

GENETIC DIVERGENCE ANALYSIS IN CHICKPEA
(*Cicer arietinum* L.)

By

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B.Sc. (AGRI.)

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MASTER OF SCIENCE

(AGRICULTURE)

IN

AGRICULTURAL BOTANY

(GENETICS AND PLANT BREEDING)



DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, LATUR
MARATHWADA AGRICULTURAL UNIVERSITY,
PARBHANI

2007

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DISSERTATION

Submitted To

*The Marathwada Agricultural University, Parbhani. In Partial
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**DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, LATUR
MARATHWADA AGRICULTURAL UNIVERSITY,
PARBHANI**

2007

Dedicated
to my
Beloved
Family,
Shinde Ajji
and my
Friends

CANDIDATE'S DECLARATION

I hereby declare that the dissertation
or part thereof, has not been
previously submitted by
me for a degree of
any University.

Place : Latur

Date : 19 / 05 / 2007


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CERTIFICATE – I

This is to certify that the dissertation entitled “**GENETIC DIVERGENCE ANALYSIS IN CHICKPEA (*Cicer arietinum* L.)**” submitted by **Shri. JADHAV RAMKRISHNA SADASHIV** to the Marathwada Agricultural University, Parbhani in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** is record of original and bonafide research work carried out by him under my guidance and supervision. It is of sufficiently high standard to warrant its presentation for the award of the said degree.

I also certify that the dissertation or part thereof has not been previously submitted by him for a degree of any university.

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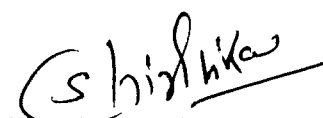
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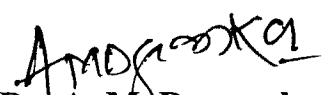
This is to certify that the dissertation entitled “**GENETIC DIVERGENCE ANALYSIS IN CHICKPEA (*Cicer arietinum* L.)**” submitted by **SHRI. JADHAV RAMKRISHNA SADASHIV** to the Marathwada Agricultural University, Parbhani in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)** has been approved by the student’s advisory committee after viva-voce examination in collaboration with the external examiner.

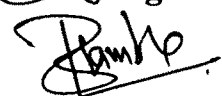

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The secrete lies in working hard, a genius is made up of one percent inspiration and ninety nine per cent perspiration.

Thomas Alva Edison

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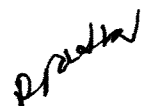
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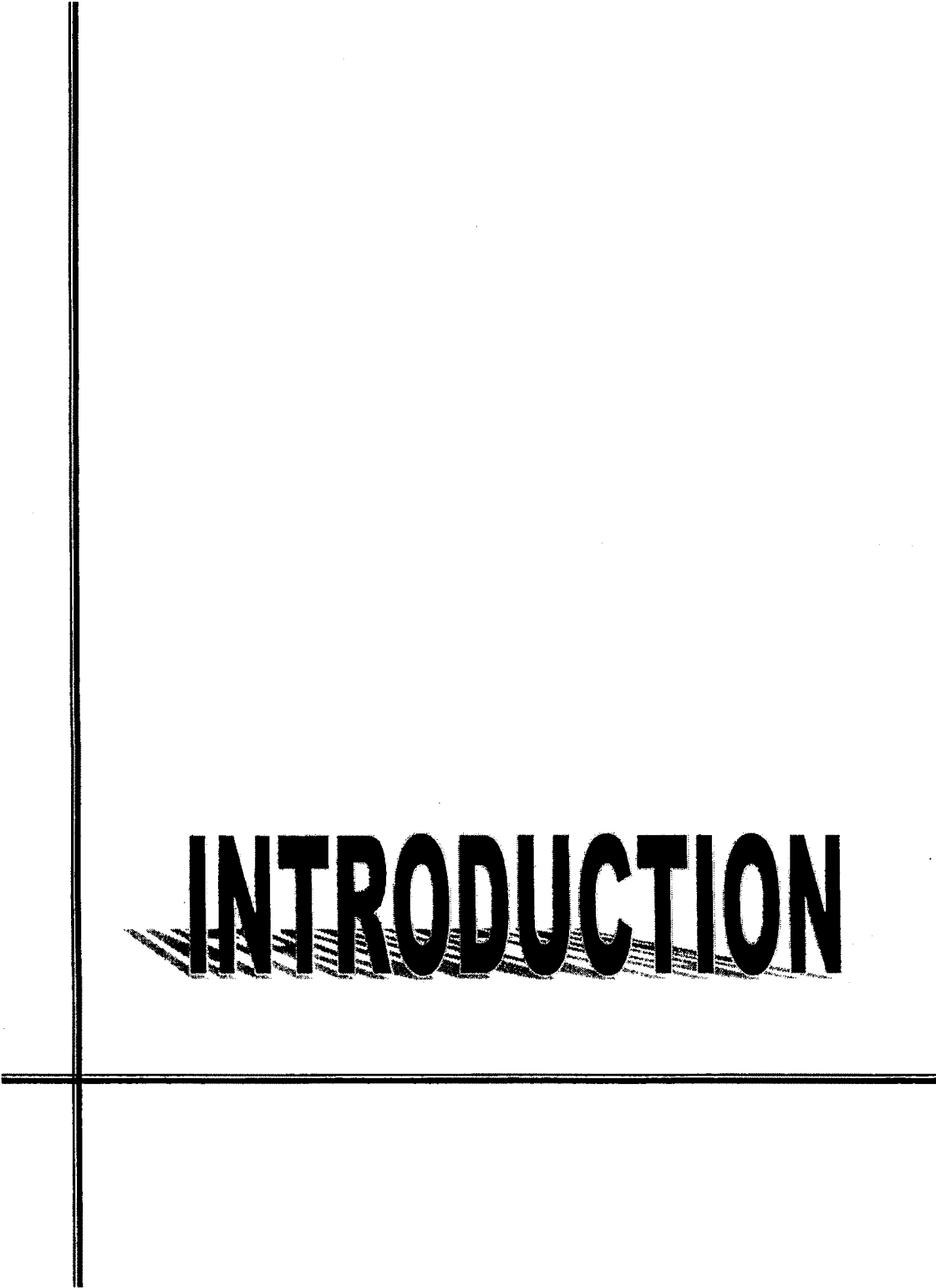
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ABBREVATIONS

*	-	Significant at 5 per cent
%	-	Per cent
**	-	Significant at 1 per cent
C.D.	-	Critical difference
cm	-	Centimeter
d.f.	-	Degrees of freedom
<i>et al.</i> ,	-	and other co-workers
Fig	-	Figure
g	-	gram
GA	-	Genetic Advance
GCV	-	Genotypic coefficient of variation
h^2 (b s)	-	Heritability (broad sense)
ha	-	hectare
M S S	-	Mean sum of squares
No.	-	Number (s)
PCV	-	Phenotypic coefficient of variation
S.E.	-	Standard error
viz.,	-	Videlicet (namely)
vs	-	Versus
$\bar{X}$	-	Mean
Σ	-	Summation



INTRODUCTION

Chapter I

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a native of India is self pollinated leguminous crop. The genus *Cicer* belongs to family leguminosae, sub-family papilionaceae. The somatic chromosome number is $2n = 16$. The genus cicer contain about 40 species out of which 31 are perennial and 9 are annuals (Ladizinsky and Adler, 1976).

Chickpea is the third most important grain legume in the world after dry beans and dry peas. It has been well recognized as a valuable source of protein particularly in developing countries. The daily per capita availability of 14 g chickpea is a source of approximately 2.3 per cent (56 kcal) energy and 4.7 per cent (2.7 g) protein to Indian population besides being a major source of calcium and iron (10-12%). Being a legume, chickpea improves physical, chemical and biological properties of soils, chickpea fixes up to 141 kg nitrogen/ha.

Chickpea cultivation is mainly confined to Asia with 90 per cent of global area and production. Besides Asia, it is also grown in North and Central America, the Mediterranean region, the West Asian and North African (WANA) region and Eastern Africa. Recently, the crop has expanded in new areas such as Australia and Canada.

It is grown mostly as rainfed crop in post rainy season in semi-arid tropics and in spring and winter season in temperate and Mediterranean types of climate, Kabuli types are mostly grown in the West Asian and North African region, the America and Europe, while desi types predominate in Asia, parts of African and Australia.

Globally, chickpea is cultivated on about 10.4 m ha adding 8.04 m tonnes of grains to the global food production. As many as 42

countries grow chickpea but a dozen countries viz., India, Pakistan, Turkey, Canada, Mexico, Iran, Australia, Ethiopia, Myanmar, Syria, Bangladesh and Spain contribute 97 per cent to the global production. India predominate the global chickpea supply as being the largest producer and consumer in the world and account for over 66 per cent of the global output.

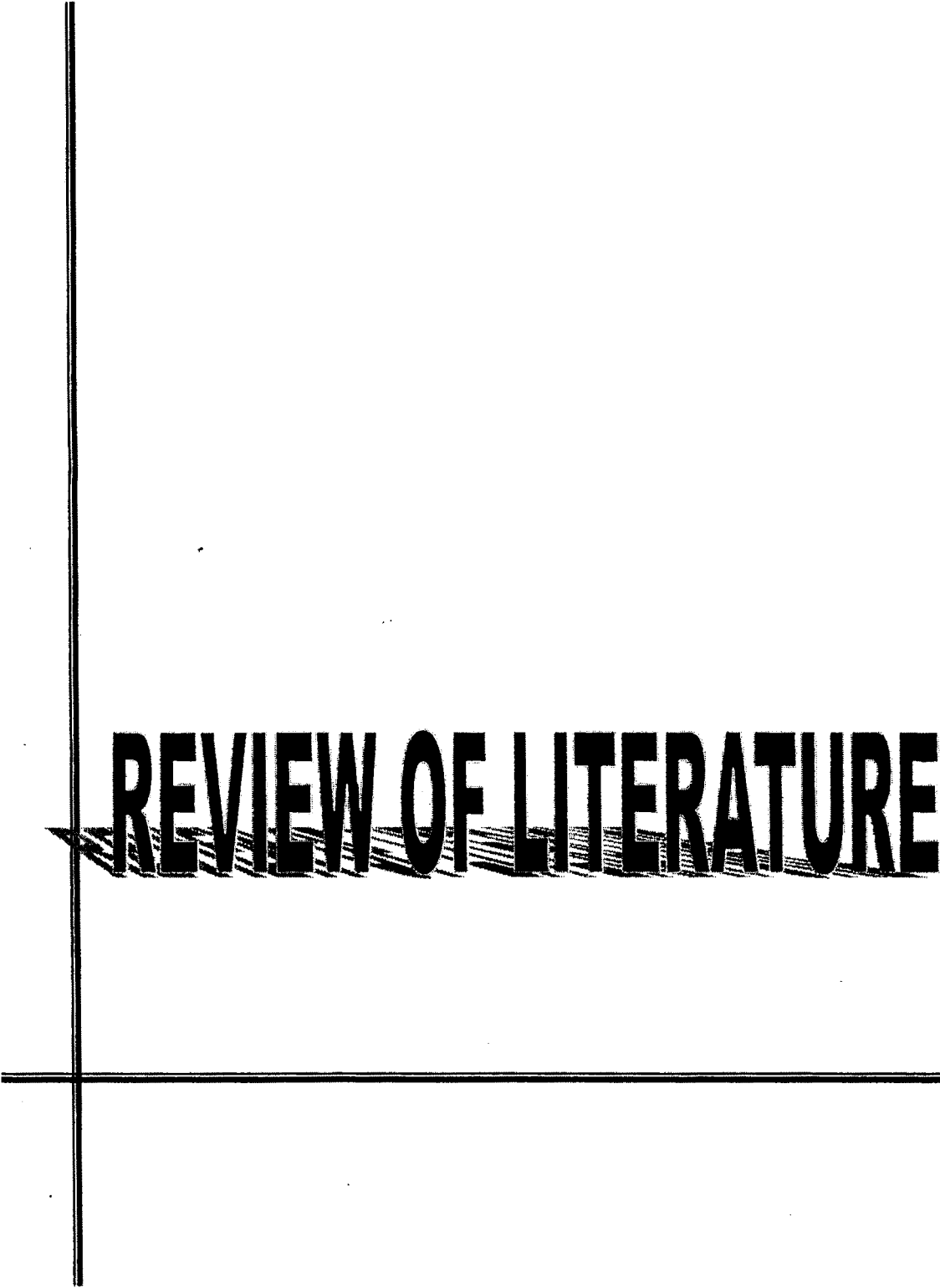
India grows chickpea on about 6.86 m ha producing 5.35 m tonnes of grain, which represents 32 per cent and 42 per cent of the national pulse acreage and production respectively. During the past 50 years, the chickpea production has gone up from 3.65 m tonnes to 5.35 m tonnes in spite of area decline from 7.51 m ha to 5.86 m ha. In India four states viz., Madhya Pradesh, Rajasthan, Uttar Pradesh and Maharashtra, together contribute 87 per cent of the production from 65 per cent area. Due to gradual expansion of rice coupled with availability of late sown wheat varieties causing substantial erosion to the chickpea area in Bihar, Haryana, Punjab, Uttar Pradesh and West Bengal. In contrast area under chickpea increased steadily in states of Southern and Central zones. In Maharashtra chickpea is grown on around 1.02 m ha area with production of 0.70 m tonnes with average productivity of 691 kg/ha as compare to world 773 kg/ha and national 844 kg/ha respectively (Anonymous, 2005).

The major production constraint that limits the realization of potential yield includes biotic and abiotic stresses. Among biotic *Fusarium* wilt, coupled with root rot complex, *Ascochyte blight*, gram pod borer are important. Among abiotic stresses, terminal drought, high temperature during reproductive stage, cold sensitivity during vegetative and flowering stage and alkalinity / salinity are major.

Systematic collection, multiplication and screening of germplasm have helped to identify useful and stable donors for key stresses in chickpea. Wild species of chickpea are rich reservoir of not only resistant genes against various biotic and abiotic stresses but also genes responsible for high yields. It is also important that considerable variability for economic trait must exist in the germplasm for better exploitation following recombination breeding or selection. The need of parental diversity in optimum magnitude to obtain superior genotypes to recover transgressive segregates has also been repeatedly emphasized. However, the genetic diversity of selected parent is not always based on factors such as geographical diversity / place of release. Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should base on sound statistical procedures such as D^2 statistics and non-hierarchical euclidean cluster analysis. These procedures characterize genetic divergence using criteria of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters.

In view of this fact, 91 chickpea genotypes evaluated for this study.

1. To estimate genetic divergence among chickpea genotype.
2. To study the contribution of characters towards genetic diversity.



REVIEW OF LITERATURE

Chapter II

REVIEW OF LITERATURE

The literature on chickpea pertaining to variability and genetic divergence reviewed below.

2.1. Genetic variability for yield and yield contributing character.

Adhikari and Pandey (1982) observed that the phenotypic coefficient of variation was higher than genotypic coefficient, being highest for seed yield, number of pods per plant, secondary branches per plant and seed weight. Although other characters such as days to flowering and seeds per pod had high heritability and genetic advance.

Khorgade *et al.* (1985) reported moderate heritability for plant height, number of pods per plant and number of branches per plant. While it was high for time to 50 per cent flowering, number of seeds per pod and seed index. Yield per plant on the other hand exhibited the lowest estimates of heritability. The character such as number of seeds per pod, time to 50 per cent flowering and to some extent number of branches per plant were high heritability and large genetic gain.

Mishra *et al.* (1988) reported high heritability for all the characters. High heritability coupled with high genetic advance expressed as mean were observed for number of secondary branches per plant, number of pods per plant, seed yield per plant, biological yield per plant and harvest index.

Singh (1988) reported magnitude of PCV ranged 3% to 20% and it was low (<10%) for days to 50 per cent flowering and days to maturity, moderate (10-20%) for plant height, number of pods per plant, biological yield and high (>20%) for 100-seed mass, yield per plant and

harvest index. Days to maturity showed a high heritability while days to 50 per cent flowering, 100-seed mass and yield per plant indicate moderate heritability. The remaining characters showed low heritability. The lowest estimate of heritability was for harvest index.

Sadhu and Mandal (1989) observed considerable range of variability for plant height, pod number, seed number, seed weight and seed yield. Estimates for heritability and expected genetic gain were high for seed weight.

Sharma *et al.* (1990) reported highest genotypic and phenotypic variation and genetic advance for secondary branches per plant, followed by 100-seed weight. Heritability was highest for 100-seed weight, days to maturity and plant height.

Singh *et al.* (1990) observed wide variation for all the characters except days to flowering, days to maturity and protein content.

Misra (1991) observed high heritability estimates for time to 50 per cent flowering, time to maturity, plant height, pods per plant and 100-seed weight. Genetic advance was high for pods per plant, moderate for branches per plant, seeds per pods and 100-seed weight. High h^2 and GA estimates were closely correlated with yield. This indicated that selection would be effective for pods per plant and seed weight.

