

**GENETIC DIVERSITY AND ASSOCIATION
STUDIES IN CHICKPEA (*Cicer arietinum* L.)**

THESIS

By

SANJAY KUMAR

Submitted to



**CHAUDHARY SARWAN KUMAR HIMACHAL PRADESH
KRISHI VISHVAVIDYALAYA PALAMPUR-176 062 (H.P.) INDIA**

IN

Partial fulfilment of the requirements for the degree

OF

**MASTER OF SCIENCE IN AGRICULTURE
(PLANT BREEDING)**

2002

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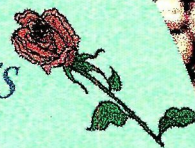
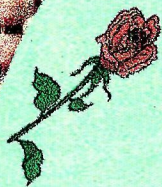
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"Lord, Thou art the Giver.

I am an humble begger .

Thou art ever so benevolent.

"Whatever I do, does not come from me.

My Lord, it is all Thy doing

"How can I ever count Thy virtues,

Who bestoweth so much on this

worthless soul !"

Dr. Anil Sirohi
Plant Breeder

Research Sub Station,
CSK HP Krishi Vishvavidyalaya,
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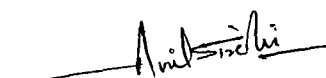
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This is to certify that the thesis entitled "**Genetic diversity and association studies in chickpea (*Cicer arietinum* L.)**" submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the subject of **Plant Breeding** of Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Mr. Sanjay Kumar** son of **Sh. Narotam Chand** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been fully acknowledged.

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Dated: 5th December, 2002.



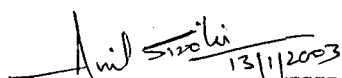
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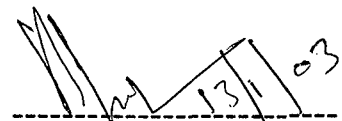
This is to certify that the thesis entitled "**Genetic diversity and association studies in chickpea (*Cicer arietinum* L.)**" submitted by **Mr. Sanjay Kumar** son of **Sh. Narotam Chand** to the Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture)** in the subject of **Plant Breeding** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.


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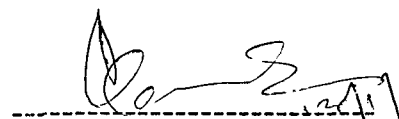
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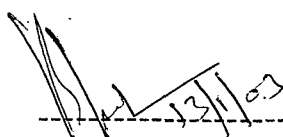
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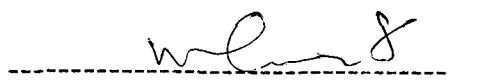
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13/11/03

Head of the Department


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Place: Palampur

Dated: the 5th December, 2002


(Sanjay Kumar Thakur)

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INTRODUCTION

Chapter-I

INTRODUCTION

Besides providing adequate nutrition, it is necessary to combat the acute protein malnutrition of the exploding human population of the world. Edible grain legumes or pulses constitute a major ingredients of vegetarian diet and offer an alternative to address protein malnutrition and supplements nutritive value of wheat and rice. Pulses are a cheap source to tackle the malnutrition of the burgeoning population in the under developed countries.

Chickpea (*Cicer arietinum* L.) is one of the most important pulse crops of the world. The crop occupies an indispensable place in our daily diet as a source of protein, fits well in cropping systems and is insensitive to drought. The resource poor farmers grow this crop in the marginal lands because of its ability to thrive better with low inputs. It stands at a comparative advantage in adapting to arid environmental conditions than many other crops.

Chickpea is known to have originated in western Asia from where it dispersed in two directions. Large seeded, owl head shaped or rounded chickpeas of white-salmon colour (*kabuli* type) were developed in the west. While small seeded having irregular shape and colours like yellow, brown, black, green etc. (*desi* types) probably

dispersed in eastern and southern parts including India. It has been suggested that western ecotype has been modified more by human selection than the eastern ecotype which has received lesser attention (Rohewal *et al.*, 1966).

India is the world's leading producer of chickpea with an area of 5200 thousand hectares and production of 3870 thousand MT. Thus, it alone accounts for about 60 per cent of the total area and production of the world, yet the average yield (741 kg/ha) is much lower as compared to many other countries (Anonymous, 2001). In Himachal Pradesh this crop covers about 2.5 thousand hectares with a production of 2.5 thousand tones (Anonymous, 1998). However, average yield of chickpea (1000 kg/ha) is much lower than its total genetic potential because of poor management practices and lack of high yielding and disease resistant varieties. Gupta (1984) has indicated that there are vast opportunities of increasing pulse production in Himachal Pradesh by introducing new high yielding and disease resistant varieties. Although in recent years efforts have been made in developing varieties suitable for cultivation in Himachal Pradesh and a number of varieties like HPG-17, Himachal Chana-1 and Himachal Chana-2 have been recommended for cultivation, yet there seems to be an ample scope for increasing its area and production by the development of high yielding and disease resistant varieties.

Genetic improvement of quantitative traits can be achieved through a clear understanding of the nature and amount of variability present in the genetic stocks and the extent to which the traits are heritable. Therefore, the estimates of various parameters for the assessment of genetic variability such as, variance, coefficient of variation, heritability, genetic advance and influence of environment on these characters will help the plant breeders devise suitable strategies to develop the desirable plant type.

Yield being the most important and complex character, is governed by polygenes and influenced by many physiological processes within the plant. It is also affected by the environment in which the plant is grown. Therefore, selection based on yield performance only may create confusion and give a biased conclusion. Consequently, rational approach towards the improvement of yield necessitates the identification of desirable components of yield. The extent and nature of association between yield and its components assumes special significance and help breeders to ascertain the real components of yield and provide an effective basis of phenotypic selection. The path coefficient analysis elucidates the intrinsic nature of observed association between yield and its attributes. It also reveals the magnitude of contribution made by different plant characters towards yield thereby, imparting confidence in selection of important yield attributes.

In plant breeding, genetic improvement of existing varieties is a continuous process. In this context, hybridization is one of the powerful tools in the hands of plant breeders for effecting varietal improvement. However, any varietal improvement through hybridization depends mainly on the selection of parents having high genetic variability so that the desirable character combinations may be selected. Multivariate analysis by means of Mahalanobis D^2 -statistic is a powerful tool in quantifying the degree of divergence among biological populations.

Keeping the above points in view, the present study was therefore, undertaken with the following objectives:

1. To assess and analyse the genetic variability in chickpea genotypes,
2. to understand the nature and association between yield and yield contributing traits, and
3. to identify suitable genotypes with wider genetic divergence and other desirable attributes for further chickpea improvement programmes.



REVIEW OF LITERATURE

Chapter-II

REVIEW OF LITERATURE

The primary aim of any breeding programme is to evolve high yielding varieties with improved quality. Thus, for obtaining superior varieties with high yield potential, the plant breeders have to deal with characters which are governed by polygenic systems and show continuous variation. For a breeder, the critical assessment of nature and magnitude of variability, association of characters with yield, path coefficient analysis and genetic diversity are most important to plan effective strategies for the improvement of characters.

The relevant reports available in the literature pertaining to various aspects included in the present study are briefly reviewed under the following sub headings:

1. Studies on genetic variability, heritability and genetic advance
2. Studies on correlation coefficients
3. Studies on path coefficient analysis
4. Genetic divergence studies
5. Reaction to diseases

2.1 Studies on genetic variability, heritability and genetic advance

Genetic variability among the genotypes is the basis for all crop improvement programmes. Sufficient genetic variability, if present, can be exploited to develop superior cultivars with desired characters under consideration. Vavilov (1951) was the first to realize that a wider range of variability in any crop provides chances of selecting the desirable types.

Information on heritability for different component of traits is essential for any crop improvement programme, as the heritable component being the consequence of genotypes, is inherited from generation to generation. Wright (1921) reported that the heritability component comprised of additive and non-additive portion and it was the former which responds to selection.

Estimation of expected genetic advance is important to have an idea of effectiveness of selection. Burton and DeVane (1953) suggested that genetic coefficient of variation in conjunction with heritability estimates gives reliable indication of the extent of improvement to be expected from selection and it was further remarked that expected genetic advance under a particular system supplies a true practical information needed by a breeder. Johnson *et al.* (1955) also found it more useful to estimate the heritability values

together with genetic advance in predicting expected progress to be achieved through selection.

Joshi (1972) observed a wide range of variability for most of the yield contributing characters viz., number of pods per plant, number of seeds per pod, branches per plant and 100-seed weight in chickpea.

Mandal and Bahl (1983) observed that biological yield showed highest phenotypic and genotypic coefficients of variability, heritability and expected genetic advance for selection. These values were reported to be moderate for economic yield and low for harvest index. The values of phenotypic and genotypic variances were close in case of 100-seed weight and days to flower. Expected genetic advance and heritability in broad sense were also high for these two characters.

Khorgade *et al.* (1985) reported high estimates of genetic advance and heritability for 100-seed weight, seeds per pod, branches per plant and days to 50 per cent flowering in chickpea. Maloo and Sharma (1987) reported high genetic advance as per cent of mean coupled with high heritability for grain yield, number of pods per plant and number of primary branches per plant. High heritability coupled with high genetic advance expressed as percentage of mean was also reported for number of secondary branches per plant, number of pods

per plant, seed yield per plant, biological yield per plant and harvest index by Mishra *et al.* (1988).

Sharma and Maloo (1988) found high estimates of heritability for all the characters studied. They also reported high genetic advance as per cent of mean coupled with high heritability for grain yield per plant, number of pods per plant and number of primary branches per plant.

High heritability coupled with high expected genetic advance was observed for 100-seed mass and seed yield per plant whereas, high heritability with moderately low genetic advance was reported for days to 50 per cent flowering and plant height by Samal and Jagadev (1989).

Singh *et al.* (1988) reported variable response of chickpea genotypes for days to flowering, plant height and primary and secondary branches per plant when shown in three different environments (normal, late and very late shown). Significant genotype x environment interaction for seed weight, plant height and days to flowering in eight *kabuli* chickpea genotypes has been also reported by Toker (1998).

Maloo and Sharma (1990) reported that mean squares due to genotypes, environments and genotype x environment interaction were highly significant for all the traits except for grain protein content

in case of environment; and grains per pod and grain protein content in case of genotype x environment. They also reported high GCV for grain yield per plant, number of pods, primary branches per plant, 100-seed weight and grain protein content but low for days to maturity, plant height and grains per pod. High genetic advance as per cent of mean together with high heritability was also reported for grain yield per plant, pods per plant, 100-grain weight, primary branches per plant and grain protein content.

Wide variation in chickpea genotypes was observed for different quantitative characters studied except for days to flowering, days to maturity and protein content by Singh *et al.* (1990).

Arora (1991) reported that mean squares due to genotypes were significant for all characters with little difference in phenotypic and genotypic coefficients of variation. He also reported high PCV and GCV values for pods per plant, 100-seed weight and seed yield per plant, and moderately high values for plant height, canopy spread, length of pod bearing branches, primary and secondary branches per plant, seeds per plant and harvest index.

Dasgupta (1992) recorded high PCV for 100-seed weight, seed yield per plant, pods per plant and seeds per plant; moderate for plant height, branches per plant and seeds per pod; and low for days to 50 per cent flowering and days to maturity. He also observed

high heritability coupled with high genetic advance for 100-seed weight and seed yield per plant.

Chavan *et al.* (1994) reported that heritability estimates were high for all the characters studied except plant breadth. High heritability coupled with high genetic advance expressed as per cent of mean were also observed for seed yield and number of pods per plant.

High estimates of genotypic coefficient of variation, broad sense heritability and genetic advance were observed for pods per plant, seeds per plant, biological yield and yield per plant by Tripathi (1998).

Kumar *et al.* (1999) reported high genotypic and phenotypic coefficients of variation for number of pods per plant, 100-seed weight, seed yield per plant and harvest index. They also reported high heritability coupled with high genetic advance as percentage of mean for number of pods per plant, 100 seed weight and seed yield per plant.

2.2 Studies on correlation coefficients

Correlation coefficient is a measure of the degree of association between the characters worked out at same time (Hays *et al.*, 1955). To raise the genetic potential of a crop, the knowledge of nature and magnitude of association among different characters is of

immense value to any breeding programme and forms a basis for selection. For selection of several character simultaneously, the knowledge of character association is helpful to avoid undesirable correlated changes in other characters. Johnson *et al.* (1955) have stressed the importance of both phenotypic and genotypic correlations among the characters in planning and evaluating breeding programmes. Correlation coefficients for a given trait vary with the genotypes studied and the environment where the test is carried out.

The earlier work done on this aspect in chickpea by various research workers is briefly reviewed below:

Paliwal *et al.* (1987) reported that seed yield per plant was positively correlated with plant height, days to 95 per cent maturity and days to 50 per cent flowering. He also reported that number of pods per plant had negative association with 100-seed weight; days to maturity had positive association with 100-seed weight; days to 50 per cent flowering had positive association with 100-seed weight, number of pods per plant.

Mishra *et al.* (1988) observed that seed yield per plant was positively associated with plant spread, number of primary and secondary branches per plant, pod bearing length, number of pods per plant, biological yield per plant and harvest index. Similarly, Sharma *et al.* (1989) also reported that seed yield was highly significantly and

positively correlated with pods per plant, number of primary and secondary branches per plant, harvest index, plant height and days to maturity. Seed yield was significantly and positively correlated with pod number and plant height whereas significantly negatively correlated with 100-seed weight as noticed by Lal *et al.* (1993).

Dasgupta *et al.* (1992) reported that seed yield was significantly and positively correlated with pods per plant, seeds per plant, 100-seed weight and seeds per pod. Positive association of seed yield with primary branches per plant, 100-seed weight, harvest index and pods per plant was observed by Rao *et al.* (1994).

Sandhu and Mangat (1995) reported significant positive correlation of seed yield per plant with primary branches, pods per plant and harvest index, and its negatively association with plant height and days to flowering.

Singh *et al.* (1997) reported significant positive association of seed yield per plant with number of pods per plant, harvest index, number of primary, secondary and tertiary branches and biological yield per plant. Positive and significant correlations of grain yield per plant with seeds per plant, pods per plant and biological yield were noticed by Chand and Singh (1997).

Tripathi (1998) reported that grain yield per plant had positive correlations with pods per plant, harvest index, nitrogen in

seed and nitrogen harvest index. He also found that biological yield had a positive correlation with days to flower, days to maturity, plant height, branches per plant and nitrogen in biomass.

Kumar *et al.* (1999) in their studies on association analysis in chickpea found that seed yield was positively and significantly associated with biological yield per plant, pods per plant, seeds per plant, 100-seed weight, plant height and canopy spread.

Wahid and Ahmed (1999) observed that plant height and pods per plant had a strong and positive association with seed yield. Significant positive correlation of seed yield with pods per plant, primary branches per plant and 100-seed weight have been reported by Khedar and Maloo (1999).

Kumar *et al.* (1999) found highly significant and positive correlations of seed yield per plant with number of pods per plant, 100-seed weight and harvest index, while plant height showed negative correlation.

Arora and Jeena (1999) reported that seed yield was significantly and positively correlated with plant height, pods per plant and biological yield per plant. They also observed that biological yield expressed positive correlation with pods per plant while days to 50 per cent flowering was found to be positively associated with days to maturity.

Jeena and Arora (2001) noticed that biological yield exhibited the highest positive significant correlation with yield followed by pods per plant, plant height and secondary branches per plant.

2.3 Studies on path coefficient analysis

The correlation simply gives the idea of the joint variation of two characters. When more variables are included in the correlated study, the interrelationship between these characters can not reveal with efficiency the actual direct or indirect effects. For finding a suitable and reliable selection index, these correlations must be analysed further and partitioned into direct and indirect effects through path analysis. Path coefficient analysis, as originally proposed by Wright (1921) measures the direct influence of one variable upon the other and permits the partitioning of the correlation coefficients into components of direct and indirect effects. Deway and Lu (1959) have opened the way for plant breeders by using for the first time, the path coefficient analysis in breeding programmes.

Maloo and Sharma (1987), Sharma *et al.* (1989) and Sandhu *et al.* (1991) found that pods per plant had the highest direct positive contribution towards seed yield. However, Sharma and Maloo (1988) reported that for two different planting dates, number of pods per plant influenced grain yield the most, followed by number of primary branches per plant and days to flowering in chickpea.

Singh *et al.* (1990) reported biological yield and harvest index to be the major direct contributors to seed yield. 100-seed weight, plant height, days to flowering and maturity, canopy width and protein content contributed to seed yield mainly through indirect effect via biological yield and harvest index. Dasgupta *et al.* (1992) observed high positive direct effect of pods per plant, seeds per plant, 100-seed weight and seeds per pod on seed yield per plant.

Arora *et al.* (1994) observed that biological yield per plant, harvest index, pods per plant and 100-seed weight had the highest positive direct effect on seed yield per plant. Similar findings were also reported by Khorgade *et al.* (1995).

Ozdemir (1996) found that seed yield per plant, secondary branches per plant and number of seeds per plant were the most important yield components with significant direct and indirect effects. He also observed that number of pods per plant had a significant and positive correlation with seed yield; although it had a negative direct effect. Its indirect effect was positive via seed number and seed yield per plant. On the other hand maximum direct contribution towards seed yield by biological yield, followed by harvest index, days to maturity and branches per plant via biological yield was recorded by Tripathi (1998).

Dasgupta *et al.* (1998) reported high positive direct and indirect effects of pods per plant, biomass per plant and harvest index on seed yield/plant. Yadav *et al.* (1999) and Kumar *et al.* (1999) also reported biological yield and harvest index to be the major direct contributors to seed yield per plant.

Singh *et al.* (1999) reported that number of pods/plant and 100-seed weight had maximum direct effect on yield. However, primary and secondary branches showed indirect effect upon yield through number of pods per plant. Pods/plant had the highest direct effect on seed yield, followed by seeds per pod, 100-seed weight and primary branches per plant as noticed by Khedar and Maloo (1999).

2.4 Genetic divergence studies

Statistical procedures such as multivariate analysis based on Mahalanobis D^2 -statistic and Canonical variate analysis (Principle Component analysis) serve as important tools in quantifying the degree of genetic divergence among all possible pairs of population at genotypic level in different crops (Rao, 1952). The analysis also provides a measurement of related contribution of different components of diversity both at intra and inter-cluster levels (Murty and Quadri 1966; Somayajulu *et al.*, 1970; Lee and Kaltsikars, 1973; Joshi and Singh, 1979 and Jatasara and Paroda, 1983). D^2 -statistic is used to

select diverse parents through a study of genetic divergence. The D^2 technique for multivariate analysis had been successfully used in a variety of crops to select genetically divergent genotypes in order to exploit heterosis and for breeding together higher frequency of desirable genes in a strain. The genotypes exhibiting higher inter-cluster distance can be utilized for inter varietal hybridization programme to exploit the available diversity for having good heterotic effect (Singh and Gautam, 1987). D^2 -statistic for getting reliable estimates of genetic divergence between population for assessing the relative contribution of different characters to the total divergence was reported by Rao (1960), Arunachalam and Ram (1967), Bhatt (1970), Upadhyay and Murty (1970), Hussaini *et al.* (1977), Arunachalam (1981), Smocek and Martineck (1987) and Singh and Gautam (1987). Consequently, stable and diverse genotypes were identified which proved to be of great significance.

Although D^2 -statistic is a quantitative measure of divergence, yet grouping pattern is arbitrary, subjective and changeable under the influence of environment (Singh and Gupta, 1979). Combined analysis over environments for taking care of the effect of genotype x environment interaction on the classification of genotypes in peas reported by Gupta *et al.* (1992).

