

Identification of Parents for Hybridisation using D² Technique in Chickpea (*Cicer arietinum* L)

THESIS



Submitted to the

**Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya,
Gwalior (M.P.)**

In partial fulfillment of the requirements for the Degree of

MASTER OF SCIENCE

In

AGRICULTURE

(PLANT BREEDING & GENETICS)

by

DEVENDRA PATEL

**Department of Plant Breeding and Genetics
Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior
College of Agriculture, Indore (M.P.)**

2017

CERTIFICATE - I

This is to certify that the thesis entitled “**Identification of Parents for Hybridisation using D² technique in Chickpea (*Cicer arietinum* L)**” submitted in partial fulfillment of the Degree of **MASTER OF SCIENCE IN AGRICULTURE (Plant Breeding & Genetics)** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by **MR. DEVENDRA PATEL** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of these investigations has been acknowledged by the scholar.

Signature

(Dr. Mridula Billore)

Chairman of the Advisory Committee

MEMBER OF STUDENT’S ADVISORY COMMITTEE

1. Chairman (Dr. Mridula Billore) : -----
2. Member (Dr. (Mrs.) Indu Swaroop) : -----
3. Member (Dr. D.K.Shrivastava) : -----
4. Member (Dr. R.K. Singh) : -----

CERTIFICATE – II

This is to certify that the thesis entitled “**Identification of Parents for Hybridisation using D² technique in Chickpea (*Cicer arietinum* L)**” submitted by **MR. Devendra Patel** to the **Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior**, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** in the **Department of Plant Breeding & Genetics** has been accepted after evaluation, by the external examiner and approved by the Student’s Advisory Committee after on oral examination on the same.

Signature

(Dr Mridula Billore)

Chairman of Advisory Committee

MEMBERS OF THE ADVISORY COMMITTEE

1. Chairman (Dr. Mridula Billore) : -----

2. Member (Dr. (Mrs.) Indu Swaroop) : -----

3. Member (Dr. D.K. Shrivastava) : -----

4. Member (Dr. R.K. Singh) : -----

Head of the Department : -----

Dean of the college : -----

Director Instruction : -----

ACKNOWLEDGEMENT

*I praise God for enabling me to accomplish this great task of thesis work in his grace for his glory. I find no words to express my sincere feelings of gratitude towards my most esteemed guide and chairman of my advisory committee, **Dr. Mridula Billore**, Professor, Department of Plant Breeding & Genetics, College of Agriculture, Indore, Now she is the Dean faculty of Agriculture at Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya , Gwalior ,who deserves my most sincere thanks and respect for inspiring and excellent guidance, contact, encouragement, unceasing interest, constructive criticism and helping attitude throughout the investigation and preparation of the manuscript.*

*With profound respect, I wish to express my sincere gratitude to **Dr. Jagdish Singh**, Head of Plant Breeding Department & Genetics and **Dr. Indu Swaroop** Senior Scientist, Department of Plant Breeding & Genetics, College of Agriculture, Indore, (M.P) for their valuable suggestions and providing necessary facilities during the experiment.*

*With profound respect, I wish to express my sincere gratitude to **Prof. A.K. Singh**, Hon'ble Vice Chancellor RVSKVV Gwalior, **Dr. R.L. Rajput**, Director Instructions (RVSKVV), **Dr. H.S. Yadav**, Director Research Services RVSKVV and **Dr. Krishna** Dean, College of Agriculture, Indore, (M.P) for providing necessary facilities during the experiment.*

I thank to all my friends Om Prakash, Deeksha, Ajay, and Rajesh Dau and others, those helped me directly or indirectly during course of investigation.

I find no rhetorical gems from the ocean of word to express my pro-founding feeling to most venerable parents Shri Shyam Lal Patel , Smt. Vimla Patel who was always present in all of my good and the bad times. I also want to express my profounding feelings to my loving elder sister Smt Om Lakshmi and my loving younger brother Tarun Patel . Thankful to my wife Smt Seema Patel for the trust and patient she shown in me , my daughter Arnika an inspiration for betterment and family who has piloted me up to this stage and whose love, devotion, blessing and care throughout my life enabled me to achieve this seemingly invincible goal.

Place: Indore

Date:

(Devendra Patel)

List of Contents

Number	<i>Title</i>	Page range
I.	Introduction	1-2
II.	Review of Literature	3-16
III.	Materials and Methods	17-34
IV.	Results	35 -61
V.	Discussion	62-72
VI.	Summary, Conclusion and Suggestions	73-77
	Bibliography	78-84
	Appendix	
	Vita	

List of Tables

Table Number	<i>Title</i>	Page Number
3.1	Meteorological data during the crop season at Indore	18
3.2	Detail of experimental materials used for present investigation	23-26
4.1	Analysis of variance for 11 characters in 250 genotypes of chickpea	36
4.2	Estimates of various parameters of genetic variability for different traits in 250 genotypes of chickpea	37-47
4.3	Estimates of genetic parameters of variations for various characters in chickpea	52
4.4	Contribution of various characters towards total divergence	54
4.5	Clustering pattern of 250 genotypes of chickpea on the basis of genetic divergence	55-57
4.6	Average intra (diagonal) and inter-cluster D^2 values among 250 genotypes of chickpea	59
4.7	Characters means of different clusters in chickpea	60

Abbreviation	Stand for
bs	Broad sense
°C	Celsius
cm	centimeter
e	Constant (2.1783)
g.	Gram
GCV	Genotypic coefficient of variance
PCV	Phenotypic coefficient of variance
GA	Genetic Advance
ha.	Hectare
h^2	Heritability
Kg.	Kilogram
K	Constant its value is 2.06 at 5% selection intensity
Min.	Minimum
Max.	Maximum
mm.	Millimeter
GM	Grand Mean
N	Number of observations
G	Number of genotypes
RH	Relative Humidity
RCBD	Randomized Complete Block Design
RBD	Randomized Block Design
r	Number of Replications
n	Degree of freedom for error + variety
Temp.	Temperature
$t_{5\%}$	Table value at 5% level of significance
$\sigma^2 p_i$	Phenotypic variance for i^{th} character

CHAPTER - I

INTRODUCTION

Chickpea is self pollinated, diploid ($2n=16$) food legume which originated in Southern Turkey (Ladizinsky and Adler 1976) and subsequent spread to India and Europe where it is grown in arid climate. Chickpea belongs to the family Papilionidae. Chickpea (*Cicer arietinum* L.) is the third most important food crop occupying first rank in area as well as production among the pulses grown in the country. It remarkably predominates among other pulse crops in terms of both area and production. The year 2015-16 observed decrease in area under chickpea (81.17 lakh ha) which was 83.10 lakh ha during 2014-15. Similarly, the chickpea production is 59.1 lakh tonnes in comparison to 70.03 lakh tonnes with the productivity of 727 kg/ha) due to unfavorable weather condition in India.

Among different pulses grown in M.P., chickpea is the premier pulse crop occupying the largest acreage of 26.21 lakh hectares with a production of 22.97 lakh tones and an average productivity of only 877 kg/ha (2015-16). The statistical data of chickpea for last three decades clearly indicate that their production has remained static fluctuating between 16 and 18.45 million tonne as against a minimum requirement of about 20 million tonne. For the present population it is of course a challenge to chickpea scientists. This situation also calls for exploring possibilities for genetic upgrading of pulses in future.

Chickpea is generally consumed as dry pulse or as green vegetable. In addition to having high protein content (20-22%), it is rich in fiber, minerals (phosphorus, calcium, magnesium, iron and zinc) and carotene. It also contains 5 % fat and 55 % carbohydrates. Its lipid fraction is high in unsaturated fatty acids. Chickpea is widely consumed as a supplement for eating. In fact it is the most essential element of diet amongst vegetarians. Due to high protein content and the important amino acid methionine, lysine and tryptophan, it is considered to be an ideal substitute for non-vegetarian foods. In combination with cereals, chickpea makes a well balanced human food. As a result there has been increase consumption of pulses.

Crop improvement depends on the magnitude of genetic variability present in the base population. Since, many characters of economic importance are highly influenced by environmental conditions; the improvement of crop mainly depends upon the amount, nature and magnitude of genetic variability present in the population, the heritable variation which creates difficulty in exercising selection. Hence, it becomes necessary to split overall variability into its heritable and non heritable components with the help of certain genetic parameters like PCV and GCV estimates, which may enable the breeders to plan out proper breeding programme.

The multivariate techniques, such as Mahalanobis generalized distance D^2 and Canonical Variate Analysis are used to quantify the nature and magnitude of divergence between populations. Further, Mahalanobis D^2 (1936) Statistics 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. Identification of potential germplasm lines from the present collection would yield desirable genotypes which will be used for further improvement of the crop. Thus, study helps in selection of diverse parents for the use in hybridization.

Keeping in view the above facts, it is imperative to carry out the present investigation entitled “Identification of parents for hybridization using D^2 technique in chickpea (*Cicer arietinum* L.)” was taken up with the following objectives:

Objectives:

1. To determine the various parameters of genetic variability in various accessions of chickpea.
2. To quantify the extent of genetic diversity existing in the gene pool using Mahalanobis D^2 analysis.
3. To identify suitable genotypes to be used as parents in hybridization programme.

CHAPTER- II

REVIEW OF LITERATURE

The success of any plant improvement programme depends on right selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the field concerned. In chickpea substantial contribution has been made to the literature regarding its genetics and breeding in the recent years. The literature pertaining to the various aspects of the present study has been reviewed under the following heads: -

- 2.1 Genetic variability
- 2.2 Heritability and Genetic Advance
- 2.3 Genetic divergence

2.1 Genetic variability

Robertson *et al.* (1997) evaluated 228 accessions of eight annual wild *Cicer* species plus 20 domesticated *kabuli* chickpea lines for 23 vegetative, flower, fruit and seed descriptors at the International Center for Agricultural Research in the Dry Areas (ICARDA), Syria, during 1993 – 94. These findings suggest that these traits underwent major changes during domestication. Although only a small sample of the cultigen was included in this study, *C. arietinum* showed greater morphological variability compared with the wild taxa.

Arora and Jeena (2001) observed highest genotypic variability for 100 seed weight followed by seed yield per plant, biological yield, secondary branches per plant and seeds per plant.

Upadhyaya *et al.* (2002) reported that the core collection consists of 1956 accessions, out of which 1465 are *desi*, 433 *kabuli*, and 58 intermediate types. The *kabuli* and intermediate types were not significantly different for growth habit and seed colour, they differed, however, significantly from *desi* types for both traits. *Desi*, *kabuli*, and intermediate types were significantly different for plant width, days to maturity, pods per plant, 100-seed weight and

plot yield. Kabuli plants have broad plant width, matured late, have lowest average number of pods, highest 100-seed weight and lowest plot yield.

Yadav *et al.* (2004) reported that the 90 genetically diverse genotypes (35 medium-sized *desi* types, 35 bold-seeded *desi* types, 10 medium-sized *kabuli* types and 10 bold-seeded *kabuli* types) were tested in several locations in the 2000-2002 seasons, under rainfed (dryland) conditions and with supplemental irrigation. The bold-seeded *desi* genotypes gave superior performance in the rainfed environment, while the bold-seeded *kabuli* genotypes out yielded the other cultivars under supplemental irrigation.

Saleem *et al.* (2005) reported that the eighteen elite genotypes (848, 4047, 810, 447, BRC-27, ILC-918, 1036, 4012, 109, 290, 5006, 932, 107, BRC-20, 406, 1028, 228 and 928) and two varieties (Bittal and CM-72) of chickpea were used to analyze the means and components of variability (genetic, phenotypic and environmental), heritability (h^2 bs), genetic advance and interrelationships (genetic and phenotypic) for yield and various other yield components. The results suggested that pods per plant, seeds per plant, 100-seed weight and total weight of plant might be useful while selecting for high yielding genotypes of chickpea. It was also suggested from the mean values of hundred seed weight, total weight of plant and seed yield per plant that chickpea genotypes 932, BRC-27 and Bittal- 98 may be used as parents in further breeding program to develop high yielding cultivars.

Meena *et al.* (2006) studied the extent of variability and association of traits related to drought tolerance in 30 chickpea (*Cicer arietinum*) genotypes. The magnitude of phenotypic co-efficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters. The phenotypic and genotypic coefficient of variation was 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.

Upadhyaya *et al.* (2007) reported that the twenty-eight early-maturing chickpea germplasm lines representing wide geographical diversity were

identified using core collection approach and evaluated with four control cultivars in five environments for 7 qualitative and 16 quantitative traits at ICRI SAT Center, Patancheru, India. Significant genotypic variance was observed for days to flowering and maturity in all the environments indicating scope for selection. Genotypes x environment interactions were significant for days to flowering and maturity and eight other agronomic traits. ICC 16641, ICC 16644, ICC 11040, ICC 11180 and ICC 12424 were very early-maturing, similar to or earlier than control cultivars Harigantars and ICCV 2. The early-maturing accessions produced on average 22.8% more seed yield than the mean of four control cultivars in the test environments. Genotypes ICC 14648, ICC 16641 and ICC 16644 had higher 100-seed weight than control cultivars, Annigeri and ICCV 2.

Ali *et al.* (2008) reported that the varietal differences among the genotypes were significant ($P < 0.01$). Phenotypic and genotypic variances were higher for plant height (33.29 & 32.45) and seed yield per plant (13.47 & 13.11).

Saki *et al.* (2009) revealed that the significant genetic variations were observed among the genotypes for days to flower, plant height, number of branches per plant, number of pods per plant, 100-seed weight and seed yield per plant. The highest genotypic variability was observed in number of seeds per pod and seed yield, followed by number of pods per plant and branches per plant, whereas days to maturity showed the lowest genotypic co-efficient of variability. In all cases, phenotypic variances were higher than the genotypic ones.

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

Parameshwarappa *et al.* (2012) reported that high variability was observed for most of the productivity related traits in E3 (irrigated 2005-06). Over all the environments, genotype ICC 6279 was found to be early flowering. For

seed yield per plant, ICC 13124 was the only top yielder in all the three environments. The genotype ICC 13124 was found promising for earliness, large seed size and high yield per plant in all the environments suggesting that this accession is best suited for both rainfed and irrigated condition during the *rabi* season.

Jha *et al.* (2012) reported that the thirty chickpea genotypes were studied for seed yield and its components for estimating genetic variability and correlation coefficient. Analysis of variance for seed yield and its component showed significant differences among the genotypes for all nine traits.

Babber *et al.* (2012) reported that total number of seeds per plant and total number of pods per plant exhibited maximum genotypic coefficient of variation.

Gul *et al.* (2013) reported that the twenty chickpea (*Cicer arietinum* L.) genotypes were evaluated for genetic potential, heritability, genetic advance and traits association of yield contributing characters during 2010-2011 at the University of Agriculture, Peshawar. Data were recorded on days to 50% flowering, pods per plant, seeds per pod, number of primary branches per plant, number of secondary branches per plant, 100-seed weight and seed yield per plant. Analysis of variance revealed significant ($P < 0.01$) variation among genotypes for all the studied characters.

