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Phenotypic Expression of Chickpea (Cicer Arietinum L.) Genotypes Under Different Environmental Conditions.

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University of Rajshahi

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PHENOTYPIC EXPRESSION OF CHICKPEA (*Cicer arietinum* L.) GENOTYPES UNDER DIFFERENT ENVIRONMENTAL CONDITIONS.

A DISSERTATION SUBMITTED TO

THE DEPARTMENT OF BOTANY, UNIVERSITY OF RAJSHAHI, BANGLADESH,
IN FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

MASTER OF PHILOSOPHY

IN

BOTANY

BY

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December 2004

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DEDICATED

TO

MY RESPECTABLE PARENTS

& MY DAUGHTER

NAHIAN

DECLARATION

I hereby declare that the entire research work now submitted as a thesis for the degree of Master of Philosophy in Botany of the University of Rajshahi, is the result of my own investigation.

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CERTIFICATE

We hereby certify that the thesis entitled " Phenotypic Expression of Chickpea (*Cicer arietinum* L.) Genotypes Under Different Environmental Conditions " has been submitted by Md. Ashraful Islam Pramanik in fulfillment for the requirements of the degree of Master of Philosphy in the Department of Botany, University of Rajshahi. It is also to certify that the research work embodied in this thesis is an original and done by Md. Ashraful Islam Pramanik and the work or part of it has not been submitted before as Candidature for any other degree.

The style and contents of the thesis have been approved and recommended for submission.

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The Author

of Rajshahi. To study phenotypic expression of chickpea (*Cicer arietinum* L.) genotypes under different environmental conditions, ten yield related characters were selected i.e. days to first flowering (DFF), number of primary branches at first flowering (NPBFF), plant height at first flowering (PHFF), plant height at maximum flowering (PHMF), number of primary branches at maximum flowering (NPBMF), number of secondary branches at maximum flowering (NSBMF), pod weight per plant (PdWPP), number of pods per plant (NPdPP), number of seeds per plant (NSPP) and seed yield per plant (SYPP). This experiment was done in three consecutive years.

Seventeen genotypes of chickpea were grown in randomized block-design with three replications under 3 different environments. The data were collected on individual plant basis. All the measurements were done in CGS system. The collected data were analyzed according to the biometrical technique. For the present analysis, mean, standard deviation (*Sd*), standard error of mean (SE), co-efficient of variability in percentage (CV%), analysis of variance, components of variations, co-efficient of variability, heritability (h^2_b), genetic advance (GA), genetic advance expressed as percentage of mean (GA%), the regression co-efficient, mean square deviation (stability) ($\overline{S}^2_{di}$) etc, were calculated.

Moderately high co-efficient of variability in percentage (CV%) was found for pod weight per plant (PdWPP) and number of seeds per plant (NSPP) in consecutive three years while low CV% was shown for plant height at maximum flowering and Plant height at first flowering in all the characters on an average of three years. The highest phenotypic variation and genotypic variation was found in NSPP. The highest phenotypic and genotypic co-

efficient of variability was observed for seed yield per plant (SYPP). The highest heritability and genetic advance as a percentage of mean (GA%) with a value of 91.609 and 85.252 respectively, were recorded for seed weight per plant (SYPP). The second highest h^2_b and GA% were recorded for pod weight per plant (PdWPP) and number of seed per plant (NSPP) with a value of 91.448 and 84.68 respectively . High heritability with genetic advance suggests that heritability was due to additive gene effect. High error component of variation causes a low estimation of heritability. Low heritability (h^2_b) and genetic advance as a percentage of mean (GA%) were shown in plant height at maximum flowering (PHMF). The highest GA% was estimated from SYPP, which suggests this character has a wide possibility for further improvement.

In the analysis of variance genotypes and environments (years) item for all the characters were found significant. The interaction between genotypes (genotype) × environment (year) was significant for all the characters except NPBFF, PHMF and NSPP. The different components of variation varied differently in different characters and phenotypic components of variation (δ_p^2) were higher than genotypic components (δ_g^2) and other components of variations. In the present materials high phenotypic values caused the high genotypic values. Large genotype value for any character is always helpful for effective selection. Phenotypic co-efficient of variability was also greater than genotypic and all other co-efficient of variabilities . The highest amount of phenotypic, genotypic and other co-efficient of variabilities indicating wide scope of selection for any trait and vice-versa.