Jahagirdar *et al.* (1994) reported high GCV and PCV for number of pods per plant. High heritability together with high genetic advance was estimated for 100-seed weight, days to 50 per cent flowering, number of secondary branches per plant and number of pods per plant.

Rao *et al.* (1994) observed highest genotypic coefficient variation for 100-seed weight followed by secondary branches per plant,

Pods per plant and seed yield per plant. High heritability and high expected genetic advance were estimated for 100-seed weight and plant height. Seed yield per pods and secondary branches per plant had relatively low heritability estimates with high genetic advance.

Rao (1996) observed genetic variability was greatest for pod weight per plant, harvest index and 100-seed weight.

Tripathi (1997) reported high genotypic coefficient of variation and broad sense heritability coupled with high genetic advance for pods per plant, seeds per plant, biological yield and yield per plant.

Kumar *et al.* (1999) observed high genotypic and phenotypic coefficient of variation for number of pods per plant, 100-seed weight, seed yield per plant and harvest index. Similarly these characters exhibited high heritability coupled with high genetic advance.

Wahid and Ahmad (1999) observed highest heritability for plant height (0.50%) followed by seed yield (0.45%) and pods per plant (0.35%). Genotypic coefficient of variation was greatest for plant height, pods per plant and seed yield. The phenotypic coefficient of variation was greater than genotypic coefficient or environmental coefficient of variation. Therefore suggested that plant height and pods per plant could be used as selection criteria for further improvement in chickpea yield.

Nimbalkar (2000) observed wide range of variability for all characters except number of days to maturity. Also showed the major portion of variance was contributed by genotypic component with the environmental component being relatively small. The genetic (58.8%) and phenotypic (49.02%) coefficient of variability and genetic advance (100.28%) were highest for 100-seed weight and lowest (2.94, 3.26 and

5.50 per cent) respectively for number of days to maturity. Heritability was highest for 100-seed weight (19.3%) and lowest for plant spread.

Sable *et al.* (2002) observed seed yield per plant, 100-seed weight and biological yield per plant possessed high amount of genotypic coefficient of variation and exhibited high estimates of genetic advance coupled with high heritability.

Nawab (2002) observed the genetic variability existed among the genotype for plant height (cm), number of pods per plant, number of seeds per plant, 100-seed weight, total weight of the plant and seed yield per plant.

Qureshi *et al.* (2004) observed highly significant differences for plant height (cm), number of primary and secondary branches per plant, number of pods per plant, 100-seed weight, biological yield per plant, harvest index and grain yield per plant.

Genetic variability for plant height, number of primary branches, number of secondary branches, number of pods per plant and total biological yield ranged from 40-90 cm, 1.5 – 6.5, 1.1 – 8.5, 1.0 – 7.5, 1.5 – 50.5 gm per plant. Whereas grain yield per plant varied from 5.5 – 25.5 gm and harvest index ranged from 10-70. The variation for days to flowering was in the range of 120-150.

Burli *et al.* (2004) found that analysis of variance revealed highly significant difference among genotype for all the characters under study. Also observed maximum range of variation for number of pods per plant followed by days to maturity and plant height. The phenotypic coefficient of variation was marginally higher than genotypic coefficient of variation for all the characters. Higher value of GCV and PCV were

observed in the grain yield per plant, number of branches per plant and plant spread.

Heritability estimates were highest for days to maturity followed by 100-seed weight, days to 50 per cent flowering and plant height. High heritability and high genetic advance is observed in 100-seed weight, days to maturity and days to 50 per cent flowering.

Ozcelik *et al.* (2004) showed that heritability for 100-seed weight, number of pods per plant, number of seeds per plant, plant height and seed yield were 79, 63, 62, 58 and 49 per cent respectively.

Arshad *et al.* (2004) showed the high heritability with low genetic advance for number of days to flowering, number of days to maturity and 100-seed weight.

2.2 Genetic divergence

2.2.1 Concept of genetic divergence

The concept of D^2 statistics for measuring the divergences between two populations were introduced by Mahalanobis (1928). It gives result based on the magnitude of divergence and is independent of size of sample.

Mahalanobis *et al.* (1949) employed D^2 statistics in a detailed study of anthropometric data of Uttar Pradesh classifying 23 groups into three major clusters. With Brahmin (B- cluster) at the top of Hindu Social Hierarchy comprising nine groups, the artisan (A – cluster) in the middle consisting of four groups and tribal (T – cluster) at the bottom consisting of ten groups.

Rao (1952) suggested the application of D^2 statistics for the assessment of genetic diversity in plant breeding.

Allard (1961) described the relationship between genetic diversity and consistency of performance in different environment by using three distinct levels of genetic diversity. He concluded that genetic diversity and productivity were completely related and the many factors determined the productivity of mixed population. According to him genetic diversity and stability on contrast appeared more simply related.

Moll *et al.* (1962) reported no relationship between geographical distribution and genetic diversity as reflected in heterosis between crosses in maize. Heterosis in maize appeared to be increased with the increased diversity. In another study, Moll *et al.* (1964) observed that heterosis increased with increases in divergence among the parent within the restricted range but extremely divergent crosses, resulted in decreased heterosis.

According to Burnaby (1966) D^2 statistic is a sum of squares of difference between corresponding mean values of two sets of suitably weighed measurements.

Murthy and Arunachalam (1966) stated that a change in the breeding structure could bring about a substantial change in character association and the pattern of genetic variability distribution genetic diversity and geographical diversity could not be directly related in many of the crops. Genetic drift and selection in different environment may cause greater diversity than geographical diversity.

2.2.2 Genetic divergence in chickpea

Katiyar (1978) studied the genetic divergence for morpho-physiological and quality determinants of yield in thirty indigenous and exotic varieties of chickpea by using Mahalanobis D^2 statistic. The varieties were grouped into seven different clusters and observed that the

clustering pattern of varieties did not follow geographical distribution. They also reported that the leaf area per plant, relative leaf weight and number of pods per plant were important for divergence.

Jain *et al.* (1981) studied genetic divergence in 36 genotypes of chickpea for ten quantitative characters grown in eight environments. These genotypes grouped into eight clusters and observed that there was considerable diversity in the material. The grouping of genotypes from different geographical areas in the some clusters confirmed that there is no parallelism between genetic diversity and geographical distribution.

Dumbre and Deshmukh (1984) studied genetic diversity in gram and found that seed size, yield per plant and duration were the most important characters contributing towards genetic diversity. They also concluded that geographical diversity did not seem to have direct association with genetic diversity.

Mishra *et al.* (1987) carried out D^2 analysis in 36 chickpea genotypes for 7 yield related traits and grouped into 8 clusters. The highest intercluster distance was observed between cluster V and VII. He also concluded that the high yielding genotypes should be selected as parents for hybridization programme from cluster I, IV and V.

Main and Bahl (1989) carried out Mahalanobis D^2 analysis of yield component in 28 populations consisting of 7 parents and 21 F_1 hybrids. It showed that there was appreciable genetic divergence among both parent and hybrids. The range of D^2 values between pair of genotypes found between 2.20 to 147.71. Clusters were not associated with geographical regions, indicating that genetic diversity was not caused by geographical isolation parents with moderate D^2 value (26.6 – 35.0) produced hybrids with the highest heterosis.

Singh and Singh (1989) evaluated 66 genotypes during 3 rabi seasons over of environments created by a combination of sowing date, spacing and fertilizer dose. Data from 9 characters were analyzed using the D^2 statistic. Highly significant differences due to genotype environment and genotype x environment interaction were shown for all characters.

Sood *et al.* (1989) derived information on genetic diversity by multivariate analysis of data on 10 yield component in 70 genotypes of chickpea. The genotypes were grouped into 15 clusters. No definite relationship between genetic diversity and geographical distribution was observed.

Samal *et al.* (1989) grouped 23 cultivars of chickpea into 6 clusters on the basis of D^2 analysis of 7 yield components. The greatest cluster distance was found between cluster 3 and 4, which had the highest yields and greatest number of pods per plant. It is suggested that crosses between cluster 3 on the one hand and cluster 4 on the other hand should exhibit high heterosis and produce segregants with higher yield.

Lal *et al.* (1989) assessed thirty strains from 8 different countries for 9 yield components. D^2 analysis grouped the strains into 6 clusters on the basis of minimum generalized distance.

Malhotra and Harris (1990) used cluster analysis of data on number of days to flowering and seed yield from 2 international trials to classify chickpea growing environment into zones. Results showed that the characterization of the genotype by locality minimized interaction within a cluster /zone and key sites should be selected from each cluster for initial evaluation of a large amount breeding material.

Mishra and Rao (1990) estimated information on genetic variability by D^2 and metroglyph analysis from data on 12 yield component in 117 genotypes. The genotypes were grouped into 13 clusters, with eleven single genotype clusters.

Khan *et al.* (1990) studied genetic diversity in 132 chickpea genotypes and indicated considerable amount of variation for grain yield and its component. Multivariate analysis of data from 7 parents and 21 F_1 hybrids indicated weak correspondence between D^2 and canonical variate analysis. As there was no relationship between heterosis over mid parent and genetic distance between parents, the traditional breeding approach of making a large number of crosses among selected parents is recommended.

Arora (1990) studied genetic divergence of 13 genotypes and 30 F_1 hybrids using Mahalanobis D^2 statistic and classified into 6 groups. No relationship was found between genetic divergence and geographical distribution. The parent ILC-613 (Tunisia) and T-3 (Uttar Pradesh, India), which were classified in different group, produced the best heterotic hybrid with high yield. This cross was subjected to an intensive selection programme over 6 generation, after which it produced a yield of 4325 kg/ha, compared with best control variety Avrodhi, which produced 3246 kg/ha.

Chaudhary *et al.* (1990) derived information on genetic distance by D^2 analysis of data in 60 chickpea genotypes grown in 3 environments, six clusters were formed in 2 of the environments while 7 clusters were formed in the third. The composition of the cluster differed between environments.

Sandhu and Gumber (1991) grouped fifty-nine strains into 12 clusters on the basis of 8 yield component using Tocher's method, with five solitary clusters. Intra cluster D^2 values ranged from 0.0 to 13.6 and intercluster distance from 15.0 to 156.5. Crossing cluster VII genotypes ICC-11321 and L-550 with the (only) cluster XI genotype ICC-11316 was recommended for the production of high yielding material.

Vijaykumar *et al.* (1991) studied genetic divergence in 104 diverse genotype (77 desi and 27 kabuli) from data on 9 characters. D^2 statistic grouped the genotypes into 6 clusters substantial diversity existed both within and between the 6 clusters. The D^2 values between the pair of genotypes ranged between 0.00 to 80.88.

Lokendra Kumar and Arora (1992) studied genetic divergence in 40 genotypes, from diverse Indian regions for yield and 17 other agronomic traits. Based on D^2 values, the genotypes were grouped into 10 clusters. No definite correlation was observed between genetic diversity and geographical origin.

Jana and Singh (1993) conducted study to test whether geographical divergence in kabuli chickpea is consistent with the proposed theory of its spread from putative center of origin. More than 4000 Kabuli chickpea accessions representing turkey and six other major chickpea growing region were grown in ICARDA, Syria and characterized for nine morphological, three phonological and four physiological characters. The discrete log-linear multivariate analysis showed two-character association, but no higher order association in any region. Multivariate principal components analysis of 11 quantitative

traits revealed that the distribution of chickpea on both sides of Turkey was consistent with the proposed pathway.

Satija *et al.* (1993) evaluated 135 lines for yield related traits using the Mahalanobis D^2 statistic and grouped in 21 clusters. In on evaluation of 28 F_1 hybrids from crosses of 8 parents, significant differences were found between hybrid, with some crosses showing good result for seed weight and pod number scores for heterosis were greater when the intercluster distance was moderate the clustering pattern was not related to geographical diversity.

Singh *et al.* (1993) derived information on genetic diversity and stability from 7 characters in 20 chickpea genotypes. Highly significant difference due to genotypes, environments and genotype x environment interaction were observed for all 7 characters the genotypes were grouped into 5 clusters on the basis of D^2 analysis. Seven genotypes were identified with high grain yield, together with stability for yield and yield related characters. Crosses among these 7 selected genotypes are recommended.

Singh and Sareen (1993) evaluated forty four desi and 16 kabuli genotypes over 3 sowing dates. Data recorded for days to 50 per cent flowering and seed yield were used for metroglyph and index score analysis. The majority of kabuli types were medium to late flowering with average yield, whereas desi types were early flowering and average yielding.

Anilkumar *et al.* (1993) studied genetic diversity for 15 photosynthetic and yield related traits in 52 true breeding advanced generation lines and 2 control varieties using Mahalanobis D^2 analysis. The study revealed very high level of diversity. The genotypes were

grouped into 9 clusters using Tocher's method. The D2 values between the pair of genotypes ranged between 53.9 to 15054.0.

Garoosi and Vojdani (1993) evaluated total 577 desi and kabuli chickpea (*Cicer arietinum*) accession of diverse Iranian origins and from various climates. For 11 characters the following result were obtained. Kabuli types showed higher diversity of quantitative characters than desi types. In relation to individual and complex characters, the best climate response patterns were shown by kabuli and desi types respectively. Number of seeds per pod, 100-seed weight, flowering duration and flower colour were the best character for type differentiation. Except between latitude and flowering duration of desi type, there was no significant correlation between the characters studied and Kabuli types had the highest degree of linkage these results show that the 2 types are independent genotypes.

Sarvaliya and Goyal (1994) studied genetic divergence in 76 genotypes of chickpea, mostly of Indian origin for the 10 agronomic characters. The genotypes were grouped into 10 clusters, with three solitary clusters. There was no relationship between geographical distribution and genetic diversity. The magnitude of intercluster distance was high than of intracluster distance.

Rao and Singh (1994) assessed 25 chickpea genotypes for genetic diversity on 10 yield component using D^2 analysis. The 25 genotypes clustered into 3 groups. The component days to flowering, days to maturity, pods per plant and 100-seed weight accounted for maximum divergence.

Pooran Chand and Singh (1995) evaluated forty chickpea genotypes for 9 yield component. The D^2 statistic grouped them into six

clusters. The genotypes of cluster VI and cluster IV were highly divergent. It is suggested that varieties of cluster IV and VI, and cluster II and VI should be hybridized in a breeding programme.

Samal and Jagdev (1996) estimated genetic divergence among 23 cultivars of chickpea for 7 yield traits. The cultivars were grouped into 6 clusters. Maximum genetic distance was recorded between cluster III and VI followed by IV and VI suggesting wide diversity among these groups.

Jethava *et al.* (1996) studied genetic divergence in 70 chickpea genotypes of different geographical origins using the Mahalanobis D^2 statistic. Results revealed considerable diversity and genotypes were grouped into 16 clusters indicating that geographical distribution and genetic diversity were not related. Seed yield per plant, number of pods per plant and 100-seed weight contributed most to genetic diversity.

Rao and Jain (1996) evaluated thirty genotype for 11 yield related characters. The genotypes were grouped into 13 clusters on the basis of D^2 analysis of data. Genetic diversity had no relationship with geographical diversity. An analysis of the percentage contribution of individual characters towards genetic diversity revealed that 100-seed weight and plant height are the major character contributing to genetic diversity in the chickpea.

Narendra Kumar (1997) analyzed genetic divergence among 60 entries of chickpea for seven developmental characters and grouped into five clusters. Grouping of entries in different cluster was not related to their geographical origin the intercluster D^2 values ranged from 8.0 to 38.2. Based on mean performance, genetic distance and clustering

pattern, hybridization involving parent from cluster II and V may give higher yielding varieties.

Shinde *et al.* (1997) studied genetic divergence in 52 genotypes for under irrigated and rainfed condition. For 10 yield related traits. The geographical origin of genotypes did not show any definite relationship with genetic diversity.

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

Deshmukh and Patil (1998) grouped fifty genotypes of chickpea into 11 clusters on the basis of Mahalanobis D^2 analysis of data on 7 yield related traits. Data are tabulated on intra-cluster and inter cluster distances.

Bhattacharya and Ganguly (1998) evaluated twenty six genotype of chickpea following normal and late sowing genotypes grown under normal sowing conditions were grouped into ten cluster and following late sowing into seven clusters. Geographical origin of genotype was not related to genetic diversity.

Arun Kumar *et al.* (1998) studied genetic divergence in 17 chickpea genotypes (five each developed via mutation breeding, interspecific hybridization with chickpea and intraspecific hybridization) on the 13 quantitative traits using D^2 analysis.

Khan (1999) evaluated 38 geographically diverse chickpea genotypes multivariate D^2 analysis grouped genotypes into 8 clusters on

the basis of yield and its component. It is concluded that hybridization among the genotypes from cluster I and II may result in high yielding progenies.

Pooran Chand (1999) estimated genetic divergence among 49 genotypes of chickpea via D^2 analysis of seven quantitative traits. The genotypes were grouped into eight clusters.

Raje and Khare (1999) evaluated 21 genotypes of chickpea varying widely in seed size, for seed yield and its component. On the basis of D^2 analysis these were grouped into 6 clusters. Moderate 100-seed weight was associated with higher seed yield per plant and had the largest contribution towards total divergence. Selection of diverse parents on the basis of seed size seemed to be effective.