Research workers like Lal *et al.* (1989), Mian and Bahl (1989), Sarvaliya and Goyal (1994), Kumar (1997) and Deshmukh and Patil (1997) reported that there was not any relationship between geographic origin and genetic diversity in chickpea. Singh *et al.* (1990) reported that composition of clusters differed between environments. Jethava *et al.* (1996) reported that geographic distribution and genetic diversity were not related. They further found that seed yield per plant, pods per plant and 100-seed weight contributed most to genetic diversity.

Gupta and Krishna (1996) reported that cluster means for all the characters in chickpea indicated considerable genetic divergence between the groups. Tripathi (1997) reported that the hybridization among genotypes from the divergence clusters identified will aid breeding for higher yields of chickpea.

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

Sirohi *et al.* (1999) reported a wide range of genetic divergence in 25 genotypes of chickpea for 6 yield related traits. The cultivars within a cluster showed smaller D^2 values than those belonging to two different clusters. They also reported that 100-seed

weight and seed yield per plant were chiefly responsible for genetic divergence.

2.5 Reaction to diseases

Chickpea suffers from a number of abiotic and biotic stresses which cause severe yield losses leading to yield instability (Solh *et al.*, 1994). Among these diseases such as wilt, root rots, collar rot, stunt, *Ascochyta* blight and rust, and insect-pests such as pod borer (*Heliothis armigera*) are the major biotic stresses. Among these biotic stresses also, *Ascochyta* blight and collar rot cause tremendous losses to the chickpea crops every year. Two main breeding approaches i.e. to breed short duration varieties that can escape their attack and to breed and select genuinely resistant plant can be followed to mitigate losses from these stresses (Rheenen *et al.*, 1990).

Identification of resistance sources against these stresses is a prerequisite for any breeding programme aiming at the development of resistant cultivars. The work done in this direction by earlier researchers is cited as follows.

2.5.1 *Ascochyta* blight

Dey and Singh (1992) reported that the dissemination and development of *Ascochyta* blight in chickpea is greatly favoured by

high relative humidity and rain associated with strong wind whereas, dry conditions inhibit the disease development. Importance of rain and wind current in disease dissemination and development were also reported by Luthra *et al.* (1935), Singh (1984) and Katelaer *et al.* (1988).

Haware *et al.* (1995) reported that the occurrence and severity of *Ascochyta rabiei* was influenced by environmental factors. Kalia (1984) reported that *Ascochyta* blight considerably reduced the chickpea growing area in Himachal Pradesh. The area under the most popular variety, C-235 had shrunk drastically due to its susceptibility to this disease.

Five to 50 per cent yield losses due to *Ascochyta* blight were reported by Nene and Reddy (1987). Reddy and Singh (1990) reported a direct association between disease rating of *Ascochyta* blight and yield in chickpea. The increase in disease directly led to reduction in yield.

Singh and Sood (1990) observed that none of the lines could be rated as immune or resistant out of 75 germplasm lines of chickpea screened for resistance to *Ascochyta* blight. However some of the lines were observed to be moderately resistant or tolerant.

Source of resistance to *Ascochyta* blight in *desi* and *Kabuli* germplasm of chickpea has been reported by Lal and Amin (1992),

Jimenez Diaz *et al.* (1993), Gaur and Singh (1996) and Haware (1998).

Singh *et al.* (1998) reported that the none of the lines was treated as highly resistant out of 165 chickpea lines screened for resistance to *Ascochyta* blight. However, three lines ICCX-810800, ICC-13816 and PBG-1 were rated as resistant and 21 lines were moderately resistant.

Pratap (1999), in his studies on 38 early maturing genotypes of chickpea, found 3 genotypes to be highly resistant to *Ascochyta* blight and recommended their use in hybridization programmes. He also found 22 genotypes to be moderately resistant.

2.5.2 Collar rot

Seedling mortality in chickpea ranging from 54.7 to 95 per cent due to *Sclerotium rolfsii* have been reported by Mathur and Sinha (1970) and Kotasthane *et al.* (1976).

Gurha *et al.* (1982) in his studies on 165 chickpea cultivars found none of the cultivars to be immune, however 20 showed tolerance when screened against collar rot pathogen in pot trials.

Among 43 cultivars screened against *Sclerotium rolfsii* in pot and lab tests, RSG-130 and RSG-132 were found resistant and RSG-191 was found moderately resistant by Chitale *et al.* (1990). Similarly,

Sugha *et al.* (1991) observed that none of the 210 lines inoculated in pot experiments was tolerant or even moderately tolerant to *Sclerotium rolfsii*, indicating the need for screening more material in order to identify possible source of resistance. They also reported that during 1989-90, collar rot was widely prevalent in Mandi, Bilaspur, Una and Solan districts of Himachal Pradesh.



MATERIAL AND METHODS

Chapter-III

MATERIAL AND METHODS

The material and methods used in the present study are discussed in detail under the following headings:

3.1 Experimental material

The experimental material of the present investigation comprised 53 genetically diverse true breeding genotypes of chickpea (*Cicer arietinum* L.), including three standard checks viz., HPG-17, C-235 and Himachal Chana-2. The genotypes and their sources are given in Table 3.1.

3.2 Location of trial and weather conditions

The present investigation was carried out at the CSK HPKV, Research Sub Station, Berthin, Distt. Bilaspur, Himachal Pradesh, situated at an elevation of about 625 meters above mean sea level with 31°12'30" to 31°35'30" N latitude and 76°23'45" to 76°55'40" E longitude, representing the sub-montane low hill subtropical zone of Himachal Pradesh. The weekly meteorological data recorded during the cropping seasons 2000-01 and 2001-02 are given in Appendix-I.

Table 3.1 List of fifty three genotypes of chickpea under study

Sr.No.	Genotype	Source
1.	HPG-54	CSK HPKV, Research Sub Station, Berthin.
2.	HPG-78	-do-
3.	HPG-100	-do-
4.	HPG-124	-do-
5.	HPG-127	-do-
6.	HPG-129	-do-
7.	HPG-130	-do-
8.	HPG-131	-do-
9.	HPG-132	-do-
10.	HPG-133	-do-
11.	HPG-134	-do-
12.	HPG-135	-do-
13.	HPG-136	-do-
14.	HPG-137	-do-
15.	HPG-138	-do-
16.	HPG-142	-do-
17.	HPG-143	-do-
18.	HPG-144	-do-
19.	HPG-145	-do-
20.	HPG-147	-do-
21.	HPG-149	-do-
22.	HPG-150	-do-
23.	H-82-2	CSS Haryana Agricultural University, Hissar
24.	H-94-1	-do-
25.	H-94-83	-do-
26.	H-96-51	-do-
27.	H-208	-do-

Contd.....

Sr.No.	Genotype	Source
28.	GL-87069	Punjab Agricultural University, Ludhiana
29.	GL-87129	-do-
30.	GL-90104	-do-
31.	GL-90169	-do-
32.	GNG-580	Rajasthan Agricultural University, Bikaner
33.	CSG-8943	Indian Institute of Pulses Research, Kanpur
34.	CSG-9505	-do-
35.	PBG-1	Punjab Agricultural University, Ludhiana
36.	Pusa-372	Indian Agricultural Research Institute, New Delhi.
37.	ICC-15851	ICRISAT, Hyderabad
38.	ICC-15599	-do-
39.	ICCV-89701	-do-
40.	BGD-112	University of Agricultural Sciences, Dharwad
41.	BG-1007	Indian Agricultural Research Institute, New Delhi.
42.	BG-1086	-do-
43.	BG-1102	-do-
44.	KW-118	Bharari
45.	165	CCS Haryana Agricultural University, Hissar
46.	Avrodhi	Indian Institute of Pulses Research, Kanpur
47.	JG-9	Jawaharlal Nehru Krishi Vishvavidyalaya, Jabalpur
48.	L-550	Punjab Agricultural University, Ludhiana
49.	TCP-40	Indian Institute of Pulses Research, Kanpur
50.	WGG-9550	West Bengal
51.	HPG-17	CSK HPKV, Research Sub Station, Berthin.
52.	C-235	Punjab Agricultural University, Ludhiana
53.	Himachal Chana-2	CSK HPKV, Research Sub Station, Berthin.

3.3 Methods

The experimental trial was laid out in randomized complete block design with three replications each during *rabi* 2000-01 and 2001-02. Each plot comprised of 2 rows of 2.0 m length spaced 30 cm apart with plant to plant spacing of 10 cm.

The crop was grown under rainfed condition following recommended package of practices.

3.4 Recording of experimental data

Replication-wise data on the basis of five randomly taken competitive plants were recorded in each environment for all the traits except days to 50 per cent flowering, days to 75 per cent maturity, *Ascochyta* blight and collar rot for which data were recorded on plot basis.

3.4.1 Yield and its related traits

i. Seed yield per plant (g)

The average yield of five random plants was recorded in grams after threshing.

ii. Biological yield per plant (g)

Five randomly taken plants were harvested at maturity at the ground level and sun dried. The average weight of the whole plant was recorded.

iii. Harvest index

Proportion of economic yield (seed yield) to the total biological yield expressed as percentage was taken for this traits.

iv. 100-seed weight

A random sample of one hundred grains was taken from each genotype in each replication and weight was recorded.

v. Pods per plant

Number of pods per plant were counted at the time of maturity from the randomly taken plants per plot.

vi. Seeds per pod

Number of seeds in five random pods per plant of five randomly taken plants per plot, were counted and averaged to per pod.

3.4.2 Structural traits**i. Plant height (cm)**

The total height of a plant from ground level to the tip of main shoot was measured at the time of maturity.

ii. Primary branches per plant

Number of branches emerging from the main shoot of five randomly taken plants were counted and averaged to per plant.

3.4.3 Phenological traits

i. Days to 50 per cent flowering

It was recorded as number of days taken from the date of sowing to the 50 per cent blooming of plants in each plot.

ii. Days to 75 per cent maturity

It was recorded as number of days taken from the date of sowing to the 75 per cent maturity in each plot.

3.4.4 Diseases

i. *Ascochyta* blight

Infection caused by *Ascochyta rabiei* (Pass.) Labrousse in the form of water soaked lesions which turn roundish with brown margin and yellowish grey centre was observed on leaves, stems and pods of chickpea. Data were recorded on the basis of 1 to 9 scale given by Nene *et al.* (1981); where,

- 1 No lesions (resistant)
- 3 Lesions visible on few plants upon careful examination, no stem girdling. (moderately resistant)
- 5 Lesions visible on many plants with stem girdling on few plants; little damage (tolerant)
- 7 Lesions present on almost all plants; 50 per cent plants with stem girdling; death of a few plants; damage conspicuous (moderately susceptible)

- 9 Lesions very common on all plants; stem girdling on more than 50 per cent plants; death of most plants; damage more than 75 per cent (susceptible)

ii. Collar rot (*Sclerotium rolfsii* Sacc.)

The pathogen attacks more commonly at seedling stage in the collar region. The plants turn yellow and show wilting symptoms. Careful examination of such plants reveals rotting at collar region and white strands are seen growing over the affected tissue. The disease incidence was recorded as per the following arbitrary scale and the categorisation of genotypes was done as under:

- 1 No mortality (resistant)
3 Less than 2 per cent plants affected (moderately resistant)
5 3–5 per cent plants affected (tolerant)
7 6–10 per cent plants affected (moderately susceptible)
9 More than 10 per cent plants affected (susceptible)

3.5 Statistical analysis

The mean values of the genotypes in each replication for yield and yield contributing characters were used for statistical analysis.

3.5.1 Analysis of variance

The data for different characters were statistically analysed as per the procedure outlined by Panse and Sukhatme (1985). Separate

statistical analysis was done characterwise under each environment and combined over environments.

3.5.1.1 Analysis of variance for individual environments

The analysis of variance for individual environments was based on the following linear model of Fisher (1954).

$$y_{ij} = m + g_i + r_j + e_{ij}$$

where,

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

m = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error associated with the i^{th} genotype in the j^{th} replication

Analysis of variance

Source	df	MS	Expected MS	'F' cal
Replication	$r-1$	M_r	$\sigma^2_e + g\sigma^2_r$	M_r/M_e
Genotypes	$g-1$	M_g	$\sigma^2_e + r\sigma^2_g$	M_g/M_e
Error	$(r-1)(g-1)$	M_e	σ^2_e	
Total	$(rg-1)$			

where,

- r = number of replications
- g = number of genotypes
- σ^2_r = variance due to replications
- σ^2_g = variance due to genotypes
- σ^2_e = experimental error variance

The genotypic and phenotypic variances were calculated as below:

$$\text{Genotypic variance } (\sigma^2_g) = Mg - Me/r$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

$$\text{Error variance } (\sigma^2_e) = Me$$

Standard errors

$$\text{Standard error of mean } SE(m) = \pm (Me/r)^{1/2}$$

$$\text{Standard error of difference } SE(d) = \pm (2Me/r)^{1/2}$$

Critical differences

For comparing the means of any two genotypes:

$$CD \text{ at } 5\% = SE(d) \times 't' \text{ value at } 5\% \text{ level of significance at error d.f.}$$

Coefficient of variation

$$CV (\%) = \{(Me)^{1/2} / \text{Grand mean}\} \times 100$$

Estimation of parameters of variability in individual environments

The following parameters were estimated following Burton and De Vane (1953) and Johnson *et al.* (1955).

(I) Genotypic coefficient of variation (GCV%) = $(\sigma_g/\bar{x}) \times 100$

(II) Phenotypic coefficient of variation (PCV%) = $(\sigma_p/\bar{x}) \times 100$

where,

σ_g = genotypic standard deviation

σ_p = phenotypic standard deviation

$\bar{x}$ = grand mean

(III) Heritability in broad sense ($h^2\%$) = $\{\sigma^2_g / (\sigma^2_g + \sigma^2_e/r)\} \times 100$

(IV) Genetic advance (ΔA) = $K \times \sigma_p \times h^2$

where,

K = Selection differential at 5% selection intensity, ($K=2.06$)

(V) Genetic advance as percentage of mean ($GA\%$) = $(GA/\bar{x}) \times 100$

3.5.1.2 Analysis of variance for combined over environments

Analysis of variance

Source	d.f.	MS	Expected MS	'F' cal
Replication	(r-1)	Mr	$\sigma^2_e + gy\sigma^2_r$	Mr/Me
Environments	(y-1)	My	$\sigma^2_e + rg\sigma^2_e + r\sigma^2_{gy}$	My/Me
Replication x Environments	(r-1)(y-1)	Mry	$\sigma^2_e + g\sigma^2_{ry}$	Mry/Me
Genotype	(g-1)	Mg	$\sigma^2_e + r\sigma^2_{gy} + y\sigma^2_g$	Mg/Me
Genotype x Environment	(g-1)(y-1)	Mgy	$\sigma^2_e + r\sigma^2_{gy}$	Mgy/Me
Error	y(r-1)(g-1)	Me	σ^2_e	

where,

r = number of replications

g = number of genotypes

y = number of environments

σ^2_e = Error variance = Me

σ^2_g = Genotypic variance = Mg

σ^2_r = Variance due to replication = Mr

σ^2_y = Variance due to environment = My

σ^2_{ry} = Variance due to replication x environment = Mry

σ^2_{gy} = Variance due to genotype x environment = Mgy

The genotypic and phenotypic variance were calculated as below:

Genotypic variance (σ^2_g) = $(Mg - Mgy)/ry$

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_{gy} + \sigma^2_e$

Error variance (σ^2_e) = Me

Genotypic x environment interaction variance (σ^2_{gy}) = $(Mgy - Me)/r$

Standard errors

Standard error of mean $SE(m) = \pm (Me/ry)^{1/2}$

Standard error of difference $SE(d) = \pm (2Me/ry)^{1/2}$

Critical difference

For comparing the means of any two genotypes

CD at 5% = $SE(d) \times 't'$ value at 5% level of significance at combined error d.f.

Coefficient of variation

$$CV(\%) = \{(\text{Me})^{1/2} / \text{Grand mean}\} \times 100$$

Estimation of parameters of variability in combined over environments

- (I) Genotypic coefficient of variation (GCV%) = $(\sigma_g / \bar{x}) \times 100$
- (II) Phenotypic coefficient of variation (PCV%) = $\{(\sigma_g + \sigma_{gy} + \sigma_e) / \bar{x}\} \times 100$
- (III) Heritability (h^2) in broad sense (%) = $\{\sigma_g^2 / (\sigma_g^2 + \sigma_{gy}^2 + \sigma_e^2)\} \times 100$
- (IV) Genetic advance (GA) at 5% selection intensity = $K (\sigma_g + \sigma_{gy} + \sigma_e) \times h^2$
- (V) Genetic advance as percentage of mean (GA%) = $(GA / \bar{x}) \times 100$

where,

σ_g = genotypic standard deviation

σ_{gy} = genotypic x environment standard deviation

σ_e = error standard deviation

For convenience following classifications were used for describing various parameters of variability in the text:

PCV and GCV	> 25%	High
	10-25%	Moderate
	< 10%	Low
Heritability (h^2)	> 80%	High
	60-80%	Moderate
	< 60%	Low

Genetic advance > 30% High
 20-30% Moderate
 < 20% Low

3.5.2 Estimation of correlation coefficients

Phenotypic and environmental coefficients of correlation were worked out following analysis of covariance involving all possible paired combinations among the characters studies.

Analysis of covariance

Source	d.f.	Mean sum of products	Expected mean sum of products
Replication	(r-1)	Mr_{xy}	$\sigma_{e_{xy}} + \sigma_{r_{xy}}$
Genotypes	(g-1)	Mg_{xy}	$\sigma_{e_{xy}} + \sigma_{g_{xy}}$
Error	(r-1)(g-1)	Me_{xy}	$\sigma_{e_{xy}}$

The genotypic, phenotypic and environmental covariances were calculated as follows:

$$\sigma_{g_{xy}} = (Mg_{xy} - Me_{xy})/r$$

$$\sigma_{p_{xy}} = \sigma_{g_{xy}} + \sigma_{e_{xy}}$$

$$\sigma_{e_{xy}} = Me_{xy}$$

where,

$$r = \text{number of replications}$$

$$g = \text{number of genotypes}$$

- $\sigma_{g_{xy}}$ = genotypic covariance between traits x and y
 $\sigma_{p_{xy}}$ = phenotypic covariance between traits x and y
 $\sigma_{e_{xy}}$ = environmental covariance between traits x and y
 $M_{g_{xy}}$ = mean sum of squares due to genotypes from the analysis of covariance between traits x and y
 $M_{e_{xy}}$ = mean sum of squares due to error from the analysis of covariance between traits x and y

The phenotypic, genotypic and environmental coefficients of correlation were computed as per the methods suggested by Al-Jibouri *et al.* (1958) as under:

Phenotypic coefficient of correlation ($r_{p_{xy}}$)

$$r_{p_{xy}} = \sigma_{p_{xy}} / (\sigma^2_{p_x} \times \sigma^2_{p_y})^{1/2}$$

where,

- $\sigma_{p_{xy}}$ = phenotypic covariance between two traits x and y
 $\sigma^2_{p_x}$ = phenotypic variance of trait x
 $\sigma^2_{p_y}$ = phenotypic variance of trait y.

Genotypic coefficient of correlation ($r_{g_{xy}}$)

$$r_{g_{xy}} = \sigma_{g_{xy}} / (\sigma^2_{g_x} \times \sigma^2_{g_y})^{1/2}$$

where,

- $\sigma_{g_{xy}}$ = genotypic covariance between two traits x and y.
 $\sigma^2_{g_x}$ = genotypic variance of trait x
 $\sigma^2_{g_y}$ = genotypic variance of trait y

Environmental coefficient of correlation ($r_{e_{xy}}$)

$$r_{e_{xy}} = \sigma_{e_{xy}} / (\sigma^2_{e_x} \times \sigma^2_{e_y})^{1/2}$$

where,

$\sigma_{e_{xy}}$ = environmental covariance between trait x and y

$\sigma^2_{e_x}$ = environmental variance of trait x

$\sigma^2_{e_y}$ = environmental variance of trait y

3.5.3 Test of significance

The significance of phenotypic coefficient of correlation at (g-2) degree of freedom where, 'g' is the number of genotypes, and environmental coefficient of correlation at {(r-1)(g-1)-1} degree of freedom, where, 'r' and 'g' stand for number of replication and genotypes respectively, were tested at 5 per cent level of significance against the table values of correlation coefficient (Fisher and Yates, 1963).

