# $D^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea (*Cicer* arietinum) under rainfed conditions

## THESIS

***Submitted to the***

**Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,**

**Gwalior**

**In partial fulfilment of the requirement for the degree of**

**MASTER OF SCIENCE**

***In***

**AGRICULTURE**
**(PLANT BREEDING AND GENETICS)**

***By***

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**Gwalior (M.P.)**

**2011-2012**

# CERTIFICATE – I

This is to certify that the thesis entitled **“D$^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea (*Cicer* arietinum) under rainfed conditions”** submitted in partial fulfilment of the requirement of the degree of **Master of Science in Agriculture (Plant Breeding & Genetics)** of the Rajamata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by **Mr. Jitendra Jaiswal** under my guidance and supervision. The subject of the thesis has been approved by Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any degree or diploma (Certificate awarded etc.) or has been published/published part has been fully acknowledged. All the assistance and help received during the course of investigation has been acknowledged by him.

*Place : Gwalior*
**Date :**

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**Thesis approved by the Student’s Advisory Committee**

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| **Member** | **(V.B. Singh)** | __________________ |

## CERTIFICATE – II

**This is to certify that the thesis entitled "$D^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea** (*Cicer* arietinum) under rainfed conditions" **submitted by** Mr. Jitendra Jaiswal **to the** Rajamata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior **in partial fulfilment of the requirements for the degree of** Master of Science in Agriculture (Plant Breeding & Genetics) **in the** Department of Plant Breeding & Genetics, College of Agriculture, Gwalior **has been, after evaluation, approved by the External Examiner and by the Student's Advisory Committee after an oral examination of the same.**

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**Director of Instructions (Y.M. Kool)** ________________

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**Date:**

**Place: Gwalior** **(Jitendra Jaiswal)**

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# CHAPTER-I

# INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the fifth most important food legume crop in the world after soybean, groundnut, dry beans and peas. Chickpea is the premier pulse crop of Indian subcontinent. India is the largest chickpea producer as well as consumer in the world. India grows chickpea on about 6.67 million ha area, which is 30% of the total area under pulses and total production of chick pea is producing 5.3 million tones, which represents 38% of the total pulse production in country. The world's total production of chickpea is around 8.5 million metric tones annually and is grown over 10 million hectares of land approximately. It is grown in the drier areas of the country. Chickpea producing states in India are Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra and Andhra Pradesh. Madhya Pradesh produces the major share of around 40% in the Indian production of around 5.3 million tones. Since 1990 a rise in the productivity of chickpea in India has been observed from 614 kg per hectare to 735 kg per hectare.

Crop improvement depends on the magnitude of genetic variability present in the base population .The expected improvement in yield components primarily depends on the nature and magnitude of heritable variation. Selection based on a single character may not always effective. On the other hand, it is very cumbersome process for a breeder to consider a large number of component characters simultaneously in selection procedure. The role of genetic diversity and its significance have been recognised for the selection of desirable parents in breeding programme to obtain high heterotic response and transgressive segregants.

The use of multivariate techniques, such as Mahalanobis' generalized distance $D^2$ and Canonical Variate Analysis, to quantify the nature and magnitude of divergence between populations and to understand the course of evolution has been emphasized in the past two decades. Further, Mahalanobis' $D^2$ statistic, not only provides a powerful tool for quantifying the degree of divergence between biological populations at genotypic level but also helps in identifying parents for hybridization programme. Thus, study of genetic diversity shall help in selection of diverse parents for their use in hybridization as heterosis is known to depend on extent of genetic diversity between parents.

The variability of biological population is an outcome of genetic constitution of the individuals making up of that population in relation to prevailing environments. A survey of genetic variability with the help of suitable parameters such as genetic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to start an efficient breeding programme. Some of the characters are known to be highly associated among them and with seed yield. The analysis of the relationships among these characters and their associations with seed yield is essential to establish selection criteria. When more characters are involved in correlation study, it becomes difficult to ascertain the characters which really contribute toward yield. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters (Singh *et al.* 1990).

Keeping the above facts in mind the present study has been undertaken with the following objectives:

1. To evaluate the genetic variability.
2. To estimate the correlation between yield and its attributing characters.
3. To estimate the path coefficient analysis at phenotypic and genotypic level.
4. Genetic divergence study among genotypes under study.

# CHAPTER - II

# REVIEW OF LITERATURE

The relevant literature related to the present investigation has been reviewed under the following heads:

2.1 Variability , heritability and genetic advance

2.2 Character association

2.3 Path coefficient analysis

2.4 Genetic divergence

**2.1 Parameters of genetic variability:**

**2.1.1. Genetic variation:**

Nimbalkar (2000) observed in chickpea that genotypic (48.84%) and phenotypic (49.02%) coefficients of variation were highest for 100-grain weight and lowest for days to maturity.

Arora and Jeena (2001) studied 40 genetically diverse genotypes of chickpea and reported that the highest genetic variability was expressed by 100 seed weight, followed by primary branches per plant and seeds per plant.

Jeena and Arora (2001) worked on 36 genetically diverse chickpea genotypes and observed highest genotypic variability for 100 seed weight followed by seed yield per plant, biological yield, and seeds per plant.

Kumar *et al.* (2001a) studied 26 genetically diverse genotypes of chickpea and reported that pods per plant exhibited the highest amount of genetic variability, followed by seed yield per plant, 100 seed weight, seeds per pod, plant height and biological yield per plant.

Saleem *et al.* (2002) studied a set of 20 chickpea elite genotypes including two check varieties and reported that the genotypes showed highly significant differences for all the characters studied.

Shaukat *et al.* (2002) studied 20 elite lines of chickpea planted in Pakistan to estimate the genetic variability for different quantitative traits *viz.,* days to flower initiation, days to flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, total weight of plant, pods per plant and seed yield per plant reported that the secondary branches per plant, total weight of plant, pods per plant and seed yield per plant reflected good response to selection. Genotypic differences were found to be significant for all quantitative characters studied.

Parshuram *et al.* (2003a) studied 16 chickpea cultivars and observed that phenotypic coefficient of variation ranged from 4.01% for days to maturity to 58.62% for number of seeds per plant. The genotypic coefficient of variation was low for all characters except plant height and number of leaves per plant indicating low environmental impact for both characters.

Yadav *et al.* (2003) studied 33 divergent genotypes of chickpea (*C. arietinum*) and observed maximum variability for harvest index, biological yield, grain yield per plant, and 100-seed weight.

Ajinder *et al.* (2004) studied genetic variability, heritability and genetic advance for grain yield and its components in 30 genotypes of *Desi* chickpea under normal and late sown conditions in Rabi 2001-2002. The results showed that 100 seed weight had comparable phenotypic and genotypic coefficients of variation under both sowing conditions.

Brar *et al.* (2004) evaluated chickpea genotypes for seed yield and its components viz., days to flowering, days to maturity, plant height, primary branches per plant, pods per plant, 100 seed weight. The genotypes differed significantly for all the characters studied.

Jahagirdar (2005) concluded that the biparental mating was attempted in $F_2$ of BDN-9-3 x ICCV 2 cross of chickpea in an experiment in Badnapur, Maharashtra, India, during *rabi* 2001-02. The biparental population had better mean performance than the selfed for all the characters namely plant height, primary branches per plant, secondary branches per plant, number of pods per plant, 100-seed weight and seed yield per plant.

Jeena *et al.* (2005) carried out the variability study in 80 genetically diverse chickpea genotypes. A high amount of genetic variability was expressed by pods per plant, 100-seed weight, biological yield per plant and seed yield per plant.

Meena *et al.* (2006) studied the extent of genetic variability and association of traits related to drought tolerance in 30 chickpea *(Cicer arietinum*) genotypes. The magnitude of phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters. The phenotypic and genotypic coefficients of variation were highest for 100-seed weight followed by seed yield, while days to maturity (2.12 and 2.03) showed the lowest PCV and GCV, respectively.

Dubey and Shrivastava (2007) carried out the variability study in 40 genotypes. High estimates of genotypic coefficient of variation were observed for grain yield per plant, followed by number of pods per plant, number of primary branches and harvest index.

Lokare *et al.* (2007) studied 60 genotypes and showed a wide range of variation for seed yield per plant, 100- seed weight and number of pods per plant while moderate variation was observed for number of fruiting branches per plant, protein content and starch content.

Thakur and Sirohi (2008) studied fifty three genotypes and reported that phenotypic and genotypic coefficients of variation were high for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight.

Dwevedi and Lal (2009) reported 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 (PCV and GCV), followed by Biological yield per plant and 100 Seed weight.

Tomar and Singh (2009) evaluated forty five genotypes of chickpea and reported that genotypic and phenotypic co-efficients of variation were maximum for number of seeds/plant.

Vaghela *et al.* (2009) studied parameters of variability in fifty diverse genotypes of kabuli chickpea (*Cicer arietinum* L.). Analysis of variance revealed significant genotypic differences for all the ten characters with wide range of variations. Estimates of genotypic and phenotypic coefficients of variation were high for seed yield per plant and number of pods per plant.

Borate et al. (2010) observed 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 seeds. PCV showed higher values than GCV for all characters.

**2.1.2 Heritability and Expected genetic Advance**

Chauhan and Singh (2000) observed that the seeds/pod and secondary branches/plant showed high heritability with high genetic gain making these characters fit for direct selection for improving yield.

Jeena and Arora (2000) worked on forty genotypes of chickpea and found that selection is likely to be effective for 100 seed weight, pods per plant, seed yield per plant, followed by harvest index, and seeds per pod.

Nimbalkar (2000) observed highest genetic advance for 100-grain weight and lowest for days to maturity. Heritability was highest for 100-grain weight (99.3%) and lowest for plant spread (61.8%).

Arora and Jeena (2001) studied 40 genetically diverse genotypes of chickpea and reported that 100 seed weight, followed by primary branches per plant and seeds per plant exhibited high genetic advance with high heritability.

Jeena and Arora (2001) observed that 100 seed weight exhibited high genetic advance with high heritability.

Kumar *et al.* (2001a) reported that pods per plant showed the highest heritability and expected genetic advance.

Albinbas (2002) reported high heratibility in broad sense for 100 seed weight (78.7%) and seed yield (77.7%).

Arshad *et al.* (2002) reported low heritability percentage coupled with low and moderate genetic advancement has been observed for primary and secondary branches, respectively. Additionally, they indicated that these traits were greatly influenced by environment.

Noor *et al.* (2003) reported medium to high genetic advance for days to flowering, maturity, secondary branch number, and 100 seed weight. Where as for other characters, low to medium heritability was observed along with low to high genetic advance.

Parshuram *et al.* (2003a) estimated that the heritability was high for number branches per plant, days to 50% flowering, days to maturity and 100 seed weight. Genetic advance was high for number of pods per plant, pod weight, number of seeds, seed weight per plant and 100 seed weight indicating the greater effects of additive genes.

