule G 171112, BDNG 2017-44, BDNG 2017-06, BDNG 2016-2, AKG 1301, AKG 1402, Phule G 171103, Phule G 171113, Digvijay, Vijay and Vishal exhibited resistant reaction for *Fusarium* wilt. However five genotypes *viz.*, BDNG 2017-49, BDNG 2015-1, AKG 1506, Phule G 171101 and BDNG 2018-1 found to be moderately resistant towards *Fusarium oxysporum* f.sp. *ciceri* pathogen. Moreover one genotype *viz.*, BDNG 21-1 exhibited susceptible reaction,

while remaining three genotypes viz., BDNG 2017-23 and AKG 1401 showed highly susceptible reaction for wilt pathogen. Eight genotypes viz. Phule G 16115, Phule G 1115-13-6, BDNG 2017-21, AKG 1303, Phule G 16312, Phule G 0739, Phule G 171104 and Phule G 171105 showed asymptomatic respond. The check varieties Digvijay, Vijay and Vishal showed resistance reaction towards wilt disease.

The sources of resistance to *Fusarium* wilt in chickpea breeding materials are not uncommon and a number of workers have reported the occurrence of high level of resistance to *Fusarium* wilt (Pathak *et al.*, 1982; Zote *et al.*, 1983; Iqbal *et al.* 1993; Iftikhar *et al.* 1997). screened 31 chickpea lines and found all of them to be highly resistant to wilt disease. In present investigation, it was found that at seedling stage, some of the genotypes were resistant whereas at reproductive stage, majority of the genotypes appeared to be susceptible. Various workers have already reported variation in response of genotypes at two stages (Nene *et al.*, 1981, Haware *et al.*, 1992). Iqbal *et al.* (2005) observed considerable variation among genotypes while evaluating 51 chickpea genotypes against *Fusarium* wilt under artificial disease conditions. Similar study was conducted by Ayyub *et al.* (2003) who reported high level of resistance to *Fusarium* wilt in chickpea germplasm originating from different sources. Bakhsh *et al.* (2007) reported 3 genotypes with disease incidence 0%, 6.7% and 8.3% as resistant, 4 with disease incidence of 18.2 to 20% as tolerant and 151 with disease incidence of 25% to 100% as susceptible at reported out of 100 genotypes, 44 showed reproductive stage. Kumar *et al.* (2013) resistant reaction, 11 MR, 22 tolerant, 15 moderately susceptible and 8 susceptible to *Fusarium* wilt. Same results were also reported by Shah *et al.* (2015) and Kumar *et al.* (2015).

5 . SUMMARY AND CONCLUSION

The present experiment entitle “Assessment of chickpea (*Cicer arietinum* L.) genotypes against *Fusarium* wilt” was conducted during rabi season with objectives viz., to assess the chickpea genotypes against *fusarium* wilt resistance and to study the correlation between yield and yield contributing characters in chickpea.

Thirty three genotypes of chickpea were evaluated in a randomized block design with two replications in one season. Eleven characters were studied viz., days to 50 per cent flowering, days to maturity, plant height (cm), plant spread (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), seed yield per plant (g), and wilt incidence. The results obtained are summarized and concluded as below.

5. 1 SUMMARY

5.1.1 Genetic Variability and Heritability

The range of variability, genotypic and phenotypic coefficient of variation, heritability percentage and genetic advance as per cent of mean were worked out. The characters days to maturity exhibited highest range of variability followed by number of pods per plant, plant height, seed yield per plant, plant spread, days to 50 per cent flowering, 100 seed weight. The variability was lowest for number of seeds per pod followed by number of primary branches per plant, number of secondary branches per plant. The estimates of genotypic as well as phenotypic coefficient of variation were highest for number of pods per plant and genotypic coefficient of variation was lowest in number of seeds per pod as well as phenotypic coefficient of variation lowest in days to 50% flowering. High heritability estimates associated with high genetic advance as per cent of mean were observed for number of pods per plant, plant spread and seed yield per plant. Characters viz., days to 50 per cent flowering and 100 seed weight showed high heritability accompanied with low genetic advance.

5.1.2 Correlation Studies

Correlation studies at both genotypic and phenotypic levels were made to resolve the direction and magnitude of association among characters. The significant positive correlation was reported between seed yield per plant with number of pods per plant at both genotypic and phenotypic level. It also showed significant positive correlation between seed yield and plant height, number of secondary branches per plant and plant spread at phenotypic level. It was observed that genotypic correlation coefficient were higher than corresponding phenotypic ones for most of the characters. The non significant positive correlation was reported between seed

yield per plant and days to maturity, number of primary branches per plant, number of seeds per pod and 100 seed weight. However days to 50 per cent flowering, showed non-significant negative correlation with seed yield per plant at genotypic as well as phenotypic level.

