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

by

MISS. GIRI SHWETA RAMESH

(Reg. No. 011/043)

A Thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH

RAHURI- 413 722, DIST. AHMEDNAGAR

MAHARASHTRA, INDIA

In partial fulfillment of the requirements for the degree

Of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY

POST GRADUATE INSTITUTE

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CANDIDATE'S DECLARATION

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

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Date: / / 2013

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CERTIFICATE

This is to certify that the thesis entitled, **"GENETIC DIVERSITY AND PATH COEFFICIENT ANALYSIS IN CHICKPEA (** *Cicer arietinum L.).* **"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra State in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY**, embodies the results of a piece of *bonafide* research work carried out by **MISS. GIRI SHWETA RAMESH,** under my guidance and supervision and that no part of the thesis has been submitted for any other Degree, Diploma in other form.

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

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Place: MPKV, Rahuri **(S.G.BORKAR)**
Date: / / 2013

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"Words provide wings to our ideas but not always can words express our feelings in words or languages".

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Place: M.P.K.V., Rahuri (S.R.GIRI)
Date:

CONTENTS

Sr. No.	Title	Page No.
CANDIDATE'S DECLARATION		iii
i.	Research Guide	iv
ii.	Associate Dean (PGI)	v
ACKNOWLEDGEMENT		vi
LIST OF CONTENTS		viii
LIST OF TABLE		x
LIST OF FIGURES		xi
LIST OF ABBREVIATIONS		xii
ABSTRACT		xiii
1.INTRODUCTION		1
2. REVIEW OF LITERATURE		5
2.1 Variability and genetic parameters		5
2.2 Correlation and path coefficient analysis		13
	2.2.1 Correlation and Path coefficient analysis in chickpea	13
2.3 Genetic diversity		21
	2.3.1 Concept of genetic diversity	21
	2.3.2 Genetic divergence in Chickpea	22
3. MATERIALS AND METHODS		33
3.1 Material		33
3.2 Experimental design		33
3.3 Cultural practices		34

3.4 Observations recorded 34
3.5 Statistical methodology 35

4. EXPERIMENTAL RESULTS 46
4.1 Genetic variability and heritability 46
4.2 Correlation studies 50
4.3 Genotypic path coefficient analysis 52
4.4 Genetic divergence 54

5. DISCUSSION 57
5.1 Variability and genetic parameters 57
5.2 Correlations 60
5.3 Path coefficient analysis 62
5.4 Genetic divergence 64

6. SUMMARY AND CONCLUSIONS 69
6.1 Variability and genetic parameters 69
6.2 Correlations 70
6.3 Path coefficient analysis 70
6.4 Genetic divergence 71

7. LITERATURE CITED 74
8. VITA 83

LIST OF TABLES

Sr. No.	Title	Between Page
1.	List of 52 genotypes of chickpea along with their sources	33-34
2.	Analysis of variance for different characters studied in chickpea	45-46
3.	Mean performance of different characters in fifty two genotypes of chickpea	46-47
4.	Estimation of genotypic, phenotypic, environmental variances, genotypic, phenotypic, coefficient of variation, heritability and genetic advance for various characters studied in chickpea.	49-50
5.	Genotypic correlation coefficient of nine character studied in chickpea.	50-51
6.	Direct and indirect effects of nine characters on seed yield studied in chickpea.	52-53
7.	Grouping of 52 chickpea genotypes in different clusters.	54-55
8.	Average intra and inter cluster D^2 values	54-55
9.	Average intra and inter cluster D values	54-55
10.	Cluster means for the nine characters studied in chickpea	54-55
11.	Percent contribution of different characters to total diversity in chickpea	54-55

LIST OF FIGURES

Fig. No.	Title	Between pages
1.	Graphical comparision of GCV and PCV of nine characters studied in chickpea	49-50
2.	Graphical comparision of heritability and expected genetic advance over mean of nine characters in chickpea.	49-50
3.	Path diagram	52-53
4.	Cluster diagram	54-55
5.	Per cent contribution of nine characters in total diversity of chickpea	54-55

LIST OF ABBREVIATIONS

%	:	Per cent
b.s.	:	Broad sense
@	:	At the rate of
/	:	Per
C.D.	:	Critical Differences
cm	:	Centimeter(s)
C.V.	:	Coefficient of variation
D.F.	:	Degrees of freedom
et al.	:	et alli (and others)
EMP	:	Error mean sum of products
g	:	gram
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
GMP	:	Genotypic mean sum of products
h^2	:	heritability
i.e.	:	That is
M.S.S.	:	Mean sum of squares
No.	:	Number
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
SE	:	Standard error
viz.,	:	Namely
σ^2	:	Variance

ABSTRACT

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RAHURI-413 722

2013

Research Guide	:	**Dr. D.V.KUSALKAR**
Department	:	**Agricultural Botany**
Major discipline	:	**Genetics and Plant Breeding**

The investigation on genetic studies of germplasms in chickpea (*Cicer arietinum L.*) was conducted on 52 genotypes of chickpea to know the variability, interrelationship among yield and its components, their direct and indirect effects on seed yield and genetic divergence among various genotypes of chickpea.

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

A wide range of variation was observed for the characters days to 50% flowering, days to maturity, plant height, number of secondary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant however, narrow range of variability was observed for number of primary branches per plant, number of seeds per pod.

Genotypic and phenotypic coefficient of variation were higher for seed yield per plant followed by plant height, number of pods per plant and number of secondary branches, while their estimates were lowest for number of seeds per pod, days to maturity. Heritability in broad sense was highest for seed yield per plant. High heritability associated with high genetic advance as percent of mean observed for number of primary, secondary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant suggesting that selection of these traits would be effective for the desired improvement in chickpea.

Genotypic correlation coefficients were found to be of higher magnitude than the corresponding phenotypic ones. The characters, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod were significantly and positively associated with seed yield per plant.

Number of seeds per pod, number of pods per plant, number of secondary branches per plant showed positive direct effects on seed yield while number of primary branches per plant showed negative direct effects.

The D^2 statistics showed that there was adequate diversity among the genotypes with D^2 values ranging from 20.52 to 985.96. On the basis of D^2 values, fifty two genotypes studied were grouped into six (6) clusters. On the basis of inter and intra cluster distance, cluster means *per se* performance, the genotypes viz., IC-275426, IC-275427, IC-275445, IC-327024, IC-327031, IC- IC-327056, IC-327029, IC-327035 and IC-275429 were identified for their use in hybridization programme.

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1. INTRODUCTION

Pulses occupy unique position in Indian Agriculture because of their characteristics of maintaining and restoring soil fertility, besides high nutritive value. Pulses restore soil fertility through biological nitrogen fixation with the help of symbiotic bacteria *Rhizobium* in roots in addition to enhancing sustainability of agricultural system. Among the pulses, chickpea is important *Rabi* crop of India.

Like other pulse crops, chickpea has multiple functions in the traditional farming systems in many developing countries. Nearly 90 % of the crop is cultivated under rainfed condition on receding soil moisture and on marginal lands. It is an important source of human food and animal feed and it also helps in the management of soil fertility.

Chickpea *(Cicer arietinum L.*) is traditionally grown in many parts of the world since ancient time, both in Asia and Europe. It is known to have originated in western Asia. It belongs to genus *Cicer* and tribe Cicereae and subfamily Papilionaceae of family Leguminaceae. It is relatively small genus with 39 known species distributed mainly in central and western Asia of which two are found to be cultivated in India. They are *Cicer arietinum* (2n=16) which is most widely cultivated and *Cicer songaricum* (2n=16) cultivated in western temperate and Alpine regions of Himalaya. (Anonymous, 1950).

Chickpea is one of the most important *Rabi* pulse crops in Asia. It is well adapted to grow on residual soil moisture in the post rainy season because of its deep and prolific root system. India is largest producer (25%), importer (20%) and

consumer (20%) of Pulses in the world. In Pulses, chickpea accommodates third position in the world (Anonymous, 2006).

Chickpea seed contains on an average 22% protein, 4.5% fat, 63% carbohydrates, 8% crude fiber, 2.7% ash and 358 calories (Miao *et al.*, 2009). Being fairly tolerant to soil moisture stress, they occupy important position in different cropping systems. Chickpea is of two types, *desi* and *kabuli*. The *desi* types are generally small seed with coloured seed coat and angular seed shape, while *kabuli* are generally large seeded with dirty white or creamy white seed colour and ram head shape, the two types are botanically similar but there are strong consumer preference for one or the other. In general *kabuli* type chickpea have higher protein content than *desi* types but they are low yielder. The main constituent of protein is globulin. It is mostly used in the form of *'dhal'*. About 75% of the total production is consumed as *dhal* in India. The whole grains are also eaten raw or boiled and roasted. Chickpea has got special importance in diet and is consumed in a variety of ways. It is mostly used in the form of *dhal* (flour or parched). In other aspects, *dhal* obtained after milling either from chickpea or from red gram, forms a major part of regular diet of vegetarian. Chickpea flour is cheap source for the preparation of different forms of Indian confectionery; tender leaves are used as vegetable, while dry plant parts above ground are used as cattle feed. Exudation from leaves called "amb" contains oxalic and mallic acids which possess medicinal value and used for intestinal disorders, stomach aches, blood purification etc., and germinating seeds are prophylactic against scurvy disease.

The *kabuli* chickpea or *kabuli chana* is one of the different forms or types of chickpea, which is comparatively bold

in size and shape, cream coloured with thin seed coat and wrinkled. Generally kabuli chickpea is used for the purpose of roasted chana "Chhole" as a best pulse for curry preparation and also uses as raw or green for direct consumption. Therefore, because of various domestic uses of chickpea (*i.e. shev, ladu, pakoda, parched seed*, etc.) there is wide scope for production of chickpea and developing small scale industries.

As far as human diet is concerned the protein requirement for normal individual's health is about 25 g per day for which about 120 g of *dhal* is required in one's daily diet. Along with this, chickpea is important in the agriculture as it is legume crop it has unique place in the cropping sequence regarding improving the soil nutrient content (especially Nitrogen) and microbial activity etc.

In India, chickpea was grown on 8.75 million ha area with total production of 8.25 million tons with an average productivity of 943 kg per hectare (Anonymous, 2011). In case of Maharashtra, chickpea was grown on 13.95 lakh ha area with total production of 13.01 lakh tons with an average productivity of 933 kg per hectare (Anonymous, 2011). Chickpea occupies 35 per cent of total area under pulses and producing about 44 per cent of total pulses production in India.

Though India is the largest producer of this crop, its productivity is low as compared to countries like Italy, Turkey, Iran, etc. There is a good scope to improve the productivity of this crop by varietal improvement and adopting the improved production technology on larger areas of the country.

The real yield potential of the crop can be exploited through varietals improvement programme which needs the information regarding the range of existing genetic variability

and the relationship of the various economically important characters in the promising genetic stock available with the breeder. Genetic variation present in germplasm arrays and the genetic relationships among genotypes are very useful for efficient conservation as well as utilization of genetic resources in breeding programme. Evaluation of germplasm increases the efficiency to make desirable selection whereas diversity index provides the information regarding the extent of variation present in the population.

In chickpea, association of one or more characters influenced by a large number of genes is elaborated statistically by correlation coefficients. Genotypic correlation coefficient provides a measure of genotypes conjugation between characters. The methods of partitioning the correlation into direct and indirect effects by path coefficients analysis was suggested by Wright (1921). It provides useful information on the relative merit of the traits in the selection criterion.

The present investigations were therefore conducted to assess the genetic variation, trait association and significance contribution of each trait towards yield and also their contribution towards genetic diversity with the following objectives.

1. To study the extent of variability.
2. To study the character association between yield and yield components and their direct and indirect effect on seed yield.

2. REVIEW OF LITERATURE

The literature pertaining to the present investigation has been reviewed under the following headings:

2.1 Variability and genetic parameters

2.2 Correlation and path analysis

2.3 Genetic diversity

2.1 Variability and genetic parameters

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

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

Dumbre *et al.* (1984) worked out the genetic variability in sixteen cultivars of chickpea for nine quantitative characters and reported the highest range of variability for pods per plant (10.4 – 95.8) followed by days to maturity (87.0 - 125.0) and lowest for seeds per pod (1.01 – 1.4). Genotypic coefficients of variation were highest for seed yield per plant showing large amount of variability in the material for this character. High heritability with higher genetic advance was observed for the

characters, seeds per pod, seed yield per plant and 100 seed weight.

Maloo and Sharma (1987) analyzed twenty one diverse varieties of gram for estimation of variability parameters. The estimates of genotypic coefficients of variation ranged from 1.58 (for days to maturity) to 40.26 (for seed yield per plant). High genetic advance as per cent of mean coupled with high heritability were recorded for seed yield, number of pods per plant and number of primary branches per plant.

Jivani and Yadavendra (1988) estimated high heritability parameters for seed yield per plant and nine yield related traits in 42 genetically diverse genotypes of *Cicer arietinum* and observed that, both coefficients of variation were high for pods per plant and 100 seed weight, plant height, days to flowering and maturity, pods per plant, 100 seed weight and harvest index and high heritability estimates. The greatest genetic gains were expected for 100 seed weight, pods per plant and days to flowering.

Samal and Jagdev (1989) showed high PCV and GCV for seed weight and yield and moderately high for plant height and days to flowering indicating relatively low influence of environment on these characters. High heritability coupled with high genetic advance was observed for seed mass and yield which may be due to the high additive gene effects and selection pressure could be probably applied on these traits for yield improvement.

Sandhu *et al.* (1989) observed that grain yield per plant had maximum amount of genetic variation (53.74 %) followed by pods per plant (40.56 %) and 100 seed weight (22.16 %). The protein content showed minimum amount of genotypic

variation (6.06 %) while seeds per pod (14.87 %) showed moderate amount of genetic variation. The heritability estimates for different characters ranged from 11.92 per cent for primary branches to 88.11 per cent for seed yield, the heritability for protein content was sufficiently high (73.81 %) while it was medium for pods/plant (39.36 %). The genetic advance as percentage of mean was highest for grain yield (103.86) while it was lowest for (8.04) primary branches and seeds per pod.

