Genetic Evaluation of Chickpea Genotypes Suitable for Late Sowing Condition

THESIS

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Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur

**In partial fulfillment of the requirements for
the Degree of**

MASTER OF SCIENCE

In

**AGRICULTURE
(GENETICS AND PLANT BREEDING)**

By

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2018

CERTIFICATE- I

This is to certify that the thesis entitled, **“Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition”** submitted in partial fulfilment of the requirement for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Genetics and Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. Babita Bajya** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instructions.

All the assistance and help received during the course of the investigation has been acknowledged by her.

Place: Jabalpur	**Dr. Anita Babbar**
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CERTIFICATE-II

This is to certify that the thesis entitled, **"Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition"** submitted by **Mr. Babita Bajya** to the Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Genetics and Plant Breeding)** in the Department of **Plant Breeding and Genetics** has been, after evaluation, approved by the External Examiner and by the Student's Advisory Committee after an oral examination on the same.

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I, **Babita Bajya** S/o Mr. **Babulal Bajya** Certify the work embodied in thesis entitled "**Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition**" is my own first hand bonafide work carried out by me under the guidance of **Dr. Anita Babbar** at Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur during **2017-2018**.

The matter embodied in the thesis has not been submitted for the award of any other degree/diploma. Due credit has been made to all the assistance and help.

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I, also abide myself with the decision taken by my advisor for the publication of material extracted from the thesis work and subsequent improvement, on mutually beneficial basis, provided the due credit is given, thereof.

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Date: / /2018 **(Babita Bajya)**

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Abbreviations

% - percentage

√ - square root

Σ - summation

‘t’ test - student ‘t’ test

cm - centimeter

et al., - and others

g - gram

ha - hectare

SE - standard error

viz. - namely

DFF - days to 50% flowering

DM - days to maturity

PH - Plant height

NEPPP - number of effective pods/plant

TNPP - number of pods/plant

SYPP - seed yield/ plant

NSPP - number of seeds/plant

NSPPod - number of seeds/pod

BY - biological yield/plant

HI - harvest index

100-SW - 100-Seed weight

Prot. - protein content

Carbo. - carbohydrate content

RWC - relative water content

CHL(SPAD 502) - cholorophyll content index

MSI - membrane stability index

PCV - Phenotypic coefficient of variation

GCV - Genotypic coefficient of variation

% - Percentage

± - Plus or minus

√	-	Square root
Σ	-	Summation
>	-	More than
<	-	Less than
-	-	Hyphen
()	-	Parenthesis
:	-	Colon
;	-	Semicolon
,	-	Coma
/	-	Oblique
.	-	Full stop
Fig.	-	Figure
i.e.	-	That is
SD	-	Standard Deviation
mha	-	million hectare
ml	-	milliliter
mt	-	million ton
g	-	gram

INTRODUCTION

Chickpea [*Cicer arietinum* (L.) $2n = 2x = 16$] belongs to genus *Cicer,* tribe Cicereae, family Fabaceae, and subfamily Papilionaceae. It is commonly called gram, Bengal gram or garbanzo bean, is most important cool season food legume in the world after common bean (*Phaseolus vulgaris* L.) and field pea (*Pisum sativum* L.). It originated in southeastern Turkey (Ladizinsky, 1975) and is an annual, self-pollinating, diploid pulse crop with a genome size of ~738 Mbp. Based on seed size and color, cultivated chickpeas are of two types: Macrosperma *(kabuli* type) and Microsperma *(desi* type).

Kabuli type is generally grown in the temperate region, while desi type chickpea is grown in the semi arid tropics. It is the most important rabi crop, which is predominantly grown in the vast rainfed areas of the country. Chickpea is one of the cheapest and readily available sources of protein (25) along with fats (1.4%), carbohydrates (57-60%), ash (4.8%) and (4.9-15.6%) moisture. It helps in making up the deficiency of cereal diets, as well as being an important source of human food and animal feed, It also helps to improve soil fertility, particularly in drylands.

Chickpea covers 11.7mha area and 9.3mt production in over 45 countries of the world. India is the largest chickpea producer accounting a share of about 67% in global chickpea production with about 9.93 mha area, 9.53 mt production and 960 kg/ha productivity. Distribution of chickpea in six states *viz*., Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka and Andhra Pradesh together contribute 91% of the production and 90% of the area of the country. In M.P., it covers 3017 thousand ha area with a production of 3364 thousand tonnes and an average productivity 1115 kg/ha which is the highest among different pulses crop (Anonymous, 2017).

Chickpea area under late sown conditions is increasing, particularly in northern and central India, due to inclusion of chickpea in new cropping systems and intense sequential cropping practices. Late sowing is compensated through shortening of their vegetative phase and flowering occurs at temperatures more conducive to subsequent pod development.

Rice fields are mostly vacated late up to the end of November making the available varieties of chickpea unfit for sowing under late conditions (rice- follow). Early maturing chickpea, however can be taken under late sown situation (rice-follow) when availability of water is not enough for wheat cultivation. Inclusion of chickpea in rice- wheat system not only brings qualitative change in the production base for long term sustainability, but also protects the environment from the risks associated with high input agriculture. The late sown conditions are characterized by low temperature at seedling and high temperature at the time of grain development. Low temperature at initial stage of crop growth results in poor and slow vegetative growth, whereas, high temperature at the end of season leads to forced maturity.

Chickpea is cultivated in India mostly in rainfed situation. It is also grown in irrigated condition under late sown condition. Now a day, farmer used to cultivate the chickpea in the month of December after harvesting of rice and potato. In such condition farmers need early genotypes tolerant to terminal heat with average production. In recent year chickpea varieties are available for late sown condition (December sown) but there is lacking of chickpea variety suitable for very late sown condition. Chickpea with low production cost, wide climatic adaptation, use in crop rotation and atmospheric nitrogen fixation ability is considered as one of the most important legume plants in sustainable agriculture system.

Gene pool of chickpea with 39 species include, 31 perennial and 8 annual land races, mutants, cultivars and wild type of *cice*r. Chickpea has high variation for different quality and quantity traits, included ideal plant type (tall type), shape and colour of grain, flower colour, podding, colour of seed coat, earliness, resistance to disease and pests, which helps breeders to release improved and advanced lines and varieties (Dasgupta et al.,1987; Singh, 1997). Genetic diversity can be accessed by characterizing morphological plant traits. Magnitude of variation present among gene pool entries can be evaluated through multivariate methods such as cluster analysis, D^2 statistics and principal component analysis (Malik *et al*., 2014). According to Sharma (1998). The objectives in many plant-breeding programmes are the selection of genotype which gives consistence performance over a wide range of environments.

Keeping this in view, the present investigation has been planned under late sowing condition with the following objectives:-

1. To characterize genotypes on the basis of morphological traits
2. To study the genetic parameters of variability for yield and its attributing traits
3. To assess the correlation coefficient and estimate the direct and indirect effect of various components on seed yield
4. To estimate the genetic divergence using D^2 analysis
5. To rank the genotypes on the basis of principle component analysis of yield and its attributing traits

REVIEW OF LITERATURE

The main objective of plant breeding is to increase the yielding ability as well as quality of produce in any crop varieties. Crop improvement depends on the magnitude of genetic variability and extent to which desired characters are heritable. Germplasm provides the base material for crop improvement, therefore collection, evaluation and cataloguing of germplasm is of utmost importance to have a dynamic crop improvement programme.

Characterization of cultivars is based on different agro-morphological traits is the most important step in the genetic improvement. This has in turn attracted the attention of plant breeders to study genetic aspects of economically important characters such as yield and its component traits. It is necessary to understand the genetic architecture of various characters of economic importance and interrelationship among them.

The available, relevant literature related to various biometrical parameter of present investigation **"**Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition**"** has been reviewed under the following heads:

2.1 Genetic parameters

2.1.1 Coefficient of variation

2.1.2 Heritability

2.1.3 Genetic advance

2.2. Correlation analysis

2.3. Path coefficient analysis

2.4. Genetic divergence

2.5 Principle component analysis

2.1 Genetic parameters

Existence of genetic variability is the primary requirement of any crop improvement program. The efficiency of selection largely depends upon magnitude of genetic variability present in the plant population. Thus the success of genetic improvement in any character depends on the nature of variability present in the gene pool for that character. Hence an insight into the magnitude of variability present in the gene pool of a crop species is of great importance to plant breeder for starting a judicious plant breeding programme. Various parameters of genetic variability are mean, range, standard deviation, coefficient of variation, heritability and genetic advance. Related available literature for genetic variability on chickpea is as follows:

2.1.1 Coefficient of variation

It is the simple measure of variability. Coefficient of variation partitions the total variation into phenotypic, genotypic and environmental components. The study of components of genetic variance helps in further partitioning of genetic variance into additive, dominance and epistatic components. A magnitude of these components is a measure of the type of gene action involved in the expression of various traits. Information about gene action helps in deciding a breeding procedure for genetic improvement of a trait. The idea of partitioning of variance was given by Fisher (1918) further many workers also suggested various technique for estimation of components of variation.

Khorgade et al. (1985) studied 32 genotypes of chickpea and observed the highest genotypic coefficient of variation for 100 seed weight and lowest for plant height.

Sharma et al. (1990) reported high genotypic coefficient of variation for number of pods per plant, seed yield per plant, 100 seed weight and number of branches per plant in chickpea.

Sandhu et al. (1991) worked on genetically diverse lines of chickpea and revealed that grain yield, pods per plant and 100 seed weight had maximum genotypic coefficient of variation.

Tripathi and Arora (1991) studied high phenotypic coefficient of variation for biological yield and seed yield per plant in chickpea.

Kumar and Balasubramanian. (1991) analyzed data derived from eleven metric traits of chickpea in three environments and observed high genotypic coefficient of variation for seed weight, harvest index and number of pods per plant.

Mishra and yadav (1994) reported genetic parameters in 32 genotypes of chickpea and reported high range and coefficient of variation for number of pods per plant, plant height, seed yield per plant and number of branches per plant indicated better scope for improvement through simple selection.

Rao and Singh (1994) found sixteen bold seeded chickpea genotypes for developmental traits and reported maximum variability for seed yield followed by harvest index and biological yield.

Arora and Jeena (2001) evaluated 40 genotypes of chickpea for genotypic and phenotypic coefficient of variation for 18 quantitative characters and found the highest genetic coefficient of variation in 100 seed weight, followed by primary branches per plant and seeds per plant.

Kumar et al. (2001) analyzed 26 genotypes for genotypic and phenotypic coefficient of variation for 12 quantitative characters, in which pods per plant exhibited the highest amount of genetic variability, followed by secondary branches per plant, seed yield per plant, 100 seed weight primary branches per plant and number of seeds per plant.

Jeena and Arora (2001) studied 96 chickpea genotypes and found high genotypic and phenotypic coefficient of variation for 100 seed weight.

Ali per plant, total weight of a plant, pods per plant and seed yield per plant which reflects that these traits response to selection.

Usmani et al. (2005) evaluated 30 genotypes and found high phenotypic coefficient of variation for et al. (2002) found maximum genetic coefficient of variation for secondary branches pod bearing length, seed yield per plant, plant height, harvest index (%) and number of pods per plant showed high genotypic coefficient of variation.

Durga et al. (2007) studied genetic variability on yield and yield components of chickpea revealed maximum genotypic coefficient of variation for branches per plant, followed by pods per plant and seed yield.

Kaul et.al. (2007) studied 150 exotic germplasm accessions, high variability observed for traits, viz., yield per plant, pods per plant and 100 seed weight, respectively. While moderate variability was detected for plant height.

Upadhaya et al. (2007) studied 14 agronomic traits in two seasons to identify diverse agronomically superior chickpea germplasm, Genotypes differed significantly for days to maturity, basal secondary branches, pods per plant, seed yield, and 100-seed weight. In comparison to controls, 12 accessions flowered early, 15 produced greater seed yield, and 29 had greater 100-seed weight.

Vaghela et al. (2008) evaluated fifty genotypes of Kabuli chickpea (Cicer arietinum L.) and estimated high genotypic coefficient of variation for seed yield per plant and number of pods per plant.

Sreelakshmi et al. (2010) evaluated genetic variability on yield and yield components of chickpea and found high genotypic and phenotypic coefficient of variation for seed yield, number of pods per plant and number of fruiting branches per plant, indicated additive gene action for these traits.

Akhtar et al. (2011) observed high phenotypic coefficient of variation (PCV) for days to flowering, days to maturity, plant height and seed yield than genotypic coefficient of variation, which means that the expression of these traits are more influenced by environmental effects. It is therefore, suggested that the grain yield could be improved by using the 100-seed weight and number of pods per plant as selection criterion in chickpea.

Babbar et al. (2012) studied forty four promising lines of chickpea under late sown condition. The maximum genotypic coefficient of variation was noticed for total number of seeds per plant and total number of pods per plant.

Nizama (2013) evaluated 50 genotypes of chickpea and found high genotypic and phenotypic coefficient of variation for pods per plant, seed yield per plant, harvest index and secondary branches per plant, whereas moderate for plant height, 100-seed weight and days to 50% flowering and low for seeds per pod, primary branches per plant, protein content and days to maturity. The GCV was observed high for pods per plant, followed by seed yield per plant and 100-seed weight.

Aarif et al. (2014) revealed high phenotypic coefficient of variation for 100-seed weight, followed by seed yield per plant and secondary branches per plant.

Yadav et al. (2015) observed high genotypic and phenotypic coefficients of variation for plant height, leaf length, leaflet length, leaflet width, number of primary branches/plant, number of secondary branches/ plant, number of pods/plant, pod length, pod width, 100-seed weight and seed yield/plant.

Desai et al. (2015) observed highest genotypic coefficient of variation for 100-seed weight, followed by methionine content, number of pods per plant, seed yield per plant and number of seeds per pod.

2.1.2 Heritability

Heritability in broad sense is the ratio of genotypic variance to total variance (phenotypic variance). It is calculated from total genetic variance which is consists of additive, dominance and epistatic variances. It is good index of the transmission of characters from parents to their off spring. The estimates of broad sense heritability help the plant breeder in selection of elite genotypes from homozygous populations.

Jivani and Yadavendra (1989) studied 42 diverse genotypes of chickpea and observed high heritability for 100 seed weight and harvest index.

Sharma et al. (1990) evaluated 70 genotypes of chickpea and reported high heritability for days to maturity, plant weight, 100 seed weight and number of branches per plant.

Kumar and Balasubramanian (1991) found high heritability for 100 seed weight, harvest index, effective pods per plant and low heritability in case of number of branches per plant and days to maturity on the basis of three environments in chickpea.

Jeena and Arora (2001) reported high heritability for 100- seed weight, followed by primary branches per plant and seeds per plant.

Patel and Babbar (2004) evaluated 24 chickpea genotypes and high heritability coupled with high genetic advance as percentage of mean was found for biological yield per plant in desi chickpea; seed yield per plant, harvest index, biological yield per plant in kabuli chickpea.

Arshad et al. (2004) noted high heritability for secondary branches and biological yield coupled with high genetic advance revealed that additive gene effects are important in determining these characters.

Jeena et al. (2005) observed high heritability for pods per plant, 100- seed weight, biological yield per plant and seed yield per plant.

Saleem et al. (2005) studied eighteen elite genotypes and observed high heritability for pods per plant, seeds per plant, 100-seed weight and total weight of plant.

Usmani et al. (2005) noticed high heritability for yield contributing traits viz., pod bearing length, seed yield per plant, plant height and harvest index.

Durga et al. (2007) noticed high heritability for days to 50% flowering and test weight indicating that improvement is possible through direct selection in respect of these traits.

Vaghela et al. (2008) found that heritability was higher for all the traits except plant height in chickpea.

Sidramappa et al. (2008) found high heritability for pods per plant, seed yield per plant, seed weight, days to 50% flowering, days to pod initiation and plant height.

Khan et al. (2011) estimates high heritability for days to 50% flowering followed by biological yield per plant, plant height, 100 seed weight, grain yield per plant and days to maturity.

Singh et al. (2012) evaluated 26 genotypes over four environments. High estimates of heritability were observed for 100-seed weight, number of pods per plant, number of branches per plant, plant height, seed yield and number of seeds per pod.

Nizama (2013) revealed high heritability estimates for protein content, 100-seed weight, pods per plant, harvest index, seed yield per plant, days to 50% flowering and secondary branches per plant.

Aarif et al. (2014) observed high heritability for 100-seed weight.

Mallu et al. (2014) found highest estimates of broad sense heritability for 100 seed weight, followed by days to 50 % flowering and plant height.

Desai et al. (2015) observed high heritability for methionine content, 100-seed weight, pods per plant and days to flowering.

Mohammadi and Talebi (2015) found high heritability values for number of seeds per plant, 100-seed weight and plant biomass.

Yadav et al. (2015) found high heritability for number of primary branches, number of secondary branches, plant height, pod length, and pods/plant indicating the influence of environment for these traits. Low heritability percentage has been observed for days to maturity indicated that this trait was greatly influenced by environment.

2.1.3 Genetic Advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. It helps in understanding the type of gene action involved in the expression of various polygenic characters and deciding a breeding procedure for the genetic improvement of various polygenic traits by determining the gene actions.

Patil and Phadnis (1977) studied 81 lines of chickpea and reported the highest genetic advance for number of pods per plant and 100 seed weight.

Pundir et al. (1991) studied 25 diverse genotypes of chickpea and observed high genetic advance as percentage of mean for seed size, seed yield and number of seeds per pod and low for number of pods per plant and days to flowering.

Gupta et al. (1992) estimated high genetic advance as percentage of mean for 100 seed weight and seed yield and moderate for number of seeds per plant, number of pods per plant and number of seeds per pod. However, it was low for plant height, days to 50 percent flowering, number of branches per plant and days to maturity.

Arora and Jeena (2001) evaluated 40 genotypes of chickpea for 18 quantitative characters. High genetic advance was noted for 100 seed weight, followed by primary branches per plant and seeds per plant.

Kumar et al. (2001) analyzed 26 genotypes and found that pods per plant, primary branches per plant and number of seeds per plant showed the maximum heritability.

Pratap et al. (2004) assessed 38 genetically diverse early maturing chickpea genotypes in four different environments, revealed that seed yield, 100 seed weight and biological yield showed high genetic advance.

Jeena et al. (2005) observed that pods per plant, 100-seed weight, biological yield per plant and seed yield per plant had high genetic advance.

Usmani et al. (2005) exhibited high genetic advance for seed yield per plant, plant height and harvest index (%).

Durga et al. (2007) observed high genetic advance for days to 50% flowering; pods per plant and seed yield indicate additive gene effects control these traits.

Vaghela et al. (2008) found high genetic advance expressed as a percentage of mean for seed yield per plant and number of pods per plant.

Alwawi and choumane (2010) achieved high genetic advance for seeds yield per plant.

Babbar et al. (2012) evaluated forty four promising lines of chickpea under late sown. Days to 50% flowering, days to maturity, plant height, 100 seed weight and seed yield per plant was showed high heritability coupled with medium genetic advance as percentage of mean, whereas number of seeds per plant and number of pods per plant showing medium heritability and high genetic advance as percentage of mean.

Sewak et al. (2012) evaluated 495 accessions of chickpea, and found wide range of variability 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.

Gul et al. (2013) observed high genetic advance for pods per plant, seed yield per plant, primary branches per plant and secondary branches per plant.

Singh and Singh (2013) reported high genetic advance as percent of mean for seed yield per plant, number of seeds per pod and number of pods per plant.

Nizama (2013) observed high genetic advance as percentage of mean for 100-seed weight, followed by pods per plant and seed yield per plant.

Kuldeep et al. (2014) reported high genetic advance as percentage of mean for seed yield per plant, followed by 100 - seed weight, harvest index, number of effective pods per plant, total number of pods per plant and number of secondary branches, while moderate genetic advance was observed for plant height, seeds per pod and days to flower initiation.

Naveed et al. (2015) observed high to moderate estimates of heritability and genetic advance for fusarium wilt incidence, days to 50% flowering, total branches per plant, pods per plant, 100-seed weight, grain yield and harvest index.

2.2 Correlation analysis

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables. A positive value of correlation shows that the changes of two variables are in same direction, whereas in negative correlation movements of two variables are in opposite direction. It measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. There are three types of correlation viz., phenotypic, genotypic and environmental. Phenotypic correlation is the observable correlation between two variables. It includes both genotypic and environmental effects. Genotypic correlation on the other hand measures the inherent association between two variables. It may be either due to pleotropic action of genes or linkage, more likely both or developmentally induced relationships. The need of correlation coefficient was suggested by Galton (1988). He also described the degree of association between variables. Searle (1961) described the mathematical application of correlation at phenotypic, genotypic and environmental level. The literatures available on correlation analysis in chickpea are listed below:

Khorgade (1985) revealed seed yield was positively significantly correlated with 100-seed weight, number of branches, pods per plant and negatively correlated with days to 50% flowering and number of seeds per plant.

Paliwal et al. (1987) reported seed yield per plant was positively correlated with plant height, days to maturity and days to flowering.

Mishra et al. (1988) evaluated 117 genotypes of chickpea that seed yield per plant had positive association with number of branches per plant, number of pods per plant, biological yield per plant and harvest index.