Vivek Kumar *et al.* (1999) identified diverse and desirable genotypes in terms of inter cluster distances and mean performance, non-hierarchical clustering approach for seven quantitative characters among 50 chickpea genotype. All genotypes grouped into 7 clusters. The intra cluster distance ranged from 0.00 (cluster II and III) to 1.90 (cluster VI).

Harisatyanarayana and Reddy (2000) estimated genetic divergence among 31 genotypes of chickpea for ten characters. The 31 genotypes were grouped into seven clusters based on the mean performance, genetic divergence and clustering pattern. The intercluster D^2 value ranged from 22.6 to 36.8.

Sivakumar and Muthiah (2001) studied genetic divergence among 126 chickpea cultivars by Mahalanobis D^2 statistics and grouped into seven clusters. The highest divergence observed in clusters IV and VII while the lowest was between cluster IV and V. The intercluster distance varied from 0 to 2.99. Cluster III included Kabuli types quite

diverse from the desi types and this was again confirmed in the canonical root square analysis.

Dharshan Lal *et al.* (2001) conducted a study to determine the genetic diversity among chickpea genotypes for future use in hybridization programme for yield improvement. The average cluster means for 11 characters carried out.

Nimbalkar and Harer (2001) recorded genetic divergence in 40 genotypes of chickpea from 7 countries (32 indigenous and 8 exotic). The genotypes were clusters into 16 groups. Out of these, 10 clusters were monogenetic. The D^2 values between all possible pair of 40 genotypes ranged between 12.62 and 3979.93. There was no parallelism between genetic divergence and geographical distribution of genotypes, which was revealed by grouping of genotypes from different origins into same cluster vice-versa. The 32 indigenous genotypes were spread into 13 and 8 exotics were spread into 8 distinct clusters. Variance of cluster means indicated pod per plant followed by plant height, and 100-grain weight were main characters contributing to the genetic divergence.

Jeena and Arora (2002) determined genetic divergence of 36 chickpea genotypes in terms of 16 characters including seed yield following Tocher's method, which described by Rao (1952) based on Mahalanobis statistics. Genotypes of similar origin in different cluster suggested the influence of human intervention and eco-geographical distribution. Excluding single genotype cluster, the other entire clusters were heterogeneous. A defined relationship between genetic diversity and geographical origin was not established.

Narendra Singh (2002) analysed 300 kabuli chickpea accessions diverse geographical background for 7 distinct traits and

grouped into 10 clusters. The average distances of cluster member from cluster centroids ranged from 1.563 to 2.290 it was maximum in cluster I and minimum in cluster III. Therefore, utilizing the genotypes from these cluster in hybridization programme, the putative transgressive segregates can be obtained. There was no parallelism between genetic and geographical diversity.

Abdul *et al.* (2003) evaluated thirty genotypes of chickpea for 10 quantitative traits using multivariate technical cluster analysis also confirmed the findings of principal component analysis. The promising accessions may be chosen from particular groups or cluster for hybridization programmes. Clusters with superior agronomic types identified may be exploited for genetic potential to transfer the desirable genes to improve yield potential of the crop.

Dasgupta and Singh (2003) evaluated genetic diversity among 23 advanced lines of chickpea and 2 control cultivars using Mahalanobis D^2 distance statistics and seed storage protein profile banding by SDS - PAGE. Data on 10 characters recorded. The lines were classified into 8 clusters based on D^2 values.

Mardi *et al.* (2003) evaluated 418 desi chickpea landraces for genetic diversity in yield and yield components factor analysis showed that yield components, and the size of seeds and pods contributed approximately 50 per cent to the total variation.

Kashyap and Rastogi (2003) studied genetic divergence for seed yield and its component in 60 germplasm accession. The analysis of variance revealed significant difference among the genotypes for each character under study. The genotypes were grouped into 6 clusters and

the maximum intra-cluster distance was observed in cluster I comprising 14 genotypes. Cluster III and VI were identified as genetically divergent.

Yadava *et al.* (2003) evaluated twenty nine newly developed chickpea genotypes for genetic diversity for consumer's quality traits. Seven clusters were obtained, among which cultivars in cluster V and VII were more divergent than others. On and soaked 100-seed weight, seed volume after soaking, hydration capacity and swelling capacity contributed more to diversity than other traits.

Raval and Dobariya (2004) determined the genetic divergence of 52 chickpea genotype and grouped into 15 clusters. Enormous diversity was observed as indicated by wide range of D^2 values. No parallelism was observed between geographical distribution and genetic diversity. The different cluster was superior based on seed yield per plant, days to 50 per cent flowering, days to maturity, plant height, plant spread, number of primary and secondary branches per plant, number of pods per plant, biological yield per plant, number of sees per pod, 100-seed weight, harvest index and protein content. It will be fruitful to intercross the genotypes from cluster X, XIII and I with those of cluster XIV and XII for the generation of promising derivatives and wide spectrum genetic variability for yield improvement in chickpea.

Kanaka Durga *et al.* (2005) revealed significant differences among 132 chickpea genotype for yield and its component characters using D^2 statistic analysis and were grouped into nine clusters. Crossing the genotypes from clusters I and VIII may lead to maximum diversity in the segregating populations and development of high yielding varieties.

Shrivastava *et al.* (2005) evaluated two hundred ten germplasm lines and three checks for 9 yield and other related traits. On

the basis of data on genetic divergence and mean performance of yield and other traits. Five divers and superior genotypes were selected. Therefore, these genotypes may be involved in multiple crossing programmes to recover transgressive segregants.

Jeena *et al.* (2005) evaluated 80 chickpea genotypes collected from different geographical areas for eighteen characters using D^2 statistic analysis and grouped into eleven clusters. No definite relationship was observed between genetic diversity and geographical distribution. Based on intercluster distances, crossing between BGM-419 and KPG-33 are expected to produce a broad spectrum of variability in segregating generation to isolate transgressive segregants for yield and its components.

Patel *et al.* (2006) grouped 24 genotypes into 4 clusters. Inter-cluster mean revealed the difference in the value for particular character between the groups indicating importance of particular cluster for choosing desirable parents for hybridization programme. The contribution towards genetic divergence by different trait showed that days to 100% flowering and 100 seed weight contributed maximum towards genetic divergence.

Vijay Prakash (2006) studied genetic divergence in 81 genotypes using data on eight characters using D^2 statistics and grouped into 10 clusters. The character grain yield per plant, 100 seed weight and seed per pod were major contributors towards genetic divergence.

2.3 Contribution of characters towards genetic divergence

Katiyar (1978) reported that the leaf area per plant, relative leaf weight and number of pods per plant were important for divergence.

Dumbre and Deshmukh (1984) found that seed size, yield per plant and duration were the most important characters contributing towards genetic diversity.

Garoosi and Vojdani (1993) found that number of seeds per pod, 100-seed weight, flowering duration and flower colour were the best characters for type differentiation.

Rao and Singh (1994) observed that the component days to flowering, days to maturity, pods per plant and 100-seed weight accounted for maximum divergence.

Jethava *et al.* (1996) reported that seed yield per plant, number of pods per plant and 100-seed weight contributed most to genetic diversity.

Rao and Jain (1996) analyzed percentage contribution of individual characters towards genetic diversity and revealed that 100 seed weight and plant height was the major character contributing to genetic diversity in the chickpea.

Arun Kumar *et al.* (1998) found that days to 50 per cent flowering, maturity, biological yield per plant and harvest index contributed nothing towards genetic divergence. On the other hand the character internode length (31.62 %) followed by 100 seed weight (26.47 %) and protein content (25 %) contributed maximum towards genetic divergence. The remaining five characters contributed very low to this parameter.

Raje and Khare (1999) found that moderate 100 seed weight was associated with higher seed yield per plant and had the largest contribution towards total divergence. Selection of diverse parents on the basis of seed size seemed to be effective.

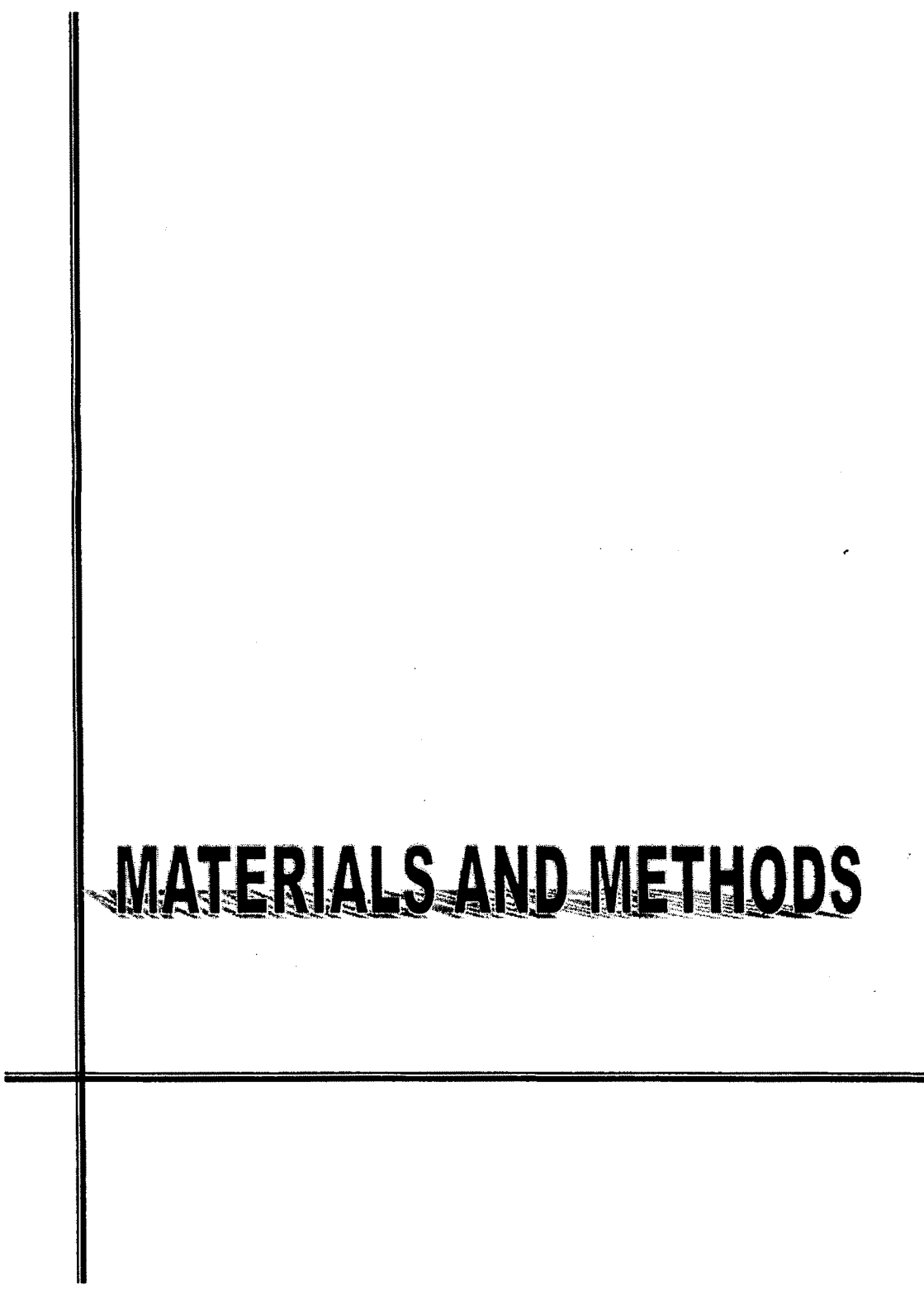
Nimbalkar and Harer (2001) reported that variance of cluster means indicated pod per plant followed by plant height and 100 grain weight were main characters contributing to the genetic divergence.

Mardi *et al.* (2003) showed that yield components the size of seeds and pods contributed approximately 50 per cent to the total variation.

Yadava *et al.* (2003) reported that soaked 100-seed weight, seed volume after soaking hydration capacity and swelling capacity contributed more to diversity than other traits.

Patel *et al.* (2006) showed that days to 100 per cent flowering and 100 seed weight contributed maximum towards genetic divergence.

Vijay Prakash (2006) reported that characters grain yield per plant, 100 seed weight and seed per pod were major contributors towards genetic divergence.



MATERIALS AND METHODS

Chapter III

MATERIALS AND METHODS

3.1 Experimental materials

The experimental material for the present investigation consisting of ninety one germplasm lines including four checks of chickpea collected from ARS, Badnapur and ICRISAT, Hyderabad were sown during Rabi 2006-2007. Details have been given in Table 1.

Table 1 : Name and sources of the germplasm lines.

Sr. No. Name		Source	Remark
1	2	3	4
1	B-24	ARS, Badnapur	Deshi
2	B-27	ARS, Badnapur	Deshi
3	B-29	ARS, Badnapur	Deshi
4	B-30	ARS, Badnapur	Deshi
5	B-31	ARS, Badnapur	Deshi
6	B-32	ARS, Badnapur	Deshi
7	B-34	ARS, Badnapur	Deshi
8	B-46	ARS, Badnapur	Deshi
9	B-48	ARS, Badnapur	Deshi
10	B-49	ARS, Badnapur	Deshi
11	B-47	ARS, Badnapur	Deshi
12	B-50	ARS, Badnapur	Deshi
13	B-51	ARS, Badnapur	Deshi
14	BCP-91	ARS, Badnapur	Deshi
15	B-56	ARS, Badnapur	Deshi
16	B-57	ARS, Badnapur	Deshi
17	B-58	ARS, Badnapur	Deshi
18	B-59	ARS, Badnapur	Deshi
19	B-65	ARS, Badnapur	Deshi
20	B-69	ARS, Badnapur	Deshi
21	BCP-97	ARS, Badnapur	Deshi
22	B-609	ARS, Badnapur	Deshi

1	2	3	4
23	B-611	ARS, Badnapur	Deshi
24	B-621	ARS, Badnapur	Deshi
25	B-630	ARS, Badnapur	Deshi
26	B-636	ARS, Badnapur	Deshi
27	B-701	ARS, Badnapur	Deshi
28	B-768	ARS, Badnapur	Deshi
29	BCP-17	ARS, Badnapur	Deshi
30	BCP-36	ARS, Badnapur	Deshi
31	BCP-73	ARS, Badnapur	Deshi
32	BCP-54-1	ARS, Badnapur	Deshi
33	BCP-54-2	ARS, Badnapur	Deshi
34	DG-1	ARS, Badnapur	Deshi
35	G-20	ARS, Badnapur	Deshi
36	G-22	ARS, Badnapur	Deshi
37	G-25	ARS, Badnapur	Deshi
38	G-26	ARS, Badnapur	Deshi
39	G-33	ARS, Badnapur	Deshi
40	G-38	ARS, Badnapur	Kabuli
41	G-40	ARS, Badnapur	Deshi
42	G-41	ARS, Badnapur	Deshi
43	G-42	ARS, Badnapur	Deshi
44	G-44	ARS, Badnapur	Deshi
45	G-45	ARS, Badnapur	Deshi
46	G-57	ARS, Badnapur	Deshi
47	G-63	ARS, Badnapur	Deshi
48	G-64	ARS, Badnapur	Deshi
49	G-70	ARS, Badnapur	Deshi
50	G-72	ARS, Badnapur	Deshi
51	G-73	ARS, Badnapur	Deshi
52	G-74	ARS, Badnapur	Deshi
53	G-77	ARS, Badnapur	Deshi
54	G-78	ARS, Badnapur	Deshi
55	G-79	ARS, Badnapur	Deshi
56	G-80	ARS, Badnapur	Kabuli
57	G-81	ARS, Badnapur	Deshi

1	2	3	4
58	G-82	ARS, Badnapur	Deshi
59	G-83	ARS, Badnapur	Deshi
60	G-84	ARS, Badnapur	Deshi
61	G-85	ARS, Badnapur	Deshi
62	G-87	ARS, Badnapur	Deshi
63	G-88	ARS, Badnapur	Kabuli
64	G-90	ARS, Badnapur	Kabuli
65	G-91	ARS, Badnapur	Kabuli
66	G-92	ARS, Badnapur	Deshi
67	G-94	ARS, Badnapur	Kabuli
68	G-95	ARS, Badnapur	Kabuli
69	GTP-11	ARS, Badnapur	Deshi
70	HP-1	ARS, Badnapur	Deshi
71	L-1	ARS, Badnapur	Deshi
72	L-2	ARS, Badnapur	Deshi
73	L-3	ARS, Badnapur	Deshi
74	L-102	ICRISAT, Hyderabad	Deshi
75	L-104	ICRISAT, Hyderabad	Deshi
76	L-108	ICRISAT, Hyderabad	Deshi
77	L-109	ICRISAT, Hyderabad	Deshi
78	L-111	ICRISAT, Hyderabad	Deshi
79	L-112	ICRISAT, Hyderabad	Deshi
80	L-113	ICRISAT, Hyderabad	Deshi
81	L-201	ICRISAT, Hyderabad	Deshi
82	L-202	ICRISAT, Hyderabad	Deshi
83	L-302	ICRISAT, Hyderabad	Deshi
84	L-303	ICRISAT, Hyderabad	Deshi
85	L-305	ICRISAT, Hyderabad	Deshi
86	L-311	ICRISAT, Hyderabad	Deshi
87	L-313	ICRISAT, Hyderabad	Deshi
88	Annegiri (C)	ICRISAT, Hyderabad	Deshi
89	G-12(C)	ARS, Badnapur	Deshi
90	BDN-9-3 (C)	ARS, Badnapur	Deshi
91	BDNG-797 (C)	ARS, Badnapur	Deshi

3.2 Experimental Details

The experiment was conducted during rabi, 2006-2007 at the Experimental Farm, Department of Agril. Botany, College of Agriculture, Latur. The experimental details are as follows.