This investigation includes genotype environment interaction on the magnitude of V × E interaction vis-a-vis stability performance of seventeen chickpea genotypes. The ten quantitative characters such as DFF, NPBFF, PHFF, PHMF, NPBMF, NSBMF, PdWPP, NPdPP, NSPP and SYPP were studied under different environments in 3 years. Regression analysis of variance showed that the item genotype was highly significant for all the characters and noted that the genotypes were different among the genotypes. The role of V × E interaction has long been of great importance to the breeder for selection of genotype. The V × E was also significant for all the characters except NPBMF. The significant E + (V × E) indicated the different reaction of genotypes with the change of environments. The significant V × E (linear) component indicated that the genotypes studied responded differently in different environments i.e, different years. The linear component of V × E interaction indicated that genotypes differed significantly with respect to their response (b_i) and stability $\left(\overline{S}^2_{di}\right)$.

On the basis of the above mentioned criteria the genotypes (genotype) which should stable performance i.e., adaptable to all environment were genotypes 6 and 40 for NPBFF, genotypes 3 and 22 for PHMF, genotypes 36 and 45 for NPBMF due to their high mean performance $\left(\overline{X}\right)$, average b_i values and non-significant $\overline{S}^2_{di}$ values.

Some genotypes such as genotype 45 for DFF, PHFF and NPBFF, genotypes 33 and 40 for NPBFF, genotype 6 for PHMF, genotypes 33, 38 and 40 for NPBMF, genotypes 22 and 31 for NSBMF, genotypes 3 and 18 for

PdWPP, genotypes 3, 18 and 31 for SYPP were stable and adapted to favourable environments.

From the above statement and from the results obtained in this study, it could be indicated that breeders are likely to select suitable genotypes by growing them under different environmental conditions which might be able to increase the yield potential. Thus these genotypes might be considered as most stable with the change of environments and could be used preferably for the future-breeding programme.

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INTRODUCTION

1. INTRODUCTION

The present civilization is the gift of science. It is the supreme cause of development all over the world. So, it goes without having that only science can make Bangladesh in to a developed country indeed. Bangladesh has a vast population in comparison with its area. To remove the want of food and nutrition for the added population, research work is needed in the field of agriculture.

Plants are part and parcel of our life. Plants are useful to us in many ways. They give us oxygen, food, medicine, fuel, furniture and shelter and maintain our ecological balance. So, plants are very important to human life.

In Bangladesh pulse is an important name in our food list. Here, it comes next to rice. As a result, the significance of pulse as a food is unquestionable. Infact, it is considered an alternative to meat and fish as it contains more protein than many other vegetables. Apart from protein, pulse also contains carbohydrate, fat and mineral salt. Hence, the research of such a crop is undoubtedly required in our country. The research, which has been going on, is utterly negligible to the requirement. Among pulses chickpea is one of them and a popular foodstuff. It is rich in nutrient and energy. There are many kinds of chickpeas in Bangladesh. Each variety does not fit in with any environment. Moreover, the best quality has to be chosen to have more production. To select the best quality and to develop it, modern research is a must.

Food materials are the most essential commodities for the survival of the human being next to breath. Food materials are six kinds of elements such as protein, carbohydrate, fat, minerals, vitamin and water. We get all this materials from plant. Though some food come from animal but this supplier on plant. So, plant is the main source of food for human and animal.

Pulses are main source of protein. Protein is an important component of food and the basis of life. In our country the major part of our population suffer from malnutrition mainly due to deficiency of protein, owing to expensive price of animal protein like meat and fish. Malnutrition and protein deficiency are the root cause of ill health. Besides Bangladesh is a food shortage country in the world. In the next century we will be facing with the challenge of growing enough food for increasing people. To solve the situation more crops are to be grown specially pulse crops and pulse are taken in daily diet.

Pulses also provides most effective proteinceous fodder for cattle and poultry. Some pulses are also grown for forage purpose. Pulse is important as replenisher of soil nitrogen. Legumes and Biological Nitrogen Fixation are very important in the developing world, whence much of the increase in food production must come to accommodate increasing world population. It is essential that tropical legumes be exploited to replace fertilizer nitrogen, to avoid compounding recalcitrant environmental problems of local and global proportions. The higher protein content in legumes is directly correlated with the presence of nodules on the root containing nitrogen fixing bacteria which live in symbiotic association with the pulse leguminous crops not only fixed

elemental nitrogen towards the benefit of the following crop but also save nitrate leaching during precipitation (Jones 1939). Among the pulse crops *Phaseolaris* spp fixed 80-120 kg nitrogen per hectare.

