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# **Assessment of Diversity in Genetic Stock of Chickpea (*Cicer arietinum* L.)**



**THESIS**

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*In*

**AGRICULTURE**

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*By*

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**2018**

**CERTIFICATE - I**

This is to certify that the thesis entitled **“Assessment of Diversity in Genetic Stock of Chickpea (*Cicer arietinum* L.)”** submitted in partial fulfillment of the Degree of **MASTER OF SCIENCE IN AGRICULTURE (Genetics and Plant Breeding)** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafide research work carried out by **Mr. Lokendra Singh Rajput** 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.

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This is to certify that the thesis entitled “**Assessment of Diversity in Genetic Stock of Chickpea (*Cicer arietinum* L.)**” submitted by **Mr. Lokendra Singh Rajput** 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 Genetics and Plant Breeding** has been accepted after evaluation by the external examiner and approved by the Student’s Advisory Committee after oral examination.

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Place: Sehore

Date:

**(Lokendra Singh Rajput )**

**LIST OF CONTENTS**

<b>Number</b>	<b>Title</b>	<b>Page No.</b>
I.	Introduction	1-3
II.	Review of Literature	4-17
III.	Material and Methods	18-30
IV.	Results	31-48
V.	Discussion	49-60
VI.	Summary, Conclusion and Suggestions for further work	61-63
	Bibliography	64-67
	Appendices	i-v
	Vita	

## LIST OF TABLES

Table no.	Title	Page no.
3.1	Meteorological information (week wise) during entire crop season of the year 2017-18 at Sehore, (M.P.).	19
3.2	Physico-chemical properties of soil collected from the experimental field	20
3.3	Details of treatments used in the study	21
3.4	ANOVA for Randomized Completely Block Design	25
4.1	Categorization of chickpea genetic stocks based on plant vigor	32
4.2	Categorization of chickpea genetic stocks based on leaf colour	33
4.3	Name of chickpea genotypes genetic stocks and grouped on the basis of flower colour	34
4.4	Categorization of chickpea genetic stocks based on plant growth habit	35
4.5	Analysis of variance (mean sum of square) for different yield characters in chickpea (mean sum of squares)	36
4.6	Estimates of genetic parameters of variations for quantitative characters in chickpea	39
4.7	Estimates of genotypic and phenotypic correlation coefficients among seed yield and its attributing traits in chickpea	42
4.8	Genotypic and phenotypic path coefficients showing direct and indirect effects of different characters on seed yield plant <sup>-1</sup> (g) in chickpea	44
4.9	Characters means of different clusters in chickpea	46
4.10	Clustering pattern of 200 genotypes of chickpea on the basis of genetic divergence	47
4.11	Average intra (diagonal) and inter-cluster D2 values among 200 genotypes of chickpea	48

LIST OF FIGURES

Figure no.	Title	After Page no.
1	Categorization of chickpea genetic stocks based on plant vigor	32
2	<b>Categorization of chickpea genetic stocks based on leaf colour</b>	33
3	<b>Categorization of chickpea genetic stocks based on flower</b>	34
4	<b>: Categorization of chickpea genetic stocks based on plant growth</b>	35

## **CHAPTER I**

### **INTRODUCTION**

Chickpea (*Cicer arietinum* L.) is the third most important cool season food legume in the world after dry beans and peas. It has been cultivated mainly in the Indian subcontinent, West Asia, and North Africa, but recently large acreages have been introduced in the Americas and Australia. Chickpea is a self pollinated and diploid ( $2n = 2x = 16$ ) legume crop primary grown by resource-poor farmer of semi arid region of the world (Varsheny *et al.*, 2017). It serves as an important source of protein in human diet and plays an important role in the enrichment of soil fertility. Two main types of chickpea cultivars are grown globally– *kabuli* and *desi*, representing two diverse gene pools. The *kabuli* types are generally grown in the Mediterranean region including Southern Europe, Western Asia and Northern Africa and the *desi* types are grown mainly in Ethiopia and Indian subcontinent. *Desi* chickpeas are characterized by angular seed shape, dark seed coat, pink flowers, anthocyanin pigmentation of stem, rough seed surface and either semi-erect or semi-spreading growth habit, whereas *kabuli* types generally have owl shaped seeds, beige coloured seeds, white flowers, smooth seed surface, lack of anthocyanin pigmentation and semi-spreading growth habit (Pundir *et al.*, 1985).

Chickpea cover an area of 81.914 lakh hectare and produced 71.699lakh tones in India during 2014-15. It is the most important rabi pulse crop in Madhya Pradesh and covering an area of 28.53 lakh hectares with annual production of 29.64 lakh tonnes. Its average productivity is 1039 kg/ha (Anonymous, 2016).

This crop is used predominantly as a pulse, but the manner of use varies with seed type and between regions. In the Indian subcontinent, the *desi* types are generally milled to remove the testa and produce a split pea composed solely of cotyledonary tissue known as 'dhal'. Dhal is utilized either in the preparation of a thin spiced porridge of the same name, which forms an accompaniment to most Indian meals, or further ground to flour ('besan') for the preparation of fried, sweet or savoury snacks or besan curry. Whole chickpea seeds are spiced,

soaked, roasted or fried and eaten in North Indians as 'chhole'. Kabuli and green-seeded desi types are principally utilized whole in soups, curries and stews. Outside the Indian subcontinent, the predominantly kabuli types are consumed as whole seeds in soups and stews or, increasingly, in developed countries, in salads as a 'health' food. In the Mediterranean area, cooked seeds are mixed with sesame oil and other flavouring to prepare a savory paste served as a side-dish and eaten with unleavened bread as an accompaniment to main meals (Smithson *et al.*, 1985).

Crop improvement is based on available genetic variability and extent to which the desirable characters are heritable. Hence, studies on genetic variability with the help of suitable genetic parameters become indispensable for an effective breeding programme. Measurement of existing variability in plant population has been the basic requirement of plant breeding. Heritability and genetic advance have been proved useful in predicting the gain through selection. Yield is very complex entity influenced by several yield components sensitive to the environmental fluctuations. Thus, the selection based on yield components will have better chance of success. It is therefore, necessary to know the types and nature of yield components and their inter relationship. The correlation coefficient analysis provides information on their relative importance of various contributing characters. Path analysis splits the correlation coefficient into the measures of direct and indirect effects and determines the direct and indirect contribution of various characters towards yield. Its high economic importance, the productivity of chickpea remains low and the potential reason may be a lack of determinate and high yielding varieties resistant to wilt. It warrants an urgent need for development of high yielding varieties with determinate growth habit. Recombination breeding and trait manipulation are potential alternatives to develop such desirable genotypes which in turn require suitable parents for crossing programme. Assessment of existing genetic diversity following multivariate analysis like diversity.

The knowledge of genetic diversity helps in the tagging of germplasm, identification of gene stock and establishment of core collections Upadhyaya et al.(2007). If the parents selected for hybridization have diverse background the more are the chances of improving the characters under consideration (Chowdhury *et al.*,2002). Criteria for estimation of the genetic diversity can be different, including morphological traits (Upadhaya *et al.*,2007) or molecular markers (Rao *et al.*, 2007). Quantitative traits provide an estimate of genetic diversity and numerical taxonomic techniques including principal component and cluster analyses have been successfully used to classify and measure the pattern of genetic diversity in germplasm (Ghafoor *et al.*, 2001). Principal component and cluster analysis procedures were found to be efficient to assess genetic diversity for agro-morphological traits in chickpea and were reported by many research workers (Parameshwarappa *et al.*, 2011; Nihal and Adak, 2012).

Aspects covered in this study are useful in crop improvement because they help plant breeders in many ways in identification of qualitative and quantitative traits. Keeping evaluation and utilization of germplasm in consideration presents investigation “Assessment of diversity in genetic stock of chickpea (*Cicer arietinum* L.)” was carried out with the following objectives:

1. To characterizes and classify the chickpea genetic stocks into different groups for morphological traits
2. To characterize and grouping of chickpea genetic stocks into various categories for yield traits.
3. To determine the extent of heritable genetic variation for quantitative traits.
4. To know the relationship between seed yield and its contributing characters in chickpea.
5. To assess diversity in genetic stock.

## **CHAPTER II**

### **REVIEW OF LITERATURE**

The success of any plant improvement programme mainly depends on the right selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the concerned field. 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 Range and mean performance
- 2.2 Coefficient of variation
- 2.3 Heritability and genetic advance
- 2.4 Correlation coefficient analysis
- 2.5 Path coefficient analysis
- 2.6 Genetic divergence

#### **2.1 Range and mean performance**

Malik *et al.* (2010) reported studying twenty chickpea genotypes 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 plant<sup>-1</sup> followed by secondary branches plant<sup>-1</sup>, biological yield, grain yield and harvest index.

Kanouni *et al.* (2012) reported that the analysis of variance for seed yield, 100-seed weight, pods plant<sup>-1</sup>, plant height and days to maturity indicated that genotypic differences were significant. Seed yield ranged from 266 kg ha<sup>-1</sup> (FLIP06-58C) to 1020 kg ha<sup>-1</sup> (FLIP 06-60C).

Ramanappa *et al.* (2013) reported investigating one hundred and seventy nine chickpea genotypes, evaluated for genetic variability in qualitative and quantitative traits of economic importance in simple lattice design with two replications. Analysis of data revealed that the genotypes exhibited highly significant differences for days to 50 % flowering, plant height (cm), number of

primary branches, number of pods plant<sup>-1</sup>, days to maturity, 100 seed weight (g) and grain yield plant<sup>-1</sup> (g). A considerable variation between genotypes for qualitative traits such as early plant vigour, growth habit, seed colour, seed shape and testa texture was also recorded. Genetic variability for plant height, number of primary branches, number of pods plant<sup>-1</sup> and 100 seed weight ranged from 23.2–49.6 cm, 1.8–5.6, 12.4–66.4 and 9.0–30.0 respectively whereas grain yield plant<sup>-1</sup> varied from 1.7–30.0g, while the variation for days to flowering were in the range of 44.0–76.0 and 89.0–114.0 for days to maturity.

Sharma *et al.* (2013) studied genetic analysis for seed size in three crosses of chickpea (*Cicer arietinum* L.). Seed size (determined by 100-seed weight) is an important component of trade and yield in chickpea.

Peerzada *et al.* (2014) reported that the thirty six genotypes of chickpea were evaluated to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. The genotype RKG135 recorded highest mean performance for number of pods plant<sup>-1</sup> (94.60) while, genotype NBEG 13 recorded highest mean performance (56.67) for plant height. Highest mean performance for seed yield q ha<sup>-1</sup> (19.61) was recorded in genotype RVSSG 1, while, genotype H 04-75 recorded highest mean performance (126.33) for days to maturity. Genotype BG 3004 showed highest mean performance for 100 seed weight (28.85) and number of branches plant<sup>-1</sup> (5.00).

Naveed *et al.* (2015) revealed that the sixty accessions were laid out in an alpha lattice design with two replications. Analysis of variance for various traits revealed significant diversity among the genotypes which can be exploited for the development of superior chickpea segregants in productivity improvement programs.

Roy *et al.* (2016) revealed while evaluating forty three chickpea genotypes (*Cicer arietinum* L.) at Calcutta University's experimental farm during *rabi* season 2014-2015 to estimate genetic parameters and nature of relationships of seed yield and its component characters, pronounced variation existed among the chickpea genotypes regarding all the characters (plant height, branches plant<sup>-1</sup>,

pods plant<sup>-1</sup>, 100 seed weight, harvest index and seed yield plant<sup>-1</sup>) except pod length and seeds pod<sup>-1</sup>.

Bhanu *et al.* (2017) reported that the significant genetic variations were observed among the genotypes for days to flower, days to maturity, plant height, number of branches plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100-seed weight and seed yield plant<sup>-1</sup>.

Mannur *et al.* (2017) reported that the analysis of variance showed that mean sum of squares due to genotypes were highly significant for most of the characters in advance generation of green chickpea.

Srivastava *et al.* (2017) reported that the analysis of variance revealed significant differences among the genotypes for all the characters studied.

Nawaz *et al.* (2018) reported that the analysis of variance showed significant differences among the F<sub>6</sub> chickpea lines for all the studied traits. Line C2-P7-1-1 showed maximum mean value for days to maturity (123.7), seed pod<sup>-1</sup> (1.9) and harvest index (27.7%), whereas, line C2-P8-2-5 exhibited maximum mean value for plant height (68.3 cm), primary branches plant<sup>-1</sup> (3.8) and biological yield (2010.6 kg ha<sup>-1</sup>). Maximum pods plant<sup>-1</sup> (28.8) was attained by line C2-P8-3-1, whereas, maximum secondary branches plant<sup>-1</sup> (8.8) were noted for C2-P8-3-4. Moreover, C2-P7-1-8 exhibited maximum mean value for 100 seed weight (25.9 g) and grain yield (463.8 kg ha<sup>-1</sup>).

### **2.2 Coefficient of variation**

Dwevedi and Gaibriyal (2009) reported that the number of pods plant<sup>-1</sup> had maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by 100 seed weight.

Parhe *et al.* (2010) evaluated fifty one genotypes of chickpea to study the nature and magnitude of genetic diversity. Seed yield plant<sup>-1</sup> had maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by 100 seed weight.

Kanouni *et al.* (2012) reported that the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) and the environmental coefficient of variation (ECV) for all traits. The PCV was highest

for plant vigor (32.24%), followed by seed yield (28.47%) and pods plant<sup>-1</sup> (27.59%). Similarly, the GCV was highest for plant vigor, followed by seed yield and pods plant<sup>-1</sup>. The GCV and PCV were lowest for days to maturity, followed by days to flowering and 100-seed weight.

Ramanappa *et al.* (2013) reported that the magnitude of the phenotypic coefficient of variation (PCV) was slightly higher than their corresponding genotypic coefficient variation (GCV) for all the characters indicated least influence of environment in the expression of these traits. The grain yield plant<sup>-1</sup> and number pods plant<sup>-1</sup> recorded higher PCV of 39.20% and 35.83% respectively and GCV of 30.95% and 29.62% respectively compared to other traits. Grain yield is highly dependent character; hence the coefficient of variability also showed the cumulative effects and resulted in higher magnitude.

Peerzada *et al.* (2014) evaluated thirty six genotypes of chickpea to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters. High genotypic (31.68) and phenotypic (31.82) coefficient of variance were recorded for pods plant<sup>-1</sup>.

Peerzada *et al.* (2015) studied the phenotypic and genotypic variances, heritability in broad sense ( $h^2$ ), genetic advance and genetic gain were conducted for yield and yield contributing traits for 11 characters in 12 genotypes of chickpea (kabuli), taken from IIPR, Kanpur, India, in a randomized block design with three replications. High genotypic and phenotypic coefficients of variability were observed for seed yield ( $q\ ha^{-1}$ ), number of pods plant<sup>-1</sup>, 100-seed weight and seed yield plant<sup>-1</sup>.

Roy *et al.* (2016) revealed in the study of forty three chickpea genotypes (*Cicer arietinum* L.) that the coefficient of variability showed cumulative effects and higher magnitude among all the genotypes. The estimates of variation revealed that GCV was smaller than PCV indicating that the apparent variation was not only due to genetic changes but also due to the favorable influence of environment. GCV was estimated to be high for branches plant<sup>-1</sup>, seed yield plant<sup>-1</sup>, pods plant<sup>-1</sup>, harvest index, pod length and 100 seed weight. Estimates of PCV showed a similar trend for all the above mentioned traits.

Tiwari *et al.* (2016) evaluated the thirty eight chickpea varieties were to find out genetic variability, genetic association and path coefficient analysis for grain yield and its attributing characters. Both genotypic and phenotypic variances were highly significant for all the traits with little higher phenotypic coefficient of variation. The low differences between the phenotypic and genotypic coefficients of variations indicated low environmental influences on the expression of these characters.

Hussain *et al.* (2016) revealed that the number of pods plant<sup>-1</sup>, 100-grain weight, biological yield plant<sup>-1</sup> and grain yield plant<sup>-1</sup> exhibited maximum genetic variation. Genotypic and phenotypic coefficient of variation (GCV and PCV %) was highest for grain yield plant<sup>-1</sup> (19.73 and 20.10) followed by number of pods plant<sup>-1</sup> (18.90 and 19.58), biological yield plant<sup>-1</sup> (13.56 and 14.81) and 100-grain weight (11.60 and 12.25), respectively.

Bhanu *et al.* (2017) reported the highest genotypic variances for number of pods plant<sup>-1</sup> (212.18), followed by plant height (60.90cm), and 100 seed weight (12.42g) , while the lowest genotypic variance was found for seeds pod<sup>-1</sup> and primary branches. The highest phenotypic variances were found for pods plant<sup>-1</sup>, plant height and days to flowering, while lowest for seeds pod<sup>-1</sup>. The highest environmental variance was found for pods plant<sup>-1</sup> while lowest for seeds pod<sup>-1</sup>. The highest genotypic and phenotypic coefficient of variances was found for seed yield plant<sup>-1</sup> while lowest genotypic coefficient of variance was found for days to maturity.

Mannur *et al.* (2017) reported that the high amount of variability was observed for both phenotypic and genotypic coefficient of variability.

### **2.3 Heritability and genetic advance**

Dwevedi and Gaibriyal (2009) reported moderate to high degree of heritability and genetic advance for number of pods plant<sup>-1</sup>, harvest index and biological yield. The genotypes KPJ 59, PBJ 1 and Pusa 329 were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

Parhe *et al.* (2010) examined fifty one genotypes of chickpea to study the nature and magnitude of genetic diversity. High magnitude of heritability (broad sense) was recorded for 100 seed weight. High heritability coupled with high genetic advance was observed for number of pods plant<sup>-1</sup>, 100 seed weight, days to 50% flowering and plant height suggesting the role of additive gene effect and possibilities of achieving high genetic progress through selection. 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.

Kanouni *et al.* (2012) reported high heritability of days to maturity and days to flowering than the heritability of the other traits.