Design	:	Augmented Randomized Block Design (Augmented R.B.D.)
Treatments	:	91 (87 germplasm lines + 4 checks)
Block	:	Three
Plot size	:	0.45 x 3.0 m. (one row of 3 m length)
Fertilizer	:	25 kg N + 50 Kg P ₂ O ₅ /ha
Spacing	:	Row to row: 45 cm. Plant to plant: 15 cm.
Date of sowing	:	11 / 10 / 2006

The experiment consisting 87 germplasm lines and four standard checks viz., BDN-9-3, BDNG-797, Annegiri and G-12 was sown in a Augmented Randomized Block Design with three blocks, each block consist of 33 genotypes (29 germplasm lines and 4 check/control lines) The experiment was conducted at experimental farm of Departmental of Agricultural Botany, College of Agriculture, Latur during rabi 2006-2007 under rainfed condition. The sowing was carried out in a single row plot of 3 meter length following the spacing of 45 cm and 15 cm between row to row and plant to plant respectively. The method of sowing was dibbling. One plant per hill maintained by thinning at 15 days after sowing the recommended dose of fertilizer 25 kg N + 50 kg P₂O₅/ha was applied at the time of sowing. All other cultural

practices and plant protection measures were undertaken to maintain the crop health.

3.3 Observations Recorded

Five plants / genotype were selected at random for recording observations on following character in each replication and averages were calculated.

3.3.1 Days to 50 per cent flowering

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

3.3.2 Days to maturity

Number of days required from the date of sowing to the maturity of crop recorded as days to maturity.

3.3.3 Plant height (cm)

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

3.3.4 Number of primary branches per plant

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

3.3.5 Number of secondary branches per plant

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

3.3.6 Number of pods per plant

The total numbers of pods were counted from five plants at maturity and average was worked out.

3.3.7 Number of seeds per pod

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

3.3.8 Number of seed per plant

Total number of seeds of five plants calculated and average was worked out.

3.3.9 100-seed weight (g)

It was recorded by weighing randomly selected 100-seeds.

3.3.10 Harvest index (%)

It's the ratio of economical yield to biological yield and expressed as percentage.

$$\text{Harvest index} = \frac{\text{Economical yield}}{\text{Biological yield}} \times 100$$

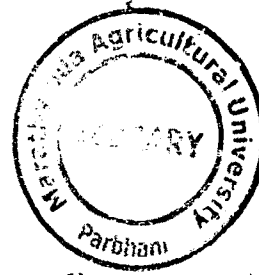
Whereas,

Biological yield = seed yield + dry matter

Economical yield = seed yield per plant.

3.3.11 Seed yield per plant (g)

The weight of seed obtained as a mean from the seed of the five selected plants.



3.4 Statistical methods

3.4.1 Analysis of variance

Experiment is conducted according to Augmented Randomized Block Design as propounded by Federer (1956) where whole field is divided distinctly into b blocks. The randomization is done such that all the checks and a part of test genotypes fall only once, thus only checks were replicated and test varieties are non-replicated. The advantage of such stratification (block formation) of area is to reduce the EMS by apportioning the block effect.

The skeletal of ANOVA for Augmented R.B.D.

Source of variation	d f	SS	MSS	F
Block	$b-1$	bSS	bMS	bMS/EMS
Entries	$e-1$	eSS	eMS	eMS/EMS
Checks	$c-1$	cSS	cMS	cMS / EMS
Varieties	$v-1$	vSS	vMS	vMS /EMS
Check vs. Varieties	1	$csSS$	$cvMS$	$cvMS/EMS$
Error	$(c-1)(b-1)=6$	ESS	EMS	--

The different component of ANOVA can be calculated as follow. However adjustment of means of varieties must be done before ANOVA with help of following effects.

T 5226

- 1) **Block effects** $(b_j) = 1/c (T_{bj} - \bar{C} - Tvb_j)$ ($j=1$ to b)

Where,

- c = Number of check
 Tb_j = Total of j^{th} block for the character
 C = Sum of mean of check in all block
 Tvb_j = Total of varieties in j^{th} block
 J = Number of block i.e. 1 to b

2. Mean effect (m) = $1/e (GT - (b-1) \bar{C} - \sum_1^n n_j b_j)$

Where,

- e = total number of entries
 GT = Grand total of all entries.
 b = Number of block
 $\bar{C}$ = Sum of mean of check in all block
 n_j = The number of v occurring in j^{th} block
 if n_j is the same in all block then $m = 1/e (GT - (b-1) \bar{C})$

3. Check effect

$$(C_i) = \bar{C}_i - m \quad (i = 1 \text{ to } c)$$

Where,

$$\bar{C}_i = \text{mean of } i^{\text{th}} \text{ check in all replication}$$

4. Adjusted mean (v_i') and genotypic effect (v_i'') are computed as under

a) Adjusted mean

$$(v_i') = v_i - b_j$$

Where,

- v_i = unadjusted mean
 b_j = Block effect of the block where v_i falls in

b) Genotypic effect

$$v_i'' = v_i' - m$$

Where,

V_i'' = Genotypic effect

V_i' = Adjusted mean

m = Mean effect

Genotypic effect is utilized for the further calculation of error sum of square.

5. Standard error

Following four types of standard error calculated as following

a) SE d_1 (between any two check mean) i.e. $C_i - C_j$

$$= \frac{\sqrt{2 \text{ EMS}}}{b}$$

Where,

EMS = Error means square

b = number of block

b) S.E. d_2 (between any two means of test varieties i.e. $B_i V_i - B_j V_j$)

$$= \sqrt{2 \text{ EMS}}$$

c) S.E. d_3 (between any two entries of same block) i.e. $B_i V_i - B_j V_j$

$$= \frac{\sqrt{2 \text{ EMS} (1 + \frac{1}{c})}}{c}$$

Where,

c = Number of check

d) S.E. d_4 (between mean of check and a test variety i.e. $C_i - V_j$)

$$= \sqrt{2 \text{ EMS } \left(1 + \frac{1}{b} + \frac{1}{c} + \frac{1}{bc}\right)}$$

C.D. is then calculated using these SEds x t at 5% or 1% level (d.f.=6) i.e. 2.447 as the case may be.

3.4.2 Estimation of mean and range

For each character, the mean values were worked out by dividing the total by corresponding number of observations.

$$\bar{X} = \frac{1}{n} \sum_{i=1}^n (X_i)$$

Where,

$\bar{X}$ = Mean of character

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

n = Number of observations.

The lowest and highest values of mean of each character represented the range.

3.4.3 Estimation of component of variance

The software package performs the analysis of data generated from block design. The treatment sum of square is portioned into different component of interest viz., 1) among the test material 2) among control treatment 3) among the test material and control treatment is obtained by maximizing the efficiency per observation for making test vs. control (s) comparison. The package generate randomized layout of an

Augmented randomized complete block (RCB) design and Augmented complete block design with equal and unequal block size.

In this design lack of replication is compensated by mean adjustment (Pimentel-Gomes, 1987). In this case analysis of variance is performed with adjusted means of the regular treatment, derived from the analysis of each Augmented R.B.D., considering treatment effect fixed. The package perform the analysis of variance by Restriction maximum likelihood method (REML) (Corbeil and Searle , 1976)

In mixed model analysis of variance can be represented for a vector of observation y as,

$$Y = X\mu + U\beta + e$$

Where,

μ = is a vector of all fixed effect, X and U are representative of design matrices and e is vector of residual error of term having variance δ^2 their and the different variance of the element of β are the variances of component of model.

$$\text{Environmental variance } (\delta^2 e) = \text{EMS}$$

$$\text{Phenotypic variance } (\delta^2 p) = \delta^2 g + \delta^2 e$$

Where,

$$\text{EMS} = \text{Error mean sum of square}$$

$$\delta^2 g = \text{genotypic variance.}$$

$$\delta^2 p = \text{phenotypic variance.}$$

3.4.4 Estimation of coefficient of variation

The genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated by following formula (Burton, 1952)

i) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\delta^2 g}}{\bar{X}} \times 100$$

Where,

$\delta^2 g$ = genotypic variance.

$\bar{X}$ = Mean of character

ii) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\delta^2 p}}{\bar{X}} \times 100$$

Where,

$\delta^2 p$ = phenotypic variance.

$\bar{X}$ = Mean of character

3.4.5 Estimation of heritability

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

$$h^2(b s) = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Where,

$\delta^2 g$ = genotypic variance.

$\delta^2 p$ = phenotypic variance.

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

Low heritability	-	5-10%
Medium heritability	-	10-30%
High heritability	-	>30 %

3.4.6 Genetic advance (G A)

The genetic advance at 5 percent selection intensity was calculated for each character using the formula suggested by Johnson *et al.* (1955).

$$1. \quad \text{Genetic advance (G A)} = K. \delta p. h^2$$

Where,

K = Selection differential at 5per cent level i.e., 2.06.

δp = phenotypic standard deviation

h^2 = heritability

The expected genetic advance in percentage of mean was calculated as,

$$2. \quad \text{EGA} = \frac{\text{G A}}{\bar{X}} \times 100$$

Where,

EGA = Expected genetic advance

GA = Genetic advance

$\bar{X}$ = General mean of character

3.5 Genetic divergence

D^2 analysis

The analysis of divergence was carried out by D^2 statistics proposed by Mahalanobis (1936), as described by Rao (1952). Analysis

of variance for individual character studied was worked out as per Augmented RBD analysis to test the significance of differences among the genotypes. The character showing significant differences were only used for further analysis of D^2 statistics.

3.5.1 Wilk's criteria

After testing the differences among the population for the eleven characters, a simultaneous test of significant of differences between the mean value of number of correlated variables with regard to pooled effect of character considered together was carried out using Wilk's criteria 'A' (Wilk's 1932) which was estimated using the relationship.

$$A = \frac{(E)}{(E + V)}$$

Where,

E = the determinant of the experiment error sum of squares and sum of products of matrix and,

E + V = the determinant of experimental error sum of squares and sum of product matrix,

Significance of wilk's criteria (A) was tested by X^2 as :

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

Where,

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

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

= total number of observation -1

P = Number of character

q = k-1

k = Number of genotypes.

Significant of values were tested by taking D^2 values as X^2 value and is tested against tabulated value of X^2 for 'p' degree of freedom.

Where,

p = number of characters considered,

Wilk' criteria, $X^2_{pq} = V = 6830.92$ for 990 d.f. and further analysis was carried out after confirming significance.

3.5.2 Mahalanobis generalized distance (D^2)

The generalized distance between any two populations is defined as

$$D^2 = \sum \sum \lambda_{ij} \delta_i \cdot \delta_j$$

Where,

δ_i = Reciprocal matrix to the common dispersion matrix

δ_j = Difference between the mean value of the two populations for the i^{th} character

This quantity is determined by D^2 statistic as

$$D^2 = \sum \sum \lambda_{sij} \delta_i \cdot \delta_j$$

Where,

S_{ij} , δ_i , δ_j are the sample estimates of λ_{ij} , δ_i and δ_j respectively, since this formula for computation requires inversion of seventh order determinant and then evaluation of 7 (7+1) terms, whose sum is D^2 .

3.5.3 Computation of D^2 values

For each combination, mean deviation i.e.

$$Y_i^{-1} - Y_i^{-2}$$

Where,

$i = 1, 2 \dots p$ was computed and the D^2 was calculated as sum of squares of these deviation i.e. $\sum [Y_i^{-1} - Y_i^{-2}]^2$

3.5.4 Determination of population constellations

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

A simple method suggested by Tocher (Chaudhary and Singh, 1977) for cluster formation is to sort with two closely related groups and final third group which has the smaller average D^2 value from the first two. Similarly the fourth group is chosen to have the smaller average D^2 value from the first three and so on. While proceeding further from cluster formation, if at any stage, the average D^2 value of a group appears to be high than those already listed, then this group does not fit in that format group and taken out of that cluster. The varieties included in the first cluster are then omitted and the rest are treated similarly to form next cluster.

3.5.5 Average intra cluster distances

The intra cluster distance were calculated as

$$\frac{\sum D_i^2}{n}$$

Where,

D_i^2 = sum of distances between all possible combinations.

n = Population included in cluster.

3.5.6 Average intercluster distances

The procedure followed for calculating intercluster distances was first to measure the distances between cluster I and II, between I and III, between I and IV and so on. Likewise the clusters were taken one by

one and the distances between other clusters were calculated. The average intercluster distance were then calculated as,

$$\frac{\sum D_i^2}{n_i n_j}$$

Where,

n_i = Number of population in cluster 'i'

n_j = Number of population in cluster 'j'

RESULTS

CHAPTER – IV

RESULTS

The results obtained in the investigation are presented in this chapter under the following sub-headings.

1. Analysis of variance
2. Mean performance
3. Genetic parameters
 - i) Variance component
 - ii) Estimates of variability parameters (GCV, PCV).
 - iii) Heritability.
 - iv) Genetic advance
 - v) Genetic advance as percent of mean (expected GA)
4. Genetic divergence

4.1 Analysis of variance

Analysis of variance was worked out to assess the variation in germplasm lines for eleven characters. The significance was tested with application of 'F' test. Analysis of variance for eleven characters consisting of block mean squares, entries mean squares, check mean squares, varieties mean square, check vs. varieties mean squares and error mean squares. The analysis of variances showed differences among block, entries, check, varieties and check vs. varieties for all characters. This indicate significant differences exist among the germplasm lines for yield and yield contributing characters (Table- 2).

Table 2 : Augmented RBD ANOVA for different character studied in chickpea.

Source of variation	d. f.	Days to 50 % flowering	Days to maturity	Number of primary branches per plant	Number of secondary branches per plant	Plant height (cm)	Number of pods per plant	Number of seeds per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)
Mean Sum of Square												
Block	2	9.7378*	9.1408	3.7814*	3.7948*	14.8149*	0.7039	1.7040	0.0122*	6.7934*	0.8461	1.5169*
Entries	90	56.3093**	97.9254**	4.6636*	2.8674*	21.4453**	73.9052**	72.8627*	0.0917**	40.0771**	54.3140**	4.1771**
Checks	3	8.8254*	21.6388**	5.8319*	3.9897*	52.8036**	310.1422**	284.5277**	0.0788**	47.8163**	96.5131**	6.0141**
Varities	86	57.9281**	98.4410**	3.9439*	2.8611*	20.4524**	64.5995**	64.9735*	0.0930**	40.2378**	48.8342**	4.1071**
Checks vs. varieties	1	68.3556**	282.4452**	8.3088*	0.0441*	12.7546*	165.4848**	116.3409**	0.0146**	5.0326*	399.0269**	4.6909**
Error	6	1.4709	2.58	0.6817	0.5223	1.17	2.79	4.88	0.0010	0.6286	2.1907	0.2249

* Significant at 5 percent level

** significant at 1 percent level

4.2 Mean performance and range of variability

The mean performance of germplasm line under study for eleven characters is given in Table 3, while estimates of range are given in Table 4.

4.2.1 Days to 50 per cent flowering

The days to 50 per cent flowering ranged from 32.25 to 76.25 days with the mean of 44.05 in case of germplasm lines and from 40.00 to 43.00 days in checks with mean of 41.50. Among the lines G-20 (32.25), B-24 (32.25), G-79 (32.25), DG-1 (35.25) GTP-11 (35.50), HP-1 (35.50) and L-108 (35.50) were showed early days to 50 per cent flowering. However, a higher days to 50 per cent flowering was observed in germplasm line G-63 (76.25), G-78 (69.25) and G-83 (68.25). Genotypes viz., B-24, B-701, DG-1, G-20, G-79, GTP-11, HP-1, L-108 were significantly superior in days to early flowering over check Annegiri. Twenty-two genotypes recorded more days to 50 percent flowering than mean performance.

4.2.2 Days to maturity

The days to maturity ranged from 59.83 to 115.58 days with mean of 80.75 and 72 to 78.33 days with mean of 75.58 in case of germplasm lines and checks respectively. Among the lines B-49 (59.83), G-88 (60.58), HP-1 (67.58), B-24 (67.83), DG-1 (68.58) and G-38 (68.58) showed early maturity while late maturity was observed in G-63 (115.58), L313 (109.58), BCP-17 (94.83), L-111 (96.58) and L-303 (92.58). Genotypes B-49 and G-88 were significantly superior in days to early maturity over the check BDN-9-3. Thirty-six genotypes recorded more days to maturity than mean performance.