Jain *et al.* (2013) reported that the thirty newly bred and diverse genotypes were tested to assess the heritable variation and yield factors in chickpea. Highly significant differences among the genotypes were noted for all characters studied.

Shweta *et al.* (2013) reported that the thirty genotypes of chickpea were evaluated to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. A high degree of significant variation was observed for all the characters studied except seeds per pod. The phenotypic and genotypic coefficients of variation were found maximum for seed yield per plant followed by pods per plant and seeds per pod whereas minimum for days to maturity.

Kuldeep *et al.* (2014) reported that the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes for various traits. The High GCV and PCV were observed for seed yield per plant, 100-seed weight, harvest index, number of effective pods per plant, total number of pods per plant and number of secondary branches per plant.

Aarif *et al.* (2014) reported that the twenty two genotypes of *kabuli* chickpea were tested to assess variability, heritability, genetic advance, correlation and path analysis between yield and yield components. Among the different yield attributing traits, 100-seed weight had the highest magnitude of genotypic coefficient of variation, whereas, phenotypic coefficient of variation was found high for 100-seed weight followed by seed yield per plant and secondary branches per plant.

Sharanappa *et al.* (2014) reported that an experiment was conducted during 2008 and 2009 to study the nature and magnitude of genetic parameters and its utilization in designing a conceptual ideotype in chickpea. The estimates of genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability, genetic advance as well as correlation coefficients were worked out in thirty chickpea genotypes for nine plant type related traits. High genotypic coefficient of variation was observed for internode distance followed by seed yield per plant and harvest index.

Desai *et al.* (2015) reported that the extent of genetic variability in indigenous collection of 48 different chickpea genotypes for yield, nutritional quality and other agronomic characters. The analysis of variance revealed that existence of considerable genetic differences among the genotypes for all the characters. The highest genotypic coefficient of variation was observed for 100-seed weight (22.95) followed by number of pods per plant (19.41), seed yield per plant (13.63) and number of seeds per pod (13.18).

Parhe *et al.* (2015) reported that the seed yield per plant had maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by 100 seed weight.

2.2 Heritability and Genetic Advance

Chouhan *et al.* (2000) observed the highest variability for seeds per pod in chickpea. The seeds per pod and secondary branches per plant showed high heritability with high genetic gain making these characters to be selected for improving yield.

Nimbalkar (2000) observed in chickpea that genetic and phenotypic coefficients of variability and genetic advance were highest for 100 – grain weight and lowest for days to maturity. Heritability was highest for 100-grain weight and lowest for plant spread.

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

Kumar *et al.* (2001) reported that pods per plant exhibited the highest genetic variability, followed by secondary branches per plant, seed yield per plant, 100 seed weight, seeds per pods, plant height and biological yield per plant, pods per plant and also showed high heritability and expected genetic advance.

Yadav *et al.* (2003) studied 33 divergent genotypes of chickpea and observed maximum variability for harvest index, biological yield, grain yield per plant and 100-seed weight. Low to very high heritability coupled with genetic advance was observed for most of the quantitative characters, indicating the involvement of non-additive gene action.

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. These characters also exhibited high predicted genetic advance with high heritability.

Yadeta *et al.* (2006) reported that the high heritability estimates (39-48%) were obtained for days to flowering, days to first pod maturity, percent pod maturity at four months after planting and days to maturity based on offspring-parent (F_4 and F_3 generations) regression and/or analysis of variance for the RIL population. The predicted gain from selection as a percentage of the population

mean was low (5% or less) for these key components of crop duration owing to the low variability detected within the populations, the exception being percent pod maturity. To maximize gain from selection in these traits, it is therefore, essential to increase genetic variability among the progenies, potentially through multi-parent crosses that may involve gene introgression from across *desi* and *kabuli* types of chickpea and from wild progenitors.

Yücel *et al.* (2006) recorded highest genotypic variance estimates for 1000 seed weight, followed by seed number per plant. Heritability estimates for seed number, 1000 seed weight, and number of pods were greater than those for the other traits.

Ali *et al.* (2008) reported that the broad sense heritability estimates were the highest for plant height (97.4) and seed yield per plant (97.3). Genetic advance was higher for seed yield per plant (27.42) and plant height (14.51). High heritability for both the traits coupled with high genetic advance revealed that additive genetic effects were important for these characters.

Sidramappa *et al.* (2008) reported that the highly significant variation was observed for yield and other component traits. The RIL population showed high range of expression transcending the limits of parental values for some important traits like seed weight, pods per plant and seed yield per plant. Heritable variation was high in respect of seed weight (92.60) compared to pods per plant (74.10) and seed yield per plant (79.90). High variability followed by high estimates of heritability was observed for pods per plant, seed yield per plant, seed weight, days to 50% flowering, days to pod initiation and plant height. It was therefore concluded that selection for these traits in the material studied would be useful in the genetic improvement of these traits.

Alwawi *et al.* (2009) reported that the heritability for protein content varied from 0.83 to 0.93 which indicated the presence of a notable proportion of total variability due to genetic causes. A high genetic advantage (51.5-62.7%) for seed yield per plant was also noted. Environmental variance (σ^2_e) was very low for days to maturity and protein content. Differences between genotypic and phenotypic coefficient of variability were very small.

Saki *et al.* (2009) revealed that the high heritability coupled with high genetic advance was observed for seed yield per plant, pods per plant, 100-seed weight and dry weight per plant, which indicates that selection could be effective for these traits. Considerable heritability was observed in pod length, seeds per pod and days to flowering.

Babber *et al.* (2012) reported that days to 50% flowering, days to maturity, plant height, 100 seed weight and seed yield per plant showing high heritability coupled with medium genetic advance as percentage of mean, whereas, damage pod percentage, number of seeds per plant and number of pods per plant showing medium heritability and high genetic advance as percentage of mean.

Dar *et al.* (2012) reported that 100-seed weight, seed per plant and seed yield per plant exhibited high heritability with moderate to high genetic advance.

Gul *et al.* (2013) reported that broad sense heritability estimates were highest for pods per plant (0.88), primary branches per plant (0.83), 100-seed weight (0.82), seed yield per plant (0.75) and secondary branches per plant (0.77). Genetic advance was higher for pods per plant (40.14), seed yield per plant (38.24%), primary branches per plant (36.64%) and secondary branches per plant (30.25%).

Jain *et al.* (2013) reported that the thirty newly bred and diverse genotypes were tested to assess the heritable variation and yield factors in chickpea. Seed yield per plant, harvest index, and 100 seed weight exhibited high heritability and moderate to high estimates of genetic advance as percentage of mean.

Shweta *et al.* (2013) reported that the thirty genotypes of chickpea were evaluated to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. High heritability estimates with high genetic advance as percentage of mean were observed for secondary branches per plant, seed yield per plant, 100-seed weight, pods per plant and plant height that could be improved by simple selection.

Kuldeep *et al.* (2014) reported that the high heritability with high genetic advance as percentage of mean was noted for seed yield per plant, followed by

100 -seed weight, harvest index, number of effective pods per plant and total number of pods per plant indicated that selection may be effective for this character.

Sharanappa *et al.* (2014) reported that an experiment was conducted during 2008 and 2009 to study the nature and magnitude of genetic parameters and its utilization in designing a conceptual ideotype in chickpea. The traits plant height, angle between primary branches and ground, angle between primary branches and secondary branches, number of pods per plant, biological yield per plant and harvest index exhibited high heritability coupled with high expected genetic advance indicating the scope for improvement and genetic gain through the selection of these traits.

Aarif *et al.* (2014) reported that the high heritability coupled with high genetic advance was exhibited for 100-seed weight.

Thakur *et al.* (2015) reported that the high heritability and genetic advance as percentage of mean for 100-seed weight and low heritability coupled with low genetic advance for plant height, primary branches per plant, secondary branches per plant, pod bearing length, days to maturity, pod length, seeds per pod, biological yield, harvest index indicating high impact of environmental conditions on these characters.

Parhe *et al.* (2015) reported that the high magnitude of heritability (broad sense) was recorded for 100 seed weight. High heritability coupled with high genetic advance was observed for number of pod per plant, 100 seed weight, days to 50% flowering and plant height suggesting that, the role of additive gene effect and possibilities of achieving high genetic progress through selection.

Desai *et al.* (2015) reported that the high heritability coupled with high genetic advance was observed for 100- seed weight, pods per plant and days to flowering indicating the predominance of additive gene action. Heritability in broad sense ranged from 50.31 per cent for seed yield per plant to 99.69 per cent for methionine content. The expected genetic advance for number of pods per plant and 100-seed weight was very high. The results demonstrated ample

scope for improving seed yield in chickpea through selection of 100-seed weight, pods per plant and days to flowering.

Bharadwaj *et al.* (2016) observed high heritability coupled with high genetic advance as per cent of mean for days to fifty per cent flowering and 100 seed weight, while high heritability with moderate genetic advance for days to maturity. Plant height and grain yield per plant showed low to moderate heritability coupled with low to moderate genetic advance as percent mean.

2.3 Genetic divergence

Raje and Khare (1999) evaluated 21 genotypes of chickpea varying widely in seed size, yield and its components. On the basis of D^2 analysis, these were grouped into 6 clusters. The highest inter cluster-distance was observed between clusters IV and V. The traits *viz.*, 100 seed weight was associated with higher seed yield per plant and had the largest contribution towards total divergence. The study concluded that the selection of diverse parents on the basis of seed size seems to be effective.

Sharma (1999) studied the genetic divergence of 70 (48 indigenous and 28 exotic) varieties of chickpea which grouped into 18 different clusters. The study indicated no parallelism between geographical distribution and genetic diversity.

Harisatyanarayana and Reddy (2000) studied the genetic divergence among 31 chickpea genotypes and observed that the genotypes were grouped into seven 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 cluster IV and VII. The Inter-cluster D^2 values ranged from 22.6 to 36.8.

Nimbalkar and Harer (2001) studied genetic diversity in 40 genotypes of chickpea collected from 7 countries (32 indigenous and 8 exotic) and found that 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 32 clusters. Variance of cluster means indicated that pods per plant followed by plant height and 100 seed weight were the main characters contributing to the genetic divergence.

Sivakumar and Muthiah (2001) studied genetic divergence using Mahalanobis' D^2 statistics with 126 chickpea cultivars available in the germplasm pool. 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. The intercluster divergence varied from 0 to 2.99. The highest intercluster distance was in cluster I with 108 genotypes. Cluster III included *kabuli* types which were quite diverse from the *desi* types and this were again confirmed in the canonical root square analysis.

Dasgupta and Singh (2003) reported that inter cluster distance highest between clusters V and VIII and lowest between clusters II and III. High genetic diversity was observed among the genotypes based on cluster mean distance.

Kashyap and Rastogi (2003) studied genetic divergence using D^2 technique for seed yield and its components in 60 chickpea germplasm accessions. The genotypes were grouped into 6 clusters and the maximum intra-cluster distance was observed in cluster I comprising 14 genotypes. Cluster III and VI were identified as genetically divergent.

Pandey *et al.* (2003) studied genetic divergence as measured by D^2 technique for seed yield and its components in 56 genotypes of chickpea. The genotypes were grouped into six clusters and the maximum intra-cluster distance was observed in cluster II comprising five genotypes. Clusters IV and V followed by I and IV, III and IV were identified as genetically divergent.

Durga *et al.* (2005) studied genetic diversity in chickpea with 132 genotypes. The genotypes were grouped into nine clusters. Cluster I was the largest, comprising of 20 genotypes, followed by clusters V and VII with 16 and 15 genotypes, respectively. Maximum intra - cluster distance was observed in cluster VI followed by cluster IV, cluster I and cluster IX. Maximum inter cluster distance was noticed between clusters I and VIII. Crossing the genotypes

between the clusters I and VIII may lead to maximum diversity in the segregating population and development of high yielding

Klaudia *et al.* (2005) reported that the variation in 20 morphological and agronomical traits has been evaluated in a set of chickpea genetic resources from four countries. Data indicated that differences between accessions in leaf, flower, pod, and seed traits and characteristics, as well as in vegetation period. Multivariate analysis of these data segregated chickpeas into groups. Polymorphism in seed glutelins was absent, while variation in seed prolamines was very limited. DNA amplification patterns have been analyzed by semi-arbitrary primers and by specific microsatellite primers. Only some of semi-arbitrary primers generated usable DNA banding patterns, moreover interpretation of these patterns can be more or less difficult.

Sirkarvar *et al.* (2006) studied cluster analysis among 204 genotypes of chickpea excluding checks for nine quantitative traits revealed considerable genetic diversity in the material. Cluster III consisted of maximum 38 genotypes followed by cluster X which consisted of 35 genotypes whereas, cluster I consisted of two genotypes the maximum inter cluster distance was recorded between clusters I and IX followed by clusters I and V and I and VI.

Upadhyaya *et al.* (2007) reported that the cluster analysis delineated three clusters, which differed significantly for all the traits. First cluster comprised three controls, ICCV 96029, Harigantars, ICCV 2 and two germplasm lines, ICC 16644 and ICC 16641, second cluster comprised 13 germplasm lines and control cultivar Annigeri, and third cluster comprised 13 germplasm lines. Maturity was main basis of delineation of the first cluster from others. Plot yield and its associated traits were the main basis for delineation of the second cluster from the others. Identification of these diverse early-maturing lines would be useful in breeding broad-based, early-maturing and high-yielding cultivars.

Devendrappa *et al.* (2008) recorded that days to physiological maturity and seed yield per plant contributed maximum to the total divergence. Maximum inter cluster distance was observed between Cluster VIII and X followed by Cluster IX and X, suggesting maximum diversity between them.

Dwevedi and Lal (2009) recorded that the cluster I showed largest cluster with 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.

Malik *et al.* (2010) reported that the cluster diagram based on Euclidean dissimilarity placed all the genotypes in three clusters at 50% linkage distance. Cluster I, II and III possessed 8, 5 and 7 genotypes, respectively. Means of various traits for each character showed that genotypes with maximum number of secondary branches, pods per plant, biological yield and seed yield per plant were placed together in cluster III. Genotypes with maximum harvest index and 100 seed weight were placed in cluster II and I, respectively.

Sial *et al.* (2010) observed that hybridization among genotypes from diverse clusters having maximum inter cluster distance. The best two pairs of clusters in order of merit for giving meaningful recombination were identified to be cluster V (BG 1043, H 86-18) and cluster VI (BKG 5020, RSG 799).

Tomar *et al.* (2011) reported that maximum intra-cluster distance was observed in cluster VIII, followed by cluster VI, cluster IV and cluster I. Maximum inter-cluster distance was noticed between cluster IV and VIII. Crossing between genotypes from the cluster IV and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

Singh *et al.* (2012) carried out an investigation among the 64 genotypes of chickpea that included 60 interspecific derivatives, their parents and two standard checks, to study the nature and magnitude of genetic divergence using Mahalanobis D^2 statistics. Highest inter-cluster distance was recorded between cluster VI and IX, while highest intra cluster distance was found among the genotypes of cluster VIII. Characters like biological yield per plot, seed yield per plot and days to 50 per cent flowering contributed maximum towards the genetic diversity.