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

Pundhir *et al.* (1991) reported considerable variation for days to flowering (46.00 – 71.00) pods per plant (14.0-91.0), 100 seed weight (5.00 – 60.94), seed yield (204.00 – 3333 kg/ha) and protein (17.00 – 23.00) in chickpea germplasm. Estimates of high heritability and genetic advance as per cent of mean were highest for seed size whereas heritability was lowest for pods per plant and genetic advance was lowest for protein content.

Sandhu *et al.* (1991) observed a wide range of variability for grain yield, plant height, secondary branches, pods per plant

and 100 seed weight and low for primary branches, seeds per pod and protein content in 55 diverse lines of chickpea. They also, observed that, grain yield followed by pods per plant and 100 seed weight had maximum genetic variation. The heritability estimates for different characters ranged from 8.4 % (primary branches) to 86.1 % (seed yield) and the characters protein content, plant height and 100 seed weight had considerably high estimates of variability. The genetic advance as per cent of mean was highest (73.44 %) for seed yield; however, it was lowest for primary branches.

Jahagirdar *et al.* (1994) reported high genotypic and phenotypic coefficients of variation for number of pods per plant and moderately high values of genetic variability for days to 50 % flowering, plant height and number of primary branches per plant. High values of heritability coupled with high genetic advance were observed for 100 grain weight, days to 50 % flowering, number of secondary branches per plant and number of pods per plant.

Singh *et al.* (1994) crossed JG-62 (a double podded *Cicer arietinum* genotype) and MS-24 (genotype with pods containing 2-3 seeds) and along with their F_1s, F_2s backcrossed progenies were evaluated during post rainy season. Analysis of variance showed significant difference between parents and backcrossed generations but not between F_1s, F_2s and back crosses indicating absence of maternal effects. The narrow sense heritability for seeds per pod was estimated to 59 per cent.

Mathur and Mathur (1996) Estimated of genetic parameters and interrelationship of quantitative traits in chickpea studied genotypic and phenotypic coefficients of variations, heritability and expected genetic advance for grain

yield and its contributing characters in 34 varieties of chickpea (*Cicer arietinum*) during *rabi* season. They reported the highest values of genotypic and phenotypic coefficients were obtained for 1000 seed weight. High heritability for all characters was recorded. Seed weight and grain yield per plant had good values of genetic advance with high heritability. Seed yield per plant showed significant positive correlation with pods per plant and 1000 seed weight but was negatively correlated with plant height and days to flowering.

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

Gumber *et al.* (2002) studied 30 genotypes of chickpea and observed highest heritability in pods per plant (78.0 %) followed by secondary branches (71.5 %) and 100 seed weight (69.4 %). The estimate of phenotypic coefficient of variation (PCV) was highest for seed yield (38.64 %) and seeds per pod (13.33 %).

Muhammad *et al.* (2004) studied variability, heritability, genetic advance, correlation coefficients and path coefficients for yield and its components were conducted in 24 advance lines of chickpea. Grain yield had positive and significant correlation with plant height, pods per plant, 100-seed weight and biological yield. High direct effects were

contributed by biological yield and harvest index although the later had negative association with grain yield.

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

Dwevedi and Gaibriyal (2009) carried out an investigation among the 25 genotypes of chickpea to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 statistics. The data were recorded on ten important quantitative traits from the genotypes raised in Randomized Block Design having three replications. The twenty five chickpea genotypes were grouped into six clusters. Three characters viz., harvest index, 100 seed weight and number of pods per plant contributed maximum in manifestation of genetic diversity. Number of pods per plant had maximum phenotypic and genotypic coefficient of variation, followed by biological yield per plant and 100 seed weight.

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

genetic advance was observed for grain yield. Plant height, dry matter, days to 50% flowering and days to maturity indicated high additive gene effects.

Moulla (2010) showed that effect of location (L.) and season (E) was highly significant ($P<0.01$) while the interaction among locations, seasons and genotypes (L×E×G) was not significant ($P>0.05$). The heritability for protein content varied from 0.83 to 0.93 which indicated the presence of a considerable proportion of total variability due to genetic causes, high GA 51.5 - 62.7 per cent for seed yield per plant. σ^2e was very low for days to maturity and protein content. The difference between GCV and PCV of variability was very small.

Parameshwarappa *et al.* (2011) carried out investigation on chickpea germplasm lines representing minicore collection obtained from ICRISAT, Patancheru (A.P.) for assessing genetic variability under three environments. Considerably high variability was observed for most of the productivity related traits in E_3 (irrigated 2005-06). This was evidenced by high range of mean performance for different traits in E_3 compared to E_1 (rainfed 2004-05) and E_2 (rainfed 2005-06). Moderately high heritability and genetic advance (GA) was observed for much productivity related traits under E_3.The higher PCV, although heritability was reduced or remained same as that under E_2. These findings revealed the importance of productivity related traits giving more response under E_3 than E_1 and E_2 for better expression for CI in chickpea.

Dar *et al.* (2012) carried out studies under field conditions to estimate genetic variability and interrelationship among various yield components in thirty diverse germplasm lines of chickpea. High heritability with moderate to high genetic

advance was recorded for 100-seed weight, seed per plant and seed yield per plant. Correlation and path analysis indicated that number of pods per plant, number of branches per plant; plant height and 100-seed weight could be useful as selection indices. The high PCV and GCV were recorded in 100-seed weight followed by number of pods per plant, seed yield plant height and days to 50% flowering.

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

Shrivastava *et al.* (2012) carried out investigation to identify superior genotypes of chickpea on the basis of yield and milling quality traits grown under rice follow condition during genetic coefficient of variation, heritability and genetic advance were observed. Seed yield shared positive and significant association with harvest index number of pod per plant, primary branches per plant and secondary branches per plant. High GCV and PCV were shown by 100-seed weight, seed yield per plant, number of pods per plant, harvest index, and low values recorded for days to 50% flowering.

2.2 Correlation and path analysis

In the improvement of any crop, the knowledge of association of one or more characters associated with yield is useful in selecting the individual. Such association between plant characters is statistically elaborated by correlation coefficients. But the correlation between the dependent and independent characters and the direct and indirect effects of the independent characters are completely separate things. Sometimes, the correlation between two characters may be highly positive but the direct effect of the independent characters on the dependent one may be negative. Hence, mere correlation can not serve the purpose of selection in crop improvement programme.

Therefore, the method of partitioning the direct and indirect effects of the independent characters on the dependent character i.e. path coefficient analysis was detailed by Wright (1921).

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

2.2.1 Correlation and path analysis in chickpea

Maloo and Sharma (1987) recorded data on seed yield per plant and seven yield related traits for 21 diverse varieties of gram and from path analysis it was observed that pods per plant had the highest direct effect on seed yield followed by 100 seed weight and days to flowering.

Paliwal *et al.* (1987) 100 seed weight had the highest positive direct effect on yield, followed by pods per plant, seeds per pod and days to 95 per cent maturity. The seed yield per plant was positively correlated with plant height, days to 95 per cent maturity and days to 50 per cent flowering. Pods per plant

and seeds per pod were recommended as selection criteria to improve the yield.

Jivani and Yadarendra (1988) studied correlation and path analysis in forty two genetically diverse chickpea genotypes. Genotypes planted on three dates and showed that yield was significant positively correlated with branches per plant (r = 0.2), pods per plant (r = 0.4), 100 seed weight (r = 0.3) and harvest index (r = 0.3). It was suggested that branches and pods per plant, 100 seed weight and harvest index could indirect selection for improving seed yield.

Khorgade (1988) reported that seed yield was significant and positively correlated with 100 seed weight, number of seeds per pod. Path analysis indicated that selection would be based on branches, pods per plant and 100 seed weight.

Reddy and Rao (1988) observed that seed and pod numbers per plant were positively associated with yield per plant and path coefficient analysis indicated positive direct influence of seed number per plant and 100 seed weight on yield.

Gupta and Krishna (1989) studied association and path analysis in F_2 generation of ten crosses of chickpea and found that seed yield was positively correlated with pods per plant followed by branches per plant. Correlations of these traits among themselves were also positive but non significant in most of the population studied. Path analysis revealed that, seeds per plant and 100 seed weight were the component characters of seed yield in chickpea. Therefore, while selecting plants from segregating generations; greater emphasis should be given on seeds per plant and 100 seed weight.

Tagore and Singh (1990) studied two hundred associations accessions of *Cicer arietinum* under normal (N) and better (B) input situation. Seed yield was significantly and positively associated with primary branches, pods per plant, seeds per plant, 100 seed weight and harvest index under B. Correlation of yield per plant with number of primary branches, seeds per pod and 100 seed weight was stronger under B than under N. Number of primary branches had the greatest direct effect on yield followed by harvest index, pods per plant, 100 seed weight and plant height under B.

Jadhav *et al.* (1992) observed that seed yield had highly significant positive association with yield contributing characters except plant height suggesting that all these characters had certain inherent relationship with seed yield. Path coefficient analysis indicated that dry matter production per plant had a maximum positive direct effect on seed yield followed by number of pods and seeds per pod, while plant height, number of branches and weight of root nodules per plant had a negative direct effect on seed yield.

Jain *et al.* (1992) studied multiple correlation and regression in fourteen varieties of Bengal gram and indicated that a combination of two or three variables *viz.,* seed weight, seed number, pod number, branches per plant, number of days to first flowering and number of days to maturity were better than other combinations of the character for the improvement of gram.

Lal *et al.* (1993) studied correlation and path analysis for seven yield components in 59 genotypes of chickpea. Seed yield was significantly and positively correlated with pod number and plant height and revealed significantly negative correlation

with 100 seed weight. Pod number had the most direct effect on yield followed by plant height.

Varghese *et al.* (1993) observed significant positive correlation of seed yield with pod weight (0.99), biological yield (0.95), pods/plant (0.64) and 100 seed weight (0.53) and significant negative correlation with harvest index (-0.73). Path analysis indicated high positive direct effects of pod weight (1.20), shelling percentage (0.22), biological yield (0.07) and harvest index (0.05) on seed yield. Pods per plant and 100 seed weight influenced seed yield via pod weight. Hence, pod weight, 100 seed weight and pods per plant are considered as important yield components in selection for better genotypes in grams.

Arora and Kumar (1994) studied correlation and path analysis in 40 genotypes of chickpea and showed that seed yield per plant had significant and positive association with biological yield per plant, pods per plant, plant height, 100 seed weight and plant spread. Path coefficient analysis indicated that biological yield, pods per plant, harvest index and 100 seed weight had the highest direct effect on seed yield.

Deshmukh and Patil (1995) reported a significant positive association of seed yield with plant height, branches per plant, 100 seed weight, pods per plant and biological yield per plant showed highly significant positive association with seed yield. Plant height showed highly significant association with pods per plant.

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

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

Khedar and Maloo (1999) derived information on yield correlations from path analysis of data on 7 yield related traits in 40 genetically diverse genotypes of chickpea. Seed yield was significant and positively correlated with pods per plant, primary branches per plant and 100 seed weight. Path analysis indicated that pods per plant had the highest direct effect on seed yield followed by seeds per pod, 100 seed weight and primary branches per plant.

Guler *et al.* (2001) examined five chickpea lines for relationships between the yield and yield components. In the studied characteristics, significant positive relationships were found between the number of seeds per pod and the number of pods per plant; and seed yield per unit area. Significant negative relationships were determined between the number of pods per plant and 100 seed weight; between the number of seed yield per unit area and 100 seed weight. The total determining coefficients linking seed yield per plant and seed yield per unit area were 0.773 (77.3 %) and 0.488 (48.8 %), respectively. The total

determining coefficient related to 100 seed weight was 0.896 (89.6 %) in the same model.

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

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

Muhammad Arshad *et al.* (2004) studied variability, heritability, genetic advance, correlation coefficient and path coefficient for yield and its components in 24 advance lines of chickpea. High heritability with low genetic advance of days to flowering, days to maturity and 100 seed weight indicated the influence of dominant and epistatic genes for these traits. High

heritability of secondary branches and biological yield coupled with high genotypic advance revealed that additive gene effects are important in determining these characters. Grain yield had positive and significant correlation with plant height, pods per plant, 100 seed weight and biological yield. High direct effects were contributed by biological yield and harvest index although the later had negative association with grain yield.

Talebi *et al.* (2007) carried out correlation and path analysis of yield and yield components of chickpea under dryland condition. 36 genotypes were tested during the 2005-06 season for their yield performance. In the examined characteristics, positive and significant relationship were found statistically between 100 seed weight and plant height, number of secondary branches and plant height, days to heading and days to maturity and number of primary and secondary branches, seed yield and number of pods per plant and number of seeds per pod, seed yield and biomass and harvest index. Negative and significant relationships were determined statistically number of pods per plant and 100 seed weight, between seeds per pod and number of secondary branches. Harvest Index had the greatest direct effect on seed yield. (PC = 0.901). Also, its indirect effect on seed yield more positive through plant height, number of pods per plant, number of seeds per pod and biomass, but negative and low through days to heading and maturity, 100 seed weight and number of primary branches. The selection for high seed yield should be based on biomass and harvest index.

Zena *et al.* (2008) studied path coefficient analysis for enhancing yield of chickpea. Thirty six genotypes of chickpea were tested in RBD for total 12 quantitative characters including

yield path coefficient analysis was carried out to determine the effect of various production factors on yield. Biological yield had shown highest direct effect on the seed yield which was followed by test weight, yield index, initial flowering period, maturity periods, secondary branches per plant and per pod seeds respectively. While 50 % flowering period has shown negative direct effect on the yield of gram.

Ali *et al.* (2009) studied twenty chickpea genotypes for evaluation of selection criteria using correlation coefficient and path analysis. The genotype exhibited highly significant differences ($P<0.01$) for all the traits studied. The results of correlation analysis revealed that grain yield per plant had significant genotypic and phenotypic relationship with primary branches, pods per plant and seeds per plant.

Thakur *and* Sirohi (2009) studied correlation and path coefficient analysis in chickpea under different seasons. They studied 53 chickpea genotypes over two seasons to find out association among characters to assess the direct and indirect contribution of nine characters on seed yield. Correlation studies indicated that seed yield per plant exhibited stable positive association with biological yield per plant, pods per plant, primary branches per plant, plant height and harvest index at genotypic and phenotypic levels in individually as well as combined over seasons. Path analysis revealed high positive and direct influence of biological yield per plant with seed yield per plant followed by harvest index and pods per plant in individuals as well as combined over seasons. Therefore, selection for high biological yield and harvest index would lead to high seed yield and selection for pods per plant, primary branches per plant and plant height would facilitate for high biological yield.