Ramanappa *et al.* (2013) observed high estimates of heritability along with high variation for 100 seed weight, number of pods plant<sup>-1</sup>, days to 50% flowering, grain yield plant<sup>-1</sup>, number of primary branches plant<sup>-1</sup> and plant height. High heritability in broad sense coupled with high genetic advance as per cent mean was recorded for grain yield plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, 100 seed weight and days to 50% flowering suggesting that these traits under the control of additive gene action and potential possibilities exist for the improvement of these traits through simple selection. Moderate genetic advance for plant height, number of primary branches and days to maturity could be due to low genetic variability for these traits. However, a high heritability value for these traits suggests that to some extent selection will be an effective strategy in improving these traits.

Peerzada *et al.* (2014) reported in thirty six genotypes of chickpea were evaluated to study the magnitude of genetic variability, heritability and genetic advance in yield and yield contributing characters, high heritability (99.8%) coupled with high genetic advance (52.19%) for seed yield q ha<sup>-1</sup> and highest genetic gain (64.97%) for number of pods plant<sup>-1</sup>. Hence, these characters indicate the presence of a considerable proportion of total variability due to

genetic causes and may serve as effective selection parameter during breeding program for crop improvement.

Faiz and Aslam (2015) studied twenty chickpea genotypes including four varieties evaluated for the existence of genetic variability and to know the interrelationship among yield traits under study during 2013-2014, at University of Agriculture, Faisalabad. Heritability estimates were higher for all characters, except number of days to maturity and number of grains plant<sup>-1</sup>, which exhibited moderate heritability. Hundred seed weight, plant height, total plant weight and primary branches plant<sup>-1</sup> would be the suitable selection criteria to accomplish better grain yield in chickpea.

Naveed *et al.* (2015) revealed high to moderate estimates of heritability and genetic advance for days to 50% flowering, total branches plant<sup>-1</sup>, pods plant<sup>-1</sup>, 100-seed weight and grain yield.

Peerzada *et al.* (2015) estimated phenotypic and genotypic variances, heritability in broad sense ( $h^2$ ), genetic advance and genetic gain for yield and yield contributing traits for 11 characters in 12 genotypes of chickpea (kabuli), taken from IIPR, Kanpur, India, in a randomized block design with three replications. Number of pods plant<sup>-1</sup>, days to maturity and 100-seed weight were characterized by high broad sense heritability. High value of genetic advance was recorded for number of pods plant<sup>-1</sup>, biological yield plant<sup>-1</sup> and harvest index and highest genetic gain was recorded for number of pods plant<sup>-1</sup>. Hence, these characters indicate the presence of a considerable proportion of total variability due to genetic causes and may serve as effective selection parameter during breeding programme for crop improvement.

Roy *et al.* (2016) revealed high magnitude of heritability as well as high genetic advance for the traits viz., plant height, harvest index, pods plant<sup>-1</sup>, seed yield plant<sup>-1</sup> and 100 seed weight in evaluating 43 genotypes of chickpea suggesting the control of additive gene effects and effective selection could be possible for improvement of these characters.

Tiwari *et al.* (2016) examined thirty eight chickpea varieties to find out genetic variability, genetic association and path coefficient analysis for grain yield

and its attributing characters. High heritability coupled with high genetic advance were obtained with harvest index, seeds pod<sup>-1</sup>, total number of pods plant<sup>-1</sup>, seed yield plant<sup>-1</sup> and days to maturity.

Salgotra (2016) observed high heritability along with high genetic advance for traits viz., number of pods plant<sup>-1</sup>, pod length and 100 seed weight. High heritability along with moderate genetic advance were observed for plant height and seed yield plant<sup>-1</sup> indicated that these traits are governed by additive-gene action and continued selection in subsequent generations will be highly responsive.

Hussain *et al.* (2016) revealed high heritability value associated with high genetic advance expressed as percentage of mean for number of pods plant<sup>-1</sup> (93.19 and 37.59), 100-grain weight (89.67 and 22.62), biological yield plant<sup>-1</sup> (83.83 and 25.58) and grain yield plant<sup>-1</sup> (96.40 and 39.91). Therefore, these traits can be considered as the most favourable attribute for their improvement due to the contribution of additive gene action and consequently high expected genetic gain from selection.

Bhanu *et al.* (2017) reported the highest heritability for 100 seed weight (99%). Greater heritability estimates for such traits as 100 seed weight, seed yield plant<sup>-1</sup> and pods plant<sup>-1</sup> indicate that these characters can be used as the genetic parameters for the improvement and selection of high yielding genotypes. The genetic advance under selection was considerable for number of pods plant<sup>-1</sup> (45.52%) and 100 seed weight (48.33%) indicating that the improvement of the trait through selection is possible. High heritability coupled with high genetic advance observed in case of pods plant<sup>-1</sup> and 100 seed weight indicated that these characters were governed largely through the additive gene effect.

Mannur *et al.* (2017) reported that the broad sense heritability estimates were highest for biological yield per plant (85.76%), number of seeds pod<sup>-1</sup> (72.94%), seed yield plant<sup>-1</sup> (67.44%), test weight (66.55%), leaflet size (60.01%) and plant height (52.76%). Genetic advance was higher for biological yield plant<sup>-1</sup> (11.45%), test weight (9.93%), days to 50 per cent flowering (9.84%) and plant

height (6.01%). High heritability with high genetic advance per cent mean was observed for number of seeds pod<sup>-1</sup>, biological yield plant<sup>-1</sup>, test weight and seed yield plant<sup>-1</sup>, whereas low heritability with low genetic advance per cent mean was observed for the traits like, number of pods plant<sup>-1</sup> and number of primary branches plant<sup>-1</sup>. The remaining traits like, leaflet size, plant height, basal height and number of secondary branches plant<sup>-1</sup> recorded moderate heritability coupled with moderate genetic advance per cent mean.

Srivastava *et al.* (2017) reported that the number of pods plant<sup>-1</sup> followed by days to maturity and seed-index exhibited high estimates of heritability (bs) as well as genetic advance. Seed-index and number of pods plant<sup>-1</sup> exhibited high estimates of genetic advance expressed as percent of mean.

Nawaz *et al.* (2018) reported that the genetic variances of all the traits were greater than environmental variances. Genetic advance was for days to maturity (15.46%), plant height (5.98%), primary branches plant<sup>-1</sup> (0.60%), secondary branches plant<sup>-1</sup> (1.67%), pods plant<sup>-1</sup> (5.81%), seeds pod<sup>-1</sup>(0.24%). 100 Seed weight (3.17%), seed yield (209.58%), biological yield (598.45%) and harvest index (7.00%). It could be concluded that high values of heritability and genetic advance for a characters like secondary branches plant<sup>-1</sup> & pods plant<sup>-1</sup> suggested appropriate selection criteria and could be effective in a future breeding programs.

### **2.4 Correlation coefficient**

Thakur and Sirohi (2009) reported that the seed yield plant<sup>-1</sup> exhibited stable positive association with biological yield plant<sup>-1</sup>, pods plant<sup>-1</sup>, primary branches plant<sup>-1</sup>, plant height and harvest index at genotypic and phenotypic levels in individually as well as combined over seasons.

Malik *et al.* (2010) observed highly significant and positive correlation of grain yield with biological yield, secondary branches and number of pods plant<sup>-1</sup>. Secondary branches were positively correlated with number of pods plant<sup>-1</sup> and grain yield plant<sup>-1</sup>, whereas it was negatively associated with 100 grain weight.

Ali *et al.* (2011) in the correlation studies, observed that biomass plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, number of seeds pod<sup>-1</sup> and 100-seed weight have positive and significant correlation at genotypic level but positive and highly significant at phenotypic level. Whereas days to flowering, days to maturity, primary branches plant<sup>-1</sup>, secondary branches plant<sup>-1</sup> were positively correlated with the grain yield plant<sup>-1</sup> at genotypic and phenotypic levels. Plant height was negative and non-significantly correlated with grain yield plant<sup>-1</sup> at both genotypic and phenotypic levels.

Kanouni *et al.* (2012) observed the positive significant relationships between seed yield plant<sup>-1</sup> and traits pods plant<sup>-1</sup>, 100-seed weight and plant height.

Ramanappa *et al.* (2013) reported that the grain yield had highly significant positive association with number of pods plant<sup>-1</sup>, number of primary branches, plant height, and number of seeds pod<sup>-1</sup> at phenotypic level. However, days to maturity was negatively correlated with grain yield.

Mushtaq *et al.* (2013) in the correlation studies, showed that the correlation was positive for plant height, total weight of plant, secondary branches plant<sup>-1</sup> and pods plant<sup>-1</sup>. It was significant at genotypic level but maximally significant at phenotypic level. The correlations were positive for days to flowering, primary branches plant<sup>-1</sup>, grains pod<sup>-1</sup>, days to maturity and 100-grains weight at genotypic and phenotypic levels.

Roy *et al.* (2016) revealed in the study of forty three chickpea genotypes (*Cicer arietinum* L.) positive and significant relationships with pods plant<sup>-1</sup>, 100 seed weight and harvest index whereas the other traits showed positive but non-significant relationship with seed yield.

Salgotra (2016) in a correlation studies, revealed that seed yield plant<sup>-1</sup> were significantly and positively correlated with plant height, number of pods plant<sup>-1</sup>, number of seeds pod<sup>-1</sup>, 100 seed weight and negatively correlated with number of secondary branches and days to fifty percent flowering.

Petrova and Desheva (2016) investigated correlation and path-coefficient analyses for seed yield and yield components in 96 genotypes of chickpea of

different origin. Seed yield  $\text{m}^2$  area correlated positively and significantly with plant height, first pod height, number of branches on main stem, number of pods  $\text{plant}^{-1}$  and number of seeds  $\text{plant}^{-1}$ .

Tadesse *et al.* (2016) studied the relationships among yield and some yield components using correlation and path coefficient analysis in desi chickpea grown under rainfed conditions. Correlation studies revealed that seed yield was significantly and positively correlated with days to flowering, days to maturity, number of pods  $\text{plant}^{-1}$ , number of seeds  $\text{pod}^{-1}$ , stand count at harvest, plant height and biomass.

Tiwari *et al.* (2016) evaluated the thirty eight chickpea varieties to find out genetic variability, genetic association and path coefficient analysis for grain yield and its attributing characters. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Harvest index, 100-seed weight, seeds  $\text{pod}^{-1}$ , number of effective pods  $\text{plant}^{-1}$ , total number of pods  $\text{plant}^{-1}$ , number of primary branches  $\text{plant}^{-1}$  and plant height were the most important characters, which possessed positive association with seed yield  $\text{plant}^{-1}$ .

Bhanu *et al.* (2017) noted that the values of genotypic correlation were higher than their phenotypic counterparts suggesting a strong inherent association for the traits studied and phenotypic selection may be rewarding. Seed yield was positively and significantly correlated with number of primary branches, number of secondary branches and number of pods  $\text{plant}^{-1}$ .

Srivastava *et al.* (2017) reported that the correlation coefficient analysis revealed that seed yield  $\text{plant}^{-1}$  exhibited significant and positive correlation both at genotypic and phenotypic level with biological yield  $\text{plant}^{-1}$ , harvest-index only at genotypic level with number of pods  $\text{plant}^{-1}$ . Hence, these characters may serve as effective selection criterion for yield improvement in chickpea.

### **2.5 Path coefficient**

Thakur and Sirohi (2009) revealed high positive and direct influence of biological yield  $\text{plant}^{-1}$  with seed yield  $\text{plant}^{-1}$  followed by harvest index and pods  $\text{plant}^{-1}$  in individual as well as combined over seasons. Pods  $\text{plant}^{-1}$ , primary

branches plant<sup>-1</sup> and plant height contributed to seed yield mainly through indirect effect *via* biological yield. Therefore, selection for high biological yield and harvest index would lead to high seed yield and selection for pods plant<sup>-1</sup>, primary branches plant<sup>-1</sup> and plant height would facilitate for high biological yield.

Kanouni *et al.* (2012) reported that 100-seed weight, plant height and pods plant<sup>-1</sup> exhibited high positive direct effects for seed yield. Vigor, days to maturity and 100-seed weight showed the highest direct influence. Therefore, this research suggests that pod plant<sup>-1</sup> can be good selection criteria for improving seed yield plant<sup>-1</sup> in chickpea.

Mushtaq *et al.* (2013) observed that days to flowering had maximum direct influence on seed yield plant<sup>-1</sup> followed by total weight of plant, 100-grains weight, primary branches and plant height. These are important parameters for selecting maximum yielding genotypes in chickpea.

Roy *et al.* (2016) that all the traits, with the exception of plant height and branches plant<sup>-1</sup>, had positive direct effect on yield. Pods plant<sup>-1</sup>, 100 seed weight, harvest index, pod length and seeds pod<sup>-1</sup> due to its highly positive both direct and indirect effect on seed yield could provide a good selection criteria for high yielding chickpea lines.

Tiwari *et al.* (2016) revealed that among the different yield contributing characters harvest index, 100-seed weight, seeds pod<sup>-1</sup>, total number of pods plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, plant height, days to maturity and days to 50% flowering influenced seed yield plant<sup>-1</sup> directly. Thus, selection for yield in chickpea through these characters would be effective.

Petrova and Desheva (2016) observed that the number of seeds plant<sup>-1</sup>, plant height and number of branches on main stem had the strongest positive direct effect on the seed yield m<sup>2</sup> area. The relations between these characters can be used as selection criteria in a breeding study aimed at improving the high yielding cultivars for that region.

Tadesse *et al.* (2016) examined in the path coefficient analysis based on seed yield, as a dependent variable, revealed that biomass had the greatest direct effect on seed yield, followed by stand count at harvest and plant height.

Both correlation and path analyses indicated that biomass, stand count at harvest and plant height were the major direct contributors to seed yield. Thus, the present study suggests that more biomass production, stand count at harvest and plant height is major yield factors in selecting high yielding desi chickpea cultivars.

Bhanu *et al.* (2017) reported in the path coefficient analysis based on seed yield, as a dependent variable, showed that pods plant<sup>-1</sup> had the greatest direct effect on seed yield (0.81) followed by number of secondary branches. Both correlation and path analysis indicated that pods plant<sup>-1</sup> and number of secondary branches were the major direct contributors to seed yield.

### **2.6 Genetic divergence**

Dwevedi and Gaibriyal (2009) recorded data on ten important quantitative traits from the genotypes. The twenty five chickpea genotypes were grouped into six clusters. 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 plant<sup>-1</sup> contributed maximum in manifestation of genetic diversity. The genotypes KPJ 59, PBJ 1 and Pusa 329 were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

Malik *et al.* (2010) observed 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 plant<sup>-1</sup>, biological yield and seed yield plant<sup>-1</sup> were placed together in cluster III. Genotypes with maximum harvest index and 100 seed weight were placed in cluster II and I, respectively.

Parhe *et al.* (2010) reported in fifty one genotypes of chickpea carried out to study the nature and magnitude of genetic divergence using Mahalanobis's D<sup>2</sup> Statistics. The fifty one chickpea genotypes were grouped into five clusters. Cluster I was largest with forty genotypes followed by cluster II with eight

genotypes. The maximum inter-cluster distance was observed between cluster I and V, followed by cluster II and V suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters viz. 100 seed weight, number of pods plant<sup>-1</sup> and days to 50% flowering contributed maximum 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.

Naveed *et al.* (2015) revealed that the cluster analysis classified the chickpea genotypes into 3 clusters with maximum 33 genotypes in cluster II. Cluster I comprised of drought tolerant accessions based on canopy temperature while cluster III consisted of bold seeded genotypes regarding 100-seed weight. Cluster II incorporated wilt resistant, early flowering yet late maturing genotypes having highest pods plant<sup>-1</sup>, grain yield and harvest index. D<sup>2</sup> statistics further confirmed the versatility of cluster II genotypes over cluster I and III for most of the studied characters.

Kushwaha *et al.* (2017) studied eighty four genotypes of chickpea and classified into 8 clusters. The inter-cluster distances were greater than intra cluster distances indicating a considerable amount of genetic variability in the studied material. Maximum inter cluster distance was between cluster V & cluster VIII (22.935) while minimum inter cluster distance (6.589) was observed between cluster II & cluster IV indicating presence of diversity in these clusters. The cluster V showed maximum intra cluster D<sup>2</sup> values (5.645). Cluster VIII which consists of 8 genotypes showed maximum mean value for number of pods plant<sup>-1</sup> and seed yield plant<sup>-1</sup> may be of importance for yield characters. Diverse clusters namely, V and VIII consists of diverse parents hold good promise for potential hybrids for desirable characters and thereby creating greater possibilities of obtaining early type high yielders.

## **CHAPTER III**

### **MATERIALS AND METHODS**

This chapter comprises the details about the materials used and the methods adopted during the course of present investigation entitled “Assessment of diversity in genetic stock of chickpea (*Cicer arietinum* L.)” was carried out in Rabi season during the year 2017-18.

#### **3.1 Experimental site**

The present experiment was laid out in the field of R.A.K. College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Sehore during Rabi season, 2017-18.

#### **3.2 Location and climate**

Sehore is situated at the latitude of 27.05° East and an altitude of 497.8 meters above the mean sea level. It lies in the western track of Vindhyan Plateau agro-climatic zone of Madhya Pradesh and enjoy sub tropical climate. The average annual rainfall is 1031 mm, which is mostly received during July and August. The average maximum temperature is 46°C and minimum temperature 6.8°C. The average annual relative humidity is 74%.

The meteorological parameter during the crop season such as minimum and maximum temperature, relative humidity, rainfall and number of rainy days were recorded at Meteorological observatory R.A.K. College of Agriculture, Sehore (M.P.) are presented in Table 3.1.

The data (Table 3.1 and Fig. 1) indicate that the total rainfall received during crop growth period was 39.6 mm in 3 rainy days. There were no rains during SMW 40, 42 - 06 and 08 – 14. The minimum and maximum temperature during crop growth period varied 7.2 °C to 23.3 °C and from 23.8 °C to 34.7 °C, with season's average values of 12.8 °C and 28.0 °C respectively. The relative humidity morning and evening ranged between 59.7 to 90.0 % and 15.6 to 60.7% with season's average of 73.7% and 28.6% respectively.

Table 3.1: Meteorological information (week wise) during entire crop season of the year 2017-18 at Sehore, (M.P.).