Tripathi and Arora (1991) reported seed yield per plant was positively associated with biological yield, number of branches per plant, harvest index and number of seeds per pod.

Dasgupta et al. (1992) found seed yield was significantly positively correlated with number of pods per plant, harvest index and number of branches per plant, 100-seed weight and seeds per pod, while days to maturity exhibited negative correlation with seed yield. The inter-correlation between pods per plant and seeds per plant was positive.

Chavan et al. (1994) reported positive correlation of days to flowering and days to maturity with seed yield per plant.

Vijaylakshmi et al. (2000) evaluated two chickpea crosses, P 9623X T39-1 and RS 11X T39-1 by using desi, Kabuli and intermediate type parents and reported that seed yield of both crosses was positively correlated with number of pods, number of seeds, primary branches and secondary branches per plant.

Guler et al. (2001) found positive and significant relationships 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, the number of seeds per pod, the number of seeds per plant; between the number of seeds per pod and seed yield per unit area; between the number of seeds per plant and seed yield per unit area. Negative and significant relationships were determined statistically between the number of pods per plant and 100 seed weight, between the number of seeds per pod and 100 seed weight, between the number of seeds per plant and 100 seed weight, between seed yield per unit area and 100 seed weight.

Singh et al. (2001) revealed positive association of primary branches, secondary branches, number of pods per plant with grain yield.

Yadav and Haquae (2001) observed seed yield was positively associated with number of seeds per pod and days to maturity but negatively correlated with days to 50 % flowering.

Rao (2001) assessed 21 vascular wilt resistant chickpea genotypes and reported biological yield were positively correlated with seed yield. Biological yield and 100 seed weight had significant positive association with harvest index.

Singh and Singh (2002) analyzed 40 genetically diverse genotypes of chickpea and revealed positive and significant association of number of secondary branches, number of pods per plant, plant height, days to flowering, days to maturity and test weight per plant with seed yield.

Patel (2003) found seed yield per plant shared positive association with biological yield, pod weight per plant, number of pods per plant, pod bearing length, plant height, days to flower initiation, days to pod intiation,50% podding, end of flowering and days to maturity.

Babbar and Patel (2005) estimated genetic correlation of 24 genotypes, and revealed positive significant association of seed yield with biological yield, pod weight per plant, number of pods per plant and days to maturity.

Jeena et al. (2005) noted seed yield was significantly and positively correlated with plant height, pods per plant, 100 seed weight, biological yield per plant and harvest index.

Yadava and Singh (2008) reported to identified the traits determining tolerance against drought and temperature in chickpea through correlation by evaluating 16 genotypes in 6 environments created by adjusting the moisture availability for 3 subsequent years. Harvest index and 100-seed weight showed positive and significant association with seed yield in all the environments.

Ali et al. (2010) reported pods per plant, seeds per pod and 100-seed weight were positive and significant at genotypic level but positive and highly significant at phenotypic level with biological yield per plant. Days to flowering were negative and non-significantly correlated with grain yield per plant at both genotypic and phenotypic levels.

Meena et al. (2010) observed correlation coefficient and suggested that selection of plants with high or more plant height, total number of branches per plant, number of pods per plant, biological yield and harvest index would be effective in identifying genotypes with high seed yield.

Sreelakshmi et al. (2010) exhibited significant positive correlation for days to 50% flowering, days to maturity and number of pods per plant with seed yield.

Mishra and Babbar (2011) observed seed yield per plant was positively and significantly correlated with effective pods per plant, seeds per pod, biological yield per plant,100 seed weight and harvest index in normal and late sown. Seven heat tolerant genotypes were identified i.e. Dilagi, ICC 9942, ICCV 10, ICCV 07115, JG 130 and JG11.

Akhtar et al. (2011) evaluated 20 advance genotypes of chickpea and observed, significant and positive correlations between yield and 100-seed weight, number of pods per plant and plant height.

Ahmad et al. (2012) studied four morphological traits the average coefficient of variation was calculated as 56.8% with significant correlation among yield traits.

Babbar et al. (2012) evaluated forty four promising lines of chickpea under late sown condition. Seed yield per plant showed high significant positive correlation with total number of seeds per plant, total number of pods per plant, biological yield, plant height and 100 seed weight. Whereas, significant negative correlation with days to 50% flowering.

Pandey et al. (2013) reported that grain yield per plant was positively and significantly correlated with days to flowering, plant height, number of branches per plant, number of pods per plant and 100 seed weight

Mishra and Babbar (2014) observed that positive and significant correlation of seed yield per plant was found with harvest index, number of total pods per plant, number of effective pods per plant, seed size and biological yield per plant under timely and late sown conditions.

Malik et al. (2014) observed high variances for days to flowering, maturity, plant height, biological yield and harvest index. These traits showed positive significant correlation with yield.

Aarif et al. (2014) observed that seed yield per plant exhibited significant positive association with primary branches per plant, secondary branches per plant, pods per plant, biological yield per plant and harvest index; and significant negative correlation with days to maturity at genotypic level.

Jadhav et al. (2014) revealed that seed yield per plant exhibited positive and significant correlation with plant height, number of branches per plant, pods per plant, number of seeds per plant,100 seed weight and harvest index at both genotypic and phenotypic level.

Sarker et al. (2014) revealed that seed weight per plant expressed positive significant correlation with number of primary branches, number of secondary branches, number of pods per plant, pod weight per plant and number of seeds per plant at genotypic level. In phenotypic level, seed yield showed positive significant correlation with number of pods per plant, pod weight per plant and number of seeds per plant. Highest positive direct effect was observed for number of seeds per plant, followed by pod weight per plant and 1000-seed weight at genotypic level.

Bala et al. (2015) revealed significant positive associations of pods per plant, harvest index, biological yield per plant and primary branches per plant with seed yield per plant.

Tesfamichael et al. (2015) found significant positive correlation of seed yield per ha with biomass yield per ha, pods per plant, plant canopy width and secondary branches per plant.

Shafique (2016) observed that harvest index and number of seeds per plant had a significant and positive association with seed yield.

2.3 Path coefficient analysis

The path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measure of direct and indirect effects .Path analysis measure the cause of association of two variables. It is based on all possible simple correlation among various characters. It help in determining yield contributing characters and useful in indirect selection. Path analysis is an extension of the regression model, used to test the fit of the correlation matrix against two or more causal models which are being compared. The concept of path analysis was developed by Wright (1921). Path coefficient analysis is applied for assessment by Dewey and Lu (1959) in crested wheat grass. The literature available on path analysis in chickpea is listed below:

Paliwal et al. (1987) found that 100 seed weight had the highest positive direct effect on seed yield per plant followed by number of seeds per plant and days to maturity.

Sontakey et al. (1991) indicated the importance of number of pods per plant, number of seeds per pod and 100-seed weight in the improvement of seed yield as these traits showed high direct effect on yield.

Dasgupta et al. (1992) reported that number of pods per plant, number of seeds per plant, 100-seed weight registered high positive direct effects on yield. The indirect effects of number of pods per plant, number of seeds per plant and number of seeds per pod were high and positive.

Bhambotia et al. (1994) revealed pods per plant and plant height had considerable positive direct effects on seed yield.

Ozdemir (1996) showed number of seeds per plant the most important yield components and have significant direct and indirect effects.

Cinsoy and Yaman (1998) evaluated 125 chickpea varieties for 17 yield components at various locations in Turkey and found significant correlation between pods per plant and seed weight per plant. Direct effects of pod length and seeds per pod on seed weight were also significant.

Rao and Kumar (2000) reported number of pods per plant, 100 seed weight, plant height, days to 50% flowering had high positive direct effect on seed yield.

Singh et al. (2001) observed that days to maturity and number of primary branches per plant had high indirect effect on seed yield via number of pods per plant although direct effect was negative.

Muhammad et al. (2002) studied that number of pods per plant had maximum positive direct effect on seed yield. The other traits in the study also exhibited considerable indirect effect on the seed yield through number of pods per plant. It was concluded that number of pods per plant and 100 seed weight could be used as selection criteria to improve the yield.

Patel (2003) revealed that biological yield, 50% podding and harvest index had high direct effect on seed yield in desi chickpea. Biological yield, harvest index and pod initiation showed high positive direct effect on seed yield per plant in kabuli chickpea, whereas 50% podding, days to flower initiation had positive direct effect on seed yield per plant in gulabi chickpea.

Babbar and Patel (2005) revealed through path coefficient analysis that biological yield per plant, 50% podding and harvest index showed maximum direct contribution on seed yield.

Talebi et al. (2007) observed that harvest index had greatest direct effect on seed yield and its indirect effect on seed yield was positive through plant height, number of seeds per pod and biomass, but negative and low through days to maturity, 100 seed weight and number of primary branches.

Farshadfer and Farshadfer (2008) revealed pod number with, seed number, 100 seed weight had highest direct effect on seed yield.

Yadava and Singh (2008) revealed that harvest index and 100-seed weight were the major and stable yield factors under both moisture stress and non-stress environments.

Shukla and Babbar (2011) studied association and path coefficient analysis of various morpho-phenological characters with yield in thirty heat tolerant lines under three environments. Very high magnitude of genotype x environment interaction were found in yield and its component characters .

Shrivastava et al. (2012) studied that biological yield, harvest index, days to maturity, effective pods per plant and seeds per pod exhibited maximum direct positive effect on seed yield per plant under rice fallow condition. Kuldeep et al. (2014) revealed that number of effective pods per plant and 100- seed weight had maximum direct effect on seed yield.

Bala et al. (2015) found that biological yield per plant and harvest index exhibited positive and high direct effects on seed yield per plant.

Joshi and Yasin (2015) found that biological yield per plant exerted maximum direct effect on seed yield, followed by harvest index. Days to 50%

flowering and days to maturity had negative indirect effect on seed yield via. biological yield and harvest index.

Chandra et al. (2015) studied the M_3 and M_4 generations and found that harvest index and biological yield per plant had high (maximum) direct effect on seed yield per plant in both generations.

Mohammadi and Talebi (2015) found that number of seeds per plant, 100-seed weight and plant biomass had a positive direct effect on seed yield.

Shafique et al. (2016) revealed that maximum positive direct effect toward seed yield was exerted by number of pods per plant with 52.87% ratio.

2.4. Genetic divergence

This is one of the potent techniques for assessment of genetic divergence in various breeding materials. Genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. It helps in selection of genetically divergent parents for their exploitation in hybridization progrrammes. It measures the degree of diversification and determines the relative proportion of each component character to the total divergence. The forces of differentiation are measured at two levels i.e. inter-cluster and intra-cluster levels. This technique provides reliable estimates of divergence and a large number of germplasm lines can be evaluated at a time for genetic diversity by this technique.

Yadav et al. (1991) studied genetic divergence amongst 38 chickpea varieties of India by applying Mahalanobis D^2 statistics for 14 yield components. Three clusters were formed. D^2 analysis revealed that the geographical diversity of 38 genotypes has no relationship with the genetic diversity.

Rao and Singh (1994) evaluated genetic diversity of 25 genotypes for 10 characters and grouped them into three clusters. Days to flowering, days to maturity and 100 seed weight accounted for maximum divergence. JG 315, JG 86-8, and JG 86-22 were identified as genetically diverse parents with agronomic value. Cluster III had high yield and small seeded genotype.

Gupta and Krishna (1996) studied 29 diverse genotypes of chickpea and grouped into 7 clusters. Comparison of cluster mean for all the characters indicated considerable genetic divergence between the groups.

Tripathi (1997) observed genetic diversity of hundred chickpea genotypes. The genotypes were grouped into 12 clusters on the basis of yield and yield components.

Pooran Chand (1999) studied genetic divergence among 49 genotypes of chickpea was estimated for 7 quantitative traits. The genotypes were grouped into 8 clusters.

Harisatyanarayan and Reddy (2001) studied genetic divergence among 31 chickpea types and grouped into 7 clusters, cluster I was largest with 14 genotypes. The maximum genetic divergence was recorded between cluster IV and VII.

Jeena et al. (2005) grouped 80 genotypes into 11 clusters. The highest number of genotype were included in cluster I (60), followed by cluster II (7). No definite relationship was observed between genetic diversity and geographic distribution.

Singh et al. (2006) recorded maximum inter cluster distance between cluster I and VI followed by cluster I and V and I and IV. Hence genotype belonging to different clusters can be used as parent for hybridization programme for the development of high yielding chickpea genotype.

Upadhaya et al. (2007) observed 39 selected accessions and two control cultivars (Annigeri and L 550) were grouped by into three clusters. Cluster I consisted of early maturing large-seeded kabuli types, cluster 2 early and late maturing desi types, and cluster III late maturing intermediate and kabuli types. Clusters II and III accessions had small to medium sized seeds. These accessions can be used in chickpea breeding programs to develop high yielding desi and kabuli cultivars with a broad genetic base.

Dwivedi and Gaibriyal (2009) grouped 25 genotypes of chickpea in 6 clusters and observed highest inter-cluster distance between cluster II and IV. Three characters viz., 100 seed weight, number of pods per plant contributed maximum in manifestation of genetic diversity.

Hahid et al. (2010) shows means of various traits for each characters that genotype with maximum number of secondary branches, pods per plant, biological yield, seed yield per plant were placed together in cluster II and genotype with maximum harvest index and 100 seed weight were placed in cluster II and I.

Sreelakshmi et al. (2010) studied 40 genotypes were grouped into 8 clusters. Out of which cluster I and II had maximum number, with seven genotypes each. Among the characters, seed yield contributed maximum towards genetic divergence. .

Pandey et al. (2013) reported the percentage contribution of individual characters towards genetic diversity .It was revealed that days to flowering, 100-seed weight and number of pods per plant were the major characters contributing traits to genetic diversity.

Parameshwarappa et al. (2012) grouped genotypes into 20, 16 and 25 clusters in E1, E2 and E3, respectively. Genotypes of cluster XIX (ICC13124) had the highest mean value for pod number and earliness in E1. In E2, the genotypes of cluster XV (ICC12654) and XVI (ICC9848) were superior in respect of plant height, pods per plant and 100 seed weight, respectively. In E3, the genotype of cluster XVI (ICC13124) had the highest mean value for seed yield.

Syed et al. (2012) estimated genetic diversity of 27 chickpea genotypes and were grouped 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.

Jinvani et al. (2013) revealed that seed yield per plant, 100-seed weight and number of pods per plant contributed more than 63% towards total genetic divergence.

Pandey et al. (2013) reported the percentage contribution of individual characters towards genetic diversity and found that days to flowering, 100-seed weight and number of pods per plant were the major characters contributing to genetic diversity.

Parashi et al. (2013) studied genetic diversity in sixty chickpea genotypes using D^2 statistics and grouped 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 (D2 =194.04), followed by cluster XI and XIII (D2 = 156.50), cluster VI and XIII (D2 = 130.64) and cluster IV and XI (D2 =

119.46). Three characters viz., yield per plant (34.29%), stomatal conductance (27.97%) and number of pods per plant (16.33%) contributed maximum towards genetic diversity.

Gaikwad et al. (2014) revealed that pods per plant, number of secondary branches per plant, 100-seed weight and days to 50% flowering contributed maximum to the divergence.

2.5. Principal component analysis

Principal component analysis (PCA) involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The principle component analysis is a multivariate analysis used to study kind of variation present in the selected population. In chickpea more PCA studies is made on pure breeding lines like germplasm lines, while these are not reported in segregating population.

Muniraja et al (2011) conducted principal component analysis among genotypes showed that the first two PC axes explained 44.2%of total multivariate variation with first five PC axes exclaiming 74.2%. The PC 1 separates genotypes on number of pods per plant, seed yield per plant, plant height and number of secondary branches per plant, while PC2 separated on days to maturity, days to 50 per cent flowering and percent pod damage.

Shahid et al. (2012) reported that the first 4 principal components accounted for 71.99% of the total variation. Seed yield, biological yield, pods plant per plant, secondary branches and plant height in chickpea showed positive relation with the first component (PC1). Days to flowering, days to maturity, 100-seed weight showed positive correlation with the second component (PC2).

Malik et al. (2014) studied genetic diversity of 113 desi chickpea genotypes through principal component analysis. The first 4 principal components accounted for 71.99% of the total variation. Seed yield, biological yield, pods per plant, secondary branches and plant height in chickpea showed positive relation with the first component (PC1). Days to flowering, days to maturity, 100-seed weight showed positive correlation with the second component (PC2). The grouping of genotypes would be of practical value to chickpea breeders in identifying the genotype with desired trait for utilization in breeding program for genetic improvement.

Naveed et al. (2015) grouped 60 chickpea genotypes into ten PCs based on Principal component analysis. First four PCs out of total ten achieved eigen values > 1 and explained 75.5% of overall variability. Days to 50% flowering, 100-seed weight and grain yield contributed highest weight on PC1 that explained 31.80% of total variation. PC2 described 21.60% of digression and was mainly related to pods per plant, plant height and canopy temperature.

Mallu et al. (2015) studied genetic diversity among 58 chickpea genotypes using Principal component analysis. The first four principal components explained significant proportion of the total variations and accounted for 77.04 % variation. The first principal component was positively associated with days to flowering, plant spread, plant height, number of primary and secondary branches per plant, days to maturity, pods per plant, pod length, biomass and seed yield. The second principal component was positively related with plant spread, pod length, plant height, pod filling period, pods per plant, seed yield and 100 seed weight.

Temesgen et al. (2015) studied genetic divergence among 49 kabuli chickpea genotypes through Principal component analysis and revealed that four principal components PC1 to PC4 with eigen values 6.35, 3.02, 1.61 and 1.01 respectively, have accounted for 79.92% of the total variation. The first two principal components PC1 and PC2 with values of 42.31% and 20.11% respectively contributed more to the total variation.

MATERIAL AND METHODS

The material and methods pertaining to the thesis entitled **"Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition"** are given as below:

3.1 Experimental site

The experiment was carried at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur (Madhya Pradesh). The experimental area occupied was quite uniform in respect of topography.

3.2 Climate and Weather

Jabalpur is situated at 23.90ºN latitude and 79.58ºE longitude at an altitude of 411.87 m above the mean sea level. This region has subtropical, semi-arid climate. The main features are hot and dry summer season. Jabalpur traditionally comes under rice - wheat crop zone of Madhya Pradesh and classified as "Kymore plateau and Satpura hills agro-climatic zone". The maximum temperature during the month of May and June reaches up to 46ºC, whereas minimum temperature goes below 6ºC in the month of December or January. The average rainfall in this region is 1107.1 mm which is mostly received during monsoon season between mid - June to end of October with little occasional showers in other seasons.

3.3 Experimental material and methods

Experimental material consisted of 36 genotypes, were obtained from AICRP on chickpea, JNKVV, Jabalpur during *Rabi*, 2015. The experiment was conducted in Randomized Complete Block Design. The details are as follows :

Experimental details:

Number of genotypes	36
Experimental design	Randomized Complete Block Design
Season	*Rabi* (2015-16)
Sowing date	10.12.2015
Number of replications	3
Row to row spacing	30 cm
Row length	4 m
Rows / plot	4

Fertilizer was applied in the ratio of 20 N: 60 P_2O_5: 40 K_2O kg/ha. The experiment was conducted with recommended agronomic practices for normal crop growth. The list of genotypes is given in table 3.2. Observations were recorded as per the DUS guidelines proposed for chickpea. Observations were recorded for quantitative traits on five random competitive plants selected from each plot.

Table 3.1 Meteorological data during entire crop season : 2015-16

Monthly Week	Meteorological weeks	Temp. max.	Temp. min.	Sun Shine hrs.	Rainfall (mm)	RH (Morning)	RH (Evening)	Wind Speed	Evaporation (mm)	Rainy days
3 to 9 Dec.	49	28.1	9.2	7.8	0.0	92.0	30.0	2.0	2.1	0
10 to 16 Dec.	50	26.6	9.2	7.6	0.0	82.0	32.0	3.0	2.3	0
17 to 23 Dec.	51	24.1	7.0	7.0	0.0	86.0	37.0	2.8	2.0	0
24 to 31 Dec.	52	24.2	5.4	8.6	0.0	91.0	25.0	1.5	2.0	0
1 to 7 Jan.	1	27.5	7.9	8.5	0.0	88.0	27.0	1.8	1.8	0
8 to 14 Jan.	2	26.7	8.0	7.7	0.0	81.0	32.0	1.7	2.1	0
15 to 21 Jan.	3	22.2	11.5	5.4	12.2	92.0	65.0	3.5	1.3	2
22 to 28 Jan.	4	23.3	4.2	9.6	0.0	94.0	29.0	2.3	1.9	0
29 to 4 Feb.	5	27.7	9.3	9.3	0.0	92.0	35.0	2.8	2.5	0
5 to 11 Feb.	6	26.4	8.4	8.3	0.0	84.0	34.0	3.2	2.8	0
12 to 18 Feb.	7	28.5	11.3	6.9	0.0	88.0	40.0	3.3	2.6	0
19 to 25 Feb.	8	30.2	11.8	7.4	0.0	90.0	32.0	2.7	3.0	0
26 to 4 March	9	30.5	13.4	8.5	0.0	97.0	39.0	3.3	2.8	0
5 to 11 March	10	31.9	17.0	8.0	29.6	88.0	47.0	3.5	3.4	2
12 to 18 March	11	30.9	15.9	8.7	6.5	85.0	37.9	4.1	3.9	2
19 to 25 March	12	34.5	14.1	10.2	0.0	67.1	18.0	3.3	5.3	0
26 to 1 April	13	35.8	16.4	10.0	8.0	78.3	17.6	2.3	4.7	1
2 to 8 April	14	39.1	20.1	9.1	0.0	62.3	18.4	3.0	6.5	0
9 to 15 April	15	38.9	19.6	10.2	0.0	56.3	12.3	3.8	7.7	0
16 to 22 April	16	41.1	21.9	10.5	0.0	48.2	12.4	5.0	8.8	0

Table 3.2 Genotypes of chickpea used as experimental material

S.No.	GENOTYPES
1	CSJ887
2	NBeG 507
3	BG 3067
4	RKG 13-155
5	PG 158
6	H 12-62
7	PBC 501
8	JSC 55
9	JG 24
10	IPC 2012-49
11	Phule G13110
12	GL 12003
13	RKG 13-180
14	JG 74315-14
15	CSJ884
16	NDG 14-24
17	H 12-55
18	GNG 2304
19	Phule G0719-10
20	GJG 1319
21	BG 3068
22	JSC 56
23	NBeG 511
24	GNG 2219
25	RVSSG 38
26	IPC 2012-98
27	GL29098
28	PBC 510
29	JG24
30	JG24-1
31	RVG 203
32	GNG 2261
33	PG 0104
34	GL 12021
35	IPC 2010-134
36	RVG 202

3.3 Observations recorded

3.3.1 Quantitative characters

Observations were recorded on five randomly selected plants from each plot and average has been taken.