Borate and Dalvi (2010) studied correlation and path coefficient analysis for thirteen characters in 30 chickpea genotypes. Character association studies indicated that number of pods per plant, seeds per pod, 100 seed weight, dry matter percentage per plant and days to maturity were having highly significant positive association with seed yield. However, path coefficient analysis revealed that number of pods per plant had highest direct positive effect on seed yield followed by dry matter per plant.

Kobraee *et al.* (2010) carried out investigation of correlation analysis and relationships between grain yield and other quantitative traits in 3 chickpea cultivars on 3 sowing date. A 3 × 3 factorial experiment in RCBD (i.e. Randomized Complete Block Design) format with 3 replications was conducted. The results showed that both sowing date and cultivar had significant effect on seed yield and yield components of chickpea. Early planted chickpea produced the highest plant height distance of first pod from the earth surface, number of sub branches, number of pods per plant, number of seeds per plant, 100 seed weight, grain yield, biological yield and harvest index. There was significant difference between cultivars for seed yield. Results showed that number of seeds per plant, number of pods per plant, plant height and biological yield had the highest positive correlation with grain yield. The number of seeds per plant had high and positive direct effects on seed yield.

2.3 Genetic diversity

2.3.1 Concept of genetic diversity

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

divergence and is independent of size of the sample. It measures a generalized distance between any two pairs of groups and classifies the breeding material into useful groups. The genetic distance has a definite role in an efficient choice of parents for hybridization. Selection of parents based on the extent of genetic divergence has been successfully utilized by different workers in various crops. Genetic divergence is the genetic differences as observed between individuals or genetic stocks with respect to individual trait or array of traits. The inherent variations are called as genetic variations and produce genetic diversity. No consistent relationship was observed between genetic diversity and geographical diversity.

Mahalanobis *et al.* (1936) employed D^2 statistic in detailed study of Anthropometric data of Uttar Pradesh classifying in 23 groups and into three major clusters i.e. Brahmin (B-cluster) of the top of the Hindu social hierarchy comprising nine groups, the Artisan (A-cluster) in the middle consisting of four groups and the Trival (T-cluster) at the 40 bottom consisting of ten groups.

2.3.2 Genetic divergence in chickpea

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

Mishra *et al.* (1987) studied genetic divergence in 36 genotypes and were grouped into 8 clusters. Cluster I had the

maximum number of genotypes. The highest inter cluster distance was observed between cluster V and VII.

Lal *et al.* (1989) assessed thirty strains of chickpea from 8 different countries for 9 yield components. Genetic divergence (D^2) analysis grouped the stains into 6 clusters on the basis of minimum generalised distance. No relationship was noted between geographic origin and genetic diversity.

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

Singh et al. (1990) Correlation and path analysis in segregating generations of chickpea studied Three thousand two hundred and sixty seven *kabuli* chickpea germplasm accessions were grown. Observations were recorded on seed yield and 14 other characters. 41 Correlation and path coefficient analyses were done to find out associations among characters and to assess the direct and indirect contribution of each character to seed yield. Large variation was observed for all the characters studied except days to flowering, days to maturity and protein content. Correlation and path coefficient analyses showed that biological yield and harvest index were the major direct contributors to seed yield.

Sandhu and Gumber (1991) studied genetic divergence in 59 diverse strains of chickpea using Mahalanobis D^2 technique. The material exhibited wide genetic diversity in all the characters studied resulting 12 clusters. The maximum of 28

strains were grouped in cluster I, five clusters (VIII and XII) had only one strain each. Cluster mean for various yield components revealed that three clusters i.e. II, IV and IX had high mean values for seed yield, harvest index, 100-seed weight, seeds per pod and secondary branches while the strains of cluster III and VI had low mean values for pod per pant, seeds per pod and seed yield.

Vijaykumar *et al.* (1991) studied genetic diversity in 104 genotypes of chickpea based on the data of two environments using generalised distance and obtained six clusters comprising all the genotypes. The first cluster was largest with 89 genotypes. They further observed that the clustering pattern was neither related to geographical origin of the genotypes nor to the two cultivar groups *viz.,* '*desi*' and' *kabuli*'.

Kumar and Arora (1992) had grouped 40 genotypes into ten clusters on the basis of D^2 values and they observed that, there was no definite relationship between genetic diversity and geographical distribution.

Singh (1993) studied genetic divergence among 44 *desi* and 16 *kabuli* genotypes of chickpea. The metroglyph index score and 42 the D^2-statistic analysis were applied to select the maximum divergence of the 60 genotypes. The metroglyph index score revealed that the majority of the *kabuli* types were medium to late in flowering and medium in seed yield, whereas the *desi* type were early in flowering and medium in seed yield. For D^2 values, the maximum genetic distances were measured as 10.55 (L-144 and L-214), 13.66 (L-144 and JG-84) and 7.70 (L-532 and No.132) in environments I, II and III, respectively.

Sarvaliya and Goyal (1995) studied genetic divergence among 76 chickpea genotypes and significant variation was found among genotypes for all the characters. On the basis of D^2 analysis, 76 genotypes were grouped in 10 clusters. The cluster I was the largest comprising 35 genotypes of different origin. Cluster II possessed 20 genotypes whereas III and IV accommodated 8 and 4 genotypes, respectively. The clusters V, VI and VII had 2 genotypes each, while the remaining clusters were of single genotype. The intracluster distance was lowest in cluster V (D=6.72) and highest in cluster II (D=15.83). The maximum intercluster distance (D) was observed between cluster V and IX (60.50) followed by cluster VII and X (60.49) while the closest proximity was noticed between cluster I and VIII (19.52). Considerable variations for characters among single and multigenotypic clusters were observed.

Gupta and Krishna (1996) studied genetic divergence among twenty nine diverse genotypes of Bengal gram and the genotypes were grouped into seven different clusters. Comparison of cluster mean for all the characters indicated considerable genetic divergence between the groups. Cluster VI had minimum values of cluster mean for days to flowering, plant height and days to maturity, while the value of 43 cluster mean of this cluster was observed minimum for 100 seed weight. Cluster V had maximum value of cluster mean for plant height, days to maturity, duration of reproductive phase and 100 seed weight; while the mean value of this cluster was observed minimum for number of effective branches, total number of branches and harvest index. The useful segregants would be expected from the crosses of KGD-1169/TAKI-9218, H-90-64/GNG-968 and BKG- 109/GL-88341.

Jethava *et al.* (1996) studied genetic divergence using Mahalanobis's D^2 statistic among 70 genotypes of different ecogeographic regions and revealed considerable diversity. The genotypes were grouped into 16 clusters indicating that the geographic distribution and genetic diversity were not related. Seed yield per plant, number of pods per plant and 100 seed weight contributed maximum to genetic diversity. The cluster XII showed high genetic divergence with cluster XVI and VIII.

Kumar (1997) studied the genetic divergence among 60 genotypes of chickpea for seven developmental characters. The genotypes were grouped into five clusters. Grouping of genotypes in different clusters was not related to their geographical origin. The intracluster D^2 values ranged from 8 to 38.2. Based on mean performance, genetic distance and clustering pattern, hybridization involving parents from clusters II and V may give higher, yielding varieties.

Tripathi (1997) evaluated 100 genotypes of chickpea from several world-wide locations for 13 agronomic characters to study patterns of genetic divergence using multivariate D^2 analysis. The genotypes were grouped into 12 clusters on the basis of yield and yield components. Hybridization among genotypes from the diverse clusters identified will aid breeding for higher yields of chickpea.

Kumar *et al.* (1998) studied the genetic divergence among the 17 chickpea genotypes, 5 each developed through mutation breeding and intra and interspecific hybridization and two standard checks in chickpea. The genotypes were grouped into 5 clusters. Cluster II, I and III had 6, 5 and 4 genotypes, respectively and cluster IV and V had only one genotype each. The genotypes falling in cluster III had the maximum divergence

which were closely followed by those of clusters II and I. The maximum and minimum divergence was revealed between clusters II and V and between III and V, respectively. In general, the cluster II and V exhibited high and low mean values, respectively for most of the characters. It has been suggested that for varietal improvement the hybridization among the genotypes of divergent clusters should be done rather than depending on those genotypes of the cluster having maximum divergence.

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

Singh K.B. *et al.* (1998) Collected data on 228 accessions of 8 annual wild *Cicer* species and 20 cultivated chickpea check lines and were evaluated for diversity in response to 6 of the most serious biotic and abiotic stresses which reduce crop yield and production stability of chickpea.

Sirohi *et al.* (1999) studied genetic divergence in 25 genotypes of chickpea for six yield related traits and the genotypes were grouped into 7 clusters. The cultivars within a cluster showed smaller D^2 values than those belonging to two different clusters. 100-seed weight 45 and seed yield per plant were chiefly responsible for genetic divergence. Based on inter-cluster distances, crossing of cluster IV genotypes with V, VI and VII was suggested to get maximum heterotic effect in F1 and a broad spectrum of variability in the segregating generations to isolate superior individuals for yield and its components.

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

Lal *et al.* (2001) studied the genetic divergence among 33 genotypes of chickpea using Mahalanobis's D^2 statistic and the genotypes were grouped into 5 clusters. The cluster IV was the largest and consisted of 12 genotypes followed by cluster III which had 10 genotypes. The cluster I had 7 genotypes while cluster IV accounted only 3 genotypes. Cluster II was unique in having only one genotype. The grouping pattern did not show any relationship between genetic divergence and geographic diversity. They concluded that the genotypes included in the diverse clusters namely, II and V hold good promise as parents for obtaining potential hybrids and thereby creating greater variability for these characters to improve the yield.

Nimbalkar and Harer (2001) studied genetic divergence among 40 chickpea genotypes from seven countries

comprising of 32 indigenous and 8 exotic and the genotypes were grouped into 16 clusters. D^2 values between all possible pair of 40 genotypes ranged between12.62 to 3979.93. Out of 16 clusters, 10 clusters were monogenotypic. Cluster II was the largest comprising of 12 genotypes followed by cluster I and IV containing 9 and 3 genotypes, respectively. The remaining 3 clusters contained 2 genotypes each. Maximum inter cluster distance was between cluster XVI and III (D=62.50). The clusters IX and X exhibited minimum inter cluster distance (12.15). Maximum intra cluster distance (11.30) was observed for cluster VI indicating heterogeneous nature of the genotypes. Variance of cluster means indicated pods per plant followed by plant height and 100 grain weight were the main traits contributing to the genetic divergence. The tentative breeding programme, based on the moderate genetic distance was suggested.

Noor *et al.* (2003) reported phenotypic and genotypic variances, heritability in broad sense, genetic advance; correlation and path coefficient analysis were conducted for yield and yield components in 30 genotypes of chickpea under rainfed conditions. Medium to high genetic advance was observed for days to flowering, maturity, secondary branches and 100 seed weight, whereas for other characters, low to medium heritability was observed along with low to high genetic advance. Improvement of these traits through direct selection could be limited from germplasm used in the present study. It was concluded that to improve grain yield emphasis should 47 be given on development of chickpea cultivars with higher seed weight and biological yield.

Sandhu *et al.* (2006) studied genetic diversity in 90 genotypes of chickpea was assessed in 3 environments using

Mahalnobis's D^2 statistic. The genotypes were grouped into 10 clusters; 3 of which were more genetically divergent than others. Common genotypes were sorted out within a cluster for combination of environments and pooled data over environments.

Verma *et al.* (2008) studied genetic diversity in 108 genotypes of chickpea were divided into four different groups of cultivars. The plantings of these cultivars were carried out in three diverse and contrasting environments viz. normal, medium and planting. All diverse genotypes were planted in a randomized block design with three replications in a four row plot. Single plant observations were recorded for quantitative traits. Statistical analysis was carried out for superior performance of different traits, which revealed highly significant differences for all the traits under different planting environments.

Dwevedi and Gaibryal (2009) an investigation carried out among the 25 genotypes of chickpea to study the nature and 48 magnitude of genetic divergence using Mahalanobis's D^2 statistics. The data were recorded on ten important quantitative traits from the genotypes raised in RBD having 3 replications. 25 genotypes were grouped into six clusters. There characters viz. harvest Index, 100 seed wt and number of pods per plant contributed maximum in manifestation of genetic diversity.

Malik *et al.* (2010) studied twenty chickpea genotypes for various yield parameters to estimate correlation coefficients and linkage distance. Analysis of variance of yield and its components revealed significant differences between genotypes for six out of nine traits studied. Maximum variations were recorded for pods per plant followed by secondary branches per plant, biological yield and grain yield and harvest index. Highly

significant and positive correlation of grain yield was found with biological yield, secondary branches and number of pods per plant. Secondary branches were positively correlated with number of pods per plant and grain yield per plant where as, it was negatively associated with low grain weight. Cluster I, II and III possessed 8, 5 and 7 genotypes respectively. Means of various traits for each character showed that genotypes with maximum number of secondary branches per plant number of pods per plant, biological yield and seed yield per plant were placed together in cluster III. Genotypes with maximum harvest index and 100 seed weight were placed in cluster II and I respectively.

Moulla *et al.* (2010) showed that effect of location (L.) and season (E) was highly significant (P<0.01) while the interaction among locations, seasons and genotypes (LxExG) was not significant (P>0.05). The heritability for protein content varied from (0.83%) to (0.93%) which indicated the presence of a considerable proportion of total variability due to 49 genetic causes, high GA 51.5 - 62.7% for seed yield per plant. 62e was very low for days to maturity and protein content. The difference between GCV and PCV of variability was very small.

Tomar *et al.* (2011) presented investigation aimed at ascertaining the nature and the magnitude of genetic diversity among the set of chickpea genotypes. Forty five genotypes of chickpea were grown in twelve environments and subsequently analyzed in order to select potential parents for hybridization. Based on D^2 values, 45 genotypes were grouped into eight clusters. Cluster V consisted 8 genotypes followed by cluster VIII and VI, which had 7and 6 genotypes, respectively. Maximum intracluster distance (2.89) was observed in cluster VIII, followed by cluster VI (2.58), cluster IV (2.34), cluster I (2.33). Maximum

intercluster distance was noticed between cluster IV and VIII (6.38). Crossing between genotypes from the cluster IV and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

Sewak *et al.* (2012) observed that genetic diversity among 495 accessions of chickpea collected from different agro-ecological zones of India was assessed for several qualitative and quantitative traits. It was observed that primary branches had highly significance positive genotypic correlation with 100 seed weight and seed yield per plant. Days to maturity showed positive genotypic association with 100 seed weight, primary branches and seed yield per plant. Days to 50% flowering showed significant negative genotypic association with primary braches and 100 seed weight.