SMW	Date & Month	Temperature (°C)		Relative humidity (%)		Rainfall (mm)	No. of rainy days
		Max.	Min.	Morning	Evening		
40	Oct. 01–07	34.7	20.4	72.9	60.7	0.0	0.0
41	Oct. 08–14	32.3	23.3	68.6	50.6	22.1	2.0
42	Oct. 15–21	34.3	18.6	79.0	24.4	0.0	0.0
43	Oct. 22–28	32.4	16.7	67.9	22.7	0.0	0.0
44	Oct. 29–Nov.04	30.8	14.2	60.8	16.3	0.0	0.0
45	Nov. 05–11	28.8	13.3	80.9	26.9	0.0	0.0
46	Nov.12–18	27.3	13.8	78.9	26.5	0.0	0.0
47	Nov.19–25	25.9	13.4	74.3	24.6	0.0	0.0
48	Nov.26 –Dec. 02	27.4	9.9	79.1	22.1	0.0	0.0
49	Dec.03-09	24.3	11.4	69.0	31.2	0.0	0.0
50	Dec.10-16	25.8	12.7	73.9	34.4	0.0	0.0
51	Dec.17-23	24.2	9.4	70.4	30.2	0.0	0.0
52	Dec.24-31	24.7	8.0	80.3	27.4	0.0	0.0
1	Jan. 01-07	23.8	7.8	82.2	31.7	0.0	0.0
2	Jan.8-14	24.1	8.7	75.4	28.0	0.0	0.0
3	Jan.15-21	27.0	12.4	61.3	26.7	0.0	0.0
4	Jan.22-28	25.3	7.2	75.9	23.4	0.0	0.0
5	Jan.29- Feb.04	28.7	9.8	75.0	18.9	0.0	0.0
6	Feb.05-11	27.0	12.0	72.9	26.7	0.0	0.0
7	Feb.12-18	26.6	11.4	90.0	31.3	17.5	1.0
8	Feb.19-25	31.8	14.1	59.7	15.6	0.0	0.0

### 3.3 Soil

The soil of the experimental field was clay loam Vertisol with 42.6% clay, 61.8% silt and 21.5% sand with pH ranging from 6.9. The soil was very low in available nitrogen, medium in available phosphorus and high in available potassium. 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 a 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

<b>SN</b>	<b>Composition</b>	<b>Content</b>	<b>Category</b>	<b>Method used</b>
<b>A. Mechanical composition</b>				
1	Sand (%)	21.50	-	Bouyoucos Hydrometer method (Piper, 1967)
2	Silt (%)	31.80	-	
3	Clay (%)	42.60	-	
4	Textural class		Clayey	
<b>B. Chemical composition</b>				
<b>S.N</b>	<b>Analysis</b>	<b>Values</b>	<b>Category</b>	<b>Method adopted</b>
1.	Soil pH	6.9	Normal	Glass electrode method (pH meter) (Jackson, 1967)
2.	Electrical conductivity (ds/m)	0.49	Normal	Conductivity meter at 25°C (Jackson, 1967)
3.	Organic carbon (%)	0.42	Low	Wakley and Black rapid titration method (Wakley and Black 1934)
4.	Available Nitrogen (kg N /ha)	149.8	Very low	Alkaline permanganate method (Jackson 1967)
5.	Available phosphorus (kg P <sub>2</sub> O <sub>5</sub> /ha)	12.10	Medium	Olsen's method (Jackson, 1967)
6.	Available potash (kg K <sub>2</sub> O /ha)	346.5	High	Flame photometer (Jackson, 1967)

### **3.4 Experimental material**

The experimental materials for this study comprised 200 genotypes of chickpea are presented in Table 3.3.

**Table 3.3: Details of treatments used in the study**

<b>S.No.</b>	<b>Genotypes</b>	<b>S.No.</b>	<b>Genotypes</b>	<b>S.No.</b>	<b>Genotypes</b>	<b>S.No.</b>	<b>Genotypes</b>
1.	ICC1000	51	ICC14787	101	ICC5021	151	ICCV93954
2.	ICC10393	52	ICC14881	102	ICC504	152	ICCV95311
3.	ICC10504	53	ICC15080	103	ICC5086	153	ICCV95703
4.	ICC10546	54	ICC15184	104	ICC5119	154	IG10224
5.	ICC10950	55	ICC1520	105	ICC512	155	IG10578
6.	ICC11059	56	ICC153	106	ICC531	156	IG10633
7.	ICC11091	57	ICC15347	107	ICC5391	157	IG5875
8.	ICC11258	58	ICC15455	108	ICC5504	158	IG5990
9.	ICC11266	59	ICC15489	109	ICC5541	159	IG5995
10.	ICC11330	60	ICC15547	110	ICC5581	160	IG6408
11.	ICC11424	61	ICC15551	111	ICC5686	161	IG69441
12.	ICC1148	62	ICC15614	112	ICC5697	162	IG69597
13.	ICC11507	63	ICC15714	113	ICC5755	163	IG70413
14.	ICC11766	64	ICC15834	114	ICC5886	164	IG70505
15.	ICC11867	65	ICC15844	115	ICC5899	165	IG70746
16.	ICC11879	66	ICC16187	116	ICC6122	166	IG70985
17.	ICC11904	67	ICC16201	117	ICC6140	167	IG70990
18.	ICC1205	68	ICC16244	118	ICC6155	168	IG71790
19.	ICC12159	69	ICC16245	119	ICC6300	169	IG71799
20.	ICC12258	70	ICC16579	120	ICC6659	170	IG71814
21.	ICC1228	71	ICC16637	121	ICC6831	171	IG71887
22.	ICC12310	72	ICC16644	122	ICC6970	172	IG71926
23.	ICC1232	73	ICC16706	123	ICC7098	173	IG71941
24.	ICC12323	74	ICC16822	124	ICC7269	174	IG71945
25.	ICC12600	75	ICC16947	125	ICC7302	175	IG71967
26.	ICC12691	76	ICC2	126	ICC7380	176	IG72042
27.	ICC128	77	ICC2086	127	ICC7479	177	IG73287
28.	ICC12856	78	ICC2113	128	ICC75	178	IG73322
29.	ICC12879	79	ICC2338	129	ICC7737	179	IG7333
30.	ICC12888	80	ICC2516	130	ICC793	180	IG73334
31.	ICC1296	81	ICC26	131	ICC8284	181	IG73341
32.	ICC13095	82	ICC2629	132	ICC8397	182	IG73458
33.	ICC13185	83	ICC2796	133	ICC8449	183	IG74094
34.	ICC13200	84	ICC2893	134	ICC8660	184	IG7432
35.	ICC13245	85	ICC3411	135	ICC871	185	IG7634
36.	ICC1356	86	ICC3458	136	ICC8723	186	IG9262
37.	ICC13764	87	ICC3491	137	ICC8923	187	IG9330
38.	ICC13964	88	ICC353	138	ICC8962	188	IG9740
39.	ICC14051	89	ICC3539	139	ICC9020	189	IG9810
40.	ICC14199	90	ICC3613	140	ICC9023	190	SAGLK102
41.	ICC14225	91	ICC3705	141	ICC952	191	JG11
42.	ICC14226	92	ICC3834	142	ICC9728	192	SAGL 01
43.	ICC14344	93	ICC4233	143	ICC981	193	KAK2
44.	ICC14411	94	ICC4359	144	ICC991	194	SAGL 101
45.	ICC14426	95	ICC4411	145	ICC9917	195	L550
46.	ICC14446	96	ICC455	146	ICCV10	196	SGLK 101
47.	ICC14469	97	ICC4567	147	ICCV10	197	SAGLK109
48.	ICC14484	98	ICC4893	148	ICCV10	198	SAGLK 20
49.	ICC1470	99	ICC4946	149	ICCV91106	199	SAGL 6
50.	ICC14710	100	ICC4984	150	ICCV92944	200	SAGL1

## **3.5 Experimental details**

### **3.5.1 Design of experiment**

The experiment was laid out in Randomized Complete Block Design (RCBD) with two replications. Each replication consists of 200 genotypes. All the genotypes were randomized separately in each replication. The other details are given as below:-

Design	:	Randomized Complete Block Design
Replication	:	Two
No. of genotypes	:	200
Row to row distance	:	30.0 cm
Plant to plant distance	:	10.0 cm
Row length	:	4 m
Number of plants for observation per plot	:	5
Season	:	Rabi 2017-18
Date of sowing	:	10 – 10 - 2017

## **3.6 Agronomical operations:**

### **3.6.1 Field preparation and sowing**

In order to get good tilth of the soil for sowing one cross cultivation was done by tractor drawn cultivator followed by two harrowing and one planking before sowing of seed.

In the beginning of the experiment, seeds were dibbled. After two weeks of sowing, thinning was carried out to maintain plant to plant distance. All the recommended package of practices was followed to raise healthy crop.

### **3.6.2 Irrigation**

The first sprinkler irrigation was given immediately after sowing to ensure proper germination. Second irrigation was given at 45 days after sowing.

### **3.6.3 Intercultural operations**

The experimental plots were kept weed free. Two hand weeding was done.

### **3.6.4 Fertilizer Application**

Nitrogen, phosphorus and potassium were applied, as per the doses through urea, single super phosphate and murate of potash respectively. A uniform dose of 20 kg N/ha, 45 kg P<sub>2</sub>O<sub>5</sub>/ha, and 25 kg K<sub>2</sub>O/ha was applied to all the genotypes. Full quantity of phosphorus and potassium fertilizer along with one-third of nitrogen was applied before sowing of seeds.

### **3.7 Sampling**

Randomly five plants were taken randomly in each replication for each genotype for recording observations.

### **3.8 Observation recorded**

The data recorded on various parameters were subdivided into two categories (Qualitative and Quantitative) during the period of experimentation. The data were recorded as per standard procedure (Chickpea descriptor used for recording observations).

#### **(A) Qualitative observation**

##### **3.8.1 Plant vigour**

The plant vigour of different genotypes was recorded on the basis of visual observation.

- Very good
- Good
- Vigorous
- Poor

##### **3.8.2 Leaf colour**

The colour of leaf of different genotypes was recorded on the basis of visual observation.

- Dark green
- Green
- Light green

##### **3.8.3 Flower colour**

The colour of flowers of different genotypes was recorded on the basis of visual observation.

- Pink
- White
- Blue

### **3.8.4 Plant growth habit**

The plant growth habit of different genotypes was recorded on the basis of visual observation.

- Erect
- Semi erect
- Semi spreading
- Spreading

## **(B) Quantitative observation**

### **3.8.5 Days to 50% flowering**

Number of days beginning from the sowing to the date when 50 per cent of the plants flowered in a row of genotype was recorded.

### **3.8.6 Days to maturity**

The number of days beginning from sowing to the day when maturity was counted for each genotype.

### **3.8.7 Secondary branches plant<sup>-1</sup>**

The numbers of secondary branches arising from the main stem of each tagged plant was counted at the harvesting stage.

### **3.8.8 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 harvest.

### **3.8.9 Pods plant<sup>-1</sup>**

The number of pods harvested from five randomly taken plants in each genotype was collected counted and average pods per plant were calculated.

### **3.8.10 Seed index (g)**

The weight of 100 seeds was recorded separately with the help of weighing balance and average was worked out for each genotypes.

### **3.8.11 Seed yield plant<sup>-1</sup> (g)**

The weight of the seeds of the tagged plants was recorded and the average weight of the seeds per plant was calculated in g.

**3.9 Statistical methodology**

The data obtained in respect of all the characters has been subjected to the following statistical analyses.

**3.9.1 Mean:** It was calculated by using following formula.

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

Where,

$\sum x$  = The sum of all the observation

$n$  = Number of observation

**3.9.2 Analysis of variance**

The data based on the mean of individual plants selected for observation were statistically analysed to find out overall total variability present in the material under study for each character and for all the populations. The first and foremost step is to carry out analysis of variance to test the significance of differences among the populations. The analysis of variance was carried out as per methods suggested by Panse and Sukhatme (1989). The skeleton of analysis of variance used was as follows:

**Table 3.4: ANOVA for Randomized Completely Block Design**

Source of variation	d.f.	Sum of square	Mean sum of square	F value	F <sub>t</sub> 5% or 1% table value
Replication	r-1	RSS	RMS	RMS/EMS	-
Genotypes	g-1	GSS	GMS	GMS/EMS	-
Error	(r-1)(g-1)	ESS	EMS	-	-
<b>Total</b>	<b>rg-1</b>	<b>TSS</b>	-	-	-

where,

r = Number of replications

g = Number of genotypes

D.F. = Degree of freedom

## RVSKVV/Thesis/M.Sc./No. 1712

RSS = Replication sum of square

GSS = Genotype sum of square

ESS = Error sum of square

TSS = Total sum of square

RMS = Replication mean sum of square

GMS = Genotype 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 requires computing C.D.

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

$$SE_{m \pm} = \sqrt{\frac{EMS}{r}}$$

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

CD at 5% prob. Level =  $SE_{diff} \times t_{5\%}$  table value

where,

C.V. % = Coefficient of variation

$SE_{m \pm}$  = Standard error of means

SE diff = Standard error of difference

GM = Grand mean

C.D. = Critical difference

$t_{5\%}$  = t, table value 5% probability level at error d.f.

**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 were calculated by conventional method

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

n

Where,

$\Sigma x_i$  = The sum of all the observation for  $i^{\text{th}}$  character.

n = Number of observations.

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

The component of variance was calculated as follows

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

$$\sigma^2 g_i = M_i - E_i$$

$$\sigma^2 e_i = E_i$$

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

Where,

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

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

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

Phenotypic and genotypic coefficient 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)

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

Where,

$x_i$  = General mean of the  $i^{\text{th}}$  character under consideration.

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

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

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

$$\text{Genetic advance (GA)} = K \cdot P_i \cdot h^2_i$$

Genetic advance as percentage of mean was calculated as follows:

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

Where,

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

$P_i$  = Phenotypic standard deviation of the  $i^{\text{th}}$  character.

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

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

### **Correlation coefficients**

Correlation coefficients were calculated in all possible combinations taking all the characters in to consideration at genotypic, phenotypic and environmental levels by using the formula as proposed by Miller *et al.* (1958).

$$\frac{\sum xy - \frac{\sum x \sum y}{n}}$$

$$r = \frac{\text{Cov}(X, Y)}{\sqrt{(\sum x^2 - \frac{(\sum x)^2}{n}) (\sum y^2 - \frac{(\sum y)^2}{n})}}$$

Where,

r = Correlation coefficient

n = Number of treatments

X and Y = Character under study

Genotypic, phenotypic and environmental correlations were computed by substituting corresponding variance and covariance in the above formula, e.g.

$r_G(X_i, X_j)$	=	$\frac{G \text{ Cov } (X_i, X_j)}{\sqrt{V_G(X_i) \cdot V_G(X_j)}}$
-----------------	---	--

$r_P(X_i, X_j)$	=	$\frac{P \text{ Cov } (X_i, X_j)}{\sqrt{V_P(X_i) \cdot V_P(X_j)}}$
-----------------	---	--

$r_E(X_i, X_j)$	=	$\frac{E \text{ Cov } (X_i, X_j)}{\sqrt{V_E(X_i) \cdot V_E(X_j)}}$
-----------------	---	--

**Testing of correlations:**

The phenotypic correlations are tested for their significance by following formula based on “t” test:

$$T_e = \frac{r}{\sqrt{\frac{n-2}{1-R^2}}} \quad \text{at } (n-2) \text{ d.f.}$$

Where,

N= Number of treatments.

R= phenotypic correlations coefficient.

The calculated value of “t” is compared with table of “t” at (n-2) d.f. If the calculated value is equal to or greater than table value, it is significant at given probability level. If  $t_c < t_\tau$ , it is non significant.

**Path coefficient analysis**

Path coefficients analysis was worked out to show the cause and effect relationship between yield and various yield components and to partition the total correlation coefficient into direct and indirect effects. This procedure was developed by Wright (1921) and followed by Dewey and Lu (1959).

Path coefficients are the standardized partial regression coefficients and as such measure the direct influence of one variable upon another variable and permits partition of correlation coefficient into components of direct and indirect effects. The sum of the direct and all possible indirect effects via all other traits must be equal to correlation coefficient of dependent traits with independent characters under consideration.

Path coefficients were obtained by setting simultaneous equations which express basic relationship between correlation and path coefficient analysis.

1.  $r_{1,y} = P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + \dots + r_{1,10} P_{10,y}$
2.  $r_{2,y} = P_{2,y} + r_{2,1} P_{1,y} + r_{2,2} P_{3,y} + \dots + r_{2,10} P_{10,y}$
10.  $r_{10,y} = P_{10,y} + r_{10,1} P_{1,y} + r_{10,2} P_{3,y} + \dots + r_{10,9} P_{9,y}$

Where,

1, 2, ..... 10 are the component characters and y is dependent upon which direct and indirect effects are studied.

Unexplained variation of the residual effect was obtained from the following equation:

$$R = \sqrt{1 - \sum di r_{ij}}$$

Where,

R = Residual effect.

di = Direct effect of the i<sup>th</sup> character.

## **RVSKVV/Thesis/M.Sc./No. 1712**

$r_{ij}$  = Correlation coefficient between the  $i^{\text{th}}$  character and  $j^{\text{th}}$  dependent character.

Direct and indirect effects of bulb yield per plant were calculated at both genotypic and phenotypic levels.

### **Diversity Analysis**

Clustering of genotypes was performed by K means clustering method was proposed by Wogstaff *et al.* (2001) . The X-STAT software was used for K means clustering. The grouping of its genotypes was based on similarity index.