From the economic point of view in our country this protein requirement is mainly maintained from the " Green World " i.e. from the cereals, pulses and other than from animal sources. The protein pulse is commonly known as vegetables protein. Plant protein are the major substitute for animal protein and in this context, grain legumes occupy an important place as source of dietary protein. On an average about 80% of protein and 90% of calories are consumed by man in the developing countries which are supplied by plants. Among plants, pulses are grown and consumed largely in Bangladesh, moreover, pulse grain are less expensive compared to animal source of protein and thus considered poor man's meal.

Table-1 : Acreage, production and yield rate of different pulses :

Pulses	1999 – 2000			2000 – 2001			2001 – 2002		
	Acreage (000)	Production (000mt)	Per acre yield(mt)	Acreage (000)	Production (000mt)	Per acre yield(mt)	Acreage (000)	Production (000mt)	Per acre yield(mt)
Gram	41	12	0.29	40	12	0.30	38	11	0.29
Arahar	13	3	0.21	10	2	0.20	-	-	-
Moog	136	36	0.26	130	34	0.26	-	-	-
Masur	412	128	0.31	106	126	0.31	388	115	0.30
Mashkali	71	21	0.30	67	20	0.24	65	19	0.29
Kheshari	499	166	0.33	462	155	0.33	499	147	0.33
Garikali	-	-	-	-	-	-	-	-	-
Motor	45	14	0.31	42	14	0.33	-	-	-
Other pulse	14	4	0.24	13	3	0.23	-	-	-

Source : Monthly Statistical Bulletin, Bangladesh March- 2002.

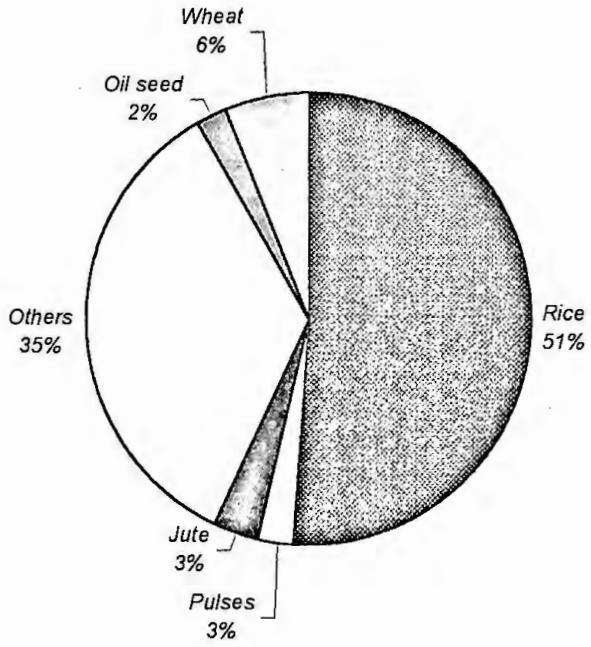

Fig. 1. Pie chart showing production of different field crops of Bangladesh.

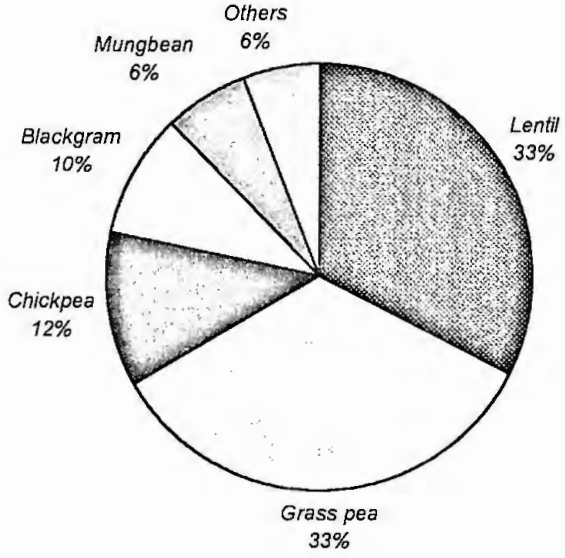

Fig. 2 : Pie chart showing production of different pulses of Bangladesh .

Protein is a component part of life. Genetic code and genetic material are formed of protein. Hence the importance of protein in the nutrition needs no elaboration. Therefore, it is obvious that most of the people of Bangladesh are deprived of protein, which is urgently necessary for the proper growth of the baby. Pulses have the remarkable quality of supplementing the cereal proteins since they are rich in an amino acid , which is generally deficient in cereals. Pulses also contain fair amount of minerals and vitamins.

Beside protein, there are a large number of calcium's iron and thiamin in pulses. Pulses are good sources of vitamin B (except riboflavin). Vitamin C is also synthesized from some pulses (chickpea). The chemical compositions of some select pulse is shown in tables 2 and 3.