3. MATERIAL AND METHODS

The present investigation entitled, "Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)" was conducted at Pulses Improvement Project, MPKV, Rahuri, during *rabi* season of 2011-12. The details of the material used, methods adopted and statistical analysis followed during the investigations are described below.

3.1 Material

The experimental material used for study consisted of 50 genotypes of chickpea which were obtained from the NBPGR, New Delhi. The list of genotypes is given in Table 1.

3.2 Experimental design

During *Rabi* 2011-12, 50 genotypes and 2 varieties of chickpea and Vishal, Digvijay as checks were evaluated in a Randomized Block Design with two replications. Each genotype was sown in single row of 4 m length with spacing 30 cm between row and 10 cm within rows. 50 genotypes were collected from NBPGR, New Delhi.

Table 1. List of 52 genotypes of Chickpea

IC-275426	IC-275444	IC-327030	IC-327045
IC-275427	IC-275445	IC-327031	IC-327046
IC-275428	IC-275446	IC-327032	IC-327047
IC-275429	IC-327015	IC-327034	IC-327048
IC-275430	IC-327016	IC-327035	IC-327052
IC-275432	IC-327018	IC-327036	IC-327053
IC-275433	IC-327019	IC-327037	IC-327054
IC-275434	IC-327020	IC-327038	IC-327056

IC-275435	IC-327021	IC-327039	IC-327057
IC-275437	IC-327024	IC-327040	IC-327060
IC-275438	IC-327026	IC-327041	IC-327061
IC-275440	IC-327027	IC-327043	Digvijay (Check)
IC-275443	IC-327029	IC-327044	Vishal (Check)

3.3 Cultural practices

The land selected for the experiment was medium black which was brought to fine tilth. The fertilizer @ 25 kg N/ha in the form of urea and 50 kg P_2O_5/ha in the form of single super phosphate were applied as a basal dose at the time of sowing. In order to facilitate easy and better germination, a light irrigation was given after sowing.

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

3.4 Observations recorded

Five competitive plants per genotype were selected at random for recording observations on following characters except days to 50% flowering and days to maturity,in each replication and averages were worked out for statistical analysis.

3.4.1 Days to 50 per cent flowering

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

3.4.2 Days to maturity

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

3.4.3 Plant height (cm)

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

3.4.4 Number of primary branches per plant

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

3.4.5 Number of secondary branches per plant

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

3.4.6 Number of pods per plant

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

3.4.7 Number of seeds per pod

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

3.4.8 100 seed weight (g)

It was recorded by weighing randomly selected 100 seeds.

3.4.9 Seed yield per plant (g)

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

3.5 Statistical methodology

3.5.1 Assessment of variability

a. Analysis of variance

The data collected on individual characters were subjected to the method of analysis of variance commonly

applicable to the Randomized Block Design (Panse and Sukhatme, 1967).

The genotypic mean square (GMS) was tested against error mean square (EMS) by 'F' test for n_1 = (g-1) and n_2 = (r-1) (g-1) degrees of freedom, where, g = number of genotypes and r = number of replications. The characters showing significant differences were subjected to further analysis.

b. Estimation of mean and range

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

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

Where, $\overline{X}$ = Mean of character

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

n = Number of observations

The lowest and highest value of mean of each character represents the range.

c. Estimation of components of variation

The analysis of phenotypic and genotypic variances was calculated by as per Johnson *et al.* (1955) as below.

Environmental variance (σ^2_e) = EMS

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

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d. Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952).

i) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2_g}}{\overline{X}} \times 100$$

Where,

σ^2_g = Genotypic variance and,

$\overline{X}$ = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2_p}}{\overline{X}} \times 100$$

Where,

σ^2_p = Phenotypic variance,

$\overline{X}$ = Mean of character

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

e. Estimation of heritability (B.S.) (h^2)

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

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

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

Low heritability = < 10 %

Moderate heritability = 10-30 %

High heritability = > 30 %

f. Genetic advance (G.A.)

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

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

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

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

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

Where,

G.A. = Genetic advance

$\overline{X}$ = Character mean

GA (As percentage of mean) were classified as

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

3.5.2 Correlation

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

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

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

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

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

The phenotypic correlation coefficient (rp) was calculated as:

$$r\ p_{1.2} = \frac{\text{COV. } p_{1.2}}{\sqrt{(\sigma^2\ p_1).(\sigma^2\ p_2)}}$$

Where,

r $p_{1.2}$ = Phenotypic correlation coefficient between character 1 and 2

COV. $p_{1.2}$ = Phenotypic covariance between character 1 and 2

$\sigma^2\ p_1$ & $\sigma^2\ p_2$ = Phenotypic variance of character 1 and 2 respectively.

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

The genotypic correlation coefficient (rg) was calculated as:

$$r\ g_{1.2} = \frac{\text{COV. } g_{1.2}}{\sqrt{(\sigma^2\ g_1).(\sigma^2\ g_2)}}$$

Where,

$rg_{1.2}$ =Genotypic correlation coefficient between character 1 and 2

COV. $g_{1.2}$ = Genotypic covariance between character 1 and 2

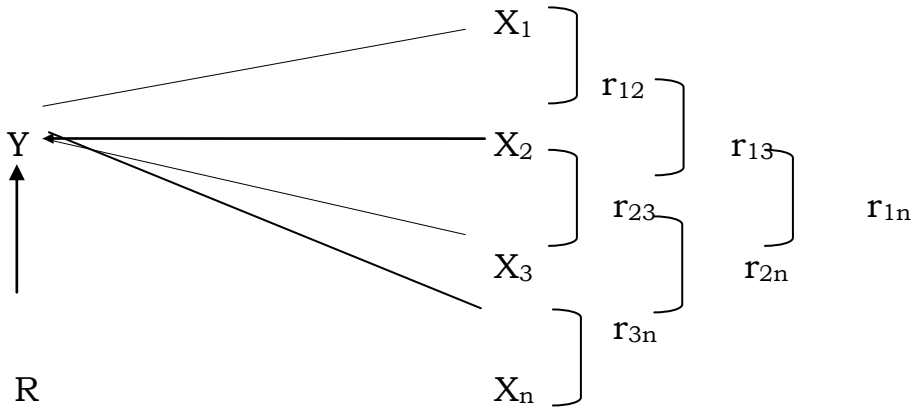
$\sigma^2 g_1$ & $\sigma^2 g_2$ = Genotypic variance of character 1 and 2 respectively.

The significance of correlation was tested by't' test.

3.5.3 Path coefficient analysis

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

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



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

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

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

Where,

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

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

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

Matrix A Matrix B C

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

Where,

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

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

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

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

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

Where, i = 1 to 10

j = 1 to 10

P_{iy} = P_{1y}, P_{2y}, ……, P_{ny}

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

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

Where,

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

P_{1y}, P_{2y}, ……, P_{ny} = Path values

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

3.5.4. Genetic diversity

D^2 analysis

The analysis of divergence was carried out by D^2 statistics of Mahalanobis's (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per R.B.D., to test significance of differences among the genotypes. The characters exhibiting 61 significant differences were only used for further analysis of D^2 statistic. The analysis of co-variance for the character pairs, based on plot averages was carried out (Cochran and Cox, 1957)

a. Wilk's criteria

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

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

Where,

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

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

Significance of Wilk's criteria (Λ) was estimated by X^2 as,

$$X^2_{pq} = V = - m \cdot \log_e \Lambda$$

Where,

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

$n = N_1 + \ldots\ldots + N_{k-1}$

= Total number of observations - 1

P = Number of significant characters

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

k = Number of varieties/genotypes

Calculated X^2 values were tested against X^2 table value at pq degrees of freedom.

b. Mahalanobis' generalized distance (D^2)

The generalized distance between any two populations is defined as :

$$\Delta_2 = \Sigma\Sigma\lambda ij.\ \delta i.\ \delta j$$

Where,

λij = Reciprocal matrix to the common dispersion matrix

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

δj = Transpose δi

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

$$D^2 = \Sigma\Sigma\delta ij\ .\ di\ .\ dj$$

Where,

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

Since this formula for computation requires the inversion of eleventh order determinant and then evaluation of 11 (11+1)/2 terms, whose sum is D^2.

c. Computation of D^2 values

For each combination, mean deviation i.e. $\overline{Yi_1} - \overline{Yi_2}$ with i = 1, 2, ..., P, was computed and the D^2 was calculated as sum of the squares of these deviations i.e. $\Sigma(\overline{Yi_1} - \overline{Yi_2})$

(For each combination among 60 genotypes D^2 values were calculated. Thus, total 60 (59)/2 numbers of D^2 values were worked out).

d. Determination of population constellations

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

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

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

e. Average intra-cluster distance

The intra-cluster distances were calculated as

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

Where,

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

n = number of genotypes included in a cluster

f. Average inter-cluster distances

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

$$D^2 = \frac{\Sigma Dij^2}{(ni.\ nj)}$$

Where,

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

ni = Number of genotypes in cluster i and

nj = Number of genotypes in cluster j

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

g. Cluster diagram

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

4. EXPERIMENTAL RESULTS

The results obtained in the present investigation entitled, "Genetic diversity and path coefficient analysis in *chickpea* (*Cicer arietinum* L.)" are presented in this chapter.

4.1 Genetic variability and heritability

The analysis of variance revealed significant genotypic differences for all the characters studied indicating the presence of substantial amount of variability (Table 2.).

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

Sr. no.	**Characters**	**Mean sum of square (M.S.S)**	**Mean sum of square (M.S.S)**
		Genotype	**Error**
		(d.f.=51)	**(d.f.=51)**
1.	Days to 50% flowering	14.64**	0.745
2.	Days to maturity	10.05**	0.551
3.	Plant height	79.59**	1.09
4.	Number of primary branches/plant	0.31**	0.01
5.	Number of secondary branches/plant	3.99**	0.1
6.	Number of pods/plant	101.43**	3.17
7.	Number of seeds/pod	0.01**	0.0006
8.	100 seed weight	11.60**	0.34
9.	Seed yield/plant	16.62**	0.18

* Significant at 5 % level

** Significant at 1 % level

4.1.2 Mean performance and the range of variability

The mean values of genotypes for different characters studies are presented in Table 3., while the estimates of range are given in Table 4.

4.1.2.1 Days to 50% flowering

The variation in days to 50% flowering ranged between 44.5 to 56.5 days. IC-275435 (44.5 days) took least number of days while 56.5 days were taken by IC-275445. The genotypes IC-327037(47.50) and IC-327032(47.50) were observed to be promising for earliness in flowering. The general mean performance of this character was 50.33 days.

4.1.2.2 Days to maturity

The variation in days to maturity ranged between 100 to 111 days. Vishal variety matured in least number of days (100.0) while IC-275428 matured very late (111.0) days. The genotypes IC-327032 and IC-327056, were observed promising for earliness in days to maturity. The general mean performance for this character was 106.67 days.

4.1.2.3 Plant height (cm)

The plant height was maximum in case of IC-327041, while it was minimum in case of IC-327027. The value recorded for maximum height was 58.00 cm while minimum height was 36.3cm. The significant genotypes were IC-275426 and IC-327045. The general mean performance for this character was 47.43 cm.

4.1.2.4 Number of primary branches per plant

Number of primary branches per plant ranged between 3.1 to 5.1, IC-327027 recorded minimum number of primary branches per plant while Vishal variety had the maximum branches per plant. Significant genotypes were IC-

275426 and IC-327045. The general mean performance for this character was 3.92.

4.1.2.5 Number of secondary branches per plant

Number of secondary branches per plant was observed minimum in case of IC-327027, while maximum in case of IC-275426. The lowest value observed was 8.1 while highest was 14.00.The genotypes IC-327052, IC-327061 and IC-275445 genotypes were the significant and the general mean performance for this character was 10.91.

4.1.2.6 Number of pods per plant

Number of pods per plant was ranged between 39.00 to 69.00.IC-275428 was recorded with lowest number of pods per plant while IC-327041 with maximum number of pods per plant than the average mean performance. The genotypes IC-275427 and IC-327061 were observed the significant and the general mean performance for this character was 53.51.

4.1.2.7 Number of seeds per pod

Number of seeds per pod was minimum in case of genotypes such as IC-327015 and IC-275437, while maximum in case of Vishal variety. The lowest number of seeds per pod was 1.00 while maximum seeds per pod were 1.4 and the general mean performance for this character was 1.027.

4.1.2.8 100 seed weight (g)

The variation for 100 seed weight ranged between 18.5 g (IC-327032) to 28.25g (IC-275445). The genotypes IC-327031 and IC-275426 are the significant and the general mean performance for this character was 23.01g.

4.1.2 .9 Seed yield per plant (g)

The mean seed yield per plant among the genotypes studied, ranged between 8.00 g to 20.25 g. The minimum seed

yield per plant was recorded by IC-327032 (8.00 g), while the maximum seed yield per plant was recorded by Vishal variety (20.25 g). The genotypes IC-275426, IC-275427and IC-327041 were significant for the further improvement. The general mean performance for this character was 12.36 g.

4.1.3 Estimates of components of variation

The estimates of genotypic, phenotypic and environmental variances for different character studied are presented in Table 4.

The magnitude of genotypic variance was highest for number of pods per plant (49.12) followed by plant height (39.25). The phenotypic variances, however, ranged between 0.006-52.30, its estimate was of higher magnitude for number of pods per plant (52.30) followed by plant height (40.34). The environmental variances ranged between 0.001-3.17, its estimate was of higher magnitude for number of pods per plant (3.177) followed by plant height (1.09).

4.1.4 Genotypic and phenotypic coefficients of variation

The estimates of genotypic and phenotypic coefficients of variation are presented in Table 4.

Genotypic coefficient of variation (GCV) was highest for seed yield per plant (23.19), followed by plant height (13.20), number of pods per plant (13.09), number of secondary branches per plant (12.66). Whereas, phenotypic coefficient of variation (PCV) was highest in case of seed yield per plant (23.45), followed by number of pods per plant (13.51), and number of secondary branches per plant (13.25).