**CHAPTER IV  
RESULTS**

The results obtained from the present investigation “Assessment of diversity in genetic stock of chickpea (*Cicer arietinum* L.)” are presented under the following heads

4.1 Characterization of chickpea genetic stocks on the basis of qualitative traits

4.2 Quantitative traits analysis

4.3 Analysis of variance

4.4 Genetic Variability analysis

4.3.1 Range and Mean performance

4.3.2 Coefficient of variation

4.3.3 Heritability

4.3.4 Genetic advance

4.5 Association analysis

4.4.1 Correlation coefficient analysis

4.4.2 Path coefficient analysis

4.6 Genetic divergence

4.5.1 Grouping of genotypes in to various clusters

4.5.2 Inter and intra cluster distance

4.5.3 Cluster mean

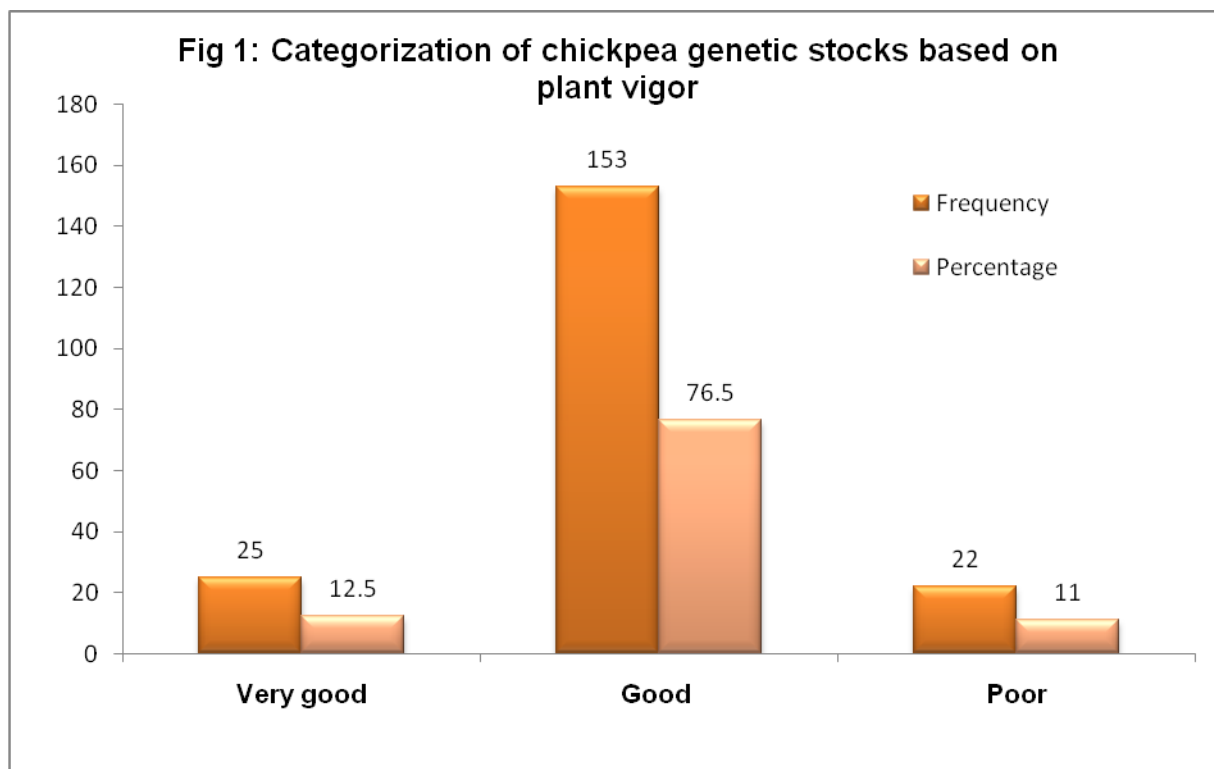
**4.1 Characterization of chickpea genetic stocks on the basis of qualitative traits**

Characterization of chickpea genetic stocks into different groups based on morphological traits at plant level are as follows.

**4.1 Plant vigor**

**Table 4.1: Categorization of chickpea genetic stocks based on plant vigor**

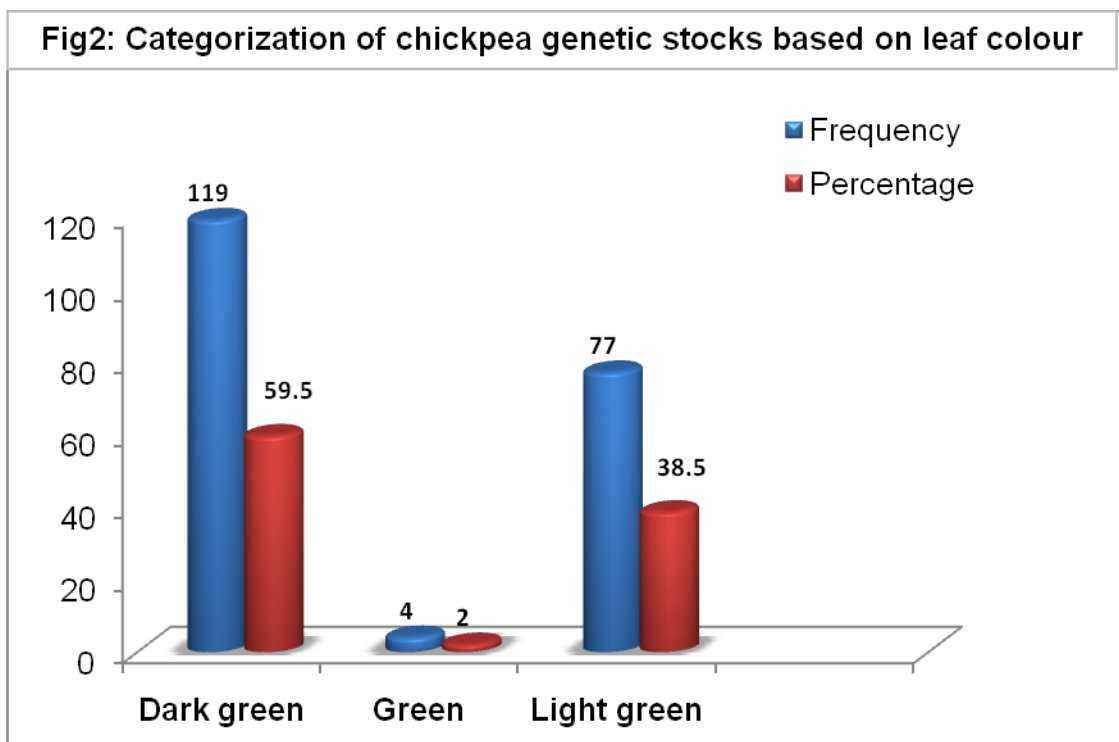
<b>Very good</b>	<b>Good</b>	<b>Poor</b>
ICC1000, ICC12879, ICC13200, ICC1356, ICC14446, ICC14710, ICC15844, ICC16245, ICC16822, ICC3613 ICC3705 ICC4233 ICC7269, ICC75, ICC8923, ICCV92944, ICCV95703, IG70413, IG71799, IG73287, IG73341, SAGLK 2, KAK2, L550.	ICC10393, ICC10546, ICC10950, ICC11059, ICC11091, ICC11258, ICC11266, ICC11330, ICC11424, ICC11507, ICC11766, ICC11867, ICC11879, ICC11904, ICC1205, ICC12159, ICC12258, ICC12310, ICC1232, ICC12323, ICC12600, ICC12691, ICC128, ICC12856, ICC12888, ICC1296, ICC13095, ICC13185, ICC13245, ICC13764, ICC13964, ICC14051, ICC14199, ICC14225, ICC14226, ICC14344, ICC14411, ICC14426, ICC14469, ICC14484, ICC1470, ICC14787, ICC14881, ICC15080, ICC15184, ICC1520, ICC15347, ICC15455, ICC15489, ICC15547, ICC15551, ICC15614, ICC15714, ICC16187, ICC16201, ICC16579, ICC16637, ICC16644, ICC16706, ICC16947, ICC2, ICC2113, ICC2338, ICC2516, ICC26, ICC2796, ICC2893, ICC3411, ICC3458, ICC353, ICC3539, ICC3834, ICC4359, ICC4411, ICC455, ICC4893, ICC4946, ICC4984, ICC5021, ICC504, ICC5086, ICC531 ICC5391 ICC5504 ICC5541 ICC5581 ICC5686 ICC5697 ICC5755 ICC5899 ICC6122 ICC6140 ICC6155 ICC6300 ICC6659 ICC6831 ICC6970 ICC7098 ICC7302 ICC7479 ICC793 ICC8284 ICC8397 ICC8449 ICC8660 ICC871 ICC8723 ICC8962 ICC9023 ICC9728 ICC981 ICC991, ICCV10, ICCV10, ICCV10, ICCV91106, ICCV93954, ICCV95311, IG10578, IG10633, IG5995, IG6408, IG69597,IG70505, IG70746, IG70985, IG70990, IG71790, IG71814, IG71887, IG71941, IG71945, IG71967, IG72042, IG73322, IG7333, IG73334, IG73458, IG74094, IG7432, IG7634, IG9262, IG9330, IG9740, IG9810, SAGL 1, JG11, KAK2, SAGLK 102, L550, ICC2086.	ICC1148, ICC1228, ICC153, ICC10504, ICC15834, ICC16244, ICC2629, ICC3491, ICC4567, ICC5119, ICC512, ICC5886, ICC7380, ICC7737, ICC9020, ICC952, ICC9917, IG10224, IG5875, IG5990, IG69441, IG71926.



**4.2 Leaf colour**

**Table 4.2: Categorization of chickpea genetic stocks based on leaf colour**

<b>Dark green</b>	<b>Green</b>	<b>Light green</b>
ICC1000, ICC10393, ICC10504, ICC10950, ICC11091, ICC11258, ICC11330, ICC1148, ICC11507, ICC11867, ICC1205, ICC12258, ICC12310, ICC1232, ICC12691, ICC128, ICC12856, ICC12879, ICC12888, ICC13095, ICC13185, ICC1356, ICC13764, ICC13964, ICC14051, ICC14344, ICC14411, ICC14469, ICC14484, ICC1470, ICC14787, ICC14881, ICC1520, ICC153, ICC15347, ICC15455, ICC15551, ICC15714, ICC15834, ICC16187, ICC16201, ICC16244, ICC16579, ICC16644, ICC16822, ICC2, ICC2086, ICC2113, ICC2338, ICC26, ICC2629, ICC3458, ICC353, ICC3539, ICC3613, ICC4359, ICC4567, ICC4893, ICC4946, ICC5021, ICC504, ICC5086, ICC512, ICC531, ICC5391, ICC5504, ICC5541, ICC5581, ICC5686, ICC5697, ICC5755, ICC5886, ICC6140, ICC6300, ICC6659, ICC7302, ICC7380, ICC7479, ICC75, ICC7737, ICC793, ICC8397, ICC871, ICC8923, ICC8962, ICC9020, ICC9023, ICC952, ICC981, ICC991, ICC9917, ICCV10, ICCV91106, ICCV92944, ICCV95311, ICCV95703, IG10224, IG5990, IG5995, IG69441, IG70413, IG70505, IG70746, IG71790, IG71799, IG71887, IG71941, IG72042, IG7333, IG73458, IG74094, IG7432, IG9330, IG9740, SAGL 9, JG11, L550, SAGLK 109.	ICC10546, ICC11424, ICC11766, L550.	ICC11059, ICC11266, ICC11879, ICC11904, ICC12159, ICC1228, ICC12323, ICC12600, ICC1296, ICC13200, ICC13245, ICC14199, ICC14225, ICC14226, ICC14426, ICC14446, ICC14710, ICC15080, ICC15489, ICC15547, ICC15614, ICC15184, ICC15844, ICC16245, ICC16637, ICC16706, ICC16947, ICC2516, ICC2796, ICC2893, ICC3411, ICC3491, ICC3705, ICC3834, ICC4233, ICC4411, ICC455, ICC4984, ICC5119, ICC5899, ICC6122, ICC6155, ICC6831, ICC6970, ICC7098, ICC7269, ICC8284, ICC8449, ICC8660, ICC8723, ICC9728, ICCV10, ICCV10, ICCV93954, IG10578, IG10633, IG5875, IG6408, IG69597, IG70985, IG70990, IG71814, IG71926, IG71945, IG71967, IG73287, IG73322, IG73334, IG73341, IG7634, IG9262, IG9810, JG11, SAGLK 4, KAK2.

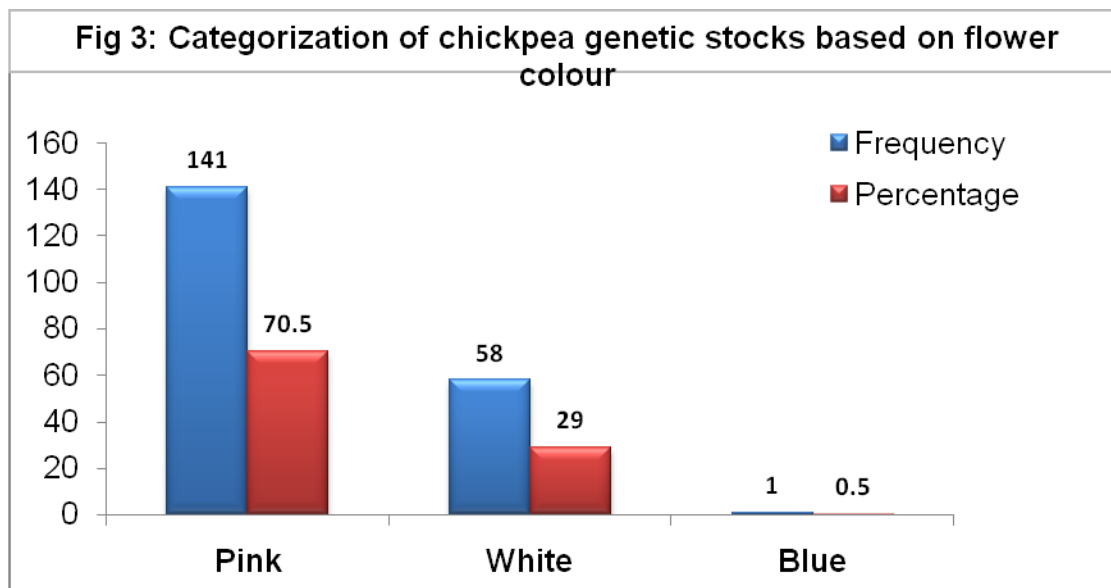


#### 4.3 Flower colour

**Table 4.3: Name of chickpea genotypes genetic stocks and grouped on the basis of flower colour**

Pink	White	Blue
ICC1000, ICC10393, ICC10504, ICC10546, ICC10950, ICC11059, ICC11091, ICC11258, ICC11330, ICC11424, ICC1148, ICC11507, ICC11867, ICC1205, ICC12159, ICC12258, ICC1228, ICC12310, ICC12323, ICC12600, ICC12691, ICC128, ICC12856, ICC12879, ICC12888, ICC1296, ICC13095, ICC13185, ICC13200, ICC1356, ICC13964, ICC14051, ICC14225, ICC14226, ICC14344, ICC14411, ICC14426, ICC14446, ICC14469, ICC14484, ICC1470, ICC14710, ICC14787, ICC14881, ICC15080, ICC15184, ICC1520, ICC153, ICC15347, ICC15455, ICC15547, ICC15614, ICC15714, ICC15844, ICC16201, ICC16244, ICC16245, ICC16706, ICC16947, ICC2, ICC2086, ICC2113, ICC2516, ICC26, ICC2629, ICC2796, ICC2893, ICC3411, ICC3458, ICC3491, ICC353, ICC3539, ICC3613, ICC3705, ICC3834, ICC4233, ICC4359, ICC4411, ICC455, ICC4567, ICC4893, ICC4946, ICC4984, ICC5021, ICC504, ICC5086, ICC512, ICC531, ICC5391, ICC5504, ICC5541, ICC5581, ICC5686, ICC5697,	ICC11266, ICC11766, ICC11879, ICC11904, ICC1232, ICC13245, ICC13764, ICC14199, ICC15489, ICC15551, ICC15834, ICC16187, ICC16579, ICC16637, ICC16644, ICC16822, ICC2338, ICC5119, ICC6140, ICC6300, ICC6831, ICC7269, ICC8284, ICC8660, ICC8923, ICC8962, ICCV95311, IG10224, IG10578, IG10633, IG5875, IG5990, IG5995, IG70505, IG70746, IG71790, IG71814, IG71887, IG71941, IG71967, IG72042, IG73287, IG7333, IG73334, IG73341, IG73458, IG74094, IG7432, IG9262, IG9330, IG9740, IG9810,	ICC839 7

ICC5755, ICC5886, ICC5899, ICC6122, ICC6155, ICC6659, ICC6970, ICC7098, ICC7302, ICC7380, ICC7479, ICC75, ICC7737, ICC793, ICC8449, ICC871, ICC8723, ICC9020, ICC9023, ICC952, ICC9728, ICC981, ICC991, ICC9917, ICCV10, ICCV10, ICCV10, ICCV91106, ICCV92944, ICCV93954, ICCV95703, IG6408, IG69441, IG69597, IG70413, IG70985, IG70990, IG71799, IG71926, IG71945, IG73322, IG7634, SAGL101, L550.	SAGLK 42 , SAGLK 121.	
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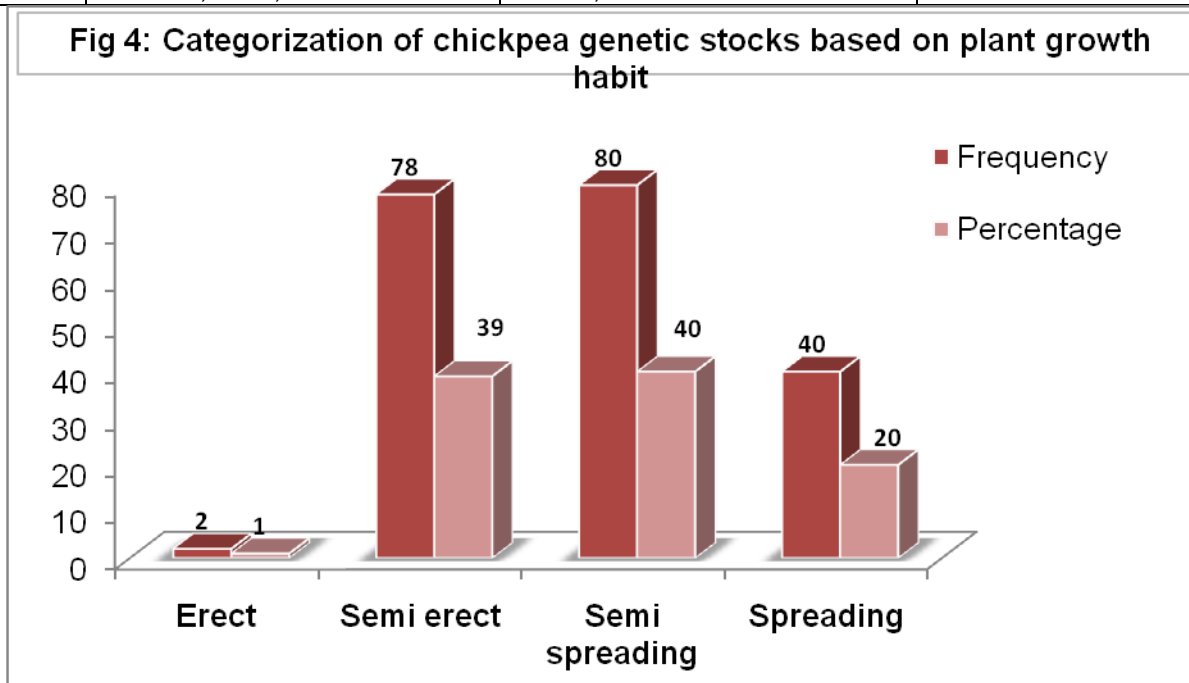