3.5.4 Path coefficient analysis

The path coefficients were calculated by employing the method suggested by Dewey and Lu (1959). This was accomplished by solving a set of equations of the form:

$$P_{y_1} + P_{y_2 r_{12}} + P_{y_3 r_{13}} + \dots + P_{y_n r_{1n}} = r_{y_1}$$

$$P_{y_1 r_{12}} + P_{y_2} + P_{y_3 r_{23}} + \dots + P_{y_n r_{2n}} = r_{y_2}$$

:

:

$$P_{y_1 r_{n1}} + P_{y_2 r_{n2}} + P_{y_3 r_{n3}} + \dots + P_{y_n} = r_{y_n}$$

where,

$P_{y_1}, P_{y_2}, \dots, P_{y_n}$ are the direct path effects of 1, 2, ..., n variables on the dependent variable 'y'.

$r_{12}, r_{13}, \dots, r_{n(n-1)}$ are the possible coefficients of correlation between various independent variables and $r_{y_1}, r_{y_2}, \dots, r_{y_n}$ are the coefficients of correlation of independent variables with dependent variable 'y'.

The degree of determination ($P^2_x R$ of such variable/variables on the dependent variable was calculated as follows:

$$\text{Residual effects } (P_{X_R}) = (1-R^2)^{\frac{1}{2}}$$

where,

$$R^2 = \sum_{i=1}^n P_{iy} r_{iy}$$

3.5.5 Estimation of genetic diversity

A measure of group distance based on multiple characters was given by Mahalanobis, 1928 (c.f. Rao, 1952).

With $x_1, x_2, x_3, \dots, x_p$ as the multiple measurements available on each individual and $d_1, d_2, d_3, \dots, d_p$ as $x_1^{-1} - x_1^{-2}, x_2^{-1} - x_2^{-2}, \dots, x_p^{-1} - x_p^{-2}$, respectively, being the difference in the means of two populations, Mahalanobis' D^2 -statistics is defined as follows:

$$pD^2 = b_1 d_1 + b_2 d_2 + \dots + b_p d_p$$

Here, the b_i value are to be estimated such that the ratio of variance between the populations to the variance within the populations is maximized. In terms of variances and covariances, the D^2 value is obtained as follows:

$$pD^2 = W^{ij} (x_i^{-1} - x_i^{-2}) (x_j^{-1} - x_j^{-2})$$

where,

W^{ij} is the inverse of estimated variance co-variance matrix.

3.5.6 Test of significance

Using 'V' statistic which, in turn, utilizes Wilk's criteria, a simultaneous test of differences between mean values of a number of correlated variables/characters at 'pq' d.f. (where p=number of variables/characters and q=number of germplasm-1) done as suggested by Rao (1952).

3.5.7 Testing the significance of D^2 values

The D^2 values obtained for a pair of population was taken as the calculated value of χ^2 and was tested against the tabulated value of χ^2 for 'p' d.f., where p is the number of characters considered.

3.5.8 Grouping of genotypes into various clusters

Using D^2 values, different genotypes were grouped into various clusters following Toucher's method as suggested by Rao (1952).

3.5.9 Average intra and inter-cluster distances

$$\text{Average intra-cluster } D^2 = \sum D_i^2 / n$$

where,

$\sum D_i^2$ = sum of all distances between all possible combinations (n) of the genotypes included in the cluster.

$$\text{Average inter-cluster distance } D^2 = \sum D_{ij}^2 / n_i \cdot n_j$$

where,

$\sum D_{ij}^2$ = sum of all distances between all possible combinations ($n_i \cdot n_j$) of the genotypes between the clusters.

n_i = number of genotypes in i^{th} cluster

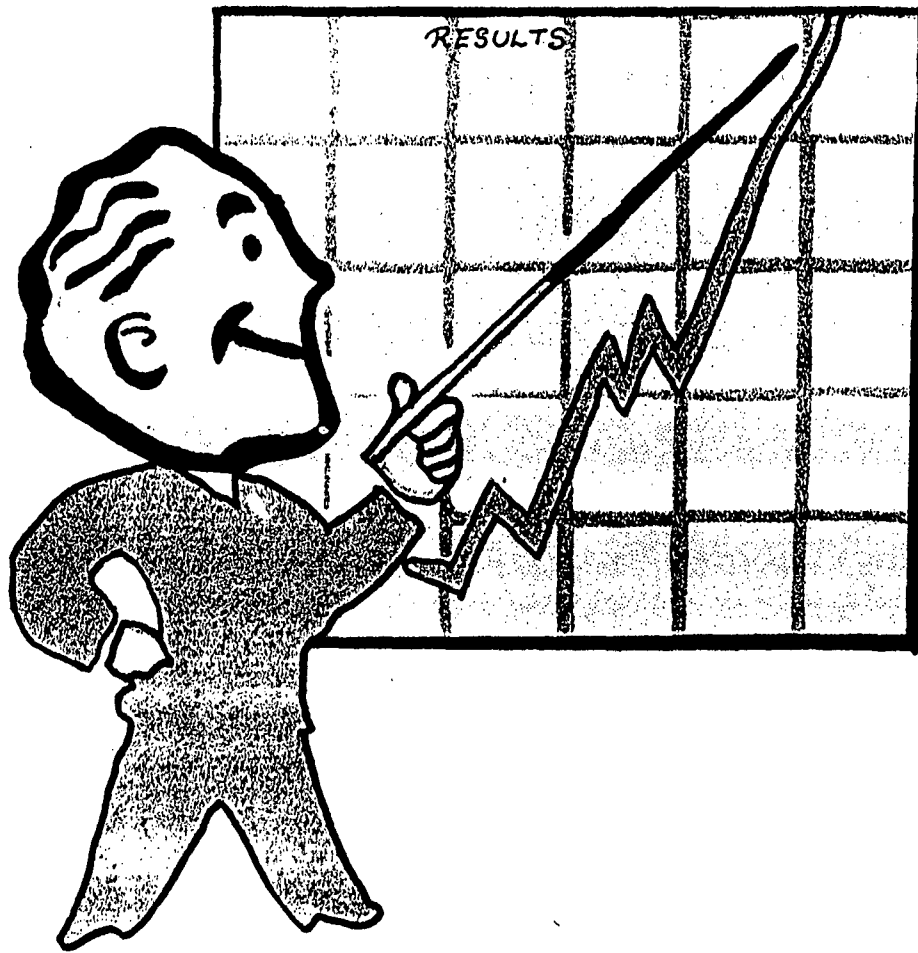
n_j = number of genotypes in j^{th} cluster

3.5.10 Cluster mean

Character means of chickpea genotypes falling under different clusters in individual as well as combined over environments were also calculated.

3.5.11 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of $d_i = Y_i^j - Y_i^k$ values. Rank 1 was given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of characters. The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first.



RESULTS

Chapter-IV

RESULTS

The results obtained on various aspects to understand the nature and magnitude of variation, correlation and path coefficients for seed yield and other related traits, genetic divergence under two environments viz., environment I (*rabi* 2000-01), environment II (*rabi* 2001-02) and combined over environments, along with the evaluation of chickpea genotypes for resistance to *Ascochyta* blight and collar rot diseases are presented below:

4.1 Studies on the nature and magnitude of variation for seed yield and other related traits

The results obtained on the nature and magnitude of variation for seed yield and other related traits are given below:

4.1.1 Analysis of variance

Mean values of 53 chickpea genotypes in environment I (*rabi*, 2000-01), environment II (*rabi*, 2001-02) and combined over environments observed for different characters studied along with their standard error and critical differences are presented in Annexure-II to IV.

Analysis of variance for the randomized block design with respect to 53 genotypes of chickpea revealed significant differences among the material used in the present investigation for all the ten characters studied viz., seed yield per plant, biological yield per plant, plant height, pods per plant, seeds per pod, primary branches per plant, days to 50 per cent flowering, days to 75 per cent maturity, 100-seed weight and harvest index under both the individual environments as well as combined over environments (Table 4.1). Analysis of variance in combined over environments also showed significant differences due to environment for seed yield per plant, plant height, pods per plant, primary branches per plant and days to 75 per cent maturity whereas, variation due to genotype x environment interaction was significant for biological yield per plant, plant height, primary branches per plant, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight.

4.1.2 Estimates of parameters of variability

The estimates of parameters of variability viz., grand mean, range of variation, phenotypic coefficient of variation, genotypic coefficient of variation, heritability in broad sense and expected genetic advance expressed as percentage of mean for different traits studied in environment-I, environment-II and combined over environments (Tables 4.2 to 4.4) are described in detail as below:

Table 4.1 Analysis of variance for different traits in environment I, environment II and combined over environments

Source of variation	df.	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
Environment I											
Replication	2	1.850	6.480	10.844	26.164	0.001	0.039	5.125	0.750	0.056	1.641
Genotype	52	29.859**	121.169**	173.454*	530.576**	0.142**	0.398**	195.519**	73.451**	98.399**	93.481**
Error	104	1.481	5.215	6.090	45.585	0.002	0.060	3.670	2.793	0.032	22.151
Environment II											
Replication	2	0.781	0.666	14.403	41.533	0.002	0.009	8.250	11.750	0.236	9.218
Genotype	52	26.948**	109.181**	158.351**	586.948**	0.125**	0.294**	168.620**	53.788*	94.390**	116.236**
Error	104	0.570	3.679	8.964	41.532	0.007	0.030	3.264	2.754	0.282	13.514
Combined over environments											
Environments	1	8.851**	15.211	65.062**	458.875**	0.001	0.367**	0.500	5233.000**	0.070	27.500
Replication	2	1.127	4.917	9.375	12.250	0.001	0.014	11.250*	9.500*	0.230	5.375
Environment X Replication	2	1.504	2.242	15.906	17.594	0.002	0.034	2.250	3.500	0.066	5.344
Genotype	52	55.493**	222.185**	308.747**	1062.800**	0.265**	0.612**	344.705**	106.115**	192.351**	187.878**
Genotype X Environments	52	1.315	8.166**	23.060**	54.726	0.002	0.080**	19.439**	20.942**	0.438**	21.835
Error	208	1.026	4.447	7.527	43.558	0.005	0.045	3.466	2.817	0.157	17.834

* Significant at 5% level

** Significant at 1% level

4.1.2.1 Phenotypic coefficients of variation (PCV)

High PCV (>25 %) was observed for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight in both the environments I and II as well as combined over environments. Primary branches per plant, plant height, seeds per pod and harvest index showed moderate PCV (10-25%), whereas, both phenological traits namely, days to 50 per cent flowering and days to 75 per cent maturity recorded low PCV (< 10%) in both the environments I and II as well as combined over environments.

4.1.2.2 Genotypic coefficient of variation (GCV)

High GCV (> 25%) was observed for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight in both the environments I and II as well as combined over environments. Plant height, primary branches per plant, seeds per pod and harvest index showed moderate GCV (10 - 25%), whereas, days to 50 per cent flowering and days to 75 per cent maturity recorded low GCV (< 10%) in both the environments I and II as well as combined over environments.

4.1.2.3 Heritability (h^2)

High heritability (> 80%) was observed for 100-seed weight, seeds per pod, plant height, days to 50 per cent flowering, days to

Table 4.2 Mean performance and parameters of variability for various traits studied in environment I

Character	Mean $\pm$ SE (m)	Range		PCV (%)	GCV (%)	h ² bs (%)	Genetic advance (% of mean)
		Min.	Max.				
Seed yield/plant (g)	7.872 $\pm$ 0.70	2.89	16.93	42.02	39.07	86.5	74.82
Biological yield/plant (g)	16.104 $\pm$ 1.32	5.48	40.32	41.13	38.61	88.1	74.64
Plant height (cm)	42.826 $\pm$ 1.42	28.60	57.73	18.37	17.44	90.2	34.11
Pods/plant	37.362 $\pm$ 3.90	13.00	71.87	38.53	34.03	78.0	61.91
Seeds/pod	1.561 $\pm$ 0.03	1.21	2.04	14.16	13.82	95.3	27.55
Primary branches/plant	2.253 $\pm$ 0.14	1.73	4.00	18.47	14.91	65.2	24.85
Days to 50% flowering	127.264 $\pm$ 1.11	105.00	144.67	6.46	6.28	94.6	12.59
Days to 75% maturity	170.817 $\pm$ 0.97	159.33	179.33	3.00	2.84	89.4	5.53
100-seed weight	18.848 $\pm$ 0.11	11.03	30.52	30.40	30.38	99.9	62.55
Harvest index (%)	48.976 $\pm$ 2.72	39.84	61.91	13.84	9.96	51.8	14.76

Table 4.3 Mean performance and parameters of variability for various traits studied in environment II

Character	Mean $\pm$ SE (m)	Range		PCV (%)	GCV (%)	h ² bs (%)	Genetic advance (% of mean)
		Min.	Max.				
Seed yield/plant (g)	7.539 $\pm$ 0.44	2.39	15.18	40.59	39.33	93.9	78.52
Biological yield/plant (g)	15.666 $\pm$ 1.11	3.97	37.78	39.78	37.85	90.5	74.17
Plant height (cm)	43.731 $\pm$ 1.73	29.80	56.87	17.53	16.14	84.7	30.59
Pods/plant	34.959 $\pm$ 3.72	11.00	71.33	42.75	38.57	81.4	71.68
Seeds/pod	1.557 $\pm$ 0.049	1.20	2.00	13.86	12.77	84.8	24.41
Primary branches/plant	2.184 $\pm$ 0.10	1.93	3.93	15.76	13.56	74.0	24.27
Days to 50% flowering	127.283 $\pm$ 0.104	103.33	144.67	6.00	5.83	94.4	11.67
Days to 75% maturity	162.704 $\pm$ 0.958	151.00	171.00	2.73	2.53	86.1	4.84
100-seed weight	18.816 $\pm$ 0.307	11.04	30.15	29.90	29.77	99.1	61.06
Harvest index (%)	48.391 $\pm$ 2.122	36.02	60.91	14.28	12.09	71.7	21.09

Table 4.4 Mean performance and parameters of variability for various traits studied in combined over environments

Character	Mean $\pm$ SE (m)	Range		PCV (%)	GCV (%)	h^2bs (%)	Genetic advance (% of mean)
		Min.	Max.				
Seed yield/plant (g)	7.706 $\pm$ 0.41	2.64	16.06	41.15	39.00	89.8	76.18
Biological yield/plant (g)	15.885 $\pm$ 0.86	4.72	39.05	39.87	37.60	88.9	73.02
Plant height (cm)	43.278 $\pm$ 1.12	29.20	56.90	17.16	15.94	86.3	30.52
Pods/plant	36.161 $\pm$ 2.69	12.00	71.60	40.22	35.85	79.4	65.79
Seeds/pod	1.559 $\pm$ 0.028	1.99	2.02	14.12	13.42	90.3	26.29
Primary branches/plant	2.219 $\pm$ 0.087	1.90	3.97	16.52	13.43	66.1	22.53
Days to 50% flowering	127.274 $\pm$ 0.76	115.67	144.67	5.97	5.79	94.0	11.55
Days to 75% maturity	166.761 $\pm$ 0.69	155.17	173.33	2.47	2.26	83.4	4.25
100-seed weight	18.832 $\pm$ 0.162	11.04	30.33	30.11	30.03	99.5	61.70
Harvest index (%)	48.684 $\pm$ 1.72	37.93	60.71	13.86	10.81	60.8	17.36

75 per cent maturity, biological yield per plant, seed yield per plant and pods per plant in both the environments I and II as well as combined over environments except pods per plant for which heritability was moderate (60 - 80%) in environment I. Primary branches per plant and harvest index showed moderate heritability in both the environments I and II as well as combined over environments except harvest index for which heritability was low (< 60%) in environment I.

4.1.2.4 Genetic advance (GA)

Expected genetic advance expressed as percentage of mean was observed high (> 30%) for seed yield per plant, biological yield per plant, pods per plant, 100-seed weight and plant height in environments I, II and combined over environments. Moderate GA (20 - 30%) was observed for seeds per pod and primary branches per plant in individual environments as well as combined over environments. Similarly, it was also moderate for harvest index in environment II. Other characters viz., days to 50 per cent flowering, days to 75 per cent maturity and harvest index showed low GA in environments I, II and combined over environments except harvest index in environment II.

4.2 Studies on correlation among seed yield and other traits

In order to understand the nature of correlations among seed yield per plant and other traits, estimates of correlation coefficients at phenotypic, genotypic and environmental levels and direct and indirect effects through path analysis were computed and the results obtained are presented below:

4.2.1 Estimates of correlation coefficients at phenotypic, genotypic and environmental levels

The results on correlations, computed at phenotypic, genotypic and environmental levels for all possible paired combinations among 10 traits, in each environment and combined over environments are presented in Tables 4.5, and 4.6 and described as under:

4.2.1.1 Estimates of correlation coefficients at phenotypic level

At phenotypic level, seed yield per plant exhibited significant and positive correlation with biological yield per plant followed by pods per plant, primary branches per plant and plant height in both the environments I and II as well as combined over environments. Significant and positive correlation of seed yield per plant with 100-seed weight was also observed but only in environment I. Correlations between seed yield per plant and harvest index was also significant and positive in environment I and combined over environments.

Table 4.5 Estimates of correlation coefficient at Phenotypic (P), genotypic (G) and environmental (E) levels among different traits studied of chickpea in E-1 and E-II

Character		Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary plant branches/	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
Seed yield/ yield (g)	P		0.942*	0.461*	0.810*	-0.158	0.502*	0.038	-0.101	0.273*	0.272*
	G		0.958	0.475	0.825	-0.202	0.558	0.045	-0.120	0.293	0.259
	E		0.831*	0.357*	0.765*	0.326*	0.383*	-0.036	0.040	0.059	0.386*
Biological yield/plant (g)	P	0.938*		0.603*	0.749*	-0.231	0.487*	0.120	-0.002	0.372*	-0.041
	G	0.952		0.635	0.756	-0.271	0.561	0.132	-0.016	0.397	-0.012
	E	0.787*		0.341*	0.758*	0.228*	0.304*	-0.009	0.109	0.013	-0.136
Plant height (cm)	P	0.369*	0.529*		0.202	-0.208	0.147	0.441*	0.296*	0.558*	-0.354*
	G	0.388	0.559		0.197	-0.229	0.175	0.464	0.305	0.589*	-0.548
	E	0.235*	0.329*		0.248*	0.064	0.069	0.176	0.216*	-0.083	0.095
Pods/plant	P	0.783*	0.697*	0.086		-0.141	0.494*	-0.137	-0.164	-0.080	0.211
	G	0.828	0.717	0.086		-0.188	0.542	-0.158	-0.207	-0.089	0.272
	E	0.552*	0.614*	0.087		0.215*	0.389*	-0.010	0.055	-0.105	0.116
Seeds/pod	P	-0.096	-0.137	0.044	-0.025		-0.194	-0.160	-0.062	-0.596*	0.200
	G	-0.129	-0.171	-0.046	-0.059		-0.243	-0.171	-0.078	-0.610	0.241
	E	0.198*	0.105	-0.033	0.143		-0.023	0.044	0.144	-0.144	0.205*

Contd.....