In general, the phenotypic coefficients of variation (PCV) were greater than genotypic coefficient of variation (GCV).

4.1.5 Heritability and genetic advance

The estimates of heritability in broad sense and genetic advance are presented in Table 4.

The range of heritability in broad sense for the characters studied was between 88.1 to 97.8 per cent. It is evident that almost all the characters exhibited high heritability (> 60 %). Maximum heritability was observed for seed yield per plant (97.8). Genetic advance ranged from 0.177 to 17.93 with the highest estimate in case of number of pods per plant (17.93) and lowest in case of number of seeds per pod (0.177). The heritability and genetic advance as a per cent of mean were higher for seed yield per plant (60.55), number of pods per plant (33.5).

4.2 Correlation studies

The genotypic and phenotypic correlations for nine characters studied are presented in Table 5.

The only significant correlations either in positive or negative direction are described in this chapter.

In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlations.

4.2.1 Association of seed yield with its components

It is revealed from Table 5., that seed yield per plant has significant positive correlation with number of pods per plant followed by number of secondary branches per plant, number of primary branches per plant, number of seeds per pod, seed yield per plant, 100-seed weight, days to 50 % flowering, days to maturity and plant height at both genotypic and phenotypic levels.

4.2.2 Interrelationship of yield components

4.2.2.1 Days to 50% flowering

Days to 50% flowering showed positive genotypic (rg =0.71) and phenotypic (rp =0.65) correlations with days to maturity and 100 seed weight (rg = 0.53, rp = 0.47), number of secondary branches per plant (rg = 0.43, rp = 0.38) number of pods per plant (rg = 0.42, rp = 0.41) while it was significant negatively correlated with number of seeds per pod (rg = -0.04, rp =-0.05) at both the genotypic and phenotypic levels.

4.2.2.2 Days to maturity

Days to maturity exhibited significant positive association with 100 seed weight (rg = 0.28, rp =0.25) number of secondary branches (rg = 0.07, rp =0.06) at both the levels and negative association with number of primary branches per plant (rg = -0.15, rp =-0.15), number of seed per pod (rg =-0.39, rp =-0.35) at both the levels.

4.2.2.3 Plant height

The correlation of plant height with seed yield per plant was significantly positive at both genotypic ((rg = 0.87, rp =0.86) levels. Further, it showed positive correlation with number of pods per plant, number of primary branches per plant, number of secondary branches per plant.

4.2.2.4 Number of primary branches per plant

The number of primary branches per plant showed highly significant positive correlations at both genotypic and phenotypic levels with number of secondary branches per plant (rg = 0.78, rp =0.75), seed yield per plant(rg = 0.72, rp =0.67), number of pods per plant, number of seeds per pod, 100 seed weight.

4.2.2.5 Number of secondary branches per plant

The number of secondary branches per plant showed positive and significant correlation with number of pods per plant (rg = 0.87, rp =0.82), seed yield per plant, (rg = 0.81, rp =0.77), 100-seed weight at genotypic and phenotypic level.

4.2.2.6 Number of pods per plant

The number of pods per plant showed highly significant correlation with seed yield per plant (rg = 0.85, rp = 0.82), while it was positively correlated with 100 seed weight (rg= 0.67, rp = 0.63) at both genotypic and phenotypic level.

4.2.2.7 Number of seeds per pod

The number of seeds per pod was positively correlated with seed yield per plant at both levels (rg = 0.69, rp =0.64), 100-seed weight.

4.2.2.8 100 seed weight

100 seed weight was positively correlated with seed yield per plant (rg = 0.82, rp =0.78).

Among the inter relationship of yield components it is evident that the number of secondary branches and pods per plant were significant and positively associated with each other. Similarly, numbers of primary branches, number of seed per pod were negatively correlated with most of the characters.

4.3 Genotypic path coefficient analysis

To find out the direct and indirect contribution from each of the characters towards seed yield per plant, path coefficient analysis was carried out. The genotypic correlation coefficients being more important were only partitioned into direct and indirect effects which are presented in Table 6.

4.3.1 Seed yield vs. days to 50 % flowering

Days to 50 % flowering showed positive direct effect (0.04) and it had positive indirect effects with almost all the characters except number of seeds per pod thus leading to significant positive correlation with seed yield (0.46).

4.3.2 Seed yield vs. days to maturity

Days to maturity showed positive direct effect (0.10). The positive indirect effect with almost all the characters except number of primary branches per plant thus leading to significant positive correlation with seed yield (0.06)

4.3.3 Seed yield vs. plant height

The plant height showed positive direct effect (0.06) on seed yield. It has positive indirect effect through number of pods per plant (0.06), number of secondary branches (0.05) followed by no. of seeds per pod (0.02). The total correlation with seed yield per plant was positive (0.87).

4.3.4 Seed yield vs. number of primary branches per plant

The number of primary branches per plant showed negative direct effect (-0.03) on seed yield. Its indirect effect through only days to maturity was positive. It has negative indirect effect through no. of secondary branches, no. of pods per plant, 100-seed weight. The total correlation with yield was positive (0.72).

4.3.5 Seed yield vs. number of secondary branches per plant

It showed positive direct effect on seed yield (0.18). Its indirect effect through plant height (0.15), number of pods per plant was highest and positive followed by100-seed weight (0.11), no. of seeds per pod (0.07) and days to 50% flowering (0.07). It showed positive significant correlation with seed yield per plant (0.81).

4.3.6 Seed yield vs. number of pods per plant

Number of pods per plant showed positive and significant correlation with seed yield (0.85). It had positive and high direct effect on grain yield (0.29). The indirect effect through plant height (0.26) and secondary branches per plant (0.25), number of seeds per pod (0.12), were positive.

4.3.7 Yield vs. number of seeds per pod

Number of seeds per pod showed maximum positive direct effect (0.43) on seed yield. Its indirect effects via all the characters are positive. The total correlation with yield was positive (0.69)

4.3.8 Yield vs. 100 seed weight

The 100 seed weight showed positive direct effect on seed yield (0.23). It showed positive indirect effects through days to 50% flowering, days to maturity, plant height and number of primary branches per plant, number of secondary branches per plant and number of pods per plant. The total correlation with yield was positive (0.82)

4.4 Genetic divergence

Genetic divergence analysis is a powerful tool in quantifying the degree of divergence between biological populations and to assess the relative contribution of different components to the total divergence. The present investigation aimed at ascertaining the nature and magnitude of genetic diversity among the set of chickpea genotypes.

4.4.1 Mahalanobis's generalized distance (D^2)

Wilk's criterion showed significant differences between the genotypes for the pooled effect of eleven characters studied (Wilk's criteria X^2= 21856.7 for 459 d.f.), hence, further analysis was done to calculate D^2 values. The D^2 values for all

the possible pairs of comparison between 52 genotypes were calculated.

4.4.2 Clustering pattern of the genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values studied is presented in Table 7.

The 52 genotypes were grouped in six clusters. Cluster I had highest number of genotypes (37) followed by cluster III with 10 genotypes, cluster VI with 2 genotypes, cluster II, IV and cluster V were solitary.

4.4.3 Intra and inter-cluster divergence

The average intra and inter cluster D^2 values and D values are presented in Table 8 and 9, respectively.

The maximum statistical distance (D) was found between the clusters, IV and VI (31.40) followed by the clusters, II and VI (29.93), V and VI (29.85), III and IV (25.91). An examination of intra cluster divergence among the six clusters revealed that, cluster III had maximum intra cluster distance (D=9.26) followed by cluster VI (9.12) while the intra cluster distance among the genotypes of the cluster I was the lowest (7.75). As the clusters II, IV and V were solitary, there was no intra cluster divergence. The mutual relationship among the clusters has been diagrammatically shown in Fig. 4.

4.4.4 Cluster means for different characters

The cluster means for the nine characters studied are presented in Table 10.

A considerable inter-cluster variation was observed among the cluster means for the characters number of pods per plant, 100- seed weight and seed yield per plant.

Cluster means for days to 50% flowering varied from 46.00 (V) to 54.43 (III). The cluster mean for days to maturity

ranged between 100.75 (VI) to 108.35 (III). The highest cluster mean for plant height was (56.33) observed in cluster III and lowest for cluster II (36.3). The cluster mean for number of primary branches was ranged from 3.10 (cluster II) to 4.85 (cluster VI). The cluster mean for secondary branches per plant ranged between 8.10 (IV) to 12.83 (III). The cluster mean for number of pods per plant was observed maximum 64.5 (cluster VI) and it was minimum in cluster II (41.00). The cluster mean for number of seeds per pod was maximum in the cluster VI (1.33) and minimum (1.00) in clusters II, IV, V. The cluster mean value for 100 seed weight was maximum (25.97) in cluster III and minimum (18.50) in cluster IV. The cluster mean for seed yield per plant ranged between 8.00(IV) to 19.63(VI).

The hybridization between the genotypes of same cluster thus, may not provide good segregants. The crosses may attempted between the genotypes of the clusters separated by maximum intercluster distance this can give desirable transgressive segregates. Taking into account the cluster means for important yield components, the various clusters which can provide the desired parents for further hybridization programme, for improvement in characters are listed below.

Cluster I	:	IC-275429, IC-275430, IC-275440, IC-327029, IC-327035.
Cluster III	:	IC-275426, IC-275427, IC-275445, IC-327024, IC-327031, IC-327041.
Cluster V	:	IC-327056 .

5. DISCUSSION

Plant breeding deals with management of genetic variability. Hence, assessment of genetic variability, study of character association and genetic diversity in the available germplasm is of immense value to design a selection programme and to identify the superior, genetically diverse genotypes to be used as parents in future hybridization programme. It is therefore necessary to classify and utilize this variability systematically for genetic upgradation of biological population. Similarly, the assessment of the magnitude and direction of association between different yield contributing characters especially with yield is useful in selecting desired genotypes on the basis of their phenotypic values. Simple correlation coefficients in this direction are of limiting value. Hence, it is important to study the cause and effect relationship between yield and its component characters through correlation and path analysis studies.

In the present investigation, 52 diverse genotypes of Chickpea collected from Pulses Improvement Project, MPKV Rahuri, were evaluated to assess the amount of genetic variability. Correlation and path analysis were also worked out to study the associations between component characters and the direct and indirect path coefficients of the component characters on yield; and to study the genetic divergence. The results obtained on these aspects are presented in chapter four and are discussed in this chapter under appropriate headings.

5.1 Variability and genetic parameters

There can be little doubt that the existence of genetic variability is advantageous to the evolutionary survival of a species. Yield improvement in any crop can be brought about

through plant breeding but necessary variability upon which selection is to be practiced must be available in the genetic material. Therefore, before proceeding for any plant breeding programme, the plant breeder must survey and assess the variability present with respect to yield and its attributes. The variability for a given agronomic or yield component character can be estimated through variance, coefficients of variability i.e. GCV and PCV, heritability, genetic advance and genetic advance as a per cent of mean.

5.1.1 Range of variability

A wide range of variability was observed for all the characters except number of primary branches per plant and number of seeds per pod. The character number of pods per plant exhibited highest range of variability followed by plant height, days to 50 per cent flowering, days to maturity, seed yield per plant, 100 seed weight. Number of secondary branches per plant showed moderate amount of variability while it was lowest for number of primary branches per plant and number of seeds per pod. Similar results were obtained by Sharma *et al.* (1990), Sandhu and Gumber (1991), Mathur and Mathur (1996), Gumber *et al.* (2002), Borate *et al.* (2010), Malik *et al.* (2010).

5.1.2 Genotypic and phenotypic coefficient of variation

The estimates of GCV and PCV for all the characters studied showed little difference. The magnitude of PCV was higher than GCV for all the characters indicating that the apparent variation is not only due to genotypes but also due to influence of environment. Selection for such traits sometimes may be misleading. The estimates of genotypic as well as phenotypic coefficients of variation in the present study were highest for seed yield per plant followed by plant height, pods per

plant, number of secondary branches per plant, 100-seed weight and number of primary branches per plant.

Mathur and Mathur (1996) reported highest values of GCV and PCV for 100 seed weight. Sable *et al.* (2000) reported high estimates of PCV for seed yield per plant, 100 seed weight and biological yield per plant. Sable et al. (2000) reported high estimates of GCV seed yield per plant, 100 seed weight. While, Gumber et al. (2002) reported high estimates of PCV for seed yield per plant and seeds per pod. Dwevedi and Gaibriyal (2009) also reported maximum GCV and PCV in number of pods per plant. While as Borate *et al.* (2010), also reported highest values for GCV and PCV for number of pods per plant.

5.1.3 Heritability and genetic advance

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicators of heritable portion of the variation (Burton 1952). The broad sense heritability includes the contribution additive gene effects and allelic interaction due to epistasis. Johnson *et al.* (1955) pointed out that in a selection programme heritability values as well as estimates of genetic advance are more useful than heritability alone. Burton (1952) suggested that genetic coefficient of variation and heritability estimates together give better idea about the amount of genetic advance expected through selection.

In the present investigation, seed yield per plant (97.8 %) followed by plant height (97.3%) and 100-seed weight (94.3%) and all other characters showed high estimates of heritability (b.s.) of all attributes. High heritability coupled with high genetic advance (as % of mean) was observed for number of pods per plant, plant height, number of primary and secondary branches

per plant, seed yield per plant and 100 seed weight indicating that these traits are under control of additive gene action and potential possibilities exist for the improvement of these traits through simple selection where findings supported by similar noting of Dumbre *et al.* (1984), Maloo and Sharma (1987), Samal and Jagdev (1989), Arora (1991), Sable *et al.* (2000), Gumber *et al.* (2002), Borate *et al.* (2010) and Dar (2012). Moderate to low genetic advances for other traits was due to low genetic variability. For characters *viz.,* days to 50 per cent flowering, number of seed per pod coupled with moderate genetic advance (as % of mean) indicating governance by additive gene action and selection of traits could be effective for desired genetic improvement. Similar results were obtained by Gumber *et al.* (2002), Moulla (2010).

A character day to maturity was observed with high heritability associated with low genetic advance which is an indication of dominant and epistatic nature of inheritance. High heritability is being exhibited due to favourable influence of environment rather than genotype. Hence, giving limited scope for further improvement through selection for the characters. These findings are in conformity with Sharma *et al.* (1990), Sable *et al.* (2000) Gumber *et al.* (2002) and Dar (2012).