Table 3 : Mean performance of germplasm lines (adjusted mean) and checks for yield and yield contributing characters.

Sr. No.	Genotype	Days to 50 % flowering	Days to maturity	Number of primary branches per plant	Number of secondary branches per plant	Plant Height (cm)	Number of pods per plant	Number of seeds per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13
1	B-24	32.25	67.83	4.56	3.48	42.93	28.62	30.47	1.08	20.58	73.42	5.94
2	B-27	41.25	79.83	5.17	3.78	39.53	42.22	43.75	1.04	17.28	74.57	7.40
3	B-29	37.25	77.83	4.77	4.18	33.33	32.62	33.27	1.04	18.18	73.16	6.00
4	B-30	41.25	87.83	5.37	3.38	36.53	33.42	34.87	1.00	18.88	76.50	6.38
5	B-31	41.25	83.83	3.37	3.78	32.13	24.62	24.67	1.04	15.38	72.50	5.44
6	B-32	56.25	96.83	7.17	5.18	42.13	46.47	47.07	1.00	13.78	77.18	6.63
7	B-34	47.25	91.83	4.17	4.58	33.88	32.42	33.67	1.04	14.58	70.81	4.80
8	B-46	40.25	87.83	2.37	2.08	36.73	17.42	18.87	1.04	14.88	75.06	2.62
9	B-48	37.25	77.83	3.17	2.18	39.53	22.62	27.47	1.28	14.98	63.81	4.20
10	B-49	37.25	59.83	4.07	1.78	35.53	15.02	27.27	1.08	24.78	74.14	6.83
11	B-47	42.25	85.83	5.77	2.08	48.93	18.42	18.87	1.00	14.78	54.65	2.75
12	B-50	43.25	78.83	3.77	2.78	38.93	17.62	18.67	1.06	28.48	77.27	5.36
13	B-51	42.25	75.83	5.17	2.78	35.73	17.42	18.27	1.08	28.28	66.68	5.21
14	BCP-91	44.50	85.58	3.62	3.70	35.03	28.85	29.82	1.04	29.24	67.71	7.20
15	B-56	39.25	78.83	3.36	1.58	33.73	8.42	10.46	1.04	19.58	62.65	2.07
16	B-57	41.25	79.83	6.07	2.18	40.93	16.62	17.87	1.04	12.18	48.63	2.01
17	B-58	39.25	70.83	3.47	2.58	39.33	19.22	20.87	1.00	34.08	74.30	6.54
18	B-59	43.25	75.83	3.77	2.38	36.73	22.62	23.47	1.04	26.58	75.46	6.03
19	B-65	39.25	80.83	5.47	4.38	40.73	33.02	34.27	1.04	18.18	68.24	6.07
20	B-69	40.25	79.83	7.07	3.18	40.33	35.02	36.27	1.08	16.38	75.40	5.82
21	BCP-97	41.25	86.83	6.47	2.58	35.13	18.47	20.27	1.08	23.68	59.36	4.39
22	B-609	41.25	74.83	2.77	2.78	40.73	13.42	15.47	1.12	16.28	58.74	2.36
23	B-611	51.25	89.83	3.27	3.38	42.73	24.55	26.67	1.04	27.28	77.27	7.35

1	2	3	4	5	6	7	8	9	10	11	12	13
24	B-621	43.25	80.83	4.87	3.18	36.33	22.42	23.07	1.08	27.88	78.68	6.49
25	B-630	43.25	87.83	7.37	4.58	38.93	32.02	32.27	1.04	18.76	73.75	6.07
26	B-636	55.25	93.83	4.97	3.28	47.93	28.42	29.57	1.12	25.98	75.07	7.42
27	B-701	35.25	69.83	5.77	3.18	32.13	30.62	31.67	1.00	23.18	73.61	7.15
28	B-768	41.25	78.83	6.17	6.38	33.93	37.02	39.27	1.04	28.58	71.82	10.64
29	BCP-17	57.25	94.83	4.17	4.58	40.53	19.02	20.27	1.04	35.48	61.88	6.81
30	BCP-36	47.25	81.83	5.57	1.98	39.73	15.82	17.67	1.12	25.28	70.59	4.51
31	BCP-73	52.25	91.58	6.62	5.71	41.43	35.77	38.42	1.08	16.45	69.96	5.77
32	BCP-54-1	42.25	85.58	5.02	2.31	36.63	17.47	20.42	1.08	27.75	71.50	4.87
33	BCP-54-2	42.25	72.58	5.62	2.11	39.13	20.27	22.62	1.28	28.05	71.64	6.23
34	DG-1	35.25	68.58	6.22	1.51	34.23	28.47	31.62	1.02	12.85	68.78	3.95
35	G-20	32.25	70.58	3.22	2.41	32.03	24.27	27.22	1.07	18.45	78.75	4.57
36	G-22	42.25	78.58	5.02	3.71	42.63	22.77	26.02	1.12	20.25	67.64	5.17
37	G-25	44.25	86.58	6.82	5.21	36.03	25.27	27.82	0.99	25.65	62.15	6.44
38	G-26	42.25	81.58	2.62	1.51	33.83	9.07	11.22	1.08	23.55	76.63	2.66
39	G-33	51.25	92.58	9.02	2.41	32.53	18.27	21.02	1.04	17.15	67.72	3.18
40	G-38	39.25	68.58	4.62	2.31	39.63	19.47	22.82	1.00	36.15	74.12	8.29
41	G-40	42.25	79.58	3.42	2.71	46.63	23.27	32.92	1.39	23.75	71.83	7.63
42	G-41	39.25	73.58	5.32	1.11	36.63	13.67	14.62	1.03	34.75	68.97	5.00
43	G-42	44.25	79.58	3.82	3.31	38.23	19.47	23.42	1.04	26.15	72.11	8.78
44	G-44	42.25	77.58	5.22	2.41	47.83	24.06	26.02	1.12	22.05	71.19	5.62
45	G-45	36.25	72.58	3.42	3.31	39.23	22.67	26.22	1.11	18.25	74.37	4.69
46	G-57	43.25	84.58	3.82	2.31	32.63	16.67	17.82	1.04	21.65	62.95	3.66
47	G-63	76.25	115.58	7.42	8.11	40.53	47.22	49.02	1.04	27.35	70.37	12.46
48	G-64	42.25	77.58	5.42	3.51	31.23	31.27	34.22	1.08	32.65	78.68	10.83
49	G-70	42.25	76.58	4.83	2.31	34.43	22.67	25.22	1.00	21.02	68.00	5.21
50	G-72	44.25	80.58	3.52	1.71	31.08	15.47	18.02	1.08	21.15	68.85	3.38
51	G-73	42.25	81.58	7.42	3.61	31.43	31.47	35.42	1.08	20.65	78.39	7.12
52	G-74	48.25	75.58	4.52	3.71	34.53	31.67	34.22	1.00	19.35	63.30	6.04
53	G-77	41.25	74.58	3.82	2.71	30.43	24.87	26.82	1.00	18.55	76.84	5.59

1	2	3	4	5	6	7	8	9	10	11	12	13
54	G-78	49.25	79.58	5.42	6.11	39.23	34.47	40.62	1.16	19.65	70.68	7.75
55	G-79	32.25	77.58	4.22	2.31	32.03	25.87	36.22	1.56	16.75	75.87	5.89
56	G-80	37.25	80.58	6.42	2.71	36.63	24.47	25.82	1.00	36.85	75.21	8.95
57	G-81	51.25	76.58	3.62	2.71	32.23	20.47	22.02	1.08	24.25	73.75	5.25
58	G-82	40.25	88.58	4.82	2.30	41.23	24.07	25.82	1.00	13.15	61.96	3.17
59	G-83	48.25	81.58	6.82	4.11	38.43	32.67	34.42	1.04	16.75	74.49	5.61
60	G-84	39.50	79.58	3.81	3.41	31.03	31.92	33.72	1.00	20.08	72.25	6.45
61	G-85	42.50	73.58	4.61	2.61	39.23	11.72	15.12	1.26	29.78	77.58	4.53
62	G-87	48.50	87.58	5.61	2.51	43.63	19.52	22.12	1.04	27.58	73.85	5.36
63	G-88	43.50	60.58	2.82	2.21	36.78	13.27	14.52	1.04	27.58	64.68	3.59
64	G-90	36.50	81.58	6.22	2.81	38.23	25.72	28.52	1.08	29.48	75.11	7.40
65	G-91	48.50	79.58	3.82	5.91	41.63	30.72	31.72	1.00	20.38	70.32	6.52
66	G-92	43.50	71.58	4.72	3.91	42.78	27.02	31.12	1.20	22.58	65.68	6.01
67	G-94	43.50	85.58	6.22	2.91	36.23	21.92	24.52	1.08	33.78	76.33	7.42
68	G-95	40.50	84.58	8.22	2.51	43.63	25.02	26.12	1.04	38.18	79.68	10.11
69	GTP-11	35.50	69.58	4.12	4.71	31.43	23.12	29.12	1.12	12.28	69.96	3.56
70	HP-1	35.50	67.58	5.82	2.51	32.43	22.32	26.92	1.28	15.98	74.72	4.30
71	L-1	39.50	74.58	3.42	3.91	38.83	26.92	27.72	1.04	25.58	71.32	6.89
72	L-2	46.50	96.58	4.22	3.61	43.83	32.92	35.52	1.08	27.52	78.88	9.40
73	L-3	50.50	90.58	2.82	2.61	38.03	19.82	24.72	1.08	16.52	67.54	3.19
74	L-102	58.50	98.58	3.22	2.71	35.23	24.72	25.11	1.00	14.75	70.70	3.60
75	L-104	42.50	79.58	4.42	2.91	32.43	24.92	25.52	1.04	17.18	71.15	4.24
76	L-108	35.50	79.58	5.12	5.51	31.23	30.32	32.52	1.08	18.68	60.79	6.05
77	L-109	43.50	85.58	4.22	2.61	40.23	15.92	17.52	1.04	16.98	54.60	2.60
78	L-111	56.50	96.58	5.42	4.61	39.36	37.72	38.12	1.00	19.88	73.68	7.10
79	L-112	40.50	74.58	5.62	6.61	46.03	36.92	38.12	1.00	22.58	68.61	8.39
80	L-113	44.50	79.58	3.42	7.61	34.83	34.92	39.92	1.24	15.38	69.60	5.73
81	L-201	38.50	79.58	4.22	2.51	30.23	27.12	28.52	1.00	17.78	62.30	4.79
82	L-202	41.50	77.58	3.62	2.51	27.43	21.72	24.12	1.04	16.28	70.50	3.50

1	2	3	4	5	6	7	8	9	10	11	12	13
83	L-302	44.50	77.58	5.22	3.31	35.83	26.52	29.52	1.00	17.48	68.34	5.15
84	L-303	48.50	92.58	7.42	7.51	41.43	40.92	41.52	1.04	17.28	70.68	7.13
85	L-305	46.50	78.58	3.42	2.51	40.23	24.72	26.72	1.00	15.78	65.50	3.85
86	L-311	46.50	98.58	4.12	2.21	40.23	24.72	26.72	1.20	15.78	65.50	3.85
87	L-313	56.50	109.58	5.42	8.61	34.83	39.12	42.52	1.04	16.98	71.44	6.68
88	Annegiri(C)	40.00	76.66	4.33	2.63	40.80	19.47	21.33	1.08	28.00	76.68	5.45
89	G-12(C)	40.67	78.33	5.40	2.96	38.80	25.47	27.60	1.00	22.57	76.30	5.70
90	BDN-9-3 (C)	43.00	72.00	6.93	5.60	34.40	43.40	44.40	1.04	19.13	77.28	6.50
91	BDNG-797 (C)	42.33	75.33	6.30	3.69	31.53	29.53	31.13	1.12	20.00	71.68	5.91
Mean		43.85	80.37	4.85	3.40	37.69	25.67	27.91	1.08	21.51	71.19	5.63

Comparison

Ci-Cj	S.E. $\pm$	0.5717	0.7571	0.38.92	0.3406	0.5099	0.7874	1.0413	0.0149	0.3737	0.6978	0.2236
	C.D. at 5%	1.3988	1.8526	0.9533	0.8336	1.2477	1.9267	2.5482	0.0364	0.9145	1.7073	0.5470
Bivi-Bivj	S.E. $\pm$	1.9176	0.2539	1.3054	1.1426	1.7102	2.6410	3.4928	0.05	1.2535	2.3402	0.7498
	C.D. at 5%	4.6920	0.6213	3.1942	2.7961	4.1850	6.4625	8.5470	0.1224	3.0675	5.7266	1.8347
Bivi-Bjvj	S.E. $\pm$	1.7151	2.27	1.1676	1.0220	1.5297	2.3622	3.1240	0.0447	1.1212	2.0932	0.6706
	C.D. at 5%	4.1967	5.5587	2.8571	2.5009	3.7431	5.7803	7.6446	0.1094	2.7436	5.1220	1.6413
Ci-Vj	S.E. $\pm$	1.5625	2.069	1.0637	0.9311	1.3936	2.1520	2.8461	0.0407	1.0215	1.9069	0.6110
	C.D. at 5%	3.82.33	5.0629	2.6028	2.2784	3.4102	5.2659	6.9646	0.0996	2.4996	4.6664	1.4951

4.2.3 Number of primary branches

The number of primary branches per plant ranged from 2.37 to 9.02 with the mean of 4.85 and from 4.33 to 6.93 with the mean of 5.73 in case of germplasm and check respectively. The highest number of primary branches observed in lines G-33 (9.02) followed by G-95 (8.22), L-303 (7.42), G-63 (7.42) and B-630 (7.37). The lowest number of primary branches observed in B-46 (2.36). Forty-two genotype recorded higher number of primary branches than mean performance.

4.2.4 Number of secondary branches

The number of secondary branches per plant ranged from 1.11 to 8.61 with the mean of 3.40 and 2.63 to 5.60 with the mean of 3.72 in case of germplasm and checks respectively. The highest number of secondary branches observed in lines L-313 (8.61) followed by B-786 (8.38), G-63 (8.11), L-113 (7.60) and L-303, while lowest secondary branches per plant recorded in G-41 (1.11). Genotypes G-63 and G-95 were significantly superior over the check BDN-9-3. Thirty-nine genotypes recorded higher number of secondary branches per plant than mean performance.

4.2.5 Plant height

Plant height ranged from 27.43 to 48.93 cm with the mean of 37.48 cm and 31.58 to 40.8 cm with the mean of 36.38 cm in case of germplasm and checks respectively. The lines L-202 (27.43) followed by G-77 (30.43), L-201 (30.23), and G-72 (31.08) exhibited dwarf plant height. The maximum plant height observed in B-47 (48.93) followed by

B-636 (47.93) and G-44 (47.83). Genotypes viz., B-47, B-636, G-40, G-44 and L-112 were significantly superior over the check Annegiri. Forty-five genotypes showed more height than the mean performance.

4.2.6 Number of pods per plant

Number of pods ranged from 8.42 to 47.22 with the mean of 25.51 and 19.47 to 43.40 with the mean value of 29.46 in case of germplasm and checks respectively. The maximum number of pods per plant observed in line G-63 (47.22) followed by B-32 (46.47), B-27 (42.21), L-303 (40.91), L-313 (39.12), L-111 (37.72), and B-768 (37.02). However, minimum number of pods per plant recorded in B-56 (8.42). Thirty-five genotypes recorded the high number of pods per plant as compare to mean.

4.2.7. Number of seeds per plant

Number of seeds per plants ranged from 10.47 to 49.02 with the mean of 27.80 and from 21.33 to 44.4 with the mean of 31.11 in the case of germplasm and checks respectively. The maximum number of seeds per plant recorded in G-63 (49.02) followed by B-32 (47.07), B-27 (43.75), L-303 (41.56) and G-78 (40.62). However, minimum number of seed per plant recorded in B-56 (10.47). Thirty-nine genotypes recorded more number of seed per plant than mean performance.

4.2.8 Number of seeds per pod

Number of seeds per pod ranged from 0.998 to 1.56 with the mean of 1.07 and 1.00 to 1.12 with the mean of 1.06 in the case of germplasm lines and check respectively. The highest number of seeds per pod observed in G-79 (1.56) followed by G-40 (1.40), B-48 (1.28),

BCP-54-2 (1.28), HP-1 (1.28) and G-85 (1.26). The minimum number of seed per pod observed in G-25 (0.99), G-38 (1.00) and B-32 (1.00). genotypes. Genotypes viz., B-48, G-40, G-79, G-85, HP-1 and G-95 were significantly superior over the check BDN-G-797. Nine genotypes recorded more number of seeds per pod than the mean performance.