Some pulses are rich in protein and minerals and the most essential item for rice-based diet of Bangladesh. They are also a nutrition's food item for cattle and poultry. Above all, pulses are very important for the soil fertility of the country specially where intensive cropping system are being practical for production of food and fibre crops.

Table-2 : Proximate principles in some pulses.

Name of food stuff	% of Edible portion	% Moisture	% Protein	% Fat	% Minerals	% Fiber	% Carbohydrate	Enengykcal
Chickpea (Whole)	100	9.8	17.1	15.3	3.0	3.9	60.9	360
Chickpea (Dhal)	100	9.9	20.8	5.6	2.7	1.2	59.8	372
Chickpea (Roasted)	100	10.7	22.5	5.2	2.5	1.0	58.1	369
Blackgram (Dhal)	100	10.9	25	1.0	2	.9	55	347
Cowpea	97	13.4	24.2	1.0	3.2	3.8	54.5	323
Mungbean (Dhal)	100	10.1	24.5	1.2	3.5	0.8	59.9	348
Lathyrus	100	10.0	28.2	0.6	2.3	2.3	56.6	345
Lentil	100	12.4	25.1	0.5	2.1	0.7	56.5	343
Sweat pea (Roasted)	100	13.4	22.3	1.7	3.5	1.5	57.6	335
Soyabean	-	8.1	43.2	19.5	4.6	3.7	20.9	432
Cajanus cajan (Arhor)	-	10	20.3	2.5	4.0	2.5	55	-

Table-3 : Important minerals and vitamin in some pulses.

Name of food stuff	Calcium (mg)	Phosphorus (mg)	Iron (mg)	Carotene (mg)	Thiamine (mg)	Riboflavin (mg)	Niacin (mg)	Vitamin (mg)	Folic acid (Total) mg
Chickpea (Whole)	202	312	10.2	189	130	0.15	2.9	3	186
Chickpea (Dhal)	56	331	9.1	129	.48	0.18	2.4	1	147
Chickpea (Roasted)	58	340	9.5	113	0.20	.21	1.3	0	139
Blackgram (Dhal)	154	385	9.1	38	0.42	0.20	2.0	0	132
Cowpea	97	414	5.9	12	0.51	0.20	1.3	0	133
Mungbean (Dhal)	75	405	8.5	49	6.47	0.21	2.4	0	-
Pigeonpea (Dhal)	73	304	5.8	132	0.45	0.19	2.9	0	103
Soyabean	240	690	11.5	426	0.73	0.39	3.2	-	100
Lentil	69	293	4.8	270	0.45	0.20	2.6	0	36
Lathynus	90	317	6.3	120	0.39	0.17	2.9	0	-
Peas(Roasted)	81	345	6.4	18	0.47	0.21	3.5	0	-

Source : Gopalan *et al.* 1981.

On global basis, chickpea (*Cicer arietinum* L.) is the third most important pulse crop after beans and dry peas. Although pre-dominantly consumed as a pulse dry chickpea is also used in preparing a variety of snack foods, sweet and condiments. Green chick peas are commonly consumed as a vegetables for a short period before the crop is mature. Nutritionally, chickpea

is relatively free from various antinutritional factors, has high protein digestibility and is richer in phosphorus and calcium than other pulses.

There are various number of pulse grown in Bangladesh, presently about 1351000 acres are cultivated under pulses. This form is 3.92% of total cultivated land (Year Book of Agriculture Statistic of Bangladesh 1999). The important pulses which are cultivated in Bangladesh are *Lens esculenta*, *Lathyrus sativus*, *Vigna radiata*, *Vigna mungo*, *Pisum sativum* and *Cicer arietinum* and *Cajanus cajan* .

Most of the pulses are concentrated in a few district. Among the pulses grown in Bangladesh chickpea ranks fourth in area 41000 acres (Statistical Bulletin of Bangladesh, Sept. 2000). About 80% of the chickpea crops are grown in the five greater district of Faridpur, Jessor, Kustia, Rajshahi and Pabna.

The Common name of chickpea is gram. It belongs to the sub family papilionaceae under the family leguminosae (Fabaceae). The plant is small, much branched annual herb. Leaves even-pinnate, alternate, leaflets elliptic-ovate, dentate. Flowers solitary auxillary, small, bluish purple, on slender peduncle. Inflonescence is raceme with one or two flowers. Fruit is pod. The pod are large, elongated, slender, turgid sessile, 2 seeded, seeds obviate or subglobose, beaked.