Sable *et al.* (2003) evaluated 30 genetically diverse genotypes for genetic parameters and observed that seed yield per plant, 100 seed weight and biological yield per plant exhibited high estimates of heritability.

Yadav *et al.* (2003) observed low to very high heritability coupled with genetic advance for harvest index, biological yield, grain yield per plant, and 100-seed weight indicating the involvement of non-additive gene action.

Ajinder *et al.* (2004) studied high heritability and average genetic advance for 100 seed weight and grain yield.

Muhammad *et al. (*2004) studied heritability and genetic advance, for yield and yield components in 24 advance lines of chickpea and reported existence of high heritability with low genetic advance for number of days to flowering, number of days to maturity and 100-seed weight indicating the influence of dominant and epistatic genes for these traits.

Jeena *et al.* (2005) reported that pods per plant, 100-seed weight, biological yield per plant and seed yield per plant characters exhibited high genetic advance with high heritability.

Mohammad *et al.* (2005) evaluated eighteen elite genotypes of chickpea and 2 cultivars for yield and its components in an experiment. High heritability estimates were obtained for 100-seed weight (97.7%), plant height (96.9%), seed yield (90.9%), total weight (89.8%), pods/plant (88%), seeds/pod (87.1%) and seeds/plant (86.2%) with corresponding genetic advance of 11.3, 8.05, 8.01, 4.28, 4.06, 3.71 and 0.10 respectively.

Raval and Dobariya (2005) recorded the highest genetic advance for seed yield per plant, number of pods per plant, 100-seed weight, biological yield per plant and harvest index respectively.

Thakur and Sirohi (2008) reported that high heritability coupled with high expected genetic advance was observed for seed yield per plant, biological yield per plant, 100-seed weight, pods per plant and plant height.

Dwevedi and Lal (2009) reported moderate to high degree of heritability and genetic Advance for number of Pods per pant, Harvest index and Biological yield.

Tomar and Singh (2009) recorded high heritability in broad sense for all the traits except days to maturity and genetic advance as per cent mean was maximum for seeds/plant.

Vaghela *et al.* (2009) observed that broad sense heritability was higher for all the traits except plant height. High genetic advance expressed as percentage of mean was exhibited by seed yield per plant and number of pods per plant.

Borate et al. (2010) recorded high heritability coupled with high genetic advance for grain yield, plant height, dry matter, days to first flowering and days to maturity indicated high additive gene effects.

### 2.3.1 Character associations

Arun kumar *et al.* (2000) reported strong correlation for biological and grain yield per plant, harvest index and 100 seed weight both at genotypic and phenotypic levels. As most of the components showed positive association with yield and among themselves, it would be easier to improve yield by exercising selection for a few associated characters.

Mishra *et al.* (2000) observed that number of seeds per pod was positively correlated with seed yield.

Vijaya lakshmi *et al.* (2000) observed that *seed* yield was positively correlated with number of pods, seeds, primary branches and secondary branches per plant.

Guler *et al.* (2001) reported significant and positive correlation of seed yield with pods per plant, dry matter accumulation, 100 seed weight and harvest index in chickpea.

Yadav *et al.* (2001) reported that seed yield was positively associated with seeds per pod and days to maturity, but negatively correlated with number of branches per plant and days to 50% flowering.

Kumar *et al*. (2001b) observed that harvest index had the highest significant positive correlation with seed yield, followed by the number of pods per plant, biological yield and number of secondary branches per plant. The major yield contributing characters were number of secondary branches and pods/plants, biological yield per plant and harvesting index.

Narayan and Reddy (2002) observed a significant association between seed yield and harvest index, number of pods per plant and number of secondary branches per plant both at genotypic and phenotypic levels. It was observed that number of pods per plant, 100 seeds weight, number of seeds/ pods and harvest index had high direct effect on seed yield.

Saleem *et al.* (2002) studied that seed yield per plant was positively and significantly correlated with days to flowering, total weight of plant, number of pods per plant and 100-seed weight both at the genotypic and phenotypic levels.

Singh *et al*. (2002) observed positive and significant association of days to initial flowering, days to 50% flowering, number of primary branches, number of pods per plant and seed yield.

Parshuram et *al*. (2003b) reported that seed yield per plant was positively correlated with number of pods per plant, pod weight per plant and number of seeds per plant at the genotypic and phenotypic levels, and with plant height, number of leaves, number of branches and shelling percentage at genotypic level and it was negatively correlated with days to maturity, days to 50% flowering and 100 seed weight at the genotypic and phenotypic levels and number of leaves at the phenotypic level. It was found that number of pods / plant, pod weight / plant and number of seeds/ plant were the major components of seed yield in chickpea.

Sail *et al.* (2003) reported that the seed yield per plant was positively correlated pods per plant, biological yield per plant at the phenotypic level and seed yield was negatively correlated with days to physiological maturity, days to flowering and harvest index at the phenotypic level.

Brar *et al.* (2004) observed that seed yield showed highly significant and positive correlation with pods per plant, plant height and primary branches per plant.

Sahu *et al.* (2005) reported that number of spikes per plant and 1000 grain weight were positively and significantly correlated with the yield.

Dhameliya *et al.* (2007) observed genotypic and phenotypic correlation between days to 50% flowering and plant height was positive and significant.

Atta (2008) reported that grain yield per plant showed highly significant positive correlation with days to maturity, primary branches, secondary branches, 100 seed weight and pods per plant.

Sidramappa *et al.* (2008) reported that seed yield had a high positive correlation with pods per plant (0.779), plant height (0.637), number of branches (0.538), 100 seed weight (0.345), reproductive period (0.342) and days to maturity (0.327).

Singh *et al.* (2008) evaluated newly inbred lines in replicated trials for seed yield, days to flowering and maturity, plant height and 100-seed weight. Correlation analyses showed that increased seed size, early maturity and reduced plant height at the drought-prone location and early maturity at the drought-free location were of prime importance in increasing seed yield.

Tomar and Singh (2009) reported that the genotypic correlation co-efficient was observed to be higher than that of phenotypic correlation co-efficient indicating the existence of strong inherent association for various traits and phenotypic selection may be rewarded. Grain yield/plant exhibited stable positive association with biological yield/plant, followed by seeds/plant, pods/plant and seeds/pod at genotypic and phenotypic levels.

### 2.3.2 Path coefficient analysis

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

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

Muhammd *et al.* (2002) carried out the path analysis in twenty genotypes and study revealed that number of pods per plant had maximum positive direct effect on seed yield. The other traits in the study also exhibited considerable indirect effect on the seed yield through number of pods per plant. It was concluded that number of pods per plant and 100-seed weight could be used as selection criteria to improve the yield.

Saleem *et al.* (2002) studied that number of pods per plant had maximum positive direct effect on seed yield. The other traits in the study also exhibited considerable indirect effect on the seed yield through number of pods per plant.

Yadav *et al.* (2002) based on the results obtained from Path analysis suggested that biological yield, harvest index and 100 seed weight were the yield determinants.

Mardi *et al.* (2003) found that seed and pod weight and number of seeds per plant had the greater direct effect on plant yield thus; these parameters were considered as the major yield components. Among the yield components, the size of seeds and pods contributed approximately 50% of the total variation.

Lokare *et al.* (2007) studied 60 genotypes and revealed that pods per plant had the highest positive direct effect on seed yield followed by 100 seed weight and seeds per pod while fruiting branches per plant, protein content and starch content showed negative direct effect on seed yield.

Atta (2008) reported that pods per plant and 100 seed weight had the highest direct effect on grain yield per plant followed by secondary branches.

Sidramappa *et al.* (2008) revealed that number of pods per plant has highest direct effect (0.766) on seed yield. The characters number of pods per plant, 100 seed weight, plant height and reproductive period should be taken into consideration in breeding of high yielding gram varieties.

Singh and Sandhu (2008) reported that pods per plant, harvest index, 100- seed weight, seeds/pod and biological yield had maximum direct effect on grain yield.

## 2.4. Genetic divergence:

Harisatyanarayana and Reddy (2000) studied the genetic divergence among 31 chickpea genotypes and observed that the genotypes were grouped into 7 clusters based on mean performance, genetic divergence and clustering pattern. Cluster I was the largest with 14 genotypes. The maximum genetic distance was recorded between clusters IV and VII. The inter-cluster D values ranged from 22.6 to 36.8

Sivakumar and Muthiah (2000) measured genetic divergence by Mahalanobis $D^2$ statistics in 126 chickpea cultivars. Cultivars were grouped into seven clusters. The highest divergence was observed in clusters IV and VII while the lowest was between clusters IV and V. Cluster III included *kabuli* types which were quite diverse from the *desi* types.

Nimbalkar and Harer (2001) studied genetic diversity in 40 genotypes of chickpea collected from 7 countries (32 indigenous and 8 exotic) and found that the genotypes were genetically distinct which were grouped into 16 clusters. There was no parallelism between genetic divergence and geographical distribution of genotypes. The 32 indigenous genotypes were spread into 13 clusters and eight exotics were grouped into eight distinct clusters. Variance of cluster means indicated that pods/plant followed by plant height and 100 seed weight were the main characters contributing to the genetic divergence.

Dasgupta and Singh (2003) evaluated diversity among 23 advanced lines of chickpea and two control cultivars using Mahalanobis $D^2$ distance statistics and the lines were classified into eight clusters based on $D^2$ values. Intercluster distance was reported to be highest between clusters V and VIII, and lowest between clusters II and III. High genetic diversity was observed among the genotypes based on cluster means and the inter-cluster distance values.

Raval and Dobariya (2005) studied genetic divergence of 52 chickpea genotypes which were grouped into 15 clusters. Enormous diversity was observed as indicated by the wide range of $D^2$ - values. Cluster I showed a high mean for biological yield per plant , while cluster VI had high mean for number of seeds per pod. Cluster X and XII contained genotypes with higher mean seed yield per plant, number of primary branches per plant and harvest index. Cluster XIII was the best for per plant spread and 100 seed weight. Cluster XIV showed the lowest values for days to flowering, maturity and plant height. Cluster XV presented high mean for secondary branches, pods per plant and protein content. It will be fruitful to intercross genotypes from cluster X , XIII and I with those of clusters XIV and XII for generating promising derivatives and wide spectrum of genetic variability for yield in chickpea.

Jahagirdar (2005) evaluated $F_2$ of BDN-9-3 x ICCV 2 cross of chickpea in an experiment in Badnapur, Maharashtra, India, during rabi 2001-02. The biparental population had better mean performance than the selfed $F_3^s$ for all the characters studied *viz.;* plant height, primary branches per plant, secondary branches per plant, pods per plant, 100-seed weight and seed yield per plant.