5.2 Correlation studies

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

The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown. Even though the material used is same, the environment including fertilization, plant population, cultural practices changes the value of correlation coefficient considerably. All correlations are greatest upon poorer soils and increased fertility tends to decrease the variability (Ramiah and Rao, 1953).

The significant positive correlation was observed between seed yield per plant and plant height and number of pods per plant. These results are in agreement with Arora and Kumar (1994) and Deshmukh and Patil (1995).

It was revealed from the present study that the genotypic correlation coefficients between most of the characters were higher in magnitude than the phenotypic correlation coefficient indicating strong inheritant association between various characters studied and that the genotypic expression of the correlation was comparatively less influenced by the environmental conditions. Similar findings were also reported by Singh *et al.* (1994) and Sharma and Maloo (1987).

The simple correlation coefficient of yield and its components estimated in this study indicated that most of the traits in present investigation were positively and significantly correlated with yield(Table.5). This indicated that strong inherent association between various characters studied and forms a sound base for their practical implication. The correlation coefficient among different characters revealed that seed yield had significant positive correlation with plant height, number of

pods per plant, number of secondary branches per plant and 100-seed weight.

The significant positive correlation was reported between seed yield per plant followed by number of secondary branches per plant, number of pod per plant, number of seeds per pod; 100 seed weight, days to maturity, days to 50 per cent flowering and plant height. These results are in agreement with Paliwal *et al.* (1987), Tagore and Singh (1990), Deshmukh and Patil (1995), Muhammad Arshad *et al.* (2004), Talebi *et al.* (2007), Ali *et al.* (2009) and Kobraee (2010).

Among the yield components, number of primary and secondary branches per plant and number of pods per plant showed significant positive correlation with such other very strong association of primary and secondary branches per plant was noticed through the highly significant positive values of correlation coefficients. Both these characters were also strongly associated with the number of pods per plant. This indicates the simultaneous improvement of these characters through selection. The importance of this association as also reported by Singh *et al.* (1994) and Sandhu (1991).

5.3 Path coefficient analysis

It provides basis for selection of superior genotypes from the diverse breeding populations. Seed yield is the product of interaction of component traits. Apart from correlation studies, path coefficient analysis is important to obtain information about different ways in which the component characters influences the seed yield.

Results showed that the number of seeds per pod with direct effect (0.43) was greatest factor affecting seed yield. Therefore, for selection programs for improving seed yield in

chickpea genotypes, number of seeds per pod can be used as a selection index. In the present investigation path coefficient analysis revealed that number of seeds per pod had highest direct effect on seed yield followed by number of pods per plant, number of secondary branches per plant, days to 50 per cent flowering and plant height.

These direct effects are mainly responsible for significant positive association of these characters with seed yield per plant. The seed yield per plant showed significant positive association with days to maturity, plant height, number of seeds per pod and 100 seed weight which have contributed their higher indirect effect via number of secondary branches per plant and number of pods per plant which are similar to finding of Tagore and Singh (1990), Tripathi *et al.* (1995), Jeena and Arora (2002), Noor *et al.* (2003) and Talebi *et al.* (2007).

In the present study, the low residual effect (0.2102), suggested that the characters included in the study were sufficient to exploit the variability in dependent variable, the seed yield.

Based on findings of the present investigations, it can conclude that genotypes had a wide range of variability for almost all the characters studied and can be utilized for yield improvement through improvement of component traits and also involve diverse lines in crossing programme.

The correlation and path analysis studies revealed that plant height, number of secondary branches per plant, number pods per plant, 100-seed weight is important yield determining traits and they should be focus of attention while selecting desirable genotypes for higher seed yield in chickpea. So selection pressure may be applied on plant height, number of

secondary branches per plant, number pods per plant, number of seeds per pod, 100-seed weight and it will be helpful for improving the seed yield and for the development of new high yielding varieties in chickpea.

5.4 Genetic divergence

Genetic divergence which is due to genetic factors is the basis for heritable improvement. The plant breeder has always, therefore, been fascinated by great amount of diversity in crop plants. The precise information about the genetic divergence therefore, is crucial for productive breeding programme. Genetically diverse parents are known to produce high heterotic effects and consequently give desirable recombinants in breeding material. Multivariate analysis (D^2statistic) is a measure that appraises the genetic diversity quantitatively among a set of genotypes (Mahalanobis, 1928).

5.4.1 Diversity based on a set of nine characters

Pooled data were used to carry out divergence analysis using Mahalanobis D^2 statistic (1936) and fifty two genotypes were grouped into six (6) clusters according to Torcher's method as described by Rao (1952). The estimates of D^2 values ranged from 20.52 to 985.96, this clearly indicated presence of adequate diversity among the genotypes studied. Jain *et al.* (1981), Shrivastava and Gutpa (1982), Dumbre *et.al*, (1984), Dasgupta *et al.* (1987), Khan *et al.* (1987), Samal *et al.* (1989), Sandhu and Gumber (1991), Kumar and Arora (1992), Singh *et al.* (1993), Sarvaliya and Goyal (1995), Gupta and Krishna (1995), Jethava *et al.* (1996), Deshmukh and Patil (1995), Tripathi (1997), Kumar *et al.* (1998), Khan (1999), Sirohi *et al.* (1999), Sivakumar and Muthiah (2000), Lal *et al.* (2001)

and Nimbalkar and Harer (2001) reported wide genetic diversity in chickpea germplasm.

5.4.2 Cluster formation

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for selecting parents for hybridization programme. The theoretical concept behind such grouping is that the genotypes grouped into the same cluster are less diverse from each other than those belonging to different clusters (Rao, 1952). And thus crossing between the genotypes belonging to the same clusters will not give designed that the parents selected for crossing should be from different clusters. Greater the divergence between the two clusters, wider is the genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.,* 1965). Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean for the characters also need due consideration in the crop improvement programme.

The analysis showed significant differences among the genotypes for all the nine characters under study. Based on D^2 values all the genotypes were grouped in into six clusters (Table.8). There appeared sufficient variability for selecting genotypes for future breeding programme. Maximum number of genotypes (37) were included in cluster I followed by cluster III (10) and cluster VI (2) genotypes. The clusters II, IV and V were solitary. The intra-cluster distance value based on D^2 values was maximum in cluster III (D=9.26) indicating that 10 genotypes in cluster III were most divergent or more heterogeneous. Maximum inter-cluster distance was noticed between clusters IV and VI

(D=31.40) followed by II and VI (D =29.93) so genotypes from clusters II, IV and VI may lead to maximum diversity in segregating populations and development of high yielding varieties in chickpea. The pattern of distribution of 52 genotypes in various clusters revealed that there was considerable genetic diversity in the material. The genotypes from cluster IV could be utilized as parent in further breeding programme with desirable genotypes from cluster VI, III.

Mishra and Rao (1990) grouped 117 chickpea genotypes into 13 clusters. The maximum of 93 genotypes were grouped in cluster I. Eleven clusters were solitary. Sarvaliya and Goyal (1995) grouped 76 chickpea genotypes into 10 clusters. The cluster I was the largest comprising of 35 genotypes of different origin. Cluster II possessed 20 genotypes whereas III and IV accommodated 8 and 4 genotypes, respectively. The clusters V, VI and VII had 2 genotypes each, while the remaining clusters were solitary.

Deshmukh and Patil (1995) grouped 50 genotypes of chickpea into 7 clusters. Sivakumar and Muthiah (2000) grouped 126 chickpea genotypes into 7 clusters. Nimbalkar and Harer (2001) grouped 40 chickpea genotypes into 16 clusters. Out of that, 10 were solitary. D^2 values of between all possible pair of 40 genotypes ranged between12.62 to 3979.93. Critical examination of Table 1 and 7 indicated that the genotypes originating in different geographical area could form one cluster, while different genotypes evolved in the same area could be grouped into different clusters. Thus, clustering pattern of the genotypes in the present study revealed that the genetic diversity was not always related to geographical diversity.

Jethava *et al.* (1996) revealed from clustering pattern of the genotypes that genetic diversity was not always related to geographical diversity confirming the present findings. The highest inter cluster distance was found between the clusters X and XI (51.11) followed by the clusters, VI and XI (42.93), VII and XI (42.48), III and VI (42.23), IX and XI (41.61), IV and VI (41.01) and I and XI (40.20). The clustering pattern has clearly suggested the wide diversity among the genotypes. The intra cluster value was highest for cluster IV (18.73) followed by cluster II (15.18), cluster I (13.47) and lowest for cluster VI (13.08). As the clusters III, V, VII, VIII, IX, X and XI were solitary, there was no intracluster divergence. On the basis of cluster means, seed yield per plant, number of pods per plant; 100-seed weight, seed density, cooking time, protein content, starch content and amylose content appeared as the major forces of differentiation.

Nimbalkar and Harer (2001) reported that pods per plant, plant height and 100 grain weight contributed maximum to genetic divergence.

Taking into account the cluster means for important seed yield components, various clusters which can provide the desired parents for hybridization programme for improvement in the respective characters are listed below.

The hybridization between the genotypes of same cluster thus, may not provide good segregants. The crosses may attempted between the genotypes of the clusters separated by maximum inter-cluster distance this can give desirable transgressive segregates. Taking into account the cluster means for important yield components, the various clusters which can

provide the desired parents for further hybridization programme, for improvement in characters are listed below.

Cluster I	:	IC-275429, IC-275430, IC-275440, IC-327029, IC-327035.
Cluster III	:	IC-275426, IC-275427, IC-275445, IC-327024, IC-327031, IC-327041.
Cluster V	:	IC-327056 .

. Simple selection procedure will be effective for the traits such as number of pods per plant, number of secondary branches per plant, 100- seed weight, seed yield per plant as it is controlled by additive genes as evident from heritability (h^2) and genetic advance (G.A.)

6. SUMMARY AND CONCLUSIONS

In the present investigation entitled, "Genetic diversity and path coefficient analysis in chickpea (*Cicer arietinum* L.)," fifty two genotypes of Chickpea obtained from Pulses Improvement Project, M.P.K.V., Rahuri and having their origin from different parts of the country were evaluated, to study the genetic variability present among the genotypes for quantitative and qualitative characters, to study the correlation among various yield attributes, to know the direct and indirect effects of different components characters on seed yield and to study the nature and extent of genetic divergence based on quantitative and qualitative characters among the various genotypes and to provide the basis for selection of parents for the future breeding programme. Fifty two genotypes of Chickpea were evaluated in Randomized Block Design (RBD) with 2 replications. The observations were recorded on days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. The results obtained and conclusions drawn on the results are summarized as below.

Summary

6.1. Variability and genetic parameters

Adequate variability was observed among the genotypes under study with wide range of variation for most of the characters except number of seeds per pod and number of primary branches per plant. The estimates of genotypic as well as phenotypic coefficients of variation were highest seed yield per

plant followed by, number of pods per plant, plant height, number of secondary branches per plant. High heritability estimates associated with high genetic advance as a percentage of mean was observed for seed yield per plant, plant height, number of pods per plant, number of secondary branches per plant, 100-seed weight number of primary branches per plant. This indicates the scope for further selection for improvement in these characters.

6.2 . Correlations

The correlations studies indicated that in most of the cases the genotypic correlation coefficients were found to be of higher magnitude than the corresponding phenotypic ones. It indicates that the strong inherent association between various characters studied and that genotypic expression of correlation was comparatively less influenced by the environmental conditions. Further, the correlation studies indicated the importance of number of pods per plant, number of secondary branches per plant and 100 seed weight through selection is expected to result in the improvement of seed yield per plant as a result of expected correlated response, because significant positive association of these characters with seed yield was observed.

6.3. Path coefficient analysis

Results showed that the number of seeds per pod with direct effect (0.43) was greatest factor affecting seed yield. Therefore, for selection programmes for improving seed yield in chickpea genotypes, number of seeds per pod can be used as a selection index.

The correlation and path analysis studies revealed that plant height, number of secondary branches per plant, number pods per plant, 100-seed weight are the important yield determining traits and they should be taken into consideration while selecting desirable genotypes for higher seed yield in chickpea.

6.4. Genetic divergence

The D^2 values showed adequate genetic diversity among the genotypes studied. On the basis of D^2 values all the genotypes were grouped into 6 clusters with varying number of genotypes in the clusters. The clustering pattern of these genotypes does not follow the geographical distribution. The maximum genetic distance was found between the clusters IV and VI (31.40).

Cluster formation

The aim of cluster formation and measuring intra and inter cluster divergence is to provide the basis for selecting parents for hybridization programme. The theoretical concept behind such grouping is that the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to different clusters. And thus, crossing between the genotypes belonging to the same clusters will not give desired improvement, hence, the parents selected for crossing should be from different clusters. Greater the divergence between the two clusters, wider is the genetic diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis. Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean

for the characters also need due consideration in the crop improvement programme. In the present investigation, the cluster means for the nine characters studied are presented in Table 10.

A considerable inter-cluster variation was observed among the cluster means for the characters number of pods per plant, 100- seed weight and seed yield per plant. Cluster means for days to 50% flowering varied from 46.00 (V) to 54.43 (III). The cluster mean for days to maturity ranged between 100.75 (VI) to 108.35 (III). The highest cluster mean for plant height was (56.33) observed in cluster III and lowest for cluster II (36.3). The cluster mean for number of primary branches was ranged from (3.10) cluster II to cluster VI (4.85). The cluster mean for secondary branches per plant ranged between 8.60 (IV) to 12.83 (III). The cluster mean for number of pods per plant was observed maximum 64.5 (cluster VI) and it was minimum in cluster II (41.00). The cluster mean for number of seeds per pod was maximum in the cluster VI (1.33) and minimum (1.00) in clusters II, IV, V. The cluster mean value for 100 seed weight was maximum (25.97) in cluster III and minimum (18.50) in cluster IV. The cluster mean for seed yield per plant ranged between 8.00(IV) to 19.63(VI).

The hybridization between the genotypes of same cluster thus, may not provide good segregants. The crosses may be attempted between the genotypes of the clusters separated by maximum intercluster distance, this can give desirable transgressive segregates. Taking into account the cluster means for important yield components, the various clusters which can provide the desired parents for further hybridization programme, for improvement in characters are listed below.