3.3.1.1 Days to flower initiation

Number of days were counted from date of sowing to the appearance of initiation of flower on the plants of the plot was recorded.

3.3.1.2 Days to 50% flowering

From date of sowing to the stage when 50% of flowers have begun to flower in each of the plot.

3.3.1.3 Days to pod initiation

Number of days taken from date of sowing to the appearance of initiation of pod on the plants of the plot was recorded

3.3.1.4 Days to maturity

Physiological maturity was recorded from date of sowing to the stage when 90% of pods have matured and the plants turned yellow.

3.3.1.5 Plant height (cm)

The height of the plant was recorded in cm from the ground level to the tip of the main stem at the time of maturity.

3.3.1.6 Number of primary branches / plant

Numbers of branches / plant born on the ground level were counted at maturity.

3.3.1.7 Number of secondary branches / plant

Number of branches born on the primary branches / plant was counted at maturity.

3.3.1.8 Total number of pods/ plant

Total number of pods/ plant was counted at the time of maturity.

3.3.1.9 Number of effective pods/ plant

Number of filled pods/ plant was counted at the time of maturity.

3.3.1.10 Number of seeds/ plant

Number of seeds/ plant were counted at the time of maturity.

3.3.1.11 100 Seed weight (g)

100 seed were counted from the seed lot and weighted in gram. This is average of replicateddata or single observation.

3.3.1.12 Biological yield / plant (g)

Each plant was harvested from ground level and weighted in gram after sun drying.

3.3.1.13 Harvest index (%)

Harvest index was obtained by dividing the total seed yield per plant by biological yield per plant and expressed in percentage.

$$\text{Harvest index (\%)} = \frac{\text{Seed yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.3.1.14 Seed yield / plant (g)

Weight of seeds of the plant was recorded in gram.

3.4 Visual traits

Observations were recorded according to chickpea descriptor.

3.4.1 Flower color

In most of the cases pink and blue flowers have veins of a darker shade in the flag, while the tip of the keel is also darker. The classes are ranges rather than only on the shades of the reference colors. Royal horticultural society (RHS) color codes are given in the parentheses beside descriptor states.

Table 3.3 Details of flower color and code

S.N.	Color	Color codes (RHS)
1.	Blue	(violet-blue group 97 B)
2.	Light blue	(violet-blue group 97 C)
3.	Dark pink	(red- purple group 64 D)
4.	Pink	(red- purple group 63 D)
5.	Light Pink	(red- purple group 69 C)
6.	White	(white group 155 D)
7.	White- pink striped	(white group 155 D, red- purple group 63 D)

3.4.2 Foliage color

Three main groups are:

(a) Dark green
(b) Medium green
(c) Light green

3.4.3 Leaf Pattern

(a) Simple
(b) Compound
(c) Pinnate

3.4.4 Leaflet size (mm): Size of basal pairs of leaflets. Leaflet size in chickpea is grouped into three categories:

Table 3.4 Leaflet size (mm)

S.N.	Type	Size(mm)
1.	Small	<10mm long-<4mm wide
2.	Medium	10-15mm long, 4-12mm wide
3.	Large	Large>15mm long,>12mm wide

3.4.5 Plant Pigmentation

(a) Present

(b) Absent

3.4.6 Growth habit

As per chickpea descriptor 5 types of growth habits i.e. erect (0-15^0 from vertical), semi-erect (16-25^0 from vertical), semi-spreading (26-60^0 from vertical), spreading (61-80^0 from vertical) and prostrate (branches flat on the ground) found in chickpea.

3.5 Seed traits

3.5.1 Seed Type

(a) Desi chickpea

(b) Kabuli chickpea

3.5.2 Seed shape

According to chickpea descriptor, seed shapes are categorized in three types.

Type	Shape	Chickpea type
Ram’s head	Angular	Desi cultivars
Owl head	Irregular rounded	Kabuli cultivars
Pea shaped	Smooth round	Gulabi cultivars

3.5.3 Seed color

According to chickpea descriptor, Royal Horticultural Society (RHS) coded 21 colours of mature seeds (Table 3.4).

Table 3.5 Different seed coat color according to chickpea descriptor

S.N.	Color	Color codes (RHS)
1.	Black	Black group 202A, 202B; brown group 200A
2.	Brown	Grayed-orange group 177B
3.	Light brown	Grayed-orange group 177C
4.	Dark brown	Grayed-orange group 177A
5.	Reddish brown	Grayed-orange group 166C
6.	Grayish brown	Brown group 200D
7.	Salmon brown	Grayed-orange group 165C
8.	Gray	Grayed-green group 196A
9.	Brown beige	Grayed-orange group 173D
10.	Beige	Grayed-orange group 165D
11.	Yellow	Grayed-orange group 164B
12.	Light yellow	Grayed-orange group 164C
13.	Yellow brown	Grayed-orange group 165C
14.	Orange yellow	Grayed orange group 168D
15.	Orange	Grayed-orange group 168C
16.	Yellow beige	Orange-white group 159C
17.	Ivory white	Orange-white group 159C
18.	Green	Grayed-green group 191A; grey group 201A; grayed-orange group 166B)
19.	Light green	Grayed- green 193B
20.	Variegated	Grayed- green 193B
21.	Blackbrown mosaic	Back group 202A; grayed-orange group 177E

3.5.4 Seed surface

According to chickpea descriptor categories into three groups.

(a) Rough

(b) Smooth

(c) Tuberculated

3.5.5 Seed ribbing

(a) Present

(b) Absent

3.5.6 Seed size

Seed size of each genotype is observed and recorded on the basis of 100 seed weight.

Table 3.6 Seed size of desi type chickpea

Seed size	Seed weight (g)
Small seed	<18
Medium	18-22
Large seed	>22

3.6 Statistical analysis

The mean value of the recorded data were subjected to analysis of variance (ANOVA) using the statistical analysis procedures suggested by Sharma (1998).

3.6.1 Mean

It was calculated by using following formula:

$$\text{Mean} \quad (\overline{X}) = \frac{\sum_{i=1}^{n} X_i}{n}$$

Where,

$\sum x$ = sum of all observations

n = Number of observations

3.6.2 Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes.

3.6.3 Analysis of variance

The mean data on five plants were subjected to variance analysis and test of significance as per the method suggested by Sharma (1998).

The data on quantitative characters were statistically analyzed on the basis of model described for complete randomized block design.

$$Y_{ij} = (\mu + b_i + t_j + e_{ij})\, n_{ij}$$

Where,

Y_{ij} = Performance of j^{th} genotype in i^{th} block

M = General mean

b_i = i^{th} block effect

t_j = j^{th} treatment effect

e_{ij} = Random errors which are supposed to be identically and independently distributed with normal distribution having mean zero and variance σ^2_e . i = 1, ..., r, j = 1, ... , v, n_{ij} is one if the j^{th} treatment occurs in the i^{th} block and zero otherwise.

Table: 3.7. ANOVA of the experiment

Source of variation	Df	Sum of square	Mean sum of square	F value
Blocks	(b-1)	bSS	bMS	bMS/ EMS
Entries	(e-1)	eSS	eMS	eMS/ EMS
Checks	(c-1)	cSS	cMS	cMS/EMS
Varieties	(V-1)	vSS	vMS	vMS/EMS
Checks Vs. varieties	1	cvSS	cvMS	cvMS/EMS
Error	(c-1) (b-1)	ESS	EMS	
Total	(N-1)	TSS		

Where,

b = Number of blocks

e = Number of entries (e = v + c)

c = Number of checks

v = Number of varieties

MS = Mean sum of square

ESS = Error sum of square

df = degrees of freedom

SS = sum of square

EMS = Error mean sum of square

N = Number of plots (N = v + bc)

A significant value of F-test indicates that the test entries differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Coefficient of variation (CV)} = \frac{\sqrt{\text{EMS}}}{\text{G.M.}} \times 100$$

$$\text{Standard error of difference SE (between any two check means) (d)} = \sqrt{\frac{2\text{EMS}}{\text{b}}}$$

$$\text{Critical difference (cd)} = t_{(0.01)} \times \text{S.em}_{(d)}$$

Where,

G.M. = General mean

$t_{(0.01)}$ = t-value at 1% probablilty level

b = number of block

3.6.4 Coefficient of variation:

The coefficient of variation at genotypic and phenotypic levels was calculated as per the formula proposed by Burton, (1952). The phenotypic and genotypic variances were also estimated according to the method suggested by Burton and De Vane (1953) using the formula, (a) and (b).

3.6.4.1 Phenotypic coefficient of variation (PCV):

$\sigma^2_p = \sigma^2_g + \sigma^2_e$ …….. (a)

PCV = $(\sigma_p / \bar{X}) \times 100$

Where, $\sigma_p = \sqrt{\sigma^2 p}$

3.6.4.2 Genotypic coefficient of variation (GCV):

σ^2_g = MSg – MS$_e$ / r ……….. (b)

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

Where,

MS_g	=	Mean square due to genotypes or accessions
MS_e	=	Error mean square
r	=	Number of replications
σ^2_p	=	Phenotypic variance
σ_p	=	Phenotypic standard deviation
σ^2_g	=	Genotypic variance
σ_g	=	Genotypic standard deviation
σ^2_e	=	Environmental variance
$\bar{X}$	=	General mean

3.6.5 Heritability

It was calculated in broad sense by the formula proposed by Hanson et al., (1956).

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

h^2 (bs) = heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson et al. (1955).

3.6.6 Genetic advance (GA):

Genetic advance is calculated by the formula suggested by Johnson et al., (1955).

$$GA = h^2 \text{ (bs)} \times \sigma_p \times K$$

Where,

GA = Genetic advance

σ_p = Phenotypic standard deviation

h^2 (bs) = Heritability of the character

K = Selection intensity at 5% level of significance i.e., 2.06

3.6.6 Genetic advance as percent of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \text{ X } 100$$

GA was categorized as

> 35 per cent = high

25-35 per cent = moderate

< 25 per cent = low

3.6.7 Estimation of correlation coefficients:

All correlation coefficients were calculated at genotypic and phenotypic levels using the formula suggested by Miller et al., (1958).

$$r\, \boldsymbol{X_i X_j} = \frac{\mathrm{Cov}\, X_i X_j}{\sqrt{(\mathrm{Var}\, X_i)\cdot(\mathrm{Var}\, X_j)}}$$

Where,

$r\, x_i x_j$ = Coefficient of correlation between characters X_i and X_j

Cov (X_iX_j) = Covariance between characters X_i and X_j

Var (X_i) = Variance of character X_i

Var (X_j) = Variance of character X_j

Genotypic and phenotypic correlation coefficients were compared by substituting the corresponding variance and covariance for all the observed characteristics.

$$\text{Genotypic } r(X_jY_j) = \frac{\text{Genotypic cov } X_iY_i}{\sqrt{\sigma_g^2(Xi)\sigma_g^2(Yi)}}$$

$$\text{Phenotypic } r(X_jY_j) = \frac{\text{Genotypic cov } X_iY_i}{\sqrt{\sigma_p^2(Xi)\sigma_p^2(Yi)}}$$

Where,

σ^2g (x_i) = Genotypic variance of character x_i

σ^2g (y_i) = Genotypic variance of character y_i

σ^2p (x_i) = Phenotypic variance of character x_i

σ^2p (y_i) = Phenotypic variance of character y_i

Testing of correlation coefficient for significance: To test the significance of correlation coefficient, t-value was computed and compared with the tabulated value of 't' at (n-2) degree of freedom at 5% and 1% level of probability.

$$\text{'}t_c\text{'} = \frac{r}{\sqrt{1-r^2}}\sqrt{n-2}$$

Where,

t_c = Calculated value of t

r = Estimated value of correlation coefficient

n = Number of paired observations

3.6.8 Path coefficient analysis:

Path coefficients are standardized partial regression coefficients and as such provide the means to direct influence of one character upon another character. It also permits partitioning of correlation coefficient into direct and indirect effects via other character. For the path coefficient analysis the method originally proposed by Wright (1921), which was further modified by Dewey and Lu (1959). The cause and effect relationship is well defined in path coefficient analysis. It is possible to represent the whole system of variables in the form of a diagram known as path diagram.

Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. In other words; it is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects, *i.e.*, it measures the direct and indirect contribution of various independent characters on a dependent character.

Wright (1921), proposed the original technique in which analysis was carried out by modified method devised by Dewey and Lu. (1959). Following set of simultaneously equations were formed and solved for estimating direct and indirect effects. Genotypic path coefficients were calculated separately for yield and yield components. The dependent variable was yield per plant. The unexplained variation in the dependent variable was obtained as residual factor from the following equation.

$$r_1Y = P_1Y + r_{12}\, P_2Y + r_{13}\, P_3\, Y + \ldots\ldots\ldots\ldots\ldots + r_1i\, P_1Y.$$

$$r_2Y = r_{21}\, P_1Y + P_2\, Y + r_{23}\, P_3Y + \ldots\ldots\ldots\ldots\ldots + r_{21}\, p_1Y.$$

$$r_ky = r_{k1}\, P_1Y + r_{k2}\, P_2Y + r_{k3}P_3Y + \ldots\ldots\ldots\ldots + r_k\, P_kY.$$

Where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to i and dependent character Y.

P_1Y to P_kY = Direct effect of characters 1 to i on character Y.

r_{12} to $r_{k-1,}$ = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under-

$$\begin{array}{ccc} A & C & \\ \begin{bmatrix} r_1Y \\ r_2Y \\ \cdot \\ \cdot \\ r_kY \end{bmatrix} & \begin{bmatrix} 1 & r_{12} & r_{13} \ldots\ldots r_{1i} \\ r_{21} & 1 & r_{23} \ldots\ldots r_{2i} \\ \cdot & & \\ \cdot & & \\ r_{k1} & r_{k2} & r_{k3} \quad\quad 1 \end{bmatrix} & \begin{bmatrix} P_1Y \\ P_2Y \\ \cdot \\ \cdot \\ P_kY \end{bmatrix} \end{array}$$

Then, $B = [C]^{-1} A$

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \ldots\ldots C_{1i} \\ C_{21} & C_{22} & C_{23} \quad\quad C_{2i} \\ \cdot & & \\ \cdot & & \\ C_{i1} & C_{i2} & C_{i3} \quad\quad C_{ii} \end{bmatrix}$$

Then the direct effects were calculated as follows-

$$P_1Y = \sum_{i=1}^{k} C_{1i}\, r_i y$$

$$P_2Y = \sum_{i=1}^{k} C_{2i}\, r_{iy}$$

$$P_kY = \sum_{i=1}^{k} C_{ki} r_k y$$

Residual effect: Residual effect was obtained as per formula given below:

$$R = \sqrt{1 - E_{di} r_{ji}}$$

Where,

d_i = Direct effect of character

r_{ij}= Correlation coefficient of i^{th} character with j^{th} character

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

>1.00 = Very high

0.3-0.99 = High

0.2-0.29 = Moderate

0.1-0.19 = Low

0.0-0.09 = Negligible

3.6.9 Genetic divergence

Mahalanobis (1928) defines D^2 analysis as follows:

$$D^2P = b_1d_1+b_2d_2+\text{--------------}\ b_pd_p$$

A resource for group distance based on multiple characters with X_1, X_2, X_3…………X_p as the multiple measurements available on each individual and d_1, d_2 ………..d_p as $\bar{x}^1{}_{1.}$ $\bar{x}^2{}_2$ ………… $\bar{x}^1{}_{p.}$ $\bar{x}^2{}_p$ respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula.

$$D^2 = \sum wij \sum (\bar{x}^1_i - \bar{x}^2_i)(\bar{x}^1_i - \bar{x}^2_i)$$

Where,

Wij is the inverse of estimated variance and covariance matrix

3.6.9.1 Step to estimate D^2 value

3.6.9.1.1 Collection of data

Data were collected considering "V" population and "P" characters which have been measured on each individual.

3.6.9.1.2 Test of significance

According to Wilk's criteria a simultaneous test of difference between mean values of number of correlated variance is done.

Using pivotal condensation method, the determinant of error and error variety matrix will be calculated.

$$A = \left|\frac{W}{S}\right| = \left|\frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}\right|$$

$$V\text{ (State)} = -m \log e = -\ [n\ \frac{(p+g+1)}{2}]\ \log e$$

Where,

$M = n - (p+q+1)/2$

P = number of variance or character

Q = degree of freedom for population

N = degree of freedom for error + variety

E = constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

3.6.9.1.3 Transformation of correlated values

Transformation was done by using pivotal consideration method. The correlated variables were first transformed into uncorrelated once and D^2 values were calculated.

3.6.9.2 Computation of D^2 values

The D^2 value obtained for a pair of population was taken as the calculated value of X^2 and tested against the tabulated value of X^2 at “P” degree of freedom, where “P” was considered as the number of characters.

3.6.9.3 Contribution of individual characters towards divergence

In all combination, each character was ranked on the basis of di = Yij – Yik values and rank 1 was given to the highest mean difference where “P” was considered as the number of characters.

3.6.9.4 Grouping of genotypes into various clusters by Tocher's method

Populations are grouped in order to their relative genetic distance from each other, in the first step grouping of different varieties into distinct clusters. The two populations having the least distance from each other from the first two populations is added, then comes the fourth population and so on. There is disrupt increase in the average D^2 at certain stage by adding a particular population, and then this population is not added in the cluster.

Similarly, second cluster is formed. The process is continues till all the populations are included into one or other cluster.

3.6.9.5 Average intra cluster distance

The formula was used for measuring the intra cluster distance as follows:

$$\sum Di^2/n$$

Where,

$\sum Di^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

3.6.9.6 Average inter cluster distance

First of all, the distance clusters were measured. The clusters were taken one by one and their distances from other cluster were calculated.

RESULT

The experimental result of present investigation has been given under following headings:

4.1 Characterization

4.2 Analysis of variance

4.2 Parameter of genetic variability

  4.2.1 Range and mean performance for different characters

  4.2.2 Genotypic and phenotypic coefficient of variation

  4.2.3 Heritability (%)

  4.2.4 Genetic advance as percentage of mean

4.3 Correlation coefficient analysis

4.4 Path coefficient analysis

4.5 Genetic divergence

4.6 Principle components analysis

4.1 Characterization

The frequency distributions of eleven morphological characters (discontinuous variable) are summarized in Table 4.1. Visual traits of 36 genotypes at plant and seed level were studied and results are presented in table 4.1.

4.1.1 Plant level

4.1.1.1 Foliage color

As per chickpea descriptor, in the present investigation the variation found in the foliage color can be categorized under two type's *viz*., light green and dark green. Out of 36 accessions, 20 accessions had light green foliage color (CSJ887, RKG 13-155, H 12-62, PBC 501, JSC 55, GL 12003, JG 74315-14, CSJ884, H 12-55, BG 3068, NbeG 511, GNG 2299, RVSSG 38, GL29098, JG24, JG24-1, PG 0104, GL 12021, IPC 2010-134, RVG 202 and 16accessions had dark green foliage color (NbeG 511,BG 3067, PG 158, JG 24, IPC 2012-49, Phule G13110, RKG 13-180, NDG 14-24, GNG 2304, Phule G0719-10, GJG 1319, JSC 56, IPC 2012-98, PBC 510,RVG 203, GNG 2261) (Table 4.1).

4.1.1.2 Leaflet size (mm)

Out of 36 accessions under study, 21 accessions were reported to have small leaflet size, 8 accessions were medium and remaining 7 accessions (BG 3067, JG 24, RKG 13-180, NDG 14-24, GJG 1319, JG24 and JG24-1) had large leaflet size (Table 4.1).