Jeena *et al.* (2005) recorded observations on 80 chickpea genotypes collected from different geographical areas for 18 characters during rabi 1998 at Pantnagar, Uttar Pradesh, India. The data were subjected to divergence analysis. Based on $D^2$ values, the 80 genotypes were grouped into 11 clusters. The highest number of genotypes was included in cluster I (60) followed by cluster II (7). No definite relationship was observed between genetic diversity and geographical distribution. Based on inter-cluster distances, crossing between BGM-419 and KPG33 is expected to produce a broad spectrum of variability in segregating generations to isolate transgressive segregants for yield and its components.

Dwevedi and Lal (2009) studied twenty five genotypes of chickpea which are grouped into six clusters. The cluster I shows largest cluster w ith eight genotypes. Highest inter cluster distance was observed between cluster III and cluster VI, followed by cluster I and VI. 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 (PCV and GCV), followed by biological yield per plant and 100 Seed weight. A moderate to high degree of Heritability and Genetic Advance was observed for number of pods per pant, harvest index and biological yield. The genotypes KPJ 59, PBJ 1 and Pusa 329 were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

# CHAPTER- III

# MATERIAL AND METHODS

## 3.1 Experimental site

An investigation entitled "$D^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea (*Cicer* arietinum) under rainfed conditions" was carried out during *Rabi* of 2010-2011 at Research Farm, College of Agriculture, Gwalior.

### Location and climate

Gwalior is situated in Gird Zone of Madhya Pradesh. Gwalior is situated between latitude 26º13' N and longitude 78º14' E and at an altitude of 211.51 metres above the mean sea level. It has semi-humid and subtropical climate having a temperature range of 23º to 40ºC and 4 to 29 ºC in summer and winter season respectively. In this area most of the rainfall is received during July to October. The south-western monsoon is responsible for the major part of the precipitation. The weather prevailed during the crop season were recorded from the meteorological observatory of College of Agriculture, Gwalior and have been presented in Table 3.1.

## 3.2 Experimental material

The experimental material used in the present study comprised of thirty chickpea varieties collected from different parts of the country. The variety here been listed in Table 3.2.

The experiment was laid out in a randomized block design with three replications. The material was sown on October 16, 2010 with row to row distance of 30 cm and plant to plant distance of 4 cm. All recommended package of practices were followed during the conduct of experiment.

## 3.4 Observations recorded:

### Yield characters

Observations on ten randomly chosen plants in each entry will be recorded for following characters:

**Table3.1. Mean standard weekly meteorological data during crop season 2010-11**

| Month | Standard week (2008-09) | Temperature (°C) | | Rainfall (mm) | Number of rainy days | Relative humidity (%) | Wind Velocity (km/hr) |
|---|---|---|---|---|---|---|---|
| | | Max. | Min. | | | | |
| **October 2008** | 40 | **33.02** | 22.50 | 0.00 | 0 | **86.00** | 0.51 |
| | 41 | **33.42** | 19.64 | 16.00 | 2 | **90.14** | 0.31 |
| | 42 | **33.81** | 17.28 | 0.00 | 0 | **82.85** | 0.52 |
| | 43 | **33.07** | 14.14 | 0.00 | 0 | **82.42** | 0.52 |
| **November 2008** | 44 | **33.18** | 14.85 | 0.00 | 0 | **83.42** | 0.32 |
| | 45 | **30.78** | 12.78 | 0.00 | 0 | **85.00** | 0.27 |
| | 46 | **26.21** | 13.85 | 0.00 | 0 | **90.71** | 0.08 |
| | 47 | **23.72** | 12.50 | 7.2.0 | 1 | **87.85** | 0.00 |
| **December 2008** | 48 | **20.21** | 11.28 | 0.00 | 0 | **81.00** | 0.00 |
| | 49 | **25.85** | 13.00 | 0.00 | 0 | **74.71** | 1.77 |
| | 50 | **27.37** | 14.00 | 0.00 | 0 | **83.57** | 0.84 |
| | 51 | **22.50** | 13.14 | 2.00 | 1 | **80.14** | 1.64 |
| | 52 | **25.37** | 8.71 | 0.00 | 0 | **83.37** | 1.25 |
| **January 2009** | 1 | **22.00** | 8.87 | 0.00 | 0 | **77.42** | 1.75 |
| | 2 | **19.68** | 11.92 | 28.60 | 3 | **90.14** | 2.77 |
| | 3 | **26.05** | 14.07 | 0.00 | 0 | **84.00** | 1.25 |
| | 4 | **26.40** | 9.92 | 0.00 | 0 | **77.00** | 1.52 |
| **February 2009** | 5 | **26.34** | 10.64 | 0.00 | 0 | **77.57** | 1.52 |
| | 6 | **26.14** | 11.27 | 0.00 | 0 | **65.00** | 2.38 |
| | 7 | **26.90** | 10.85 | 0.00 | 0 | **63.00** | 2.05 |
| | 8 | **31.52** | 13.78 | 0.00 | 0 | **63.71** | 2.61 |
| **March 2009** | 9 | **33.82** | 16.28 | 0.00 | 0 | **58.28** | 2.90 |
| | 10 | **34.58** | 14.50 | 0.00 | 0 | **50.42** | 3.55 |
| | 11 | **31.35** | 16.07 | 0.00 | 0 | **60.14** | 2.90 |

Sources: Meterological observatory, AICRPDA, College of Agriculture Gwalior.

1. **Plant height (cm):**

The height of main shoot of each selected plant was measured in cm from base of the plant to the terminal bud.

2. **Number of primary branches per plant:**

The number of branches emerging from the main stem was recorded.

3. **Number of pods per plant:**

It was recorded by counting the total number of pods borne on each plant.

4. **Number of seeds per pod:**

It is the ratio of number of seeds per plant and number of pods per plant.

5. **Days to 50% flowering:**

The number of days required from sowing to 50% plants of the plot to flower (anthesis) was recorded.

6. **Days to maturity:**

The number of days required from sowing to physiological maturity (i.e. 75-80% pods mature) was recorded.

7. **100 seed weight (g):**

Samples of 100 seeds were drawn randomly from bulked seed of the ten plants and were weighed in g up to second decimal place with the help of an electronic balance and mean of the samples recorded as 100-seed weight.

8. **Seed yield per plant (g):**

The pods of selected ten plants were threshed and winnowed. The seeds obtained from each plant were weighed in grams.

## 3.5 Statistical analysis

### 3.5.1. Analysis of variance

The data on various characters were subjected to statistical analysis by using appropriate model for analysis of variance and covariance as per Panse and Sukhatme (1954). The range and estimates of mean, phenotypic, genotypic and environmental variance and covariance, standard error, coefficient of variation and critical difference were obtained for all the traits. The test of significance between genotypes for various characters was tested by f test. The analysis of variance for experimental design was based on the following model.

$Y_{ij} = m + g_i + r_j + e_{ij}$ (I, j = 1…..... t)

(k = 1……….b)

Where,

$Y_{ij}$ = Phenotypic observation of $i^{th}$ genotype in $j^{th}$ replication

m = the population mean

$r_j$ = Effect of $j^{th}$ replication

$g_i'^s$ = Genotypic effects which are random variable, distributed independently andnormally as N $(0,\sigma^2 g)$

$e_{ij'}^s$ = Errors associated with the ij observations, distributed independently and normally N $(0, \sigma^2 g)$.

The mean values of each observation were used for analysis of data for randomized block design (RBD). The skeleton of ANOVA is given below:

**Table 3.2: Skeleton of ANOVA for Randomized Block Design**

| **Sources of variation** | **Degree of Freedom** | **MSS** | **'F' calculated** |
|---|---|---|---|
| Replications | (r-1) | $M_r$ | $M_r / M_e$ |
| Genotypes | (g -1) | $M_g$ | $M_g / M_e$ |
| Error | (r -1) (g – 1) | $M_e$ | |

Where,

r = Number of replications

g = Number of genotypes

$M_r$ = Mean sum of squares for replications

$M_g$ = Mean sum of squares for genotypes

$M_e$ = Error mean sum of squares

d.f = degree of freedom

### 3.5.3. Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in percent were computed by the following formulae given by Burton (1952).

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Mean}} \times 100$$

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Mean}} \times 100$$

### 3.5.4. Estimation of heritability and genetic advance:

***Heritability***

Heritability in broad sense (%) was estimated as:

$$\text{Heritability } (h^2) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

**Genetic advance**

The estimates of genetic advance from selection, G(s), were obtained by the formula suggested by Robinson *et al.* (1949):

$G(s) = k \times h^2 \times \sigma_p$

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity

$h^2$ = Heritability in broad sense

$\sigma_p$ = Phenotypic standard deviation

### 3.5.5. Estimation of correlation coefficients:

Phenotypic and genotypic correlation coefficients between characters were computed utilizing respective components of variance and co-variance, as per the formula suggested by Miller *et al.* (1958).

$$r_{xy} = \frac{\text{Covariance x, y}}{\sqrt{(\text{variance x}).(\text{variance y}}} \times 100$$

Where,

$r_{xy}$ = Correlation coefficient between characters x and y

Cov (x,y) = Co-variance of characters x and y

V(x) = Variance of character x

V(y) = Variance of character y

To test the significance of correlation coefficients, the estimated values were compared with the tabulated values at (t-2) d.f. at 0.05 and 0.01 probability level.

### 3.5.6. Path coefficient analysis:

The proportion of direct and indirect contributions of various characters to the total correlation coefficients was estimated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

To estimate various direct and indirect effects, the following sets of simultaneous equations were formed and solved.

$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots. + r_{1l}P_{ly}$

$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \ldots\ldots. + r_{2l}P_{ly}$

$r_{1y} = r_{l1}P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \ldots\ldots. + P_{ly}$

Where,

$r_{1y}$ to $r_{ly}$ = Correlation coefficient between casual factor 1 to l and dependent character y.

$r_{12}$ to $r_{l-1,l}$ = Correlation coefficient among casual factor themselves

$P_{1y}$ to $P_{ly}$ = Direct effects of characters 1 to l on character y.

Residual effect, which measures the contribution of the characters not considered in the casual scheme, was obtained as:

$$\text{Residual effect } (P_{RY}) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \Sigma P_i^2 Y + 2\Sigma P_{iy}P_{jy}R_{ij}$$

i ≠j

i>j

### 3.5.7. Multivariate analysis:

#### (a) Estimation of Wilk's (Λ) criterion:

To test the significance of difference between lines, taking all the characters simultaneously, 'V' statistic was calculated which was based on Wilk's (Λ) criterion (Wilk, 1932). The sum of squares and sum of products of error and error + variety were utilized for estimation of "Λ".

To calculate the value of "Λ" following relationship was used:

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

where,

$|E|$ was the determinant of error sum of squares and sum of products matrix and $|E+V|$ was the determinant of the "error + variety' sum of squares and sum of products matrix.