Syed *et al.* (2012) assessed the genetic diversity of 27 chickpea genotypes through Mahalanobis D^2 and Principal Component Analysis. The

genotypes under study fall into five clusters. The cluster II contained the highest number of genotypes (11) and Cluster I contained the lowest. Cluster I produced the highest mean value for number of pods per plant. The inter cluster distances were much higher than the intra cluster distances. Cluster V exhibited the highest intra cluster distance while the lowest distance was observed in cluster I. The highest inter cluster distance was observed between cluster I and II while the lowest was between cluster III and V. Considering all the characters, it was suggested that the genotypes BD 6549, BD 6603 and BD 6548 could be used as parents for future breeding programs to develop high yielding varieties of chickpea.

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

Parhe *et al.* (2015) revealed that the fifty one chickpea genotypes were grouped into five clusters. Cluster I was largest with forty genotypes followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster I and V, followed by cluster II and V suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters viz. 100 seed weight, number of pods per plant and days to 50% flowering contributed maximum in manifestation of genetic diversity. The genotypes IC-270936, IC- 487323, IC-350889, Vishal, Digvijay, IC-442831, IC-268927, IC-327656, IC-299779, EC-490044 and IC-269004 were identified as genetically diverse parents, which can be utilized for future crop improvement programme in chickpea.

Johnson *et al.* (2015) experimented 112 genotypes of chickpea to study the nature and magnitude of genetic divergence using Mahalanobis's D^2 Statistics and grouped into eight clusters. The highest inter cluster distance was

observed clusters IV and VII followed by I and VII, IV and V, I , and IV. The intra-cluster distance was observed for cluster V.

CHAPTER- III

MATERIAL AND METHODS

This chapter comprises the details about the materials used and the methods adopted during the course of present investigation entitled “Identification of parents for hybridization using D² technique in chickpea (*Cicer arietinum* L.)” was carried out during the year 2013-14.

3.1 Experimental site

The present experiment was laid out in the field of the Research Farm, Regional Research Centre on Pulses, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Indore, during 2013-14. The land topography of the experimental site was almost uniform with an adequate surface drainage. The internal drainage of the experimental site is medium.

3.2 Location and climate

Indore is situated in Malwa plateau region in the Western part of the state of Madhya Pradesh at an altitude of 567 meters above mean sea level (MSL). It is located at latitude of 22.43° N and longitude of 76°54' E. It has subtropical climate having a temperature range of 21° C to 45° C and 6° C to 31° C in summer and winter seasons, respectively. The rainfall in the region has been mostly inadequate and erratic in most of the recent past seasons. Late commencement, early withdrawal of monsoon and occurrence of two to three dry spells during the rainy season are the common features. The mean annual average rainfall is 964 mm. The meteorological data during crop growth period from the 22nd October, 2013 to 8th April, 2014 are given in Table 3.1.

The meteorological parameters during the crop season such as minimum and maximum temperature, rainfall, wind speed and relative humidity were recorded in AICRP for Dryland Agriculture; College of Agriculture, Indore (M. P.) and are presented in Table 3.1.

The data (Table 3.1) indicate that the total rainfall received during crop growth period was 44.4 mm. There were no rains during SMW 43 – 47, 49 to 6 and 10 to 14. The minimum and maximum temperature during crop growth period varied from 6.5⁰C to 19.1⁰C and from 20.3⁰C to 36.5⁰C, with season's average values of 9.9⁰C and 27.3⁰ C respectively. The relative humidity and wind speed ranged between 73.0 to 85.7 % and 1.4 to 4.8 km hrs⁻¹ respectively with season's average of 78.7% and 3.1 km hrs⁻¹.

Table 3.1: Meteorological information (week wise) during entire crop season of the year 2013-14 at Indore, (M.P.).

SMW	Month and date	RH (%)	Temp (⁰ C)		Rainfall (mm)	Wind speed (km/hrs)
			Max.	Min.		
43	October 22 – 28	80.0	31.1	15.2	0.0	1.9
44	Oct. 29 – Nov. 04	78.0	28.5	15.2	0.0	1.8
45	Nov. 05 – 11	78.0	27.0	11.7	0.0	1.9
46	Nov.12 – 18	76.0	26.7	8.4	0.0	2.0
47	Nov.19 – 25	78.0	28.6	11.2	0.0	2.3
48	Nov.26 – Dec.02	73.0	27.0	9.6	2.2	1.8
49	Dec.03 – 09	77.0	25.2	7.0	0.0	1.4
50	Dec.10 – 16	80.0	25.4	6.6	0.0	1.4
51	Dec.17 – 23	78.0	23.9	6.8	0.0	3.4
52	Dec.24 – 31	80.0	24.0	6.5	0.0	2.0
1	Jan. 01 – 07	78.7	24.8	7.8	0.0	3.4
2	Jan. 08 – 14	78.6	23.3	6.9	0.0	3.5
3	Jan. 15 – 21	79.1	23.0	6.8	0.0	4.4
4	Jan. 22 – 28	85.7	20.3	7.1	0.0	3.4
5	Jan. 29 – Feb. 04	78.4	25.2	6.6	0.0	2.2
6	Feb. 05 – 11	78.7	26.8	8.1	0.0	3.0
7	Feb.12 – 18	80.6	22.3	8.0	0.6	4.0
8	Feb.19 – 25	76.3	26.6	6.8	11.6	4.0
9	Feb.26– March 04	79.3	27.1	8.2	30.0	4.6
10	March 05 – 11	78.3	27.8	10.1	0.0	4.0
11	March 12 – 18	77.6	32.9	12.9	0.0	3.4
12	March 19 – 25	80.6	34.4	14.2	0.0	4.5
13	March 26 – April 01	81.6	36.4	17.4	0.0	4.3
14	April 02 – 08	78.0	36.5	19.1	0.0	4.8
Total		-	-	-	44.4	-
Average		78.7	27.3	9.9	-	3.1

Source: AICRP for Dryland Agriculture; College of Agriculture, Indore (M. P.)

3.3 Soil

The soil of the experimental field has been grouped under medium black clay soil (Vertisols) belonging to Kamliakhedi series, which is a member of fine, smectitic, hyperthermic family of Vertic, Ustochrepts. In order to determine the textural class and fertility status of the experimental area, the soil samples were collected randomly from each plot with the help of soil auger before sowing from the experimental field. Primary samples were mixed to prepare composite soil sample from each replication was drawn to study physico-chemical properties of the experimental field. The data pertaining to various physico-chemical properties have been presented in Table 3.2.

Table 3.2: Physico-chemical properties of soil collected from the experimental field

SN	Composition	Content	Category	Method used
A. Mechanical composition				
1	Sand (%)	10.4	-	Bouyoucos Hydrometer method (Piper, 1967)
2	Silt (%)	35.5	-	
3	Clay (%)	54.0	-	
4	Textural class		Clayey	
B. Chemical composition				
S.N	Analysis	Values	Category	Method adopted
1.	Soil pH	7.8	Slightly alkaline	Glass electrode method (pH meter) (Jackson, 1967)
2.	Electrical conductivity (ds/m)	0.32	Normal	Conductivity meter at 25°C (Jackson, 1967)
3.	Organic carbon (%)	0.26	Low	Wakley and Black rapid titration method (Wakley & Black 1934)
4.	Available Nitrogen (kg N /ha)	210.0	Low	Alkaline permanganate method (Jackson 1967)
5.	Available phosphorus (kg P ₂ O ₅ /ha)	12.6	Medium	Olsen's method (Jackson, 1967)
6.	Available potash (kg K ₂ O /ha)	425	High	Flame photometer (Jackson, 1967)

Source: - All India Co-ordinated Research Project on Salt Affected Soils and Use of Saline Water In Agriculture, Indore.

The physico-chemical analysis of soil showed that the soil of experimental site was predominantly clayey in texture. The organic carbon content (0.26%) and available nitrogen (210.0 kg ha⁻¹) were low. The available phosphorus (12.6 kg ha⁻¹) and potash (425 kg ha⁻¹) were medium and high respectively. The soil pH was (7.8) slightly alkaline. Electrical conductivity (0.32 dS m⁻¹) of soil was found normal (Table 3.2).

3.4 Experimental material

The experimental material for present study comprised 250 genotypes are presented in Table 3.4.

Table 3.3: Details of genotypes:

S.No.	Name of Genotype	S.No.	Name of Genotype
1	GVT-GP 1	126	GVT-GP 307
2	GVT-GP 2	127	GVT-GP 315
3	GVT-GP 7	128	GVT-GP 318
4	GVT-GP 8	129	GVT-GP 320
5	GVT-GP 12	130	GVT-GP 321
6	GVT-GP 13	131	GVT-GP 331
7	GVT-GP 14	132	GVT-GP 338
8	GVT-GP 18	133	GVT-GP 342
9	GVT-GP 19	134	GVT-GP 355
10	GVT-GP 25	135	GVT-GP 365
11	GVT-GP 29	136	GVT-GP 369
12	GVT-GP 29	137	GVT-GP 386
13	GVT-GP 31	138	GVT-GP 390
14	GVT-GP 38	139	GVT-GP 397
15	GVT-GP 40	140	GVT-GP 406
16	GVT-GP 42	141	GVT-GP 408
17	GVT-GP 50	142	GVT-GP 412
18	GVT-GP 73	143	GVT-GP 414
19	GV T-GP 74	144	GVT-GP 420
20	GVT-GP 88	145	GVT-GP 431
21	GVT-GP 94	146	GVT-GP 432
22	GVT-GP 96	147	GVT-GP 435
23	GVT-GP 96	148	GVT-GP 438
24	GVT-GP 99	149	GVT-GP 439
25	GVT-GP 100	150	GVT-GP 443
26	GVT-GP 101	151	GVT-GP 446

27	GVT-GP 102	152	GVT-GP 452
28	GVT-GP 104	153	GVT-GP 454
29	GVT-GP 104	154	GVT-GP 459
30	GVT-GP 105	155	GVT-GP 464
31	GVT-GP 107	156	GVT-GP 467
32	GVT-GP 108	157	GVT-GP 474
33	GVT-GP 109	158	GVT-GP 475
34	GVT-GP 110	159	GVT-GP 479
35	GVT-GP 113	160	GVT-GP 480
36	GVT-GP 115	161	GVT-GP 482
37	GVT-GP 120	162	GVT-GP 495
38	GVT-GP 123	163	GVT-GP 500
39	GVT-GP 124	164	GVT-GP 518
40	GVT-GP 131	165	GVT-GP 521
41	GVT-GP 134	166	GVT-GP 529
42	GVT-GP 139	167	GVT-GP 544
43	GVT-GP 142	168	GVT-GP 546
44	GVT-GP 143	169	GVT-GP 550
45	GVT-GP 144	170	GVT-GP 552
46	GVT-GP 147	171	GVT-GP 571
47	GVT-GP 148	172	GVT-GP 577
48	GVT-GP 153	173	GVT-GP 578
49	GVT-GP 153	174	GVT-GP 582
50	GVT-GP 154	175	GVT-GP 585
51	GVT-GP 154	176	GVT-GP 589
52	GVT-GP 157	177	GVT-GP 608
53	GVT-GP 160	178	GVT-GP 617
54	GVT-GP 163	179	GVT-GP 625
55	GVT-GP 170	180	GVT-GP 630
56	GVT-GP 171	181	GVT-GP 631
57	GVT-GP 173	182	GVT-GP 635
58	GVT-GP 174	183	GVT-GP 640
59	GVT-GP 175	184	GVT-GP 669
60	GVT-GP 177	185	GVT-GP 647
61	GVT-GP 178	186	GVT-GP 652
62	GVT-GP 179	187	GVT-GP 652
63	GVT-GP 183	188	GVT-GP 654
64	GVT-GP 183	189	GVT-GP 655
65	GVT-GP 183	190	GVT-GP 665
66	GVT-GP 186	191	GVT-GP 666
67	GVT-GP 187	192	GVT-GP 669

68	GVT-GP 189	193	GVT-GP 674
69	GVT-GP 190	194	GVT-GP 676
70	GVT-GP 193	195	GVT-GP 679
71	GVT-GP 194	196	GVT-GP 680
72	GVT-GP 195	197	GVT-GP 694
73	GVT-GP 197	198	GVT-GP 696
74	GVT-GP 200	199	GVT-GP 700
75	GVT-GP 208	200	GVT-GP 700
76	GVT-GP 210	201	GVT-GP 701
77	GVT-GP 211	202	GVT-GP 703
78	GVT-GP 213	203	GVT-GP 704
79	GVT-GP 215	204	GVT-GP 706
80	GVT-GP 217	205	GVT-GP 710
81	GVT-GP 225	206	GVT-GP 721
82	GVT-GP 226	207	GVT-GP 726
83	GVT-GP 244	208	GVT-GP 739
84	GVT-GP 245	209	GVT-GP 751
85	GVT-GP 248	210	GVT-GP 755
86	GVT-GP 249	211	GVT-GP 758
87	GVT-GP 250	212	GVT-GP 760
88	GVT-GP 251	213	GVT-GP 763
89	GVT-GP 253	214	GVT-GP 772
90	GVT-GP 256	215	GVT-GP 778
91	GVT-GP 257	216	GVT-GP 782
92	GVT-GP 258	217	GVT-GP 785
93	GVT-GP 259	218	GVT-GP 792
94	GVT-GP 262	219	GVT-GP 793
95	GVT-GP 264	220	GVT-GP 805
96	GVT-GP 267	221	GVT-GP 819
97	GVT-GP 268	222	GVT-GP 828
98	GVT-GP 270	223	GVT-GP 836
99	GVT-GP 271	224	GVT-GP 881
100	GVT-GP 272	225	GVT-GP 882
101	GVT-GP 273	226	GVT-GP 883
102	GVT-GP 274	227	GVT-GP 884
103	GVT-GP 275	228	GVT-GP 887
104	GVT-GP 276	229	GVT-GP 889
105	GVT-GP 279	230	GVT-GP 890
106	GVT-GP 281	231	GVT-GP 891
107	GVT-GP 282	232	GVT-GP 891
108	GVT-GP 284	233	GVT-GP 901

109	GVT-GP 285	234	GVT-GP 9
110	GVT-GP 285	235	GVT-GP 28
111	GVT-GP 286	236	GVT-GP 99
112	GVT-GP 289	237	GVT-GP 104
113	GVT-GP 289	238	GVT-GP 94
114	GVT-GP 290	239	GVT-GP 28
115	GVT-GP 293	240	GVT-GP 902
116	GVT-GP 294	241	GVT-GP 881
117	GVT-GP 296	242	GVT-GP 275
118	GVT-GP 298	243	GVT-GP 157
119	GVT-GP 300	244	GVT-GP 300
120	GVT-GP 301	245	GVT-GP 7
121	GVT-GP 302	246	GVT-GP 617
122	GVT-GP 304	247	GVT-GP 282
123	GVT-GP 305	248	GVT-GP 500
124	GVT-GP 306	249	GVT-GP 104
125	GVT-GP 307	250	GVT-GP K46-367

3.6 Experimental details

3.6.1 Design of experiment

The experiment was laid out in Randomized Completely Block Design (RCBD) with two replications. Each replication consists of 250 genotypes. All the genotypes were randomized separately in each replication. The details of layout is given as below:-

Crop	:	Chickpea (<i>Cicer arietinum</i> L.)
Season	:	2013-14
Date of sowing	:	28 – 10 – 2013
Design	:	Randomized Completely Block Design
Number of Replications	:	Two
Number of Accessions	:	250
Row to row distance	:	30 cm

Plant to plant distance	:	10 cm
Number of rows in each plot	:	$(0.64 \times 4.0 =) 0.24$
Number of plants per plot for observation		5
Manure and fertilizers applied	:	NPK 100:50:25 kg/ha

3.7 Agronomical Operations

3.7.1 Land preparation and sowing

The experimental area was ploughed and harrowed in order to bring the soil in well-pulverized condition. Plots were made according to the layout plan after leveling. Two rows of each genotype were sown in 4.0m long row with row to row and plant to plant spacing of 30 cm and 10 cm, respectively. After sowing, one come up irrigation was done for proper germination of seeds.