4.1.1.3 Leaf pattern

In the present study, all the genotypes have pinnate leaf pattern.

4.1.1.4 Plant height (cm)

The height of the plant can be grouped into 3 categories *viz*., short (< 45 cm), medium (45-65 cm) and tall (> 65 cm), 24 genotypes were medium stature, 10 genotypes had short and remaining 2 genotypes (JG24 and JG24-1) had tall stature.

4.1.1.5 Growth habit

As per DUS guidelines of chickpea, 5 types of growth habits were found in chickpea genotypes. Out of 36 genotypes, 30 genotypes had semi-erect type growth habit. Six genotypes *viz.,* JG 24, Phule G13110, GNG 2304, JSC 56, PG 0104 and GL 1202 had erect type growth habit.

4.1.1.6 Plant pigmentation

Anthocynin was noticed at the vegetative stage of the plant as presence or absence of any other color on the leaves and stem. Anthocynin pigmentation present one leaves and stem was recorded only presence in one entry (PBC501), whereas in rest of the entries this was absent.

4.1.1.7 Days to 50% flowering

Chickpea genotypes according to days taken to 50% flowering can be classified into four categories viz., extra early (< 40 days), early (40-60 days), medium (61-80 days) and late (> 80 days). Under the investigation, 16 genotypes had early in 50% flowering and remaining 20 genotypes had late in 50% flowering (Table 4.1)

4.1.1.8 Flower color

Out of 36 genotypes evaluated, all flowers were pink in color.

4.1.2 Seed traits

4.1.2.1 Seed coat color

Seed color is the important market preference as well as consumer acceptable trait. Royal Horticultural Society (RHS) describes 21 color codes for mature seeds of chickpea. Out of 36 genotypes studied, 11 genotypes were brown, 9 genotypes were dark brown, 6 were genotypes yellow (RKG 13-155, IPC 2012-49, GL 12003, H 12-55, GNG 2261, GL 12021) and 5 were genotypes grayish brown (GNG 2304, BG 3068, RVSSG 38, IPC 2012-98, IPC 2010-134), 3 beige (RKG 13-180, JG 74315-14, NbeG 511) and 2 genotypes were brown beige (JG24, JG24-1) (Table 4.1).

4.1.2.2 Seed shape

Seed shape is categorized into three categories, all 36 genotypes were desi types were belong to angular seed shape (Table 4.1).

4.1.2.3 Seed surface

Thirty one genotypes had smooth seed surface, whereas remaining 5 genotypes *viz.,* CSJ887, PG 158, JG 24, JG 74315-14 and GJG 1319 had rough seed surface (Table 4.1).

4.1.2.4 Seed ribbing

Seed ribbing was present in 27 genotypes and in this study were absent in 9 genotypes *viz*., BG 3067, PG 158, JSG 55, JG 24, RKG 13-180, JG24, JG24-1, JSC 56 and RVG 202.

4.1.2.5 Seed: size (weight of 100 seeds in g)

Seed size can be classified into 2 categories according to the weight of 100 seeds (seed index) *viz.,* small (<18g) medium (18-22) and large (>22g). Out of 36 genotypes 18 were reported to have small seed size, medium 4 and 14 had large seed size.

Table 4.1 Morphological characterization of chickpea genotypes

S.No.	Genotypes	Foliage colour	Leaf pattern	Growth habit	Plant pigmentation	Flower colour	Leaflet size	Seed colour	Seed surface	Seed ribbing	Seed size	Seed shape
1	CSJ887	LG	P	SE	0	P	S	B	R	+	S	A
2	NBeG 507	DG	P	SE	0	P	M	DB	S	+	L	A
3	BG 3067	DG	P	SE	0	P	L	B	S	+	M	A
4	RKG 13-155	LG	P	SE	0	P	S	Yellow	S	+	S	A
5	PG 158	DG	P	SE	0	P	M	DB	R	0	L	A
6	H 12-62	LG	P	SE	0	P	M	B	S	+	S	A
7	PBC 501	LG	P	SE	+	P	S	B	S	+	S	A
8	JSC 55	LG	P	SE	0	P	S	DB	S	0	S	A
9	JG 24	DG	P	E	0	P	L	B	R	0	L	A
10	IPC 2012-49	DG	P	SE	0	P	M	Yellow	S	+	L	A
11	Phule G13110	DG	P	SE	0	P	M	DB	S	+	L	A
12	GL 12003	LG	P	E	0	P	S	Yellow	S	+	S	A
13	RKG 13-180	DG	P	SE	0	P	L	Beige	S	0	L	A
14	JG 74315-14	LG	P	SE	0	P	S	Beige	R	+	S	A
15	CSJ884	LG	P	SE	0	P	S	DB	S	+	S	A
16	NDG 14-24	DG	P	SE	0	P	L	B	S	+	L	A
17	H 12-55	LG	P	SE	0	P	S	Yellow	S	+	S	A
18	GNG 2304	DG	P	E	0	P	S	GB	S	+	S	A
19	Phule G0719-10	DG	P	SE	0	P	S	B	S	+	M	A
20	GJG 1319	DG	P	SE	0	P	L	DB	R	+	L	A
21	BG 3068	LG	P	SE	0	P	S	GB	S	+	S	A
22	JSC 56	DG	P	E	0	P	S	DB	S	+	M	A
23	NBeG 511	LG	P	SE	0	P	S	Beige	S	+	L	A
24	GNG 2219	LG	P	SE	0	P	S	B	S	+	S	A
25	RVSSG 38	LG	P	SE	0	P	M	GB	S	+	S	A
26	IPC 2012-98	DG	P	SE	0	P	M	GB	S	+	S	A
27	GL29098	LG	P	SE	0	P	S	B	S	+	S	A
28	PBC 510	DG	P	SE	0	P	S	B	S	+	L	A
29	JG24	LG	P	SE	0	P	L	B.Beige	S	0	L	A
30	JG24-1	LG	P	SE	0	P	L	B.Beige	S	0	L	A
31	RVG 203	DG	P	SE	0	P	S	DB	S	0	M	A
32	GNG 2261	DG	P	SE	0	P	S	Yellow	S	+	S	A
33	PG 0104	LG	P	E	0	P	S	B	S	+	S	A
34	GL 12021	LG	P	E	0	P	S	Yellow	S	+	S	A
35	IPC 2010-134	LG	P	SE	0	P	M	GB	S	+	L	A
36	RVG 202	LG	P	SE	0	P	S	DB	S	0	L	A

Table 4.2. Frequency distribution of Morphological traits in chickpea

Traits	Classes	Number of entry	Percentage of entry (%)
Foliage color	Light green	20	55.5
	Dark green	16	44.4
Leaflet size	Small(<10mm)	21	58.3
	Medium(10-5mm)	8	22.2
	Large (>15mm)	7	19.4
Leaf pattern	Simple	00	0.0
	Compound	00	0.0
	Pinnate	36	100
Growth habit	Erect	6	16.7
	Semi erect	30	83.3
	Semi spreading	00	0.0
	Spreading	00	0.0
Plant height	Short (<45cm)	10	27.8
	Medium(45-65cm)	24	66.7
	Tall(>65cm)	2	5.6
Plant pigmentation	Present	1	2.8
	Absent	35	97.2
Flower color	White	00	0.0
	Pink	36	100
	Blue	00	0.0
Days to 50% flowering	Extra early (<40days)	00	0.0
	Early (40-60 days)	16	44.4
	Medium (61-80 days)	00	0.0
	Late (>80days)	20	55.6
Seed shape	Pea shaped	00	0.0
	Owl's shaped	00	0.0
	Angular	36	100
Seed color	Brown	11	30.6
	Dark brown	9	25
	Yellow	6	16.7
	Grayish brown	5	13.9
	Beige	3	8.4
	Brown beige	2	5.6
Seed surface	Smooth	31	86.1
	Rough	05	13.9
	Tuberculated	00	0.0
Seed ribbing	Present	27	75
	Absent	09	25
Seed index	Very small(<20g)	00	00
	Small(20-25g)	28	77.8
	Medium(26-35g)	00	0.0
	Large(36-45g)	08	22.2
	Very large(>45g)	00	0.0

4.2 Analysis of variance

Analysis of variance refers to the observable differences in individuals for a particular trait. To know the extent of variation of observed characters among the 36 genotypes, analysis of variance was performed and presented in (Table 4.3). Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters which revealed that there was considerable genetic variability amongst the material under study, which can be exploited through selection.

Considerable amount of variability was observed for all the traits. Maximum variability was observed for total number of pods per plant followed by effective pods per plant and lowest for number of seeds per pod (Table 4.3)

Table 4.3 Analysis of variance for yield, yield attributing and quality traits

Source of variation	Mean sum of squares										
	d.f.	FI	DFF	PI		DM	PH	PB	SB	TNPP	NEPPP
Replication	2	0.176	4.509	3.37		7.528	2.691	0.020	0.191	3.258	4.623
Treatments	35	173.717**	126.543**	118.143**		83.074**	194.341**	0.0593**	1.834**	334.360**	303.394**
Error	70	1.538	1.547	1.342		2.09	2.114	0.044	0.396	2.488	2.056

Source of variation	Mean sum of squares							
	d.f.	NSPP	100SW(g)	BY(g)	HI (%)	SYPP(g)	RWC (%)	CHLO
Replication	2	1.956	3.249	1.307	11.406	1.691	1.332	10.224
Treatments	35	436.351**	103.218**	67.389**	839.603**	28.775**	78.243**	58.589**
Error	70	1.941	1.434	1.573	1.759	0.826	2.713	4.555

**Significant at 1 % level

* Significant at 5 % level

4.3 Parameters of genetic variability

The parameter of genetic variability *viz.*, mean, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean were calculated for different traits and are presented in table (Table 4.4).

4.3.1 Mean and Range

Mean and range performance for yield component characters were summarized in Table 4.4. Days to flower initiation ranged from 38 to 64 days with an average of 51 days. Days to 50% flowering varied from 51.7 to 74 days with mean of 63 days, Days to pod initiation ranged from 58 to 83 days with mean of 68.8days; Days to maturity showed a mean value of 97.1 days and varied from 87.7 to 107.4 days. The degree of dispersion for the plant height ranged between 34.2 to 66.5 cm. with an average performance of 49.1 cm. Number of primary branches/ plant varied from 1.7 to 2.2 with average performance of 2. Number of secondary branches/ plant ranged from 3.4 to 6.8 with mean of 6. Total number of pods/ plant varied from 16.7 to 54.5 with a mean of 50.8. Number of effective pods/ plant had an average 40.5 and varied from 11.7 to 66.4. Number of seeds/ plant ranged from 15.4 to 64.9 with a mean of 45.6. 100 seed weight had an average of 20.9 g with a minimum of 12.6 g and maximum of 34.4 g. Biological yield/ plant ranged from 7.3 to 36.4 with an average performance of 35.6g. Harvest index varied from 26.3 to 104.7 with mean of 61.9. Seed yield/ plant had an average performance of 50.2 g with a range of 24.7 to 55.7g. Relative water content ranged from 45.9% to 68.3% with a mean value of 58.6%, chlorophyll content index ranged from 63.9 to 77.6 SPAD 502 with mean value of 69.7.

4.4 Genetic parameters of variability for yield and its components in chickpea genotypes

S.No.	Character	Mean	RANGE		Coefficient of variation (%)		h^2b (%)	Genetic advance	GA as % of mean 5%
			Min.	Max.	PCV (%)	GCV (%)			
1	Days to flower initiation	50.3	38.0	64.0	15.2	15.0	97.4	15.4	30.6
2	Days to 50% flowering	62.2	51.7	74.0	10.5	10.3	96.4	13.1	21.0
3	Days to pod initiation	68.8	57.7	82.7	9.2	9.0	96.7	12.6	18.3
4	Days to maturity	97.1	87.7	107.4	5.5	5.3	92.8	10.3	10.6
5	Plant height (cm)	49.1	34.2	66.5	16.5	16.3	96.8	16.2	33.0
6	Number of primary branches/plant	1.9	1.7	2.2	11.1	3.6	45.9	0.0	2.4
7	Number of secondary branches/plant	5.1	3.4	6.8	18.4	13.7	54.7	1.1	20.8
8	Total number of pods/ plant	50.8	16.7	54.5	33.2	32.5	97.8	21.4	42.1
9	Number of effective pods/plant	40.5	11.7	66.4	34.2	33.9	98.0	15.5	38.3
10	100 seed weight(g)	45.6	15.4	64.9	32.3	32.0	98.7	20.5	44.9
11	Number of seeds/ plant	20.9	12.6	34.4	28.4	27.8	95.9	11.7	56.2
12	Biological yield (g)	35.6	7.3	36.4	31.8	30.8	93.3	9.3	26.1
13	Harvest index (%)	61.9	26.3	104.7	27.0	26.9	99.4	34.3	55.4
14	Seed yield per plant(g)	50.2	24.7	55.7	35.0	33.6	91.9	8.5	16.9
15	Relative water content (%)	58.6	45.9	68.3	9.0	8.5	90.3	9.8	16.8
16	Chlorophyll content index (SPAD 502)	69.7	63.9	77.6	6.8	6.0	79.8	7.8	11.2

4.3.2 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation for yield and yield attributing traits are summarized in table 4.2. In general the phenotypic variance must be higher in magnitude than that of genotypic variance. The same trend was observed in the present investigation for all the characters.

Number of effective pods/ plant recorded the highest GCV (33.9%), followed by seed yield/ plant (33.6%), total number of pods/ plant (32.5%), number of seeds/ plant (32.0%), biological yield/ plant (30.8%), 100 seed weight (27.8%) and harvest index (26.9%).

Plant height (16.3%), days to flower initiation (15.0%), number of secondary branches/ plant (13.7%), days to 50% flowering (10.3%), days to pod initiation (9.0%), relative water content (9.0%), chlorophyll content (6.8%), days to maturity (5.3%) and number of primary branches/ plant (3.6%) were recorded low GCV.

The highest value of PCV was recorded for seed yield/ plant (35.0%), followed by number of effective pods/ plant (34.2%) total number of pods/ plant (33.2%), number of seeds/ plant (32.3%) biological yield/ plant (31.8%), 100 seed weight (28.4%) and harvest index (27.0%).

On the other hand, number of secondary branches/ plant (18.4%), plant height (16.5%), days to flower initiation (15.2%), number of primary branches/ plant (11.1%), days to 50% flowering (10.5%) , days to pod initiation (9.2%), relative water content (8.5%), chlorophyll content (6.0%) and days to maturity (5.5%) were recorded low PCV (Table 4.4).

4.3.3 Heritability

Broad sense heritability was computed for each of the characters by the variance components for estimating their relative magnitude of genotypic and phenotypic variability contributed through environmental factors. It was classified as very high (>90%), high (70-90%), moderate (50 -70%) and low (<50%). The estimates of heritability in broad sense for yield and attributing characters have been presented in Table 4.4.

In the present study, very high heritability estimate was noted for harvest index (99.4%), number of seed/ plant (98.7%), number of effective pods/ plant (98.0%) followed by total number of pods/ plant (97.8%), days to flower initiation (97.4%) and plant height (96.8%). Days to pod initiation (96.7%), days to 50% flowering (96.4%), 100 seed weight (95.9%), Biological yield/ plant (93.3%), days to maturity (92.8%), seed yield/ plant (91.9%), relative water content (90.3%), chlorophyll content (79.8%) were recorded high estimates of heritability. Number of secondary branches/plant (54.7%) recorded moderate heritability. Whereas, number of primary branches/ plant (45.9%) showed low heritability (Table 4.4).

4.3.4 Genetic advance as percentage of mean

Estimate of genetic advance as percentage of mean ranged between 2.4 % to 56.2%. The highest genetic advance as percentage of mean was recorded for 100 seed weight (56.2%) followed by harvest index (55.4%), number of seed/ plant (44.9%), total number of pods/ plant (42.1%), number of effective pods/ plant (38.3%), plant height (33.0%), days to flower initiation (30.6%), biological yield/ plant (26.1%), days to 50% flowering (21.0%), number of secondary branches/ plant (20.8%), days to pod initiation (18.3%), seed yield/ plant (16.9%), relative water content (16.8%), chlorophyll content (11.2%), days to maturity (10.6%) (Table 4.4).

While, low genetic advance as percentage of mean was recorded for the character number of primary branches/ plant (2.4%) (Table 4.4).

4.4 Correlation coefficient analysis:

Correlation coefficients were estimated between yield and its components at genotypic, phenotypic and environmental levels to know the inter-relationship among the characters. It provides information about the nature, extent and direction of selection pressure to be applied for practical consideration. In general, phenotypic correlation coefficients were higher than the genotypic correlation coefficients because of masking effect of environment on the genotypes in the expression of characters. The corresponding phenotypic correlation coefficients of different characters have been presented in Table 4.5.

4.4.1 Days to flower initiation

Days to flower initiation exhibited strong significant and positive association with days to 50% flowering (0.914), days to pod initiation (0.854) and days to maturity (0.739). It has significant and positively correlated with plant height (0.543) and number of primary branches/ plant (0.462). Whereas, this trait revealed highly significant and negative correlation with harvest index (-0.421), total number of pods/ plant (-0.374) and number of seeds/ plant (-0.303) and is significantly negative correlated with effective pods/ plant (-0.294) and 100 seed weight (-0.248).

4.4.2 Days to 50% flowering

Days to 50% flowering had strong significant and positive association with days to flower initiation (0.914) , days to pod initiation (0.914) and days to maturity (0.813). this trait had significant and positively correlation with plant height (0.604) and number of primary branches/ plant (0.496). However; this character exhibited strong significant and negative correlation with harvest index (-0.426) and total number of pods/ plant (-0.316) and is significantly negative correlated with number of seeds/ plant (-0.231) and effective pods/ plant (-0.228).

4.4.3 Days to pod initiation

Days to pod initiation showed highly significant and positive correlation with days to flower initiation (0.854), days to maturity (0.805), plant height (0.604) and number of secondary branches/ plant (0.444). However, this trait had higher significant and negative correlation with harvest index (-0.459) , total number of pods/ plant (-0.340) and 100 seed weight (-0.319) and is significantly negative correlated with effective pods/ plant (-0.245) and number of seeds/ plant (-0.195) (Table 4.5).

4.4.4 Days to maturity

Days to maturity expressed highly significant and positive correlation with days to flower initiation (0.739). However, it had significant and positive correlation with number of secondary branches/ plant (0.513) and plant height

(0.401). However; this character exhibited strong significant and negative correlation with harvest index (-0.444) (Table 4.5).

4.4.5 Plant height (cm)

Plant height showed significantly positive correlation with 100 seed weight (0.314). Number of secondary branches/ plant (0.290). Whereas, it expressed strong significant and negative correlation with total number of pods/ plant (-0.300), number of secondary branches/ plant (0.300) and number of effective pods/ plant (-0.241), while significant negative correlation with harvest index (-0.219) (Table 4.5).

Table 4.5: Phenotypic Correlation Coefficient analysis for yield and its contributing traits in chickpea

Characters	50% F	PI	DM	PH	PB	SB	P/P	EP	S/P	100SW	BY	HI	SY
Days to flower initiation	0.914**	0.854**	0.739**	0.543**	0.027	0.462**	-0.374**	-0.294*	-0.303*	-0.248*	-0.178	-0.421**	-0.475
Days to 50% flowering		0.914**	0.813**	0.604**	0.011	0.496**	-0.316**	-0.228*	-0.231*	-0.148	-0.067	-0.426**	-0.394
Days to pod initiation			0.805**	0.440**	0.024	0.444**	-0.340**	-0.245*	-0.195*	-0.319**	-0.146	-0.459**	-0.497
Days to maturity				0.401**	0.017	0.513**	-0.168	-0.126	-0.110	-0.177	-0.002	-0.444**	-0.363
Plant height (cm)					-0.049	0.290*	-0.300*	-0.241*	-0.300*	0.314**	0.233*	-0.219*	0.048
Number of primary branches/plant						0.358**	-0.037	-0.017	0.041	0.048	0.117	-0.091	0.072
Number of secondary branches/plant							-0.085	-0.012	-0.023	0.001	0.210*	-0.440**	-0.104
Total number of pods/ plant								0.943**	0.706**	0.160	0.582**	-0.033	0.582
Number of effective pods/plant									0.729**	0.143	0.591**	-0.065	0.577
100 seed weight(g)										0.011	0.506**	-0.185	0.395
Number of seeds/ plant											0.548**	0.088	0.617
Biological yield (g)												-0.361**	0.699
Harvest index (%)													0.315

** Significant at 5% and 1% level

4.4.6 Number of primary branches/ plant

Number of primary branches/ plant expressed highly significant and positive correlation with number of secondary branches/ plant (0.358).

4.4.7 Number of secondary branches/ plant

Number of secondary branches/ plant expressed highly significant and positive correlation with biological yield/ plant (0.210). However; this character exhibited strong significant and negative correlation with harvest index (-0.440).

4.4.8 Total number of pods/ plant

Total pods/ plant had highly significant and positive association with number of effective pods/ plant (0.943) followed by number of seeds/ plant (0.706) and biological yield/ plant (0.582).

4.4.9 Number of effective pods/ plant

Number of effective pods/ plant revealed highly significant positive correlation with total number of seeds/ plant (0.729), biological yield/ plant (0.591).