The seed of chickpea is one of the most highly priced pulse of Bangladesh. Dry seeds of chickpea give us enough heat and energy. Chickpea 'dhal' is very nutrition's food. The powder which we get from the dry seeds is called 'Beson' and used as in food preparation. The seed of the gram soaked in water is given to the player to make them strong. Green pods are nice to eat. The husks with broken seeds particles given to the cattle. Malic and oxalic acid in the plant parts is used medicinally.

Chickpea is a rabi seasonal crop. In Bangladesh, the crop is grown on sandy loam, alluvial to clay loam soils which are normally well drained. The farmer can be cultivated it as a single or mix with other crops. The chickpea can be grown on soil with p^H range of 6.0 to 9.0. However, it is sensitive to salinity and alkalinity. In the traditional chickpea growing areas about 60% to 65% of the crops grown under the Aus (rain fed) rice/jute fallow/chickpea cropping pattern. In this pattern, chickpea sown in early November (mid Kartic) is harvested by early March (mid Falgun) in southern part of the country. In the northern districts it is sown in mid November (early Agrahayon) and harvested in last March or early April (mid Chaittra). The remaining 35%-40% is grown under the Aman (rainy season) rice chickpea fallow cropping pattern under the late sowing condition. The yield of chickpea is 550 – 575 kg / hectare in Bangladesh.

Gram is the most important legume in Bangladesh but its per acre yield is low in our Country. In order to increase per acre yield vigorous breeding works are to be carried out. Most of its economic characters are quantitative in nature and show continuous variation.

The progress in a breeding programme depends on the magnitude of genetic variability in the available materials. The genetic variability shown by the characters can be measured from the genotypic co-efficient of variability. It is not only sufficient to determine the amount of heritable variances. The heritable portion of the variations can also be measured by the heritable estimates and genetic gains (Swarup and Chaugale, 1962).

In the present research work, characters under study are quantitative in nature and polygenic control. Ploygenes cumulate their effect to give rise greater action on a phenotype. A phenotype / character is the joint product of interaction between genotype and environment. Analysis of quantitative characters are very much complex when more than one environments are included because change in gene expression may occur with the changes of environments. These changes are observable as V × E interaction in a biometrical analysis and have long been recognize as an important source of phenotypic variation (Immer *et al.* 1934, Yates and Cochran, 1938 and Mather, 1949).

Any development through breeding programme depends upon the magnitude of genetic variability in the materials. Most agronomic and economic characters are done by following biometrical technique bound on mathematical model of Fisher *et al.* (1932) and as developed by Mather and Jinks (1971).

Eberhart and Russel 1966 used two parameters to describe the performance of a genotype over an array of environment. They proposed that the regression of each cultivars on an environmental index and function of the squired deviations from this regression would provide useful estimate of cultivates stability parameters. Stable genotype is one, which has a high mean unit regression co-efficient (b_i = 1.00) and deviation of zero $\left(\bar{S}^2_{di} = 0.000\right)$ from regression.

The second approach is based on fitting of models, specifying contributions of genotype, environment and genotype × environment interaction of generation means and variances due to contributions of additive, dominance and epistatic gene effect to the genetic and interaction components. This approach has been used by Mather (1949), Jinks (1954) and Jinks and Mather (1955) in *Nicotiana rustica* L. and latter on Bucio Alanis (1966), Bucio Alanis and Hill (1966), and Perkins and Jinks (1968).

In many traits in which a set of plant genotypes is grown over a range of environment the genotype do not behave in the same relative way in all environments. The phenomenon is known as genotype × environment (V×E) interaction. Many methods have been proposed for its statistical analysis, these having been reviewed critically by Freemen (1973) and Hill (1975).

The occurrence of genotype-environment interactions have long been provided a major challenge to obtaining a fuller understanding of the genetic control of variability. Genotype-environment interaction is the different in response of two or more genotypes to a given change in the environment. In

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other words, the relative performance of different genotypes under different environments vary indicating the existence of genotype environment interaction. As it is lender the control of gene, the breeders are able the select suitable genotype in advanced generation by growing them under different environment conditions.

A regression method to deal with this situation introduced by Yates and Cochran (1938), and this technique is now usually known as joint regression analysis. The joint regression analysis, a form of the analysis of variance has been widely used in the study of Genotype × Environment interaction. Freeman (1973) and Hill (1975) reviewed its producers and applications. In particular, genotype which vary comparatively little in different environment and so have regression co-efficient of less than unity are regarded as stable and these may be of value to the plant breeder.

Genotype environment interaction is now recognized as an important source of phenotype variation. Knowledge about the type of genotype environment interactions involved in population help the plant breeders to breed and select better genotypes.