Ten days after sowing gap filling was done. All the other recommended package of practices was followed to raise a healthy crop.

3.7.2 Irrigation

The first irrigation was given immediately after sowing to ensure proper germination of seeds. Subsequent irrigation was given at about one month interval.

3.7.3 Intercultural operations

Intercultural operations were done from time to time to keep the crop free from weed plants.

3.7.4 Fertilizer Application

Nitrogen, phosphorus and potassium were applied, through urea, single super phosphate and murate of potash respectively. Recommended and a

uniform dose of 100 kg N ha⁻¹, 50 kg P ha⁻¹ and 25 kg K ha⁻¹ was applied to all the plots.

3.7.5 Plant protection measures:

The crop was sprayed with Trizophos at 2ml/l in order to avoid the attack of *helicoverpa* caterpillar. In addition , sprayed with tilt at 1ml/l as a precautionary measure against foliar diseases.

3.8 Sampling

Five plants were randomly selected from each plot and replication for recording data.

3.9 Observations recorded

Biometrical observations on eleven traits were recorded on five randomly selected plants and the mean values were subjected to statistical analysis. The data were recorded as per standard procedure.

3.9.1 Days to 50% flowering

Number of days beginning from the sowing to the date when 50 % of the plants flowered in a plot was recorded.

3.9.2 Days to maturity

Number of days beginning from the sowing to the date when crop attained physiological maturity was recorded.

3.9.3 Plant height (cm)

The height of the main stem from the ground level to the apical bud (leaf apex) was measured with the meter scale at the time of maturity.

3.9.4 Number of primary branches per plant

The numbers of primary branches arising from the main stem of each tagged plant was counted at maturity.

3.9.5 Number of pods per plant

The numbers of pods of the each tagged plant in each genotypes were counted at maturity.

3.9.6 Number of seeds per plant

The total numbers of seeds of the each tagged plant in each genotypes were counted and average number was worked out.

3.9.7 Number of seeds per pod

It is calculated as :- No. of seeds per plant / No. of pods per plant

3.9.8 100 seed weight (g)

The weight of hundred seeds picked at random from each replication in each genotype was taken and weight and expressed in grams.

3.9.9 Biological yield per plant (g)

Dried produce of five tagged plants harvested above the ground level from each plot at maturity was weighted before threshing.

3.9.10 Harvest index (%)

Harvest index for each plant was calculated separately using the following formula and expressed in percentage.

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

3.9.11 Seed yield per plant (g)

The pods obtained from five tagged plants were threshed and weighed to obtain seed yield per plant in grams.

3.10 Statistical analysis

The data obtained in respect of all the characters were subjected to the following statistical analysis.

3.10.1 Mean: It was calculated by using following formula.

$$\text{Mean} = \frac{\sum x}{n}$$

where,

$$\sum x = \text{Sum of all the observations}$$

n = Number of observations

3.10.2 Analysis of variance

The data based on the mean of individual plants selected for observations were statistically analysed as described by Panse and Sukhatme (1967) to find out overall total variability present in the material under study for each character. The first and foremost step is to carry out analysis of variance to test the significance of differences among the populations. The skeleton of analysis of variance used was as follows:

Table 3.5: ANOVA for Randomized Completely Block Design

Source of variation	D.F.	Sum of square	Mean sum of square	F value	F _t 5% or 1% table value
Replications	r-1	RSS	RMS	RMS/EMS	-
Genotypes	G-1	GSS	GMS	GMS/EMS	-
Error	(r-1)(G-1)	ESS	EMS	-	-
Total	rG-1	TSS	-	-	-

where,

r = Number of replications

G = Number of genotypes

D.F. = Degree of freedom

RSS = Replication sum of square

GSS = Genotypes sum of square

ESS = Error sum of square

TSS = Total sum of square

RMS = Replication mean sum of square

GMS = Genotypes mean sum of square

EMS = Error mean sum of square

A significant value of F test indicates that the test entries differ significantly among themselves, which can be calculated by following formulas:-

$$C.V. = \frac{\sqrt{EMS}}{GM} \times 100$$

$$S E_m \pm = \sqrt{\frac{EMS}{r}}$$

$$SE_{diff} = \sqrt{\frac{2 EMS}{r}}$$

CD at 5% prob. Level = SE diff x $t_{5\%}$ level of significance

where,

C.V.% = Coefficient of variation

SEm ± = Standard error of means

S E diff = Standard error of difference

GM = Grand mean

C.D. = Critical difference

t 5% = t, table value 5% level of significance

3.10.3. Estimation of mean, components of variance, phenotypic, genotypic and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean

The mean of different characters was calculated by conventional method:

$$\text{Mean} = \frac{\sum x_i}{N}$$

Where,

Σx_i = The sum of all the observation for i^{th} character.

N = Number of observations.

Range was recorded by observing the lowest and the highest mean values for each character.

Table 3.6: The component of variance was calculated as follows

S. No.	Source	M.S.S.	Expected M.S.S.
1.	Replication	-	-
2.	Genotypes	M_i	$\sigma^2 e_i + r. \sigma^2 g_i$
3.	Error	E_i	$\sigma^2 e_i$

$$\sigma^2 g_i = \frac{M_i - E_i}{r}$$

$$\sigma^2 e_i = E_i$$

$$\sigma^2 p_i = \sigma^2 g_i + \sigma^2 e_i$$

where,

$\sigma^2 g_i$ = Genotypic variance for i^{th} character.

$\sigma^2 e_i$ = Environmental variance for i^{th} character.

$\sigma^2 p_i$ = Phenotypic variance for i^{th} character.

Phenotypic and genotypic coefficients of variation (expressed in %) were calculated by using the formula given by Burton (1952). Genotypic coefficient of variation (GCV) was calculated as below:

$$\text{GCV}\% = \frac{\sqrt{\sigma^2 g_i}}{\bar{X}_i} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV}\% = \frac{\sqrt{\sigma^2 p_i}}{\bar{X}_i} \times 100$$

$$\bar{X}_i$$

where,

$\bar{X}_i$ = General mean of the i^{th} character under consideration

$\sigma^2 g_i$ and $\sigma^2 p_i$ = Genotypic and phenotypic standard deviation of the i^{th} character respectively

Heritability and genetic advance

Heritability (broad sense) which is ratio of genotypic variance to the total phenotypic variance is symbolized as h^2 (BS) and expressed in percentage. Estimation of heritability was done as per the formula given by Hanson *et al.* (1956).

$$h^2 \text{ (BS)\%} = \frac{\sigma^2 g_i}{\sigma^2 p_i} \times 100$$

or

$$= \frac{\text{Genotypic variance of the } i^{\text{th}} \text{ character}}{\text{Phenotypic variance of the } i^{\text{th}} \text{ character}} \times 100$$

Phenotypic variance of the i^{th} character

Expected genetic advance was calculated by using the method suggested by Johnson *et al.* (1955) at 5% selection intensity.

$$\text{Genetic advance (GA)} = K. P_i . h_i^2$$

Genetic advance as percentage of mean was calculated as follows:

$$\frac{\text{Genetic advance}}{\bar{X}_i} \times 100$$

where,

K = Selection intensity its value at 5% selection level is 2.06

P_i = Phenotypic standard deviation of the i^{th} character

h^2_i = Broad sense heritability (fraction) of the i^{th} character

$\bar{X}_i$ = General mean of the i^{th} character under consideration

3.10.4 Genetic diversity through Mahalanobis D^2 analysis

Genetic divergence was calculated as suggested by Mahalanobis (1936). He defined D^2 as follows:

$$D^2 = b_1d_1 + b_2d_2 + \dots + b_p d_p$$

A measure for group distance based on multiple characters with $X_1 X_2 X_3 \dots \dots \dots X_p$ as the multiple measurement available on each individual and $d_1 d_2 \dots \dots \dots d_p$ as $X^1_1 - X^2_1 \dots \dots \dots X^1_p - X^2_p$ respectively, being the difference in the mean of two populations. The 'p' values are to be estimated so that the ratio of variance between the populations to the variance within the population's is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula:

$$D^2 = \sum W_{ij} \sum (X^1_i - \bar{X}^1_i) (X^1_j - \bar{X}^1_j)$$

where,

W_{ij} is the inverse of estimated variance and covariance matrix.

Steps to estimate D^2 values

Collection of data

Data are collected considering 'V' populations and 'P' characters which have been estimated on each individual.

Testing of significance

According to the Wilk's criteria, a simultaneous test of difference between mean values of number of correlated variance is done (Rao, 1948).

Using pivotal condensation method, the determinant of error and error + variety was calculated as follows:

$$A = \frac{\left| \begin{array}{c} W \\ \hline S \end{array} \right|}{\left| \begin{array}{c} \text{Determinant of error matrix} \\ \hline \text{Determinant of error + variety matrix} \end{array} \right|}$$

$$V(\text{state}) = -m \log e = - \frac{n}{2} (p+q+1) \log e$$

where,

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

p= Number of variance or characters

q= Degree of freedom for population

n= Degree of freedom for error + variety

e= Constant (2.1783)

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

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

Transformation of correlation values

The transformation is done using the pivotal condensation method. The correlated variables are first transformed into uncorrelated ones and D^2 values are calculated.

Computation of D^2 values

The D^2 values obtained for a pair of population taken as the calculated values of χ^2 tested against the tabulated value of χ^2 at 'p' is the number of characters.

Contribution of different characters towards divergence

In all combinations each character is ranked on the basis of $d_i = Y_{ij} - Y_{ik}$ values. Rank I is given to the highest mean difference where 'p' is the total number of characters.

Grouping of varieties into various clusters by Tocher method

The first step in grouping the varieties in distinct clusters is to arrange these populations in order of their relative distance from each other. All the other populations are also arranged in the similar fashion. This method suggested by Tocher is used for cluster formation. The two populations having the smallest distance from each other are considered first to which a third population having the smallest D^2 value from the first two populations is added. Then comes the nearest fourth population and so it goes on. At certain point when it is felt that after adding a particular population, there is a sudden increase in the average D^2 value, this population is not added in the cluster. Similarly a second cluster is formed. Thus the process is continued till all the populations are included into one or other clusters.

Average intra cluster distance

The following formula is used for measuring the intra cluster distance:

$$\text{Intra cluster distance} = \frac{\sum D_i^2}{N}$$

Where, D_i^2 / N is the sum of distances between all possible combinations (n) of the populations included in the cluster.

Average inter cluster distance

First of all the distances between clusters are estimated, and then clusters are taken one by one and from their other clusters.

$$\text{Inter-cluster distance} = \frac{\sum D_{ij}^2}{n_i n_j}$$

Where,

$\sum D_{ij}^2$ = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster

n_i = Number of entries in the cluster i

n_j = Number of entries in the cluster j

CHAPTER- IV

Results

The results obtained from the present investigation “Identification of parents for hybridization using D² technique in chickpea (*Cicer arietinum* L)” are presented under the following heads

4.1 Analysis of variance

4.2 Genetic variability

4.2.1 Range and mean performance

4.2.2 Variances and coefficient of variation

4.2.3 Heritability

4.2.4 Genetic advance

4.3 Genetic divergence

4.1 Analysis of variance

The analysis of variances for all the characters studied has been presented in Table 4.1. Mean square due to genotypes was highly significantly for number of seeds per plant, harvest index, days to maturity, number of pods per plant, plant height and days to 50 per cent flowering.

4.2 Genetic Variability

4.2.1 Range and mean performance of the genotypes

Range (maximum and minimum) and mean performance of the two hundred fifty genotypes of chickpea for all the eleven characters are presented in Table 4.2.

Table 4.1: Analysis of variance for various characters in chickpea (mean sum of squares).

Source of variance	D.F.	Days to 50% flowering (1)	Days to maturity (2)	Plant height (cm) (3)	Number of primary branches/plant (4)
Replications	1	6.962	0.162	18.004	0.002
Genotypes	249	41.690**	63.931**	47.606**	0.417**
Error	249	2.034	2.511	1.228	0.057

Source of variance	D.F.	Number of pods/plant (5)	Number of seeds/plant (6)	Number of seeds/pod (7)	100 seed weight (g) (8)
Replications	1	189.999	294.558	0.0008	16.456
Genotypes	249	60.495**	165.108**	0.0659**	20.687**
Error	249	8.567	0.610	0.0128	1.478

Source of variance	D.F.	Biological yield / plant (g) (9)	Harvest index (%) (10)	Seed yield/plant (g) (11)
Replications	1	76.370	981.176	77.075
Genotypes	249	14.657**	76.435**	1.583**
Error	249	0.100	5.949	0.132

4.2.1.1 Days to 50 per cent flowering

Early 50 per cent flowering was recorded in genotype GVT – GP 284 (40.00 days), while the genotype GVT – GP 9 required the maximum (63.50 days) for 50 per cent flowering. The average days for 50 per cent flowering were 53.63 days and it ranged from 40.00 to 63.50 days. 55 accessions out of 250 were recorded for 40 to 55 days to flowering while 185 and 10 accessions were recorded for 50 to 60 days and 60 to 70 days to 50% flowering respectively.

4.2.1.2 Days to maturity

Days to maturity ranged from 87.50 to 112.50 days. Genotype GVT-GP 157 was earliest for days to maturity, while GVT-GP 446 was latest for the same. The mean was calculated to be 98.32 days. 93 and 137 accessions were recorded 85 to 95 ranges of days and 95 to 105 range of days for maturity respectively. While 105 to 125 range of days for maturity recorded only 20 genotypes out of 250.

4.2.1.3 Plant height (cm)

Plant height varied from 26.20 to 53.25 cm with an overall mean performance of 44.27 cm. Genotype GVT-GP 14 was recorded the maximum plant height 53.25 cm and genotype GVT-GP 726 was exhibited the minimum 26.20 cm plant height. Only 8 accessions out of 250 were recorded for 25 to 35 centimeters to plant height while 127 and 115 accessions were recorded for 35 to 45 cm and 45 to 55 cm to plant height respectively.