4.4.10 Number of seeds/ plant

Highly significant and positive correlation of number of seeds/ plant was observed with biological yield/ plant (0.506).

4.4.11 100 seed weight (g)

100 seed weight exhibited significant and positive correlation with biological yield/ plant (0.548).

4.4.12 Biological yield/ plant (g)

Biological yield/ plant showed highly significant and negative correlation with harvest index (-0.361).

4.4.13 Harvest index (%)

Significant and negative correlation of harvest index was observed with days of pod initiation (-0.459) and days to maturity (-0.444), number of secondary branches/ plant (-0.440), days to 50% flowering (-0.426) and days to flower initiation (-0.421). Whereas, significant and negative correlation was observed for biological yield/ plant (-0.361) and plant height (-0.219).

4.4.14 Seed yield/ plant (g)

Seed yield/ plant had highly significant and positive association with biological yield/ plant (0.699), total number of pods/ plant (0.785), biological yield/ plant (0.486) and harvest index (0.481). However, it also showed significant and positive correlation with number of seeds/ pod (0.184) and plant height (0.138).

4.5 Path coefficient analysis

Path coefficient analysis, measures the direct and indirect effects of total correlation coefficient of one variable through another, at the end product was carried out by using phenotypic correlation value by keeping seed yield per plant as dependent variable.

The observed phenotypic correlation of seed yield/ plant with its contributing components was partitioned into direct and indirect effects (Table 4.6 and figure 1 & 2).

4.5.1 Direct effects

The genotypic path coefficient analysis of different yield and yield contributing traits on seed yield$^{/}$ plant revealed that traits *viz.,* biological yield/ plant exhibited highest positive direct effect (0.8674) on seed yield/ plant, followed by harvest index (0.6312) and days to flower initiation (0.1351). However, days to pod initiation (-0.0546) and days to maturity (-0.0527) showed maximum negative direct effect on seed yield/ plant.

4.5.2 Indirect effects

Days to flower initiation

Days to flower initiation showed indirect effect on days to 50% flowering (0.1265), days to pod initiation (0.1180), days to maturity (0.1040), number of secondary branches/ plant (0.0872) and plant height (0.0760). Indirect effects of harvest index were negative (-0.0575), number of pods/ plant (-0.0515) and number of seeds/ plant (0.0411) on this trait.

Days to 50% flowering

The indirect effect of days to 50% flowering was negative on days to pod initiation (-0.0473), days to flower initiation (-0.0471) and days to maturity (-0.0432). Positive indirect effect was recorded on seed yield/ plant *via* harvest index (0.0218), number of pods/ plant (0.0162) and number of effective pods/ plant (0.0118).

Days to pod initiation

Days to pod initiation showed indirect effect on days to 50% flowering (-0.0513), days to flower initiation (-0.0477) and days to maturity (-0.0460). Positive indirect effect was recorded on seed yield/ plant *via* harvest index (0.0256), number of pods/ plant (0.0189) and 100 seed weight (0.0177).

Days to maturity

Days to maturity showed indirect effect on days to 50% flowering (-0.0452), days to pod initiation (-0.0444), days to flower initiation (-0.0406), plant height (0.0224). Positive indirect effect was recorded on seed yield/ plant *via* harvest index (0.0244)

Plant height

Plant height showed negative indirect effect on number of pods/ plant (-0.0020). Other Indirect effects of this character *via* other characters were relatively low and negligible.

Number of primary branches/ plant

Numbers of secondary branches/ plant (0.0421) and biological yield/ plant (0.0253) were positive indirect effects via number of primary branches/ plant on seed yield, while low negative indirect effect via number of primary branches/ plant on harvest index (-0.0229), plant height (-0.0120), number of pods/ plant (-0.0111)

Number of secondary branches/ plant

The indirect effect of number of secondary branches/ plant on days to maturity was negative (-0.0341), days to 50% flowering (-0.0307), days to flower initiation (-0.0289) and days to pod initiation (-0.0283). Positive indirect effect was recorded on seed yield/ plant *via* harvest index (0.0270) and other characters were relatively low and negligible.

Total number of pods/ plant

The indirect effect of total number of pods/ plant via effective pods/ plant on seed yield /plant was positive (0.0978), number of seeds/ plant (0.0736), biological yield/ plant (0.0623), 100 seed weight (0.0170). Total number of pods/ plant showed low negative indirect effect on days to flower initiation (-0.0389), days to pod initiation (-0.0353) and days to 50% flowering (-0.0328).

Number of effective pods/ plant

The indirect effect of number of effective pods/ plant via number of seeds/ plant was positive and high (0.0313) indirect effect of number of pods/ plant on seed yield/ plant *via* biological yield/ plant (0.0258). Negative indirect effect was recorded on seed yield/ plant *via* total days to flower initiation (-0.0127) and plant height (-0.0103).

Number of seeds/ plant

The indirect effect of total number of pods/ plant via plant height was positive (0.0107). Indirect effect of total number of pods/ plant through number of effective pods/ plant (-0.0257) and number of pods/ plant (-0.0249) was negative.

100 - Seed weight

100-seed weight exerted high positive indirect effect on seed yield/ plant was biological yield (0.0296). Indirect effects of this trait via different traits on seed yield/ plant were days to pod initiation (-0.0163), plant height (-0.0161), days to flower initiation (-0.0129) (Table 4.6).

Biological yield/ plant

Biological yield/ plant exerted high positive indirect effect via number of effective pods/ plant (0.5319), total number of pods/ plant (0.5289), 100 seed weight (0.5111), number of seeds/ plant (0.4573) and number of primary branches/ plant (0.2519), plant height (0.2168) and number of secondary branches/ plant (0.2153) on biological yield/ plant. Negative indirect effect was recorded via harvest index (-0.3241) and days to flower initiation (-0.1612) and days to pod initiation (-0.1320).

Harvest index

The indirect effect of harvest index was positive via 100 seed weight (0.0601), total number of secondary branches/ plant (0.0270), days to pod initiation (0.0256) days to maturity (0.0244) and days to 50% flowering (0.0218) on seed yield/ plant . Negative indirect effect was recorded on seed yield/ plant *via* number of secondary branches/ plant (0.3801), days to pod initiation (-0.2958), days of maturity (-0.2924), days of 50% flowering (-0.2732), days to flower initiation (-0.2686) and biological yield/ plant (-0.2359).

Table 4.6. Genotypic Path coefficient analysis for yield and its component characters in chickpea

Characters	FI	50% F	PI	DM	PH	PB	SB	P/P	EP	S/P	100SW	BY	HI
Days to flower initiation	0.1351	0.1265	0.1180	0.1040	0.0760	0.0103	0.0872	-0.0515	-0.0408	-0.0411	-0.0348	-0.0251	-0.0575
Days to 50% flowering	-0.0471	-0.0503	-0.0473	-0.0432	-0.0313	0.0015	-0.0344	0.0162	0.0118	0.0118	0.0081	0.0035	0.0218
Days to pod initiation	-0.0477	-0.0513	-0.0546	-0.0460	-0.0250	-0.0048	-0.0345	0.0189	0.0137	0.0107	0.0177	0.0083	0.0256
Days to maturity	-0.0406	-0.0452	-0.0444	-0.0527	-0.0224	-0.0023	-0.0401	0.0094	0.0067	0.0061	0.0096	0.0004	0.0244
Plant height (cm)	0.0036	0.0040	0.0030	0.0027	0.0065	-0.0009	0.0025	-0.0020	-0.0016	-0.0020	0.0021	0.0016	-0.0014
Number of primary branches/plant	0.0066	-0.0026	0.0077	0.0037	-0.0120	0.0870	0.0421	-0.0111	-0.0045	0.0140	0.0090	0.0253	-0.0299
Number of secondary branches/plant	-0.0289	-0.0307	-0.0283	-0.0341	-0.0176	-0.0217	-0.0449	0.0051	0.0012	0.0011	-0.0007	-0.0111	0.0270
Total number of pods/ plant	-0.0389	-0.0328	-0.0353	-0.0182	-0.0310	-0.0130	-0.0117	0.1021	0.0978	0.0736	0.0170	0.0623	-0.0037
Number of effective pods/plant	-0.0127	-0.0098	-0.0106	-0.0054	-0.0103	-0.0022	-0.0011	0.0403	0.0421	0.0313	0.0063	0.0258	-0.0028
100 seed weight(g)	0.0105	0.0081	0.0068	0.0040	0.0107	-0.0056	0.0008	-0.0249	-0.0257	-0.0346	-0.0003	-0.0182	0.0064
Number of seeds/ plant	-0.0129	-0.0081	-0.0163	-0.0092	0.0161	0.0052	0.0008	0.0084	0.0075	0.0004	0.0503	0.0296	0.0048
Biological yield (g)	-0.1612	-0.0604	-0.1320	-0.0072	0.2168	0.2519	0.2153	0.5289	0.5319	0.4573	0.5111	0.8674	-0.3241
Harvest index (%)	-0.2986	-0.2732	-0.2958	-2924.0000	-0.1405	-0.1658	-0.3801	-0.0228	-0.0427	-0.1173	0.0601	-0.2359	0.6312
Seed yield / plant(g)	0.5028	-0.4260	-0.5292	-0.9339	0.0360	0.1396	-0.1981	0.6170	0.5974	0.4113	0.6555	0.7339	0.3287
Partial R	-0.0679	0.0215	0.0289	0.0208	0.0002	0.0122	0.0089	0.0630	0.0251	-0.0142	0.0329	0.6366	0.2075

4.6 Genetic divergence

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance (Mahalanobis D^2) between pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time.

4.6.1 Contribution of individual character towards genetic divergence:

The percentage contributions towards genetic divergence by all the 14 characters under study are presented in table 4.7. The percent contribution of individual characters toward the total divergence was found highest for harvest index (42.5%) followed by number of seeds/ plant (27.5%). Other characters viz days to flower initiation (10.0%), plant height (6.7%), total number of pods/ plant (4.6%), 100 seed weight (4.1%), biological yield (1.8%), number of effective pods/ plant (1.4%) and days to pod initiation (1.0%) showed low percent of contribution, whereas remaining characters exhibited very low or negligence contribution towards divergence.

Table 4.7: Contribution of different characters toward clustering in chickpea genotypes

S. N.	Character	Times Ranked 1st	Contribution %
1	**Days to flower initiation**	63	10
2	**Days to 50% flowering**	2	0.3
3	**Days to pod initiation**	6	1
4	**Days to maturity**	0	0
5	**Plant height (cm)**	42	6.7
6	**Number of primary branches/plant**	0	0
7	**Number of secondary branches/plant**	1	0.2
8	**Total number of pods/ plant**	29	4.6
9	**Number of effective pods/plant**	9	1.4
10	**100 seed weight(g)**	173	27.5
11	**Number of seeds/ plant**	26	4.1
12	**Biological yield (g)**	11	1.8
13	**Harvest index (%)**	268	42.5
14	**Seed yield per plant(g)**	0	0

4.6.2 Inter and intra cluster divergence D^2

Intra-cluster distance ranged from 0.00 to 188.54 (Table 4.8). The highest intra- cluster divergence was notes in Cluster III (188.54) followed by Cluster II (155.17), Cluster I (128.07) and Cluster IV (72.57). The highest inter cluster divergence was observed between genotypes of cluster VII and cluster VI (1619.55), followed by cluster IX and cluster VII (1591.68), cluster VIII and cluster VI (1571.25), cluster IX and cluster VIII (1375.74), cluster IX and cluster VI (1022.62), cluster IX and cluster V (1017.17), cluster III and cluster VII (1002.27), cluster VIII and III (899.93), cluster I and cluster VII (845.37) cluster VI and cluster II (771.77), cluster I and cluster VIII (766.05), cluster IV and cluster VII (733.95), cluster I and cluster IX (703.51), cluster V and cluster VIII (691.53), cluster II and cluster IX (667.63), cluster IV and cluster VIII (639.73), cluster IX and cluster IV(584.97), cluster VII and cluster V (576.82), cluster VI and III (514.38), cluster VI and IV (479.30), cluster II and cluster VIII(468.10), cluster VI and cluster V(418.33), cluster V and cluster IV(403.40) and Low inter-cluster distance was found between cluster II and cluster VII (383.30), cluster III and cluster IX(354.33), cluster V and III (350.64), cluster III and cluster II (334.59), cluster IV and cluster III (323.81), cluster II and cluster I (316.76), cluster II and cluster IV(307.20), cluster I and cluster VI (266.81), cluster III and cluster I (266.35), cluster I and cluster IV (240.51).

Table 4.8 Inter and intra cluster D^2 values for different clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	128.07	316.76	266.35	240.51	182.69	266.81	845.37	766.05	703.51
II		155.17	334.59	307.20	250.28	771.77	383.30	468.10	667.63
III			188.54	323.81	350.64	514.38	1006.44	899.93	354.33
IV				72.57	403.40	479.30	733.95	639.73	584.97
V					-0.00	418.33	576.82	691.53	1017.17
VI						0.00	1619.55	1571.25	1022.62
VII							0.00	211.42	1591.68
VIII								0.00	1375.74
IX									0.00

The cluster mean for different traits are presented in (Table 4.9). In cluster VI days to flower initiation showed maximum 57 days, whereas cluster VII showed minimum 41 days. In case of days to 50% flowering, cluster VI showed maximum and cluster VII had minimum cluster mean values of 71.6 days and 55.6 days, respectively. Days to pod initiation (78 days) recorded maximum in cluster VI, whereas minimum in cluster VII (63 days). Days to maturity was found maximum in cluster VI i.e. 106.3 days and minimum cluster mean values were observed for cluster VII 87.3 days. Plant height (65.6 cm) recorded maximum in cluster IV, whereas minimum in cluster IX (38.90 cm). Number of primary branches/ plant was found maximum in cluster III (2.04) and minimum in cluster mean values were observed for cluster V (1.80). Number of secondary branches/ plant (5.8) found maximum in cluster VI, followed by cluster V (4.43). Total number of pods/ plant (65.9) found maximum in cluster IX, followed by cluster VII (15.8), number of effective pods/ plant was noticed maximum in cluster IX (66.47), while minimum in cluster VII (11.6). Number of seeds/ plant recoded maximum in cluster IX (64.9) and minimum in cluster VII (15.4). 100 seed weight was recorded maximum in cluster IV (32.8). Biological yield/ plant (23.2g) recorded maximum value in cluster IX, while harvest index (104.6%) was observed maximum value in cluster VIII and seed yield/ plant (15.3g) was recorded maximum values in cluster IX.

Table 4.9. Cluster mean for yield and yield contributing traits of chickpea genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Days to flower initiation	56.97	44.07	47.90	54.33	51.67	57.00	41.00	53.00	42.00
Days to 50% flowering	67.82	56.83	59.38	66.67	59.00	71.67	55.67	65.33	56.00
Days to pod initiation	75.15	63.63	66.48	68.11	66.00	78.00	63.00	72.67	65.33
Days to maturity	101.24	94.80	94.19	98.56	92.67	106.33	87.33	100.00	94.00
Plant height (cm)	51.10	43.03	46.50	65.64	47.20	58.13	47.90	59.43	38.90
Number of primary branches/plant	2.01	1.97	2.04	1.92	1.80	2.00	1.90	1.90	1.90
Number of secondary branches/plant	5.65	4.48	4.84	5.62	4.43	5.80	4.47	4.87	5.03
Total number of pods/ plant	27.52	31.61	39.17	35.86	16.67	35.13	15.87	18.33	65.90
Number of effective pods/plant	27.19	27.51	35.77	33.66	15.90	27.03	11.67	16.43	66.47
100 seed weight(g)	33.22	34.56	52.49	35.74	28.33	28.90	15.47	26.33	64.90
Number of seeds/ plant	18.49	22.81	18.43	32.84	12.87	17.20	23.60	15.40	24.73
Biological yield (g)	14.18	13.47	17.79	22.23	8.43	18.40	8.27	7.30	23.20
Harvest index (%)	51.79	73.48	56.78	59.14	54.53	26.37	98.33	104.67	67.07
Seed yield per plant(g)	7.30	9.63	10.02	12.97	5.03	4.83	7.87	8.17	15.33

4.6.4 Grouping of genotypes into various clusters

Thirty six genotypes of chickpea were grouped into nine clusters based on divergence analysis. Distributions of genotypes into different clusters were presented in table 4.10.Cluster I was the largest among of all the clusters, comprising 11 genotypes followed by cluster II consisting of 10 genotypes, cluster III had 7 genotypes, cluster IV had 3 genotypes, while cluster V cluster VI, cluster VII, cluster VIII and cluster IX had only 1 genotype each.

Table 4.10. Distribution of chickpea genotypes in different clusters

Cluster No.	No.of genotypes	Genotypes
I	11	G158, GL 12021, GNG 2261, BG 3067, H 12-62, L29098, IPC 2010-134, GNG 2299, JSC 56, BG 068
II	10	JG 74315-14, RVSSG 38, NBeG 511, PBC 501, RKG 13-180, NBeG 507, GL29098, RKG 13-155, NDG 14-24, JSC 55
III	7	CSJ887, H 12-55, RVG 203, GJG 1319, IPC 2012-98, CSJ884, RVG 202
IV	3	JG24, JG24-1, JG 24
V	1	GNG 2304
VI	1	PG 0104
VII	1	Phule G13110
VIII	1	GL 12003
IX	1	Phule G0719-10

4.7. Principal component analysis (PCA)

Principle Component Analysis is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set (Massay, 1965; Jolliffie, 1986). It is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Table 4.11 Eigen values, variance % and cumulative Eigen values for corresponding 14 traits in chickpea

Traits	Principal component	Eigen value	Variability (%)	Cumulative %
Days to flower initiation	PC1	4.503	28.144	28.144
Days to 50% flowering	PC2	2.823	17.642	45.786
Days to pod initiation	PC3	1.486	9.286	55.072
Days to maturity	PC4	1.267	7.916	62.988
Plant height (cm)	PC5	1.074	6.713	69.701
Number of primary branches/plant	PC6	0.793	4.956	74.657
Number of secondary branches/plant	PC7	0.736	4.599	79.255
Total number of pods/ plant	PC8	0.631	3.945	83.2
Number of effective pods/plant	PC9	0.505	3.155	86.356
100 seed weight(g)	PC10	0.483	3.021	89.376
Number of seeds/ plant	PC11	0.458	2.861	92.237
Biological yield (g)	PC12	0.368	2.301	94.538
Harvest index (%)	PC13	0.327	2.042	96.579
Seed yield per plant(g)	PC14	0.223	1.395	97.974
Relative water content (%)	PC15	0.189	1.182	99.156
Chlorophyll content index (SPAD 502)	PC16	0.135	0.844	100

Principal components analysis is similar to another multivariate procedure called factor analysis. Traditionally, principal component analysis is performed on a square symmetric matrix. It can be a SSCP matrix (pure sums of squares and cross products), covariance matrix (scaled sums of squares and cross products), or correlation matrix (sums of squares and cross products from standardized data). The analysis results for objects of type SSCP and covariance do not differ, since these objects only differ in a global scaling factor. A correlation matrix is used if the variances of individual variants differ much, or if the units of measurement of the individual variants differ.

In present investigation PCA was performed for yield and yield contributing traits of chickpea and presented in table 4.16. Out of eighteen, only five principal components (PCs) exhibited more than 1.074 Eigen value and showed about 69.701% variability among the traits studied. The PC 1, showed 28.14%. While, PC 2 , PC 3 , PC 4 ,PC 5 exhibited 17.642 %,9.286 %,7.916 % and 6.713% variability, respectively among the genotypes for the traits under study.

PC 1 showed 28.144% variability with Eigen value 4.503, which then declined gradually. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other four PCs. So, selection of lines from this PC will be useful

Table 4.12. Interpretation of rotated component matrix for the traits having highest values in each PC

	PC1	PC2	PC3	PC4	PC5
Characteristics	Days t0 50% flowering	Number of effective pods/ plant	100 seed weight	Relative water content	Number of primary branches/ plant
	Days to pod initiation	Biological yield (g)	Plant height (cm)	Harvest index	
	Days to flower initiation	Number of pods/ plant			
	Days to maturity	Number of seeds/ plant			
	Seed yield/ plant	Chlorophyll content			
	Number of secondary branches/ plant	-			
	-	-	_	_	

Rotated component matrix under normal sown condition revealed that the PC1 which accounted for the highest variability (21.619%) was mostly related to seed yield/ plant, number of effective pods/ plant, number of pods/ plant, harvest index, biological yield/ plant, number of seed/ plant , 100 seed weight . PC 2 was dominated by days to 50% flowering, days of maturity and plant height(cm) , PC 4 were dominated by number of secondary branches/ plant , while PC5 was dominated by number of primary branches/ plant.