In Bangladesh, the soil and climatic conditions are such that the cropping pattern of chickpea does not permit its sowing at the same time all over the country. For this, V × E interaction is essential in breeding genotypes for general adaptation, particular in a crop like chickpea which is grown in diverse agroclimatic conditions.

There are different method available estimating the magnitude of V × E interaction and stability parameters. However, the model proposed by Eberhart and Russell (1966) is relatively simple and most widely used for this purpose. Accordingly in the present investigation an attempt has been made to determine the magnitude of V × E interactions vis-a-vis stability parameters for ten quantitative characters of 17 genotypes in order to select the suitable genotypes having wider adaptability for different environments.

The present investigation deals with the phenotypic and genotypic variability, heritability (in brode sense), genetic advance, stability parameters viz. regression co-efficient, mean square deviation , standard error of co-efficient in seventeen genotypes of chickpea (*Cicer arietinum* L.) and also the direct and indirect effect of component characters on yield.

CHAPTER- 2

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Literature in respect of phenotypic expression of chickpea (Cicer *arietinum L.)* genotypes under different environmental conditions are not available. In fact reports on chickpea are very few and scattered. A few number of papers has been published dealing with the problem of stability parameters of different quantitative characters on various leguminous crop plants. A brief review of literatures on the leguminous crops with others are given below.

Johansen (1909) explained the relationship between heredity and environment at first time. He proposed that environment play a significant part in determining the life situation. In an investigation with beans (Phaseolus *vulgare L.)* he showed that the phenotype was the product of both heritable and non-heritable effects and the phenotypic variation in pure was due to the environmental effect.

Fisher (1918) was the first to develop statistical method to partition variance due to quantitative character in segregating population into genetic and environmental components.

Smith (1944) thought that the quantitative characters were governed by a large number of genes, which were similar, relatively small, non-dominant and additive in nature.

Mather (1949), Mather and Jones (1958) and Stevens (1959) were separately and combindly developed the techniques to measure the genotype-environment interactive based in the mathematical model of *Fisher et al.* (1932). It involved the partitioning of the variation of quantitative data into genetic and environmental effects and their interactions. Here the degree of interaction was expressed as a linear function of the effect of environment.

Kalton *et al.* (1952) and Lebsock and Kalton (1954) estimated environmental variance within several clonal populations upon analysis, these estimates exhibited a significant difference for characters controlled by gene indicating the presence of genotype-environment interaction. In the latter studies, it was concluded that the environmental variance composed of two components viz., a true environmental effect and genotype-environment interaction.

Athwal and Gill (1964) studied crosses of gram (*Cicer arietinum* L.) and found that in three-crossed habitability in narrow sense appeared to give the best indication of the actual genetic advance. The co-habitability of yield with some other characters was substantially greater than habitability of yield alone.

Bucio Alanis (1966) studied the genotype-environment interaction in *Nicotiana rustica.* He observed that genotype-environment interaction significantly influenced the phenotypic expression.

Ananda (1968) studied the relationship between variety and environment in wheat. Analysis of variance of data from trials involving 12, varieties at 4 locations for 3 year, showed variety × location × year and variety × location

interaction were significant, indicating that the performance of varieties varied with the environments. The interaction variance was found to decrease with the increase of the number of locations.

Chandra (1968) worked on variability in gram. The estimates of components of variation for ten yield components showed that there were wide variations in the material for all the characters and that variability was affected by environment, particularly for plant height and secondary branches per plant. On the whole heritability (broad sense) values were high for number of pods per plant was low. High heritability and high genetic advance were associated in case of setting percentage, flowering duration, primary branches and number of pods per plant.

Singh and Dixit (1970) studied genetic variability which showed positive genotypic and phenotypic correlations between yield and the number of primary or secondary branches of the six morphological characters studied, plant height and number of secondary branches gave the highest heritability estimates. It was indicated by genetic advance that selection for more seeds per pod, more pods per plant and more secondary branches could be fruitful.

Lal and Mehta (1973) found genotypic variability to be present in eleven quantitative characters of 25 soybean varieties. In the study of genetic co-efficient of variation and genetic advance were found to be highest for plant height. Medium estimates of heritability were recorded for number of branches, number of pods per plant and number of seeds per pod.

Malhotra *et al.* (1974) investigated genetic variability and genotype-environment interaction in lentil. Significant differences were recorded in all six characters studied in 47 lines grown at three regional sites. The number of primary branches, number of clusters and pods per plant, plant height, 100-seed weight and yeild per plant were studied. Seed yield gave high co-efficient of genetic variation and estimated genetic advance as a percentage of mean for pod number and 100-seed weight gave high co-efficient of genetic variation and genetic advance, and moderate heritability at all three sites.