**4.4 Plant growth habit**

**Table 4.4: Categorization of chickpea genetic stocks based on plant growth habit**

Erect	Semi erect	Semi spreading	Spreading
ICC3613, ICC8923.	CC1000, ICC10504, ICC11059, ICC11258, ICC11266, ICC11424, ICC1148, ICC11507, ICC1205, ICC1228, ICC12323, ICC12691, ICC13185, ICC13245, ICC1356, ICC13964, ICC14051, ICC14226, ICC14344, ICC14426, ICC1470, ICC14710, ICC15080, ICC15184, ICC1520, ICC153, ICC16244, CC16245, ICC16637, ICC16822, CC2086, ICC2516, ICC26, CC3491, ICC353, ICC3705, CC4233, ICC455, ICC4946, CC5021, ICC5086, ICC5119, CC512, ICC531, ICC5391, CC5541, ICC5697, ICC6122, CC6300, ICC6970, ICC7269, CC7479, ICC75, ICC7737, CC9020, ICC952, ICC981, CC991, ICCV10, ICCV10,	ICC10393, ICC10546, ICC11091, ICC11330, ICC11766, ICC11879, ICC11904, ICC12159, ICC1232, ICC12600, ICC12856, ICC12888, ICC13200, ICC14199, ICC14225, ICC14411, ICC14446, ICC14484, ICC14881, ICC15489, ICC15547, ICC15551, ICC15614, ICC15834, ICC15844, ICC16187, ICC16201, ICC16947, ICC2, ICC2629, ICC2893, ICC3458, ICC3834, ICC4359, ICC4411, ICC4984, ICC504, ICC5504, ICC5686, ICC5755, ICC5886, ICC5899, ICC6155, ICC6659, ICC6831, ICC7098, ICC7380, ICC8397, ICC8449, ICC8660, ICC871, ICC8723, ICC8962, ICC9023, ICC9728, ICCV93954, ICCV95311, IG10224, IG10578,	ICC10950, ICC11867, ICC12258, ICC12310, ICC128, ICC12879, ICC1296, ICC13095, ICC13764, ICC14469, ICC14787, ICC15347, ICC15455, ICC15714, ICC16579, ICC16644, ICC16706, ICC2113, ICC2338, ICC2796, ICC3411, ICC3539, ICC4567, ICC4893, ICC5581, ICC6140, ICC7302, ICC793, ICC8284, ICC9917, ICCV10, ICCV91106, IG5875, IG5995, IG70746, IG70990, IG71814, IG73341,

CCV92944, ICCV95703, G10633, IG5990, IG69441, G69597, IG70413, IG70505, G70985, IG71967, IG73322, IG73458, IG7634, IG9810, JG11, SGKL109, L550,	IG6408, IG71790, IG71799, IG71887, IG71926, IG71941, IG71945, IG72042, IG73287, IG7333, IG73334, IG74094, IG7432, IG9262, IG9330, IG9740, SAGL6 ,	KAK2,
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#### 4.2 Analysis of variance

The analysis of variance for all the quantitative characters studies has been presented in Table 4.5. The mean differences due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the material.

**Table 4.5: Analysis of variance (mean sum of square) for different yield characters in chickpea (mean sum of squares)**

Source of variance	D.F.	Mean sum of square			
		Days to 50% flowering	Days to maturity	Secondary branches plant <sup>-1</sup>	Plant height (cm)
Replications	1	11.902	16.810	8.122	6.656
Genotypes	199	34.600**	23.135**	168.936**	83.134**
Error	199	0.827	1.448	2.956	4.015

Source of variance	D.F.	Pods plant <sup>-1</sup>	Seed index (g)	Seed yield plant <sup>-1</sup> (g)
Replications	1	3.610	139.122	31.696
Genotypes	199	1834.141**	157.891**	51.566**
Error	199	5.765	2.424	2.666

### 4.3 Genetic variability

Mean performance of the 200 genotypes for all the seven characters are depicted in Table 4.6.

#### 4.3.1 Days to 50% flowering

Days to 50 per cent flowering was recorded in genotype ICC16644 (59 days), while the genotypes IG6408, IG71926 and IG71945 required maximum 87 days for 50 per cent flowering. The average days for 50 per cent flowering were 79 days and it ranged from 59 to 87 days.

#### 4.3.2 Days to maturity

Days to maturity ranged from 115 to 135 days. Genotype ICC 14426 was earliest for days to maturity, while genotype ICC15489 was late for 20 days the same. The overall mean maturity of the accessions was 123 days.

#### 4.3.3 Secondary branches plant<sup>-1</sup>

Number of secondary branches plant<sup>-1</sup> ranged between 5.0 to 54.0 with a average performance of 16.99. The maximum (54.0) secondary branches plant<sup>-1</sup> was recorded in genotype ICC512 followed by IG9740 (51) and ICC504 (50.0), while it was recorded minimum in ICC15834 (5.0).

### **4.3.4 Plant height (cm)**

Plant height varied from 25.75 cm to 66.0 cm with an overall mean of 40.80 cm. Genotype ICC8923 recorded the maximum plant height (66 cm) followed by ICC15489 (61.10 cm), while, genotype ICC1296 exhibited the minimum of 25.75 cm plant height.

### **4.3.5 Pods plant<sup>-1</sup>**

The maximum number of pods plant<sup>-1</sup> was observed in ICC12159 (164) followed by ICC16187 (162), while it was least in genotype IG69597 (9.0). The average number of pods plant<sup>-1</sup> was 62.80 and it ranged from 9.0 to 164.

### **4.3.6 Seed index (g)**

The seed index varied from 9.19 g to 46.19 g with a mean value of 20.60 g. Genotype ICC15547 produced considerably heaviest seed and recorded maximum (46.19 g) seed index followed by IG71887 (44.25 g), while genotype ICC455 (9.19 g) had minimum seed index.

### **4.3.7 Seed yield plant<sup>-1</sup> (g)**

Maximum seed yield plant<sup>-1</sup> was recorded in genotype ICC9023 (36.79 g) which was closely followed by ICC14199 (36.39 g) and which were at par with each other. Genotype IG70985 (10.85 g) was poor yielder. The average seed yield plant<sup>-1</sup> was 16.70 g and it ranged from 10.85 g to 36.79 g.

## **4.4.2 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 studied (Table 4.7). Result indicated that the value of phenotypic coefficient of variations were of higher in magnitude than that of genotypic coefficient of variation for all the characters showing that the environment had an important role in influencing the expression of the characters.

### **4.3.2.1 Phenotypic coefficient of variations**

The phenotypic coefficient of variation ranged from 2.86% for days to maturity to 54.57% for secondary branches plant<sup>-1</sup>. The phenotypic coefficient of

variations was highest for characters viz., secondary branches plant<sup>-1</sup> (54.57%), pods plant<sup>-1</sup> (48.30%), and seed index (43.46%). However, it exhibited in low for characters like days to maturity (2.86%) followed by days to 50 per cent flowering (5.33%) and plant height (16.18%). The remaining characters such as seed yield plant<sup>-1</sup> (31.19%) exhibited moderate phenotypic coefficient of variation.

### **4.3.2.2 Genotypic coefficient of variation**

Results revealed from the Table 4.7 that genotypic coefficient of variation varied from 2.68% for days to maturity to 53.63% for secondary branches plant<sup>-1</sup>.

High genotypic coefficient of variation was noted for secondary branches plant<sup>-1</sup> (53.63%) followed by pods plant<sup>-1</sup> (48.15%) and seed index (42.80%). Days to maturity (2.68%), days to 50 per cent flowering (5.21%) and plant height (15.42%) showed lowest GCV. While, it was moderate for the characters such as seed yield plant<sup>-1</sup> (29.62%).

### **4.3.3. Heritability**

The heritability (BS) was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors. The estimates of heritability (BS) for all the characters have been discussed as follows (Table 4.7). It varied from 88.22% for days to maturity to 99.37% for pods plant<sup>-1</sup> and also 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 very high for pods plant<sup>-1</sup> (99.37%), seed index (96.98%), secondary branches plant<sup>-1</sup>(96.56), days to 50 per cent flowering (95.33), plant height (90.78) and seed yield plant<sup>-1</sup> (90.16%). It was also recorded high for days to maturity (88.22%).

Table 4.7: Estimates of genetic parameters of variations for quantitative characters in chickpea

Characters	Grand Mean	Range		Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean
		Min.	Max.	Phenotypic	Genotypic			
Days to 50% flowering	78.91	59	87	5.33	5.21	95.33	8.27	10.47
Days to maturity	122.65	115	135	2.86	2.68	88.22	6.37	5.19
Secondary branches plant <sup>-1</sup>	16.99	5	54	54.57	53.63	96.56	18.44	108.54
Plant height (cm)	40.80	25.75	66	16.18	15.42	90.78	12.35	30.26
Pods plant <sup>-1</sup>	62.80	9	164	48.30	48.15	99.37	62.09	98.87
Seed index (g)	20.60	9.19	46.19	43.46	42.80	96.98	17.89	86.82
Seed yield plant <sup>-1</sup> (g)	16.70	10.85	36.79	31.19	29.62	90.16	9.67	57.92

## **4.3.4 Genetic advance**

Based on the estimate of heritability (BS), expected genetic advance was computed on the hypothetical selection at 5 per cent best individual ( $1 \leq 2.06$ ). Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment genetic advance as percentage of mean was calculated to predict the genetic gain (Table 4.7).

Genetic advance as percentage of mean ranged between 5.19% for days to maturity to 108.54% for secondary branches plant<sup>-1</sup>. The highest estimate of genetic advance as percentage of mean was recorded for secondary branches plant<sup>-1</sup> (108.54%), pods plant<sup>-1</sup> (98.87%), seed index (86.82%) and seed yield plant<sup>-1</sup> (57.92%).

Plant height (30.26%) showed moderate value of genetic advance as percentage of mean. Whereas, low estimates were observed for days to maturity (5.19%) and days to 50 per cent flowering (10.47%).

## **4.4 Association analysis**

### **4.4.1 Correlation coefficient**

Correlation coefficients were worked out at phenotypic, genotypic and environmental levels for all possible combination of seven yield and its attributing characters (Table 4.8). Results indicated that genotypic correlation coefficient in general, were of higher magnitude than the corresponding phenotypic correlation coefficient for all the characters.

The results of phenotypic correlation coefficients have been discussed only as the genotypic and environmental correlation were mostly influenced by the environmental conditions, hence phenotypic correlation will give the correct idea about the association between two variables.

### **4.4.1 Days to 50 per cent flowering**

Days to 50 per cent flowering had highly significant and positive association with days to maturity (0.336) and plant height (0.174).

### **4.4.2 Days to maturity**

Correlation coefficient of days to maturity was exhibited significant and positive with plant height (0.309) and seed index (0.158), while, highly

significant and negative association of this character was observed with secondary branches plant<sup>-1</sup> (-0.326) and pods plant<sup>-1</sup> (-0.291).

### **4.4.3 Secondary branches plant<sup>-1</sup>**

Secondary branches plant<sup>-1</sup> expressed significant and positive correlation with pods plant<sup>-1</sup> (0.324).

### **4.4.4 Plant height (cm)**

Plant height showed significant and positive correlation with seed index (0.365). Significant and negative association of this character was observed with pods plant<sup>-1</sup> (-0.143).

### **4.4.5 Pods plant<sup>-1</sup>**

Correlation coefficient of pods plant<sup>-1</sup> exhibited significant and positive with seed yield plant<sup>-1</sup> (0.291), while, highly significant and negative association of this character was observed with seed index (-0.330).

### **4.4.6 Seed index**

Significant and positive association of seed index was observed with seed yield plant<sup>-1</sup> (0.186).

### **4.4.7 Seed yield /plant (g)**

Seed yield show genotypic and phenotypic negative correlation with days 50% flowering and days to maturity while show positive and significant correlation with plant height , pods per plant and seed index.

Table 4.8: Estimates of genotypic and phenotypic correlation coefficients among seed yield and its attributing traits in chickpea

Characters		Days to 50% flowering	Days to maturity	Secondary branches plant <sup>-1</sup>	Plant height (cm)	Pods plant <sup>-1</sup>	Seed index (g)	Seed yield plant <sup>-1</sup> (g)
Days to 50% flowering	G		0.371	-0.059	0.191	-0.038	-06	-0.124
	P		0.336**	-0.056	0.174*	-0.037	-03	-0.120
Days to maturity	G			-0.362	0.344	-0.311	0.175	-0.028
	P			-0.326**	0.309**	-0.291**	0.158*	-0.025
Secondary branches plant <sup>-1</sup>	G				0.020	0.331	0.014	0.046
	P				0.018	0.324**	0.014	0.048
Plant height (cm)	G					-0.154	0.394	0.143
	P					-0.143*	0.365**	0.122
Pods plant <sup>-1</sup>	G						-0.337	0.308
	P						-0.330**	0.291**
Seed index (g)	G							0.202
	P							0.186**

Significant at 5% level = \*

Significant at 1% level = \*\*

### **4.4.2 Path coefficient analysis**

To measure the direct as well as indirect association of one variable (cause) through another on the end product (effect), path coefficients were calculated at genotypic and phenotypic levels for all the yield attributing traits. The observed correlation coefficients of seed yield with its contributing traits were partitioned into direct and indirect effects. In the present investigation, important characters viz., seed yield plant<sup>-1</sup> have been used as dependable variables with other traits. Since the values of genotypic path are more reliable in predicting the correct idea about the direct and indirect effects of the component traits, only this has been discussed as below.

The estimates of path coefficient were furnished in the Table 4.9. In general the genotypic direct as well as indirect effects were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects. The results obtained from genotypic direct and indirect effects are presented as under.

#### **4.4.2.1 Direct effect**

Path coefficient analysis of different characters contributing towards seed yield plant<sup>-1</sup> showed that pods plant<sup>-1</sup> (0.4740) had highest positive direct effect followed by seed index (0.3118), plant height (0.1092) and days to maturity (0.0405). Whereas, days to 50 per cent flowering (-0.1461) had the highest negative direct effect on seed yield plant<sup>-1</sup> followed by secondary branches plant<sup>-1</sup> (-0.1117).

#### **4.4.2.2 Indirect effect**

##### **4.4.2.2.1 Days to 50 per cent flowering**

Days to 50 per cent flowering imparted highest positive indirect effect on seed yield plant<sup>-1</sup> via plant height (0.0209), days to maturity (0.0150) and secondary branches plant<sup>-1</sup> (0.066). However, indirect effect was visible to be highest negative via pods plant<sup>-1</sup> (-0.0180) and seed index (-0.020).

##### **4.4.2.2.2 Days to maturity**

Days to maturity revealed high values of positive indirect effect on seed yield plant<sup>-1</sup> through seed index (0.0547), secondary branches plant<sup>-1</sup> (0.0404) and plant height (0.0376). Therefore, the remaining characters showed high negative indirect effect i.e. pods plant<sup>-1</sup> (-0.1474) and days to 50% flowering (-0.0542).

**4.4.2.2.3 Secondary branches plant<sup>-1</sup>**

Secondary branches plant<sup>-1</sup> was recorded to have highest positive indirect effect on seed yield plant<sup>-1</sup> through, pods plant<sup>-1</sup> (0.1571), days to 50% flowering (087) and seed index (044). However, it was expressed high negative indirect effect via days to maturity (-0.0147).

**4.4.2.2.4 Plant height**

Plant height imparted highest positive indirect effect on seed yield plant<sup>-1</sup> via seed index (0.1228) and days to maturity (0.0139). However, indirect effect was visible to be highest negative via pods plant<sup>-1</sup> (-0.0731), and days to 50 per cent flowering (-0.0279),

**Table 4.9: Genotypic and phenotypic path coefficients showing direct and indirect effects of different characters on seed yield plant<sup>-1</sup> (g) in chickpea**

Characters		Days to 50% flowering	Days to maturity	Secondary branches plant <sup>-1</sup>	Plant height (cm)	Pods plant <sup>-1</sup>	Seed index (g)	Seed yield plant <sup>-1</sup> (g)
Days to 50 % flowering	G	<b>-0.1461</b>	0.0150	066	0.0209	-0.0180	-020	-0.124
	P	<b>-0.1383</b>	0.0150	052	0.0157	-0.0164	-010	-0.120
Days to maturity	G	-0.0542	<b>0.0405</b>	0.0404	0.0376	-0.1474	0.0547	-0.028
	P	-0.0465	<b>0.0447</b>	0.0304	0.0279	-0.1275	0.0462	-0.025
Secondary branches plant <sup>-1</sup>	G	087	-0.0147	<b>-0.1117</b>	022	0.1571	044	0.046
	P	077	-0.0146	<b>-0.0931</b>	016	0.1420	041	0.048
Plant height (cm)	G	-0.0279	0.0139	-022	<b>0.1092</b>	-0.0731	0.1228	0.143
	P	-0.0240	0.0138	-017	<b>0.0904</b>	-0.0627	0.1065	0.122
Pods plant <sup>-1</sup>	G	055	-0.0126	-0.0370	-0.0168	<b>0.4740</b>	-0.1050	0.308
	P	052	-0.0130	-0.0302	-0.0130	<b>0.4380</b>	-0.0962	0.291
Seed index (g)	G	009	071	-016	0.0430	-0.1596	<b>0.3118</b>	0.202
	P	005	071	-013	0.0330	-0.1446	<b>0.2915</b>	0.186

Residual effect Genotypic = 0.8739

Residual effect Phenotypic = 0.8923

**4.4.2.2.5 Pods plant<sup>-1</sup>**

Pods plant<sup>-1</sup> exhibited positive indirect effect via., days to 50 per cent flowering (055). Highest negative indirect effect was observed through seed index (-0.1050), secondary branches plant<sup>-1</sup> (-0.0370) and plant height (-0.0168).