Character	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary plant branches/	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
Primary branches/plant	P 0.387*	0.303*	-0.035	0.492*	-0.151		-0.113	-0.120	0.053	0.122
	G 0.414	0.311	-0.073	0.561	-0.189		-0.126	-0.142	0.066	0.101
	E 0.336*	0.309*	0.116	0.258*	-0.005		-0.103	-0.061	0.010	0.154
Days to 50% flowering	P 0.045	0.145	0.433*	-0.178	-0.122	-0.098		0.738*	0.416*	-0.225
	G 0.046	0.163	0.491	-0.187	-0.140	-0.115		0.740	0.429	-0.320
	E 0.032	-0.073	-0.064	-0.141	0.037	-0.018		0.753*	-0.119	-0.005
Days to 75% maturity	P 0.083	0.176	0.282*	-0.059	0.006	-0.105	0.818*		0.228	-0.235
	G 0.098	0.209	0.351	-0.047	0.003	-0.133	0.824		0.244	-0.336
	E -0.053	-0.076	-0.122	-0.121	0.026	0.005	0.846*		-0.175	-0.029
100-seed weight (g)	P 0.195	0.300*	0.431*	-0.202	-0.567*	-0.143	0.384*	0.248		-0.200
	G 0.201	0.315	0.474	-0.230	-0.621	-0.171	0.396	0.265		-0.280
	E 0.054	0.062	-0.071	0.109	0.057	0.065	0.061	0.080		0.061
Harvest index (%)	P 0.241	-0.079	-0.499*	0.255	0.144	0.202	-0.316*	-0.221	-0.262	
	G 0.280	0.004	-0.585	0.402	0.160	0.278	-0.406	-0.295	-0.309	
	E 0.082	-0.498*	-0.211*	-0.226*	0.091	-0.001	0.141	0.050	-0.033	

* Significant at 5 per cent level.

Values above and below the diagonal represent correlation coefficients in environment I and II, respectively.

Table 4.6 Estimates of correlation coefficient at Phenotypic (P), genotypic (G) and environmental (E) levels among different traits studied of chickpea in combined over environments

Character		Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
Seed yield/ yield (g)	P		0.940*	0.428*	0.800*	-0.118	0.470*	0.030	-0.014	0.236	0.277*
	G		0.956	0.447	0.832	-0.157	0.522	0.033	-0.017	0.248	0.298
	E		0.808*								
Biological yield/plant (g)	P			0.289*	0.671*	0.228*	0.368*	-0.010	0.004	0.043	0.285*
	G			0.571*	0.717*	-0.180	0.416*	0.123	0.095	0.342*	-0.037
	E			0.605	0.729	-0.218	0.466	0.138	0.106	0.362	0.029
Plant height (cm)	P			0.330*	0.692*	0.145	0.305*	-0.037	0.024	0.041	-0.279*
	G				0.127	-0.119	0.017	0.425*	0.280*	0.512*	-0.379*
	E				0.121	-0.135	-0.003	0.467	0.325	0.554	-0.507
Pods/plant	P				0.161	-0.002	0.088	0.047	0.031	-0.069	-0.052
	G					-0.075	0.522*	-0.180	-0.162	-0.141	0.261
	E					-0.116	0.600	-0.199	-0.192	-0.160	0.388
Seeds/pod	P					0.163	0.032	-0.072	-0.031	0.046	-0.030
	G						-0.170	-0.147	-0.014	-0.579*	0.181
	E						-0.217	-0.163	-0.026	-0.611	0.211
Primary branches/plant	P						-0.012	0.037	0.066	0.024	0.129
	G							-0.124	-0.140	-0.032	0.206
	E							-0.145	-0.179	-0.041	0.268
Days to 50% flowering	P							-0.068	-0.033	0.039	0.098
	G								0.838*	0.418*	-0.275*
	E								0.857	0.432	-0.375
Days to 75% maturity	P								0.791*	0.013	0.058
	G									0.276*	-0.265
	E									0.303	-0.375
100-seed weight (g)	P									0.010	0.007
	G										-0.232
	E										-0.298
											-0.004

* Significant at 5 per cent level.

Biological yield per plant expressed positive and significant correlations with pods per plant, followed by plant height, primary branches per plant and 100 seed weight in environments I and II as well as combined over environments.

Plant height had positive and significant correlations with 100-seed weight, days to 50 per cent flowering and days to 75 per cent maturity whereas, plant height had negative correlation with harvest index in environments I and II as well as combined over environments. Positive and significant correlations were also observed between pods per plant and primary branches per plant; days to 50 per cent flowering and days to 75 per cent maturity in both the environments I and II and over environments. Days to 50 per cent flowering also showed significant and positive association with 100-seed weight in environment II and over environments. Significant and positive correlation also existed between days to 75 per cent maturity and 100 seed weight in the combined over environments. Seeds per pod showed significant and negative correlations with 100-seed weight in environment I, II and combined over environments whereas days to 50 per cent flowering was negatively associated with harvest index in environment II and combined over environments.

4.2.1.2 Estimates of correlation coefficients at genotypic level

At the genotypic level, the estimates of correlation coefficients were generally similar to that observed at the phenotypic level, though their magnitude were slightly higher than the corresponding phenotypic correlations. Here, also seed yield per plant and pods per plant exhibited positive association with harvest index whereas, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight expressed negative correlation with harvest index in both the individual as well as combined over environments.

4.2.1.3 Estimates of correlation coefficients at environmental level

Environmental correlations in general were low in magnitude than the corresponding phenotypic as well as genotypic correlations. Positive and significant correlations were observed for seed yield per plant with biological yield per plant, pods per plant, primary branches per plant, plant height and seeds per pod in both the environments I and II as well as combined over environments. Seed yield per plant also showed positive and significant correlation with harvest index in environment I and combined over environments.

Biological yield per plant exhibited positive and significant correlation with pods per plant, plant height and primary branches per plant in environments I, II and combined over environments. Biological

yield per plant also recorded positive and significant correlation with seeds per pod in environment I only, however, it recorded significant but negative association with harvest index in environment II and combined over environments.

Positive and significant correlations were observed for plant height with pods per plant and days to 75 per cent maturity in environment I only, however, plant height had significant and negative association with harvest index in environment II. Pods per plant exhibited significant and positive association with primary branches in environments I and II; with seeds per pod in environment I and significantly negative association with harvest index in environment II. Similarly, positive and significant correlations were observed between seeds per pod and harvest index in environment I only and days to 50 per cent flowering and days to 75 per cent maturity in both the individual as well as combined over environments.

4.2.2 Estimates of direct and indirect effects

The direct and indirect effects were computed through path analysis and results so obtained are presented below:

The estimates of direct and indirect effects of different characters on seed yield per plant along with their correlation coefficients with seed yield per plant for environment I, environment II

and combined over environments are given in Tables 4.7 to 4.9, respectively.

At phenotypic level high direct contribution of biological yield followed by harvest index and pods per plant towards seed yield per plant were observed in environment I, environment II and combined over environments. Though the plant height and 100-seed weight also registered positive direct effects on seed yield per plant but the values were of low magnitude. Similar was the case of contribution by primary branches per plant in environment II. On the other hand, primary branches per plant exhibited low direct negative effect on seed yield per plant in environment I and combined over environments.

Pods per plant, plant height and primary branches per plant contributed towards seed yield mainly via biological yield in environment I, environment II and combined over environments and 100-seed weight mainly via biological yield in environment I only. Similarly biological yield per plant in environments I, II and combined over environments and harvest index in environment I and combined over environments also exhibited indirect positive effects towards seed yield per plant via pods per plant though the values were of low magnitude.

At the genotypic level also the estimates of direct and indirect effects were generally similar to those observed at phenotypic

Table 4.7 Estimates of direct and indirect effects for various traits studied towards seed yield in chickpea in environment I

Character		Biological yield/plant (g)	Plant height (cm)	Pods/plant	Seeds/pod	Primary branches/plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)	Correlation with seed yield/plant
Biological yield/plant (g)	P	0.873	0.009	0.070	-0.002	-0.003	0.005	0.000	0.001	-0.012	0.942*
	G	0.840	0.053	0.072	0.004	-0.007	0.005	0.001	-0.006	-0.004	0.958
Plant height (cm)	P	0.527	0.015	0.019	-0.001	-0.001	0.018	-0.015	0.002	-0.103	0.461*
	G	0.534	0.084	0.019	0.004	-0.002	0.016	-0.013	-0.009	-0.158	0.475
Pods/plant	P	0.654	0.003	0.093	-0.001	-0.003	-0.006	0.008	0.000	0.061	0.810*
	G	0.634	0.017	0.095	0.003	-0.007	-0.006	0.009	0.001	0.078	0.825
Seeds/pod	P	-0.202	-0.003	-0.013	0.007	0.001	-0.007	0.003	-0.002	0.058	-0.158
	G	-0.228	-0.019	-0.018	-0.016	0.003	-0.006	0.003	0.009	0.069	-0.202
Primary Branches/plant	P	0.425	0.002	0.046	-0.001	-0.007	-0.005	0.006	0.000	0.035	0.502*
	G	0.471	0.015	0.052	0.004	-0.012	-0.004	0.006	-0.001	0.029	0.558
Days to 50% flowering	P	0.104	0.007	-0.013	-0.001	0.001	-0.042	-0.038	0.001	0.065	0.038
	G	0.111	0.039	-0.015	0.003	0.002	0.036	-0.031	-0.006	-0.092	0.045
Days to 75% maturity	P	-0.002	0.005	-0.015	0.000	0.001	0.031	-0.052	0.001	-0.068	-0.101
	G	-0.014	0.026	-0.020	0.001	0.002	0.026	-0.041	-0.004	-0.097	-0.120
100-seed weight (g)	P	0.325	-0.009	-0.007	-0.004	0.000	0.017	-0.012	0.004	-0.058	0.273*
	G	0.333	0.049	-0.008	0.010	-0.001	0.015	-0.010	-0.015	-0.080	0.293
Harvest index (%)	P	-0.036	-0.005	0.020	0.001	-0.001	-0.009	0.012	-0.001	0.291	0.272*
	G	-0.010	-0.046	0.026	-0.004	-0.001	-0.011	0.014	0.004	0.288	0.259

Residual effects (P) = 0.0131; (G) = 0.0042

The bold values indicates direct effects; P = Phenotypic level and G = Genotypic level.

* Significant at 5 per cent level

Table 4.8 Estimates of direct and indirect effects for various traits studied towards seed yield in chickpea in environment II

Character		Biological yield/plant (g)	Plant height (cm)	Pods/plant	Seeds/pod	Primary branches/plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)	Correlation with seed yield/plant
Biological yield/plant (g)	P	0.859	0.025	0.071	0.000	0.005	0.009	-0.010	0.004	-0.025	0.938*
	G	0.765	0.019	0.146	-0.008	0.006	0.013	-0.017	0.027	0.001	0.952
Plant height (cm)	P	0.455	0.047	0.009	0.000	-0.001	0.026	-0.016	0.005	-0.156	0.369*
	G	0.428	0.033	0.018	-0.002	-0.001	0.040	-0.029	0.040	-0.139	0.388
Pods/plant	P	0.598	0.004	0.102	0.000	0.008	-0.011	0.003	-0.002	0.080	0.783*
	G	0.549	0.003	0.203	-0.003	0.011	-0.015	0.004	-0.020	0.096	0.828
Seeds/pod	P	-0.118	-0.002	-0.003	-0.002	-0.003	-0.007	0.000	-0.007	0.045	-0.096
	G	-0.131	-0.002	-0.012	0.045	-0.004	-0.011	0.000	-0.053	0.038	-0.129
Primary branches/plant	P	0.260	-0.002	0.050	0.000	0.017	-0.006	0.006	-0.002	0.063	0.387*
	G	0.238	-0.002	0.114	-0.009	0.020	-0.009	0.011	-0.015	0.066	0.414
Days to 50% flowering	P	0.125	0.020	-0.018	0.000	-0.002	0.059	-0.046	0.005	-0.099	0.045
	G	0.125	0.016	-0.038	-0.006	-0.002	0.082	-0.068	0.034	-0.097	0.046
Days to 75% maturity	P	0.151	0.013	-0.006	0.000	-0.002	0.049	-0.056	0.003	-0.069	0.083
	G	0.160	0.012	-0.009	0.000	-0.003	0.068	-0.082	0.023	-0.070	0.098
100-seed weight (g)	P	0.258	0.020	-0.021	0.001	-0.002	0.023	-0.014	0.012	-0.082	0.195
	G	0.241	0.016	-0.047	-0.028	-0.003	0.032	-0.022	0.085	-0.074	0.201
Harvest index (%)	P	-0.068	-0.023	0.026	0.000	0.003	-0.019	0.012	-0.003	0.312	0.241
	G	0.003	-0.020	0.082	0.007	0.006	-0.033	0.024	-0.026	0.238	0.280

Residual effects (P) = 0.0153; (G)=0.0076

The bold values indicates direct effects; P = Phenotypic level and G = Genotypic level.

* Significant at 5 per cent level

Table 4.9 Estimates of direct and indirect effects for various traits studied towards seed yield in chickpea in combined over environments

Character		Biological yield/plant (g)	Plant height (cm)	Pods/plant	Seeds/pod	Primary branches/plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)	Correlation with seed yield/plant
Biological yield/plant (g)	P	0.854	0.011	0.083	-0.002	-0.002	0.008	-0.006	0.005	-0.011	0.940*
	G	0.787	0.012	0.138	-0.008	-0.005	0.011	-0.008	0.022	0.007	0.956
Plant height (cm)	P	0.488	0.018	0.015	-0.001	0.000	0.029	-0.018	0.007	-0.109	0.428*
	G	0.476	0.021	0.023	-0.005	0.000	0.037	-0.024	0.034	-0.115	0.447
Pods/plant	P	0.613	0.002	0.116	-0.001	-0.002	-0.012	0.011	-0.002	0.075	0.800*
	G	0.573	0.002	0.190	-0.004	-0.006	-0.016	0.014	-0.010	0.088	0.832
Seeds/pod	P	-0.154	-0.002	-0.009	0.011	0.001	-0.010	0.001	-0.008	0.052	-0.118
	G	-0.171	-0.003	-0.022	0.038	0.002	-0.013	0.002	-0.037	0.048	-0.157
Primary branches/plant	P	0.356	0.000	0.060	-0.002	-0.004	-0.008	0.009	0.000	0.059	0.470*
	G	0.367	0.000	0.114	-0.008	-0.010	-0.012	0.013	-0.003	0.061	0.522
Days to 50% flowering	P	0.105	0.008	-0.021	-0.002	0.000	0.068	-0.055	0.006	-0.079	0.030
	G	0.108	0.010	-0.038	-0.006	0.001	0.079	-0.063	0.026	-0.085	0.033
Days to 75% maturity	P	0.081	0.005	-0.019	0.000	0.001	0.057	-0.066	0.004	-0.076	-0.014
	G	0.084	0.007	-0.036	-0.001	0.002	0.068	-0.073	0.018	-0.085	-0.017
100-seed weight (g)	P	0.292	0.009	-0.016	-0.006	0.000	0.028	-0.018	0.014	-0.067	0.236
	G	0.285	0.011	-0.030	-0.023	0.000	0.034	-0.022	0.061	-0.067	0.248
Harvest index (%)	P	-0.031	-0.007	0.030	0.002	-0.001	-0.019	0.017	-0.003	0.288	0.277*
	G	0.023	-0.010	0.074	0.008	-0.003	-0.030	0.027	-0.018	0.226	0.298

Residual effects (P) = 0.0134; (G)=0.0055.

The bold values indicates direct effects; P = Phenotypic level and G = Genotypic level.

* Significant at 5 per cent level

level with little variation in magnitudes in both the individual as well as combined over environments.

The magnitudes of residual effects at both phenotypic and genotypic levels were observed to be low in environment I environment II and over environments.

4.3 D²-statistics

4.3.1 Test of significance

Simultaneous test of significance based on Wilk's criteria and D²-values obtained for each pair of populations were observed to be significant in environment I, II and over environments.

4.3.2 Grouping of genotypes into clusters

On the basis of D²-values for all possible 1378 cultivar pairs, the 53 genotypes studied were grouped into 11, 8 and 7 clusters in environment I, environment II and combined over environments, respectively (Table 4.10 to 4.12).

In environment I, 9 genotypes viz., HPG-100, HPG-131, HPG-134, HPG-138, HPG-143, HPG-144, BG-1086, BG-1102 and 165 formed cluster I; 15 genotypes viz., HPG-54, HPG-78, HPG-150, H-94-83, GL-87069, GL-87129, GL-90104, GNG-580, CSG-9505, PBG-1, Pusa-372, ICC-15851, BG-1007, C-235 and JG-9 formed cluster II; 9 genotypes viz., HPG-124, HPG-132, HPG-133, HPG-135, HPG-137,

Table 4.10 Distribution of 53 genotypes of chickpea among clusters on the basis of D² - analysis in environment I

Cluster	No. of genotypes	Genotypes
I.	9	HPG-100, HPG-131, HPG-134, HPG-138, HPG-143, HPG-144, BG-1086, BG-1102, 165
II.	15	HPG-54, HPG-78, HPG-150, H-94-83, GL-87069, GL-87129, GL-90104, GNG-580, CSG-9505, PBG-1, Pusa-372, ICC-15851 BG-1007, C-235, JG-9
III.	9	HPG-124, HPG-132, HPG-133, HPG-135, HPG-137, HPG-147, HPG-149, GL-90169, Avrodhi
IV.	11	HPG-129, HPG-130, HPG-136, H-94-1, H-96-51, H-208, ICC-15599, ICCV-89701, TCP-40, WGG-95-50, Himachal Chana-2
V.	3	HPG-127, HPG-145, CSG-8943
VI.	1	H-82-2
VII.	1	L-550
VIII.	1	KW-118
IX.	1	BGD-112
X.	1	HPG-142
XI.	1	HPG-17

Table 4.11 Distribution of 53 genotypes of chickpea among clusters on the basis of D² - analysis in environment II

Cluster	No. of genotypes	Genotypes
I.	22	HPG-54, HPG-124, HPG-129, HPG-130, HPG-132, HPG-133, HPG-136, HPG-142, HPG-147, HPG-149, HPG-150, H-94-1, H-94-83, H-96-51, GL-87069, GNG-580, BGD-112, C-235, JG-9, TCP-40, WGG-95-50, Himachal Chana-2
II.	13	HPG-100, HPG-131, HPG-134, HPG-135, HPG-137, HPG-138, HPG-143, HPG-144, HPG-145, BG-1086, BG-1102, 165, L-550
III.	11	H-82-2, H-208, GL-87129, GL-90104, CSG-9505, PBG-1, Pusa-372, ICC-15851, ICC-15599, ICCV-89701, BG-1007
IV.	2	HPG-127, CSG-8943
V.	2	GL-90169, Avrodhi
VI.	1	KW-118
VII.	1	HPG-78
VIII.	1	HPG-17

Table 4.12 Distribution of 53 genotypes of chickpea among clusters on the basis of D² - analysis in combined over environments

Cluster	No. of genotypes	Genotypes
I.	15	HPG-100, HPG-131, HPG-132, HPG-133, HPG-134, HPG-135, HPG-137, HPG-138, HPG-143, HPG-144, CSG-8943, BG-1086, BG-1102, 165, L-550
II.	19	HPG-54, HPG-124, HPG-129, HPG-130, HPG-136, HPG-142, HPG-147, HPG-149, HPG-150, H-94-1, H-94-83, H-96-51, H-208, GL-87069, ICC-15599, BGD-112, TCP-40, WGG-95-50, Himachal Chana-2
III.	12	H-82-2, GL-87129, GL-90104, GNG-580, CSG-9505, PBG-1, Pusa-372, ICC-15851, ICCV-89701, BG-1007, C-235, JG-9
IV.	3	HPG-127, HPG-145, KW-118
V.	2	GL-90169, Avrodhi
VI.	1	HPG-78
VII.	1	HPG-17

HPG-147, HPG-149, GL-90169 and Avrodhi formed cluster III; 11 genotypes viz., HPG-129, HPG-130, HPG-136, H-94-1, H-96-51, H-208, ICC-15599, ICCV-89701, TCP-40, WGG-95-50 and Himachal Chana-2 formed cluster IV; 3 genotypes viz., HPG-127, HPG-145 and CSG-8943 formed cluster V; and one genotype each H-82-2, L-550, KW-118, BGD-112, HPG-142 and HPG-17 formed clusters VI, VII, VIII, IX, X and XI, respectively.