4.2.9 100 seed weight

100 seed weight ranged from 12.18 to 38.18 with the mean of 21.89 and 19.33 to 28.00 with the mean of 22.43 in the case of germplasm and check respectively. The maximum test weight recorded in line G-95 (38.18), followed by G-80 (36.85), G-38 (36.15) and BCP-17 (35.47), while lowest test weight recorded in B-57 (12.18). Genotypes viz., BCP-17, B-58, G-38, G-41, G-80, G-94 and G-95 were significantly superior over check Annegiri. Thirty-nine genotypes recorded higher 100 seed weight than mean performance.

4.2.10 Harvest index

Harvest index ranged from 48.63 to 79.68 with the mean value of 71.34 and 71.68 to 77.28 with the mean value of 75.49 in case of germplasm and check respectively. The highest harvest index recorded in G-95 (79.68) followed by L-2 (78.88), G-20 (78.75), G-64 (78.68) and G-73 (78.39), while lowest harvest index was recorded in B-57 (48.63). Genotypes viz., B-768, G-63, G-64 and G-95 were significantly superior over check BDN-9-3. Forty-seven Genotypes recorded higher harvest index than mean performance.

4.2.11 Seed yield per plant

Seed yield per plant ranged from 2.01 to 12.46 with the mean value of 5.72 and 5.45 to 8.49 with the mean value of 6.38

respectively for germplasm and check. The highest yield per plant recorded by G-63 (12.47) followed by G-64 (10.83), B-768 (10.64), G-95 (10.11) and L-2, while lowest seed yield per plant recorded by B-57 (2.01). Genotypes viz., B-768, G-63, G-64 and G-95 were significantly superior over the check BDN-9-3. Forty-eight Genotypes recorded higher seed yield per plant than mean performance.

4.3 Genetic parameters

Genetic parameters viz., the genotypic variance (δ^2g), phenotypic variance (δ^2P), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA) and expected genetic advance as per cent mean (EGA) were worked out and presented in Table 4.

4.3.1 The variance component

The amount of variation in quantitative characters is measured and expressed as variance. The whole amount of observed variation or phenotypic variation present in the character does not give true account of variation, which is non-fixable in the succeeding years of generation, while genotypic variation is the amount of fixable index from one generation to the next generation. The environmental variation varies from one place to other and such cannot be fixed up.

The magnitude of genotypic variance ranged between 0.0085 to 96.47. The days to maturity recorded highest genotypic variance (96.47) followed by number of pods per plant (61.19), Number of seeds per plant (60.02) and harvest index (55.24). The phenotypic variance ranged between 0.0095 to 99.06. The days to maturity recorded highest phenotypic variance (99.06) followed by number of seeds per plant

Table 4 : Estimation of variability parameters for different characters studied in chickpea.

Sr. No	Name of the Characters	Range	General mean	$\sigma^2 g$	$\sigma^2 p$	$\sigma^2 e$	G C V (%)	P C V (%)	$h^2(b s)$ (%)	G A	G A as % of mean
1	Days to 50 % flowering	32.25-76.25	43.85	51.80	53.27	1.47	16.41	16.64	97.24	14.62	33.33
2	Days to maturity	59.83-115.58	80.37	96.47	99.06	2.58	12.22	12.38	97.39	19.96	24.84
3	Number of primary branches per plant	2.37-9.02	4.85	0.90	1.58	0.68	19.54	25.90	56.91	1.47	30.36
4	Number of secondary branches per plant	1.11-8.61	3.40	1.77	2.29	0.52	39.12	44.53	77.19	2.41	70.80
5	Plant height (cm)	27.43-48.93	37.69	23.79	24.96	1.17	12.94	13.26	95.30	9.81	26.03
6	Number of pods per plant	8.42-47.22	25.67	61.19	63.98	2.79	30.50	31.19	95.64	15.76	61.45
7	Number of seeds per plant	10.47-49.02	27.91	60.02	64.91	4.88	27.76	28.86	92.48	15.35	54.98
8	Number of seeds per pod	0.99-1.56	1.08	0.0085	0.0095	0.0010	8.48	8.95	89.75	0.18	16.55
9	100 seed weight (g)	12.18-38.18	21.51	37.99	38.62	0.6286	28.66	28.90	98.37	15.59	58.55
10	Harvest index (%)	48.63-79.68	71.19	55.24	57.43	2.19	10.44	10.65	96.19	15.02	21.10
11	Seed yield per plant (g)	2.01-12.46	5.63	3.60	3.82	.2249	33.69	34.73	94.12	3.79	67.33



Fig. 1: Graphical comparison of GCV and PCV of 11 characters in chickpea

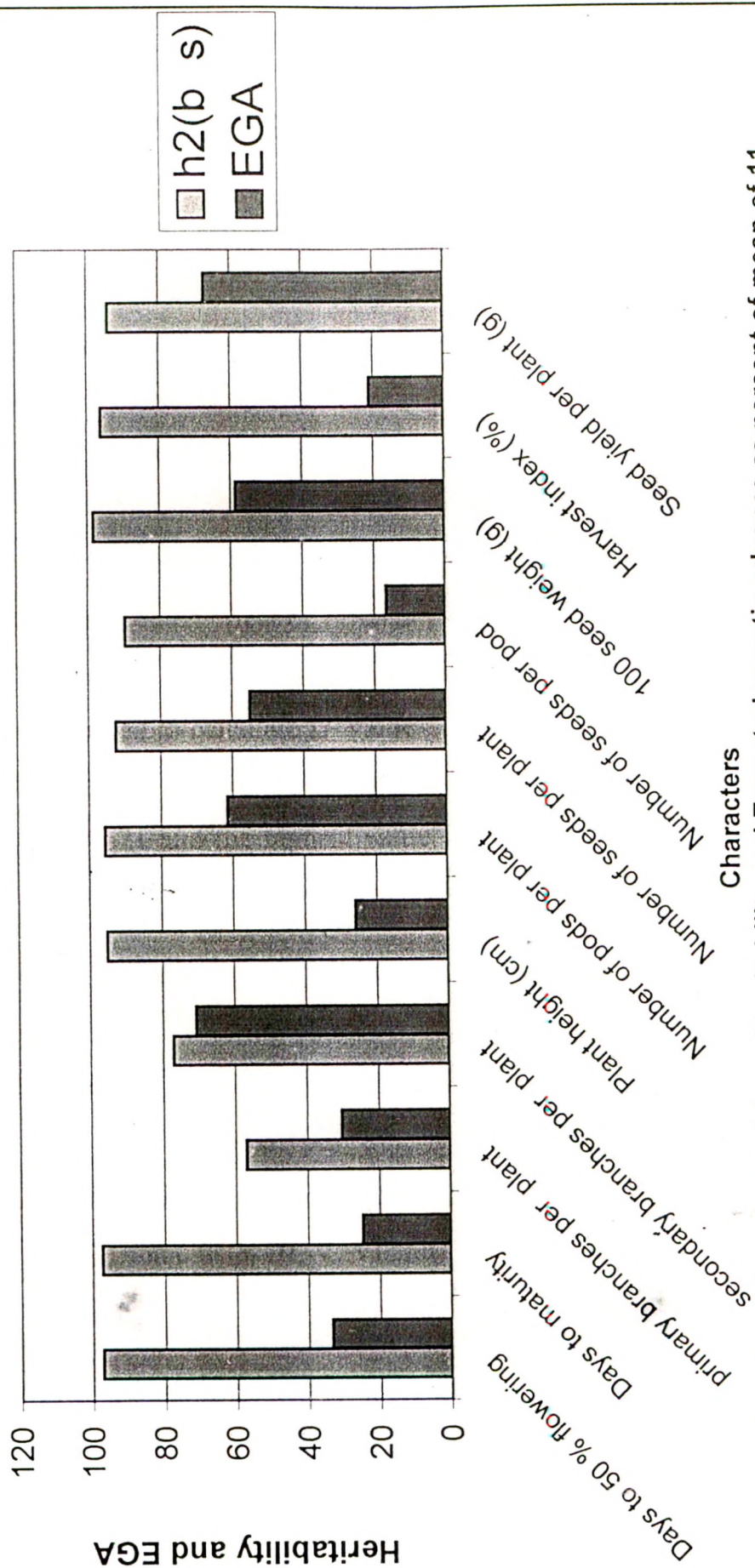


Fig. 2. Graphical comparison of heritability and Expected genetic advance as percent of mean of 11 characters in chickpea.

(64.91), number of pods per plant (63.98) and harvest index (57.43). The environmental variance ranged between 0.0010(number of seeds per pod) to 4.88 (number of seeds per plant).

4.3.2 Estimation of genotypic and phenotypic coefficient variation (GCV) and PCV)

Genotypic coefficient of variation was highest for number of secondary branches per plant (39.12) followed by seed yield per plant (33.69) and number of pods per plant (30.50). The lowest genotypic coefficient of variation recorded by number of seeds per pod (8.48). Phenotypic coefficient of variation was recorded maximum for number of secondary branches per plant (44.53), followed by seed yield per plant (34.73) and number of pods per plant (31.19). The lowest phenotypic coefficient variation recorded for number of seeds per pod (8.95). In general magnitude of phenotypic coefficient of variation was higher than the genotypic coefficient of variation.

4.3.3 Heritability and genetic advance

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

The maximum heritability (%) was observed for 100 seed weight (98.37) followed by days to maturity (97.39) and days to 50 per cent flowering (97.24). The lowest value recorded for number of primary branches per plant (56.91). High heritability (>30 %) was observed in all the characters studied. The estimates of genetic advance ranged from 0.18 to 19.96, with the highest estimates recorded for days to maturity (19.96) followed by number of pods per plant (15.76) and lowest in number of seeds per pod (0.18).

4.3.4 Expected genetic advance as percent of mean (EGA)

Expected genetic advance as percent of mean (EGA) ranged between 16.55 to 70.80. It was highest for number of secondary branches per plant (70.80) followed by seed yield per plant (67.33), number of pods per plant (61.45) and 100 seed weight (58.55). However lowest was observed in number of seeds per pod (16.55).

4.4 Genetic divergence

4.4.1 Mahalanobis generalized distances (D^2)

Wilk's criteria showed significant difference between the genotypes for pooled effect of 11 characters studied.

(Wilk's criteria, $X^2_{pq} = V = 6830.92$ for 990 d.f.). Hence the analysis was further extended to calculate D^2 values. The calculated D^2 values ranged from 4.25 to 908.43. The lowest value was between the pair genotypes B-50 and B-621 and the highest value was between the genotypes G-63 and G-79.

4.4.2 Clustering pattern of the genotypes

The clustering pattern obtained on the basis of magnitude of D^2 values studies, are presented in Table 5.

The 91 genotypes were grouped into seven clusters. The cluster I with highest number of genotypes (80) followed by cluster II (5) cluster IV (2) and cluster III, V, VI and VII with single genotypes each.

Table 5 : Composition of chickpea genotypes into different clusters by Tocher's method.

Cluster Number	Number of strains	Genotypes included
I	80	B-24, BCP-91, G-82, B-27, BCP-97, B-29, BCP-54-1, G-84, B-30, BCP-54-2, G-85, B-31, BDN-9-3, G-87, BDNG-797, B-34, DG-1, G-90, B-46, G-20, G-91, B-48, G-22, G-92, G-25, G-94, B-47, G-26, B-50, G-33, GTP-11, B-51, G-38, HP-1, B-56, G-40, L-1, B-57, G-41, L-2, B-58, G-42, L-3, B-59, G-44, L-102, B-65, G-45, L-104, B-69, G-57, L-108, L-109, B-609, G-64, B-611, G-70, L-112, B-621, G-72, L-113, B-630, G-73, L-201, B-636, G-74, L-202, B-701, G-77, L-302, B-768, L-303, L-305, BCP-36, G-80, L-311, BCP-73, G-81, G-12 and Annegiri.
II	5	G-78, G-83, L-111, B-32, L-313
III	1	G-79
IV	2	B-49, G-88
V	1	G-95
VI	1	BCP-17
VII	1	G-63

4.4.3 Inter and intra cluster divergence

The average inter-cluster and intra-cluster D and D² values are presented in Table 6.

The maximum distance (D) was found between the cluster III and VII (30.14) followed by cluster IV and VII (29.75), cluster III and VI (24.89) and cluster I and VII (23.62). The lowest distance was found between cluster V and VI (13.38). The intra cluster distance was maximum in cluster II (13.66) followed by cluster IV (12.15) with lowest

value of cluster I (11.28) and cluster III, V, VI and VII were solitary clusters.

The mutual relationship among the clusters has been shown diagrammatically in Fig. 3.

4.4.4 Cluster means for different characters

The cluster mean for the eleven characters are presented in Table 7.

A considerable inter cluster variation was observed among the cluster means for the character viz., days to 50 per cent flowering, days to maturity, number of primary branches, number of pods per plant, number of seeds per plant, 100 seed weight, harvest index and seed yield per plant.

The cluster mean for days to 50 per cent flowering varied from 32.25 (III) to 76.25 (VII). The cluster mean for days to maturity ranged from 60.21 (IV) to 115.58 (VII). The highest cluster mean for number of primary branches was observed in cluster V (8.22) and lowest in cluster IV (3.45). The cluster mean for number of pods per plant ranged from 15.15 (IV) to 46.67 (VII). The cluster mean for number of seeds per plant was observed maximum in cluster VII (49.02) and minimum in cluster VI (20.27). The cluster mean for 100 seed weight ranged from 16.75 (III) to 38.18 (V). The cluster mean for harvest index was observed maximum in cluster V (79.68) and minimum in cluster VI (61.88). The cluster mean for seed yield per plant though not showing considerable variation but maximum cluster mean observed in cluster VII (12.46) and minimum in cluster IV (5.21).

Table 6 : Inter and intra cluster D and D² values of chickpea genotypes.

Cluster No.	I	II	III	IV	V	VI	VII
I	11.28 (127.35)	16.30 (265.63)	15.40 (237.11)	15.03 (225.88)	16.63 (276.65)	16.99 (288.78)	23.62 (557.78)
II		13.66 (186.78)	21.38 (456.96)	20.95 (438.78)	21.72 (471.86)	18.64 (347.42)	17.03 (290.10)
III			0	18.29 (334.39)	22.42 (502.55)	24.89 (619.70)	30.14 (908.43)
IV				12.15 (147.85)	19.17 (367.49)	19.99 (399.83)	29.75 (884.39)
V					0	13.38 (179.01)	23.44 (549.30)
VI						0	16.58 (274.84)
VII							0

Figures in parenthesis indicates D² values.

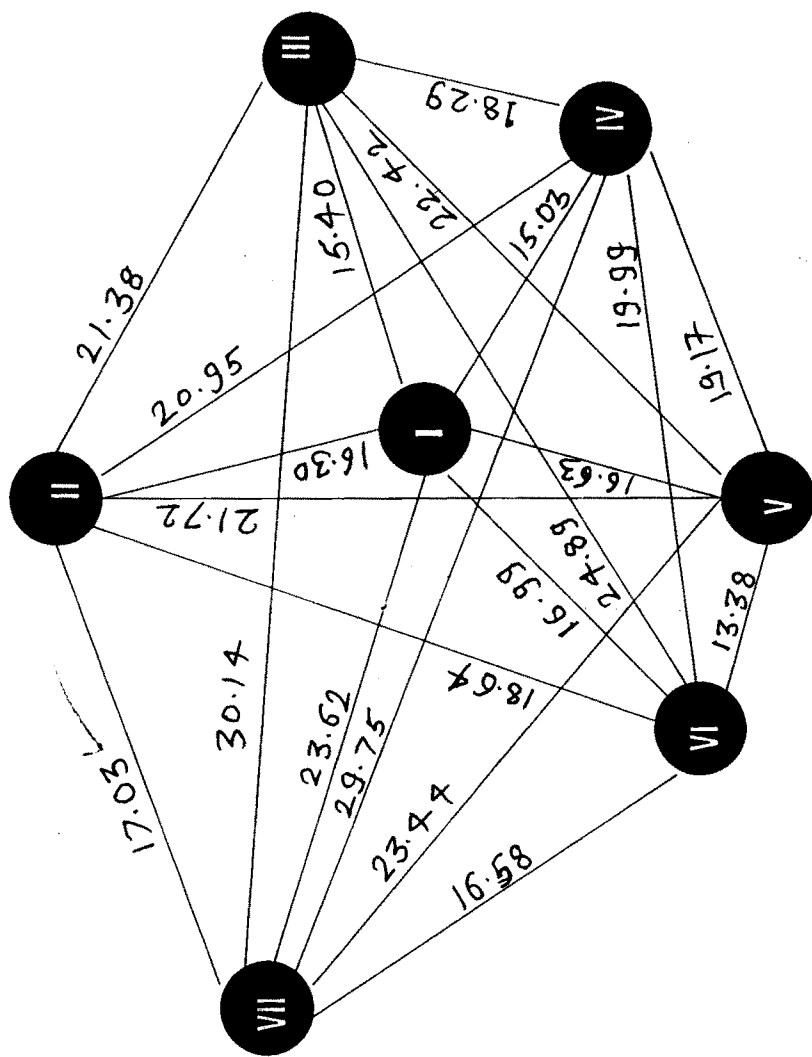


Fig. 3 Cluster diagram showing mutual relationship between clusters (Not to the scale)

Table 7: cluster mean for the characters studied in chickpea.