$\chi^2$ was used to test the significance of "Λ" as

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

where,

$$m = n - \frac{p+q+1}{2}$$ with pq degree of freedom.

where,

n = total number of observations –1,

p = number of characters,

q = k – 1, and

k = number of lines

**(b) Estimation of $D^2$-statistic:**

To estimate divergence between two lines Mahalanobis (1936) $D^2$- statistic was used. He defined generalized distance between two lines as:

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

where,

$\lambda^{ij}$ = Reciprocal matrix of the common dispersion matrix $\lambda_{ij}$,

$\delta_i$ = Difference between mean values of two lines for the $i^{th}$ character, and

$\delta_j$ = Difference between mean values of two lines for the $j^{th}$ character.

$D^2$-statistic is the sample estimate of the generalized distance which is estimated as:

$$D^2 = \sum_{i,j=1}^{P} s^{ij} d_i d_j$$

where,

$s^{ij}$ and $d_i$ are the sample estimates of $\lambda^{ij}$ and $\delta_i$, respectively. For calculating $D^2$ values inversion of matrix was required which is quite cumbersome. To overcome this difficulty original correlated, unstandardized character means ($X_i$) were transformed to uncorrelated, standardized variables ($Y_i$) by Pivotel condensation method (Rao, 1952). $D^2$ between any pairs of populations, for example population 1 and 2, was then estimated as:

$$D_p^2 = \sum_{i=1}^{p} (Y_{i1} - Y_{i2})^2$$

where,

p = number of characters used for estimation of divergence.

**(c) Determination of population constellations:**

Population constellations were determined by Tocher's method described by Rao (1952). A cluster or constellation may be explained as a group of populations or genotypes such that any two populations belonging to the same cluster showed, on the average, a smaller $D^2$ value than those belonging to different clusters.

Tocher suggested that two closely related populations of low $D^2$ value be pooled together and then a third population of similar $D^2$ value be added to this group such that it did not increase the average $D^2$ value appreciably. This process is continued. Any population, which sharply increases the average $D^2$ value should not be included in that group.

After formation of first cluster, the process is repeated to form second, third clusters, using remaining populations until all populations are included in one or the other cluster. After cluster formation average intra and inter-cluster distances were calculated. The square root of corresponding average $D^2$ values represents the distance within and between groups.

**(d) Canonical analysis:**

To visualize multidimensional picture of variability among genotypes canonical analysis was done. Canonical roots were estimated by transformation of correlated, unstandardized means into uncorrelated, standardized variables (Rao, 1952). From these uncorrelated standardized variables, matrix of variance and covariance (matrix A) was obtained by computing sums of squares and sums of products. From matrix A, matrix $(A)^p$ was derived, where p is the number of characters. The column totals of matrix $(A)^p$ were obtained and each total was divided by the highest value among them to obtain the first approximation trial vector. The canonical variates were determined by iteration. The vectors were then standardized by dividing them with correlated sum of squares of these vectors. The first root, $\lambda_1$, was calculated as the $p^{th}$ root of the highest column total of the last approximation.

The second root, $\lambda_2$, was obtained by transforming the original $(A)^p$ matrix to reduced matrix $(B)^p$. Each i × j$^{th}$ element of $(B)^p$ was calculated as: (i, j)$^{th}$ element of $(A)^p = \lambda_1 \times$ i$^{th}$ element × j$^{th}$ element of the vector.

Estimation of second and third canonical root was done following the same procedure as in the case of 'A' was followed. The utility of estimation of other roots depends on the proportions of the sum of squares accounted for by the first three roots.

# CHAPTER – IV

# Results

The experimental results of the present study have been presented under the following heads:

**(A) Univariate analysis**

1. Analysis of variance
2. Population mean and range
3. Phenotypic and genotypic coefficients of variation
4. Heritability
5. Genetic advance

**(B) Association analysis**

1. Correlation coefficient estimates
2. Path coefficient analysis

**(C) Divergence analysis**

**(A) Univariate analysis**

**1. Analysis of variance**

Analysis of variance (Table 4.1) showed that mean sum of squares due to genotypes were highly significant for the characters *viz.* plant height, number of pods per plant, days to 50% flowering, days to maturity, 100 seed weight and seed yield per plant.

**2. Population mean and range**

The values of means and range were calculated for all the characters. The values of mean and range are presented in table 4.2.

**The values of Mean and Range:**

**(i) Plant height:**

Plant height varied from 30.87 to 60.80 cm with the mean of 40.75 cm. C-529(60.80) and C-528(51.93) was most prominent.

**Table 4.1. ANOVA showing mean sum of squares for different traits in chickpea**

| Source of variation | | Replication | Treatment | Error |
|---|---|---|---|---|
| d.f. | | 2 | 29 | 58 |
| Mean sum of squares | Plant height (cm) | 8.9609 | 138.2564** | 4.8424 |
| | No. of primary branches/ plant | 0.8703 | 0.7083 | 0.3386 |
| | No. of pods/ plant | 246.0078 | 257.8559** | 88.0227 |
| | No. of seeds/ pod | 0.0312 | 0.1231 | 0.5782 |
| | Days to 50 % flowering | 1.2968 | 93.8250** | 1.4150 |
| | Days to maturity | 0.1875 | 8.7816** | 1.3268 |
| | 100 seed weight | 15.3828 | 80.6364** | 5.3539 |
| | Seed yield / plant (g) | 3.6806 | 54.4265** | 1.8902 |

* = Significant at p = 0.05

** = Significant at p = 0.01

**(ii) Number of Primary branches:**

Number of primary branches per plant varied from 3.27 to 5.20 branches and mean was 3.9 branches. C-507(5.20) and C-519(4.67) was most prominent.

**(iii) Number of pods per plant:**

The range for number of pods per plant was from 32.33 to 70.00 pods and mean was 48.62 pods. C-531(70.0) and C-528(65.33) was most prominent.

**(iv) Number of seeds per pod:**

Number of seeds per pod ranged from 1.00 to 1.67 seeds with the mean of 1.16 seeds. C-509(1.67) and C-502(1.60) was most prominent.

**(v) Days to 50% flowering:**

The range for days to 50% flowering was from 61.33 to 85.67 days and mean was 72.40 days. C-502(61.33) and C-510(62.0) was most prominent.

**(vi) Days to maturity:**

For days to maturity mean data ranged from 125.67 to 132.33 days and mean was 128.97 days. C-523(125.67) and C-511,C-522,C-526(126.67) was prominent.

**(vii) 100 Seed weight:**

The range for 100 seed weight was from 17.59 to 37.76 g and mean was 26.15 g. C-501(37.76) and C-525(37.69) was most prominent.

**(viii) Seed yield per plant:**

The range for seed yield per plant was from 8.81 to 28.64 g and mean was 15.27 g. C-531(28.64) and C-523(23.51) was most prominent.

### 3. Coefficient of variation

Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were worked out for all the characters under study and have been presented in Table 4.2.

The highest PCV was recorded for seed yield per plant (28.84%) followed by number of pods per plant (24.73%), number of seeds per pod (22.35%), 100 seed weight (21.10%), number of primary branches per plant (17.38%), plant height (17.23%), days to 50% flowering (7.84%) and it was lowest for days to maturity (1.51%).

The highest GCV was recorded for seed yield per plant (27.40%) followed by 100 seed weight (19.16%), plant height (16.36%), number of pods per plant (15.47%), number of seeds per pod (11.69%), number of primary branches per plant (8.98%), days to 50% flowering (7.67%) and it was least for days to maturity (1.22%).

The estimate of PCV was higher than their respective GCV for all the characters under study.

### 4. Heritability

Heritability in broad sense was estimated for all the characters under both the conditions and presented in table 4.2.

High heritability estimates were recorded for days to 50% flowering (95.6%), seed yield per plant (90.3%), plant height (90.2%) and 100 seed weight (82.4%). Trait namely, viz; days to maturity (65.2%) showed moderate estimate of heritability, while, it was low for number of pods per plant (39.1%), number of seeds per pod (27.4%) and number of branches per plant (26.7).

### 5. Expected genetic advance

Expected genetic advance was estimated for all the characters under study in both the conditions and presented in table 4.2.

The estimates of expected genetic advance expressed as percentage of mean (Table 4.2) was high for seed yield per plant (53.63%), 100 seed weight (35.83%) and plant height (32.02%) whereas number of pods per plant (19.95%), days to 50% flowering (15.51%) and number of seeds per pod (12.69%) exhibited its moderate estimates, while, it was lowest for number of branches per plant (9.48%) and days to maturity (2.03%).

However high heritability coupled with high expected genetic advance was observed for seed yield per plant, plant height and 100 seed weight. Therefore, these characters are showing high additive component and hence, suitable for direct selection. While days to 50% flowering recorded high heritability with moderate expected genetic advance.

**Table 4.2 Parameters of genetic variation for various characters in chickpea**

| S.No. | Characters | Mean | Range | | PCV (%) | GCV (%) | Heritability (Broad sense) (%) | Genetic Advance | Genetic advance as % of mean |
|---|---|---|---|---|---|---|---|---|---|
| | | | Min. | Max. | | | | | |
| 1 | **Plant height (cm)** | 40.75 | 30.87 | 60.80 | 17.23 | 16.36 | 90.2 | 13.05 | 32.02 |
| 2 | **No. of primary branches/ plant** | 3.9 | 3.27 | 5.20 | 17.38 | 8.98 | 26.7 | 0.37 | 9.48 |
| 3 | **No. of pods/ plant** | 48.62 | 32.33 | 70.00 | 24.73 | 15.47 | 39.1 | 9.7 | 19.95 |
| 4 | **No. of seeds/ pod** | 1.26 | 1.00 | 1.67 | 22.35 | 11.69 | 27.4 | 0.16 | 12.69 |
| 5 | **Days to 50 % flowering** | 72.40 | 61.33 | 85.67 | 7.84 | 7.67 | 95.6 | 11.18 | 15.51 |
| 6 | **Days to maturity** | 128.97 | 125.67 | 132.33 | 1.51 | 1.22 | 65.2 | 2.62 | 2.03 |
| 7 | **100 seed weight** | 26.15 | 17.59 | 37.76 | 21.10 | 19.16 | 82.4 | 9.37 | 35.83 |
| 8 | **Seed yield / plant (g)** | 15.27 | 8.81 | 28.64 | 28.84 | 27.40 | 90.3 | 8.19 | 53.63 |

## (B) ASSOCIATION ANALYSIS

### (1) Estimates of correlation coefficients

Estimates of phenotypic and genotypic correlation coefficients between chick pea yield and its contributing characters and among themselves were worked out and are presented in table 4.3, 4.4 respectively.

**Correlation coefficients between seed yield and its attributing traits in chickpea**

**(A) Correlation with yield**

**(a) At phenotypic level**

Table 4.3 revealed that seed yield per plant showed significant positive correlation with number of pods per plant (0.553), 100 seed weight (0.303), number of seeds per pod (0.244) and plant height (0.236) but it was significant and negative with days to 50% flowering (-0.247).