In environment II, cluster I was the largest one comprising 22 genotypes viz., HPG-54, HPG-124, HPG-129, HPG-130, HPG-132, HPG-133, HPG-136, HPG-142, HPG-147, HPG-149, HPG-150, H-94-1, H-94-83, H-96-51, GL-87069, GNG-580, BGD-112, C-235, JG-9, TCP-40, WGG-95-50 and Himachal Chana-2. Cluster II accommodated 13 genotypes viz., HPG-100, HPG-131, HPG-134, HPG-135, HPG-137, HPG-138, HPG-143, HPG-144, HPG-145, BG-1086, BG-1102, 165 and L-550. Eleven genotypes viz., H-82-2, H-208, GL-87129, GL-90104, CSG-9505, PBG-1, Pusa-372, ICC-15851, ICC-15599, ICCV-89701 and BG-1007 formed cluster III; 2 genotypes each, HPG-127 and CSG-8943; GL-90169 and Avrodhi formed cluster IV and V, respectively. Cluster VI, VII and VII included only one genotype each KW-118, HPG-78 and HPG-17, respectively.

In combined over environments, cluster I contained 15 genotypes viz., HPG-100, HPG-131, HPG-132, HPG-133, HPG-134,

HPG-135, HPG-137, HPG-138, HPG-143, HPG-144, CSG-8943, BG-1086, BG-1102, 165 and L-550. Cluster II comprised 19 genotypes viz., HPG-54, HPG-124, HPG-129, HPG-130, HPG-136, HPG-142, HPG-147, HPG-149, HPG-150, H-94-1, H-96-51, H-9483, H-208, GL-87069, ICC-15599, BGD-112, TCP-40, WGG-95-50 and Himachal Chana-2. 12 genotypes viz., H-82-2, GL-87129, GL-90104, GNG-580, CSG-9505, PBG-1, Rusa-372, ICC-15851, ICCV-89701, BG-1007, C-235 and JG-9 fell in cluster III whereas, cluster IV and V accommodated 3 genotypes viz., HPG-127, HPG-145 and KW-118 and 2 genotypes viz., GL-90169 and Avrodhi, respectively. Cluster number VI and VII retained only one genotype each i.e. HPG-78 and HPG-17, respectively.

4.3.3 Average intra and inter-cluster distances

Average intra and inter-cluster distances are presented in Tables 4.13 to 4.15. In environment I, highest intra-cluster distance was observed for cluster V (14.656) followed by cluster I (13.419) and cluster II (12.462). In environment II, the highest intra-cluster distance was observed for cluster V (13.943) followed by cluster III (11.769) and cluster IV (11.725). Cluster IV showed maximum intra-cluster distance (13.038) followed by cluster V (12.204) and cluster I (11.266) in the combined over environments.

Table 4.13 Average Intra and Inter-cluster values of D^2 and $\sqrt{D^2}$ among 11 clusters in environment I

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	180.063 (13.419)	5321.114 (72.946)	755.767 (27.491)	3106.044 (55.732)	811.361 (28.484)	4652.477 (68.209)	463.951 (21.539)	2100.421 (45.830)	3036.425 (55.104)	1555.374 (39.438)	324.624 (18.017)
II	155.293 (12.462)	2379.157 (48.777)	2379.157 (48.777)	453.027 (21.284)	9473.822 (97.334)	291.390 (17.070)	3157.682 (56.193)	12443.663 (111.551)	631.969 (25.139)	1319.183 (36.321)	6310.720 (79.440)
III	142.984 (11.958)	1028.644 (32.072)	1028.644 (32.072)	2639.574 (51.377)	2048.042 (42.255)	330.412 (18.177)	4804.829 (69.317)	1020.603 (31.947)	317.714 (17.824)	1203.566 (34.692)	317.714 (17.824)
IV	140.370 (11.848)	6395.517 (79.972)	6395.517 (79.972)	364.999 (19.105)	1721.819 (41.495)	9658.185 (98.276)	291.928 (17.086)	401.392 (20.035)	3921.691 (62.623)	3921.691 (62.623)	3921.691 (62.623)
V	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
VI	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
VII	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
VIII	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
IX	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
X	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)
XI	214.803 (14.656)	8335.057 (91.296)	8335.057 (91.296)	1861.647 (43.147)	571.270 (23.901)	6362.097 (79.763)	3933.160 (62.715)	673.187 (25.946)	3933.160 (62.715)	673.187 (25.946)	673.187 (25.946)

Values bolded are intra-cluster distance
Figures in parenthesis are the values of $\sqrt{D^2}$

Table 4.14 Average Intra and Inter-cluster values of D² and $\sqrt{D^2}$ among 8 clusters in environment II

Cluster	I	II	III	IV	V	VI	VII	VIII
I	124.744 (11.169)	400.090 (20.002)	241.810 (15.550)	754.322 (27.465)	328.531 (18.125)	1133.625 (33.669)	325.238 (18.034)	745.135 (27.297)
II		107.315 (10.359)	757.216 (27.517)	278.191 (16.679)	295.851 (17.200)	337.318 (18.366)	767.691 (27.707)	317.754 (17.826)
III			138.505 (11.769)	978.707 (31.284)	434.434 (20.843)	1557.115 (39.460)	414.024 (20.347)	1047.535 (32.366)
IV				137.480 (11.725)	307.945 (17.548)	344.720 (18.567)	1203.175 (34.687)	293.405 (17.129)
V					194.400 (13.943)	769.025 (27.731)	537.275 (23.179)	289.660 (17.019)
VI						—	1774.81 (42.128)	484.160 (22.004)
VII							—	1084.190 (32.927)
VIII								—

Values bolded are intra cluster distance
Figures in parenthesis are the values of $\sqrt{D^2}$

Table 4.15 Average Intra and Inter-cluster values of D^2 and $\sqrt{D^2}$ in combined over environments

Cluster	I	II	III	IV	V	VI	VII
I	125.912 (11.266)	545.857 (23.364)	1054.632 (32.475)	419.137 (20.473)	225.090 (15.003)	1034.774 (32.168)	295.448 (17.189)
II		121.518 (11.024)	216.313 (14.708)	1496.754 (38.688)	298.203 (17.269)	322.363 (17.954)	962.948 (31.031)
III			104.233 (10.209)	2262.411 (47.565)	592.742 (24.346)	283.707 (16.844)	1534.649 (39.175)
IV				169.977 (13.038)	751.023 (27.405)	2350.713 (48.484)	380.467 (19.506)
V					148.940 (12.204)	652.510 (25.544)	340.350 (18.449)
VI						—	1513.120 (38.899)
VII							—

Values bolded are intra cluster distance
Figures in parenthesis are the values of $\sqrt{D^2}$

In environment I, highest inter-cluster distance was observed between clusters II and VIII (111.551) followed by between clusters VI and VIII (109.999) and between clusters VIII and IX (98.542). The lowest value of inter-cluster distance was observed between cluster number II and VI (17.070) followed by clusters IV and IX (17.086) and between clusters III and X (7.824).

In environment II highest inter-cluster distance was observed between clusters VI and VII (42.128) followed by clusters III and VI (39.460) and between clusters IV and VII (34.687) while, the closest proximity was noticed between clusters I and III (15.550) followed by clusters II and IV (16.679).

In the combined over environments, maximum inter-cluster distance was observed between clusters IV and VI (48.484) followed by clusters III and IV (47.565) and clusters III and VII (39.175). The least inter-cluster distance was observed between clusters II and III (14.708) followed by clusters I and V (15.003) and between clusters III and VI (16.844).

4.3.4 Cluster means and contribution of individual character towards divergence

Character means of chickpea genotypes falling under different clusters in environment I, environment II and combined over environments are presented in Table 4.16 to 4.18, respectively.

Table 4.16 Cluster means of eleven clusters for ten quantitative traits in chickpea in environment I

Cluster No.	No. of genotypes	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
I	9	8.562	18.375	50.235	34.444	1.403	2.207	133.038	172.221	25.131	46.631
II	15	7.749	14.511	38.394	41.319	1.720	2.197	123.867	170.133	12.806*	52.899
III	9	7.392	15.898	46.734	33.008	1.541	2.192	134.184	174.630	20.819	46.223
IV	11	5.943	12.579	37.740	34.141	1.580	2.328	124.182	169.333	15.834	46.849
V	3	11.570	23.220	50.733	46.267	1.300	2.377	123.110	168.110	29.523	49.630
VI	1	8.710	17.970	32.130	56.070**	1.410	2.200	105.000*	162.000	14.110	48.300
VII	1	12.470	24.390	40.330	52.530	1.270	2.470	125.000	158.000*	22.890	51.450**
VIII	1	4.830*	8.290*	32.000*	17.470*	1.210*	2.070*	134.330**	177.330**	32.630**	58.560**
IX	1	8.230	16.400	52.270	31.000	2.040**	2.070*	130.000	166.000	15.950	50.190
X	1	6.180	11.960	37.330	31.670	1.590	2.070*	120.000	172.000	18.770	51.710
XI	1	16.930**	40.320**	57.730**	50.300	1.670	3.270**	132.330	177.330**	26.220	42.060*
Mean		8.961	18.537	43.239	38.929	1.521	2.314	125.913	169.735	21.335	49.501
Range	Min.	4.830	8.290	32.000	17.470	1.210	2.070	105.000	158.000	12.806	42.060
	Max	16.930	40.320	57.730	56.070	2.040	3.270	134.330	177.330	32.630	58.560

* and **: Minimum and Maximum values, respectively.

Table 4.17 Cluster means of eight clusters for ten quantitative traits in chickpea in environment II

Cluster No.	No. of genotypes	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
I	22	6.034	13.104	43.915	30.220	1.651	2.128	128.075	162.758	16.358	45.971
II	13	7.564	16.491	48.746	29.765	1.400	2.087	132.512	164.050	24.719	45.469
III	11	7.582	14.011	35.607	44.131	1.631	2.310	118.546*	159.878	13.391	55.077
IV	2	12.530	24.725	48.830	51.165	1.200	2.470**	119.500	157.835*	27.700	51.165
V	2	13.435	27.190	50.135	48.165	1.625	2.365	126.330	164.330	20.925	50.750
VI	1	4.500*	8.050*	31.330*	15.000*	1.200*	2.000*	134.670	169.670**	32.550**	56.070
VII	1	13.440	23.860	43.670	56.300**	1.560	2.730	141.670**	168.000	12.410*	56.320**
VIII	1	15.180**	37.780**	53.300**	45.670	1.670**	2.070	133.670	169.330	26.490	40.170*
Mean		10.033	20.651	44.442	40.052	1.492	2.270	129.372	164.481	21.818	50.124
Range	Min.	4.500	8.050	31.330	15.000	1.200	2.000	118.546	157.835	12.410	40.170
	Max	15.180	37.780	53.300	56.300	1.670	2.470	141.670	169.670	32.550	56.320

* and **: Minimum and Maximum values, respectively.

Table 4.18 Cluster means of seven clusters for ten quantitative traits in combined over environments

Cluster No.	No. of genotypes	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary plant branches/	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
I	15	8.008	17.273	48.333	33.005	1.389	2.189	132.167	167.421	24.122	45.944
II	19	5.879*	12.599*	41.581	30.513*	1.636	2.130	126.816	166.895	16.303	46.731
III	12	7.932	14.722	36.989*	44.600	1.693**	2.331	119.778*	163.700*	12.796*	54.153
IV	3	8.800	17.790	45.097	35.210	1.307*	2.077*	129.443	169.500	30.710**	51.123
V	2	12.765	25.455	50.415	46.510	1.615	2.415	126.670	168.585	20.970	51.185
VI	1	13.380	23.680	43.130	59.880**	1.560	2.600	141.500**	172.170	12.570	56.490**
VII	1	16.060**	39.050**	55.520**	47.980	1.670	2.670**	133.000	173.330**	26.360	41.120*
Mean		10.403	21.510	45.866	42.528	1.553	2.344	129.911	168.800	20.547	49.535
Range	Min.	5.879	12.599	36.989	30.513	1.307	2.077	119.778	163.700	12.796	41.120*
	Max.	16.060	39.050	55.520	59.880	1.693	2.670	141.500	173.330	30.710	56.490

* and **: Minimum and Maximum values, respectively.

In environment I, cluster XI showed the maximum cluster means for seed yield per plant, biological yield per plant, plant height, primary branches per plant and days to 75 per cent maturity. For days to 50 per cent flowering, days to 75 per cent maturity, 100-seed weight and harvest index, cluster VIII recorded the maximum values. This cluster also showed minimum values for seed yield per plant, biological yield per plant, plant height, pods per plant, seeds per pod and primary branches per plant. Cluster VI showed maximum values for pods per plant and cluster IX showed maximum values for seeds per pod. Similarly, minimum values for harvest index, days to 50 per cent flowering and 100-seed weight were observed for cluster XI, VI and II, respectively.

In environment II, cluster VIII recorded maximum values for seed yield per plant, biological yield per plant, plant height and seeds per pod and minimum value for harvest index. Cluster VII recorded maximum values for pods per plant, days to 50 per cent flowering and harvest index and minimum value for 100-seed weight. Maximum value were recorded for days to 50 per cent flowering and 100-seed weight in cluster VI. This cluster also showed minimum values for seed yield per plant, biological yield per plant, plant height, pods per plant, seeds per pod and primary branches per plant. Cluster IV recorded maximum value for primary branches per plant. Minimum

values for 75 per cent maturity and days to 50 per cent flowering were observed in cluster IV and cluster III, respectively.

Over environments, cluster VII recorded maximum values for seed yield per plant, biological yield per plant, plant height, primary branches per plant and days to 75 per cent maturity. Maximum values for pods per plant, days to 50 per cent flowering and harvest index were recorded in cluster VI. Similarly, maximum values for seeds per pod and 100-seed weight were observed in cluster III and IV, respectively. Minimum values for plant height, days 50 per cent flowering, days to 75 per cent maturity and 100-seed weight were recorded in cluster III; for harvest index in cluster VII; for seeds per pod and primary branches per plant in cluster IV and for seed yield, biological yield and pods per plant in cluster II.

The contribution of individual characters to the divergence has been worked out in terms of number of times it appeared first (Table 4.19). In environment I, 100-seed weight contributed maximum towards divergence (86.139 %) followed by seeds per pod (5.515%), days to 50 per cent flowering (3.483 %) and days to 75 per cent maturity (3.048 %). In environment II, 100-seed weight contributed maximum towards divergence (63.716 %) followed by days to 50 per cent flowering (11.611 %), seed yield per plant (9.869 %) and days to 75 per cent maturity (8.636 %). 100-seed weight, days to 50 per cent

Table 4.19 Contribution of individual characters to the divergence among 53 genotypes of chickpea

Trait	<u>Environment I</u>		<u>Environment II</u>		<u>Combined over environments</u>	
	No. of times ranked	Contribution (%)	No. of times ranked	Contribution (%)	No. of times ranked	Contribution (%)
Seed yield/plant (g)	12	0.871	136	9.869	57	4.136
Biological yield/plant (g)	3	0.218	0	0.0*	2	0.145
Plant height (cm)	6	0.435	19	1.379	15	1.089
Pods/plant	2	0.145	1	0.073	0*	0.0*
Seeds/pod	76	5.515	35	2.540	71	5.152
Primary branches/plant	2	0.145	19	1.379	11	0.798
Days to 50% flowering	48	3.483	160	11.611	123	8.926
Days to 75% maturity	42	3.048	119	8.636	61	4.427
100-seed weight	1187	86.139**	878	63.716**	1036	75.181**
Harvest index (%)	0	0.0*	11	0.798	2	0.145

* and ** : Minimum and Maximum values, respectively.

flowering, seeds per pod, days to 75 per cent maturity and seed yield per plant contributed towards divergence to the tune of 75.181, 8.926, 5.152, 4.427 and 4.136 per cent, respectively over environments.

4.4 Reaction to diseases

All the 53 genotypes were evaluated for their reaction to two important diseases, *Ascochyta* blight (*Ascochyta rabiei*) and collar rot (*Sclerotium rolfsii*) under field conditions and the results are given below:

4.4.1 *Ascochyta* blight

The test genotypes were screened for *Ascochyta* blight in both the environments under natural epiphytotic conditions.

Disease reaction varied from 1 to 5 on different genotypes in environment I and 1 to 7 in environment II (Table 4.20). Genotypes, HPG-17, PBG-1 and 165 on which no visible lesions developed were graded resistant; 33 genotypes viz., HPG-54, HPG-124, HPG-127, HPG-131, HPG-132, HPG-133, HPG-136, HPG-137, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-150, H-82-2, H-96-51, H-208, GL-87069, GL-87129, GL-90169, GNG-580, CSG-8943, Pusa-372, ICC-15851, ICC-15599, ICCV-89701, BGD-112, BG-1102, Avrodhi, JG-9, TCP-40, WGG-95-50 and Himachal Chana-2, with a disease score of 3 and 17 genotypes viz., HPG-78, HPG-100, HPG-129, HPG-130,

Table 4.20 Reaction of chickpea genotypes to *Ascochyta* blight in environment I and II.

Environments	Disease reaction/genotypes			
	Resistant (1)	Moderately resistant (3)	Tolerant (5)	Moderately susceptible (7) Susceptible (9)
I.	HPG-17, PBG-1, 165	HPG-54, HPG-124, HPG-127, HPG-131, HPG-132, HPG-133, HPG-136, HPG-137, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-150, H-82-2, H-96-51, H-208, GL-87069, GL-87129, GL-90169, GNG-580, CSG-8943, Pusa-372, ICC-15851, ICC-15599, ICCV-89701, BGD-112, BG-1102, Avrodhi, JG-9, TCP-40, WGG-95-50, Himachal Chana-2.	HPG-78, HPG-100, HPG-129, HPG-130, HPG-134, HPG-135, HPG-138, HPG-149, H-94-1, H-94-83, GL-90104, CSG-9505, BG-1007, BG-1086, KW-118, C-235, L-550.	
II.	HPG-17, HPG-100, HPG-124, HPG-131, HPG-132, HPG-133, GL-87069, GL-87129, GNG-580, PBG-1165, WGG-95-50, Himachal Chana-2.	HPG-54, HPG-78, HPG-127, HPG-129, HPG-130, HPG-134, HPG-135, HPG-136, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-149, HPG-150, H-82-2, H-208, CSG-8943, Pusa-372, ICC-15851, ICC-15599, ICCV-89701, BGD-112, Avrodhi, JG-9, TCP-40.	HPG-137, HPG-138, H-94-1, H-94-83, H-96-51, GL-90104, GL-90169, CSG-9505, BG-1007, BG-1086, BG-1102, KW-118, C-235.	L-550

HPG-134, HPG-135, HPG-138, HPG-149, H-94-1, H-94-83, GL-90104, CSG-9505, BG-1007, BG-1086, KW-118, C-235 and L-550 with a disease score of 5 were categorised moderately resistant and tolerant, respectively. None of the genotypes showed moderately susceptible and susceptible type of reaction in environment I.