Cluster number	Days to 50 % flowering	Days to maturity	Number of primary branches per plant	Number of secondary branches per plant	Plant height (cm)	Number of pods per plant	Number of seeds per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)
I	43.35	81.17	4.79	3.13	37.29	25.17	27.09	1.07	21.71	71.47	5.55
II	61.35	89.03	6.05	5.72	38.80	38.24	40.55	1.05	17.41	73.49	6.75
III	32.25	77.58	4.22	2.31	32.03	25.87	36.22	1.56	16.75	75.87	5.89
IV	42.88	60.21	3.45	2.00	36.16	15.15	20.90	1.04	26.18	69.41	5.21
V	40.50	84.58	8.22	2.51	43.63	25.02	26.12	1.04	38.18	79.68	10.11
VI	57.25	94.83	4.17	4.58	40.53	19.02	20.27	1.04	35.48	61.88	6.81
VII	76.25	115.58	7.42	8.11	40.53	46.67	49.02	1.08	27.35	70.37	12.46
Population mean	43.85	80.37	4.85	3.40	37.69	25.67	27.91	1.08	21.51	71.19	5.63

4.4.5 Per cent contribution of different characters to genetic divergences

The contribution towards genetic divergence by different trait worked out in terms of number of times it appeared first (Table 8). 100 seed weight (32.60%) contributed maximum towards genetic divergence. The magnitude of contribution by number of pods per plant (14.11%), harvest index (12.97%), days to 50 per cent flowering (12.26%), days to maturity (11.58%), plant height (10.06%) number of seeds per pod (3.71%) and seed yield per plant (2.44%) was moderate. Other characters number of primary branches per plant, number of secondary branches and number of seeds per plant contributed less than 1% towards genetic divergence. However, it was noticed that variation with respect to certain characters was well distributed in the material.

Table 8: Percent contribution of different characters to genetic diversity.

Character	Days to 50 percent flowering	Days to maturity	Number of primary branches per plant	Number of secondary branches per plant	Plant height (cm)	Number of pods per plant	Number of seeds per plant	Number of seeds per pod	100 seed weight (g)	Harvest index (%)	Seed yield per plant (g)	Total
Number of times appearing 1 st ranking	502	474	4	4	412	578	3	152	1335	531	100	4095
Percent contribution	12.26	11.58	0.10	0.10	10.06	14.11	0.07	3.71	32.60	12.97	2.44	100

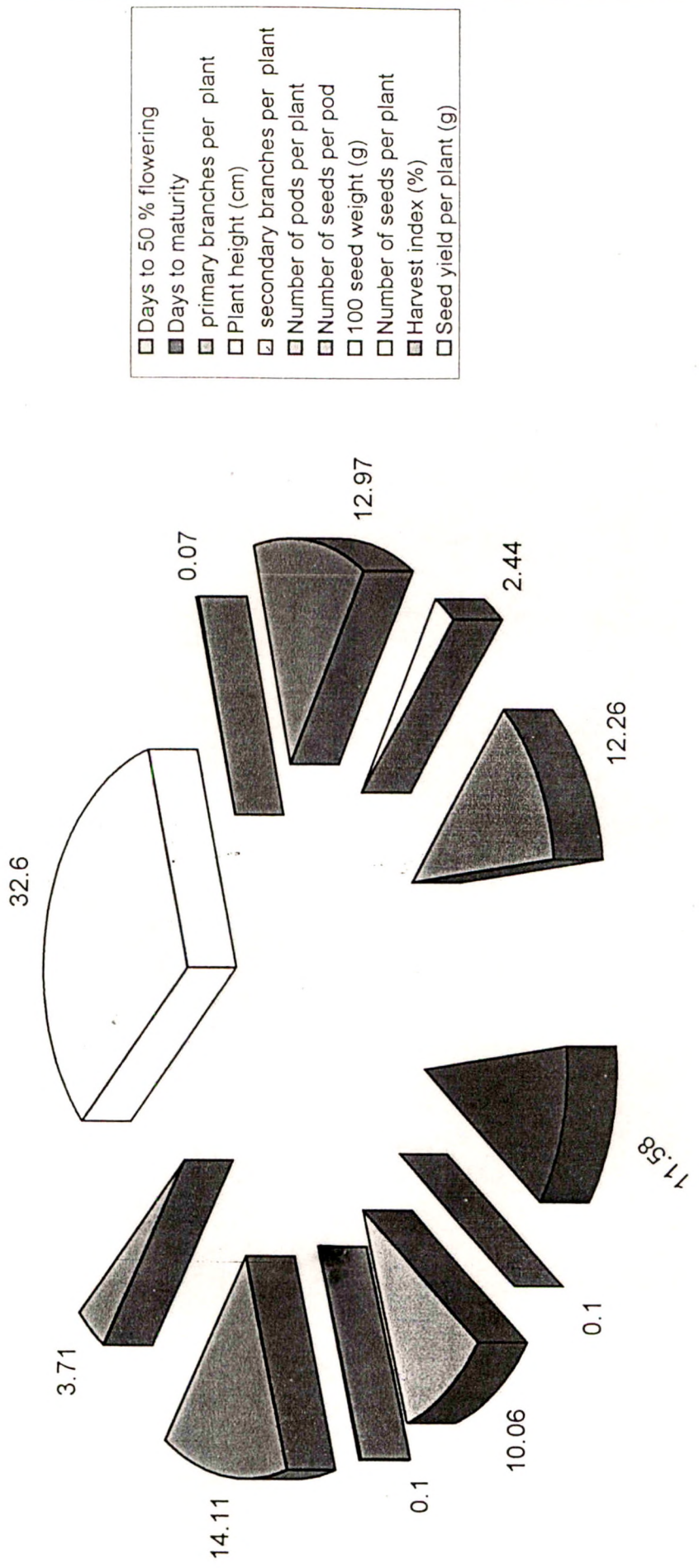
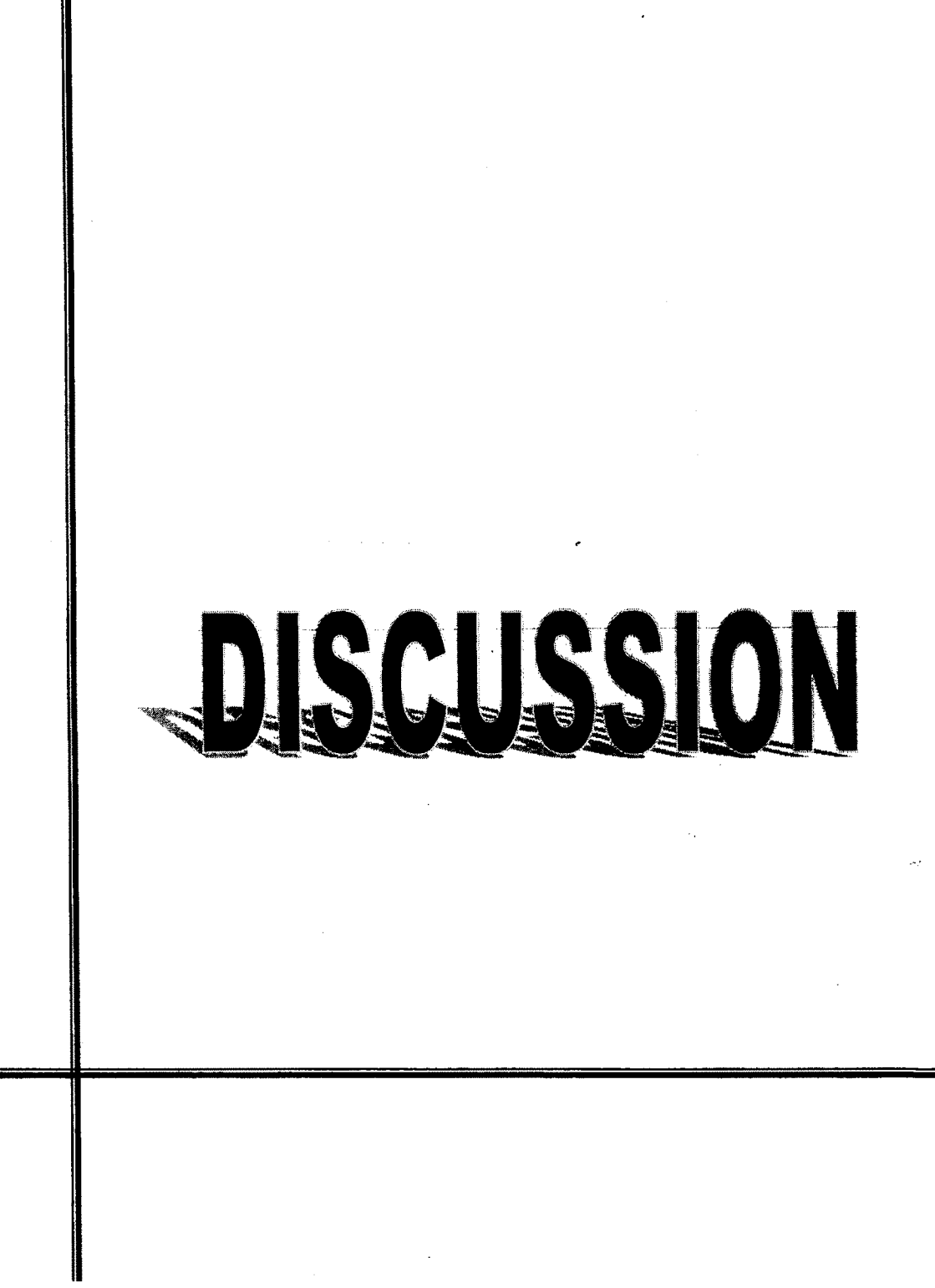


Fig. 4 Percent contribution of 11 characters to total genetic divergence in chickpea



DISCUSSION

Chapter V

DISCUSSION

Chickpea (*Cicer arietinum* L.) is the premier important pulse crop in our country. The protein content in chickpea varies from 21-25 per cent. Yield is complex character and cannot be improved by direct selection as it is influenced by a set of other character known as yield component.

In the present investigation, 91 genotypes of chickpea obtained from Agricultural Research Station, Badnapur and ICRISAT, Patancheru, Hyderabad (A.P.) consisting of 4 checks were evaluated for variation for eleven quantitative characters. The vital genetic variability along with non-genetic variation was studied for each character. Genetic diversity was assessed for grouping the genotypes into different clusters.

5.1 Analysis of variance and mean performance

Analysis of variance revealed significant differences among all the characters studied, indicating the wide range of variability among the lines. Similar results were obtained by Burli *et al.* (2004) and Qureshi *et al.* (2004). The mean performance indicated that the germplasm lines G-20, B-24, G-79, DG-1, GTP-11, HP-1 and L-108 exhibited earliness for days to 50 per cent flowering, while B-49, G-88, HP-1, B-24, DG-1 and G-38 showed early maturity. The lines L-202, G-77, G-72, L-201 exhibited dwarf plant height (27.43 – 30.23 cm). Maximum pods per plant were observed in G-63 followed by B-32, B-27 and L-303. G-63 exhibited highest seed per plant. Highest number of seed per pod recorded in line G-79 (1.56) followed by G-40, B-48, BCP-54-2, HP-1 and G-85. The lines G-95 followed by G-80, G-38 and BCP-17 recorded highest test weight. The line G-95 followed by L-2, G-20, G-64 and G-73

exhibited high harvest index. For the character seed yield per plant line G-63 followed by G-64, B-768 and G-95 recorded high yield. In germplasm lines G-33, G-95, L-303 showed maximum primary branches per plant while germplasm lines L-313, G-63, B-768, L-113 and L-303 showed maximum secondary branches per plant. Genotypes B-768, G-63, G-64, G-95, L-2 and L-111 generally showed superior performance for all characters.

5.2 Variability and genetic parameters

Plant breeding deals with the management and utilization of genetic variability. Variability refers to the presence of differences among the individuals of plant population. Variability is advantageous to the evolutionary survival of a species. Selection is also effective when there is genetic variability among the individuals of a population. Hence, insight into the magnitude of genetic variability present in a population is of paramount importance to plant breeder for starting a judicious breeding programme.

The variability for a given agronomic or yield component character can be estimated through variance, coefficients of variability i.e. GCV and PCV, heritability and genetic advance as percent of mean.

5.2.1 Range of variability

A wide range of variability was observed for all characters except number of primary branches per plant and number of seeds per pod. The character days to maturity exhibited highest range of variability followed by number of seeds per plant, number of pods per plant, days to 50 per cent flowering, harvest index, Seed yield per plant, 100 seed weight, plant height and number of secondary branches per plant. On

contrary Nimbalkar (2000) found wide range of variability for all characters except number of days to maturity. However, Burli *et al.* (2004) observed maximum range of variability for number of pods per plant followed by days to maturity and plant height. Nawab (2002) found genetic variability for plant height, number of primary branches per plant, secondary branches per plant, 100 seed weight, harvest index and seed yield per plant. Sadhu and Mandal (1989) found variability for plant height, pod number, seed number, seed weight and seed yield.

5.2.2 The variance component

Partitioning the variances into genotypic, phenotypic and environmental variances, it was observed that the major portion of variance is contributed by genotypic component, while environmental variance played very less role in variation (Table 4). The less influence of environment on character suggested the sufficient genetic variability and allows selection for individual trait. Nearly equal genotypic and phenotypic variances observed for seed yield per plant, 100 seed weight, number of seeds per pod, number of primary, secondary branches per plant and plant height, indicated variability remain unaltered by environmental condition. Whereas differences between genotypic and phenotypic variances for the characters viz., number of seeds per plant, days to maturity, harvest index and days to 50 per cent flowering revealed that variability changes under different environmental condition. These results are in conformity with previous results of Nimbalkar (2000).

5.2.3 Genotypic and phenotypic coefficient of variation

The relative value of genotypic and phenotypic coefficient of variation gives an idea about the variation present in genetic population.

The phenotypic coefficient of variance (PCV) was marginally higher than genotypic coefficient of variation (GCV) for all the characters (Table 4) indicating that the apparent variation is not only due to genotypes but also due to the little influence of environment. Therefore variability existing in these characters was mainly due to genetic factors and effective selection can be made. Higher value of GCV and PCV were observed in number of secondary branches per plant, seed yield per plant, number of pods per plant, 100 seed weight and number of seed per plant. GCV and PCV values were moderate for characters viz., number of primary branches per plant, harvest index, days to maturity, plant height and days to 50 per cent flowering, while low for number of seeds per pod. The high genetic variation estimated for seed yield per plant along with number of pods per plant, number of secondary branches per plant and 100 seed weight offer wide scope for selection. Similar results obtained for seed yield per plant by Burli *et al.* (2004). Sable *et al.* (2002) reported similar results for seed yield per plant, number of branches per plant, 100 seed weight and plant spread. On contrary Singh (1988) reported PCV values low (<10) for days to 50 % flowering, days to maturity, moderate (10-20) for plant height, number of pods per plant and biological yield and high (>20) for 100 seed mass, seed yield per plant and harvest index.

Jahagirdar *et al.* (1994) reported high estimates of GCV and PCV for number of pods per plant. Nimbalkar (2000) reported high GCV and PCV for 100 seed weight and lowest for number of days to maturity.

5.2.4 Heritability and genetic advance

Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. The heritability estimates are better

indicator in this respect. The broad sense (b s) heritability includes the contribution of additive gene effect, allelic interaction due to dominance and non-allelic due to epistasis. Heritability is a major of transmission of an attribute from one generation to the other, while genetic advance is a genetic improvement in the mean genotypic value of selected plant over the parental population as percent of mean.

Burton (1952) suggested that genotypic coefficient of variation and heritability estimates together give better idea about the amount of genetic advance expected through selection.

Johnson *et al.* (1955) pointed out that in a selection programme heritability values as well as estimates of genetic advance are more useful than heritability alone. The high heritability coupled with high genetic advance for only particular character indicates its suitability of being selected for further improvement.

In present investigation 100 seed weight, showed maximum broad sense heritability followed by days to maturity, days to 50 per cent flowering, harvest index, number of pods per plant, plant height and seed yield per plant (Table 4). It indicates that these characters is least influenced by the environmental effect, these finding are in agreement with Sharma *et al.* (1990). However Singh (1988) reported high heritability for days to maturity, moderate heritability for days to 50 % flowering, 100 seed mass, seed yield per plant and lowest for harvest index. Wahid and Ahmad (1994) reported highest heritability for plant height followed by seed yield per plant and pods per plant. Burli *et al.* (2004) reported highest heritability for days to maturity followed by 100 seed weight, days to 50 % flowering and plant height. However the selection for improvement of such character may not be useful, because

broad sense heritability based on total genetic variance, which include both fixable (additive) and non fixable (dominance and epistatic) variance. Out of these characters high heritability (b s) accompanied with high genetic advance as per cent of mean for characters viz., seed yield per plant, secondary branches per plant, 100 seed weight, number of pods per plant and number of seeds per plant, it indicate that most likely that heritability is due to additive gene effects and selection be effective. These finding are in agreement with Mishra *et al.* (1988), Jahagirdar *et al.* (1990), Rao *et al.* (1994), Adhikari and Pande (1982), Sandhu and Mandal (1989), Tripathi (1997), Kumar *et al.* (1999) and Sable *et al.* (2002). The remaining character viz., number of seeds per pod, harvest index, plant height, days to maturity and days to 50 % flowering exhibited high heritability with low genetic advance as percent of mean is indicative of non-additive gene action. Arshad (2004) found similar results for days to 50 per cent flowering and days to maturity. The high heritability was exhibited due to favorable influence of environment rather than genotype and selection for such trait may not be rewarding.