Table 4.13 Principle Component values of rotation component matrix for eighteen variables of chickpea

Traits	PCI	PC2	PC3	PC4	PC5
Days to flower initiation	**0.839**	**0.162**	0.005	0.223	-0.039
Days to 50% flowering	0.852	**0.209**	0.067	0.273	-0.088
Days to pod initiation	**0.844**	**0.158**	-0.078	0.257	0.006
Days to maturity	0.739	**0.298**	0.01	0.17	-0.026
Plant height (cm)	0.46	**0.096**	0.572	0.046	-0.203
Number of primary branches/plant	0.14	0.259	0.137	-0.289	**0.774**
Number of secondary branches/plant	0.526	0.453	0.196	**-0.139**	0.308
Number of pods/ plant	**-0.465**	0.684	-0.174	0.277	-0.035
Number of effective pods/plant	**-0.407**	0.728	-0.17	0.307	0.030
Number of seeds/ plant	**-0.343**	0.566	-0.429	0.039	0.054
100 seed weight	**-0.327**	0.232	0.618	-0.195	-0.348
Biological yield (%)	-0.234	0.745	0.295	-0.21	-0.07
Harvest index	**-0.464**	-0.378	0.103	0.479	0.065
Seed yield per plant	**-0.586**	0.345	0.431	0.184	0.056
Relative water content (%)	-0.249	-0.15	**0.228**	0.623	0.177
Chlorophyll content index (SPAD 502)	0.159	0.384	**-0.36**	-0.19	-0.398

Table 4.14 Principle Component values of rotation component matrix for 36 chickpea genotype

Observation	PC1	PC2	PC3	PC4	PC5
CSJ887	-2.150	0.451	-1.528	1.524	0.507
NBeG 507	-2.726	-1.311	1.914	-1.136	1.221
BG 3067	1.984	0.649	1.455	-1.045	2.173
RKG 13-155	-1.141	0.633	-0.565	-2.329	1.569
PG 158	4.225	0.519	1.151	0.552	0.689
H 12-62	3.648	-1.709	0.066	-0.720	1.111
PBC 501	-3.378	-1.346	0.250	-0.593	0.221
JSC 55	-0.468	1.024	2.047	0.067	-2.416
JG 24	3.773	0.791	0.299	-0.208	-1.078
IPC 2012-49	-1.861	-4.577	1.371	0.403	0.269
Phule G13110	1.431	-2.904	0.634	1.638	0.049
GL 12003	-3.334	0.227	0.744	1.572	-1.041
RKG 13-180	-1.255	-2.418	0.916	1.204	-0.241
JG 74315-14	0.215	-2.022	-1.141	-0.026	-0.731
CSJ884	-0.543	1.374	-2.380	-0.426	0.990
NDG 14-24	-1.757	-1.487	0.005	-0.890	-1.252
H 12-55	-0.373	1.505	-1.835	1.091	1.214
GNG 2304	0.486	-3.330	-1.083	-0.531	-0.336
Phule G0719-10	-4.113	4.560	-1.519	-0.063	-0.551
GJG 1319	-2.658	1.464	1.341	-1.045	0.592
BG 3068	0.300	0.858	-1.309	0.124	0.744
JSC 56	-1.348	0.515	0.198	0.338	0.404
NBeG 511	1.194	-2.345	-0.188	0.329	-0..030
GNG 2219	0.562	-0.180	-1.432	1.348	-1.375
RVSSG 38	0.118	-2.373	-1.040	1.148	-0.680
IPC 2012-98	1.961	1.003	-1.174	-0.557	0.211
GL29098	2.102	-1.302	-0.531	0.461	1.983
PBC 510	-1.538	0.235	0.016	0.983	0.363
JG24	0.770	1.876	3.378	0.958	-0.450
JG24-1	-0.094	2.719	3.887	0.702	-0.201
RVG 203	-3.747	2.728	-0.788	-0.940	-0.004
GNG 2261	2.243	0.652	-0.958	0.172	0.146
PG 0104	3.808	1.661	-0.465	-0.808	-0.748
GL 12021	4.350	0.632	-0.701	-0.389	-0.632
IPC 2010-134	2.917	1.372	-0.322	-0.357	-1.838
RVG 202	-1.250	-0.143	-0.716	-2.551	-0.850

Table 4.15 Principle Component Analysis scores of chickpea genotypes having positive >0.5 values in each PCs

	PC1	PC2	PC3	PC4	PC5
Characters	GL 12021	Phule G0719-10	JG24	Phule G13110	BG 3067
	PG 158	JSC 56	JG24-1	GL12003	GL29098
	PG 0104	JG24	JSC 55	CSJ887	RKG 13-155
	JG 24	JG24-1	NbeG 507	GNG 2299	NbeG 507
	H 12-62	PG 0104	BG 3067	RKG 13-180	H 12-55
	IPC 2010-134	H 12-55	IPC 2012-49	RVSSG 38	H 12-62
	GNG 2261	GJG 1319	GJG 1319	H 12-55	CSJ884
	GL29098	CSJ884	PG 158	PBC 510	BG 3068
	BG 3067	IPC 2010-134	RKG 13-180	JG24	PG 158
	IPC 2012-98	RVG 202	GL 12003	JG24-1	GJG 1319
	Phule G13110	IPC 2012-98	Phule G13110	CSJ884	CSJ-887
	JG24	BG 3068	-	-	-
	RVSSG 38	JG 24	-	-	-
	-	GNG 2261	-	-	-
	-	BG 3067	-	-	-
	-	RKG 13-155	-	-	-
	-	GL 12021	-	-	-
	-	PG 158	-	-	-
	-	RVG 203	-	-	-

The PC scores of each component (PC1, PC2, PC3, PC4 and PC5) under normal sown condition were presented in table 4.14. In PC1, scores ranged from 0.562(GNG 2299) to 4.350(GL 12021). Maximum value of PC1 component scores, was recorded in GL 12021(4.350) followed by PG 158,PG 0104,JG 24,H12-62,IPC 2010-134,GNG 2261,GL29098,BG 3067,IPC 2012-98,Phule

G13110,JG24 and RVSSG 38. In PC2, scores ranged from 0.515 (JSC 56) to 4.560 (Phule G0719-10). In PC3, the value ranged from 0.634 (Phule G13110) to 3.887 (JG24). While, in PC4 component scores ranged from 0.552(CSJ884) to 1.638 (Phule G13110). In PC5, the value of the component ranged from 0.507 (CSJ887) to 2.173 (BG 3067) (table 4.15).

Table 4.16. PC values of rotation component PCA scores of chickpea genotypes having negative >0.5 values in each PCs under late sown condition

	PC1	PC2	PC3	PC4	PC5
Characters	Phule G0719-10	IPC 2012-49	CSJ884	RKG 13-155	JSC 55
	JSC 56	GNG 2304	H 12-55	NbeG 507	IPC 2010-134
	PBC 501	Phule G13110	CSJ887	GJG 1319	GNG 2299
	GL 12003	RKG 13-180	Phule G0719-10	BG 3067	NDG 14-24
	NbeG 507	RVSSG 38	GNG 2299	RVG 203	JG 24
	GJG 1319	NbeG 511	BG 3068	NDG 14-24	GL 12003
	CSJ887	JG 74315-14	IPC2012-98	PG 0104	RVG 202
	IPC 2012-49	H 12-62	JG 74315-14	H 12-62	PG 0104
	NDG 14-24	NDG 14-24	GNG 2304	PBC 501	JG 74315-14
	PBC 510	PBC 501	RVSSG 38	IPC2012-98	RVSSG 38
	RVG 203	NbeG 507	GNG 2261	GNG2304	GL 12021
	RKG 13-180	GL2909	RVG 203	-	Phule G0719-10
	JSC 55	-	JSC 55	-	-
	NbeG 511	-	GL 12021	-	-
	RKG 13-155	-	RKG 13-155	-	-
	CSJ884	-	GL29098	-	-
	-	-	-	-	-
	-	-	-	-	-
	-	-	-	-	-

The PC scores of each component (PC1, PC2, PC3, PC4 and PC5) under late sown condition were presented in table 4.14. In PC1, scores ranged from -0.543(CSJ884) to -4.113(Phule G0719-10). Maximum value of PC1 component scores, was recorded in Phule G0719-10 (-4.113), followed by RVG 203, PBC 501,GL 12003,NbeG 507, GJG 1319, CSJ887,IPC 2012-49,NDG 14-24,PBC 510,JSC 56, RKG 13-180,JSC 55, NbeG 511,RKG 13-155 and CSJ884. In PC2, scores ranged from -1.302(GL29098) to -4.577 (IPC 2012-4). In PC 3, the value ranged from -0.531(GL29098) to -2.380 (CSJ-884). While, in PC 4 component scores ranged from -0.531(GNG 2304) to -2.329 (RKG 13-155). In PC 5, the value of the component ranged from -0.551 (Phule G0719-10) to -2.416 (RVG 202) (Table 4.16).

DISCUSSION

Chickpea, the world's third most important food legume crop, grown under rainfed in cool and dry climate in semi-arid regions. Production & productivity of chickpea have been stagnant since the past three decade due to several biotic and abiotic stresses like heat and drought. Seasonal temperature is an important climatic factor, which can have profound effects on the yield of chickpea. Changes in seasonal temperature affect the grain yield, mainly through phenological development processes. Winter crops like chickpea, are especially vulnerable to high temperature during reproductive stage. Chickpea area under late-sown conditions is increasing, particularly in northern and central India, due to inclusion of chickpea in new cropping systems and intense sequential cropping practices. Late sowing is compensated through shortening of their vegetative phase and flowering occurs at temperatures more conducive to subsequent pod development.

Rice fields are mostly vacated late at the end of November, making the available varieties of chickpea unfit for sowing under late conditions (rice- follow). Early maturing chickpea, however can be taken under late sown situation (rice-follow) when availability of water is not enough for wheat cultivation. Inclusion of chickpea in rice- wheat system not only brings qualitative change in the production base for long term sustainability, but also protects the environment from the risks associated with high input agriculture. The late sown conditions are characterized by low temperature at seedling and high temperature at the time of grain development. Low temperature at initial stage of crop growth results in poor and slow vegetative growth, whereas, high temperature at the end of season leads to forced maturity.

Genetic diversity within a species provides broad genetic base and wide adaptability to a population. Selection on the basis of grain yield, a polygenically controlled complex character is usually not very efficient as such, but selection based on its component characters could be more efficient. A comprehensive study of genetic architecture of quantitative and qualitative characters of economic value is essential to improve the yield potential. Improvement in yield can be achieved by genetically manipulating the morphogenetic architecture of the plant by recombination breeding or other crop improvement methods for creation of new variability.

A survey of genetic variability with the help of suitable parameters such as, genetic coefficient of variation, heritability, estimates and genetic advance are absolutely necessary to start an efficient breeding programme and helps the breeder in deriving suitable plant types by bringing improvement in quantitatively inherited traits, which will directly affects the crop yield. The analysis of the relationships among these characters and their associations with seed yield is essential to establish selection criteria.

In the present investigation an attempt has been made to understand the genetic variability among the genotypes (PCV, GCV, heritability and genetic advance), nature of association among yield attributing traits and also partition their direct and indirect effects towards seed yield. This information may be useful to the breeder to formulate appropriate breeding plans for selecting the genotype. The aim of the present investigation was to find out the appropriate yield contributing traits along with stable genotypes.

Thirty six chickpea genotypes were evaluated in this objective, considering phenological, quantitative, morphological and physiological traits.

Keeping that in view the present investigation entitled "**Genetic evaluation of chickpea genotypes suitable for late sowing condition**" was carried out under AICRP on Chickpea (Lead center), Seed Breeding Farm, Department of Genetics and Plant Breeding, J.N.K.V.V, Jabalpur during *Rabi*, 2015-16.

The discussion pertaining has been furnished under the following heads:

5.1. Morphological traits
5.2 Genetic variability
5.2.1. Phenotypic and Genotypic coefficient of variation (PCV and GCV)
5.2.2. Heritability (Broad sense) and Genetic advance (as % of mean)
5.3 Correlation coefficient
5.4 Path coefficient analysis
5.5 Genetic diversity analysis
5.5 Principal component analysis

5.1 Morphological traits

Phenology is the study of relationship between climatic factor and periodic phenomena in organism. A pattern of phenological events is variously used for characterization of vegetation type. The study of plant phenology provides knowledge about the pattern of plant growth and development as well as effect of environment and selective factors on phenological behaviors. climate change forced deviation in the length of growing periods and competition among species may change the resource use patterns in different species flowering time is an important stage in crops development because environmental condition during the reproductive phase have a major impact on final yield.

For characterization of 36 genotypes at plant level, observations were recorded for traits *viz*., foliage color, leaflet size, growth habit, plant pigmentation, leaf pattern and flower color. At seed level characters for seed shape, seed color, seed surface, seed ribbing and seed size were taken into consideration.

Out of 36 genotypes, desi type have characterized on the basis of erect/ semi-erect growth habit, pink flower color, dark/ light green foliage color, pinnate leaf pattern, small /medium/ large leaflet size, plant pigmentation, brown / brown beige /beige / yellow /grayish brown /dark brown seed color, angular /pea shape seed shape and rough to smooth seed surface. Anthocynin pigmentation present in one genotype (PBC 501) and other genotypes are absent. On the basis of phenological and high yield/ plant attributing traits, five genotypes viz., JG24-1, Phule G0719-10, JSC 56 GJG 1319 and RKG 13-180 were found promising.

Though, these morphological traits showed overlapping of expression in various combination traits, yet proved to be of great utility as identity of all the genotypes could be established individually are in agreement with the finding of Sarao et al. 2009, Kaul et al. 2007 and Upadhaya et al. 2007.

5.2 Genetic variability

Estimates of various parameters for assessment of genetic variability *viz.,* mean, range, coefficient of variation, heritability, genetic advance (as % of mean) helps the breeder in deriving suitable selection programme for the improvement in quantitatively inherited traits, which will directly effects the crop yield.

5.2.1 Phenotypic and genotypic coefficient of variation (PCV and GCV):-

The PCV was higher in magnitude than its corresponding GCV for all the observed traits. This indicates the influence of the environment on the expression of these characters.

High phenotypic and genotypic coefficient of variation were reported for Seed yield / plant followed by number of effective pods/ plant , total number of pods/plant , number of seeds/plant ,biological yield/ plant, 100 seed weight, harvest index, number of secondary branches/ plant, plant height, days to flower initiation. While, other traits *viz.*, number of primary branches/ plant, days to 50% flowering, days to pod initiation and days to maturity exhibited low phenotypic and genotypic coefficient of variation.

The findings of present investigation are in accordance with the earlier findings of Usmani et al. (2005) for seed yield / plant, plant height, harvest index, number of pods / plants; Durga et al.(2007) and Vaghela et al. (2008) for number of pods /plant, No. of seed yield / plant; Alwani et al. (2010) and Sreelakshmi et al. (2010) seed yield/ plant; Akhtar et al.(2011) for days to maturity, plant height and seed yield / plant; Babbar et al. (2012) for the character number of pods / plant and seed yield / plant; Singh et al.(2012) for number of pods /plant, plant height, seed yield / plant and 100 seed weight; Nizama et al.(2013) for pods/ plant, seed yield / plant, harvest index and number of secondary branches / plant; Kuldeep et al.(2014) for seed yield / plant, 100-seed weight, harvest index, number of effective pods / plant, number of pods / plant and number of secondary branches / plant; Aarif et al.(2014) seed yield / plant and secondary branches / plant; Yadav et al.(2015) and Desai et al.(2015) for 100 seed weight and seed yield / plant. It indicates the preponderance of additive genetic effect for these characters. Selection of these traits will be effective.

Other traits *viz.* days to 50% flowering and days to maturity exhibits low phenotypic and genotypic coefficient of variation under both the planting. Contradictory results of above findings have been reported by Dahiya et al. (2012), and Choudary et al. (2012) for days to 50% flowering; Akhtar et al.(2011) for days to maturity and days to 50% flowering.

5.2.2 Heritability (Broad sense) and Genetic advance (as % of mean)

In any crop improvement programme, the most basic information required by a breeder is the extent of the inheritance capacity of the genotype for different character under consideration. In fact, the variability of biological population is an outcome of genetic constitution of the individual make up of that population in relation to prevailing environments. Such studies enable the breeder to have maximum selection response, if the variance exhibited by the populations is largely due to additive genetic variance.

In this investigation, an attempt was made to estimate the broad sense heritability, which involves all types of gene expression, additive as well as non-additive effects, in order to draw some valid conclusion about the possibilities of the improvement of the various characters. To this reason estimate of heritability and genetic advance should be interpreted together. As the genetic advance estimates are dependent on the unit of characters under measurement, hence genetic advance expressed as percentage of mean was calculated in order to have relative comparison of expected genetic gain for quantitative characters for one generation of selection in hypothetical selection programme.

High heritability was observed for harvest index, number of seeds / plant, number of effective pods/plant, number of pods/ plant, days to flower initiation, plant height, days to pod initiation, days to 50% flowering, biological yield/ plant, days to maturity, seed yield/ plant, relative water content and chlorophyll content.

The findings of present investigation are in accordance with the earlier findings of Dahiya et al. (2012), Muhammad et al.(2013),Singh et al.(2012), Jeena et al.(2005), Saleem et al. (2005) and Tiwari et al.2013 for plant height, days to 50% flowering, days to maturity, number of pods / plant, 100 seed weight, biological yield / plant, seed yield/plant and harvest index; Rozina et al.(2011) and Khan et al.(2011)for days to 50% flowering, biological yield /plant, plant height ,100 seed weight and days to maturity; Jeena et al.(2005) for pods / plant,100 seed weight, biological yield / plant and seed yield /plant; Singh et al. (2012) for pods / plant,100 seed weight, plant height and seed yield/plant, Usmani et al. (2005) for seed yield /plant, plant height and harvest index; Gul et al. (2013) for pods/plant,100 seeds weight and seed yield / plant; Monapara and

Dhamelia, (2013) for days to maturity, plant height and seed yield/plant. Whereas, contradictory results were reported by kumar and balasubramanian, (1991)for days to maturity, Ali et al.(2012) and Vaghela, (2008) for plant height. Low heritability was recorded for number of secondary branches / plant and number of primary branches, supported by Ali et al.(2012) for seeds/pod. Whereas, contradictory results were reported by Jeena and Arora et al. (2001) for number of primary branches.

High heritability coupled with high genetic advance as percentage of mean was recorded for harvest index, number of seeds/ plant, number of pods / plant and number of effective pods / plant. Such results indicated, predominantly the presence of additive gene action in the expression of these traits and consequently chance of improving these traits through simple selection. These findings were in agreement with Durga et al. (2007) and Vaghela et al. (2008) for pods / plant; Singh and Singh. (2013), Nizama et al. (2013) and Kuldeep et al. (2014) for pods / plant; Tiwari et al. (2013) for number of seeds per pod; Desai et al. (2015) and Mohammadi and Talebi 2015 for number of seeds / plant and number of pods / plant. High genetic advance revealed that additive gene effects are important in determining these characters.

A character showing high heritability with low genetic advance mean was recorded for relative water content (%), biological yield/ plant, seed yield/ plant, chlorophyll content. These findings were in agreement with Yadav et al. (2015) for days to maturity. This reflects the presence of non-additive gene effects. Selection based on such traits may not be rewarding.

5.3 Correlation coefficient analysis

Most of the characters are associated with each other but the extent of correlation values varies with different pairs of character. A positive correlation between the desired characters is favorable to the breeder as it helps in selection. However, a negative correlation hinders the recovery of the recombinants in both characters. In such a situation any strong selection applied to a character also bring about change in other character.

In present study seed yield / plant exhibited positive and highly significant correlation with biological yield / plant, 100 seed weight, total number of pods /

plant, number of effective pods / plant, number of seeds / plant, harvest index, plant height, number of primary branches/ plant. Whereas, negative correlation was exhibited days to pod initiation, days to flower initiation, days to 50%flowering, days to maturity, number of secondary branches/ plant.

The findings of present investigation are in accordance with the earlier findings of Mishra and Babbar, (2011) and Mishra and Babbar, (2014) for number of effective pods / plant, number of seeds / pod, biological yield / plant and harvest index; Jeena et al. (2005) for number of pods plant, biological yield/ plant and harvest index; Aarif et al. (2014) fornumber of secondary branches, biological yield per plant and harvest index; Naveed et al. (2012) for number of pods per plant, number of secondary branches, number of seeds per pod; Jadhav et al. (2014) for number of pods / plant, number of seeds per pod, harvest index; Malik et al. (2014) for days to maturity, biological yield per plant and harvest index; Yadav and Singh. (2008) for harvest index and 100-seed weight; Thakur et al. (2009) for biological yield per plant and harvest index; Ali et al. (2010) for number of pods /plant and seeds per pod;Sreelakshmi et al. (2010) for days to maturity and number of pods per plant;Babbar et al. (2012) for total number of pods per plant and biological yield per plant; Kumar et al. (2012) for harvest index and number of pods per plant ;Akhtar et al. (2011) and Pandey et al.(2013) for number of pods per plant; Devasirvatham et al. (2013) and Monpara and Dhamelia, (2013) for days to maturity, Dar et al. (2012) for number of seeds per pod;Malik et al (2014) for plant height and Pandey et al. (2013) for plant height and 100 seed weight.; Sarker et al, (2014) for number of primary branches / plant; Bala et al. (2015) and Tesfamichael et al. (2015) for pods /plant; shafique et al. (2016) for harvest index and number of seeds / plant .