Thirteen genotypes viz., HPG-17, HPG-100, HPG-124, HPG-131, HPG-132, HPG-133, GL-87069, GL-87129, GNG-580, PBG-1, 165, WGG-95-50 and Himachal Chana-2 were found resistant, 26 genotypes viz., HPG-54, HPG-78, HPG-127, HPG-129, HPG-130, HPG-134, HPG-135, HPG-136, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-149, HPG-150, H-82-2, H-208, CSG-8943, Pusa-372, ICC-15599, ICC-15851, ICCV-89701, BGD-112, Avrodhi, JG-9 and TCP-40 as moderately resistant, 13 genotypes viz., HPG-137, HPG-138, H-94-1, H-94-83, H-96-51, GL-90104, GL-90169, CSG-9505, BG-1007, BG-1086, BG-1102, KW-118 and C-235, were tolerant and only one genotype, L-550 was moderately susceptible whereas, none of the genotypes showed susceptible type of reaction to *Ascochyta* blight in environment II.

4.4.2 Collar rot

The screening of genotypes against collar rot under natural epiphytotic conditions showed that none of the genotypes was

Table 4.21 Reaction of chickpea genotypes to collar rot in environment I and II

Envi- nments	Disease reaction/genotypes			
	Resistant (1)	Moderately resistant (3)	Tolerant (5)	Moderately susceptible (7) Susceptible (9)
I.	H-82-2, H-94-1, H-208, ICC-15851, ICC-15599, 165, Himachal Chana-2	HPG-17, HPG-54, HPG-78, HPG-100, HPG-124, HPG-131, HPG-132, HPG-133, HPG-134, HPG-136, HPG-137, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-149, HPG-150, H-94-83, H-96-51, GL-87069, GL-87129, CSG-9505, Pusa-372, ICCV-89701, BG-1007, BG-1086, BG-1102, KW-118, Avrodhi, L-550, TCP-40.	HPG-127, HPG-129, HPG-130, HPG-135, HPG-138, GL-90104, GL-90169, GNG-580, CSG-8943, PBG-1, BGD-112, C-235, JG-9, WGG-9550.	- -
II.	ICC-15851, ICC-15599	HPG-17, HPG-100, HPG-127, HPG-129, HPG-136, HPG-137, HPG-142, HPG-144, HPG-145, HPG-147, H-82-2, H-94-1, H-208, GL-90104, GNG-580, ICCV-89701, 165, C-235, JG-9, WGG-95-50, Himachal Chana-2.	HPG-54, HPG-78, HPG-124, HPG-130, HPG-131, HPG-132, HPG-133, HPG-134, HPG-135, HPG-138, HPG-143, HPG-149, HPG-150, H-94-83, H-96-51, GL-87069, GL-87129, GL-90169, CSG-8943, CSG-9505, PBG-1, Pusa-372, BGD-112, BG-1007, BG-1086, BG-1102, KW-118, Avrodhi, L-550, TCP-40.	

moderately susceptible or susceptible in both the environments (Table 4.21). Seven genotypes viz., H-82-2, H-94-1, H-208, ICC-15851, ICC-15599, 165 and Himachal Chana-2 were categorised as resistant; 32 genotypes viz., HPG-17, HPG-54, HPG-78, HPG-100, HPG-124, HPG-131, HPG-132, HPG-133, HPG-134, HPG-136, HPG-137, HPG-142, HPG-143, HPG-144, HPG-145, HPG-147, HPG-149, HPG-150, H-94-83, H-96-51, GL-87069, GL-87129, CSG-9505, Pusa-372, ICCV-89701, BG-1007, BG-1086, BG-1102, KW-118, Avrodhi, L-550 and TCP-40 were grouped into moderately resistant whereas remaining 14 genotypes were graded tolerant in environment I.

In environment II, genotypes ICC-15851 and ICC-15599 were grouped as resistant and 21 genotypes viz., HPG-17, HPG-100, HPG-127, HPG-129, HPG-136, HPG-137, HPG-142, HPG-144, HPG-145, HPG-147, H-82-2, H-94-1, H-208, GL-90104, GNG-580, ICCV-89701, 165, C-235, JG-9, WGG-95-50 and Himachal Chana-2 were graded as moderately resistant. The remaining 30 genotypes were categorised as tolerant.



DISCUSSION

DISCUSSION

The present dissertation on chickpea (*Cicer arietinum* L.) was aimed (i) to assess and analyse the genetic variability present in the set of genotypes (ii) to understand the association between seed yield and yield contributing traits and (iii) to facilitate the selection of parents for hybridization programme by estimating the genetic divergence, among 53 chickpea genotypes evaluated in a randomized block design with three replications during two consecutive years 2000-01 and 2001-02. The various aspects of the present study have been discussed as under for their genetic breeding implications.

5.1 Studies on the nature and magnitude of variation for seed yield and other related traits

Selection which is the basis of every breeding programme operates only on variation which is of genetic nature (Johansen, 1909). A wide range of variability present in any crop, always provides the better chances of selecting desired types (Vavilov, 1951).

The success of plant improvement lies in careful management of variability and techniques to be employed in each case, will depend upon clear understanding of the extent and nature of variability.

According to Fisher (1918), the continuous variation exhibited by quantitative traits with which most of the plant breeders have to deal with, includes the heritable and non-heritable components. The heritable component is the consequence of genotypes and the non-heritable part is mainly due to unknown environmental factors. As it is very difficult to assess the genotypes directly, it is possible only through the assessment of phenotypic expression (which is an outcome of genotype and environmental interaction) in the existing material. Therefore, the study of phenotypic variability for various traits under investigation is of great importance.

A thorough screening of the material studied under present investigation revealed (Table 4.1) sufficient variability for all the ten characters viz., seed yield per plant, biological yield per plant, plant height, pods per plant, seeds per pod, primary branches per plant, days to 50 per cent flowering, days to 75 per cent maturity, 100-seed weight and harvest index in environment I, environment II and combined over environments. High amount of genetic variability for many of these traits has also been reported by Mandal and Bahl (1983), Dahiya *et al.* (1983), Bhambota (1993) and Pratap (1999). Combined analysis of environments revealed significant mean squares due to environments with respect to seed yield per plant, plant height, pods per plant, primary branches per plant and days to 75 per cent

maturity indicating variation among the environments for these characters and thus their influence on seed yield per plant. The differential response of genotypes to varying environmental conditions is indicated by significant genotype x environment interactions for biological yield per plant, plant height, primary branches per plant, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight. Significant mean squares due to genotype x environment interactions for yield contributing traits has also been reported by Singh *et al.* (1988), Maloo and Sharma (1990) and Toker (1998).

The genotypic and phenotypic variances are of little meaning as they do not have any clear limit or ceiling, and at the same time, the categorization of the genotypic variance as low or high is difficult, rendering them unsuitable for comparison of two populations with desired precision when expressed in absolute values. To overcome this difficulty, the genotypic and phenotypic coefficients of variation which are free from the unit of measurement, can be conveniently employed for making comparison between populations and different metric traits of population. Results from the present study in this context indicated that PCV and GCV were high ($> 25\%$) for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight; moderate for plant height, seeds per pod, primary branches per plant and harvest index, and low for days to 50 per cent flowering and

days to 75 per cent maturity under both the individual environments, as well as combined over environments. Further, the present findings revealed that the estimates of PCV were generally higher than their corresponding GCV for all the characters studied. Similar findings with respect to PCV and GCV have been reported by earlier researchers also (Arora, 1991; Dasgupta *et al.*, 1992 and Yadav *et al.*, 1999). The present study indicated higher contribution of seed yield per plant, biological yield per plant, pods per plant and 100-seed weight towards genetic variability and thereby suggesting that the parents chosen on the basis of these characters may be utilized in the crossing programme for obtaining good transgressive segregants.

A useful measure of considering the ratio of genetic variance to total variance is heritability and this concept is of major importance in the development of quantitative genetics. It may be described as a measure of relative importance of heredity and environment.

The present study in this context revealed that estimates of heritability (broad sense) were high ($> 80\%$) for seed yield per plant, biological yield per plant, plant height, seeds per pod, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight in environments I and II as well as over environments. Similarly high estimates of heritability were also recorded for pods per plant in environment II and over environments. Thus, the selection made for

these traits on the basis of phenotypic expression could be relied upon. Moderate heritability (60 - 80%) was recorded for pods per plant and primary branches per plant in environment I; harvest index and primary branches per plant in environment II and combined over environments, whereas, it was low for harvest index in environment I. High heritability estimates for most of the traits studied have been reported earlier also (Mishra *et al.* 1988; Sharma and Maloo, 1988; Samal and Jagdev, 1989; Maloo and Sharma, 1990 and Chavan *et al.* 1994).

The information on heritability estimates are useful in studying the inheritance of quantitative traits as well as for planning breeding programmes with desired degree of expected genetic progress. From the present study the results revealed that the response to selection for different traits like seed yield per plant, biological yield per plant, plant height, seeds per pod, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight showed high heritability in environments I and II as well as combined over environments and therefore, needs to be given due consideration while following a selection and other seed yield improvement programmes based on their phenotypic expression.

For an effective selection, the knowledge alone on the estimates of heritability is not sufficient, and genetic advance if studied along

with heritability is more useful. In the present study, high ($> 30\%$) estimates of genetic advance expressed as per cent of mean have been observed for seed yield per plant, biological yield per plant, pods per plant, biological yield per plant, pods per plant, 100-seed weight and plant height in both the environments I and II as well as combined over environments, thereby, suggesting good response for selection based on *per se* performance. Seeds per pod and primary branches per plant showed moderate genetic advance ($20 - 30\%$) in both the individual environments as well as combined over environments. Low ($< 20\%$) estimates of genetic advance were observed for three characters viz., days to 75 per cent maturity, days to 50 per cent flowering and harvest index in environments I and II as well as combined over environments except in environment II where the moderate genetic advance was observed for harvest index thereby, suggesting poor response from selection based on *per se* performance.

In the present study, broad sense heritability was computed which includes both additive and non-additive gene effects. Therefore, heritability estimates should be considered in conjugation with genetic advance. Based on this consideration, high heritability for seed yield per plant, biological yield per plant, 100-seed weight, pods per plant and plant height coupled with high genetic advance in environment I,

environment II and combined over environments except pods per plant in environment I, indicate additive genetic control in the inheritance of these traits and selection pressure could be profitably applied on these characters for yield improvement. High heritability coupled with high genetic advance for some of these traits have also been reported earlier by Dasgupta *et al.* (1992); Maloo and Sharma (1987); Tripathi (1998) and Kumar *et al.* (1999).

High heritability with moderate or low genetic advance for seeds per pod, days to 50 per cent flowering and days to 75 per cent maturity revealed the importance of dominance and epistatic effects in the inheritance of these traits and selection for these characters would be less effective.

Therefore, on the basis of study of all the variability parameters in individual as well as combined over environments, it may be interpreted that maximum improvement through direct selection can be brought for seed yield, biological yield per plant, pods per plant and 100-seed weight.

5.2 Studies on correlation and direct and indirect effects

It has been well established that yield is one of the most important economic character, which is influenced to a great extent by the interaction of several metric traits and by the fluctuating

environmental conditions. The effectiveness of any breeding or selection programme depends upon the nature of associations between yield and other component characters, as more directly and positively a character is associated with seed yield, the more will be the success of the selection programme. Therefore, besides getting information on the nature and magnitude of variation, it is also imperative to have a knowledge on the associations of seed yield with other traits and among themselves and their causation to identify characters for defining an ideal plant type as well for increasing the efficiency of indirect selection. Estimates of phenotypic and genotypic coefficients of correlation and that of direct and indirect effects provide the base necessary for identification of traits of an ideal plant type and indirect selection.

In the present investigation, in general, phenotypic correlation estimates were higher than that of the correlations at environmental level. Similarly, the genotypic correlation estimates were generally observed to be higher than that of phenotypic correlations which indicated the inherent association among the various traits studied. However, the phenotypic expression of the correlation was influenced by the environmental factors. Seed yield per plant exhibited stable positive association with biological yield per plant followed by pods per plant, primary branches per plant and plant height at genotypic,

phenotypic and environmental levels in both the individual as well as combined over environments. Thus, it can be inferred that selection based on any one of these traits either alone or in combination, will result in identifying high yielding strains. Positive association of biological yield per plant and pods per plant with seed yield per plant observed in this investigation is in confirmation with the findings of Mishra *et al.* (1988), Singh *et al.* (1997), Chand and Singh (1997), Kumar *et al.* (1999) and Arora and Jeena (2000). Dasgupta *et al.* (1992), Rao *et al.* (1994), Sandhu and Magat (1995), Wahid and Ahmed (1999), Khedar and Maloo (1999) and Kumar *et al.* (1999) also reported positive association between seed yield per plant and pods per plant. Similarly, positive association of primary branches per plant with seed yield per plant observed in this study is also in confirmation with the findings of Mishra *et al.* (1988), Rao *et al.* (1994), Sandhu and Mangat (1995), Singh *et al.* (1997) and Khedar and Maloo (1999). Positive association of plant height with seed yield per plant was in agreement with the findings of Paliwal (1987), Sharma *et al.* (1989), Lal *et al.* (1993), Kumar *et al.* (1999) and Wahid and Ahmed (1999). Seed yield per plant also had positive and significant association with harvest index at phenotypic and environmental levels in environment I and combined over environments, and at genotypic level in environment II, whereas, positive association

between seed yield per plant and 100-seed weight was observed at phenotypic and genotypic levels in environment I only. Positive association of seed yield per plant with harvest index observed is in confirmation with the findings of Mishra *et al.* (1988), Sharma *et al.* (1989), Rao *et al.* (1994), Sandhu and Mangat (1995), Singh *et al.* (1997), Tripathi (1998) and Kumar *et al.* (1999). Similarly, positive association of 100-seed weight with seed yield per plant observed in this study is also in confirmation with the findings of Dasgupta *et al.* (1992), Rao *et al.* (1994), Kumar *et al.* (1999), Khedar and Maloo (1999) and Kumar *et al.* (1999).

Biological yield per plant exhibited positive association with pods per plant, plant height, primary branches per plant and 100-seed weight in both the environments as well as combined over environments. Positive association of biological yield with pods per plant and plant height has also been reported earlier by Chand and Singh (1997) and Jeens and Arora (2001). Similarly, Singh *et al.* (1990) and Tripathi and Arora (1991) reported positive association of biological yield per plant with plant height and 100-seed weight. Positive and significant association of plant height with 100 seed weight, days to 50 per cent flowering and days to 75 per cent maturity observed in the present investigation is in agreement with the earlier findings of Singh *et al.* (1990).

Pods per plant also showed positive and significant association with primary branches per plant at all the levels in environments I, II and combined over environments as earlier reported by Mishra *et al.* (1988) and Sharma *et al.* (1989). Pods per plant also showed positive and significant correlation with harvest index at genotypic level only in environment II and combined over environments. Further, seeds per pod had negative association with 100-seed weight. This supports the earlier studies conducted by Chand and Singh (1997) and Jeena and Arora (2001).

Days to 50 per cent flowering showed positive and significant association with days to 75 per cent maturity and 100-seed weight in environment I, environment II as well as combined over environments, however, it recorded significant but negative association with harvest index at genotypic level. Similar findings were reported earlier with respect to association of days to 50 per cent flowering with days to 75 per cent maturity (Dasgupta *et al.*, 1992 and Singh *et al.*, 1990), with 100-seed weight (Paliwal *et al.*, 1987) and harvest index (Pratap, 1999). Days to 75 per cent maturity was positively associated with 100-seed weight at phenotypic and genotypic levels over environments only. Whereas, it had negative and significant association with harvest index at genotypic level only in environments I, II as well as combined over environments. These results supplement the findings of Paliwal *et*

al. (1987) for 100-seed weight and Pratap (1999) for harvest index. 100-seed weight also reflected negative relationship with harvest index which was in agreement with the findings of Chand and Singh (1997). No association of seed yield per plant was observed with seeds per pod, days to 50 per cent flowering and days to 75 per cent maturity indicating thereby the possibility of improvement of seed yield without any adverse effect on the expression of such traits. This finding has been contrary to some of the earlier reports particularly with respect to association of seed yield per plant with days to flowering and days to maturity (Chavan *et al.* 1994; Singh *et al.*, 1990) and seeds per pod (Tripathi and Arora, 1991; Tagor and Singh, 1990) which has been shown to be positively associated with seed yield.

Based on the estimates of genotypic and phenotypic correlations, the breeder would be able to decide the method of breeding to be followed so that the useful correlation could be exploited and the undesirable ones modified by generating fresh variability to obtain new recombinants. According to Al-Jibouri *et al.* (1958), if negative association between characters is due to pleiotropic effects, it would be very difficult to obtain the desired recombinants, while if linkage is involved, special breeding programme are needed to break these linkages. Miller and Rawlings (1967 a, b) have shown that the undesirable correlations could be broken by recurrent selection

programmes, whereas Kaltsikes and Lee (1971) opined that if morphological traits are highly correlated with yield, a pedigree programme with yield per plant or plot as the selection criterion would be useful.

Thus, from the present study on correlation, it was apparent that for improvement of chickpea, 6 traits, viz., biological yield per plant, pods per plant, primary branches per plant, harvest index, 100-seed weight and plant height are important. Among these traits also, two traits viz., biological yield and pods per plant are more important since these have highest correlation coefficient values in environment I, environment II as well as combined over environments.

Even though the correlation coefficients are quite helpful in determining the components of a complex trait like yield, however, an exact picture of the relative importance of direct and indirect influence of each component character is not provided by such studies. Path coefficient analysis (Wright, 1921; Dewey and Lu, 1959) under such circumstances plays an important role in partitioning of the correlation coefficient into direct and indirect effects of a set of independent variable on the dependent variable and determines the component characters on which selection can be based for improvement in yield.

Results on the phenotypic and genotypic path coefficients revealed high direct contribution of biological yield per plant towards

seed yield per plant followed by harvest index and pods per plant in environments I, II and combined over environments. Pods per plant, plant height and primary branches per plant contributed mainly via biological yield. Indirect contribution of biological yield and harvest index via pods per plant was also observed though the values were of low magnitudes.

The positive association of biological yield per plant, harvest index and pods per plant with seed yield per plant was mainly due to their high positive direct effects. The indirect positive effects of pods per plant, plant height and primary branches per plant were mainly responsible for their positive association with seed yield per plant. The positive association of 100-seed weight with seed yield per plant in environment I, was mainly because of its positive indirect effects via biological yield per plant.

The contribution of residual effects that influenced seed yield was very low at both genotypic and phenotypic levels in environments I, II and combined over environments indicating that the characters included in the present investigation were sufficient enough to account for the variability in the dependent characters i.e. seed yield per plant.

The results discussed above indicated that, in general, biological yield per plant, harvest index and pods per plant exhibited

high positive and direct influence on seed yield per plant. Most of the other component characters contributed mainly via biological yield per plant. Similar observations have also been recorded by Singh *et al.* (1990), Arora *et al.* (1994), Khorgade *et al.* (1995), Tripathi (1998), Dasgupta *et al.* (1998), Kumar *et al.* (1999) and Yadav *et al.* (1999) in chickpea.

5.3 Studies on genetic diversity

The selection of suitable diverse parents for hybridization programme is an important feature of any crop improvement strategy for getting desired recombinants. The importance of genetic divergence in plant breeding has been emphasized by several scientists (Griffing and Lindstorm, 1954; Moll *et al.*, 1962; De Pace *et al.* 1978; Arunachalam, 1981 and Hawkes, 1981).

In the present investigation, Mahalanobis D^2 -statistic helped in grouping 53 genotypes of chickpea into 11, 8 and 7 diverse clusters in environment I, environment II and combined over environments, respectively. Genotypes from same geographical locations fell into different clusters and vice-versa indicating that clustering of populations did not follow their geographic or location distribution. Similar observations have also been reported by Sarvaliya and Goyal (1994), Kumar (1997) and Deshmukh and Patil (1997). Singh *et al.* (1979)

suggested that genetic drift and selection in different environments seems to be a cause of greater diversity rather than geographical isolation. Therefore, it is suggested that parents should be selected on the basis of total divergence for the characters used for an overall improvement in the yield. Gupta *et al.* (1992) suggested that combined analysis over environments for taking care of the effect of genotype x environment interaction on the classification of genotypes.