4.2.1.4 Number of primary branches per plant

Number of primary branches per plant ranged between 2.30 to 4.80 with a average performance of 3.99 primary branches per plant. The maximum 4.80 branches per plant were recorded in genotype GVT-GP 495, while it was recorded minimum 2.30 in GVT-GP 148. Only 7 accessions out of 250 were recorded for 2 to 3 primary branches per plant while 109 and 134 accessions were recorded for 3 to 4 and 4 to 55 primary branches per plant respectively.

4.2.1.5 Number of pods per plant

Number of pods per plant ranged from 33.50 to 65.80 with a overall mean performance of 53.79. The maximum 65.80 pods per plant were noted in

genotype GVT-GP 208, while minimum 33.50 pods per plant were exhibited in genotype GVT-GP 251. Only 3 accessions out of 250 were recorded for 30 to 40 pods per plant while 58, 159 and 30 accessions were recorded for 40 to 50, 50 to 60 and 60 to 70 numbers of pods per plant respectively.

4.2.1.6 Number of seeds per plant

Maximum number of seeds per plant was observed in GVT-GP 267 (102.60), while it was least (34.40) in genotype GVT-GP 248. The average number of seeds per plant was 68.92 and it ranged between 34.40 to 102.60 seeds per plant. Only 6 accessions out of 250 were recorded for 30 to 50 seeds per plant while 129, 111 and 4 accessions were recorded for 50 to 70, 70 to 90 and 90 to 110 numbers of seeds per plant respectively.

4.2.1.7 Number of seeds per pod

Maximum number of seeds per pod was observed in GVT-GP 88 (1.72), while it was least (0.58) in genotype GVT-GP 625. The average number of seeds per pod was 1.14 and it ranged between 0.58 to 1.72 seeds per pod. Only 56 accessions out of 250 were recorded for 0.5 to 1 seeds per pods while 188 and 6 accessions were recorded for 1 to 1.5 and 1.5 to 2 numbers of seeds per pods respectively.

4.2.1.8 100 seed weight (g)

The bold seeds were observed in genotypes GVT-GP 143 (28.57 g) and smallest in GVT-GP 131 (12.90 g). The weight of 100 seeds lied between 12.90 g to 28.57 g, while the average weight of 100 seeds was 20.79 g. 98 accessions out of 250 were recorded for 10 to 20 grams to 100 seed weight while 152 accessions were recorded 20 to 30 grams to 100 seed weight respectively.

4.2.1.9 Biological yield per plant (g)

Maximum biological yield per plant was recorded in GVT-GP 495 (31.2 g) and genotypes GVT-GP 144 (9.1 g) was lowest biological yield. The average yield per plant was 17.72 g and it ranged from 9.1 g to 31.2 g. 22 accessions out of 250 were recorded for 5 to 15 grams of biological yield per plant while 220 and 1 accessions were recorded for 15 to 25 grams and 25 to 35 grams of biological yield per plant respectively.

4.2.1.10 Harvest index (%)

The harvest index percentage varied from 21.80% to 66.30% with a mean value of 37.28%. Genotype GVT-GP 144 produced considerably more 66.30% harvest index. Whereas, genotype GVT-GP 147 was recorded minimum 21.80% harvest index. . 28 accessions out of 250 were recorded for 20 to 30 % of harvest index while 138,79 and 5 accessions were recorded 30 to 40 % , 40 to 50 % and 50 to 60 % of harvest index respectively.

4.2.1.11 Seed yield per plant (g)

Maximum seed yield per plant was recorded in GVT-GP 631(10.71 g) which was closely followed by GVT-GP 267 (9.51 g). Genotype GVT-GP 248 (3.89 g) was poor yielder. The average seed yield per plant was 6.50 g and it ranged from 3.89 g to 10.71 g. 165 accessions out of 250 were recorded for 3.5 to 6 grams of seed yield per plant while 182 and 3 accessions were recorded for 6 to 8.5 grams and 8.5 to 11 grams of seed yield per plant respectively.

4.2.2 Variances and coefficient of variations

Estimation of components of genetic parameters of variation for yield and its attributes exhibited a wide range of variation for the characters studies (Table 4.3). Result indicated that the value of phenotypic variance and phenotypic coefficient of variations were of higher in magnitude than that of genotypic variance and genotypic coefficient of variation for all the characters.

4.2.2.2 Phenotypic coefficient of variations (PCV)

The phenotypic coefficient of variation ranged from 5.86% for days to maturity to 17.62% for harvest index. The phenotypic coefficient of variations was highest for characters viz., harvest index (17.62%), number of seeds per pod (17.42%), 100 seed weight (16.04%), biological yield per plant (15.49%), seed yield per plant (15.46%), number of seeds per plant (13.25%), number of primary branches per plant (12.22%) and plant height (11.17%). Days to maturity (5.86%) exhibited the lowest estimate for the same. The rest of the characters such as days to 50 per cent flowering (8.72%) and number of pods per plant (10.06%) exhibited moderate phenotypic coefficient of variation.

Table 4.3: Estimates of genetic parameters of variations for various characters in chickpea

Characters	Grand Mean	Range		Variance			Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean
		Min.	Max.	Pheno.	Geno.	Envi.	Pheno.	Geno.			
Days to 50% flowering	53.63	40.00	63.50	21.86	19.83	2.03	8.72	8.30	90.70	8.74	16.29
Days to maturity	98.32	87.50	112.50	33.22	30.71	2.51	5.86	5.64	92.44	10.98	11.16
Plant height (cm)	44.27	26.20	53.25	24.46	23.16	1.30	11.17	10.87	94.97	9.65	21.79
No. of primary branches /plant	3.99	2.30	4.80	0.24	0.18	0.06	12.22	10.63	75.60	0.76	19.03
No. of pods/ plant	53.79	33.50	65.80	29.27	27.45	1.81	10.06	9.74	75.19	10.45	19.43
No. of seeds/ plant	68.92	34.40	102.60	83.45	81.66	1.79	13.25	13.11	99.26	18.41	26.72
No. of seeds/ pod	1.14	0.58	1.72	0.04	0.03	0.01	17.42	14.29	67.29	0.28	24.15
100 seed weight (g)	20.79	12.90	28.57	11.12	9.58	1.54	16.04	14.89	86.66	5.92	28.46
Biological yield / plant (g)	17.72	9.10	31.22	7.53	7.12	0.41	15.49	15.06	98.64	5.35	30.18
Harvest index (%)	37.28	21.80	66.30	43.16	33.27	9.89	17.62	15.47	85.56	10.43	27.98
Seed yield/ plant (g)	6.50	3.89	10.71	1.01	0.57	0.44	15.46	11.61	84.59	1.17	17.96

4.2.2.4 Genotypic coefficient of variation

It is revealed from the Table 4.3 that genotypic coefficient of variation varied from 5.64% for days to maturity to 15.47% for harvest index. High genotypic coefficient of variation was noted for harvest index (15.47%), biological yield per plant (15.06%), 100 seed weight (14.89%), number of seeds per pod (14.29%), number of seeds per plant (13.11%), seed yield per plant (11.61%), plant height (10.87%) and number of primary branches per plant (10.63%). Days to maturity (5.64%) showed lowest genotypic coefficient of variation. While it was moderate for rest of the characters such as days to 50 per cent flowering (8.30%) and number of pods per plant (9.74%).

4.2.3 Heritability

The estimates of heritability (BS) for all the characters have been discussed as follows (Table 4.3). It was partitioned as very high (above 90%), high (70 to 90%), medium (50-70%) and low (less than 50%).

Result indicated that the heritability estimates were observed very high for number of seeds per plant (99.26%), followed by biological yield per plant (98.64%), plant height (94.97%), days to maturity (92.44%) and days to 50 per cent flowering (90.70%). However, it was recorded to be high for 100 seed weight (86.66%), harvest index (85.56%), seed yield per plant (84.59%), number of primary branches per plant (75.60%) and number of pods per plant (75.19%). It was moderate for number of seeds per pod (67.29%).

4.2.4 Genetic advance

Genetic advance as percentage of mean ranged between 11.16% for days to maturity to 30.18% for biological yield per plant. The highest estimate of genetic advance as percentage of mean was recorded for biological yield per plant (30.18%), followed by 100 seed weight (28.46%), harvest index (27.98%) and number of seeds per plant (26.72%). Seed yield per plant (17.96%), number of primary branches per plant (19.03%), number of pods per plant (19.43%), plant height (21.79%) and number of seeds per pod (24.15%)

showed moderate value of genetic advance as percentage of mean. Whereas, low estimates were observed for days to maturity (11.16%) and days to 50 per cent flowering (16.29%).

4.3 Genetic divergence

D^2 statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. It measures the forces of differentiation at two levels, i.e. intra-cluster and inter-cluster levels. Analyses of covariance for all possible combination of characters were done for genetic divergence. The uncorrelated variables i.e. transformed variables when obtained by pivotal condensation method, the original mean values (x_1 to x_n) are transformed into standard divergence uncorrelated (y_1 to y_n) variables.

4.3.1 Contribution of individual characters toward divergence.

The percentage contributions of different characters towards total genetic divergence in the two hundred fifty chickpea genotypes are depicted in the Table 4.4.

Number of seeds per plant (30.08%) contributed maximum towards genetic divergence followed by biological yield per plant (19.05%), plant height (11.11%), harvest index (8.02%), number of pods per plant (8.00%), days to maturity (7.25%), days to 50 per cent flowering (6.60%), 100 seed weight (5.46%), number of primary branches per plant (1.06%) and number of seeds per pod (0.37%). The seed yield per plant did not have any contribution towards total genetic divergence.

Table 4.4: Contribution of various characters towards total divergence

S No.	Characters	Time ranked first	Contribution (%)
1	Days to 50% flowering	2055	6.60
2	Days to maturity	2257	7.25
3	Plant height (cm)	4392	11.11
4	No. of primary branches /plant	329	1.06
5	No. of pods/ plant	2490	8.00

6	No. of seeds/ plant	9362	30.08
7	No. of seeds/ pod	114	0.37
8	100 seed weight (g)	1699	5.46
9	Biological yield / plant (g)	5930	19.05
10	Harvest index (%)	2497	8.02
11	Seed yield/ plant (g)	0.01	0.00

4.3.2 Grouping of genotypes in to various clusters

The characters comprising of two hundred fifty chickpea genotypes were grouped into sixteen clusters based on divergence analysis. Distribution of genotypes into different clusters is presented in the Table 4.5. Out of these clusters, cluster VIII had large population consisting of thirty six genotypes followed by cluster X (35), cluster XV (30), cluster IV (18), cluster I (17), cluster VII (16), cluster XI (16), cluster II (13), cluster XVI (13), cluster XII (12), cluster IX (11), cluster V (9), cluster III (8), cluster VI (8), cluster XIII (5) and cluster XIV (3).

Table 4.5: Clustering pattern of two hundred fifty genotypes of chickpea on the basis of genetic divergence

S No.	Cluster	No. of genotypes	Name of genotypes
1	I	17	GVT-GP 342, GVT-GP 131, GVT-GP 474, GVT-GP 578, GVT-GP 726, GVT-GP 630, GVT-GP 144, GVT-GP 903, GVT-GP 891, GVT-GP 153, GVT-GP 338, GVT-GP 184, GVT-GP 186, GVT-GP 154, GVT-GP 179, GVT-GP 50, GVT-GP 13
2	II	13	GVT-GP 332, GVT-GP 253, GVT-GP 290, GVT-GP 386, GVT-GP 293, GVT-GP 438, GVT-GP 475, GVT-GP 31, GVT-GP 739, GVT-GP 211, GVT-GP 751, GVT-GP 96, GVT-GP 772
3	III	8	GVT-GP 635, GVT-GP 259, GVT-GP 258, GVT-GP 289, GVT-GP 264, GVT-GP 175, GVT-GP 189, GVT-GP 793
4	IV	18	GVT-GP 700, GVT-GP 758, GVT-GP 298, GVT-GP 236, GVT-GP 412, GVT-GP 467, GVT-GP 250, GVT-GP 655,

			GVT-GP 215, GVT-GP 177, GVT-GP 105, GVT-GP 890, GVT-GP 38, GVT-GP 805, GVT-GP 19, GVT-GP 887, GVT-GP 110, GVT-GP 500
5	V	9	GVT-GP 251, GVT-GP 262, GVT-GP 248, GVT-GP 647, GVT-GP 245, GVT-GP 113, GVT-GP 281, GVT-GP 190, GVT-GP 173
6	VI	8	GVT-GP 631, GVT-GP 267, GVT-GP14, GVT-GP 454, GVT-GP 443, GVT-GP 755, GVT-GP 174, GVT-GP 300
7	VII	16	GVT-GP 625, GVT-GP 103, GVT-GP 301, GVT-GP 276, GVT-GP 552, GVT-GP 225, GVT-GP 703, GVT-GP 439, GVT-GP 640, GVT-GP 307, GVT-GP 365, GVT-GP 302, GVT-GP 521, GVT-GP 270, GVT-GP 654, GVT-GP 40
8	VIII	36	GVT-GP 665, GVT-GP 459, GVT-GP 760, GVT-GP 88, GVT-GP 183, GVT-GP 390, GVT-GP 674, GVT-GP 689, GVT-GP 171, GVT-GP 763, GVT-GP 701, GVT-GP 296, GVT-GP 684, GVT-GP 355, GVT-GP 482, GVT-GP 529, GVT-GP 406, GVT-GP 25, GVT-GP 480, GVT-GP 274, GVT-GP 154, GVT-GP 143, GVT-GP 464, GVT-GP 107, GVT-GP 160, GVT-GP 142, GVT-GP 183, GVT-GP 213, GVT-GP 120, GVT-GP 305, GVT-GP 785, GVT-GP 778, GVT-GP 73, GVT-GP 279, GVT-GP 134, GVT-GP 104
9	IX	11	GVT-GP 435, GVT-GP 577, GVT-GP 495, GVT-GP 256, GVT-GP 582, GVT-GP 102, GVT-GP 331, GVT-GP 9, GVT-GP 178, GVT-GP 28, GVT-GP 157
10	X	35	GVT-GP 268, GVT-GP 414, GVT-GP 710, GVT-GP 294, GVT-GP 320, GVT-GP 271, GVT-GP 284, GVT-GP 589, GVT-GP 369, GVT-GP 518, GVT-GP 680, GVT-GP 452, GVT-GP 272, GVT-GP 585, GVT-GP 244, GVT-GP 544, GVT-GP 96, GVT-GP 546, GVT-GP 315, GVT-GP 571, GVT-GP 690, GVT-GP 27, GVT-GP 139, GVT-GP 228, GVT-GP 431, GVT-GP 217, GVT-GP 124, GVT-GP 163,

			GVT-GP 200, GVT-GP 819, GVT-GP 227, GVT-GP 18, GVT-GP 779, GVT-GP 74, GVT-GP 881
11	XI	16	GVT-GP 257, GVT-GP 187, GVT-GP 29, GVT-GP 397, GVT-GP 285, GVT-GP 194, GVT-GP 652, GVT-GP 109, GVT-GP 1, GVT-GP 889, GVT-GP 115, GVT-GP 101, GVT-GP 210, GVT-GP 197, GVT-GP 195, GVT-GP 809
12	XII	12	GVT-GP 289, GVT-GP 550, GVT-GP 249, GVT-GP 479, GVT-GP 682, GVT-GP 183, GVT-GP 321, GVT-GP 666, GVT-GP 696, GVT-GP 285, GVT-GP 99, GVT-GP 94
13	XIII	5	GVT-GP 318, GVT-GP 286, GVT-GP 408, GVT-GP 828, GVT-GP 147
14	XIV	3	GVT-GP 208, GVT-GP 123, GVT-GP 108
15	XV	30	GVT-GP 248, GVT-GP 100, GVT-GP 446, GVT-GP 608, GVT-GP 304, GVT-GP 148, GVT-GP 721, GVT-GP 700, GVT-GP 226, GVT-GP 679, GVT-GP 676, GVT-GP 420, GVT-GP 153, GVT-GP 432, GVT-GP 42, GVT-GP 704, GVT-GP 8, GVT-GP 751, GVT-GP 883, GVT-GP 782, GVT-GP 792, GVT-GP K46-367, GVT-GP 901, GVT-GP 882, GVT-GP 884, GVT-GP 306, GVT-GP 193, GVT-GP 104, GVT-GP 275, GVT-GP 282
16	XVI	13	GVT-GP 694, GVT-GP 12, GVT-GP 235, GVT-GP 836, GVT-GP 706, GVT-GP 273, GVT-GP 669, GVT-GP 170, GVT-GP 29, GVT-GP 902, GVT-GP 7, GVT-GP 617, GVT-GP 2

4.3.3 Inter and intra cluster distance

Considering the inter and intra cluster distances (Table 4.6), the highest inter cluster distance was observed between cluster II and cluster XIV (2563.57) followed by cluster II and XV (2229.76), cluster V and XIV (1685.96) and cluster II and XII (1654.20).