**(a) At genotypic level**

Table 4.4 shows that days to 50% flowering (-0.273) had negative correlation with yield while number of pods per plant (0.921), number of seeds per pod (0.501), 100 seed weight (0.365) and plant height (0.257) had positive correlation with yield.

**(B) Correlation among yield attributing characters**

**(a) At phenotypic level**

**(i) Plant height:**

Table 4.3 showed that plant height had significant positive correlation with number of seeds per pod (0.306), days to 50% flowering (0.246) and number of pod per plant (0.229).

**(ii) Number of primary branches per plant:**

Number of primary branches per plant had significant positive correlation with number of pods per plant (0.291).

**(iii) Number of pods per plant:** Number of pods per planat has significant positive correlation with number of seeds per pod (0.243).

**Table 4.3. Estimates of phenotypic correlation coefficients**

| S.No. | Characters | No. of primary branches/ plant | No. of pods/ plant | No. of seeds/ pod | Days to 50 % flowering | Days to maturity | 100 seed weight | Seed yield / plant (g) |
|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | 0.068 | 0.229* | 0.306** | 0.246* | 0.020 | -0.022 | 0.236* |
| 2 | No. of primary branches/ plant | | 0.291** | 0.103 | -0.023 | -0.034 | -0.181 | 0.028 |
| 3 | No. of pods/ plant | | | 0.243* | 0.045 | 0.091 | 0.045 | 0.553** |
| 4 | No. of seeds/ pod | | | | 0.020 | -0.228* | -0.105 | 0.244* |
| 5 | Days to 50 % flowering | | | | | 0.160 | 0.319** | -0.247* |
| 6 | Days to maturity | | | | | | 0.198 | 0.035 |
| 7 | 100 seed weight | | | | | | | 0.303** |

* = Significant at p = 0.05

** = Significant at p = 0.01

**Table 4.4. Estimates of genotypic correlation coefficients**

| S.No. | Characters | No. of primary branches/ plant | No. of pods/ plant | No. of seeds/ pod | Days to 50 % flowering | Days to maturity | 100 seed weight | Seed yield / plant (g) |
|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | 0.164 | 0.291 | 0.663 | 0.260 | -0.016 | -0.020 | 0.257 |
| 2 | No. of primary branches/ plant | | 0.670 | 0.380 | -0.028 | 0.071 | -0.400 | 0.054 |
| 3 | No. of pods/ plant | | | 0.897 | 0.049 | 0.014 | 0.113 | 0.921 |
| 4 | No. of seeds/ pod | | | | 0.026 | -0.418 | -0.183 | 0.501 |
| 5 | Days to 50 % flowering | | | | | 0.195 | -0.349 | -0.273 |
| 6 | Days to maturity | | | | | | 0.240 | 0.031 |
| 7 | 100 seed weight | | | | | | | 0.365 |

**(iv) Number of seeds per pod:**

Number of seeds per pod showed significant negative correlation with days to maturity (-0.228) and significant positive association with seed yield /plant (0.244).

**(v) Days to 50% flowering:**

Days to 50% flowering showed significant positive correlation with 100 seed weight (0.319). and negative correlation with seed yield (-0.247)

**(vi) Days to maturity:**

Days to maturity exhibited non-significant positive correlation with 100 seed weight (0.198).

**(v) 100 seed weight:**

The traits *viz.,* 100 seed weight shows non-significant positive correlation with harvest index (0.045).

## (b) At genotypic level

**(i) Plant height:**

(Table 4.4) plant height had significant positive correlation with number of seeds per pod (0.663), number of pod per plant (0.291) and days to 50% flowering (0.260).

**(ii) Number of primary branches per plant:**

Number of primary branches per plant exhibited significant positive correlation with number of pods per plant (0.690) and number of seeds per pod (0.380) while it showed significant negative correlation with 100 seed weight (-0.400).

**(iii) Number of pods per plant:**

Number of pods per plant has significant positive correlation with number of seeds per pod (0.897).

**(iv) Number of seeds per pod:**

Number of seeds per pod showed significant negative correlation with days to maturity (-0.418).

**(v) Days to 50% flowering:**

Days to 50% flowering showed significant negative correlation with 100 seed weight (-0.349).

**(vi) Days to maturity:**

Days to maturity exhibited significant positive correlation with 100 seed weight (0.240).

**(v) 100 seed weight:**

The traits *viz.,* 100 seed weight shows non-significant positive correlation with number of pods per plant (0.113).

**(2) Path coefficient analysis**

Path coefficient analysis was carried out taking seed yield per plant as a dependent variable. The correlation coefficients of seed yield and yield-attributing characters were further partitioned in to direct and indirect effects. The direct and indirect effects of seed yield attributing traits in table 4.5 and 4.6 at genotypic and phenotypic levels respectively.

**(A) Genotypic Path Coefficient analysis of yield attributing characters on seed yield**

The genotypic correlation coefficient of seed yield to yield attributing characters are further partitioned in to direct and indirect effects. The results are presented in Table 4.5.

**1. Direct effect**

Number of seeds per pod possessed the maximum direct effect of (1.601) followed by number of pods per plant (0.329), days to maturity (0.600) and 100 seed weight (0.479). It was observed that the plant height (-0.656), number of primary branches per plant (-0.080) and days to 50% flowering (-0.079) registered the negative direct effect.

## 2. Indirect effect

### (i) Plant height:

Plant height registered the maximum positive indirect effect through number of seeds per pod (1.062) while negative indirect effects exhibited by plant height through all other characters were negligible.

### (ii) Number of primary branches per plant:

Maximum positive indirect effect was found via number of seeds per pod (0.609) followed by days to maturity and days to 50% flowering whereas negative indirect effect observed by number of pods per plant (-0.220), 100 seed weight(-0.192) and plant height(-0.108).

### (iii) Number of pods per plant:

Number of pods per plant exhibited maximum positive indirect effect via number of seeds per pod (1.436) whereas the maximum negative indirect effect was registered via plant height (-0.191).

### (iv) Number of seeds per pod:

Maximum negative indirect effect was found to be via plant height (-0.435) followed by number of pods per plant and days to maturity.

### (v) Days to 50% flowering:

Days to 50% flowering showed that maximum positive indirect effect was found via days to maturity (0.117) followed by number of seeds per pod and number of branches per plant while maximum negative indirect was showed by Plant height (-0.170) and 100 seed weight.

### (vi) Days to maturity:

Days to maturity showed maximum positive indirect effect was noted via number of 100 seed weight (0.115) followed by plant height while mximum negative effect was recorded by number of seeds per pod (-0.669) and days to 50% flowering.

### (vii) 100 seed weight:

100 seed weight registered maximum positive indirect effect through days to maturity (0.144) followed by number of primary branches per plant, days to 50% flowering and plant height, whereas the maximum negative indirect effect was recorded via number of seeds per pod (-0.294) and number of pods per plant.

## 3. Residual effect:

The residual effect was found to be 0.4593.

**(C) Divergence analysis:**

The analysis of variance showing mean squares (Table 4.1) revealed highly significant differences among the accessions for all the 8 characters under investigation indicating the presence of considerable genetic variability in the experimental material. From the estimates of variances, and co-variances, v-statistic, which utilizes Wilk's criterion, a simultaneous test of all 8 characters was done, which also showed highly significant differences among thirty genotypes ($\chi^2$ = 1526.34 for 232 d.f.)

These differences suggested the existence of considerable divergence among the material under study.

**(i) $D^2$ statistic:**

The generalized distance ($D^2$ values) corresponding to 457 possible combinations between pairs of genotypes was computed. The $D^2$ values ranged from 7.12 (between genotypes 7 and 14) to 433.88 (between genotypes 2 and 22).

**Clusters of genotypes and estimates of intra and inter cluster distance:**

Using Tocher's method, as suggested by Rao (1952), 30 genotypes were grouped into 6 clusters. The genotypes included in each cluster have been reported in Table 4.7. Cluster I the contained maximum number of genotypes (8) and cluster VI contained 5 genotypes only.

**Table 4.5 Genotypic path coefficient showing direct (diagonal) and indirect effects**

| S.No. | Characters | Plant height (cm) | No. of primary branches/ plant | No. of pods/ plant | No. of seeds/ pod | Days to 50 % flowering | Days to maturity | 100 seed weight | $r_{sy}$ |
|---|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | **-0.656** | -0.013 | -0.096 | 1.062 | -0.021 | -0.009 | -0.010 | 0.257 |
| 2 | No. of primary branches/ plant | -0.108 | **-0.080** | -0.220 | 0.609 | 0.002 | 0.042 | -0.192 | 0.054 |
| 3 | No. of pods/ plant | -0.191 | -0.054 | **0.329** | 1.436 | -0.004 | 0.008 | 0.054 | 0.921 |
| 4 | No. of seeds/ pod | -0.435 | -0.030 | -0.295 | **1.601** | -0.002 | -0.251 | -0.088 | 0.501 |
| 5 | Days to 50 % flowering | -0.170 | 0.002 | -0.016 | 0.041 | **-0.079** | 0.117 | -0.167 | -0.273 |
| 6 | Days to maturity | 0.010 | -0.006 | -0.005 | -0.669 | -0.016 | **0.600** | 0.115 | 0.031 |
| 7 | 100 seed weight | 0.013 | 0.032 | -0.037 | -0.294 | 0.028 | 0.144 | **0.479** | 0.365 |

Residual effect = 0.4593

**Table 4.6 Phenotypic path coefficient showing direct (diagonal) and indirect effects**

| S.No. | Characters | Plant height (cm) | No. of primary branches/ plant | No. of pods/ plant | No. of seeds/ pod | Days to 50 % flowering | Days to maturity | 100 seed weight | $r_{sy}$ |
|---|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | **0.157** | -0.008 | 0.121 | 0.033 | -0.063 | 0.001 | -0.004 | 0.236 |
| 2 | No. of primary branches/ plant | 0.011 | **-0.119** | 0.154 | 0.011 | 0.006 | 0.001 | -0.034 | 0.028 |
| 3 | No. of pods/ plant | 0.036 | -0.035 | **0.528** | 0.026 | -0.011 | 0.001 | 0.009 | 0.553 |
| 4 | No. of seeds/ pod | 0.048 | -0.012 | 0.129 | **0.107** | -0.005 | -0.002 | -0.020 | 0.244 |
| 5 | Days to 50 % flowering | 0.039 | 0.003 | 0.024 | 0.002 | **-0.0256** | 0.001 | -0.060 | -0.247 |
| 6 | Days to maturity | 0.003 | 0.004 | 0.048 | -0.024 | -0.041 | **0.007** | 0.037 | 0.035 |
| 7 | 100 seed weight | -0.003 | 0.022 | 0.024 | -0.011 | 0.082 | 0.001 | **0.189** | 0.303 |

Residual effect = 0.5273

**Table 4.7. Populations in cluster**

| Cluster | Genotypes included in cluster | Number of population |
|---|---|---|
| I | C-505, C-513, C-516, C-532, C-533, C-534, C-535, C-537 | 8 |
| II | C-502, C-510, C-523 | 3 |
| III | C-504, C-507, C-514, C-530, JG-16 | 5 |
| IV | C-508, C-509, C-511, C-517, C-519, C-522, C-528 | 7 |
| V | C-501, C-525 | 2 |
| VI | C-520, C-521, C-526, C-529, C-531 | 5 |

The intra and inter-cluster D and $D^2$ values among the five clusters are presented in table 4.8 and 4.9. In these tables, the diagonal values denote mean intra cluster distance and off the diagonal values represent inter cluster distances.