In the present investigation also the composition of the clusters differed between environments indicating that D^2 -statistic is influenced by the environmental variation resulting in inconsistent clustering of some genotypes. Similar observations have also been reported earlier by Somayajulu *et al.* (1970), Upadhyay and Murty (1970), Jatasara and Paroda (1978), Rout *et al.* (1985), Pradhan and Roy (1990), Singh *et al.* (1990) and Gupta *et al.* (1992). These results, therefore, emphasized that in order for the clustering based on D^2 to be of any value, the experiments should be conducted over a series of environments.

100-seed weight followed by seeds per pod, days to 50 per cent flowering and days to 75 per cent maturity in environment I, 100-seed weight followed by days to 50 per cent flowering, seed yield per plant and days to 75 per cent maturity in environment II and 100-seed weight followed by days to 50 per cent flowering, seeds per

pod, days to 75 per cent maturity and seed yield per plant in combined over environments contributed most towards genetic divergence. Remaining characters contributed very little or did not contribute at all towards genetic divergence and hence were of no or very little consideration. Earlier, Sirohi *et al.* (1999) and Raje and Khare (1999) also reported that 100-seed weight and seed per plant were chiefly responsible for genetic divergence in chickpea.

The intra-cluster distance among various clusters revealed maximum intra-cluster distance for cluster V, in environment I and environment II and cluster IV in combined over environments. The lowest intra-cluster distance was observed for IV, II and III in environment I, environment II and over environments, respectively. The maximum intra-cluster distance was because of wide genetic diversity among its genotypes. The chance of developing good segregants by crossing the genotype of the same cluster showing low value for intra-cluster distance are very low. Therefore, it would be logical to attempt crosses between the genotypes of cluster separated by large inter-cluster distances.

In the present study, the maximum inter-cluster distance was recorded between clusters II and VIII (111.551) followed by clusters VI and VIII (109.999); between clusters VI and VII (42.128) followed by clusters III and VI (39.460); between cluster IV and VI (48.484)

followed by III and IV (47.565) in environment I, environment II and combined over environments, respectively. This clearly indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could very well be used in hybridization programme of chickpea for improving seed yield. The least inter-cluster distance was observed between clusters II and IV (17.070) followed by clusters IV and IX (17.080) in environment I, between clusters I and III (15.550) followed by clusters II and IV (16.679) in environment II and between cluster II and III (14.708) followed by clusters I and V (15.003) in combined over environments. The lowest inter-cluster distances indicate that the genotypes of these clusters had close relationship and hence, may not be emphasized upon to be used in hybridization programme.

Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture (Singh *et al.*, 1987). In environment I, thus, crosses between the genetically diverse genotypes of cluster II characterized by low 100-seed weight, with KW-118, the only genotype, representing cluster VIII characterized by maximum 100-seed weight, harvest index, days to flowering and days to maturity and minimum seed yield per plant, biological yield per plant, plant height pods per plant, seeds per pods and primary branches per plant are expected

to exhibit high heterosis and are also likely to produce new recombinants with desired traits. Similarly H-82-2, the only genotypes constituting cluster VI, which exhibited excellence for pods per plant and early flowering could be crossed with KW-118, to get desirable segregants with higher yield for developing short duration superior variety of chickpea. Similarly, crosses may also be attempted to get desirable results between the genotypes BGD-112 and KW-118.

In environment II, KW-118 and HPG-78 alone constituted cluster VI and VII, respectively. Cluster-VI was characterized by minimum seed yield per plant, biological yield per plant, plant height, pods per plant, seeds per pod, primary branches per plant and high 100-seed weight and being late in maturity. Whereas, cluster VII was characterized by high pods per plant, harvest index, being late in flowering and low 100-seed weight. 100-seed weight being the highest contributors towards genetic divergence thereby suggesting that crosses should be attempted between KW-118 and HPG-78 to get desirable segregants to identify suitable variety. Crosses between the genotypes of cluster III which exhibited excellence for being early in flowering with the genotype of cluster VI (KW-118) with characters which are already discussed may throw good chance of developing early maturing segregants. Similarly, mating between the genotypes of cluster I with the genotypes of cluster IV which characterized

excellence for primary branches per plant and being late in maturity would exhibit high heterosis and also likely to produce new combinations with desired traits.

In combined over environments, HPG-127, HPG-145 and KW-118, the three genotypes constituting cluster IV and characterized by lowest seeds per pod, primary branches and highest 100-seed weight could be crossed with HPG-78, the only genotype representing cluster VI characterized by high pods per plant, harvest index and being late in flowering to get desirable segregants for developing superior variety of chickpea. Similarly, the crosses between the genotypes belonging to cluster III characterized by maximum seeds per pods and minimum 100-seed weight, short plant height and being early in flowering with genotypes of cluster IV (HPG-127, HPG-145 and KW-118) would exhibit high heterosis and also likely to produce new combinations with desired traits. Similarly crosses may also be attempted between genotypes of cluster III and HPG-17 belonging to cluster VII with excellent seed yield per plant, biological yield per plant, plant height, primary branches per plant and minimum harvest index would exhibit high heterosis and also results in segregants with higher yield.

Hence, in general, divergence study suggested that crosses involving genotypes HPG-78, GL-87129, GL-90104, CSG-9505, PBG-1, Pusa-372, ICC-15851, BG-1007, H-82-2, ICCV-89701, GNG-580,

JG-9 and C-235 with KW-118 for getting desired transgressive segregants.

5.4 Reaction to disease

5.4.1 *Ascochyta* blight

Blight caused by *Ascochyta rabiei* (Pass.) Lab. is a major disease of chickpea in the submontane and low hill, subtropical zone of Himachal Pradesh (Singh and Sood, 1990). In the present studies all the 53 genotypes were evaluated for their reaction to *Ascochyta* blight under natural epiphytotic conditions. The disease development in both the years was low due to low rainfall and ranged from 1 to 5 in test genotypes. These results are in accordance with the findings of Luthra *et al.* (1935), Singh (1984), Ketelaer *et al.* (1988) and Dey and Singh (1992) and who had emphasized the importance of rain and wind current in disease dissemination and development.

The present study indicated that genotypes HPG-17, PBG-1 and 165 were resistant in both the years whereas rest of the genotypes were moderately resistant to tolerant (rating 3 - 5) in both the years of testing. Lal and Amin (1992), Gaur and Singh (1996), Haware (1998) and Singh *et al.* (1998) have enlisted large number of gram genotypes resistant to *Ascochyta* blight. Resistance of genotype PBG-1 is in accordance with the findings of Singh and

Sood (1990) and Singh *et al.* (1998). Resistance of other genotypes needs further confirmation before their exploration in future breeding programmes.

5.4.2 Collar rot

Collar rot of chickpea caused by *Sclerotium rolfsii* Sacc. is a fast spreading and destructive disease. It is reported to cause 54.7 to 95 per cent seedling mortality (Kotasthane *et al.*, 1976). During 1989-90, collar rot was widely prevalent in Mandi, Bilaspur Una and Solan districts of Himachal Pradesh (Sugha *et al.* 1991). Therefore, in the present study, all the 53 genotypes were evaluated for their reaction to collar rot. Two genotypes ICC-15851 and ICC-15599 showed high degree of resistance to collar rot pathogen in both the years. Most of the other genotypes showed moderately resistant to tolerant disease reaction. The disease is favoured by good soil moisture, high soil temperature and low organic matter in the soil (Sen Gupta and Das, 1971). There was very little rainfall in both the years which resulted in poor development of disease. Therefore, these genotypes need intensive evaluation before their exploitation in future breeding programmes.

Conclusions

- ◆ Variability Studies indicated that direct selection is highly effective for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight.
- ◆ Correlation and path coefficient analysis suggested that improvement in seed yield can be obtained by improving biological yield per plant, harvest index, pods per plant, primary branches per plant and plant height.
- ◆ Genotypes from the same geographical region fell into different clusters and vice-versa. This suggested that selection of parents for hybridization should be on genetic diversity rather than on the geographical areas.
- ◆ Clustering pattern changed with the environment which indicated that D^2 -statistics are highly influenced by the environments.
- ◆ 100-seed weight contributed most towards divergence in both individual as well as combined over environments.
- ◆ Divergence study suggested that crosses involving genotypes HPG-78, GL-87129, GL-90104, CSG-9505, PBG-1, Pusa-372, ICC-15851, BG-1007, H-82-2, ICCV-89701, GNG-580, JG-9 and C-235 with KW-118 for getting desired segregants.
- ◆ Genotypes, HPG-17, PBG-1, 165, were found to be resistant against *Ascochyta* blight whereas ICC-15851 and ICC- 15599 showed resistance to collar rot. Therefore, these can be used as donors in future hybridization programmes.



SUMMARY

Chapter-VI

SUMMARY

The objectives of the present investigation, entitled "Genetic diversity and association studies in chickpea (*Cicer arietinum* L.)" were to assess and analyse the variability present in the set of genotypes, to understand the association between yield and yield contributing traits and to facilitate the selection of parents for hybridization programme by estimating genetic diversity through Mahalanobis D²-statistic.

The present investigation was carried out on 53 genetically diverse true breeding genotypes of chickpea procured from different eco-geographic regions and three check varieties, HPG-17, C-235 and Himachal Chana-2. These genotypes were grown in randomized block design in three replications at the Research Sub-Station, Berthi of CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur during *rabi*, 2000-01 and *rabi*, 2001-02. The data were recorded on seed yield per plant and 11 other traits including reaction to diseases (*Ascochyta* blight and collar rot).

The data were analysed environment-wise and combined over environments as per Rao (1952), Burton and DeVane (1953), Fisher (1954), Johnson *et al.* (1955), Deway and Lu (1959) and Panse and

Sukhatme (1985). Grouping of chickpea genotypes into different categories to indicate the type of reaction to diseases was based on 1-9 scale given by Nene *et al.* (1981).

Analysis of variance revealed considerable differences among the genotypes for all the traits studied in both the individual as well as combined over environments. Combined analysis of variance indicated significant differences due to environments for seed yield per plant, plant height, pods per plant, primary branches per plant and days to 75 per cent maturity. The genotypic and environmental interaction was also significant for biological yield per plant, plant height, primary branches per plant, days to 50 per cent flowering, days to 75 per cent maturity and 100-seed weight.

Phenotypic and genotypic coefficient of variation were high for seed yield per plant, biological yield per plant, pods per plant and 100-seed weight; moderate for plant height, seeds per pod, primary branches per plant and harvest index whereas, these were low for days to 50 per cent flowering and days to 75 per cent maturity in both the individual as well as combined over environments.

High heritability values for 100-seed weight, seeds per pod, plant height, days to 50 per cent flowering, days to 75 per cent maturity, biological yield per plant, seed yield per plant and pods per plant in individual environments as well as combined over environments

except pods per plant in environment I, indicating thereby, lesser effect of environment on these traits. Hence, the selection made for these traits on the basis of phenotype could be relied upon.

In general, high heritability coupled with high genetic advance was observed for seed yield per plant, biological yield per plant, 100-seed weight, pods per plant and plant height showing the influence of additive gene action on these traits and hence may prove useful for effective selection.

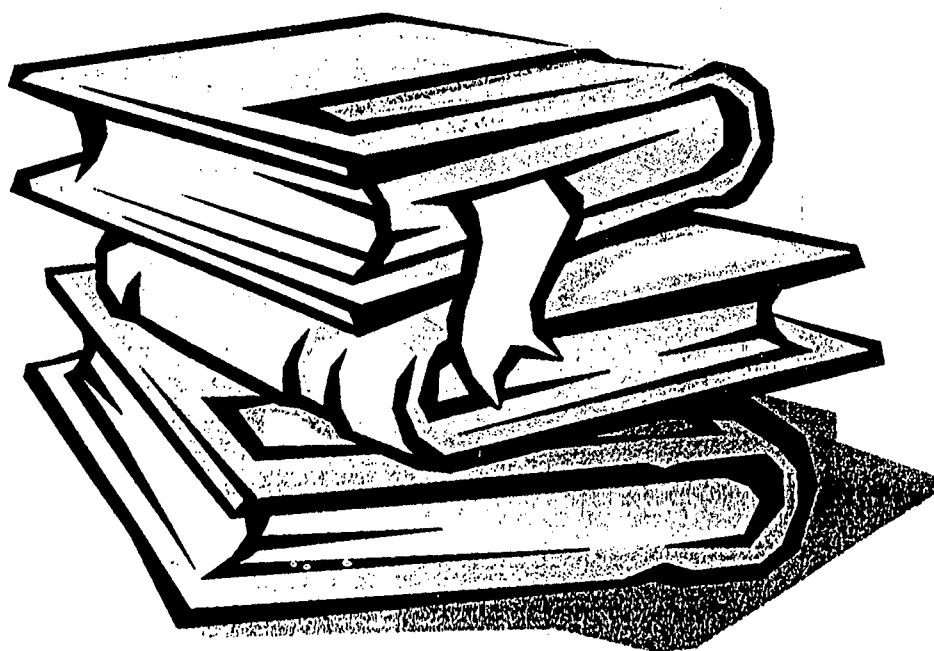
Correlation studies indicated the higher magnitude of genotypic correlations than the corresponding phenotypic ones, indicating the inherent association among the various traits. Seed yield per plant exhibited significant and strong positive association with biological yield followed by pods per plant, primary branches per plant and plant height at phenotypic, genotypic and environmental levels in the individual as well as combined over environments. The association of seed yield per plant with harvest index was also significant and positive at phenotypic and environmental level in environment I and combined over environments whereas in environment II, it was positively significant at genotypic level only. The present study on correlation indicated that higher grain yield can be obtained by increasing biological yield per plant, pods per plant, primary branches per plant, plant height and harvest index.

Path coefficient analysis revealed high positive and direct influence of biological yield per plant, harvest index and pods per plant on seed yield per plant. Pods per plant, plant height and primary branches per plant exhibited high indirect positive effect towards seed yield mainly via biological yield. Thus, effectiveness of selection for high yield could be enhanced by inclusion of biological yield as a selection criterion along with the harvest index. Besides, selection on the basis of pods per plant, plant height, primary branches per plant and 100-seed weight can lead to considerable improvement of seed yield in chickpea.

Genetic divergence studies helped in grouping 53 genotypes of chickpea in to 11, 8 and 7 diverse clusters in environment I, environment II and combined over environments, respectively. Clustering pattern did not follow their geographic or location distribution. The genotypes in a particular cluster were not totally identical in environment I, environment II and combined over environments. 100-seed weight contributed most towards divergence in both the individual as well as combined over environments. Maximum intra-cluster distance was observed in cluster V in individual environments and in cluster IV in combined over environments, indicating greater genetic divergence between the genotypes belonging to these clusters. Hence, attempting crosses between genotypes, HPG-78, GL-87129, GL-90104, CSG-9505,

PBG-1, Pusa-372, ICC-15851, BG-1007, H-82-2, ICCV-89701, GNG-580, JG-9 and C-235 with KW-118 is suggested. Crosses in the above combination are expected to provide enough genetic variability to select high yielding and stable segregants in the segregating generations.

Field screening of various genotypes revealed three genotypes viz., HPG-17, PBG-1, 165 as potential source of resistance against *Ascochyta* blight and ICC-15851 and ICC-15599 as resistance source against collar rot.



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APPENDICES

Appendix x-1

Weekly meteorological data during crop duration in years 2000-01 and 2001-02

Month/Week	Temperature (°C)				Relative humidity (%)				Rainfall (mm)	
	2000		2001		2000		2001		2000	2001
	Max.	Min	Max.	Min	Max.	Min.	Max.	Min.		
October										
40	30.7	14.1	30.8	17.3	100	55.0	100	48.7	0.0	0.0
41	31.4	12.8	31.4	14.8	100	45.3	100	39.0	0.0	0.0
42	30.5	11.0	29.3	10.2	96.8	48.4	100	38.1	0.0	0.0
43	30.0	12.2	29.3	12.8	100	51.6	100	43.0	0.0	0.0
44	27.3	12.1	28.8	14.0	100	65.8	100	41.4	0.0	59.6
November										
45	26.6	11.6	25.7	7.6	100	63.0	100	37.1	0.0	0.0
46	25.5	7.2	26.1	6.1	100	51.8	100	45.7	0.8	0.0
47	25.1	7.3	24.6	6.2	98	56.7	100	43.6	0.0	0.0
48	23.8	4.5	23.4	4.9	100	37.1	100	50.3	0.0	0.0
December										
49	23.8	2.5	23.6	4.0	100	29.4	100	47.1	0.0	0.0
50	21.4	2.5	22.1	5.6	100	55.1	100	57.0	0.0	14.0
51	23.1	4.0	20.7	4.2	100	38.7	100	55.7	0.0	3.6
52	21.8	0.3	20.4	3.8	100	37.6	100	56.7	0.0	0.0
January										
1	18.0	5.3	20.6	0.8	98	63.8	100	46.8	17.0	0.0
2	18.3	0.6	21.6	3.0	100	53.4	97.1	57.8	0.0	1.0
3	20.7	-0.2	17.2	5.6	100	37.7	100	73.8	0.0	33.2
4	21.3	0.4	17.4	2.6	100	39.1	100	62.4	0.0	9.2
5	23.4	0.2	19.5	0.9	100	34.1	100	44.7	0.0	0.0

Contd.....

Month/Week No.	Temperature (°C)				Relative humidity (%)				Rainfall (mm)	
	2001		2002		2001		2002		2001	2002
	Max.	Min.	Max.	Min.	Max.	Min.	Max.	Min.		
February										
6	23.7	0.2	17.4	5.2	100	28.0	100	60.7	0.0	21.0
7	25.0	5.8	21.7	5.9	94.6	36.3	100	64.7	0.0	25.2
8	25.7	7.0	23.9	7.2	94.1	34.8	97.4	50.7	0.5	10.4
9	24.6	3.0	20.8	6.9	97.0	29.7	100	58.0	2.0	41.0
March										
10	27.0	5.7	24.5	8.3	95.7	34.4	98.4	52.1	0.0	4.2
11	27.4	7.4	27.4	8.5	82.7	29.7	98.1	58.6	12.8	0.0
12	27.6	10.6	29.7	8.6	79.3	38.0	96.8	46.7	9.0	0.0
13	27.2	11.1	31.3	11.9	87.3	48.8	91.0	26.7	36.4	0.0
April										
14	30.6	11.0	31.9	11.2	81.4	28.4	85.4	34.0	1.2	0.0
15	30.8	14.6	32.5	11.9	82.7	40.4	89.7	29.3	11.6	0.0
16	26.9	14.1	36.3	13.3	95.4	48.7	71.7	22.0	63.2	0.0
17	34.0	14.5	33.6	14.8	76.6	32.8	77.0	29.7	0.0	39.2
18	35.6	15.7	35.7	15.2	68.3	31.3	64.3	20.7	3.4	1.8
May										
19	37.4	19.3	39.6	17.7	67.8	33.1	69.7	22.8	5.8	0.0
20	32.7	19.5	38.9	18.1	75.8	45.6	61.0	28.4	53.0	21.4
21	35.1	17.5	38.6	17.5	84.8	39.8	67.8	31.4	4.2	3.4
22	33.8	21.2	34.2	19.0	86.4	46.8	78.1	48.6	25.2	9.6

Appendix-II

Estimates of mean values for 53 genotypes with respect to 10 traits in environment-I

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
1.	HPG-54	7.71	15.11	41.10	38.14	1.69	2.33	127.33	170.00	14.10	50.83
2.	HPG-78	13.33	23.51	42.60	63.47	1.56	2.47	141.33	176.33	12.72	56.65
3.	HPG-100	7.90	19.19	53.47	34.73	1.41	2.33	130.67	172.67	24.44	41.51
4.	HPG-124	5.95	11.80	39.20	22.33	1.68	1.80	133.00	173.00	20.47	50.55
5.	HPG-127	14.49	29.35	51.40	60.80	1.23	2.13	122.33	170.33	29.32	49.41
6.	HPG-129	2.86	6.11	33.47	16.60	1.81	1.87	121.67	171.33	15.07	46.43
7.	HPG-130	4.47	10.60	40.60	29.47	1.62	2.07	128.67	174.00	15.66	42.54
8.	HPG-131	7.53	17.34	50.93	27.60	1.21	2.33	127.33	170.33	23.15	43.89
9.	HPG-132	5.27	12.65	46.00	29.77	1.41	2.13	136.00	176.00	22.26	41.46
10.	HPG-133	5.93	11.43	48.40	21.87	1.60	1.87	144.67	179.67	20.99	50.87
11.	HPG-134	9.06	21.33	55.87	44.53	1.31	1.93	133.33	173.33	26.76	42.52
12.	HPG-135	8.06	20.22	50.47	47.29	1.37	2.33	132.33	172.33	20.76	39.84
13.	HPG-136	5.25	12.85	41.20	30.07	1.56	2.27	131.33	172.33	16.77	41.11
14.	HPG-137	5.91	14.54	47.07	29.53	1.29	2.20	142.00	178.00	21.51	40.75
15.	HPG-138	6.39	12.84	43.93	22.47	1.41	2.00	138.67	179.33	23.12	50.01
16.	HPG-142	6.18	11.96	37.33	31.67	1.59	2.07	120.00	172.00	18.77	51.71
17.	HPG-143	6.51	14.37	56.93	26.67	1.67	2.27	126.00	171.00	24.12	45.49
18.	HPG-144	8.29	18.51	53.73	36.00	1.47	2.80	135.67	173.67	24.34	44.58

Contd.....