Zuberi and Gale (1975) studied the effect of soil nutrients on the expression of eleven traits of *Papaver dubium* observed significant effect of all nutrients obtained the greatest effect of Calcium. Both linear and non-linear relationship between genotype environment interactions and environmental mean were found for all the traits.

Khaleque (1975) investigated genotype × environment interactions for eighteen quantitative characters in a 5 × 5 diallel progenies of rice over two seasons. Joarder and Eunus (1977) also made a study of genotype-environment interaction shown by heading and harvesting time in *Brassica campestries* L. All of them showed that genotype environmental interactions were operative in both parental and F_2 generations and that a significant portion of these interactions was accounted for by the linear function of the environmental means. A part of the interactions was independent of this linear component. Both the linear and non-linear components were under the control of different gene systems and subjected to dominance. Interaction between the additive

component and the environmental means was greater than that of the dominant component under different environments.

Shalehuzzaman and Joarder (1979) worked on heritability, phenotypic and genotypic components of variation in soybean. The major portion of the total variance in respect of all the characters was contributed by the genotypic and genotype-environment interaction component. The yield/plant showed the highest genotype-environment co-efficient of variability but the lowest heritability.

Majid *et al.* (1982) studied forty germplasm of black gram growing in a randomized block design. Data on ten agronomic characters were taken viz. days to first flowering, days to maturity, plant height, number of primary branches/plant, number of inflorescence's/plant, number of pods/plant, pod length, number of seeds/pod, 500-seed weight and seed yield/plant. The phenotypic variances were found to be larger than the genotypic variance for all the characters.

Ashutosh *et al.* (1984) worked on genetic variability and interrelationship in eleven pure line of black gram. Some genetic parameters and interrelationship were studied for seven characters. They reported that high heritability along with high genetic advance was observed for plant height and days maturity. Two important yield contributing traits, such as pods/plant and 100-seed weight showed an appreciable percentage of heritability and genetic advance.

Rahman *et al.* (1986) worked on variability correlation and path co-efficient analysis in bottle goured (*Lagenara vulgaris* L). Genotypic and phenotypic variability were high for fruit length and number of branches per plant, but very low for number of fruits per plant and length of mainvine. Heritability (broad sense) and genetic advance in percentage of mean were high for length, fruit diameter and fruit weight per plant.

Alam (1987) studied the G×E interaction in Tossa jute. He reported significant variations due to sowing and year components. Genotypes interacted with year for base diameter and green weight. Genotype × year × sowing interactions were significant for all the characters except plant height. Major portion of the interaction was due to regression.

Sarker *et al.* (1988) worked on genotype-environment interaction in groundnut. Twenty five genotypes of ground-nut were evaluated at three different locations to determine the genotype-environment interaction vis-a-vis stability over a wide range of environment. Significant G×E interactions were observed for all the characters.

Rahman and Parth (1988) worked on variability and correlation in chickpea (*Cicer arietinum* L.) co-efficient of variation was maximum for yield/plant (50.85%) and 100-seed weight (31.40%). The lowest co-efficient of variation was observed for days to maturity (2.45%).

Hossain and Khaleque (1989) made a quantitative analysis on seventeen lines for eleven characters in chilli (*Capsicum annuum* L.). They observed that

all the characters included in the analysis were polygenic in nature. They further proposed that the lines were well differentiated in respect of the characters studied.

Khaleque *et al.* (1991) studied the variability and correlation of some chemical characteristics in chilli (*C. annuum* L). They reported that most of the chemical characteristics and yield per plant showed high GCV. All the characters except yield per plant and protein in ripe chillies under study exhibited very heritability estimates. It was also observed that variety season (G×S) interactions effect were highly significant.

Samad (1991) worked on genotype-environment interaction of six agronomical characters in fifteen rapeseed (*Brassica campestris* L) cultivars in six consecutive years. He showed that genotype-environment interactions were significantly operative in the experiment. He observed all the genotypes for plant height and number of pod/plant failed to show the stable performances, while some of the genotypes like Polar, Tori-9, Tori-7 and Sampan were predicted to show the stable performances in regard to the agronomical characters such as number of secondary branches, number of seed/pod and yield/ plant.

Khaleque *et al.* (1994) studied the variability of fourteen quantitative characters in chickpea (*Cicer arietinum* L.). They reported that low genotypic, variations were observed for all the characters except 100- seed weight and plant height at harvest. They also reported that the highest heritabitality with low genetic advance and expected genetic advance in percentage of mean were found in 100- seed weight, second highest heritability, genetic advance and

GA% were found in plant height at harvest. These characters were also showed maximum GCV. They showed strong and positive association between in plant height at harvest and 100- seed weight.