From the present investigation on correlation studies, it appeared that biological yield / plant, 100 seed weight, total number of pods/plant, number of effective pods / plant, number of seeds/plant, harvest index, plant height, number of primary branches/ plant and seed yield / plant showed significant positive relationship with most of the characters; hence these traits must be taken into consideration at the time of selection. Highly significant and positive association among the various yield attributing traits indicate immense scope for the seed yield improvement in chickpea via mentioned traits.

5.4 Path coefficient analysis

Path coefficient analysis is the most widely used biometrical technique in plant breeding. The information obtained from this technique, also helps in making selection based on component characters of yield. It helps in understanding the cause of association between two variables. It determines the direct effect of various characters on yield and also indirect effects *via* other components characters and provides the selection of superior genotypes. The path coefficient analysis, a statistical device developed by Wright 1921, is carried out at genotypic and phenotypic level by taking seed yield per plant as the dependent variable in order to see the causal factor. The genotypic direct and indirect effects were found slightly higher in magnitude as compared to phenotypic direct and indirect effects.

In the present study the genotypic path revealed that days to 50% flowering, plant height, number of secondary branches/plant, 100-seed weight, number of seeds/plant, biological yield/plant and harvest index had positive direct effect on seed yield / plant. The findings of present investigation are in accordance with the earlier findings for biological yield / plant, harvest index and number of pods/plant and harvest index; Jhadav et al. 2014 for harvest index and number of pods/plant ; Kumar et al. 2012 for days to 50% flowering and number of pods/plant; Babbar and Patel, 2005, Yucel and Anlarsal, 2010 for harvest index; Borate and Dalvi, 2010 and Kobraee et al. 2010 for number of pods per plant; Kuldeep et al. 2014 for number of effective pods per plant and Dar et al. 2012 for days to maturity; Joshi and Yasin 2015 and Chandra et al. 2015 for biological yield/plant, harvest index; Mohammadi and Talebi, 2015 for number of seeds/plant, 100-seed weight; Shafique 2016 for number of pods / plant .

Days to maturity, number of primary branches/plant, number of pods/plant, number of effective pods/plant and number of seeds/pod showed negative direct on seed yield/ plant. The findings of present investigation are in accordance with the earlier findings of Talebi et al. 2007 for days to maturity and number of primary branches; Dar et al. 2012 for days to maturity .Contradictory results were reported by Borate and Dalvi, 2010 for number of primary branches; Shrivastava et al.2012 for seeds per pod; Dar et al. 2012 for seeds per pod and plant height; Muhammad et al.2013 for number of primary branches and plant height and Hasan and Deb 2014 for plant height; Joshi and Yasin,2015 for biological yield/ plant and harvest index.

Similarly, as direct effect, the indirect effects will also find it contribution *via* different traits towards seed yield per plant. Majority of indirect effects of various independent traits *via* other traits were extremely low of either signs. The indirect effect of number of secondary branches / plant, number of pods /plant, number of effective pods / plant, 100-seed weight, number of seeds / pod, number of seeds /plant, biological yield/ plant and harvest index were positive on seed yield per plant. The findings of present investigation are in accordance with the earlier findings for number of pods/ plant, number of primary branches and plant height contributed to seed yield mainly through indirect effect *via* biological yield and Talebi et al. 2007 for plant height and number of seeds per pod.

5.4 Genetic diversity analysis

The success of breeding programme through hybridization is highly dependent on genetic divergence of parents involved. The more diverse the parents more are the chances of pronounced heterotic effects and increased spectrum of variability in the segregating generations. The present study was also aimed at analyzing the genetic divergence among the 36 genotypes and to identify the superior and divergent parental genotypes for formulating the crossing programme. Mahalanobis D^2 statistic is a powerful tool widely used by breeders in quantifying the degree of divergence at genotypic level.

5.4.1 Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence estimated was highest for carbohydrate content (%), followed by number of effective pods, number of pods/plant, days to 50% flowering and protein content (%). The findings of present investigation are in accordance with the earlier findings of Pandey et al. (2013) ,Jivani et al. (2013) for 100 seed weight and number of pods/ plant; Parashi et al. 2013 for number of pods/plant; Gaikwad et al. (2014) for 100-seed weight.

5.4.2 Grouping of genotypes into different clusters

The study comprised of 36 chickpea genotypes, which were assessed for nature and magnitude of genetic divergence based on 15 quantitative characters using Mahalanobis's D^2 statistic. On the basis of D^2 values, the 36 genotypes were grouped into 9 clusters, following Tocher's method. Cluster I, II, and cluster III were poly-genotypic and remaining clusters were mono-genotypic.

Cluster I and cluster II were poly-genotypic and remaining clusters were mono-genotypic. The findings of present investigation are in accordance with the earlier findings of Jeena et al. (2005) grouped 80 genotypes into 11 clusters. The highest number of genotype were included in cluster I (60), followed by cluster II (7); Dwevedi and Gaibriyal, (2011) grouped genotypes into 6 clusters. Cluster I, the largest cluster with 8 genotypes. Highest inter cluster distance was observed between cluster III and cluster VI; Sreelakshmiet al. (2010) studied 40 genotypes and were grouped into 8 clusters. Out of which cluster I and II have polygenotypic*;* Syed et al. 2012 grouped genotypes under study into five clusters. The cluster II contained the highest number of genotypes (11) and Cluster I contained the lowest; Parameshwarappa et al. (2011), Parashi et al. (2013) obtained 16, 15, 20, 16, 25 in E1, E2 and E3 and 13 clusters of genotypes, from 70, 52, 103 and 33 genotypes respectively, indicating presence of broad genetic diversity in their materials.

5.4.3 Cluster mean values for different characters

On the basis of cluster mean values, cluster VI had highest mean value for Days to maturity, days to pod initiation, days to 50% flowering, days to flower initiation and number of secondary branches/plant. Cluster V had highest mean value for number of seeds/pod. Cluster VIII for harvest index; cluster IX for number of pods/ plant, number of effective pods /plant, number of seeds / plant, biological yield and seed yield / plant; cluster IV for plant height, 100 seed weight; cluster III for number of primary branches. The findings of present investigation are in accordance with the earlier findings of Parameshwarappa et al. (2012), found highest mean value for days to maturity, plant height, number of seeds per pods, 100 seed weight and seed yield and Syed et al. (2012) found highest mean value for total number of pods per plant.

Therefore, intercrossing of genotypes involved in these clusters could be practiced for inducing variability in the respective characters and their rationale improvement for increasing seed yield. Based on cluster means, Rao and Singh (1994) also reported wide range of variation for days to maturity, pods per plant and 100 seed weight. Grouping of genotypes in different clusters was due to the traits viz., plant height, seed yield per plant, number of primary and secondary branches, number of seeds per pod, total number of pods per plant, followed by plant height and 100 grain weight were the main yield contributing character to genetic divergence in chickpea. On the basis of these characters superior genotypes are selected and used in hybridization programme as a donor parent.

5.4.4 Inter and intra cluster D^2 values for different clusters

Cluster II was the most diversified, having highest Intra-cluster cluster. On the basis of inter-cluster distances, the highest inter cluster divergence was observed between genotypes of cluster VI and cluster VII, followed by cluster VII and cluster IX, cluster VI and cluster VIII, cluster VIII and cluster IX, cluster VI and cluster IX, cluster V and cluster IX, cluster III and cluster VII, cluster III and VIII, cluster I and VII. That indicates existence of closer proximity between these clusters. Dwevedi and Gaibriyal, (2011) found highest inter cluster distance between cluster III and cluster VI; Parashi et al.(2013) found highest inter-cluster distance between cluster VII and cluster XIII , followed by cluster XI and XIII , cluster VI and XIII and cluster IV and XI.

5.5 Principal component analysis

Principal component analysis (PCA) involves a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The principle component analysis is a multivariate analysis used to study kind of variation present in the selected population. In chickpea more PCA studies is made on pure breeding lines like germplasm lines, while these are not reported in segregating population.

In the present study, Rotated component matrix revealed that the PC1 which accounted for the highest variability (28.144%) was mostly related to yield attributing traits like like days to 50% flowering, days to pod initiation, days to flower initiation, days to maturity, seed yield/ plant, number of secondary branches/ plant. PC 2 was dominated by phenological traits *i.e.* number of effective pods/ plant, biological yield/ plant, number of pods/ plant, number of seeds/ plant, chlorophyll content. PC 3 was dominated by physiological traits *i.e.* 100 seed weight, plant height, PC 4 was dominated by physiological traits i.e. relative water content harvest index, while PC5 was dominated by traits i.e. number of primary branches / plant.

In PC1, principal component scores ranged from 0.562(GNG 2299) to 4.350 (GL 12021). Maximum value of PC1 component scores was recorded in GL 12021 followed by followed by PG 158, PG 0104, JG 24, H 12-62, IPC 2010-134, GNG 2261, GL29098, BG 3067, IPC 2012-98, Phule G13110, JG24 and RVSSG 38. In PC2, scores ranged from 0.515 (JSC 56) to 4.560 (Phule G0719-10). In PC 3, the value ranged from 0.634 (Phule G13110) to 3.887 (JG24). In PC 4 component scores ranged from 0.552(CSJ884) to 1.638 Phule G13110). While, In PC 5, the value of the component ranged from 0.507 (CSJ887) to 2.173 (BG 3067).

The findings of present investigation are in accordance with the earlier findings of Munirajaet al.2011, the PC 1 separates genotypes on number of pods per plant, seed yield/plant, plant height and number of secondary branches / plant, while PC2 separated on days to maturity, days to 50 per cent flowering and per cent pod damage; Shahid et al.2012, found traits viz., seed yield/ plant, biological yield / plant, number of pods /plant, number of secondary branches/ plant and plant height in the first component (PC1) and days to flowering, days to maturity, 100-seed weight in the second component (PC2); Malik et al.2014, found traits viz., seed yield, biological yield, pods/ plant, secondary branches and plant height in chickpea showed positive relation with the first component (PC1). Days to flowering, days to maturity, 100-seed weight showed positive correlation with PC2; Naveed et al.2015, found traits viz., days to 50% flowering, 100-seed weight and grain yield contributed highest weight on PC1.PC2 was mainly related to pods/ plant and plant height; Mallu et al.2015, found traits viz., the first PC was positively associated with days to flowering, plant height, number of primary and secondary branches / plant. The second PC was positively related with plant height, pods/ plant, seed yield and 100-seed weight.

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER WORK

6.1 Summary

The present investigation entitled "**Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition**" was aimed at identification of phenological, morphological and quantitative traits influencing grain yield of chickpea. Experimental material comprised of 36 promising chickpea genotypes grown in Randomized Completely Block Design with three replications under All India Coordinated Research Project on Chickpea at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur during *Rabi* 2015-16.

Observation were recorded on four phenological traits *viz*., days to flower initiation, days to 50% flowering, days to pod initiation and days to maturity, ten different yield component characters *viz.,* plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/ plant, number of effective pods/ plant, number of seeds / plant, 100 seed weight (g), biological yield/plant (g), harvest index (%) and seed yield/plant (g), two physiological traits *viz*., relative water content (%), chlorophyll content index (%).

For characterization of genotypes, data were recorded on morphological traits (plant and seed level) *viz*., foliage color, leaflet size, growth habit, plant pigmentation, leaf pattern, flower color, seed shape, seed color, seed surface, seed ribbing and seed size.

To study the genetic variability, different genetic parameters *viz*., phenotypic and genotypic coefficient of variation, heritability, genetic advance as percentage of mean, genotypic and phenotypic correlation coefficient, path analysis, genetic diversity and principal component analysis were estimated. The values of phenotypic coefficient of variation for all the traits under study were higher than genotypic coefficient of variation. High genotypic and phenotypic coefficient of variation was recorded for traits viz., Seed yield/ plant, number of effective pods / plant, number of pods/ plant, number of seeds/ plant, biological yield /plant, 100- seed weight and harvest index.

High heritability coupled with high genetic advance as percentage of mean was recorded for harvest index, followed by number of seeds/ plant, number of pods/plant and number of effective pods/plant.

High heritability with moderate genetic advance as percentage of mean was recorded for plant height, days to flower initiation, days to 50% flowering, days to pod initiation, 100 seed weight and days to maturity.

High heritability with low genetic advance as percentage of mean was recorded for relative water content, biological yield, seed yield/ plant, chlorophyll content index.

Seed yield per plant shared strong significant and positive association with biological yield, 100 seed weight, number of pods/ plant, number of effective pods / plant, number of seeds /plant and harvest index. Path analysis revealed that biological yield/ plant, harvest index, days to flower initiation, number of pods/ plant and number of primary branches/ plant, whereas remaining traits showed low direct positive effect. The highest negative direct effect was exhibited by days to pod initiation.

On the basis of D^2 values, the 36 genotypes were grouped into 9 clusters. Cluster I, II, III cluster IV were poly-genotypic having 11, 10, 7 and 3 genotypes, respectively. Whereas, cluster V, VI, VII, VIII and IX were mono-genotypic.

Highest inter cluster distance was observed between genotypes of cluster VI and cluster VII, followed by cluster VII and cluster IX, cluster VI and cluster VIII, cluster VIII and cluster IX, cluster VI and cluster IX, cluster V and cluster IX, cluster III and VII, cluster III and VIII and cluster I and cluster VII.

Cluster VI had highest mean value for days to maturity, days to pod initiation, days to 50% flowering, days to flower initiation, number of secondary branches/ plant; Cluster VIII for harvest index; cluster IX for Total number of pods/ plant, number of effective pods/ plant, number of seeds/ plant**,** Biological yield/ plant, seed yield/ plant, cluster IV for plant height, 100 seed weight, cluster III for number of primary branches/ plant.

Out of sixteen, only five PC exhibited more than 1.00 Eigen value, and showed about 69.701% total variability among the traits studied. The PC 1, showed 28.144 %, while, PC 2, PC 3, PC 4, PC 5 exhibited 17.642%, 9.286%, 7.916% and 6.713% variability, respectively among the genotypes for the traits under study.

The PC1 which accounted for the highest variability (28.144%) was mostly related to yield traits like days to 50% flowering, days to pod initiation, days to flower initiation, days to maturity, seed yield/ plant, number of secondary branches/ plant. PC 2 was dominated by traits *i.e*. number of effective pods/ plant biological yield/ plant, number of pods/ plant, number of seeds/ plant, chlorophyll content, PC 3 was dominated by quantitative traits *i.e*. 100 seed weight and plant height, PC 4 was dominated by physiological traits *i.e.* relative water content, while PC5 was dominated by trait number of primary branches / plant.

6.2 Conclusions

1. High genotypic and phenotypic coefficient of variation was recorded for traits viz., Seed yield/ plant, number of effective pods / plant, number of pods/ plant, number of seeds/ plant, biological yield /plant, 100- seed weight and harvest index indicated the presence of sufficient variability in the existing material. Therefore, these characters should be considered in selection programme.
2. Harvest index, number of seeds/ plant, number of pods/ plant, number of effective pods /plant showed high heritability coupled with high genetic advance, indicating contributions of additive genetic variance. Therefore, selection for such traits may be rewarding.
3. Seed yield per plant shared strong significant and positive association with biological yield, 100 seed weight, number of pods/ plant, number of effective pods / plant, number of seeds /plant and harvest index. Hence for genetic improvement of yield, these characters should be given prime importance.
4. Path analysis revealed that biological yield/ plant, harvest index, days to flower initiation, number of pods/ plant and number of primary branches/ plant exerted maximum positive direct effect on seed yield/ plant. Hence, high biological yield/ plant and harvest index and more number of pods and primary branches should be consider for constructing plant type of chickpea.

5. The percentage contribution towards genetic divergence was found high for harvest index, number of seeds/ plant, days to flower initiation, plant height, number of pods/ plant and 100 seed weight. Thirty six genotypes were grouped into 9 clusters. Maximum inter cluster distance was observed between genotypes of cluster VII (Phule G13110) and VI (PG 0104). The hybridization between individuals belonging to these clusters may leads to the formation of superior segregates/ transgressive segregates.
6. Five genotypes viz., Phule G0719-10, GL 12012, PG 158, PG 0104 and JG 24 found superior based on phenological & yield traits, which can be used as donor for earliness and improvement in yield in hybridization programmes.
7. Out of sixteen, only five PC exhibited more than 1.00 Eigen value, and showed about 69.701% total variability among the traits studied. The PC 1, showed 28.144 %, while, PC 2, PC 3, PC 4, PC 5 exhibited 17.642%, 9.286%, 7.916% and 6.713% variability, respectively among the genotypes for the traits under study. Therefore, the genotypes from PC1 can be given due importance.
8. On the basis of Principal Component analysis, the genotypes Phule G0719-10, GL 12021, PG 158, PG 0104, JG 24 and H 12-62 have highest PC values for yield related traits. Thus, these genotypes are used for development of promising genotypes.
9. High yielding entries NBeG 507, RKG 13-180, Phule G0719-10, JG24-1, RVG 203 found suitable under late sown condition.

6.3 Suggestions for further work

1. Identified genotypes should be utilized for crop improvement.
2. Further prolonged study should be considered over years and locations to obtain more illustrating picture of different traits and identified stable accessions for sustainable chickpea production.
3. Evaluation of genotypes based on molecular markers has to be carried out.

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Appendix- I

Mean table of yield and yield contributing traits in chickpea

S.No.	ACCESSION NO.	FI	50% F	PI	DM	PH	PB	SB	P/P	EP	S/P	100SW	BY	HI	SY
1	CSJ887	48	61	67	91	46.5	2.00	3.70	46.1	43.3	57.3	16.3	13.9	68.8	9.20
2	NBeG 507	41	54	63	89	47.3	2.23	4.56	28.2	24.1	26.3	29.5	14.0	85.4	13.96
3	BG 3067	52	64	70	102	54.4	2.20	6.80	23.3	26.4	24.7	16.8	19.3	49.5	9.66
4	RKG 13-155	41	57	65	98	34.2	2.30	5.43	30.1	26.2	44.8	27.9	15.5	63.3	8.96
5	PG 158	64	74	82	107	54	2.10	6.00	25.1	22.2	25.4	22.6	15.2	51.7	7.26
6	H 12-62	61	69	76	99	53.2	2.10	5.53	18.8	18.6	16.86	15.1	9.20	48.7	4.73
7	PBC 501	38	52	59	92	39.4	2.10	4.56	39.3	35.7	35.36	18.2	11.7	78.0	8.36
8	JSC 55	38	51	57	90	41.5	1.90	4.43	34.4	26.2	38.0	24.2	15.6	58.8	9.70
9	JG 24	47	64	70	97	63.9	1.66	4.66	36.0	33.1	36.8	29.7	22.2	54.3	12.06
10	IPC 2012-49	65	73	78	104	55.3	2.00	5.53	24.8	25.0	26.3	23.6	14.6	47.4	7.36
11	Phule G13110	41	55	63	87	47.9	1.90	4.46	15.8	11.6	15.4	23.6	8.2	98.3	7.86
12	GL 12003	53	65	72	100	59.4	1.90	4.86	18.3	16.43	26.3	15.4	7.3	104.6	8.16
13	RKG 13-180	42	56	62	98	45.2	1.80	4.03	43.6	36.1	37.6	25.3	18.5	84.6	14.90

14	JG 74315-14	52	62	66	97	43.6	1.90	4.53	24.4	18.6	28.3	17.1	9.3	84.4	7.76
15	CSJ884	51	56	61	98	38.2	2.00	5.76	45.3	34.2	52.8	12.6	16.0	44.0	7.40
16	NDG 14-24	41	55	69	93	47.4	1.80	4.43	28.0	25.4	29.4	23.4	14.1	58.9	8.73
17	H 12-55	51	64	66	98	39.6	2.00	5.86	46.3	42.8	52.0	14.0	13.5	65.0	9.10
18	GNG 2304	51	59	65	92	47.2	1.80	4.43	16.6	15.9	28.3	12.8	8.4	54.5	5.03
19	Phule G0719-10	42	56	65	94	38.9	1.90	5.03	65.9	66.4	64.9	24.7	23.2	67.0	15.33
20	GJG 1319	44	56	64	92	53.2	2.10	4.56	35.2	33.3	54.2	25.6	24.1	64.8	14.8
21	BG 3068	53	64	71	98	39	2.00	5.56	35.4	34.1	45.1	16.8	15.3	58.4	9.10
22	JSC 56	47	58	65	95	49.2	2.00	5.00	38.3	33.3	43.5	22.3	16.3	56.6	10.13
S.No.	**ACCESSION NO.**	**FI**	**50% F**	**PI**	**DM**	**PH**	**PB**	**SB**	**P/P**	**EP**	**S/P**	**100SW**	**BY**	**HI**	**SY**
23	NBeG 511	48	57	66	93	42.9	2.00	3.43	24.9	22.3	27.2	22.3	12.1	68.7	7.06
24	GNG 2219	54	66	72	98	48.2	1.77	4.43	38.2	37.9	28.5	15.4	11.8	67.4	7.76
25	RVSSG 38	54	63	69	97	45.3	1.77	4.10	27.9	25.2	31.3	16.6	7.8	87.6	7.26
26	IPC 2012-98	55	68	74	102	54.9	2.10	4086	25.4	25.1	57.8	15.3	15.7	49.8	7.90
27	GL29098	55	64	74	99	47.6	2.10	5.86	18.3	25.0	37.4	14.4	9.3	59.2	4.83

28	PBC 510	44	58	66	99	43.2	1.90	5.23	35.0	34.9	47.2	23.3	15.9	64.7	9.56
29	JG24	57	67	66	103	66.6	2.00	6.00	36.1	34.5	33.8	34.4	20.0	58.2	11.13
30	JG24-1	58	68	67	94	66.5	2.10	6.20	35.4	33.3	36.5	34.4	24.4	64.9	15.70
31	RVG 203	39	53	61	90	46.3	2.10	4.43	48.5	45.5	55.1	21.3	23.5	59.4	14.06
32	GNG 2261	55	68	78	101	47.5	2.00	5.43	29.5	27.3	35.7	14.5	16.2	51.3	7.96
33	PG 0104	57	71	78	106	58.1	2.00	5.80	35.1	27.0	28.9	17.2	18.4	26.3	4.83
34	GL 12021	63	71	79	104	59.5	2.00	5.90	25.3	24.1	34.3	16.7	12.1	41.7	5.03
35	IPC 2010-134	55	71	77	104	54.1	1.80	6.10	25.3	25.0	47.3	24.8	16.4	37.4	6.40
36	RVG 202	47	56	63	87	46.3	2.0	4.70	27.2	26.1	38.0	23.6	17.6	45.4	7.70

CURRICULUM VITAE

The author of this thesis **Miss. Babita Bajya** D/o Mr. Babulal Bajya was born 15 April, 1995 at Jaipur Rajasthan.