Cluster I	:	IC-275429, IC-275430, IC-275440, IC-327029, IC-327035.
Cluster III	:	IC-275426, IC-275427, IC-275445, IC-327024, IC-327031, IC-327041.
Cluster V	:	IC-327056.

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8. VITA

Miss. Shweta Ramesh Giri

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of
MASTER OF SCIENCE (AGRICULTURE)
in
GENETICS AND PLANT BREEDING
2013

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- **Major Field :** Genetics and Plant Breeding

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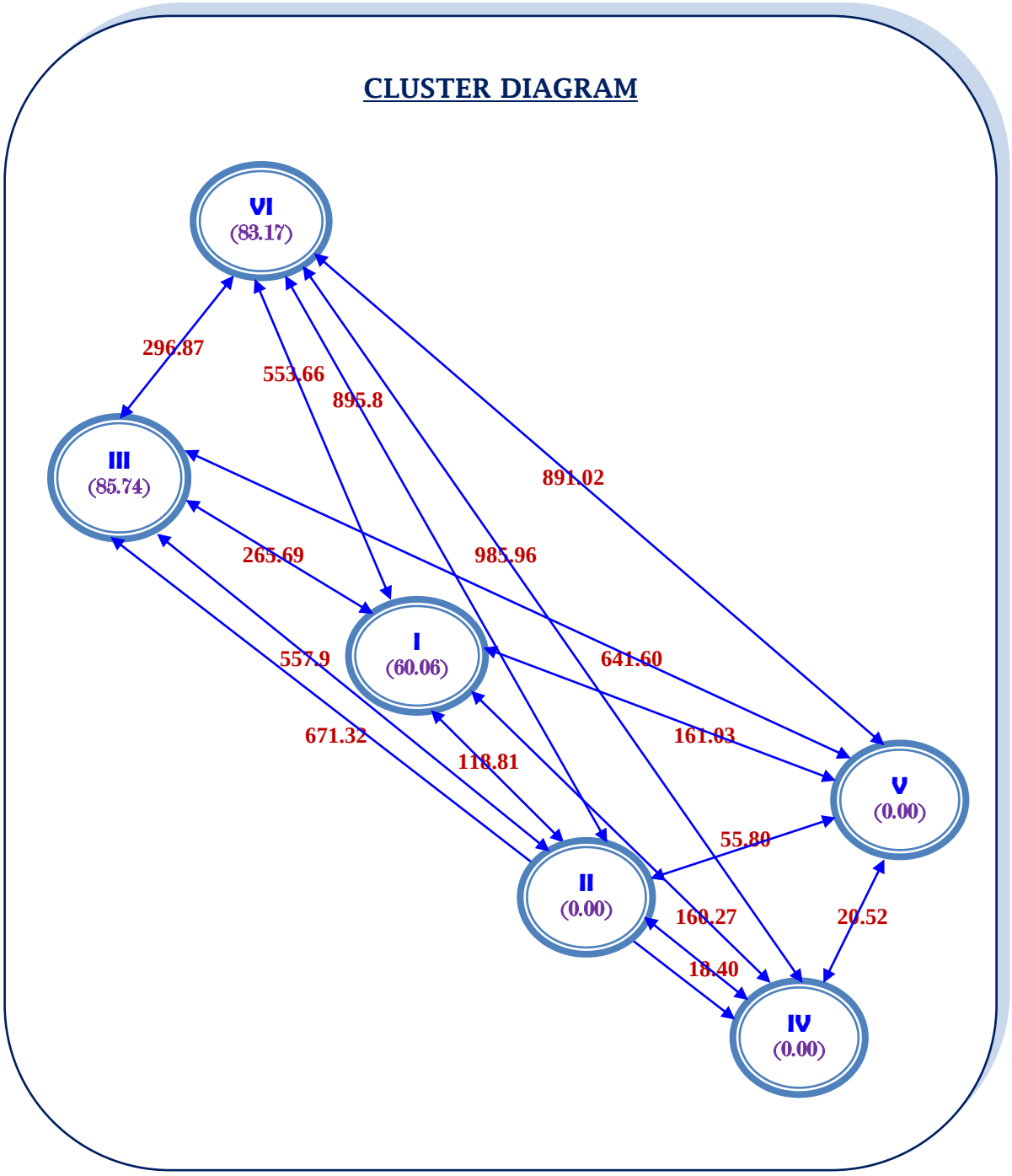
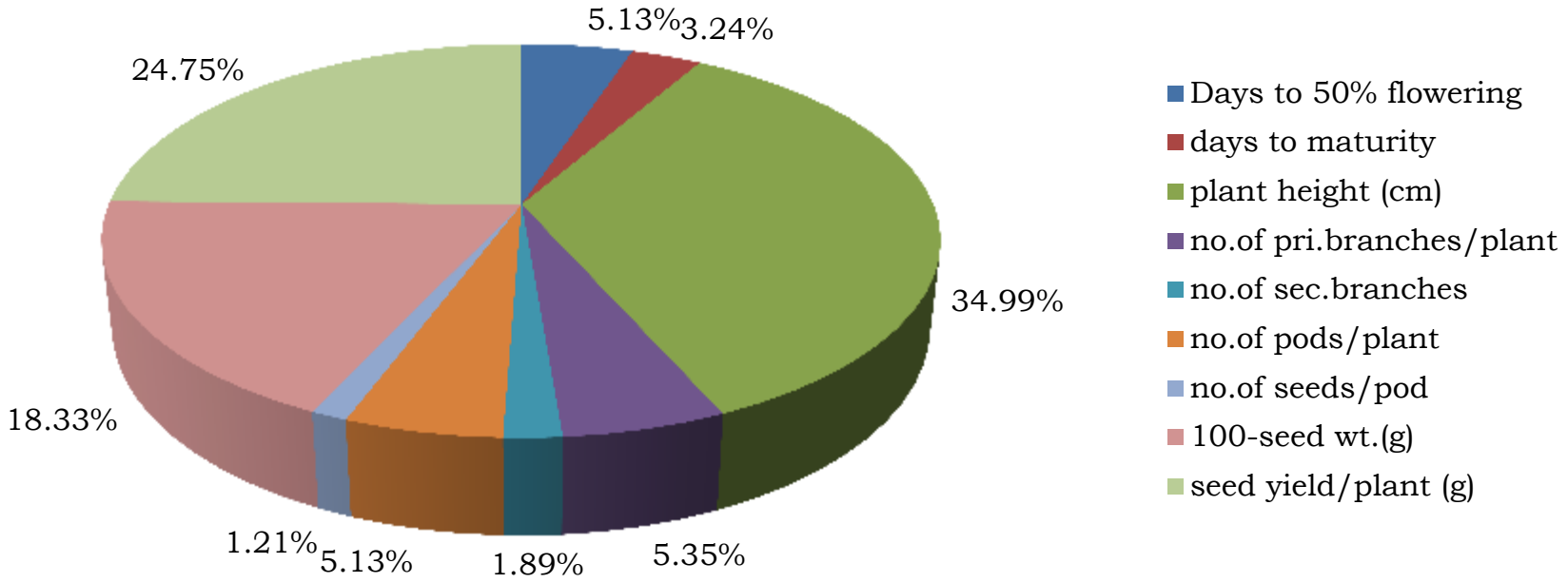


Fig.4. A cluster diagram showing interrelationship between six clusters in chick pea.

Fig.5.Percent contribution of nine characters to the total genetic diversity in chickpea



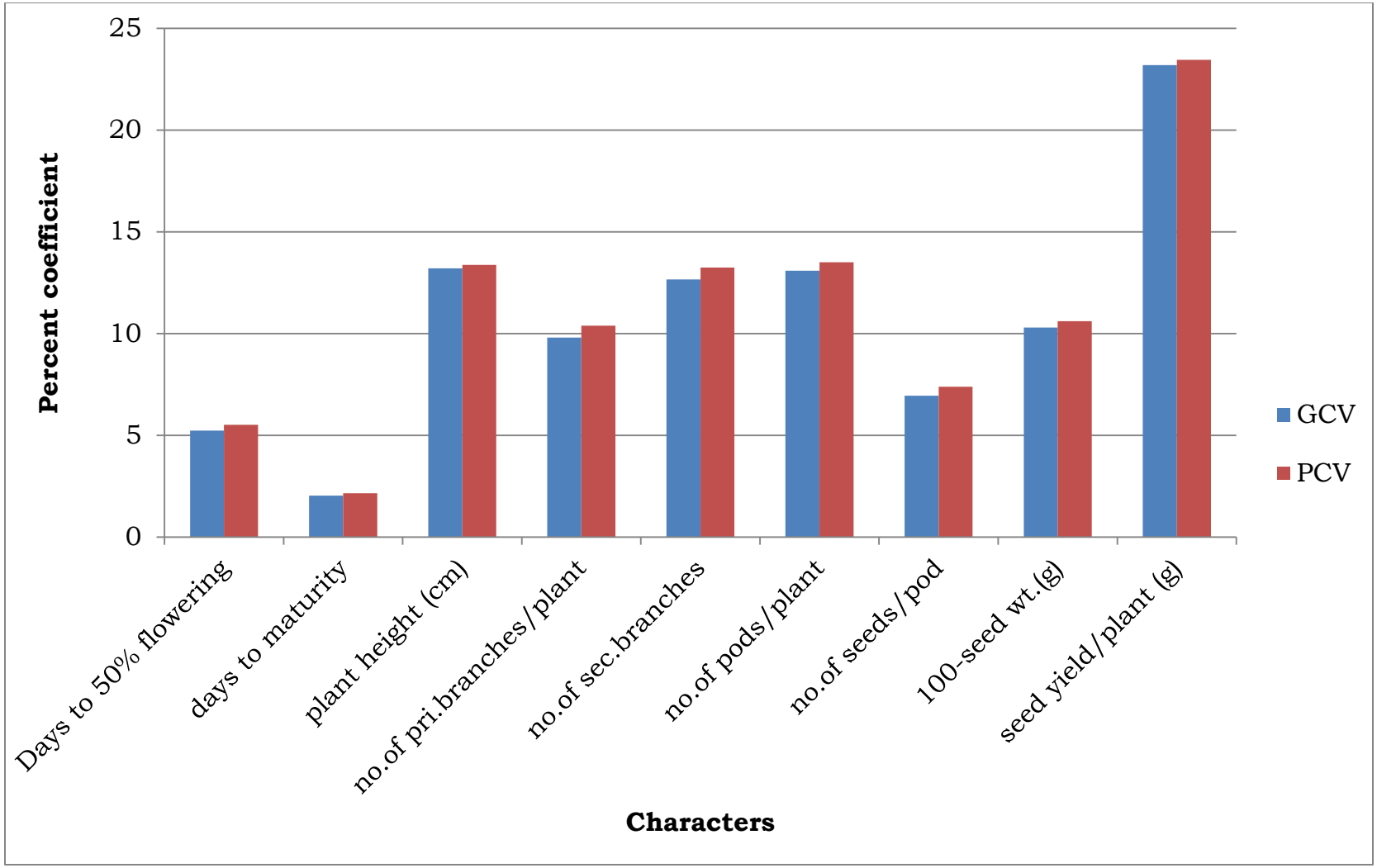


Fig.1 Graphical comparison of GCV and PCV of nine characters

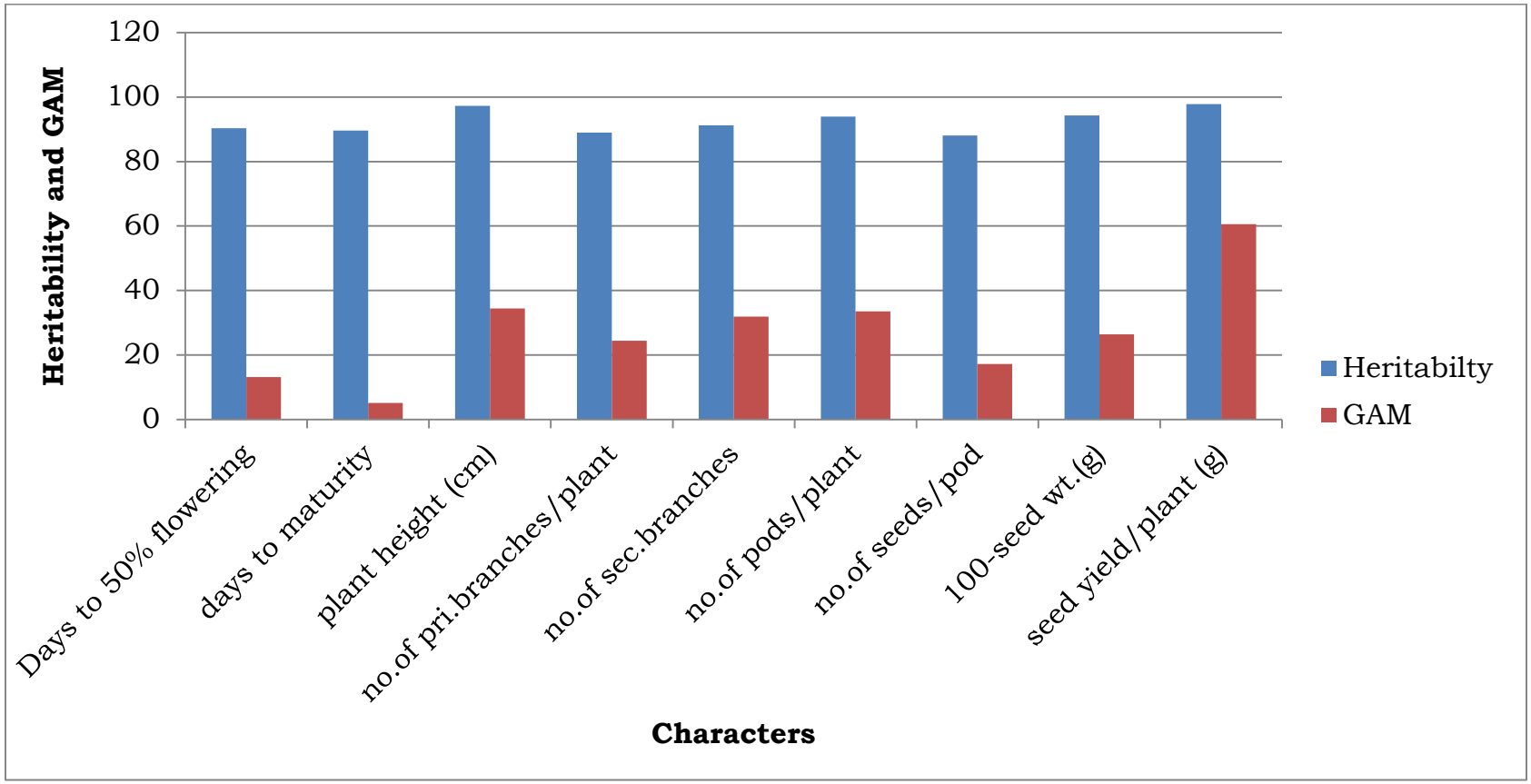


Fig.2 Graphical comparison of heritability and expected genetic advance of nine characters in chickpea

Table.6. Direct and indirect effects (genotypic) of 8 causal variables on seed yield in chickpea

Characters	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/ plant	No. of seeds/pod	100-seed wt.	Coeff. for seed yield/ plant
Days to 50% flowering	**0.04**	0.02	0.02	0.002	0.01	0.01	-0.002	0.02	0.46
Days to maturity	0.07	**0.10**	0.02	-0.01	0.007	0.0008	-0.04	0.03	0.06
Plant height(cm)	0.03	0.013	**0.06**	0.04	0.05	0.06	0.02	0.05	0.87
No. of primary branches/ plant	-0.002	0.005	-0.02	**-0.03**	-0.02	-0.02	-0.02	-0.02	0.72
No. of secondary branches/ plant	0.07	0.01	0.15	0.14	**0.18**	0.15	0.07	0.11	0.81
No. of pods/plant	0.12	0.002	0.26	0.20	0.25	**0.29**	0.12	0.19	0.85
No. of seeds/pod	-0.02	-0.17	0.17	0.25	0.17	0.18	**0.43**	0.18	0.69
100-seed wt.(g)	0.12	0.06	0.19	0.12	0.14	0.15	0.10	**0.23**	0.82

Residual effect: 0.2102

Underlined figures denote direct effect.