5.1.3 Path Coefficient Analysis

Path coefficient analysis revealed that number of pods per plant had highest direct effect (0.9510) on seed yield per plant with positive and significant followed by number of primary branches per plant (0.1225), number of secondary branches per plant (0.1132) and plant height (0.0699) are mainly responsible for positive association of these characters with seed yield per plant. The direct effect of days to 50 per cent flowering (0.0277) and its association with seed yield per plant was negative. The direct effect of days to maturity (-0.1239), plant spread (-0.1450), number of seeds per pod (-0.1356) and 100 seed weight (-0.0251) were negative however, their association with seed yield per plant was positive, indicating that they played their role via indirect effects.

5.1.4 Genetic Divergence

The D^2 values showed adequate genetic diversity among the genotypes studied. On the basis of D^2 values all the genotypes were grouped into seven different clusters with varying number of genotypes in the clusters. The clustering pattern of these genotypes did not follow geographical distribution. The maximum genetic distance (D) of 37.29 was found between the clusters III and VII followed by (D) of 35.02 by the clusters V and VII. The highest D^2 value (1445.65) was between a pair of genotype viz., Phule G 1022-10-6 and Vishal.

5.1.5 Wilt Incidence

Total thirty three chickpea genotypes along with four checks were screened in wilt sick plot of Pulses Improvement Project M.P.K.V, Rahuri. The wilt susceptible check i.e., JG-62 was sown after every two test entries to ensure high disease pressure. There was a significant variation between genotypes for their disease reaction. Out of thirty three genotypes seventeen genotypes viz., Phule G 15109, Phule G 0819-43, Phule G 16101, Phule G 1022-3, Phule G 1010-4, Phule G 1022-10-6, Phule G 171112, BDNG 2017-44, BDNG 2017-06, BDNG 2016-2, AKG 1301, AKG 1402, Phule G 171103, Phule G 171113, Digvijay, Vijay and Vishal exhibited resistant reaction for *Fusarium* wilt. However five genotypes viz., BDNG 2017-49, BDNG 2015-1, AKG 1506, Phule G 171101 and BDNG 2018-1 found to be moderately resistant towards *Fusarium oxysporum* f. sp. *ciceri* pathogen. Moreover one genotype viz., BDNG 21-1 exhibited susceptible reaction, while remaining three genotypes viz., BDNG 2017-23, AKG 1401 and JG-62 showed highly susceptible reaction for wilt pathogen. Eight genotypes viz., Phule G 16115, Phule G 1115-13-6, BDNG 2017-21, AKG 1303, Phule G 16312, Phule G 0739, Phule G

171104 and Phule G 171105 shows asymptomatic respond. The check varieties Digvijay , Vijay and Vishal showed resistance reaction towards wilt disease.

5.2 Conclusion

5.2.1 Genetic Variability and Heritability

High genotypic coefficients of variation was observed for number of pods per plant followed by seed yield per plant and number of secondary branches per plant suggested presence of more variability and can be improved by simple selection.

Characters *viz.*, number of pods per plant, days to 50 per cent flowering, and 100 seed weight showed high heritability accompanied with high genetic advance as percent of mean. It is indicative of non-additive gene action which indicated scope for selection for improvement of these characters.

5.2.2 Correlation Studies

Number of pods per plant had strong positive correlation with seed yield per plant .This indicates the simultaneous improvement of these characters through selection.

5.2.3 Path Coefficient Analysis

Number of pods per plant followed by number of primary branches per plant and number of secondary branches per plant showed positive direct effects on seed yield. So these are the important yield components suggesting direct selection and can be given importance during selection.

5.2.4 Genetic Divergence

- I. There was substantial genetic diversity present among the genotypes studied.
2. The studied thirty three genotypes of chickpea were grouped into seven clusters.
3. The pair of genotypes *viz.*, (BDNG 2017-49 and Vishal) was mostly divergent from one another.
4. On the basis of the cluster means for important yield components and inter-cluster distance the various clusters parents given in Table. 14 may be used in further hybridization programme, for different character improvement in chickpea.

Table No. 14. List of potent parents.

Sr. No	Characters	Genotype	Cluster
1	100 seed weight (g)	Phule G 171101	I
2	Number. of secondary branches plant ⁻¹	BDNG 2017-49	III
		AKG 1301	IV
3	Number of podsplant ⁻¹	Phule G 1022-10-6	V
		Vishal	VII
4	Seed yield per plant	Phule G 1115-13-6	V

5.2.5 Wilt Incidence

Out of thirty three genotypes studied seventeen genotypes including checks viz., Phule G 15109, Phule G 0819-43, Phule G 16101, Phule G 1022-3, Phule G 1010-4, Phule G 1022-10-6, Phule G 171112, BDNG 2017-44, BDNG 2017-06, BDNG 2016-2, AKG 1301, AKG 1402, Phule G 171103, Phule G 171113, Digvijay, Vijay and Vishal exhibited resistant reaction for *Fusarium* wilt. So by using these genotypes resistant varieties could be developed for *Fusarium* wilt.

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7. VITAE

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in

AGRICULTURAL BOTANY

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