The intra cluster divergence ranged from 1.516 to 2.009. The intra cluster $D^2$ values were almost parallel. While cluster IV which had the highest intra cluster $D^2$ value of 4.036 comprised 7 genotypes indicating diversity between the genotypes within the cluster. The maximum divergence at inter cluster level was observed between cluster IV and V (17.430) followed by clusters, I and VI (17.156), III and IV (15.303), V and VI (13.786), III and V (11.840), II and V (10.837), I and IV (10.374), I and V (9.175) whereas, the minimum divergence at inter cluster level was observed between clusters I and III (6.105).

**Cluster mean:**

Clusters means of all 8 characters have been presented in Table 4.8 and detailed as below:

**(a) Plant height:**

The cluster mean was highest (46.32) for cluster VI and lowest (34.11) for cluster III.

**(b) Number of primary branches/ plant:**

Cluster mean was highest (4.33) for cluster III and lowest (3.39) for cluster I.

**(c) No. of pods/ plant:**

Cluster mean was highest (62.00) for cluster VI and lowest (37.75) for cluster I.

**(d) No. of seeds/ pod:**

Cluster mean was highest (1.44) for cluster IV and lowest (1.08) for cluster III.

**(e) Days to 50 % flowering:**

Cluster mean was highest (78.00) for cluster IV and lowest (62.89) for cluster II.

**(f) Days to maturity:**

Cluster mean was highest (131.17) for cluster V and lowest (128.11) for cluster II.

**(g) 100 seed weight:**

Cluster mean was highest (37.73) for cluster V and lowest (22.55) for cluster III.

**(h) Seed yield/ plant (g):**

Cluster mean was highest (22.61) for cluster VI and lowest (12.67) for cluster I.

**(d) Cluster characteristics:**

Table 4.10 revealed that Cluster I did not show desirable mean level for any of the characters under study.

Cluster II was characterized by days to 50% flowering (62.89) and days to maturity (128.11) which had the lowest mean value for this trait.

Cluster III was characterized by number of primary branches per plant (4.33) which had highest mean value for this trait.

Cluster IV was characterized by the highest value for number of seeds per pod (1.44).

**Table 4.8. Average intra and inter-cluster distance (D-values) of different clusters in chickpea**

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 1.879 | 3.008 | 2.471 | 3.221 | 3.117 | 4.142 |
| II | | 1.547 | 2.927 | 3.065 | 3.292 | 2.857 |
| III | | | 1.722 | 3.912 | 3.441 | 2.716 |
| IV | | | | 2.009 | 4.175 | 2.790 |
| V | | | | | 1.516 | 3.713 |
| VI | | | | | | 1.954 |

**Table 4.9. Inter and intra (diagonal) cluster divergence ($D^2$) in chickpea**

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 3.530 | 9.084 | 6.105 | 10.374 | 9.715 | 17.156 |
| II | | 2.393 | 8.567 | 9.394 | 10.837 | 8.265 |
| III | | | 2.965 | 15.303 | 11.840 | 7.376 |
| IV | | | | 4.036 | 17.430 | 7.784 |
| V | | | | | 2.298 | 13.786 |
| VI | | | | | | 3.818 |

Table 4.10. Cluster means for 10 characters

| S.No. | characters | I | II | III | IV | V | VI | Range (difference between max. and min.) |
|---|---|---|---|---|---|---|---|---|
| 1 | Plant height (cm) | 38.91 | 40.76 | 34.11 | 44.69 | 37.13 | 46.32 | 12.21 |
| 2 | No. of primary branches/ plant | 3.39 | 4.02 | 4.33 | 4.19 | 3.83 | 3.89 | 0.94 |
| 3 | No. of pods/ plant | 37.75 | 47.00 | 47.13 | 52.62 | 50.83 | 62.00 | 24.25 |
| 4 | No. of seeds/ pod | 1.10 | 1.40 | 1.08 | 1.44 | 1.13 | 1.43 | 0.36 |
| 5 | Days to 50 % flowering | 72.42 | 62.89 | 72.00 | 78.00 | 68.50 | 72.20 | 15.11 |
| 6 | Days to maturity | 128.83 | 128.11 | 129.40 | 128.57 | 131.17 | 129.00 | 3.06 |
| 7 | 100 seed weight | 27.00 | 26.96 | 22.55 | 23.19 | 37.73 | 27.41 | 14.18 |
| 8 | Seed yield/plant (g) | 12.67 | 16.98 | 13.24 | 13.54 | 15.97 | 22.61 | 9.94 |

Cluster V was characterized by the highest value for 100 seed weight (37.73).

Cluster VI was characterized by the highest value for plant height (46.32) number of pods per plant (62.00) and Seed yield per plant (22.61).

**(ii) Canonical analysis:**

How far the divergence between the genotypes arrived at $D^2$ values agrees with those determined by the use of canonical analysis method was also examined. This method dealt with the replacement of the measurements of a number of mutually correlated characters by relatively few measurements obtained as linear combinations of large number of such measurements. The divergence as determined by canonical analysis following the procedure given by Rao (1952), the standardized best linear functions (canonical vectors) were obtained and are presented in Table 4.11. Of the total variation, the first root alone accounted for 48.94% and is the major axis of differentiation. Further, first two roots together accounted for 73.30% of the diversity indicating that the difference for these traits in these genotypes was nearly complete in the two phases. It was observed spositions in $D^2$ analysis.

From the coefficients of 1st canonical root, it was found that primary axis was based on days to 50% flowering, seed yield per plant, plant height and 100 seed weight.

The coefficients of canonical root II revealed that the 2nd axis was mainly concerned with plant height, seed yield per plant, days to 50% flowering and number of seeds per plant.

With respect to the relative importance of different characters under study, it would be apparent from the absolute size of coefficients that days to 50% flowering (0.8934), seed yield per plant (0.4128), plant height (0.1230) and 100 seed weight (0.1089) were important in the primary axis of differentiation and in the secondary axis of differentiation, plant height (0.7307), seed yield per plant (0.5767), days to 50% flowering (0.1939) and number of seeds per pod (0.1882) were important.

**Table 4.11. Values of first two canonical vectors, which supply the best linear function of variates**

| Characters | Canonical roots | |
|---|---|---|
| | CR I | CR II |
| Plant height (cm) | 0.1230 | 0.7307 |
| No. of primary branches/ plant | 0.0045 | 0.0476 |
| No. of pods/ plant | -0.0636 | -0.0103 |
| No. of seeds/ pod | -0.0038 | 0.1882 |
| Days to 50 % flowering | 0.8934 | 0.1939 |
| Days to maturity | 0.0174 | -0.1115 |
| 100 seed weight | 0.1089 | -0.2137 |
| Seed yield/plant (g) | 0.4128 | 0.5767 |
| **Percentage of variation observed** | **48.94** | **24.36** |

# CHAPTER – V

# DISCUSSION

An investigation entitled "$D^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea (Cicer arietinum) under rainfed conditions"was carried out during Rabi of 2010-2011 at Research Farm, College of Agriculture, Gwalior.

The results of the work have been discussed in this chapter in conjunction with the findings of other workers. The discussion is confined to the relevant topics, *viz.* variability, heritability, genetic advance, association analysis and genetic divergence.

**Variability**

A broad spectrum of variability is a key factor for success of a plant-breeding programme because it provides an opportunity to the plant breeder for making desired improvement in population by increasing the frequency of desirable individuals. Wide range of variability for traits is also necessary to isolate significantly superior genotypes for commercial cultivation or to be used as parents in hybridization programme for combination breeding or to develop high yielding hybrid varieties or to create useful genetic variability for further improvement.

Wide range of variability was observed in the experimental material for all the traits under study. The values of mean and range revealed that there is wide variability among genotypes for most of the characters. The variation was uniformly distributed on the both sides of the means for each character, indicating normal distribution in the population for all characters. The value of mean sum of squares due to genotypes was significant for all the traits under stress and non-stress conditions except for number of seeds per pod in non-stress situation. This suggests that the experimental material differed significantly amongst them.

High estimates of PCV was observed for seed yield per plant followed by number of pods per plant, number of seeds per pod, 100 seed weight, number of primary branches per plant, plant height and days to 50% flowering. Similar trend was observed at genotypic level also. Thus, the present investigation revealed that there is sufficient genetic variability exist in the population and a lot of scope for achieving desirable improvement.

The difference between PCV and GCV was negligible/ low for seed yield per plant, 100 seed weight, plant height and days to 50% flowering. This suggests that the expression of these traits were least affected by the environmental factors and their phenotype is the true representative of its genotype. Further, the selection on the basis of *per se* performance will be effective.

The results were in the agreement with the findings of Nimbalkar (2000), Arora and Jeena (2001), Arora and Jeena (2001), Kumar *et al.* (2001a), Yadav *et al.* (2003), Ajinder *et al.* (2004), Jeena *et al.* (2005), Meena *et al.* (2006), Dubey and Shrivastava (2007) , Lokare *et al.* (2007), Thakur and Sirohi (2008), Dwevedi and Lal (2009), Tomar and Singh (2009) , Vaghela *et al.* (2009) and Borate et al. (2010).

**Heritability**

The total variability, which is present in the population, will not be transmitted; only its heritable portion will be transmitted to the next generation. The knowledge of heritable proportion of genetic variability present in the population can be obtained by another genetic parameter that is heritability estimates.

Heritability estimate in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. It is an index of transmission of a character from parents to their offspring. It helps the plant breeders in the selection of superior genotypes from the genetically variable population. Robinson *et al.* (1949) had classified heritability estimate in broad sense as high (above 70%), medium (50-70%) and low (below 50%).

The estimates of heritability are influenced by various factors such as sample size, sampling methods, effects of linkage, method of estimation and population density etc and other biotic and abiotic factors that effect the expression of the characters in the population. Thus, heritability estimate is not only the property of the characters alone but it is the property of population and environmental factors. When the estimate of heritability was high indicating the phenotypic appearance would provides a close measure of genotypic value and thus, a breeder can make selection on the basis of *per se* performance of the individuals.