Thus selection for character viz., number of pods per plant, number of secondary branches per plant, 100 seed weight and seed yield per plant with high GCV, high heritability and high genetic advance as percent of mean will be effective.

5.3 Genetic divergence

Genetic divergence, which is due to genetic factor, is the basis for heritable improvement. The plant breeder have always therefore, has been fascinated by great amount by diversity in crop plants. The precise information about the genetic divergence is therefore crucial for effective breeding programme. The genetically diverse parents are

known to produce higher heterotic effect and consequently give desirable recombinants in the breeding material. Multivariate analysis (D^2 statistics) is a measure that appraises the genetic variability quantitatively among set of genotype (Mahalonobis, 1928).

5.3.1 Diversity based on a set of eleven characters

The estimates of D^2 values ranged from 4.25 to 908.43. This clearly indicates the presence of adequate diversity between genotypes studies. Main and Bahl (1989), Vijaykumar *et al.* (1991), Anilkumar *et al.* (1993), Jethava *et al.* (1996) and Nimbalkar and Harer (2001) also reported wide genetic diversity in chickpea germplasm.

The highest D^2 value was observed between genotype G-63 and G-79 (908.43), while the lowest (4.25) was between genotype B-50 and B-621.

5.3.2 Cluster formation

The aim of cluster formation and finding out inter and intra cluster divergence is to provide the basis for selection of parents for hybridization programme. As accumulation of different desirable traits spread over diverse genotype is important to rapid advance in yield improvement of any crop. The theoretical concept behind such grouping is that the genotypes grouped into the same cluster presumably are less diverse from each other than those belonging to different clusters. (Rao, 1952) and thus crossing between the genotypes belonging to the same cluster will not give expected desired heterotic response and segregants in further generations. Consequently breeding programme should be so designed that the parents selected from different cluster, because greater the distance between two clusters, wider is the genetic

diversity in the genotypes. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis (Moll *et al.* 1964). Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean for the character also need due consideration in crop improvement programme. In the present investigation based on the procedure described by Rao (1952), the values of " D^2 " between pairs of populations were worked out (Table 5). Following Tocher's method (Singh and Chaudhary, 1977), the populations were then grouped into seven clusters, maximum genotypes (80) were included in cluster I followed by cluster II (5), IV (2) and Cluster III, V, VI, VII with single genotype each (Table 5). Similar results found by Battachary and Ganguly(1998), Vijaykumar *et al.* (1991) reported 89 genotypes in Ist cluster with two solitary clusters. Mishtra and Rao (1990) reported eleven single variety clusters. Sandhu and Gumber (1991) reported five solitary clusters. Sarvaliya and Goyal (1994) reported three solitary clusters, while Nimbalkar and Harer (2001) reported ten solitary clusters.

5.3.3 Inter and intra cluster divergence

The highest inter cluster distance was found between the cluster III and VII ($D = 30.14$) followed by cluster IV and VII ($D = 29.75$) and between cluster III and VI (24.89). The closest proximity was found between cluster V and VI (13.38). The intra cluster distance was maximum in cluster II (13.66) indicating that this cluster is more heterogeneous. Sandhu and Gumber (1991) found similar results for intra cluster distances. Vijaykumar (1994) found 1.90 as highest intra cluster distance. Cluster VII showed maximum genetic distance to all other clusters and cluster I showed maximum closeness to all other

clusters, indicating maximum number of common gene complex. Estimate of average intra and inter cluster distances (D^2 values) revealed that the genotypes of same cluster that little divergence from each other with respect to aggregate effect of eleven characters. As the genotypes of same cluster are closely related therefore it is suggested that crosses should be attempted between genotypes belonging to cluster (III and VII) separated by large inter cluster distances. Similar results were found by Samal *et al.* (1989), Sandhu and Gumber (1991), Pooran chand and Singh (1995) and Narendra singh (2002). Sometimes parents separated by moderate D^2 values generally showed the higher heterosis for different characters (Mian and Bahl (1989).

5.3.4 Cluster means for different characters

Cluster means indicated substantial variation among the clusters. The differences among cluster though observed for all characters, but were more pronounced for characters viz., days to 50 per cent flowering, days to maturity, number of pods per plant and 100 seed weight. The cluster mean revealed that cluster III and VII varied considerably for most of the character from each other, as cluster III showed early days to 50 per cent flowering, early maturity, lowest plant height and highest number of seeds per pod, while cluster VII showed high cluster mean for all character except number of seeds per pod and 100 seed weight. Thus both cluster exhibit extreme limit for characters and may give useful sergregants in further generation after hybridization. Cluster mean revealed the differences in value for particular character between the groups indicating importance of particular cluster for choosing desirable parent for hybridization programme. Raval and Dobariya (2004) and Patel *et al.* (2006) found similar results

for clusters mean of characters. On the basis of cluster mean characters viz., days to 50 per cent flowering, days to maturity, number of pods per plant and 100 seed weight appeared as the major force of differentiation.

5.3.5 Per cent contribution of different characters to genetic divergences

In present investigation the character 100 seed weight contributed maximum towards the genetic divergence followed by number of pods per plant, harvest index, days to 50 per cent flowering and days to maturity contributed moderately. Similar results were found by Raj and Khare (1999), Yadava *et al.* (2003), Patel *et al.* (2006) and by Rao and Jain (1996) for 100 seed weight. Number of secondary, primary branches per plant and number of seed per plant contributes less than 1%. Samal *et al.* (1989) reported the contribution of 100 seed weight, seed yield per plant and days to 50 per cent flowering to the total divergence. Nimbalkar and Harer (2001) reported genetic divergence due to plant height and 100 seed weight. Garoosi and Vojdani (1993) reported that number of seeds per pod, 100 seed weight, flowering duration and flower colour were the best characters for type differentiation. Vijayprakash (2006) reported that the character grain yield per plant, 100 seed weight and seed per pod were major contributor towards genetic divergence. Khan *et al.* (1990) observed that the characters like days to 50 per cent flowering, number of effective branches, harvest index, days to reproductive phase and seed size contributed more to divergence.

Taking into account the cluster means for important yield component, the various clusters, which can provide the desired parents for further hybridization programme for improvement of character, are listed below.

Character	Cluster
Days to 50 per cent flowering	III, V, I
Days to maturity	IV, III
Primary branches per plant	V, VII, II
Secondary branches per plant	VII, II
Pods per plants	VII, III, II
Number of seeds per pod	III
100 seed weight	V, VI
Seed yield per plant	VII, V

Genotypes included into the clusters.

Cluster I	B-48, B-29, B-701, G-20, DG-1, GTP-11, G-64.
Cluster II	G-78, G-83, B-32, L-111, L-313.
Cluster III	G-79
Cluster IV	B-49, G-88
Cluster V	G-95
Cluster VI	BCP-17
Cluster VII	G-63.

SUMMARY

Chapter VI

SUMMARY AND CONCLUSION

The present investigation entitled “Genetic divergence analysis in chickpea (*Cicer arietinum* L.)” was conducted during rabi season of 2006-2007 to estimate the extent of genetic variability, heritability, genetic advance, genetic advance as percent of mean, genetic divergence and contribution of different characters towards the divergence.

Ninety-one genotypes of chickpea including four checks viz. BDN-9-3, BDNG-797, Annegiri and G-12 evaluated in Augmented randomized block design (Augmented R.B.D.) with three blocks. Data were recorded on eleven characters viz. days to 50 percent flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height, number of pods per plant, number of seed per plant, number of seeds per pod, 100 seed weight (g), harvest index (%) and seed yield per plant (g).

The data was analyzed and results obtained were summarized below.

6.1 Analysis of variance showed significant differences for all the characters among germplasm lines indicating the presence of wide genetic variability in material.

6.2 On the basis of mean performance the highest seed yield per plant was observed in line G-63 (12.47) followed by G-64 (10.83), B-768 (10.64). Whereas maximum number of pods per plant observed in G-63 (47.22) followed by B-32 (46.47), B-27 (42.21) and L-303 (40.91). Highest number of seeds per plant observed in G-63 (49.02) followed by B-32 (47.07), B-27 (43.75), L-303 (41.56). Maximum 100 seed weight

was observed in G-95 (38.18) followed by G-80 (36.85), G-38 (36.15) and BCP-17 (35.48). Number of seed per pod observed in G-79 (1.56) followed by G-40 (1.40) and B-48 (1.28). For days to 50 per cent flowering line G-20 (32.25), B-24 (32.25), G-79 (32.25) showed early flowering while B-49 (59.83) followed by G-88 (60.58), DG-1 (68.38) showed early maturity. Genotypes B-768, G-63, G-64, G-95, L-2, and L-111 generally showed superior performance for all characters. This genotypes can be utilize for further breeding progamme as a parent.

6.3 A wide range of variability was observed for all character except number of seeds per pod. The days to maturity exhibited highest range of variability followed by number of seed plant, number of pod per plants, days to 50 per cent flowering, harvest index, seed yield per plant, 100 seed weight and plant height.

6.4 Equal genotypic and phenotypic variance observed for seed yield per plant, 100 seed weight, number of seed per pod, number of primacy and secondary branches per plant and plant height. Whereas difference found for number of seeds per plant, days to maturity, harvest index and days to 50 per cent flowering. Former unaltered by environmental condition later revealed changes under different environmental condition.

6.5 High value of GCV and PCV were observed in number branches per plant, seed yield per plant, number of pod per plant, 100 seed weight and number of seeds per plant. GCV and PCV values were very low for character viz., number of seeds per pod, harvest index, days to maturity plant height and days to 50 per cent flowering.

6.6 High heritability estimates observed in 100 seed weight followed by days to maturity, days to 50 per cent flowering, harvest index, number of pods per plant.

6.7 High heritability estimates associated with high genetic advance as percentage of mean was observed for seed yield per plant, secondary branches per plant, 100 seed weight, number of pod per plant, number of seeds per plant indicative of additive gene effect and selection be effective, remaining characters with high heritability (b s) and low genetic advance that indicate predominant role of non additive gene action.

6.8 Character with high GCV, high heritability and high genetic advance as parent of mean viz., number of pods per plant, number of secondary branches per plant, 100 seed weight, seed yield per plant will be effective.

6.9 The D^2 values showed adequate diversity among the genotypes. On the basis of D^2 value all the genotypes were grouped into seven clusters. The maximum genetic distance (D^2) of 30.14 was found between the cluster III and VII. The maximum D^2 value of 908.43 was observed in the pair of genotypes viz., G-63 and G-79 and lowest value of D^2 4.25 was observed between B-50 and B-621. The genotypes included into the different cluster having high character value therefore selected for further breeding programme. Genotypes G-79 (III), B-49 (IV), G-92, G-80 (I) were early in days to 50 per cent flowering. Genotypes G-88, B-49 (IV) and G-79 (III) showed early maturity. Genotype G-95 (IV), G-63 (VII), B-32, G-83 (II) recorded high primary branches per plant, while G-63 (VII) showed highest secondary branches per plant. Genotypes G-63 (VII), B-32, L-111, L-313 (II) showed superior

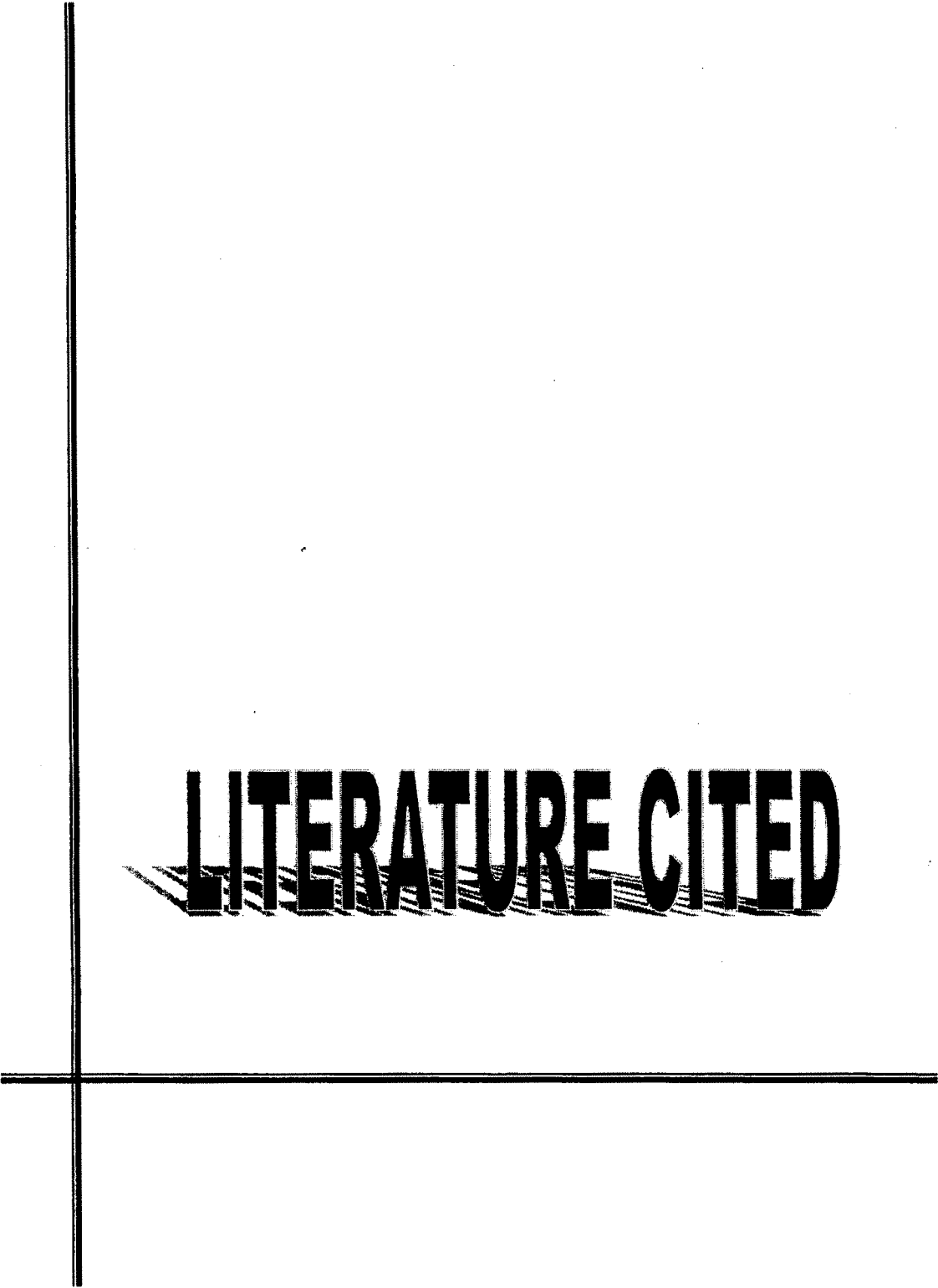
performance for number of pods per plant. Genotypes G-79 (III) showed highest number of seeds per pod. Genotypes G-95 (V), BCP-17 (VI), G-63 (VII) showed superior performance for 100 seed weight. In case of seed yield per plant genotype BDN-9-3 (I), L-111, L-313 (II), BCP-17 (VI) and G-95 (V) showed superior performance. In case of harvest index genotype G-95 (III), G-83, B-32 (I) showed superior performance.

6.10 The contribution towards genetic divergence by different trait worked out in terms of number of times it appeared first. 100 seed weight (32.60%) contributed maximum towards genetic divergence. The magnitude of contribution by number of pods per plant (14.11%), harvest index (12.97%), days to 50 per cent flowering (12.26%), days to maturity (11.58%), plant height (10.06%) number of seeds per pod (3.71%) and seed yield per plant (2.44%) was moderate. Other characters number of primary branches per plant, number of secondary branches and number of seeds per plant contributed less than 1% towards genetic divergence.

CONCLUSION

1. Analysis of variance proved the significant differences for all characters indicating the presence of wide variability in material.
2. The characters number of pods per plant, number of secondary branches per plant, 100 seed weight and seed yield per plant showed high GCV, heritability and high genetic advance as per cent of mean indicating additive gene effect and selection will be effective.

3. In present investigation the character 100 seed weight contributed maximum towards the genetic divergence followed by number of pods per plant, harvest index, days to 50 per cent flowering and days to maturity contributed moderately.
4. On the basis of mean performance and genotypes included into different cluster, genotype G-95, G-63, G-79, B-32, BCP-17, L-111 and L-313 are useful for further improvement in chickpea as parents for hybridization programme.



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