The inter cluster distance was the least between clusters VII and IX (171.68), cluster VI and VIII (175.58), cluster VI and VII (186.92), cluster XI and XII (188.93), cluster IV and VI (201.16), cluster IX and XI (208.59) and cluster III and IV (235.61). Cluster II was highly divergent from clusters XIV, XI and XII, i.e. 1388.04, 1258.5 and 1185.0, respectively, and cluster I and XIV (1547.03), cluster I and XV (1526.61) were observed to be the nearest.

Maximum intra cluster distance was revealed in cluster XIV (300.77) followed by cluster V (280.82), cluster XV (256.38), cluster X (220.64) and cluster XVI (176.39). The least (84.7 and 88.52) intra cluster distance was expressed by cluster XI and VI.

4.3.4 Cluster mean

As regards to the values for cluster mean for all the traits were summarized and presented in Table 4.7. The higher average inter cluster mean was exhibited in days to maturity followed by number of seeds per plant, days to 50 per cent flowering, number of pods per plant, harvest index, plant height, 100 seed weight and biological yield per plant. Highest mean value for a large number of characters was exhibited in cluster VI [viz. days to maturity (101.31), plant height (49.77), number of primary branches per plant (4.33) and number of seeds per plant (89.68)] followed by cluster XIV [viz. number of primary branches per plant (4.33), number of pods per plant (64.38) and seed yield per plant (8.38)] cluster I for harvest index (46.81), cluster III for days to 50 per cent flowering (55.06), cluster V for number of seeds per pod (1.23), cluster VII for 100 seed weight (21.71) and cluster IX for biological yield per plant (24.01). However, cluster V expressed the least mean values for number of primary branches per plant (3.78), number of pods per plant (43.14), number of seeds per plant (46.05), biological yield per plant (13.47) and seed yield per plant (4.74), followed by

Table 4.7: Characters means of different clusters in chickpea

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Biological yield / plant (g)	Harvest index (%)	Seed yield/ plant (g)
Cluster I	54.32	101.05	43.86	3.96	48.16	68.38	1.11	20.86	14.12	<u>46.81</u>	6.51
Cluster II	52.07	96.65	43.90	3.94	52.34	57.74	1.12	20.87	17.73	31.83	5.64
Cluster III	<u>55.06</u>	95.62	43.61	4.16	49.82	80.87	1.12	19.74	15.55	46.64	7.24
Cluster IV	54.77	99.66	46.33	4.19	56.15	75.00	1.16	20.73	17.93	38.94	6.98
Cluster V	53.50	97.61	42.80	3.78	<u>43.14</u>	<u>46.05</u>	<u>1.23</u>	20.60	<u>13.47</u>	35.43	4.74
Cluster VI	54.68	<u>101.31</u>	49.77	<u>4.33</u>	57.36	<u>89.68</u>	1.12	19.23	19.39	41.74	8.11
Cluster VII	<u>50.65</u>	95.62	<u>41.92</u>	3.93	47.17	59.50	<u>1.07</u>	<u>21.71</u>	15.08	39.85	<u>5.98</u>
Cluster VIII	54.40	99.86	43.61	3.95	53.00	70.39	1.17	21.69	16.60	40.46	6.74
Cluster IX	54.72	98.09	43.27	3.99	59.42	74.19	1.13	21.47	24.01	27.75	6.66
Cluster X	51.98	96.97	43.22	<u>3.85</u>	52.08	64.87	1.18	21.60	16.69	38.26	6.38
Cluster XI	54.18	97.90	45.94	<u>3.85</u>	57.01	64.59	1.06	21.26	19.72	31.88	6.29
Cluster XII	55.04	99.83	45.18	4.12	59.85	76.26	1.16	<u>19.18</u>	20.21	33.38	6.75
Cluster XIII	50.70	97.60	42.80	3.94	56.08	55.22	1.02	21.17	22.11	<u>25.58</u>	5.65
Cluster XIV	51.83	<u>93.66</u>	49.18	<u>4.33</u>	<u>64.38</u>	87.75	1.08	19.12	<u>23.48</u>	35.70	<u>8.38</u>
Cluster XV	54.13	97.16	<u>43.94</u>	4.01	55.97	70.31	1.12	19.98	18.93	33.70	6.38
Cluster XVI	54.65	100.80	45.91	4.06	59.25	78.26	1.12	18.94	18.51	37.58	6.96

cluster VII for days to 50 per cent flowering (50.65) and plant height (41.92), cluster XIII for number of seeds per pod (1.02) and harvest index (25.58), cluster XIV for days to maturity (93.66) and cluster XVI for 100 seed weight (18.94). Whereas, cluster II, IV, VIII, X, XI, XII and XV did not exhibit any highest or lowest mean values for any of the characters.

CHAPTER - V

DISCUSSION

The experimental findings of the present investigation “Identification of parents for hybridization using D² technique in chickpea (*Cicer arietinum* L)” have been discussed on the following heads in the light of the available literature.

5.1 Study for Genetic Variability

5.1.1 Analysis of Variance

5.1.2 Genetic variability

5.1.2.1. Range and mean performance

5.1.2.2 Coefficient of variation

5.1.2.3 Heritability in Broad Sense

5.1.2.4 Genetic advance as % of mean

5.2. Genetic divergence

5.1 Study for Genetic Variability

5.1.1 Analysis of variance

The main objective of the present investigation was to study the diversity present in two hundred fifty genotypes of chickpea. The mean sum of square due to genotypes was highly significant for all the characters, indicating the presence of genetic variability in the experimental material. The present findings were in agreement with those of the findings of Upadhyaya et al. (2002), Ali et al. (2008), Malik et al. (2010), Jha et al. (2012), Gul et al. (2013), Jain et al. (2013), Shweta et al. (2013), Kuldeep et al. (2014) and Desai et al. (2015) for all the traits.

5.1.2 Genetic variability

5.1.2.1 Mean performance of the genotypes

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for number of seeds per plant (34.35 – 102.60), followed by harvest index (21.80 – 66.30%), number of

pods per plant (33.50 – 65.75), plant height (26.20 – 53.25cm), days to maturity (87.50 – 112.50 days), days to 50 per cent flowering (40.00 – 63.50 days), biological yield per plant (9.10 – 31.22 g), 100 seeds weight (12.90 g – 28.57 g) and seed yield per plant (3.89 – 10.71 g). The present findings were in agreement with those of the findings of Arora and Jeena (2001) for number of seeds per plant, Malik *et al.* (2010) for harvest index, Saki *et al.* (2009) and Malik *et al.* (2010) for number of pods per plant, Saki *et al.* (2009) for plant height, Saki *et al.* (2009) and Parameshwarappa *et al.* (2012) for days to 50 per cent flowering, Arora and Jeena (2001) and Malik *et al.* (2010) for biological yield per plant, Arora and Jeena (2001), Upadhyaya *et al.* (2007) and Saki *et al.* (2009) for 100 seeds weight, Arora and Jeena (2001), Upadhyaya *et al.* (2007), Saki *et al.* (2009), Malik *et al.* (2010) and Parameshwarappa *et al.* (2012) for seed yield per plant

5.1.2.2 Coefficient of variation

In the present finding phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however the differences was narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The finding of Meena *et al.* (2006), Saki *et al.* (2009) were similar to that of the present findings.

5.2.2.2 Phenotypic coefficient of variations

The phenotypic coefficient of variation ranged from 5.86% for days to maturity to 17.62% for harvest index. The phenotypic coefficient of variations was highest for characters viz., harvest index (17.62%), number of seeds per pod (17.42%), 100 seed weight (16.04%), biological yield per plant (15.49%), seed yield per plant (15.46%), number of seeds per plant (13.25%), number of primary branches per plant (12.22%) and plant height (11.17%), indicated that these characters would respond to selection. The findings are in close harmony with the result of Meena *et al.* (2006), Aarif *et al.* (2014) and Parhe *et al.* (2015) for 100 seed weight, Meena *et al.* (2006), Aarif *et*

al. (2014),) and Parhe *et al.* (2015) for seed yield per plant, for number of primary branches per plant.

However, it was exhibited in low for characters like days to maturity (5.86%), which indicated that there is limited scope for improvement. The findings are in close harmony with the result of Meena *et al.* (2006) for days to maturity.

The rest of the characters such as days to 50 per cent flowering (8.72%) and number of pods per plant (10.06%) exhibited moderate phenotypic coefficient of variation.

5.2.2.4 Genotypic coefficient of variation

It is revealed from the Table 4.3 that genotypic coefficient of variation varied from 5.64% for days to maturity to 15.47% for harvest index. High genotypic coefficient of variation was noted for harvest index (15.47%), biological yield per plant (15.06%), 100 seed weight (14.89%), number of seeds per pod (14.29%), number of seeds per plant (13.11%), seed yield per plant (11.61%), plant height (10.87%) and number of primary branches per plant (10.63%). The findings are in close harmony with the result of Meena *et al.* (2006), Kuldeep *et al.* (2014), Aarif *et al.* (2014), Desai *et al.* (2015) and Parhe *et al.* (2015) for 100 seed weight, Meena *et al.* (2006), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Sharanappa *et al.* (2014), Desai *et al.* (2015) and Parhe *et al.* (2015) for seed yield per plant, Babber *et al.* (2012) for number of seeds per plant, Shweta *et al.* (2013) and Desai *et al.* (2015) for number of seeds per pod, Kuldeep *et al.* (2014) and Sharanappa *et al.* (2014) for harvest index, Gul *et al.* (2013) for number of primary branches per plant. The high values of GCV suggested greater phenotypic genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection.

Days to maturity (5.64%) showed lowest genotypic coefficient of variation. The finding of Meena *et al.* (2006), Saki *et al.* (2009) and Shweta *et al.* (2013) for days to maturity was similar to the present finding which indicated that there is limited scope for improvement.

While it was moderate for rest of the characters such as days to 50 per cent flowering (8.30%) and number of pods per plant (9.74%). The finding of Desai *et al.* (2015) for number of pods per plant was similar to the present finding.

5.1.2.3 Heritability in Broad Sense

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as very high (more than 90%), high (more than 70- 90%), medium (50-70%) and low (less than 50%).

Result indicated that the heritability estimates were observed very high for number of seeds per plant (99.26%), followed by biological yield per plant (98.64%), plant height (94.97%), days to maturity (92.44%) and days to 50 per cent flowering (90.70%). However, it was recorded to be high for 100 seed weight (86.66%), harvest index (85.56%), seed yield per plant (84.59%), number of primary branches per plant (75.60%) and number of pods per plant (75.19%). The results were in close proximate to that of Yadeta *et al.* (2006), Sidramappa *et al.* (2008), Saki *et al.* (2009), Babber *et al.* (2012), Parhe *et al.* (2015) and Desai *et al.* (2015) for days to 50 per cent flowering, Yadeta *et al.* (2006) and Babber *et al.* (2012) for days to maturity, Ali *et al.* (2008), Sidramappa *et al.* (2008), Babber *et al.* (2012), Shweta *et al.* (2013), Sharanappa *et al.* (2014) and Parhe *et al.* (2015) for plant height, Gul *et al.* (2013), Ramya *et al.* (2014) and Sharanappa *et al.* (2014) for number of primary branches per plant Jeena *et al.* (2005), Yücel *et al.* (2006), Sidramappa *et al.* (2008), Saki *et al.* (2009), Gul *et al.* (2013), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Sharanappa *et al.* (2014), Parhe *et al.* (2015) and Desai *et al.* (2015) for number of pods per plant, Yücel *et al.* (2006) and Dar *et al.* (2012) for number of seeds per plant, Nimbalkar (2000), Arora and Jeena (2001), Jeena *et al.* (2005), Yücel *et al.*

(2006), Saki *et al.* (2009), Babber *et al.* (2012), Dar *et al.* (2012), Gul *et al.* (2013), Jain *et al.* (2013), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Aarif *et al.* (2014), Thakur *et al.* (2015), Parhe *et al.* (2015) and Desai *et al.* (2015) for 100 seed weight, Jeena *et al.* (2005), Sidramappa *et al.* (2008) and Sharanappa *et al.* (2014) for biological yield per plant, Jain *et al.* (2013), Kuldeep *et al.* (2014) and Sharanappa *et al.* (2014) for harvest index, Jeena *et al.* (2005), Ali *et al.* (2008), Sidramappa *et al.* (2008), Saki *et al.* (2009), Babber *et al.* (2012), Dar *et al.* (2012), Gul *et al.* (2013), Jain *et al.* (2013), Shweta *et al.* (2013), Kuldeep *et al.* (2014) for seed yield per plant. High values of broad sense heritability for the above characters expressed that they were least influenced by environmental modification. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

It was moderate for number of seeds per pod (67.29%), which indicated that selection based on phenotypic performance would be rewarding. The results were in close proximate to that of Saki *et al.* (2009) for number of seeds per pod,

5.2.4 Genetic advance as percentage of mean

Heritability however indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson *et al.*, 1955). Estimates of genetic advance helps to predict the extent of improvement that can be achieved for improving the different characters. The estimated values of genetic advance as percent of mean were classified as high (more than 25%), moderate (15 - 25%) and low (less than 15%).