Table.4. Estimation of range, genotypic variance, phenotypic and environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (b.s.), genetic advance (GA), GA as% of mean

Characters	Range	Genotypic variance	Phenotypic variance	Environmental variance	GCV	PCV	Heritability (b.s.) %	Genetic advance (GA)	GA as % of mean
Days to 50% flowering	44.5-56.5	6.951	7.69	0.74	5.23	5.51	90.3	6.61	13.14
Days to maturity	100-111	4.75	5.30	0.55	2.04	2.15	89.6	5.44	5.10
Plant height (cm)	36.3-58	39.25	40.34	1.09	13.20	13.38	97.3	16.31	34.39
No. of primary branches/ plant	3.1-5.1	0.14	0.16	0.018	9.80	10.39	89.0	0.95	24.40
No. of secondary branches/ plant	8.1-14.00	1.90	2.091	0.18	12.66	13.25	91.2	3.48	31.92
No. of pods/ plant	39-69	49.12	52.30	3.17	13.09	13.51	93.9	17.93	33.50
No. of seeds/pod	1.00-1.4	0.005	0.006	0.001	6.94	7.39	88.1	0.17	17.20
100-seed wt (g)	18.5-28.25	5.630	5.97	0.34	10.30	10.61	94.3	6.08	26.42
Seed yield/ plant	8.00-20.25	8.22	8.40	0.18	23.19	23.45	97.8	7.48	60.55

Table.5. Estimation of Genotypic and Phenotypic coefficient of correlation in chickpea.

Sr. no.		Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/plant	No. of seeds/pod	100-seed wt.	Seed yield/plant
1.	G	1.00	0.71**	0.56**	0.05	0.43**	0.42**	-0.04	0.53**	0.46**
	P	1.00	0.65**	0.52**	0.04	0.38**	0.41**	-0.05	0.47**	0.42**
2.	G		1.00	0.20*	-0.15	0.07	0.007	-0.39	0.28*	0.06
	P		1.00	0.19*	-0.15	0.06	0.01	-0.35	0.25*	0.05
3.	G			1.00	0.66*	0.85**	0.89**	0.40**	0.82**	0.87**
	P			1.00	0.62*	0.81**	0.86**	0.36**	0.78**	0.86**
4.	G				1.00	0.78**	0.68**	0.58**	0.54**	0.72**
	P				1.00	0.75**	0.64**	0.52**	0.47**	0.67**
5.	G					1.00	0.87**	0.39**	0.63**	0.81**
	P					1.00	0.82**	0.37**	0.58**	0.77**
6.	G						1.00	0.43**	0.67**	0.85**
	P						1.00	0.38**	0.63**	0.82**
7.	G							1.00	0.43**	0.69**
	P							1.00	0.37**	0.64**
8.	G								1.00	0.82**
	P								1.00	0.78**
9.	G									1.00
	P									1.00

G: Genotypic correlation coefficient P: Phenotypic correlation coefficient

*, ** indicate 5% and 1% level of significant respectively

Table.3. Mean performance of different characters studied in chickpea genotypes

Sr. no.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	No. of pods/ plant	No. of seeds/ pod	100-seed wt.(g)	Seed yield/ plant (g)
1.	IC-275426	54.50	107.5	57.50	4.75	14.00	61.00	1.15	25.65	17.65
2.	IC-275427	55.50	110.5	55.00	4.10	12.75	66.00	1.05	27.75	17.59
3	IC-275428	50.75	111.0	39.50	3.40	8.55	39.00	1.00	20.40	9.75
4.	IC-275429	49.00	107.5	52.00	4.00	11.50	57.50	1.00	24.90	12.60
5.	IC-275430	48.50	108.0	47.50	4.10	9.50	49.00	1.05	25.70	12.25
6.	IC-275432	49.00	107.5	49.00	3.95	11.75	57.00	1.00	22.60	11.75
7.	IC-275433	49.50	107.0	45.45	3.35	10.75	50.00	1.05	21.00	11.90
8.	IC-275434	54.00	109.0	55.50	4.35	13.00	59.00	1.10	25.40	17.00
9.	IC-275435	44.50	105.0	40.10	3.95	10.25	41.00	1.00	22.40	10.00
10.	IC-275437	48.50	106.0	39.50	4.15	11.50	48.00	1.00	21.75	10.40
11.	IC-275438	51.50	109.5	44.50	3.15	9.25	49.50	1.00	24.80	11.50
12.	IC-275440	49.50	108.0	49.00	4.35	11.25	57.00	1.00	23.60	12.95
13.	IC-275443	55.50	110.0	43.50	3.70	10.50	46.00	1.00	23.75	11.00
14.	IC-275444	49.00	104.5	45.50	4.10	11.50	52.00	1.00	20.60	10.50
15.	IC-275445	56.50	110.5	59.00	4.25	13.25	64.00	1.00	28.25	19.25
16.	IC-275446	48.50	105.0	47.50	4.35	11.10	51.00	1.00	24.50	11.70
17.	IC-327015	48.50	106.0	54.50	4.15	12.95	55.00	1.00	23.40	12.25
18.	IC-327016	48.50	106.5	40.50	3.50	9.65	50.00	1.00	20.50	10.25
19.	IC-327018	53.00	108.0	49.50	3.90	10.75	55.00	1.00	23.40	12.25
20.	IC-327019	48.50	105.0	42.00	3.50	9.00	49.00	1.00	23.25	11.20
21.	IC-327020	50.50	105.5	39.00	3.55	9.50	46.00	1.00	19.50	9.65
22.	IC-327021	50.00	105.5	43.00	3.50	9.25	46.00	1.00	24.60	10.75
23.	IC-327024	55.25	110.0	52.75	3.65	10.50	56.00	1.00	24.40	13.25
24.	IC-327026	49.00	105.0	41.50	3.65	10.25	51.00	1.00	21.90	10.25
25.	IC-327027	49.50	105.5	36.30	3.10	8.10	41.00	1.00	19.50	8.65
26.	IC-327029	51.50	106.5	52.50	4.00	11.50	57.50	1.00	24.40	13.40
27.	IC-327030	51.50	109.0	40.70	3.80	10.25	50.00	1.00	19.60	9.70
28.	IC-327031	54.00	107.5	56.00	3.90	12.75	61.00	1.20	27.75	16.50

Table.3. contd……

29.	IC-327032	47.50	103.5	36.50	3.35	8.60	44.00	1.00	18.50	8.00
30.	IC-327034	48.50	106.5	45.50	4.00	10.00	53.50	1.00	24.50	11.75
31.	IC-327035	49.50	107.0	48.00	4.10	11.90	61.00	1.00	21.95	12.50
32.	IC-327036	49.00	106.0	38.00	3.50	10.10	44.50	1.00	21.50	9.45
33.	IC-327037	47.50	106.5	42.30	4.15	10.10	49.00	1.00	21.00	9.73
34.	IC-327038	50.50	105.5	45.50	3.35	9.40	50.00	1.00	22.40	11.25
35.	IC-327039	49.50	107.0	43.25	3.65	9.80	49.50	1.00	19.40	9.73
36.	IC-327040	51.50	106.5	48.00	3.55	9.25	49.00	1.00	22.85	11.25
37.	IC-327041	51.50	107.0	58.00	4.10	13.10	69.00	1.00	24.50	17.25
38.	IC-327043	51.50	108.5	43.50	3.85	10.40	52.00	1.00	20.30	10.25
39.	IC-327044	47.50	105.5	48.00	3.85	10.15	51.00	1.10	22.40	11.70
40.	IC-327045	55.50	110.0	56.50	4.50	12.90	63.00	1.05	27.25	15.25
41.	IC-327046	50.00	107.0	49.85	4.30	11.00	56.00	1.00	22.50	12.45
42.	IC-327047	49.50	106.5	46.00	3.75	10.15	51.00	1.00	22.75	10.85
43.	IC-327048	51.00	106.0	51.10	4.00	11.00	57.00	1.00	22.25	12.50
44.	IC-327052	53.50	105.5	57.50	4.10	13.00	62.00	1.00	25.75	14.50
45.	IC-327053	48.00	108.0	47.00	4.05	11.10	55.00	1.00	22.90	11.65
46.	IC-327054	49.50	104.5	45.50	3.90	10.50	55.00	1.00	20.50	10.25
47.	IC-327056	46.00	101.5	37.25	3.90	10.60	50.00	1.00	18.75	8.90
48.	IC-327057	50.00	108.5	45.25	4.05	10.70	43.00	1.00	20.75	11.25
49.	IC-327060	49.00	105.0	53.50	4.20	11.00	57.00	1.05	25.40	13.10
50.	IC-327061	54.00	106.0	55.50	4.10	13.00	66.50	1.00	23.25	14.25
51.	Digvijay(ch.)	46.50	101.0	53.50	4.60	12.90	64.00	1.25	24.60	19.00
52.	Vishal (ch.)	47.00	100.5	53.50	5.10	12.10	65.00	1.40	26.00	20.25
53.	**Mean**	**50.33**	**106.67**	**47.43**	**3.92**	**10.91**	**53.51**	**1.02**	**23.01**	**12.36**
54.	**S.E**	**0.61**	**0.52**	**0.73**	**0.09**	**0.30**	**1.26**	**0.01**	**0.41**	**0.30**
55.	**C.D.5%**	**1.73**	**1.49**	**2.09**	**0.27**	**0.85**	**3.57**	**0.05**	**1.17**	**0.86**
56.	**C.V.**	**1.71**	**0.69**	**2.20**	**3.44**	**3.92**	**3.33**	**2.54**	**2.53**	**3.47**

Table7. Grouping of Chickpea genotypes in different clusters

Cluster No.	No. of strains	Genotype included in the cluster
I	37	IC-275428, IC-275429, IC-275430, IC-275432, IC-275433, IC-275435,IC-275437, IC-275438, IC-275440, IC-275443, IC-27544, IC-275446,IC-327015, IC-327016, IC-327018, IC-327019, IC-327020, IC-327021, IC-327026, IC-327029, IC-327030, IC-327034, IC-327035, IC-327036, IC 327037, IC-327038, IC-327039, IC-327040, IC-327043, IC-327044, IC-327046, IC-327047, IC-327048, IC-327053, IC-327054, IC-327057, IC-327060.
II	01	IC-327027
III	10	IC-275426, IC-275434, IC-275427, IC-275445, IC- 327024, IC- 327031, IC- 327041, IC-327045, IC-327052, IC- 327061.
IV	01	IC-327032
V	01	IC-327056
VI	02	Vishal, Digvijay

Table 8. Average intra and inter cluster (D^2) values

Cluster No.	I	II	III	IV	V	VI
I	60.06	118.81	265.69	160.27	161.03	553.66
II		0.00	557.9	18.40	55.80	895.80
III			85.74	671.32	641.60	296.87
IV				0.00	20.52	985.96
V					0.00	891.02
VI						83.17

Table 9. Average intra and inter cluster distance (D) values

Cluster No.	I	II	III	IV	V	VI
I	7.75	10.90	16.30	12.66	12.69	25.53
II		0.00	23.62	4.29	7.47	29.93
III			9.26	25.91	25.33	17.23
IV				0.00	4.53	31.40
V					0.00	29.85
VI						9.12

Table10. Cluster means for nine characters studied in chickpea.

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50% flowering	49.64	49.50	54.43	47.50	46.00	46.75
Days to maturity	106.8	105.5	108.3	103.5	101.5	100.7
Plant height (cm)	45.58	36.30	56.33	36.50	37.25	53.50
No. of primary branches/plant	3.8	3.1	4.1	3.3	3.9	4.8
No. of secondary branches/plant	10.4	8.1	12.8	8.6	10.6	12.5
No. of pods/plant	51.1	41.0	62.7	44.0	50.0	64.5
No. of seeds/pod	1.01	1.00	1.06	1.00	1.00	1.33
100-seed weight (g)	22.4	19.5	25.9	18.5	18.7	25.3
Seed yield/plant (g)	11.2	8.6	16.2	8.0	8.9	19.6

Table 11. Percent contribution of different characters to the genetic diversity

Sr. no.	Characters	% Contribution
1.	Days to 50% flowering	5.13
2.	Days to maturity	3.24
3.	Plant height	34.99
4.	Number of primary branches/plant	5.35
5.	Number of secondary branches/plant	1.89
6.	Number of pods/plant	5.13
7.	Number of seeds/pod	1.21
8.	100 seed weight	18.33
9.	Seed yield/plant	24.75
	Total	100