She joined the College of Agriculture, Lalsot, Rajasthan in the year 2010 and successfully completed the degree of B.Sc. (Ag) in June, 2014 with (6.7 OGPA out of 10.00 point scale). After graduation author completed the M.Sc. (Ag.) degree in Department of Plant Breeding and Genetics with (OGPA) in the year 2017-18.

S.No.	Institutions
1.	JNKVV, Jabalpur
2.	COA, Lalsot, Rajasthan
3.	Shri Shyam Bal Niketan School, Rajasthan
4.	Rajdhani Public School, Rajasthan

She has got the following degrees

S.No.	Degree granted	University / Board	Year
1.	M.Sc. (Ag.)	JNKVV, Jabalpur	2018
2.	B.Sc. (Ag.)	COA, Lalsot, Rajasthan	2014
3.	12th	Shri Shyam Bal Niketan School, Rajasthan	2010
4.	10th	Rajdhani Public School, Rajasthan	2008

Awards

For the partial fulfillment of the master degree programme she was allotted a research problem on "**Genetic evaluation of Chickpea Genotypes Suitable for Late Sowing Condition"** which was successfully conducted by her and being submitted in the form of thesis.

Foliage colour – Dark green & medium green

Leaflet size- Small, medium & large

Flower colour- Pink & white

Growth habit- Erect & semi-erect

Seed shape – Angular and Pea shaped

Seed colour- Dark brown, Light brown and Light Yellow

Plate 1: Photographs of various morphological traits of the experimental material

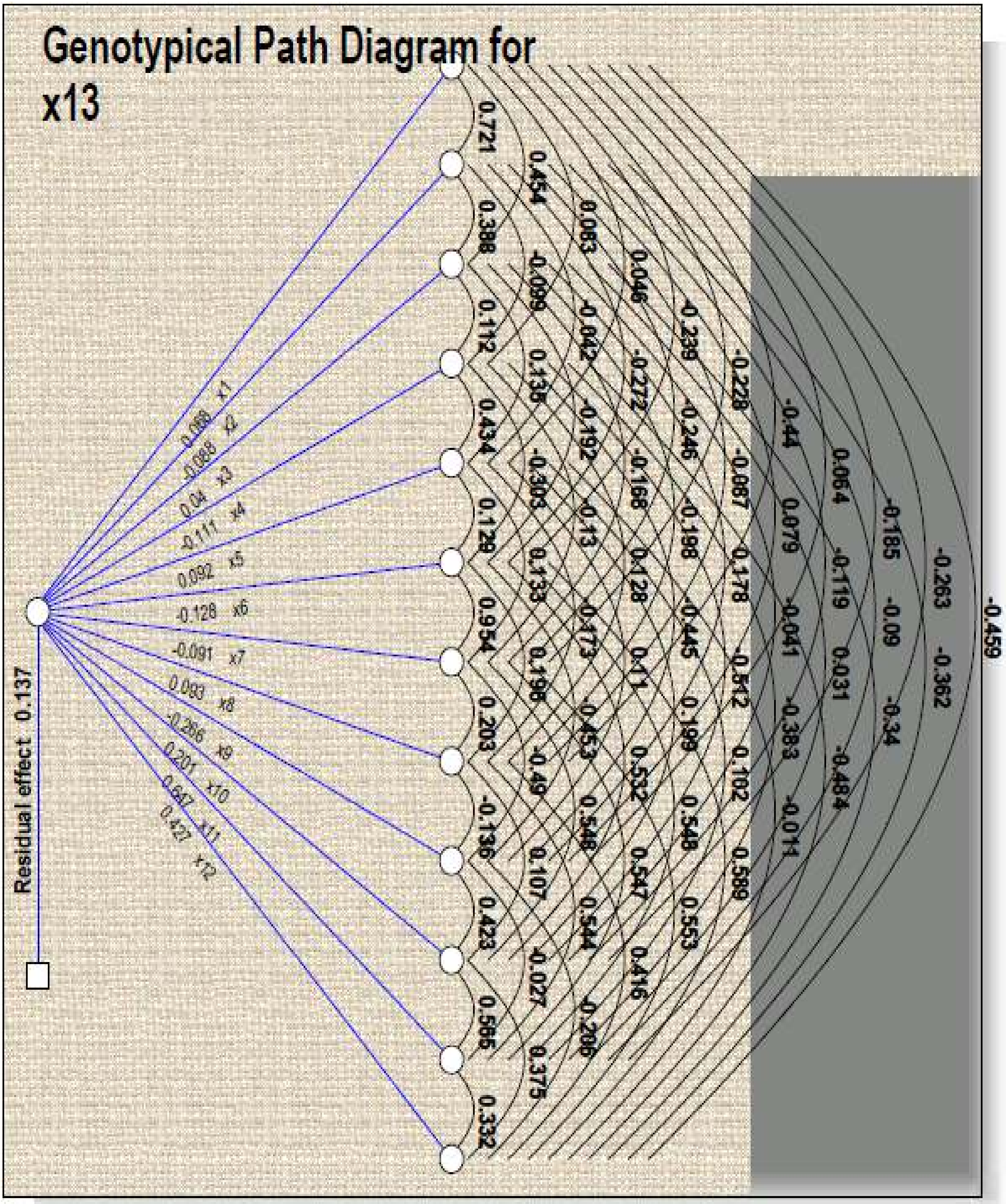

Figure 2: Genotypic path diagram

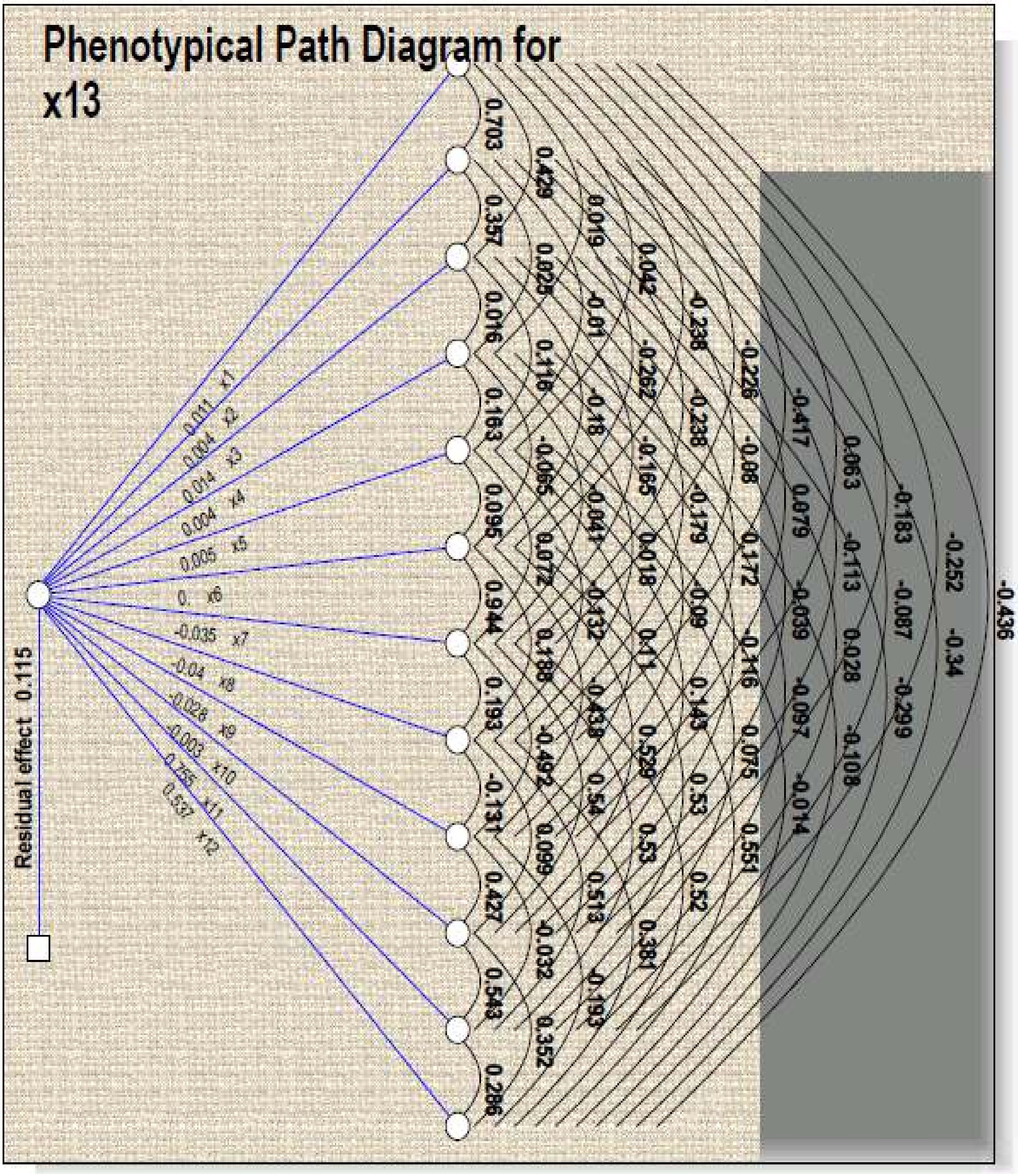

Figure 1: Phenotypic path diagram

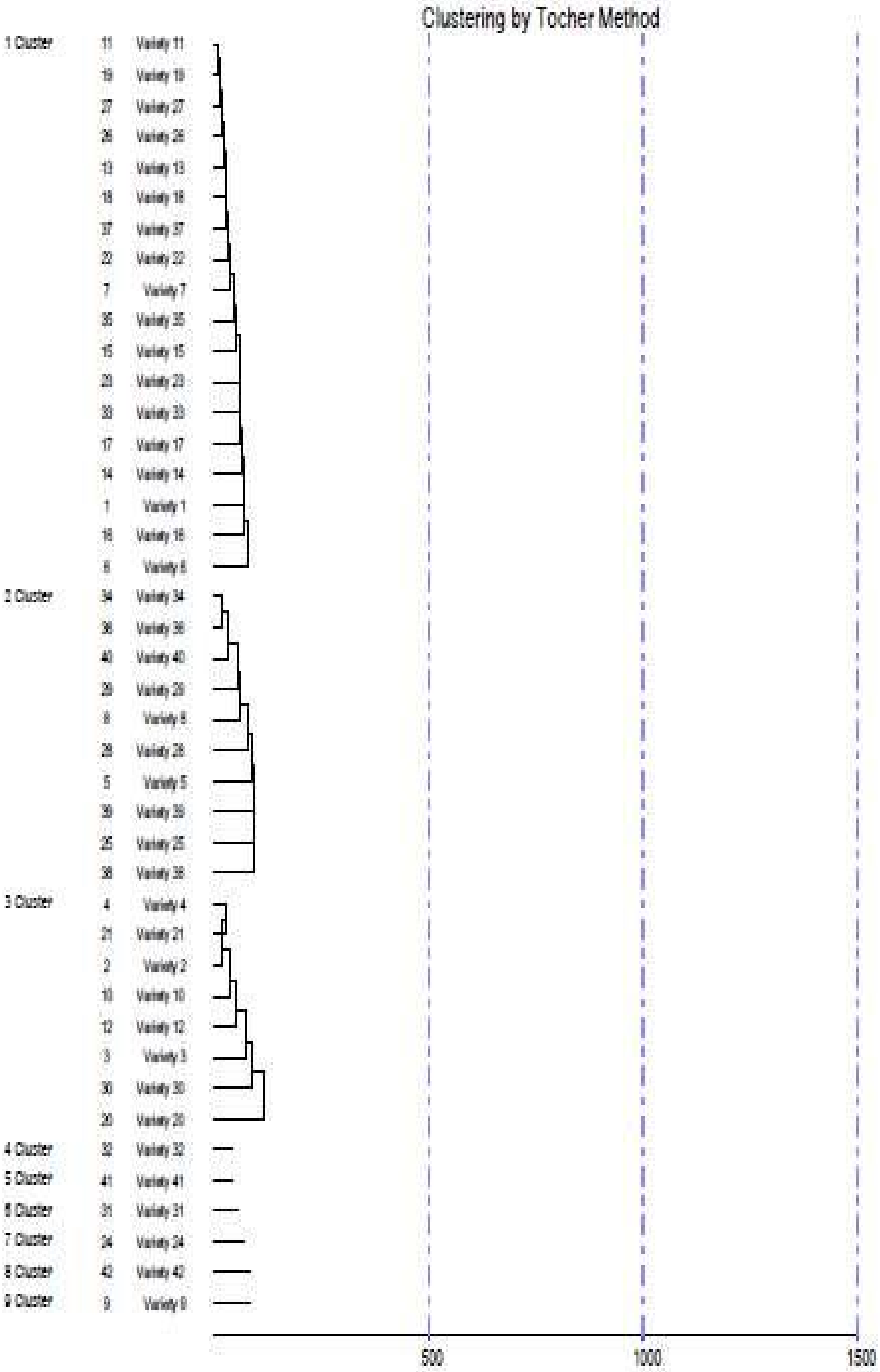

Figure 3: Clustering by Tocher Method

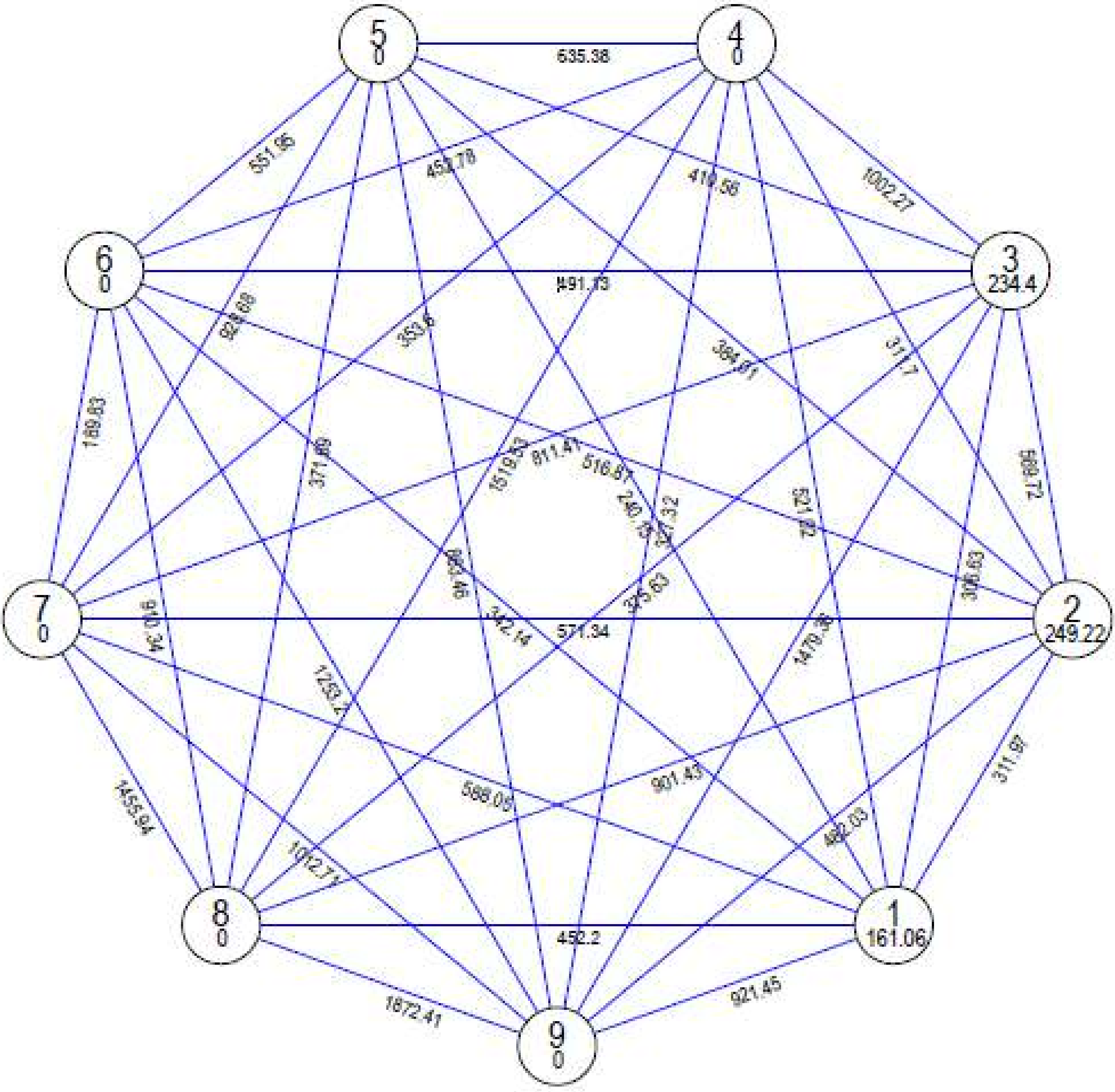

Figure4: Mahalnobis Euclidean Distance

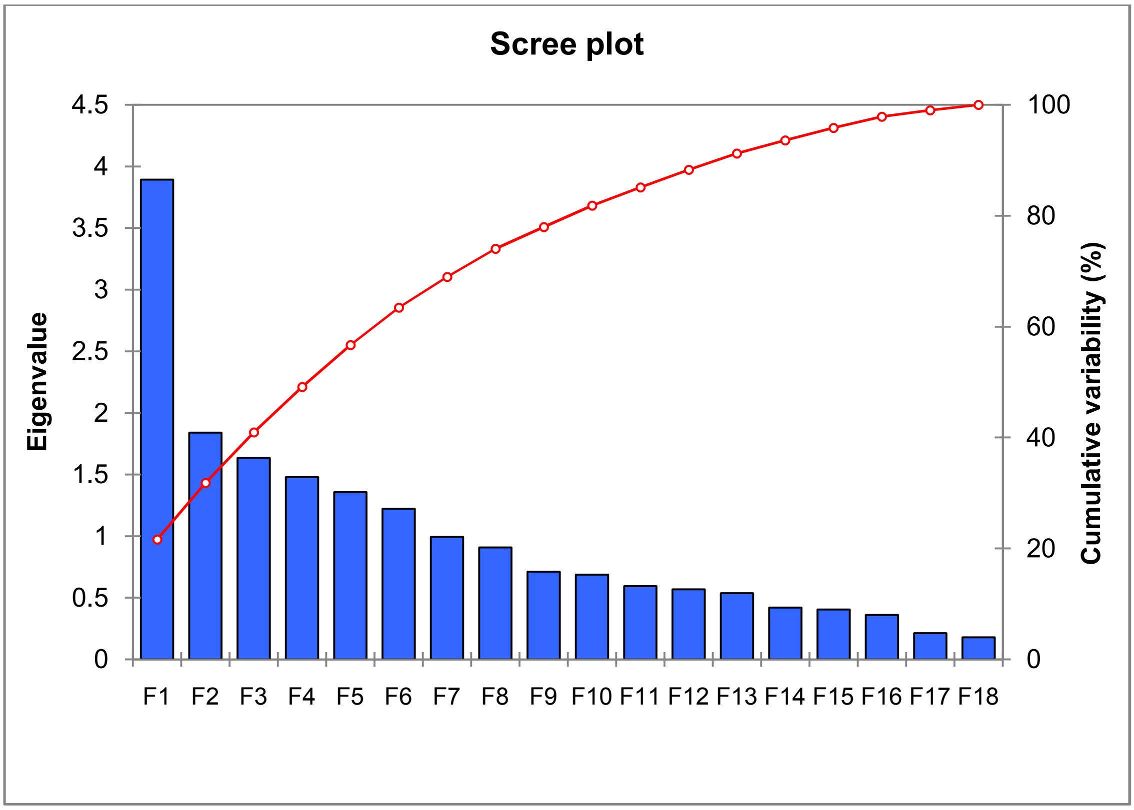

Figure 5: Scree plot between eigen value and principal components