Genetic advance as percentage of mean ranged between 11.16% for days to maturity to 30.18% for biological yield per plant. The highest estimate of genetic advance as percentage of mean was recorded for biological yield per plant (30.18%), followed by 100 seed weight (28.46%), harvest index (27.98%) and number of seeds per plant (26.72%). The results were in consonance with Babber *et al.* (2012) and Dar *et al.* (2012) for number of

seeds per plant, Nimbalkar (2000), Arora and Jeena (2001), Jeena *et al.* (2005), Saki *et al.* (2009), Dar *et al.* (2012), Jain *et al.* (2013), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Aarif *et al.* (2014), Thakur *et al.* (2015), Parhe *et al.* (2015) and Desai *et al.* (2015) for 100 seed weight), Jeena *et al.* (2005) and Sharanappa *et al.* (2014) for biological yield per plant, Jain *et al.* (2013) and Kuldeep *et al.* (2014) for harvest index.

Seed yield per plant (17.96%), number of primary branches per plant (19.03%), number of pods per plant (19.43%), plant height (21.79%) and number of seeds per pod (24.15%) showed moderate value of genetic advance as percentage of mean. The findings were in agreement to the findings of Ali *et al.* (2008), Babber *et al.* (2012), Shweta *et al.* (2013), Sharanappa *et al.* (2014) and Parhe *et al.* (2015) for plant height, Gul *et al.* (2013), Sharanappa *et al.* (2014) for number of primary branches per plant, Jeena *et al.* (2005), Saki *et al.* (2009), Gul *et al.* (2013), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Sharanappa *et al.* (2014), Parhe *et al.* (2015) and Desai *et al.* (2015) for number of pods per plant, Jeena *et al.* (2005), Ali *et al.* (2008), Alwawi *et al.* (2009), Saki *et al.* (2009), Babber *et al.* (2012), Dar *et al.* (2012), Gul *et al.* (2013), Jain *et al.* (2013), Shweta *et al.* (2013) and Kuldeep *et al.* (2014) for seed yield per plant.

Whereas, low estimates were observed for days to maturity (11.16%) and days to 50 per cent flowering (16.29%). The findings were in agreement to Nimbalkar (2000) and Thakur *et al.* (2015) for days to maturity.

High heritability coupled with high genetic advance for traits like biological yield per plant, followed by 100 seed weight, harvest index and number of seeds per plant. It is suggested that the desired improvement can be achieved by simple selection procedures in the experimental populations.. The findings were in agreement to the findings of Jeena *et al.* (2005) and Sharanappa *et al.* (2014) for biological yield per plant, Arora and Jeena (2001), Jeena *et al.* (2005), Saki *et al.* (2009), Shweta *et al.* (2013), Kuldeep *et al.* (2014), Aarif *et al.* (2014), Thakur *et al.* (2015), Parhe *et al.* (2015) and Desai *et al.* (2015) for 100 seed weight, Kuldeep *et al.* (2014) and Sharanappa *et al.* (2014) for harvest index.

High heritability supplemented with moderate genetic advances as percentage of mean were manifested by seed yield per plant, number of

primary branches per plant, number of pods per plant, plant height and number of seeds per pod, which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about. The findings were in agreement to the findings of Babber *et al.* (2012), Dar *et al.* (2012) and Jain *et al.* (2013) for seed yield per plant, Babber *et al.* (2012), for plant height.

High heritability supplemented with low genetic advances as percentage of mean was manifested by days to 50 per cent flowering and days to maturity. This revealed the predominance of non-additive gene action in the expression of these characters. These findings corroborated the earlier findings of Thakur *et al.* (2015) for days to maturity.

5.3 Genetic divergence

D^2 statistic helps in the selection of genetically divergent parents for their exploitation in hybridization programmes. The technique measures the degree of diversification and determines the relative proportion of each components character to the total divergence. It measures the forces of differentiation at two levels i.e. intra cluster and inter cluster levels. It provides reliable estimates of genetic divergence and a large number of germplasm lines can be evaluated at time for genetic diversity by this technique. In the present investigation, 250 genotypes were grouped into 16 clusters using tocher methods. The intra and inter cluster distance was calculated by using D^2 values.

5.3.1 Contribution of individual characters toward divergence

The variance of cluster mean of different characters indicated that there is a significant variation for all the characters. Hence, characters like number of seeds per plant (30.08%) followed by biological yield per plant (19.05%), plant height (11.11%), harvest index (8.02%), number of pods per plant (8.00%), days to maturity (7.25%), days to 50 per cent flowering (6.60%), 100 seed weight (5.46%), number of primary branches per plant (1.06%) and number of seeds per pod (0.37%) contributed more towards genetic divergence. The seed yield per plant did not have any contribution towards total genetic divergence. These findings corroborated with the earlier

findings of Raje and Khare (1999) reported the 100 seed weight was associated with higher seed yield per plant and had the largest contribution towards total divergence. Nimbalkar and Harer (2001) they found that variance of cluster means indicated that pods per plant followed by plant height and 100 seed weight were the main characters contributing to the genetic divergence. Devendrappa *et al.* (2008) recorded that days to physiological maturity and seed yield per plant contributed maximum to the total divergence. Dwevedi and Lal (2009) recorded that the three characters viz. harvest Index, 100 seed weight and number of pods per plant contributed maximum in manifestation of genetic diversity. Singh *et al.* (2012) reported characters like biological yield per plot, seed yield per plot and days to 50 per cent flowering contributed maximum towards the genetic diversity. Parhe *et al.* (2015) revealed that the three characters viz. 100 seed weight, number of pods per plant and days to 50% flowering contributed maximum in manifestation of genetic diversity.

5.3.2 Grouping of genotypes in to various clusters

The maximum number of genotypes (36) was found in the cluster VIII followed by

cluster X (35), cluster XV (30), cluster IV (18), cluster I (17), cluster VII (16), cluster XI (16), cluster II (13), cluster XVI (13), cluster XII (12), cluster IX (11), cluster V (9), cluster III (8), cluster VI (8), cluster XIII (5) and cluster XIV (3). From the composition of genotypes of most of the clusters, it was found that the genotypes included in clusters are heterogeneous in terms of their origins. These results revealed that geographic diversity might not be an important factor in determining genetic divergence. These finding are in agreement with the results obtained by Raje and Khare (1999), Sharma (1999), Harisatyanarayana and Reddy (2000), Nimbalkar and Harer (2001), Sivakumar and Muthiah (2001), Kashyap and Rastogi (2003), Pandey *et al.* (2003), Durga *et al.* (2005), Sirkarvar *et al.* (2006), Upadhyaya *et al.* (2007), Dwevedi and Lal (2009), Malik *et al.* (2010), Syed *et al.* (2012), Jain and Indapurker (2013) and Parhe *et al.* (2015).

5.3.3 Inter and intra cluster distance

The inter cluster distances were found higher than the intra cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was observed between cluster II and cluster XIV followed by cluster II and XV, cluster V and XIV and cluster II and XII. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregants. These finding are in agreement with the results obtained by Raje and Khare (1999), Harisatyanarayana and Reddy (2000), Sivakumar and Muthiah (2001), Dasgupta and Singh (2003), Kashyap and Rastogi (2003), Pandey *et al.* (2003), Durga *et al.* (2005), Sirkarvar *et al.* (2006), Devendrappa *et al.* (2008), Dwevedi and Lal (2009), Sial *et al.* (2010), Tomar *et al.* (2011), Singh *et al.* (2012), Syed *et al.* (2012), Jain and Indapurker (2013) and Parhe *et al.* (2015).

The minimum distance between clusters VII and IX, cluster VI and VIII, cluster VI and VII and cluster XI and XII indicated that they were genetically closure clusters. Selection of parents from such clusters may be avoided because it may result in narrow genetic base. These finding are in agreement with the results obtained by Sivakumar and Muthiah (2001), Dasgupta and Singh (2003) and Syed *et al.* (2012).

The highest genetic diversity in cluster XIV (300.77) followed by cluster V (280.82), cluster XV (256.38), cluster X (220.64) and cluster XVI (176.39) may be due to both natural and artificial selection forces among the genotypes. The least (84.7 and 88.52) intra cluster distance was expressed by cluster XI and VI. The present results are in accordance with the findings of Kashyap and Rastogi (2003), Pandey *et al.* (2003), Durga *et al.* (2005), Tomar *et al.* (2011), Singh *et al.* (2012) and Syed *et al.* (2012).

5.3.4 Cluster mean

The higher average inter cluster mean was exhibited in days to maturity followed by number of seeds per plant, days to 50 per cent flowering, number of pods per plant, harvest index, plant height, 100 seed weight and

biological yield per plant. Highest mean value for a large number of characters was exhibited in cluster VI [viz. days to maturity, plant height, number of primary branches per plant and number of seeds per plant] followed by cluster XIV [viz. number of primary branches per plant, number of pods per plant and seed yield per plant] cluster I for harvest index, cluster III for days to 50 per cent flowering, cluster V for number of seeds per pod, cluster VII for 100 seed weight and cluster IX for biological yield per plant. The present results are in accordance with the findings of Dasgupta and Singh (2003), Upadhyaya *et al.* (2007), Malik *et al.* (2010), Syed *et al.* (2012) and Jain and Indapurker (2013).

5.3.5 Genotypes identified as parents in hybridization programme

Crossing among the genotypes in cluster II (GVT-GP 332, GVT-GP 253, GVT-GP 290, GVT-GP 386, GVT-GP 293, GVT-GP 438, GVT-GP 475, GVT-GP 31, GVT-GP 739, GVT-GP 211, GVT-GP 751, GVT-GP 96, GVT-GP 772) and cluster XIV (GVT-GP 208, GVT-GP 123, GVT-GP 108) were identified as genetically diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in chickpea.

CHAPTER- VI

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FUTURE WORK

6.1 Summary

The present investigation “Identification of parents for hybridization using D² technique in chickpea (*Cicer arietinum* L.)” was carried out during rabi season of 2014-15 at the Research Farm, Regional Research Centre on Pulses, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Indore (M.P.). The experimental material for the present investigation was comprised of 250 genotypes of chickpea. These genotypes were sown in Randomized Complete Block Design with two replications, to observe eleven biometrical observations and to estimate the various parameters of genetic variability and genetic divergence. Observations were recorded on the basis of five random competitive plants selected from each genotype separately for eleven traits were evaluated as per standard procedure. On the basis of results, the present investigation is summarized as follows:

The estimates of mean sum of square due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material.

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for number of seeds per plant, followed by harvest index, number of pods per plant, plant height, days to maturity, days to 50 percent flowering, biological yield per plant, 100 seeds weight and seed yield per plant.

The present study revealed that the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits which might be due to interaction of the genotypes with the environment to some degree or other explaining environmental factors influencing the expression of these characters. High phenotypic and genotypic coefficient of variation was observed for

harvest index, biological yield per plant, 100 seed weight, number of seeds per pod, number of seeds per plant, seed yield per plant, plant height and number of primary branches per plant, which suggests greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. However, days to maturity showed low estimates of genotypic and phenotypic coefficient of variation indicating their limited scope for improvement.

High heritability coupled with high genetic advance for traits like biological yield per plant, followed by 100 seed weight, harvest index and number of seeds per plant. Suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

High heritability supplemented with moderate genetic advances as percentage of mean were manifested by seed yield per plant, number of primary branches per plant, number of pods per plant, plant height and number of seeds per pod, which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about.

High heritability coupled with low genetic advance as percentage of mean was observed for days to 50 percent flowering and days to maturity. This revealed the predominance of non-additive gene action in the expression of these characters.

The multivariate analysis provides valuable information on the extent of variation present in the crop under improvement. Selection of parent based on individual attributes may not be as advantageous as the one based on a number of important traits collectively. In any breeding programme inclusion of such genetically diverse parent is essential to generate variability and desirable recombinants.

On the basis of D^2 analysis the 250 genotypes were grouped into 16 clusters, irrespective of the geographic divergence, indicating on parallelism between geographic and genetic diversity.

Number of seeds per plant showed maximum contribution towards total divergence followed by biological yield per plant, plant height, harvest index, number of pods per plant, days to maturity, days to 50 percent flowering and 100 seed weight. These traits should be given utmost consideration for the purpose of further selection and choice of parents for improvement programme.

Intra cluster distance was maximum in cluster XIV and the minimum inter cluster distance was recorded between cluster VII and IX, while the maximum inter cluster distance was exhibited by cluster II and cluster XIV followed by cluster II and XV. It would therefore logical to make crosses between genotypes belonging to these different clusters separately by high estimated statistical distance to create wider spectrum of variability and to exploit hybrid vigour.

The inter cluster mean was wide for days to maturity followed by number of seeds per plant, days to 50 per cent flowering, number of pods per plant, harvest index, plant height, 100 seed weight and biological yield per plant, thus strongly indicated that traits which showed the variation are responsible for the variability in open pollinated and hybrid cultivars.

Crossing among the genotypes in cluster II (GVT-GP 332, GVT-GP 253, GVT-GP 290, GVT-GP 386, GVT-GP 293, GVT-GP 438, GVT-GP 475, GVT-GP 31, GVT-GP 739, GVT-GP 211, GVT-GP 751, GVT-GP 96, GVT-GP 772) and cluster XIV (GVT-GP 208, GVT-GP 123, GVT-GP 108) were identified as genetically diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in chickpea.

6.2 Conclusion

Analysis of variance revealed highly significant variance for all the traits depicting greater variability in the existing material.

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for number of seeds per plant, followed by harvest index, number of pods per plant, plant height, days

to maturity, days to 50 per cent flowering, biological yield per plant, 100 seeds weight and seed yield per plant.

The PCV was higher than the GCV for all the characters. High PCV and GCV was observed for harvest index, biological yield per plant, 100 seed weight, number of seeds per pod, number of seeds per plant, seed yield per plant, plant height and number of primary branches per plant, indicating greater diversity for these traits and their further improvement through selection.

High heritability coupled with high genetic advance for traits like biological yield per plant, followed by 100 seed weight, harvest index and number of seeds per plant. Suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

Study of genetic divergence revealed a high inter cluster distance between cluster II and cluster XIV suggesting there by that genotypes i.e. GVT-GP 332, GVT-GP 253, GVT-GP 290, GVT-GP 386, GVT-GP 293, GVT-GP 438, GVT-GP 475, GVT-GP 31, GVT-GP 739, GVT-GP 211, GVT-GP 751, GVT-GP 96, GVT-GP 772 and GVT-GP 208, GVT-GP 123, GVT-GP 108 may be considered in a crossing programme to get better segregants for improvement of chickpea. Also high contribution of characters such as number of seeds per plant, biological yield per plant, plant height, harvest index, number of pods per plant, days to maturity, days to 50 percent flowering and 100 seed weight towards total divergence suggested selection of parents based on these characters for exploitation of hybrid vigour.