In present investigation high estimates of heritability in broad sense were observed for days to 50% flowering, seed yield per plant, plant height and 100 seed weight. However days to maturity showed moderate heritability.

The present findings were in conformity with the findings of Nimbalkar (2000) for 100 seed weight, Jeena and Arora (2001) for 100 seed weight, Albinbas (2002) for 100 seed weight and seed yield, Sable *et al.* (2003) for seed yield per plant and 100 seed weight, Jeena *et al.* (2005) for 100-seed weight and seed yield per plant, Mohammad *et al.* (2005) for plant height, 100-seed weight and seed yield, Thakur and Sirohi (2008) for seed yield per plant, 100-seed weight and plant height, Tomar and Singh (2009) for plant height, seed yield per plant and 100 seed weight and Borate et al. (2010) for plant height in chickpea.

**Expected Genetic advance**

The improvement showed by the population, which is expected by selection for a character was estimate of another genetic parameters, that is genetic advance. It measures genetic gain under selection. It is influenced by the genetic variability present in the base population for the particular trait; heritability estimate for the character under selection and the proportion of individuals selected that is selection intensity. Since, the genetic advance is affected by the unit of measurement, genetic advances as percentage of mean was calculated which is free from unit and it will facilitate the comparison of genetic gain for various characters.

The estimates of expected genetic advance was high for seed yield per plant, 100 seed weight and plant height whereas, number of pods per plant, days to 50% flowering; and number of seeds per pod had moderate estimates of expected genetic advance; number of branches per plant and days to maturity possessed low values for expected genetic advance.

High heritability coupled with high expected genetic advance was observed for seed yield per plant, plant height and 100 seed weight. While, days to 50% flowering had high heritability with moderate expected genetic advance suggesting the additive gene action plays important role in the expression of these traits. The desirable improvement can be achieved by simple selection procedure.

The present results were in agreement with the findings of Jeena and Arora (2000) for 100 seed weight and seed yield per plant, Nimbalkar (2000) for 100-grain weight, Jeena and Arora (2001) for 100 seed weight, Jeena *et al.* (2005) for 100-seed weight and seed yield per plant, Raval and Dobariya (2005) for seed yield per plant and 100-seed weight, Thakur and Sirohi (2008) for seed yield per plant, 100-seed weight and plant height, Tomar and Singh (2009) for plant height, seed yield per plant and 100 seed weight and Borate et al. (2010) for plant height in chickpea.

**Correlation coefficients**

Yield is an important and a complex quantitative trait, which is, governed by large number of genes with small individual gene effects and the expression of individual genes is greatly influenced by environmental factors. Thus, the desired improvement for seed yield can only be achieved indirectly i.e., by practicing selection for characters that are highly heritable and exhibiting strong and positive association with seed yield.

Correlation is the relationship between two attributes and the strength of relationship is measured in terms of correlation coefficient, its limits range from minus unity to plus unity.

If increase in one variable result in the increase of other variable, the relationship is positive and if it results in the decrease of other variable, the association is said to be negative. The two variables are said to be uncorrelated if any changes in one variable does not affect the other variable.

Knowledge of correlation helps a plant breeder to determine the methodology to improve a particular trait that is not readily amenable to direct selection and so indirect selection becomes inevitable. It also provides information about the correlated response to directional selection to predict genetic advance and thus can be used as selection index for operating more efficient selection programme.

Correlation could be phenotypic, genotypic or environmental. Phenotypic correlation between values directly measured on individuals and includes genetic and non-genetic effects. Genotypic correlation shows the relationship between breeding values and accounts for only genetic causes, which could be pleiotropy, linkage or gene frequency disequilibrium. Environmental correlation indicates the relationship between non-genetic values and which were arises due to the fact that several observations were affected by the same amount of environment. Therefore, the knowledge of correlations is of great significance.

The estimates of phenotypic correlation coefficients revealed that seed yield per plant was positively correlated with number of pods per plant, 100 seed weight, number of seeds per pod and plant height. This suggested that improvement in any one of them through direct selection would result in improvement in seed yield per plant.

The appearance of correlation at genotypic level indicated that these characters were highly influenced by the environment. Such characters need to be carefully included in selection indices to exploit correlated response.

Arun kumar *et al.* (2000), Mishra *et al.* (2000), Vijaya lakshmi *et al.* (2000), Guler *et al.* (2001), Yadav et *al*. (2001), Kumar *et al*. (2001b), Narayan and Reddy (2002), Saleem *et al.* (2002), Singh *et al*. (2002), Sail *et al.* (2003), Brar *et al.* (2004), Atta (2008), Sidramappa *et al.* (2008) and Tomar and Singh (2009) also reported similar results.

**Path coefficient analysis**

In order to achieve clear-cut picture of cause and effect relationship of yield attributes, their extent of correlation studies is not sufficient. Path analysis devised by Wright (1921) provided measures of direct and indirect effects of trait on yield splitting the correlation coefficient in to direct and indirect effects.

The results of path coefficient analysis based on genotypic coefficients taking seed yield as dependent variable, indicated that the traits namely, number of seeds per pod**,** number of pods per plant, days to maturity and 100 seed weight exhibited strong positive direct effects on seed yield. Number of pods per plant, number of seeds per pod and 100 seed weight showed strong positive correlation and also exhibited positive direct effect on yield. It revealed that true relationship of these traits with seed yield existed and hence, direct selection for these characters would be rewarding for improvement in yield. However the direct effects indicated by traits like plant height, number of primary branches per plant and days to 50% flowering were found to be negative and very low in magnitude.

Number of pods per plant revealed positive direct effect and strong correlation on seed yield *via* plant height, number of primary branches per plant and number of seeds per pod. Number of seeds per pod had positive direct effect on seed yield but its strong correlation with seed yield may be ascribed to the fact that this character had positive effects via plant height and number of pods per plant. 100 seed weight revealed strong correlation and positive direct effect on seed yield *via* number of days to 50% flowering. Days to maturity has positive direct effect on seed yield *via* 100 seed weight.

The residual effects were negligible for path coefficient of yield attributing characters. This indicated that most of the components traits, which contribute for seed yield, have been included in the present investigation.

It could be concluded from the present investigation that the characters like number of seeds per pod, number of pods per plant and 100 seed weight possessed strong positive association and high magnitude of positive direct effects on seed yield. Moreover the indirect effects of most of the characters *via* these characters were positive. Thus these traits were conceded as the most important yield attributing characters.

The present results were in agreement with the findings of Rao and Kumar (2000) for number of pods per plant and 100 seed weight, Yadav *et al.* (2002) for 100 seed weight, Mardi *et al.* (2003) for number of seeds per pod, Lokare *et al.* (2007) for number of pods per plant, number of seeds per pod and 100 seed weight, Sidramappa *et al.* (2008) for number of pods per plant and Singh and Sandhu (2008) for 100- seed weight and number of seeds per pod.

**Genetic divergence:**

The choice of parents is of paramount importance in any breeding programme. It is rather a difficult task for a plant breeder. Selection of parents on the basis of *per se* performance is good but there is a possibility of related lines being chosen resulting in limited or no advances under selection and, therefore, there is a need for emphasis on a wide genetic base by the utilization of world collection on genetic criterion. Selection of parents on the basis of geographical diversity is another way of choosing parents and this has led to success in some cases but these needs to be supplemented with genetic diversity. The measures based on genetic criteria qualifying diversity have become important in classifying material for the use by the breeders. Further, the genetic divergence among the parents is important because a cross involving genetically diverse parents is likely to produce high heterotic effect and also a broad spectrum of variability could be expected in the segregating generations. The assessment of divergence for a set of genotypes using multivariate analysis like distance analysis, canonical analysis etc. has been attempted and effectively utilized in a number of crop plants with diverse breeding systems (Murty and Arunachalam, 1966). Thus, the genetic divergence has a definite role to play for efficient choice of parents for hybridization programme.

The analysis of variance revealed highly significant differences among genotypes for almost all the eight characters studied. The dispersion amongst variables for the aggregate effect of the eight characters as tested by Wilk's criterion was also highly significant indicating existence of considerable divergence in the material under study.

Genetic differences among genotypes were quantified by estimating $D^2$ statistics. The $D^2$ values ranged from 7.12 (between genotypes 7 and 14) to 433.88 (between genotypes 2 and 22).

The estimates of $D^2$ values varied substantially from 7.12 to 433.88. The maximum divergence ($D^2$ = 433.88) was recorded between genotype C-502 and C-529. A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization. On the other hand, minimum divergence ($D^2$=7.12) was observed between genotypes C-509 and C-519 which did not differ significantly from each other, these may be related in their evolution.

Using Tocher's method as suggested by Rao (1952), 30 genotypes were grouped into 6 clusters. Cluster I the contained maximum number of genotypes (8) and cluster V contained 2 genotypes only.

Comparison of inter and intra cluster distances for each population revealed that cluster IV and V were most divergent followed by clusters, I and VI, III and IV, V and VI, III and V, II and V, I and IV, I and V. Crosses between lines carefully selected from these clusters are expected to throw a wide range of segregants.

In the present study, $D^2$ cluster means and inter cluster divergence were utilized for the choice of parents and deciding the cross combinations which are likely to produce the highest possible variability and high heterotic effect for various economic characters. Cluster means for the 8 traits of all the 6 clusters were worked out. It was found that Cluster VI had the highest value for plant height, number of pods per plant and Seed yield per plant. Cluster V had highest mean value for 100 seed weight. Cluster IV had the highest mean value for number of seeds per pod. Cluster III had the highest mean value for number of primary branches per plant. Cluster II had lowest mean value for days to 50% flowering and days to maturity.

To improve any particular trait donor for hybridization could be chosen from an appropriate cluster.

The following genotypes of marked mean performance from the selected clusters may serve as parents for hybridization programmes.

| Cluster | Characters | Genotypes |
|---|---|---|
| II | Early in days to 50% flowering | C-502 |
| | Early maturity | C-523 |
| III | Higher number of primary branches per plant | C-507 |
| IV | more number of seeds per pod | C-509 |
| V | Higher 100 seed weight | C-501 |
| VI | Higher number of pods per plant and high seed yield | C-531 |
| | Tallness | C-529 |

**Canonical analysis:**

Mahalanobis (1936) generalized distance $D^2$ statistic, is a useful measure of genetic divergence among genotypes. It provides degree of divergence based on multiple variables. However, it does not provide any indication about the quantum of contribution of each character towards the total genetic divergence. Further, it is difficult to classify characters, by $D^2$ statistic, into major or secondary traits, based on their contribution to the total genetic divergence. Canonical analysis is another useful technique to analyse genetic divergence based on multivariate analysis. It not only discerns the genetic divergence but also supplies information about relative contribution of the traits under study.

In present study, canonical analysis was carried out to classify all the thirty chick pea genotypes and to verify the clustering pattern on the basis of $D^2$ values. First two roots were considered for this study. The variability explained by the first two roots was 73.30% per cent of the total variability.