**4.4.2.2.6 Seed index**

Seed index exhibited significant positive indirect effect via. plant height (0.0430) and days to maturity (071). Highest negative indirect effect was observed through pods plant<sup>-1</sup> (-0.1596).

### **4.4.2.2.7 Seed yield (g)**

Seed yield show negative indirect effect with days to 50% flowering and days to maturity while positive indirect effect with plant height , pods/plant and seed index.

## **4.5 Genetic divergence**

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.

### **4.5.3 Cluster mean**

As regards to the values for cluster mean for all the traits are summarized in Table 4.12. The higher average inter cluster mean was exhibited in days to maturity followed by pods plant<sup>-1</sup>, days to 50 per cent flowering and plant height.

Highest mean value for a large number of characters was exhibited in cluster VI [viz. days to maturity (123.98) and seed index (33.42)] followed by cluster VIII [viz. days to 50 per cent flowering (80.92) and seed yield plant<sup>-1</sup> (25.81)] cluster I for plant height (46.03), cluster V for pods plant<sup>-1</sup> (120.91) and cluster VII for secondary branches plant<sup>-1</sup> (39.73).

However, cluster II expressed the least mean values for plant height (37.71) and secondary branches plant<sup>-1</sup> (12.01), followed by cluster III for seed index (13.76), cluster IV for seed yield plant<sup>-1</sup> (14.20), cluster V for days to 50 per cent flowering (77.74), cluster VI for pods plant<sup>-1</sup> (29.52) and cluster VIII for days to maturity (120.17).

Table 4.12: Characters means of different clusters in chickpea

Characters	Days to 50% flowering	Days to maturity	Secondary branches plant <sup>-1</sup>	Plant height (cm)	Pods plant <sup>-1</sup>	Seed index (g)	Seed yield plant <sup>-1</sup> (g)
Cluster I	80	123	16.00	46.03	55.02	29.28	17.69
Cluster II	79	123	12.01	37.71	35.23	16.18	15.60
Cluster III	79	122	15.52	39.24	88.13	13.76	15.21
Cluster IV	78	122	14.68	38.92	66.85	15.46	14.20
Cluster V	77	121	21.91	39.28	120.91	17.22	21.91
Cluster VI	78	123	15.69	45.29	29.52	33.42	16.04
Cluster VII	79	120	39.73	40.69	70.27	18.29	15.76
Cluster VIII	80	120	20.25	41.41	82.67	28.40	25.81

#### 4.5.1 Grouping of genotypes in to various clusters

The 200 chickpea genotypes on the basis of 7 characters were grouped into eight clusters based on divergence analysis. Distribution of genotypes into different clusters is presented in the Table 4.10.

Table 4.10: Clustering pattern of 200 genotypes of chickpea on the basis of genetic divergence

S. No.	Cluster	No. of genotypes	Name of genotypes
1	I	27	ICC1000, ICC11879, ICC12323, ICC14226, ICC14446, ICC15489, ICC15844, ICC16579, ICC4233, ICC5119, ICC5541, ICC5686, ICC6155, ICCV92944, ICCV95311, IG5995, IG70505, IG70746, IG70985, IG71887, IG71926, IG72042, IG7333, IG73458, IG7634, IG9262 and KAK2.
2	II	43	ICC10393, ICC11059, ICC11091, ICC11507, ICC12600, ICC12879, ICC13095, ICC1356, ICC13964, ICC14051, ICC14344, ICC1470, ICC14710, ICC14881, ICC15184, ICC1520, ICC15347, ICC15614, ICC15834, ICC16245, ICC16706, ICC2113, ICC2516, ICC2629, ICC2796, ICC2893, ICC3834, ICC4567, ICC5755, ICC6140, ICC6300, ICC7098, ICC8284, ICC8449, ICC871, ICC8723, ICC981, ICCV10, ICCV93954, IG6408, JG11, JG11 and L550.

3	III	27	ICC10504, ICC10546, ICC11330, ICC11424, ICC1148, ICC1205, ICC12691, ICC12888, ICC1296, ICC13245, ICC13764, ICC14787, ICC15714, ICC16947, ICC2, ICC2086, ICC4359, ICC455, ICC5021, ICC5581, ICC5886, ICC7302, ICC75, ICC8397, ICC9728, ICCV95703 and IG71799.
4	IV	34	ICC10950, ICC11258, ICC11867, ICC12258, ICC1228, ICC12310, ICC12856, ICC14411, ICC14426, ICC14469, ICC15080, ICC16244, ICC16644, ICC26, ICC3411, ICC3491, ICC353, ICC3613, ICC3705, ICC4411, ICC4893, ICC4946, ICC4984, ICC531, ICC6970, ICC7380, ICC7737, ICC8660, ICC9020, ICCV91106, IG10224, IG74094, JG11 and L550.
5	V	23	ICC11266, ICC12159, ICC1232, ICC13185, ICC14225, ICC14484, ICC153, ICC16187, ICC16201, ICC2338, ICC3458, ICC5086, ICC5391, ICC5899, ICC6122, ICC6659, ICC9023, ICC991, ICCV10, ICCV10, IG69441, IG7432 and JG11.
6	VI	29	ICC11766, ICC11904, ICC13200, ICC14199, ICC15547, ICC15551, ICC16637, ICC16822, ICC5504, ICC6831, ICC8923, ICC8962, IG10578, IG10633, IG5875, IG5990, IG69597, IG70413, IG70990, IG71814, IG71941, IG71967, IG73287, IG73322, IG73341, IG9810, and KAK2.
7	VII	11	ICC128, ICC3539, ICC504, ICC512, ICC7479, ICC793, ICC952, ICC9917, IG73334, IG9740 and L550.
8	VIII	6	ICC15455, ICC5697, IG71790, ICC7269, IG71945 and IG9330.

Out of these clusters, cluster II had large population consisting of forty three genotypes followed by cluster IV (34), cluster VI (29), cluster I and III (27 each), cluster V (23), cluster VII (11) and lowest population exhibited in cluster VIII (6).

#### **4.5.2 Inter and intra cluster distance**

Considering the inter and intra cluster distances (Table 4.11), the highest inter cluster distance was observed between cluster V and cluster VI (86.792) followed by cluster II and V (80.282), cluster I and V (60.259), cluster III and VI (57.265), cluster V and VII (55.843), cluster VI and VIII (53.067) and cluster II and III (50.342).

## RVSKVV/Thesis/M.Sc./No. 1712

The inter cluster distance was the least between clusters II and VI (13.118), cluster III and IV (20.151) and cluster I and IV (21.096). Cluster VI and cluster V were highly divergent from clusters II (13.118) to cluster V (86.792) and clusters III (31.213) to cluster II (80.282), respectively, and clusters I and IV (21.096) and cluster III and IV (20.151) were observed to be the nearest.

**Table 4.11: Average intra (diagonal) and inter-cluster D2 values among 200 genotypes of chickpea**

Cluster	I	II	III	IV	V	VI	VII	VIII
I	13.834	27.698	32.444	21.096	60.259	28.775	37.481	26.783
II		13.174	50.342	32.224	80.282	13.118	47.784	50.167
III			12.159	20.151	31.213	57.265	33.977	22.657
IV				10.790	50.026	40.441	30.210	27.145
V					20.967	86.792	55.843	40.466
VI						16.463	52.731	53.067
VII							15.376	36.685
VIII								12.255

Maximum intra cluster distance was revealed in cluster V (20.967) followed by cluster VI (16.463) and cluster VII (15.376). The minimum (10.790) intra cluster distance was expressed by cluster IV.

## **CHAPTER V**

### **DISCUSSION**

The experimental findings of the present investigation “Assessment of diversity in genetic stock of chickpea (*Cicer arietinum* L.)” have been discussed on the following heads in the light of the available literature.

#### **5.1 Characterization of chickpea genetic stocks into different groups based on morphological traits**

Characterization of genetic stocks of chickpea was performed based on morphological characters of plant and flower. Distinguishing genotypes on the basis of morphological characters is one of the most common criteria.

##### **5.1.1 Plant vigor**

A wide range of variation exhibited for plant vigor. Based on plant vigor, chickpea genetic stocks were categorized into three group's i.e. very good (25 frequency and 12.5 percentage), good (153 frequency and 76.5 percentage) and poor (22 frequency and 11 percentage). These observations are in agreement with the result of Ramanappa *et al.* (2013).

##### **5.1.2 Leaf colour**

Considerable variability was observed for leaf colour i.e. dark green (119 frequency and 59.5 percentage), green (4 frequency and 2 percentage) and light green (77 frequency and 38.5 percentage). These observations are in agreement with the result of Salgotra (2016) and Hussain *et al.* (2016).

##### **5.1.3 Flower colour**

Based on intensity of flower colour, genotypes were categorized as pink (141 frequency and 70.5 percentage), white (58 frequency and 29 percentage) and blue (1 frequency and 0.5 percentage). These observations are in agreement with the result of Ramanappa *et al.* (2013)

##### **5.1.4 Plant growth habit**

A wide variation was exhibited for plant growth habit (Table 4.4). Chickpea genetic stocks were categorized into four group's i.e. erect (2 frequency and 1 percentage), semi erect (78 frequency and 39 percentage) semi spreading (80 frequency and 40 percentage) and spreading (40 frequency and 20 percentage). The findings are in agreement with the result of Nawaj (2018) and Srivastav *et al.* (2017) .

## 5.2 Analysis of variance

The main objective of the present investigation was to study the diversity present in 200 genetic stocks of chickpea. The estimates of mean sum of square due to genotypes were highly significant for all the characters (Table 4.5), indicating the presence of genetic diversity in the existing material. The findings of Malik *et al.* (2010), Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Naveed *et al.* (2015), Roy *et al.* (2016), Mannur *et al.* (2017), Srivastava *et al.* (2017) and Nawaz *et al.* (2018) are similar to that of the present findings.

## 5.3 Genetic variability

### 5.3.1 Mean performance of the genotypes

The mean performance of the genotypes revealed a wide range of variability for all the characters. The variation was highest for pods plant<sup>-1</sup> (9.0 to 164.5), secondary branches plant<sup>-1</sup> (15.0 to 54.0), plant height (25.75 to 66.0 cm), seed index (9.19 to 46.19 g), days to 50 per cent flowering (59.5 to 87.5 days), seed yield plant<sup>-1</sup> (10.85 to 36.79 g) and days to maturity (115.0 to 135.5 days). The findings were quite similar to as reported by Malik *et al.* (2010), Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for pods plant<sup>-1</sup>, Malik *et al.* (2010), Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for secondary branches plant<sup>-1</sup>, Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for plant height, Ramanappa *et al.* (2013), Sharma *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for seed index, Ramanappa *et al.* (2013) and Bhanu *et al.* (2017) for days to 50 per cent flowering, Malik *et al.* (2010), Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for seed yield plant<sup>-1</sup>, Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Bhanu *et al.* (2017) and Nawaz *et al.* (2018) for days to maturity.

### 5.3.2 Coefficient of variation

In the present findings 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 effective on the basis of phenotypic performance. The finding of Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Roy *et al.* (2016), Tiwari *et al.* (2016) and Mannur *et al.* (2017) were similar to that of the present findings.

### **5.3.2.1 Phenotypic and genotypic coefficient of variations**

The phenotypic and genotypic coefficient of variation range from 2.86% and 2.68% for days to maturity to 54.57% and 53.63% for secondary branches plant<sup>-1</sup>, respectively. The phenotypic and genotypic coefficient of variations was highest for characters viz., secondary branches plant<sup>-1</sup>, pods plant<sup>-1</sup> and seed index, indicating that selection can be predicted to improvement in the chickpea for these characters. The findings are in close harmony with the result of Roy *et al.* (2016) for secondary branches plant<sup>-1</sup>, Dwevedi and Gaibriyal (2009), Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Peerzada *et al.* (2015), Roy *et al.* (2016), Hussain *et al.* (2016) and Bhanu *et al.* (2017) for pods plant<sup>-1</sup>, Dwevedi and Gaibriyal (2009), Parhe *et al.* (2010), Peerzada *et al.* (2015), Roy *et al.* (2016), Hussain *et al.* (2016) and Bhanu *et al.* (2017) for seed index.

However, it exhibited in low for characters like days to maturity followed by days to 50 per cent flowering and plant height which indicated that there is limited scope for improvement. The findings are in agreement with the result of Kanouni *et al.* (2012) and Bhanu *et al.* (2017) for days to maturity, Kanouni *et al.* (2012) for days to 50 per cent flowering, Bhanu *et al.* (2017) for plant height.

The remaining characters such as seed yield plant<sup>-1</sup> (31.19%) exhibited moderate phenotypic coefficient of variation. The finding of Parhe *et al.* (2010), Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Peerzada *et al.* (2015), Roy *et al.* (2016), Hussain *et al.* (2016) and Bhanu *et al.* (2017) for most of the characters was similar to the present finding.

### **5.3.3 Heritability**

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 (70- 90%), medium (50-70%) and low (less than 50%).

The value of heritability (broad sense) was recorded very high for pods plant<sup>-1</sup> (99.37%), seed index (96.98%), secondary branches plant<sup>-1</sup>(96.56), days to 50 per cent flowering (95.33), plant height (90.78) and seed yield plant<sup>-1</sup> (90.16%). However, it was recorded high for days to maturity (88.22%). The results were in close proximate to that of Dwevedi and Gaibriyal (2009) Ramanappa *et al.* (2013), Naveed *et al.* (2015), Peerzada *et al.* (2015), Bhanu *et al.* (2017) and Srivastava *et al.* (2017) for pods plant<sup>-1</sup>, Parhe *et al.* (2010), Ramanappa *et al.* (2013), Naveed *et al.* (2015), Peerzada *et al.* (2015), Bhanu *et al.* (2017), Mannur *et al.* (2017) and Srivastava *et al.* (2017) for seed index, Naveed *et al.* (2015) for secondary branches plant<sup>-1</sup>, Kanouni *et al.* (2012), Ramanappa *et al.* (2013) and Naveed *et al.* (2015) for days to 50 per cent flowering, Ramanappa *et al.* (2013) and Mannur *et al.* (2017) for plant height, Ramanappa *et al.* (2013), Naveed *et al.* (2015), Bhanu *et al.* (2017) and Mannur *et al.* (2017) for seed yield plant<sup>-1</sup>. High values of broad sense heritability for these 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.

### **5.3.4 Genetic advance**

Heritability 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 per cent of mean were classified as high (more than 50%), moderate (30-50%) and low (less than 30%).

Genetic advance as percentage of mean ranged between 5.19% for days to maturity to 108.54% for secondary branches plant<sup>-1</sup>. The highest estimate of genetic advance as percentage of mean was recorded for secondary branches plant<sup>-1</sup>, pods plant<sup>-1</sup>, seed index and seed yield plant<sup>-1</sup>. The results were in consonance with Nawaz *et al.* (2018) for secondary branches plant<sup>-1</sup>, Dwevedi and Gaibriyal (2009), Peerzada *et al.* (2015), Bhanu *et al.* (2017) and Srivastava *et al.* (2017) for pods plant<sup>-1</sup>, Bhanu *et al.* (2017), Mannur *et al.* (2017) and Srivastava *et al.* (2017) for seed index, Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Roy *et al.* (2016), Tiwari *et al.* (2016), Hussain *et al.* (2016) and Mannur *et al.* (2017) for seed yield plant<sup>-1</sup>.

Plant height showed moderate value of genetic advance as percentage of mean. The findings were in agreement to the findings of Salgotra (2016) and Mannur *et al.* (2017). Whereas, low estimates were observed for days to maturity and days to 50 per cent flowering.

High heritability coupled with high genetic advance for traits like secondary branches plant<sup>-1</sup>, followed by pods plant<sup>-1</sup>, seed index and seed yield plant<sup>-1</sup>. 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. The findings were in agreement to the findings of Nawaz *et al.* (2018) for secondary branches plant<sup>-1</sup>, Parhe *et al.* (2010), Ramanappa *et al.* (2013), Peerzada *et al.* (2014), Roy *et al.* (2016), Tiwari *et al.* (2016), Salgotra (2016), Hussain *et al.* (2016), Bhanu *et al.* (2017), Srivastava *et al.* (2017) and Nawaz *et al.* (2018) for pods plant<sup>-1</sup>, Parhe *et al.* (2010), Ramanappa *et al.* (2013), Roy *et al.* (2016), Salgotra (2016), Hussain *et al.* (2016), Bhanu *et al.* (2017), Mannur *et al.* (2017) and Srivastava *et al.* (2017) for seed index, for seed yield plant<sup>-1</sup>.

High heritability supplemented with moderate genetic advances as percentage of mean were manifested by plant height 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 Salgotra (2016) and Mannur *et al.* (2017).

High heritability coupled with low genetic advance as percentage of mean was observed for days to maturity and days to 50 per cent flowering.

This revealed the predominance of non-additive gene action in the expression of these characters.

### **5.4 Correlation coefficient analysis**

A wide range of variation in quantitative characters provides the basis for selection in plant breeding programme. The knowledge of association among the characters is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. Correlation coefficient provides a clear picture of the extent of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component characters help in improving the efficiency of selection for yield by making proper choice and balancing one component with another.

The magnitude of genotypic correlation was higher than the phenotypic correlation for all the traits that indicated inherent association between various characters. The findings were in agreement to Tiwari *et al.* (2016) and Bhanu *et al.* (2017).