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
19.	HPG-145	7.93	18.50	53.40	34.20	1.49	2.13	130.67	172.67	30.52	43.29
20.	HPG-147	5.42	11.33	43.00	32.31	1.48	2.33	131.33	172.00	19.26	47.45
21.	HPG-149	5.81	13.68	45.07	24.27	1.82	2.13	134.33	175.00	20.08	41.90
22.	HPG-150	6.07	14.54	47.00	44.60	1.40	2.07	130.67	177.67	13.89	41.95
23.	H-82-2	8.71	17.97	32.13	56.07	1.41	2.20	105.00	162.00	14.11	48.30
24.	H-94-1	5.65	12.10	43.40	28.00	1.44	2.27	121.00	171.00	15.29	46.84
25.	H-94-83	5.73	12.51	42.07	34.60	1.82	1.73	126.00	175.67	14.22	45.94
26.	H-96-51	3.86	9.08	33.67	23.87	1.41	1.87	121.00	169.67	16.25	42.52
27.	H-208	12.58	25.02	45.47	71.87	1.38	2.53	121.33	169.00	16.03	50.31
28.	GL-87069	5.46	11.52	38.47	26.20	1.78	2.20	124.00	173.33	13.10	46.49
29.	GL-87129	9.78	16.05	40.33	46.27	2.01	2.07	120.00	168.00	11.98	60.94
30.	GL-90104	5.15	9.22	29.67	32.33	1.66	2.20	125.00	174.67	12.58	56.34
31.	GL-90169	11.31	20.37	45.40	39.17	1.69	2.47	119.00	169.00	21.81	55.60
32.	GNG-580	7.44	14.33	44.13	34.93	1.74	2.27	115.33	159.33	12.64	51.74
33.	CSG-8943	12.29	21.81	47.40	43.80	1.18	2.87	116.33	161.33	28.73	56.19
34.	CSG-9505	3.53	7.54	34.13	22.67	1.84	1.93	117.00	167.00	12.20	46.48
35.	PBG-1	10.89	19.90	36.67	52.93	1.77	2.27	117.67	163.67	13.49	54.74
36.	Pusa-372	7.51	13.17	35.00	43.60	1.58	2.27	118.00	167.00	13.22	56.46
37.	ICC-15851	5.32	9.48	28.60	31.80	1.57	2.13	117.00	167.00	11.03	57.52

Contd.....

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
38.	ICC-15599	2.89	5.48	29.40	13.00	1.65	2.33	118.00	166.00	15.34	52.67
39.	ICCV-89701	11.20	21.03	35.93	65.80	1.41	4.00	120.00	168.00	15.64	53.65
40.	BGD-112	8.23	16.40	52.27	31.00	2.04	2.07	130.00	166.00	15.95	50.19
41.	BG-1007	9.68	18.00	38.87	58.60	1.65	2.47	125.67	171.33	12.64	53.77
42.	BG-1086	9.57	19.05	47.33	30.67	1.36	2.07	132.33	168.33	25.66	50.14
43.	BG-1102	9.28	19.86	45.40	39.60	1.32	2.00	128.67	165.33	26.29	46.79
44.	KW-118	4.83	8.29	32.00	17.47	1.21	2.07	134.33	177.33	32.63	58.56
45.	165	12.53	22.89	44.53	47.73	1.47	2.13	144.67	176.00	25.30	54.75
46.	Avrothi	12.87	27.06	56.00	50.53	1.53	2.47	135.00	176.67	20.23	47.64
47.	JG-9	9.39	16.11	39.07	47.27	1.85	2.27	130.00	172.00	12.74	58.42
48.	L-550	12.47	24.39	40.33	52.53	1.27	2.47	125.00	158.00	22.89	51.45
49.	TCP-40	5.29	11.93	38.80	34.20	1.35	2.47	128.00	168.00	15.94	44.37
50.	WGG-9550	4.13	8.57	30.93	24.20	1.79	1.93	131.00	166.00	15.51	48.62
51.	HPG-17	16.93	40.32	57.73	50.30	1.67	3.27	132.33	177.33	26.22	42.06
52.	C-235	9.24	16.68	40.20	42.37	1.88	2.27	123.00	169.00	11.54	55.22
53.	Himachal Chana-2	7.19	15.60	42.27	38.47	1.96	2.00	124.00	167.33	16.67	46.28

SE(m)±		0.703	1.32	1.424	3.898	0.028	0.141	1.106	0.965	0.963	2.717
CD at 5%		1.973	3.701	3.999	10.943	0.078	0.398	3.105	2.709	0.294	7.628

Appendix-III

Estimates of mean values for 53 genotypes with respect to 10 traits in environment-II

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
1.	HPG-54	8.56	16.03	43.43	38.80	1.66	2.00	128.33	161.67	14.07	53.41
2.	HPG-78	13.44	23.86	43.67	56.30	1.56	2.73	141.67	168.00	12.41	56.32
3.	HPG-100	7.63	16.57	50.33	30.00	1.39	2.13	131.00	165.00	24.32	46.29
4.	HPG-124	6.40	14.99	50.93	24.07	1.61	2.20	133.33	167.33	20.36	42.72
5.	HPG-127	13.34	26.83	53.33	58.00	1.22	2.07	122.33	162.67	29.10	50.43
6.	HPG-129	3.71	9.40	45.47	15.87	1.82	2.00	131.33	165.67	15.36	39.29
7.	HPG-130	4.72	10.38	39.07	27.20	1.61	2.20	133.00	164.33	16.07	45.06
8.	HPG-131	5.58	14.36	47.17	21.20	1.41	2.00	126.67	162.33	23.93	39.00
9.	HPG-132	5.60	13.26	42.53	27.60	1.43	2.07	131.00	163.67	21.61	42.28
10.	HPG-133	5.28	12.68	46.70	22.27	1.59	1.93	131.33	162.33	21.22	41.79
11.	HPG-134	6.75	14.92	50.60	22.33	1.32	1.93	132.00	163.00	26.10	45.03
12.	HPG-135	4.56	12.65	54.17	18.27	1.35	2.07	132.67	162.33	21.08	36.02
13.	HPG-136	5.33	11.23	40.33	23.47	1.51	2.07	125.67	159.67	16.91	47.51
14.	HPG-137	5.63	14.92	47.73	31.00	1.28	2.27	142.33	171.00	21.56	38.78
15.	HPG-138	6.15	14.83	44.80	20.83	1.40	1.93	130.33	161.33	26.38	41.48
16.	HPG-142	7.40	15.60	45.67	32.33	1.59	2.07	129.00	162.33	18.81	47.43
17.	HPG-143	7.49	16.51	56.87	27.20	1.68	2.07	131.00	165.00	25.14	45.23
18.	HPG-144	7.31	16.55	52.87	30.07	1.49	2.20	131.33	161.00	24.48	44.40

Contd.....

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
19.	HPG-145	7.70	15.73	49.10	25.80	1.49	2.07	132.33	164.33	30.15	48.97
20.	HPG-147	6.74	15.10	46.67	30.40	1.49	2.07	133.00	164.33	19.82	44.79
21.	HPG-149	5.69	13.04	49.20	26.67	1.83	2.27	126.67	161.00	20.17	43.67
22.	HPG-150	6.02	14.02	43.73	38.33	1.41	2.20	128.33	164.00	13.71	43.13
23.	H-82-2	8.62	18.00	31.67	57.67	1.41	2.07	103.33	151.67	14.07	48.12
24.	H-94-1	5.28	11.75	45.77	25.00	1.45	2.40	121.67	162.00	15.32	45.89
25.	H-94-83	5.55	12.00	44.07	29.73	1.83	1.93	127.00	165.67	15.44	46.06
26.	H-96-51	3.73	9.62	33.67	25.67	1.41	1.93	121.33	162.00	16.13	39.82
27.	H-208	12.23	23.67	50.00	71.33	1.41	2.47	121.67	161.00	16.00	51.75
28.	GL-87069	5.43	10.56	38.00	25.03	1.78	2.33	123.00	160.00	13.07	51.07
29.	GL-87129	9.21	15.27	41.67	44.00	1.97	2.00	120.00	160.33	11.97	60.47
30.	GL-90104	5.59	9.43	31.57	30.33	1.68	2.07	125.33	167.00	12.51	59.76
31.	GL-90169	12.07	21.59	43.60	39.33	1.68	2.33	118.33	160.33	21.71	56.20
32.	GNG-580	7.30	13.70	44.67	37.33	1.74	2.07	116.00	151.00	12.65	53.40
33.	CSG-8943	11.72	22.62	44.33	44.33	1.18	2.87	116.67	153.00	26.30	51.90
34.	CSG-9505	3.57	7.53	35.57	21.67	1.83	2.00	117.67	159.00	12.22	47.44
35.	PBG-1	9.71	17.46	35.33	50.60	1.77	2.20	117.67	157.00	13.04	55.60
36.	Pusa-372	7.52	12.53	33.40	41.67	1.59	2.33	116.67	158.33	13.46	60.05
37.	ICC-15851	4.98	8.78	29.80	31.67	1.59	2.07	117.33	158.00	11.04	57.17

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
38.	ICC-15599	2.39	3.97	26.00	11.00	1.66	2.00	118.00	158.33	15.10	60.91
39.	ICCV-89701	10.56	19.48	36.67	63.17	1.40	3.93	119.67	159.67	15.15	54.20
40.	BGD-112	7.51	15.77	52.27	29.40	2.00	2.07	129.33	162.33	15.98	47.63
41.	BG-1007	9.02	18.00	40.00	62.33	1.63	2.27	126.67	168.33	12.76	50.38
42.	BG-1086	9.28	18.21	49.13	30.33	1.35	2.00	132.33	165.00	25.60	50.92
43.	BG-1102	7.39	15.86	46.93	28.33	1.30	1.93	128.67	161.33	26.33	46.39
44.	KW-118	4.50	8.05	31.33	15.00	1.20	2.00	134.37	169.67	32.55	56.07
45.	165	11.65	21.50	43.00	52.00	1.47	2.20	144.67	169.33	23.56	54.50
46.	Avrodhi	14.80	32.79	56.67	57.00	1.57	2.40	134.33	168.33	20.14	45.30
47.	JG-9	7.70	14.17	39.33	40.67	1.83	2.27	130.67	165.00	12.69	54.53
48.	L-550	11.21	21.77	41.00	49.59	1.28	2.33	127.33	161.67	22.72	54.09
49.	TCP-40	4.78	10.48	38.00	32.67	1.33	2.40	129.33	159.67	15.98	45.80
50.	WGG-9550	4.27	9.28	38.53	22.67	1.72	2.00	133.00	165.67	16.16	46.32
51.	HPG-17	15.18	37.78	53.30	45.67	1.67	2.07	133.67	169.33	26.49	40.17
52.	C-235	8.74	19.52	53.33	54.67	1.87	2.33	130.00	165.33	11.69	44.96
53.	Himachal Chana-2	7.02	15.70	44.77	35.00	1.81	2.00	123.33	165.67	16.66	44.81

SE(m)±		0.436	1.107	1.728	3.721	0.049	0.101	0.104	0.958	2.824	2.122
CD at 5%		1.224	3.109	4.853	10.455	0.136	0.285	2.928	2.690	0.861	0.596

Appendix- IV

Estimates of mean values for 53 genotypes with respect to 10 traits in pooled over environments

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
1.	HPG-54	8.14	15.57	42.27	38.47	1.68	2.17	127.83	165.83	14.09	52.12
2.	HPG-78	13.38	23.68	43.13	59.88	1.56	2.60	141.50	172.17	12.57	56.49
3.	HPG-100	7.76	17.88	51.90	32.37	1.40	2.23	130.83	168.83	24.38	43.90
4.	HPG-124	6.17	13.39	45.07	23.20	1.65	2.00	133.17	170.17	20.41	46.63
5.	HPG-127	13.92	28.09	52.37	59.40	1.23	2.10	122.33	166.50	29.21	49.92
6.	HPG-129	3.28	7.75	39.47	16.23	1.81	1.93	126.50	168.50	15.21	42.86
7.	HPG-130	4.60	10.49	39.83	28.33	1.62	2.13	130.83	169.17	15.86	43.80
8.	HPG-131	6.55	15.85	49.05	24.40	1.31	2.17	127.00	166.33	23.54	41.44
9.	HPG-132	5.44	12.95	44.27	28.68	1.42	2.10	134.50	169.83	21.93	41.87
10.	HPG-133	5.61	12.05	44.55	22.07	1.59	1.90	138.00	171.00	21.11	46.33
11.	HPG-134	7.91	18.12	53.23	33.43	1.32	1.93	132.67	168.17	26.43	43.77
12.	HPG-135	6.31	16.44	52.32	32.78	1.36	2.20	132.50	167.33	20.92	37.93
13.	HPG-136	5.29	12.04	40.77	26.77	1.53	2.17	128.50	166.00	16.84	44.31
14.	HPG-137	5.77	14.73	47.40	30.27	1.29	2.23	142.17	174.50	21.54	39.77
15.	HPG-138	6.27	13.84	44.37	21.65	1.41	1.97	134.50	170.33	26.25	45.74
16.	HPG-142	6.79	13.78	41.50	32.00	1.59	2.07	124.50	167.17	18.79	49.57
17.	HPG-143	7.00	15.44	56.90	26.93	1.67	2.17	128.50	168.00	24.63	45.36
18.	HPG-144	7.80	17.53	53.30	33.03	1.48	2.50	133.50	167.33	24.41	44.49

Contd.....

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
19.	HPG-145	7.82	17.11	51.25	30.00	1.49	2.10	131.50	168.50	30.33	46.13
20.	HPG-147	6.08	13.21	44.83	31.35	1.49	2.20	132.17	168.17	19.54	46.12
21.	HPG-149	5.75	13.36	47.13	25.47	1.82	2.20	130.50	168.00	20.13	42.79
22.	HPG-150	6.04	14.28	45.37	41.47	1.41	2.13	129.50	170.83	13.80	42.54
23.	H-82-2	8.66	17.98	31.90	56.87	1.41	2.13	104.17	156.83	14.09	48.21
24.	H-94-1	5.46	11.93	44.58	26.50	1.44	2.33	121.33	166.50	15.31	46.37
25.	H-94-83	5.64	12.26	43.07	32.17	1.82	1.83	126.50	170.67	14.83	46.00
26.	H-96-51	3.79	9.35	33.67	24.77	1.41	1.90	121.17	165.83	16.19	41.17
27.	H-208	12.41	24.34	47.73	71.60	1.39	2.50	121.50	165.00	16.02	51.03
28.	GL-87069	5.44	11.04	38.23	25.62	1.78	2.27	123.50	166.67	13.09	48.78
29.	GL-87129	9.50	15.66	41.00	45.13	1.99	2.03	120.00	164.17	11.98	60.71
30.	GL-90104	5.37	9.32	30.62	31.33	1.67	2.13	125.17	170.83	12.54	58.05
31.	GL-90169	11.69	20.98	44.50	39.25	1.68	2.40	118.67	164.67	21.76	55.90
32.	GNG-580	7.37	14.01	44.40	36.13	1.74	2.17	115.67	155.17	12.65	52.57
33.	CSG-8943	12.01	22.21	45.87	44.07	1.18	2.87	116.50	157.17	27.51	54.04
34.	CSG-9505	3.55	7.54	34.85	22.17	1.83	1.97	117.33	163.00	12.21	46.96
35.	PBG-1	10.30	18.68	36.00	51.77	1.77	2.23	117.67	160.33	13.27	55.17
36.	Pusa-372	7.52	12.85	34.20	42.63	1.58	2.30	117.33	162.67	13.34	58.26
37.	ICC-15851	5.15	9.13	29.20	31.73	1.58	2.10	117.17	162.50	11.04	57.35

Contd.....

Sr. No.	Genotype	Seed yield/ plant (g)	Biological yield/plant (g)	Plant height (cm)	Pods/ plant	Seeds/ pod	Primary branches/ plant	Days to 50% flowering	Days to 75% maturity	100-seed weight (g)	Harvest index (%)
38.	ICC-15599	2.64	4.72	27.70	12.00	1.65	2.17	118.00	162.17	15.22	56.79
39.	ICCV-89701	10.88	20.26	36.30	64.48	1.40	3.97	119.83	163.83	15.39	53.93
40.	BGD-112	7.87	16.09	52.27	30.20	2.02	2.07	129.67	164.17	15.96	48.91
41.	BG-1007	9.35	18.00	39.43	60.47	1.64	2.37	126.17	169.83	12.70	52.07
42.	BG-1086	9.42	18.63	48.23	30.50	1.35	2.03	132.33	166.67	25.63	50.53
43.	BG-1102	8.34	17.86	46.17	33.97	1.31	1.97	128.67	163.33	26.31	46.59
44.	KW-118	4.66	8.17	31.67	16.23	1.20	2.03	134.50	173.50	32.59	57.32
45.	165	12.09	22.20	43.77	49.87	1.47	2.17	144.67	172.67	24.43	54.63
46.	Avrodhi	13.84	29.93	56.33	53.77	1.55	2.43	134.67	172.50	20.18	46.47
47.	JG-9	8.54	15.14	39.20	43.97	1.84	2.27	130.33	168.50	12.72	56.47
48.	L-550	11.84	23.08	40.67	51.06	1.27	2.40	126.17	159.83	22.81	52.77
49.	TCP-40	5.03	11.20	38.40	33.43	1.34	2.43	128.67	163.83	15.96	45.09
50.	WGG-9550	4.20	8.93	34.73	23.43	1.75	1.97	132.00	165.83	15.84	47.47
51.	HPG-17	16.06	39.05	55.52	47.98	1.67	2.67	133.00	173.33	26.36	41.12
52.	C-235	8.99	18.10	46.77	48.52	1.87	2.30	126.50	167.17	11.62	50.09
53.	Himachal Chana-2	7.11	15.65	43.52	36.73	1.88	2.00	123.67	166.50	16.66	45.54

SE(m)±		0.41	0.86	1.12	2.69	0.028	0.087	0.76	1.007	0.162	1.72
CD at 5%		1.146	2.386	3.105	7.468	0.078	0.242	2.107	1.899	0.449	4.779