6.3 Suggestions for further work

1. Stability of distinct traits of chickpea should be established over the years.
2. Traits identified for high heritability coupled with high to moderate genetic gain may be considered in selection for the improvement of crop.

3. Selection of parent for improvement work in chickpea on the basis of D^2 analysis may be considered as high inter cluster distance between cluster II and cluster XIV.
4. The genotypes showing greater yield potential with other desirable qualities may be tested under different agro climatic conditions and those found suitable could be recommended for general cultivation.
5. DNA finger printing may be used for differentiating the genotypes.

BIBLIOGRAPHY

- Aarif, M.; Rastogi, N.K.; Johnson, P.L. and Chandrakar, P.K. (2014). Genetic analysis of seed yield and its attributing traits in *kabuli* chickpea (*Cicer arietinum* L.). *Journal of Food Legumes*. 27 (1): 24-27.
- Ali, M.A.; Nawab,N.N.; Rasool, G. and Saleem,M. (2008). Estimates of variability and correlations for quantitative traits in *Cicer arietinum*. *J. Agri. Soc. Sc.*, 4: 177–79.
- Alwawi,Hayel; Mouhammad Moulla and Wafaa Choumane (2009). Genotype-environment interaction and genetic parameters in chickpea (*Cicer arietinum* L.) landraces. *Middle East Journal of Scientific Research*. 4 (3): 231-236.
- Arora, P.P. and Jeena, A.S. (2001). Genetic variability studies in chickpea. *Legume Research*. 24 (2): 137-138.
- Babbar, Anita; Prakash, Vijay; Tiwari, Prakash and Iquebal, M.A. (2012). Genetic variability for chickpea under late sown season. *Legume Research*. 35 (1): 1-7.
- Bharadwaj, C.; Singhal, T.,T.;Tripathi,S.;Roorkiwal, M.;Gour,R. and Varshney, R.(2016). Heritability and genetic advance for yield traits in a training Population of Chickpea. *National seminar on omics technologies for better food and nutrition*.
- Burton, G.W. (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong.* 1: 227-283.
- Chouhan, M.P. and Singh, I.S. (2000). Identifying chickpea genotypes for yield and yield contributes in salt affected soil. *Legume Research*. 23 (3): 199-200.
- Dar, S.A.; Ishfaq, A.; Khan, M. H.; Pir, F. A.; Ali, Gowhar and Manzar, Abu (2012). Studies on genetic variability and interrelationship for yield and yield component characters in chickpea. *Trends in Biosci.* 5 (2): 119-121.
- Dasgupta, T. and Singh, Mukesh (2003). Diversity in advanced breeding lines of chickpea, Intl. *Chickpea News letter*. (10): 38-41.

- Desai, Kamla; Tank, C.J.; Gami, R.A.; Patel, A.M. and Chauhan, R.M. (2015). Genetic variability in indigenous collection of chickpea (*Cicer arietinum* L.) genotypes for seed yield and quality traits. *The Ecoscan* 9 (1 & 2): 59-62.
- Devendrappa, J.; Viswanatha, K.P.; Mallikarjun, B.P.; Ambika, D.S. and Gavisiddappa, Choudki V. M. (2008). Assessment of genetic diversity in chickpea (*Cicer arietinum* L.) *Am.-Eu. J. Sustain Agric.* 2 (3): 205-211.
- Durga K. Kanaka; Rao, Y. Koteswara and Reddy M.V. (2005). Genetic divergence in chickpea. *Legume Research* 28 (4): 250-255.
- Dwevedi, K.K. and Lal, G.M. (2009). Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.). *Asian J. of Agric. Sci.* 1 (1): 7-8.
- Gul, R.; Khan, H.; Bibi, M.; Ain, Q.U. and Imran, B. (2013). Genetic analysis and interrelationship of yield attributing traits in chickpea (*Cicer arietinum* L.). *The Journal of Animal & Plant Sciences.* 23 (2): 521-526.
- Hanson, C.H.; Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating population of Korean Lespedeza. *Agron. J.* 48: 268-272.
- Harisatyanarayan, N and Reddy, N.S. (2000). Genetic diversity in chickpea. *Journal Research ANGRAU.* 24 (4): 31-33.
- Jackson, M.L. (1967). Soil chemical analysis, Pub. Prentice Hall India, New Delhi, pp. 87-93.
- Jain, Sudhanshu and Indapurkar, Y. M. (2013). Assessment of genetic divergence in chickpea genotypes. *Trends in Biosci.* 6 (1): 68-69.
- Jain, Sudhanshu; Srivastava, S.C.; Indapurkar, Y.M. and Yadava, H.S. (2013). Assessment of heritable components in chickpea (*Cicer arietinum* L.). *Journal of Food Legumes.* 26 (3 & 4): 134-136.
- Jeena, A.S.; Arora, P.P. and Ojha, O.P. (2005). Variability and correlation studies for yield and its components in chickpea. *Legume Res.* 28 (2): 146-148.
- Jha, Uday Chand; Singh, D.P. and Lavanya, G. Roopa (2012). Assessment of genetic variability and correlation of important yield related traits in chickpea (*Cicer arietinum* L.). *Legume Res.* 35 (4): 341 – 344.

- Johnson, H.W.; Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-318.
- Johnson, P.L.; Sharma, R.N. and Nanda, H.C. (2015). Genetic diversity and association analysis for yield traits in chickpea (*Cicer arietinum* L.) Under rice based cropping system. *The Bioscience* **10** (2): 879-884.
- Kashyap, O.K. and Rastogi, N.K. (2003). Genetic divergence in chickpea. *Journal of Plant Genetic Resources*. **16** (1): 1-3.
- Klaudia, Jomova; Benkova, Michaela; Zakova, Maria; Gregova, Edita and Kraic, Jan (2005). [Clustering of chickpea \(Cicer arietinum L.\) accessions](#). *Genetic Resources & Crop Evolution*. **52** (8): 1039-1048.
- Kuldeep, Rajkumar; Pandey, Suneeta, Babbar, Anita and Mishra, D.K. (2014). Genetic variability, character association and path coefficient analysis in chickpea grown under heat stress conditions. *Electronic Journal of Plant Breeding*. **5** (4): 812-819.
- Kumar, S.; Arora, P.P. and Jeena, A.S. (2001). Genetic variability studies for quantitative traits in chickpea. *Legume Research*. **21** (4): 263-264.
- Ladizinsky, G. and Adler, A. (1976). Genetic relationship among the annual species of *Cicer arietinum* L. *Theoretical and Applied Genetics* **48**: 197-203.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci., India*. **2**: 49-55.
- Malik, S.R.; Bakhsh, A.; Asif, M.A.; Iqbal, U. and Iqbal, S.M., (2010). Assessment of genetic variability and interrelationship among some agronomic traits in chickpea. *Int. J. Agric. Biol.* **12**: 81-85.
- Meena, H.S.; Kumar, J. and Yadav, S.S. (2006). Diallel analysis for components of genetic variation on traits related to drought tolerance in chickpea (*Cicer arietinum* L.). *Indian J. Genet.* **66** (2): 173.
- Nimbalkar, R.D. (2000). Genetic variability and heritability studies and scope for improvement in chickpea. *Journal of Maharashtra Agriculture Univ.* **25** (1): 109-110.
- Nimbalkar, R.D. and Harer, P.N. (2001). Genetic diversity in chickpea. *Journal Maharashtra Agricultural University*. **26** (1): 206-207.

- Pandey, R.L.; Rastogi, N.K. and Prasad, G.V. (2003). Genetic divergence in chickpea. *Indian Journal of Plant Genetic Resources*. 16(1):64-67.
- Panse, V.G. and Sukhatme, P.V. (1967). Statistical methods for Agricultural workers, *ICAR, Publication New Delhi*. pp.152-161.
- Parameshwarappa, S.G.; Salimath, P.M.; Upadhyaya, H.D.; Patil S.S. and Kajjidoni, S.T. (2012). Genetic variability studies in minicore collection of chickpea (*Cicer arietinum* L.) under different environments. *Karnataka J. Agric. Sc.* 25 (3): 305-308.
- Parhe, Sachin D.; Harer, P.N. and Nagawade, D.R. (2014). Investigation of genetic divergence in chickpea (*Cicer arietinum* L.) genotypes. *The bioscan* (Supplement on Genetics and Plant Breeding). 9 (2): 879-882.
- Piper, C.S. (1967). Soil and plant analysis. *Uni.of Adelaide*, Australia. Hans Publishers, Bombay.
- Raje, R.S. and Khare, D. (1999). Genetic divergence in relation to seed size in chickpea. *Advances Plant Sciences*. 12 (1): 111-114.
- Rao, C.R. (1948). The utilization of multiple measurements in problem of biological classification. *J. Roy. Stat. Soc.* 10 (B): 159-203.
- Robertson, L.D.; Ocampo, B. and Singh, K.B. (1997). Morphological variation in wild annual *Cicer* species in comparison to the cultigen. *Euphytica*. 95 (3): 309-319.
- Saki, A.I.; Zaman, M.A. Tuhina-Khatun. M.; Kamal, M.M. and Hasina Begum (2009). Genetic variability, correlation and path co-efficient analysis for agronomic traits in chickpea (*Cicer arietinum* L.). *The Agriculturists*. 7 (1&2): 12-21.
- Saleem, Muhammad; Asif Zafar; Muhammad Ahsan and Muhammad Aslam (2005). Interrelationships and variability studies for grain yield and its various components in chickpea (*Cicer arietinum* L.). *Journal of Agriculture & Social Sciences*. 1 (3): 266–269.
- Sharanappa, S.D.; Kumar, J.; Meena, H.P.; Bharadwaj, C.; Jagadeesh, H.M. Raghvendra, K.P. and Singh, Avinash (2014). Studies on heritability and genetic advance in chickpea (*Cicer arietinum* L.). *Journal of Food Legumes*. 27 (1): 71-73.
- Sharma, H.M. (1998). Genetic divergence in chickpea (*Cicer arietinum* L.) in . M.Sc. (Ag.) Thesis, submitted to JNKVV, Jabalpur.

- Shweta; Yadav, A.K. and Yadav, R.K. (2013). Studies on genetic variability, heritability and genetic advance in chickpea (*Cicer arietinum* L.) *Journal of Food Legumes*. 26 (**3 & 4**): 139-140.
- Sial, P.; Pradhan, B.; Sarangi, D.N.; Bastia, D.N. and Mishra, T.K. (2010). Genetic divergence in chickpea. *Environment and Ecology*. 28 (3A): 1848-1851.
- Sidramappa, S.A.; Patil, P.M.; Salimath and Kajjidoni, S.T. (2008). Genetic variation for productivity and its related traits in a recombinant inbred lines population of chickpea. *Karnataka J. Agric. Sci.* 21(**4**): 488-490.
- Singh, Rupinder Pal; Singh, Inderjit; Singh, Sarvjeet and Sandhu, J.S. (2012). Assessment of genetic diversity among interspecific derivatives in chickpea. *J. of Food Legumes*. 25 (**2**): 150-152.
- Sirkarvar, Vinod Singh; Sharma, R.N. and Payasi, Devendra (2006). Genetic divergence analysis for seed yield and its components in chickpea (*Cicer arietinum* L.). *Indian J. Pl. Genet. Resources*. 19 (**2**): 215-217.
- Sivakumar, S. and Muthiah, A. (2001). Genetic divergence in chickpea germplasms. *Madras Agril. Journal*. 87 (**1/3**): 48-50.
- Syed, M.A.; Islam, M.R.; Hossain, M.S.; Alam, M.M. and Amin, M.N. (2012). Genetic divergence in chickpea (*Cicer arietinum* L.). *Bangladesh Journal Agricultural Research*. 37 (**1**): 129-136.
- Thakur T.S.; Johnson P.L. and Nanda H.C. (2015). Evaluation of desi chickpea (*Cicer arietinum* L.) genotypes for yield and yield contributing traits under rainfed rice based cropping ecosystem of Chhattisgarh. *Journal of Food Legumes*. 28 (**2**): 21-26.
- Tomar, O.K.; Singh, Devi and Singh, Dharendra (2011). Genetic divergence in chickpea. *J. Food Legumes*. 24 (**4**): 296-298.
- Upadhyaya, H.D.; Salimath, P.M.; Gowda, C.L.L. and Singh, Sube (2007). [New early-maturing germplasm lines for utilization in chickpea improvement](#). *Euphytica*. 157 (**1- 2**): 195-208.
- Upadhyaya, Hari D.; Ortiz, Rodomiro; Bramel, Paula J. and Singh, Sube (2002). [Phenotypic diversity for morphological and agronomic characteristics in chickpea core collection](#). *Euphytica*. 123 (**3**): 333-342.
- Walkley, A.J. and Black, J.A. (1934). Estimation of organic carbon by chromic acid titration method. *Soil Science*, **37**: 29-38.

- Yadav, J.K.; Singh, H.L. and Kumar, R. (2003). Determining selection components in chickpea (*C.arietinum*). *Plant Archi.* 3 (1): 125-128.
- Yadav, S.S.; Kumar, J.; Turner, Neil C.; Berger, Jens; Redden, Robert; McNeil, David; Materne, Michael; Knights, E.J. and Bahl, P.N. (2004). [Breeding for improved productivity, multiple resistance and wide adaptation in chickpea \(*Cicer arietinum* L.\)](#). *Plant Genetic Resources: Characterization & Utilization.* 2 (3): 181-187.
- Yadeta, Anbessa; Tom, Warkentin; Albert, Vandenberg and Bandara, Manjula (2006). Heritability and predicted gain from selection in components of crop duration in divergent chickpea cross populations. *Euphytica.* 152 (1): 1-8.
- Yücel, Derya Özveren; Anlarsal, Adem Emin and Yücel, Celal (2006). Genetic variability, correlation and path analysis of yield, and yield components in chickpea (*Cicer Arietinum* L.). *Turkish J. of Agric. and Forestry Sci.* 30 (3): 183-188.

VITA

The author of the thesis **Mr. Devendra Patel** s/o Shri Shyam Lal Patel was Born on 14th October, 1987 at Teh. – Damoh , Dist.- Damoh (M.P.)

He received higher secondary education at Narsingharh, Dist. Damoh (M.P.). He passed Senior Secondary School Certificate Examination from CBSE Board ,New Dehli.in 2006

He completed his B.Sc. (Ag.) from R.A.K. College of Agriculture, Sehore (M.P.) in the year 2012 achieving 7.27 OGPA out of 10.0 scale.

After completing graduation he was selected for M.Sc. (Ag.) degree program in “Plant Breeding and Genetics” and Partial fulfillment of the requirements for the award of the same, he was allotted with an interesting topic “Identification of Parents for Hybridisation using D² technique in chickpea (*Cicer arietinum* L)” which was duly completed by him and presented in this thesis .

He is now submitting thesis after completing the course with 7.31 OGPA out of 10.0 point scale.

Devendra Patel