#### **5.4.1 Seed yield plant<sup>-1</sup> (g)**

In the present findings correlation coefficient of seed yield plant<sup>-1</sup> was recorded highly significant and positive with pods plant<sup>-1</sup> and seed index. The highest positive and significant correlation coefficient of seed yield plant<sup>-1</sup> was noted with pods plant<sup>-1</sup> and seed index indicating that these characters is the primary yield determinant in chickpea. These findings corroborated the earlier findings of Ali *et al.* (2011), Kanouni *et al.* (2012), Roy *et al.* (2016), Salgotra (2016), Tadesse *et al.* (2016) and Tiwari *et al.* (2016) for pods plant<sup>-1</sup> and seed index, Thakur and Sirohi (2009), Malik *et al.* (2010), Ramanappa *et al.* (2013), Petrova and Desheva (2016), Bhanu *et al.* (2017) and Srivastava *et al.* (2017) for pods plant<sup>-1</sup>.

### **5.4.2 Days to 50 per cent flowering**

Days to 50 per cent flowering was recorded highly significant and positive association with days to maturity and plant height.

### **5.4.3 Days to maturity**

Correlation coefficient of days to maturity was exhibited significant and positive with plant height and seed index, while, highly significant and negative association of this character was observed with secondary branches plant<sup>-1</sup> and pods plant<sup>-1</sup>.

### **5.4.4 Secondary branches plant<sup>-1</sup>**

Secondary branches plant<sup>-1</sup> expressed significant and positive correlation with pods plant<sup>-1</sup>. These findings corroborated the earlier finding of Malik *et al.* (2010).

### **5.4.5 Plant height (cm)**

Plant height showed significant and positive correlation with seed index. Significant and negative association of this character was observed with pods plant<sup>-1</sup>. This indicates the importance of this character in selection. The positive correlation of plant height with seed index indicates that allocation and translocation of photosynthates from the source to the sink.

### **5.4.6 Pods plant<sup>-1</sup>**

Correlation coefficient of pods plant<sup>-1</sup> was exhibited significant and positive with seed yield plant<sup>-1</sup>, while, highly significant and negative association of this character was observed with seed index. These findings corroborated the earlier finding of Thakur and Sirohi (2009), Malik *et al.* (2010), Ali *et al.* (2011), Kanouni *et al.* (2012), Ramanappa *et al.* (2013), Roy *et al.* (2016), Salgotra (2016), Petrova and Desheva (2016), Tadesse *et al.* (2016), Tiwari *et al.* (2016), Bhanu *et al.* (2017) and Srivastava *et al.* (2017).

### **5.4.7 Seed index**

Significant and positive association of seed index was observed with seed yield plant<sup>-1</sup>. These findings corroborated the earlier finding of Ali *et al.* (2011), Kanouni *et al.* (2012), Roy *et al.* (2016), Salgotra (2016), Tadesse *et al.* (2016) and Tiwari *et al.* (2016).

## **5.5. Path coefficient analysis**

Correlation coefficients are the indication of simple association between variables. In a biological system, however the relationship may exist in a very complex form. It is therefore, essential to study the relationship among variable in a comprehensive way. Path coefficient analysis is a power full tool, which enable portioning of the given relationships in its further components. In other words, it takes into account not only the relationship of component characters with the dependent character, but simultaneously takes care of its relationship with other component also. Thus, it helps in understanding the causal system in a better way because it enables portioning the total correlations coefficient into direct and indirect effects of various characters.

In the present investigation path coefficient analysis was carried out for characters under study using genotypic and phenotypic correlation coefficient and taking seed yield plant<sup>-1</sup> as dependable variables, in order to see the causal factor and so as to identify the components which are responsible for producing seed yield plant<sup>-1</sup>. In general the genotypic direct as well as indirect effects were slightly higher in magnitude as compared to corresponding phenotypic direct and indirect effects indicating that the masking effect of the environment.

Path coefficient analysis of different characters contributing towards seed yield plant<sup>-1</sup> showed that pods plant<sup>-1</sup> had highest positive direct effect followed by seed index, plant height and days to maturity. The characters pods plant<sup>-1</sup>, seed index and plant height had correlation coefficient values positive and at par with their direct effect on seed yield plant<sup>-1</sup>. This indicates true relationships with seed yield plant<sup>-1</sup> and direct selection for these traits would result in higher breeding efficiency for improving yield. Thus, these traits might be reckoned as the most important component trait for seed yield plant<sup>-1</sup>. The results are in propinquity with Thakur and Sirohi (2009), Kanouni *et al.* (2012), Tiwari *et al.* (2016) and Bhanu *et al.* (2017) for pods plant<sup>-1</sup>, Kanouni *et al.* (2012), Mushtaq *et al.* (2013) and Tiwari *et al.* (2016) for seed index, Kanouni *et al.* (2012), Mushtaq *et al.* (2013), Roy *et al.* (2016), Tiwari *et al.* (2016), Petrova and Desheva (2016) and Tadesse *et al.* (2016) for plant height and Tiwari *et al.* (2016) for days to maturity.

Whereas, days to 50 per cent flowering had the highest negative direct effect on seed yield plant<sup>-1</sup> followed by secondary branches plant<sup>-1</sup>. Secondary branches plant<sup>-1</sup> was positively correlated to it. This indicated that the indirect effect was the cause of correlation and the indirect causal factors are to be considered simultaneously for selection. Days to 50 per cent flowering imparted a negative direct effect on seed yield plant<sup>-1</sup>, as well as they were negatively correlated to it. Under such circumstance direct selection for this character should be avoided, instead indirect selection should be followed. The results are in propinquity with Mushtaq *et al.* (2013) and Tiwari *et al.* (2016) for days to 50 per cent flowering and Roy *et al.* (2016), Tiwari *et al.* (2016), Tiwari *et al.* (2016), Petrova and Desheva (2016) and Bhanu *et al.* (2017) for secondary branches plant<sup>-1</sup>.

The estimated residual effect of genotype is being 0. 8739. The 12.61 % variability was observed in yield contributing traits such as days to 50 per cent flowering, days to maturity, secondary branches plant<sup>-1</sup>, plant height, pods plant<sup>-1</sup> and seed index on seed yield plant<sup>-1</sup>. the probably reason for this very low and non-significant correlation of days to 50 per cent flowering, days to maturity, secondary branches plant<sup>-1</sup> and plant height with seed yield plant<sup>-1</sup>.

Path coefficient analysis revealed that pods plant<sup>-1</sup>, seed index and plant height are the most important characters contributing towards seed yield and hence purposeful and balanced selection based on these characters would be made rewarding for improvement of chickpea. Direct selection of secondary branches plant<sup>-1</sup> and days to 50 per cent flowering should be avoided instead of indirect selection.

### **5.6 Genetic divergence**

Diversity analysis 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, 200 genotypes were grouped into 8 clusters using tocher methods. The intra and inter cluster distance was calculated by using diversity analysis.

### **5.6.1 Grouping of genotypes in to various clusters**

The maximum number of genotypes (43) was found in the cluster II followed by cluster IV (34), cluster VI (29), cluster I and III (27 each), cluster V (23), cluster VII (11) and lowest population exhibited in cluster VIII (6). 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 Dwevedi and Gaibriyal (2009), Malik *et al.* (2010), Parhe *et al.* (2010), Mehandi *et al.* (2015), Naveed *et al.* (2015) and Kushwaha *et al.* (2017).

### **5.6.2 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 V and cluster VI (86.792) followed by cluster II and V (80.282), cluster I and V (60.259), cluster III and VI (57.265), cluster V and VII (55.843), cluster VI and VIII (53.067) and cluster II and III (50.342). 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 Dwevedi and Gaibriyal (2009), Malik *et al.* (2010), Parhe *et al.* (2010), Naveed *et al.* (2015) and Kushwaha *et al.* (2017).

The inter cluster distance was the least between clusters II and VI (13.118), cluster III and IV (20.151) and cluster I and IV (21.096) 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 Kushwaha *et al.* (2017).

Cluster VI and cluster V were highly divergent from clusters II (13.118) to cluster V (86.792) and clusters III (31.213) to cluster II (80.282), respectively, may be due to both natural and artificial selection forces among the genotypes.

Maximum intra cluster distance was revealed in cluster V (20.967) followed by cluster VI (16.463) and cluster VII (15.376). The minimum (10.790) intra cluster distance was expressed by cluster IV. These findings are in agreement with the results obtained by Kushwaha *et al.* (2017).

### **5.6.3 Cluster mean**

Highest mean value for a large number of characters was exhibited in cluster VI [viz. days to maturity (123.98) and seed index (33.42)] followed by cluster VIII [viz. days to 50 per cent flowering (80.92) and seed yield plant<sup>-1</sup> (25.81)] cluster I for plant height (46.03), cluster V for pods plant<sup>-1</sup> (120.91) and cluster VII for secondary branches plant<sup>-1</sup> (39.73). The present results are in accordance with the findings of Dwevedi and Gaibriyal (2009), Malik *et al.* (2010), Parhe *et al.* (2010) and Kushwaha *et al.* (2017).

### **5.6.4 Genotypes identified as parents in hybridization programme**

Amongst the 200 genotypes of eight distinct clusters formed which are sowing diversity in cluster I is closely related to cluster IV Cluster VII Cluster II Cluster IV and highly dissimilar or distinct for cluster III Cluster VIII and cluster V The present results are in accordance with the findings of Parhe *et al.* (2010) and Kushwaha *et al.* (2017).

**CHAPTER VI**  
**SUMMARY, CONCLUSION AND SUGGESTIONS FOR**  
**FUTURE WORK**

**6.1 Summary**

The present investigation “Assessment of diversity in genetic stock of chickpea (*Cicer arietinum* L.)” was carried out during *Rabi* season of 2017-2018 in the field of R.A.K. College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Sehore (M.P.). The experimental material for the present investigation comprised of 200 accessions of Desi and Kabuli chickpea. These genotypes were sown in Randomized Complete Block Design with two replications, to observe qualitative and quantitative observation. Observations were recorded on the basis of five random competitive plants selected from each genotype separately for qualitative and quantitative characters and were evaluated as per standard procedure with the following objectives:

6. To characterizes and classify the chickpea genetic stocks into different groups for morphological traits
7. To characterize and grouping of chickpea genetic stocks into various categories for yield traits.
8. To determine the extent of heritable genetic variation for quantitative traits.
9. To know the relationship between seed yield and its contributing characters in chickpea.
10. To assess diversity in genetic stock.

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 quantitative 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 pods plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, plant height and seed index.
- 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 effective on the basis of phenotypic performance.
- High heritability coupled with high genetic advance for traits like secondary branches plant<sup>-1</sup>, followed by pods plant<sup>-1</sup>, seed index and seed yield plant<sup>-1</sup>. suggested the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters might be governed by additive gene actions.
- High heritability coupled with low genetic advance as percentage of mean was observed for days to maturity and days to 50 per cent flowering. This revealed the predominance of non-additive gene action in the expression of these characters.
- The correlation coefficient of seed yield plant<sup>-1</sup> was recorded highly significant and positive with pods plant<sup>-1</sup> and seed index. The highest positive and significant correlation coefficient of seed yield plant<sup>-1</sup> was noted with pods plant<sup>-1</sup> and seed index indicating that these characters is the primary yield determinant in chickpea yield through these components could be achieved.
- Path coefficient analysis of different characters contributing towards seed yield plant<sup>-1</sup> showed that pods plant<sup>-1</sup> had highest positive direct effect followed by seed index, plant height and days to maturity and correlation coefficient values of these characters are positive and at par with their direct

effect on seed yield plant<sup>-1</sup>. This indicates true relationships with seed yield plant<sup>-1</sup> and direct selection for these traits would result in higher breeding efficiency for improving yield. Thus, these traits might be reckoned as the most important component trait for seed yield plant<sup>-1</sup>. Whereas, days to 50 per cent flowering had the highest negative direct effect on seed yield plant<sup>-1</sup> followed by secondary branches plant<sup>-1</sup>. Secondary branches plant<sup>-1</sup> was positively correlated to it indicated that the indirect effect was the cause of correlation and the indirect causal factors are to be considered simultaneously for selection. Days to 50 per cent flowering imparted a negative direct effect on seed yield plant<sup>-1</sup>, as well as they were negatively correlated to it. Under such circumstance direct selection for this character should be avoided, instead indirect selection should be followed.

- On the basis of diversity analysis the 200 genotypes were grouped into eight clusters.
- 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 V and cluster VI followed by cluster II and V, cluster I and V, cluster III and VI, cluster V and VII, cluster VI and VIII and cluster II and III. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregants.
- Maximum intra cluster distance was revealed in cluster V followed by cluster VI and cluster VII. Highest mean value for a large number of characters was exhibited in cluster VI [viz. days to maturity and seed index] followed by cluster VIII [viz. days to 50 per cent flowering and seed yield plant<sup>-1</sup>] cluster I for plant height, cluster V for pods plant<sup>-1</sup> and cluster VII for secondary branches plant<sup>-1</sup>.
- Crossing among the genotypes in cluster V and cluster VI 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**

Plant vigor, leaf colour and plant growth habit are the most stable and uniform distinguishing characters for verification of genetic stocks of chickpea. Flower colours are the uniform characters but their expressions are observed by the some degree of fluctuating environment. Therefore, these traits should be used only as an indicator not as marker to verify the genetic purity.

The PCV was higher than the GCV for all the characters. The phenotypic and genotypic coefficient of variations was highest for characters viz., secondary branches plant<sup>-1</sup>, pods plant<sup>-1</sup> and seed index, indicating that selection can be predicted to improvement in the chickpea for these characters.

Path coefficient analysis revealed that pods plant<sup>-1</sup>, seed index and plant height are the most important characters contributing towards seed yield and hence purposeful and balanced selection based on these characters would be made rewarding for improvement of chickpea. Direct selection of secondary branches plant<sup>-1</sup> and days to 50 per cent flowering should be avoided instead of indirect selection.

Study of genetic divergence revealed a high inter cluster distance between cluster V and those genetically diverse parents, can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in chickpea.

### **6.3 Suggestions for further work**

1. Traits identified for high heritability coupled with high or moderate genetic gain may be considered well in selection for the improvement of crop.
2. Characters having desirable association and direct effects with seed yield should be given due consideration for genetic improvement in chickpea.
3. 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.

**REFERENCES**

- Ali, Qurban; Muhammad Hammad Nadeem Tahir; Hafeez Ahmad Sadaqat; Saeed Arshad; Jahenzeb Farooq; Muhammad Ahsan; Muhammad Waseem and Amjad Iqbal (2011). Genetic variability and correlation analysis for quantitative traits in chickpea genotypes (*Cicer arietinum* L.). *Journal of Bacteriology Research*. **3** (1): 6-9.
- Anonymous (2016). Pulses in India Retrospect and Prospects; Published by Govt of India, Directorate of Pulses Development, Vindhyachal Bhavan, Bhopal. Publication No.: DPD/ Pub.1/ Vol. 2/2016.
- Bhanu, A. Nishant; Singh, M.N.; Tharu, Rajendra and Saroj, S.K. (2017). Genetic variability, correlation and path coefficient analysis for quantitative traits in chickpea genotypes. *Indian J. Agric. Res.* **51** (5): 425-430.
- Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. 6<sup>th</sup> *Int. Grassland Cong.* **1**: 227-285.
- Dewey, D.R. and Lu, K.H. (1959). Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **57**: 515 – 518.
- Dwevedi, K. K. and Gaibriyal, M. Lal (2009). Assessment of genetic diversity of cultivated chickpea (*Cicer arietinum* L.). *Asian Journal of Agricultural Sciences*. **1** (1): 7-8.
- Fiaz , Sajid Fiaz and Aslam, Muhammad (2015). Interrelationship among yield and yield contributing traits in chickpea (*Cicer arietinum* L.) *Bangladesh J. Pl. Breed. Genet.* **28** (2): 39-46.
- Ghafoor, A., A. Sharif, Z. Ahmad, M.A. Zahid and M.A. Rabbani (2001). Genetic diversity in Blackgram (*Vigna mungo*(L.) Hepper). *Field Crops Res.*, 69: 183-190
- Hanson, C.H.; Robinson, H.F. and Comstock, R.E. (1956). Bimetric studies of yield in segregating population of Korean Lespedeza. *Agronomy Journal*. **48**: 268-272.
- Hussain, N.; Ghaffar, A.; Aslam, M.; Hussain, K. and Naeem-ud-Din (2016). Assessment of genetic variation and mode of inheritance of some

- quantitative traits in chickpea (*Cicer arietinum* L.). *The Journal of Animal and Plant Sciences*. **26** (5): 1334-1338.
- Johnson, H.W.; Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetics and environment variability in soybean. *Agronomy Journal*. **47**: 314-318.
- Kanouni, H.; Shahab, M. R.; Imtiaz, M. and Khalili, M. (2012). Genetic variation in drought tolerance in chickpea (*Cicer arietinum* L.) genotypes. *Crop Breeding Journal*. **2** (2): 133-138.
- Kushwaha, Asha; Jain, Sudhanshu; Yasin, M. and Singh A.K. (2017). Assessing genetic diversity in chickpea for crop improvement. *International Journal of Agriculture Sciences*. **9** (37): 4563-4565.
- Malik, Shahid Riaz; Ahmad Bakhsh, M.; Ahsan Asif; Umer Iqbal and Iqbal, S.M. (2010). Assessment of genetic variability and interrelationship among some agronomic traits in chickpea. *International Journal of Agriculture and Biology*. **12** (1): 81–85.
- Mannur, Honnappa, D.M.; Shankergoud, I.; Nidagundi, J.M.; Muniswamy, S. and Muttappa, Hosamani (2017). Genetic variability and heritability study for quantitative traits in advance generation (F<sub>5</sub>) of cross between green seeded desi (GKB-10) and white Kabuli (MNK-1) chickpea genotypes (*Cicer arietinum* L.). *International Journal of Science and Nature*. **8** (4): 874 – 878.
- Miller, D.A.; Williams, J.C.; Robinson, H.F. and Comstock, K.B. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implication in selection. *Agronomy Journal*. **50**: 126-131.
- Mushtaq, Muhammad Adnan; Bajwa, Muhammad Maqsood and Muhammad Saleem (2013). Estimation of genetic variability and path analysis of grain yield and its components in chickpea (*Cicer arietinum* L.). *International Journal of Scientific and Engineering Research*. **4** (1): 1-4.
- Naveed, Muhammad; Chaudhry, Muhammad Shafiq; Muhammad Rafiq, and Muhammad Afzal Zahid (2015). Genetic diversity in new chickpea accessions for *fusarium* wilt resistance, canopy temperature and yield components under drought milieus. *Australian Journal of Crop Science*. **9** (6): 538-544.