The coefficient of canonical root -1 revealed that the primary axis rotated around days to 50% flowering, seed yield per plant, plant height and 100 seed weight. These traits thus, were primarily responsible for variation between genotypes. It indicated that these yield components were the major traits for genetic divergence. Therefore, greater significance needs to be attached to these traits during selection.

The estimates of coefficients of canonical root II revealed that the second axis was primarily concerned with plant height, seed yield per plant, days to 50% flowering and number of seeds per plant.

It could be concluded that these traits contributed moderately to the genetic differences and thus, be given careful attention while selecting parents to improve these traits.

# CHAPTER – VI

# SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FURTHER STUDY

The present investigation "$D^2$ analysis and characters association studies for seed yield, its contributing traits in chickpea (*Cicer* arietinum) under rainfed conditions"was carried out during *Rabi* of 2010-2011 at Research Farm, College of Agriculture, Gwalior. The genotypes were grown in Randomized Block design with three replications.

The observations were recorded on plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, days to 50% flowering, days to maturity, 100 seed weight and seed yield per plant. The data on all characters were subjected to statistical analysis. The summarized findings of the investigation have been presented here under:

**Summary:-**

Analysis of variance revealed highly significant differences among genotypes for all the characters at univariate. Estimates of population mean were high and range was wide for most of the traits. Trend of variability at genotypic level was similar to that observed at phenotypic level for most of the characters. The genotypic coefficient of variation was highest for seed yield per plant, number of pods per plant, number of seeds per pod, 100 seed weight, number of primary branches per plant, plant height and days to 50% flowering.

The estimates of heritability in broad sense for most of the traits were high. High estimates of heritability were observed for days to 50% flowering, seed yield per plant, plant height and 100 seed weight.

The expected genetic advance as percent of mean was highest for high for seed yield per plant, 100 seed weight and plant height.

High heritability coupled with high expected genetic advance was observed for seed yield per plant, plant height and 100 seed weight.

The estimates of correlation coefficients revealed that seed yield per plant was positively correlated with number of pods per plant, 100 seed weight, number of seeds per pod and plant height. This suggested that improvement in any one of them through direct selection would result in improvement in seed yield per plant.

Path association revealed that the characters like number of seeds per pod**,** number of pods per plant, days to maturity and 100 seed weight exhibiting positive correlation and high magnitude of positive direct effects on seed yield should be given due weightage in the constitution of selection index.

Wilk's criterion revealed highly significant differences among genotypes studied, at multivariate level and indicated the existence of considerable divergence among the genotypes. Based on $D^2$ statistic, all the 30 genotypes were grouped into 6 clusters. Cluster I contained the maximum number of genotypes (8) and minimum cluster V had 2 genotypes. The maximum divergence was observed between cluster IV and V and the minimum between cluster I and III. The highest average intra cluster distance was recorded for cluster IV and the lowest for cluster V.

Canonical analysis revealed that days to 50% flowering, seed yield per plant, plant height and 100 seed weight were the major traits causing genetic divergence among genotypes.

**Conclusions**

- The characters namely, seed yield per plant, number of pods per plant, number of seeds per pod, 100 seed weight, number of primary branches per plant, plant height and days to 50% flowering exhibited wide range and high PCV and GCV offering ample scope for improvement through selection. Besides this, these characters also had narrow differences between the values of PCV and GCV showing least influence of environment.

- High heritability coupled with high genetic advance observed for seed yield per plant, plant height and 100 seed weight indicated that these traits are governed by additive gene action. Hence, there are good chances of improvement of these traits through direct selection.

- On the basis of association and path coefficient analysis number of seeds per pod**,** number of pods per plant and 100 seed weight were found to be major component traits that contribute towards seed yield. Hence, due weightage should be given while practicing selection for identifying high yielding strains.

- The maximum divergence ($D^2$ = 433.88) was recorded between genotype C-502 and C-529. These two genotypes also showed significant differences between them in respect of most of the characters. A cross between these two genotypes is expected to give a heterotic hybrid and wide spectrum of variability. Therefore, these genotypes may be used as parents for hybridization.

- The coefficient of canonical root I revealed that the primary axis rotated around days to 50% flowering, seed yield per plant, plant height and 100 seed weight thus was primarily responsible for variation between genotypes. It indicated that number of 1000 grain weight was the major yield component for genetic divergence. Therefore, greater significance needs to be attached to this trait during selection.

- The estimates of coefficients of canonical root II revealed that the second axis was primarily concerned with plant height, seed yield per plant, days to 50% flowering and number of seeds per pod. Thus, these traits contributed moderately to the genetic differences and thus be given careful attention while selecting parents to improve these traits.

- The accessions C-501, C-502, C-507, C-509, C-523, C-529 and C-531 may serve as potential parents for hybridization programme in improvement of potentiality of the high yielding, early maturing and tallest genotypes.

**Suggestions for further work:**

The following suggestions have been made for further study:-

❖ The genetic variability reported for different characters in relation to yield should be exploited.

❖ Characters showing high heritability with high genetic advance should be utilized in selection.

❖ A better crop ideotype should be developed using findings from association analysis.

❖ The promising stable genotypes identified can be tested for combining ability and inheritance of yield and its contributing traits for further use in breeding programme.

❖ These genotypes may be tested for genetic diversity study for one or two more years so as to derive some concrete conclusions regarding diversity spectrum.

❖ Genotypes from different clusters, identified for a specific character may be used as parent for breeding programme with an objective to improve the specific character.

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## Appendix : Mean performance for yield and its components of 30 genotypes of Chickpea

| S. No. | Variety | Plant height | Number of branches / plant | Number of pods / plant | Number of seeds per pod | Days to 50% flowering | Days to maturity | 100 seed weight | Seed yield per plant |
|---|---|---|---|---|---|---|---|---|---|
| 1 | C- 501 | 38.40 | 4.40 | 53.33 | 1.07 | 64.33 | 130.67 | 37.76 | 17.21 |
| 2 | C- 502 | 35.27 | 3.87 | 48.67 | 1.60 | 61.33 | 127.00 | 25.57 | 16.89 |
| 3 | C- 504 | 33.40 | 3.80 | 47.33 | 1.13 | 72.33 | 128.67 | 24.36 | 16.17 |
| 4 | C- 505 | 34.67 | 3.73 | 44.33 | 1.00 | 70.33 | 127.67 | 32.62 | 12.92 |
| 5 | C- 507 | 31.60 | 5.20 | 49.00 | 1.13 | 70.67 | 127.33 | 22.36 | 12.03 |
| 6 | C- 508 | 34.47 | 3.73 | 58.67 | 1.27 | 85.67 | 129.67 | 20.94 | 15.53 |
| 7 | C- 509 | 38.20 | 4.00 | 49.67 | 1.67 | 72.67 | 128.33 | 24.38 | 13.68 |
| 8 | C- 510 | 43.60 | 4.13 | 49.00 | 1.40 | 62.00 | 130.67 | 27.76 | 17.91 |
| 9 | C- 511 | 43.47 | 4.13 | 50.67 | 1.53 | 80.00 | 126.67 | 26.21 | 12.45 |
| 10 | C- 513 | 43.33 | 3.33 | 38.33 | 1.13 | 69.33 | 128.00 | 32.97 | 16.58 |
| 11 | C- 514 | 31.13 | 4.53 | 50.00 | 1.00 | 72.67 | 132.33 | 25.86 | 12.71 |
| 12 | C- 516 | 43.33 | 3.33 | 36.00 | 1.00 | 74.33 | 128.67 | 26.16 | 8.81 |
| 13 | C- 517 | 47.33 | 4.33 | 47.00 | 1.33 | 78.33 | 130.33 | 17.59 | 10.50 |
| 14 | C- 519 | 41.47 | 4.67 | 58.00 | 1.47 | 72.67 | 129.00 | 21.95 | 15.61 |
| 15 | C- 520 | 44.87 | 4.07 | 53.33 | 1.53 | 72.67 | 129.33 | 28.28 | 18.86 |
| 16 | C- 521 | 45.47 | 3.60 | 60.67 | 1.33 | 71.67 | 130.00 | 27.42 | 18.59 |
| 17 | C- 522 | 47.07 | 4.27 | 59.00 | 1.40 | 75.67 | 126.67 | 22.56 | 13.18 |
| 18 | C- 523 | 41.87 | 3.47 | 60.67 | 1.53 | 72.67 | 125.67 | 27.13 | 23.51 |
| 19 | C- 525 | 35.87 | 3.27 | 48.33 | 1.20 | 72.67 | 131.67 | 37.69 | 14.73 |
| 20 | C- 526 | 43.40 | 4.07 | 43.33 | 1.20 | 65.33 | 126.67 | 27.56 | 16.14 |

**Contd…**

| S. No. | Variety | Plant height | Number of branches / plant | Number of pods / plant | Number of seeds per pod | Days to 50% flowering | Days to maturity | 100 seed weight | Seed yield per plant |
|---|---|---|---|---|---|---|---|---|---|
| 21 | C- 528 | 51.93 | 4.27 | 65.33 | 1.47 | 70.33 | 128.00 | 22.07 | 23.43 |
| 22 | C- 529 | 60.80 | 4.20 | 45.33 | 1.40 | 81.00 | 129.33 | 28.71 | 13.85 |
| 23 | C- 530 | 35.07 | 3.80 | 44.33 | 1.07 | 69.00 | 128.33 | 21.17 | 13.41 |
| 24 | C- 531 | 47.47 | 4.07 | 70.00 | 1.27 | 73.67 | 132.00 | 32.15 | 28.64 |
| 25 | C- 532 | 30.87 | 3.27 | 39.67 | 1.00 | 68.00 | 128.67 | 29.72 | 16.21 |
| 26 | C- 533 | 31.53 | 3.33 | 34.00 | 1.00 | 72.67 | 128.33 | 22.47 | 11.58 |
| 27 | C- 534 | 41.60 | 3.27 | 37.67 | 1.13 | 81.67 | 131.67 | 28.14 | 11.79 |
| 28 | C- 535 | 41.53 | 3.27 | 39.67 | 1.33 | 66.33 | 128.67 | 27.42 | 12.56 |
| 29 | C- 537 | 44.40 | 3.60 | 32.33 | 1.20 | 76.67 | 129.00 | 16.53 | 10.94 |
| 30 | J.G.-16 (check) | 39.33 | 4.30 | 45.00 | 1.07 | 75.33 | 130.33 | 19.02 | 11.86 |
|  | **S.E.m (d) ±** | 1.79 | 0.47 | 7.66 | 0.19 | 0.97 | 0.94 | 1.89 | 1.12 |

# VITA

The author of the these thesis jitendra jaiswal S/o Shri Ramesh Jaiswal was born on 4 September, 1985 at Khargone

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