- Nawaz, Muhammad Kashif; Amir Sohail, Tanvir Burni, Shahzad Ali, Manzoor, Sada Bahar and Quaid Hussain (2018). Assessment of genetic variability, heritability and genetic advance in F<sub>6</sub> population of desi chickpea (*Cicer aretinum*). *Pure and Applied Biology*. **7** (1): 194-200.
- Panes, V.G. and Sukhatme, P.V. (1989). Statistical methods for Agricultural workers, 3<sup>rd</sup> edition, ICAR, New Delhi 70--99.
- Parhe, Sachin D.; Harer, P. N. and Nagawade, D. R. (2014). Investigation of genetic divergence in chickpea (*Cicer arietinum* L.) genotypes. *The Bioscan*. **9** (2): 879-882.
- Peerzada, Ovais Hamid; Chaurasia, A. K. and Anzer. U. I. (2015). Evaluation of chickpea germplasm (*Cicer kabulium* L.) for yield and yield attributing traits. *Annals of Biology*. **31** (1): 64-67.
- Peerzada, Ovais Hamid; Chaurasia, A. K. and Naqueshbandi Irshad Ahmad (2014). Evaluation of chickpea germplasm (Desi) (*Cicer arietinum* L.) for yield and yield contributing traits. *The Bioscan*. **9** (4): 1805-1809.
- Petrova, Sonia D. and Desheva, Gergana N. (2016). Path coefficient and correlation analyses of quantitative characters in Chickpea (*Cicer arietinum*). *Phytologia Balcanica*. **22** (2): 243 – 246.
- Ramanappa, T. M.; Chandrashekar, K. and Nuthan, D. (2013). Analysis of variability for economically important traits in chickpea (*Cicer arietinum* L.). *International Journal of Research in Applied, Natural and Social Sciences*. **1** (3): 133-140.
- Rao, C.R. (1948). The utilization of multiple measurements in problem of biological classification. *J. Roy. Stat. Soc.* **10** (B): 159-203.
- Rao L.S., P. Usha Rani, P.S. Deshmukh, P.A. Kumar and S.K.Panguluri (2007). RAPD and ISSR fingerprinting in cultivated chickpea (*Cicer arietinum* L.) and its wild progenitor *Cicer reticulatum* Ladizinsky. *Genet. Resour. Crop Evol.*, **54**: 1235–1244
- Roy, Anindita; Ghosh, Sanhita and Kundagrami, S. (2015). Genetic approach and biometrical association of yield attributing traits in chickpea (*Cicer arietinum* L.). *International Journal of Science and Research*. **5** (7): 2208-2212.

- Salgotra, S.K. (2016). Association studies for seed yield and its attributing traits in desi chickpea (*Cicer arietinum* L.) varieties . *Legume Genomics and Genetics*. **7** (3): 1-4.
- Sharma, S.; Upadhyaya, H. D.; Gowda, C. L. L.; Kumar, S. and Singh, S. (2013). Genetic analysis for seed size in three crosses of chickpea (*Cicer arietinum* L.). *Can. J. Plant Sci.* **93**: 387–395.
- Srivastava, Saurabh; Lavanya, G. Roopa and Lal, G.M. (2017). Genetic variability and character association for seed yield in chickpea (*C. arietinum* L.). *J. of Pharmacognosy and Phytochemistry.* **6** (4):748-750.
- Tadesse, Megersa; Fikre, Asnake; Eshete, Million; Girma, Nigusie; Korbu, Lijalem; Mohamed, Ridwan; Bekele, Dagnachew; Funga,Assefa and Ojiewo, Chris O. (2016). Correlation and path coefficient analysis for various quantitative traits in desi chickpea genotypes under rainfed conditions in Ethiopia. *Journal of Agricultural Science.* **8** (12): 112-118.
- Thakur, Sanjay K. and Sirohi, Anil (2009). Correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) under different seasons. *Legume Res.* **32** (1): 1-6.
- Tiwari, Akanksha; Babbar Anita and Pal, Namita (2016). Genetic variability, correlation and path analysis in yield and yield components in chickpea (*Cicer arietinum* L.) genotypes under late sown condition. *International Journal of Agriculture Sciences.* **8** (54): 2884-2886.
- Wagstaff,K.; Cardie ,C; Ragees, S and Schroedl, S. (2001). Constrained K means clustering with background knowledge. In Pruc. 18<sup>th</sup> International Conference on Machine Lessening
- Wright, S. (1921). System of mating. *Genetics.* **6**: 111- 178

## Appendix

Mean performance of quantitative traits in genetic stock of chickpea

Genotypes	Days to 50% flowering	Days to maturity	Secondary branches plant <sup>-1</sup>	Plant height (cm)	Pods plant <sup>-1</sup>	Seed index (g)	Seed yield plant <sup>-1</sup> (g)
ICC1000	81	121	30	49.95	53	19.85	19.72
ICC10393	78	125	6	32.70	26	14.13	15.99
ICC10504	82	120	10	32.15	76	12.82	12.14
ICC10546	79.	122	20	33.65	92	13.55	14.05
ICC10950	79	120	24	32.55	61	11.64	14.60
ICC11059	74	115	16	35.00	42	13.00	13.21
ICC11091	75	125	8	37.60	15	15.69	18.56
ICC11258	79	121	22	43.20	71	13.81	14.99
ICC11266	81	122	16	48.00	121	29.43	31.67
ICC11330	79	125	11	36.70	91	12.45	13.71
ICC11424	81	124	22	43.10	82	15.01	16.06
ICC1148	81	124	18	35.75	90	11.63	11.75
ICC11507	86	125	12	37.75	48	11.60	14.45
ICC11766	83	121	25	39.00	40	32.66	14.95
ICC11867	78	125	13	43.45	63	21.81	16.63
ICC11879	78	126	14	46.80	46	28.99	22.82
ICC11904	81	128	14	48.15	31	26.61	17.52
ICC1205	82	126	11	37.40	84	14.90	12.38
ICC12159	77	119	34	36.85	164	23.65	30.99
ICC12258	77	123	24	38.55	70	13.59	13.13
ICC1228	87	124	12	37.65	66	13.02	14.45
ICC12310	75	120	16	40.90	71	14.70	17.73
ICC1232	80	125	19	41.00	138	12.03	17.94
ICC12323	82	124	16	54.25	55	24.64	17.12
ICC12600	80	124	8	36.10	37	9.80	16.00
ICC12691	77	120	20	52.65	83	10.62	17.36
ICC128	78	119	45	43.00	69	12.40	12.87
ICC12856	79	124	12	31.00	54	10.08	11.39
ICC12879	69	125	9	37.30	33	14.80	23.45
ICC12888	78	120	12	36.10	82	11.90	13.78
ICC1296	78	121	9	<b>25.75</b>	90	16.13	14.00
ICC13095	79	121	13	34.00	47	13.03	11.68
ICC13185	79	121	12	37.25	107	12.85	19.03
ICC13200	68	125	8	40.40	21	25.60	17.78
ICC13245	80	130	12	44.65	73	14.74	15.63
ICC1356	78	121	11	36.00	48	11.79	13.63
ICC13764	80	123	12	44.75	81	11.33	16.70

## RVSKVV/Thesis/M.Sc./No. 1712

ICC13964	78	119	8	35.00	35	12.57	15.90
ICC14051	78	120	8	35.85	42	12.18	16.34
ICC14199	80	127	14	44.40	38	42.31	36.39
ICC14225	77	124	12	34.05	103	11.33	15.16
ICC14226	78	124	8	46.65	53	19.39	13.90
ICC14344	78	128	13	40.75	36	17.82	16.54
ICC14411	78	125	14	33.90	57	13.69	14.86
ICC14426	73	<b>115</b>	22	32.80	71	11.80	11.39
ICC14446	87	127	17	51.60	65	38.18	21.76
ICC14469	77	121	20	37.00	66	12.05	14.35
ICC14484	78	120	13	35.15	114	14.19	21.79
ICC1470	80	126	8	35.60	43	17.62	14.46
ICC14710	78	119	13	33.95	33	19.75	22.99
ICC14787	83	119	23	41.75	96	15.15	18.48
ICC14881	78	121	12	35.60	21	10.47	15.85
ICC15080	78	121	10	34.00	64	14.29	12.35
ICC15184	78	125	8	38.15	17	16.90	21.19
ICC1520	80	124	6	37.80	39	13.58	15.34
ICC153	86	125	8	34.45	41	15.68	15.07
ICC15347	80	125	16	39.40	105	12.44	11.65
ICC15455	80	121	20	34.80	85	28.12	16.97
ICC15489	78	135	18	61.10	62	34.14	23.41
ICC15547	87	127	14	47.10	35	46.19	13.78
ICC15551	75	122	28	41.00	42	27.13	12.34
ICC15614	69	125	8	34.75	34	14.07	21.00
ICC15714	79	125	8	46.75	74	20.18	17.58
ICC15834	78	121	<b>5</b>	37.40	33	19.43	14.00
ICC15844	82	125	9	44.35	43	26.68	14.57
ICC16187	75	118	43	32.10	162	10.53	22.75
ICC16201	78	124	17	39.20	116	15.90	19.22
ICC16244	81	125	12	43.85	71	11.58	14.37
ICC16245	80	124	11	46.80	41	20.60	14.20
ICC16579	81	126	26	41.60	52	33.84	15.19
ICC16637	79	124	7	43.40	16	30.68	14.06
ICC16644	<b>59</b>	119	14	27.65	61	21.60	17.06
ICC16706	76	127	10	37.90	18	14.94	15.38
ICC16822	85	123	24	38.40	31	42.49	12.16
ICC16947	75	115	21	33.85	99	16.30	19.74
ICC2	79	123	31	35.60	94	12.88	16.55
ICC2086	75	118	20	32.45	84	13.68	14.14
ICC2113	79	122	21	37.40	16	17.98	13.42
ICC2338	79	123	41	53.60	113	16.52	22.43

## RVSKVV/Thesis/M.Sc./No. 1712

ICC2516	80	128	10	40.75	34	15.29	13.19
ICC26	78	127	12	43.60	73	15.70	14.91
ICC2629	86	124	10	31.65	40	11.33	11.22
ICC2796	86	128	9	40.60	27	12.74	19.48
ICC2893	81	121	11	45.95	42	19.48	14.41
ICC3411	79	120	13	42.90	74	14.26	13.08
ICC3458	76	115	28	32.80	114	14.42	13.38
ICC3491	80	122	12	48.90	69	15.88	13.55
ICC353	78	119	10	39.85	70	12.28	14.44
ICC3539	79	123	34	52.65	64	17.16	12.72
ICC3613	78	120	11	44.15	70	11.43	11.09
ICC3705	68	119	14	43.15	65	24.53	14.87
ICC3834	78	119	10	32.00	27	13.00	14.36
ICC4233	78	120	11	54.00	54	14.73	15.98
ICC4359	79	122	24	37.40	94	11.83	13.88
ICC4411	75	117	17	41.30	66	12.83	13.44
ICC455	76	118	18	36.10	84	<b>9.19</b>	13.14
ICC4567	79	122	26	34.20	41	16.43	11.30
ICC4893	79	124	23	36.20	53	15.98	12.18
ICC4946	83	124	8	42.15	73	14.00	14.88
ICC4984	78	126	20	37.15	66	16.33	14.16
ICC5021	78	124	12	41.10	81	11.47	11.75
ICC504	79	127	50	42.80	86	12.47	14.68
ICC5086	76	117	22	45.35	115	13.02	16.96
ICC5119	81	124	14	37.00	61	28.93	19.18
ICC512	80	121	54	36.75	71	10.73	20.63
ICC531	86	123	15	35.10	65	14.63	13.74
ICC5391	79	120	11	37.10	106	12.80	12.83
ICC5504	76	116	31	42.60	35	27.37	13.20
ICC5541	81	120	23	54.00	53	22.73	12.44
ICC5581	78	119	13	34.10	102	11.68	15.23
ICC5686	81	125	15	41.00	64	25.48	22.39
ICC5697	75	117	21	34.85	76	26.01	25.43
ICC5755	75	116	17	31.15	39	15.02	12.82
ICC5886	77	122	16	33.75	85	16.33	13.48
ICC5899	78	125	12	40.45	125	25.08	31.59
ICC6122	77	120	10	38.05	108	27.95	32.83
ICC6140	80	123	27	37.25	34	21.00	14.04
ICC6155	82	124	14	47.95	57	23.35	17.15
ICC6300	81	124	9	43.75	40	14.38	15.17
ICC6659	76	116	23	31.15	143	13.00	16.97
ICC6831	76	124	21	45.60	23	30.86	12.69

## RVSKVV/Thesis/M.Sc./No. 1712

ICC6970	82	125	10	55.00	65	14.10	13.37
ICC7098	81	128	10	41.35	37	14.28	14.23
ICC7269	83	123	14	51.30	83	37.98	28.96
ICC7302	78	121	16	42.35	86	14.09	15.03
ICC7380	79	124	12	37.60	65	16.28	14.58
ICC7479	82	119	31	44.15	78	12.53	15.78
ICC75	77	120	11	37.40	104	15.56	16.59
ICC7737	81	122	9	41.90	70	16.28	14.25
ICC793	79	119	37	37.90	59	15.92	19.92
ICC8284	80	125	17	46.85	36	18.47	15.36
ICC8397	78	124	14	51.00	82	14.18	14.71
ICC8449	86	126	9	42.35	31	25.88	14.35
ICC8660	81	127	8	43.30	70	15.74	15.71
ICC871	78	121	21	39.00	46	15.87	14.13
ICC8723	87	128	13	46.30	34	23.41	13.55
ICC8923	83	123	14	66.00	36	24.94	17.53
ICC8962	76	123	22	47.00	34	40.79	12.56
ICC9020	77	117	16	27.00	76	13.05	13.57
ICC9023	78	124	10	37.35	127	12.05	36.79
ICC952	79	121	32	31.15	65	22.54	11.53
ICC9728	81	122	10	47.30	105	15.45	14.46
ICC981	82	129	7	33.60	37	13.10	12.83
ICC991	80	125	45	42.05	104	15.08	15.13
ICC9917	80	119	29	36.80	77	13.83	13.98
ICCV10	78	119	32	45.30	104	18.17	23.52
ICCV10	69	121	15	37.95	120	16.00	28.78
ICCV10	68	119	9	42.25	19	15.84	29.12
ICCV91106	78	120	16	36.00	67	15.94	14.13
ICCV92944	68	121	8	45.65	49	24.81	29.29
ICCV93954	78	120	16	35.85	44	21.23	13.88
ICCV95311	77	120	17	43.40	60	35.82	23.21
ICCV95703	78	119	11	41.35	84	15.13	24.00
IG10224	80	120	17	35.00	73	22.20	15.53
IG10578	79	121	24	41.75	42	33.69	15.02
IG10633	81	127	10	42.80	27	26.13	15.31
IG5875	81	124	7	41.90	29	34.54	13.22
IG5990	79	119	26	46.15	36	30.90	13.01
IG5995	78	122	19	34.55	54	32.99	14.15
IG6408	87	126	7	35.15	15	23.02	13.68
IG69441	81	126	9	41.95	119	22.40	21.05
IG69597	79	127	11	54.00	9	18.95	13.43
IG70413	81	124	10	47.30	23	21.28	14.73

## RVSKVV/Thesis/M.Sc./No. 1712

IG70505	81	124	15	44.30	64	37.58	14.81
IG70746	83	119	32	50.85	52	28.72	12.06
IG70985	82	123	11	52.30	49	31.35	<b>10.85</b>
IG70990	81	125	14	52.15	36	29.49	33.26
IG71790	82	117	31	35.75	86	21.95	28.82
IG71799	78	124	8	44.60	95	13.40	14.33
IG71814	80	130	12	44.15	30	41.35	12.24
IG71887	76	123	15	47.35	53	44.25	16.08
IG71926	87	121	10	36.40	45	34.85	19.94
IG71941	73	120	21	43.65	37	41.76	17.04
IG71945	87	124	14	46.00	83	24.19	28.61
IG71967	80	122	14	35.35	35	37.63	14.28
IG72042	81	122	13	48.10	57	27.75	13.39
IG73287	81	127	8	47.60	19	33.00	14.35
IG73322	78	120	6	43.60	13	38.78	14.60
IG73333	78	119	26	35.10	48	28.46	12.40
IG73334	79	116	41	37.05	62	32.26	20.08
IG73341	79	129	8	43.95	19	36.52	12.12
IG73458	80	121	18	44.80	66	25.23	23.61
IG74094	82	122	10	35.05	65	19.88	14.48
IG7432	76	117	31	44.65	121	26.54	14.80
IG7634	82	123	15	47.90	59	30.64	15.18
IG9262	77	125	8	37.10	46	28.00	15.48
IG9330	76	118	20	45.75	81	32.15	26.08
IG9740	76	122	51	48.10	66	34.03	17.64
IG9810	80	124	8	53.00	17	33.75	17.29
JG11	73	116	21	43.45	41	18.28	13.68
JG11	73	117	13	31.05	43	20.60	13.65
JG11	77	120	8	35.40	54	21.03	14.68
JG11	73	117	26	32.30	126	20.31	26.77
KAK2	61	124	8	44.75	34	37.65	11.13
KAK2	63	120	16	39.90	40	41.04	15.71
KAK2	68	121	22	47.00	22	35.17	23.48
KAK2	78	125	15	44.75	60	38.83	21.62
L550	77	121	29	37.20	72	17.37	13.00
L550	80	124	12	45.95	68	19.84	15.05
L550	80	129	12	37.10	48	19.06	17.08
S.Em±	0.64	0.85	1.21	1.41	1.70	1.10	1.15
C.D.5% level	1.92	2.55	3.63	4.23	5.1	3.30	3.45

**VITA**

The author of this thesis **Lokendra Singh Rajput** S/o **Shri Rajmal Singh Rajput** was born on 01/01/1990 at Ujain(M.P.).

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During all the period of education, from schooling to post graduation he was very sincere and honest towards studies and works.