Begum (1995) studied on variability and heritability in chickpea (*Cicer arietinum* L.). She investigated fourteen quantitative characters. In her investigation, among all the characters only 100- seed weight showed highest heritability and co-efficient of variability and this character also showed positive correlation with other characters.

Shafiyoul (1997) studied on genotype-environment interaction of some morphological characters under soil moisture stress condition in chickpea (*Cicer arietinum* L.). In the genotype-environment interaction, he estimated regression co-efficient, genotypic and environmental and joint regression analysis. Genotype and environmental items were significant for all the characters. Joint regression analysis indicated that linear portion of V×E interaction was not significant for most of the characters. With above average regression value for most of the genotypes showed that they would likely respond in better environment only. However, varieties ICCV-92133 in 1993-94 PAO-299/3603 in 1993-94 for plant height at first flower, ICCL-83105 for plant height at maximum flower in 1993-94 and all the genotypes for number of secondary branches at first flower in two years (1993-94 and 1994-95) with average regression value and less standard error indicated that they are likely to be stable in varied environmental condition.

Yan (1999) with doubled haploid (DH) population of 123 lines from IR-64p Azucena analyzed the genotype × environment (G × E) interaction for

eight plant type traits in rice (*Oryza sativa* L.). The total genetic effects were partitioned into genetic main effects and G×E interaction effect. These two kinds of predicted effects were used in mapping quantitative trait loci (QTLs). Four to nine QTLs affecting different plant type traits were detected. Results indicated that all common some also by G×E interaction effects. Some genomic regions identified significant QTLs in only one environment, some also showed genetic main effects. Those QTLs with genetic main effects could be used in marker-assisted selection only for specific environments. In most cases, the pairs of traits with a high genetic correlation shared more common QTLs regions than those pairs of traits with a lower genetic correlation.

Islam *et al.* (2000) studied eighteen chickpea (*Cicer arietinum* L.) lines for germination test for the characters such as the length of radicle (LR) and the length of plumule (LP). The response of individual genotypes was determined by the analysis of joint regression on the mean values of genotype over a range of days (days considered as environment). The analysis showed that the response of seedling growth in all 18 chickpea lines was linear as the regression and regression co-efficient were significant for all the genotypes. The differences between the genotypes both for plumule and radicle were largely due to different environment as environment item was highly significant. Moreover, significant genotype environment interaction indicated that different genotypes responded differently in different days.

K.A. Sarkar *et al.* (2000) an investigation on genotype × environment interaction for seed yield and three yield contributing characters showed that the varieties interacted significantly with the environment and this interaction was accounted for by the linear function of the environmental means. Some of the interactions were independent of this linear component. Genotypes, Akbar and Sonora with high mean performance, regression coefficients greater than 1.00 together with high $S^2_{d_i}$ values were found to be suitable for favourable environments. Kanchan and Aghrani with average mean performance, average response and low $S^2_{d_i}$ values were suitable for all environments.

E. Haque *et al.* (2002) the performance of five traits in 21 near isogenic lines (NILs) of wheat were evaluated at six different agroenvironments. The NILs of wheat were considered as different genotypes and the sowing dates were treated as different environments. The significant genotype × environment (G × E) interaction indicated for estimating the stability parameters. The significant E + (G × E) component indicated the differential reaction of genotypes upon the environment. Both the significant linear and nonlinear (Pooled deviation) components of G × E interaction for yield traits suggested that the genotypes differed significantly with respect to their response (b_i) and the stability $(S^2_{d_i})$. From the estimation of stability parameters the genotypes 14 for effective tillers/plant; 1, 11, 12 and 20 for spike let no./spike; 3, 5, 7 and 11 for grain no/spike; 4, 11 and 19 for 100-grain weight and 11, 14 and 20 for grain yield/plant were found to be most stable and suitable for all the environments. Thus, the yield potency might be increased by developing the stable and good performer in appropriate environments.

M.A. Islam *et al.* (2004) the present investigation deals with the study of comparison of G × E models for selection of stable genotypes in chilli (*Capsicum annuum* L.). The materials were seven chilli vanehes, viz. abbreviatum, annuum, acuminatum, nigra, conoides, cersiformis and fasciculatum which were tested for ten quantitative characters, such as number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), number of leaf at first flower (NLFF), leaf area at first flower (LAFF), plant height at first flower (PHFF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), number of leaf at maximum flower (NLMF), leaf area at maximum flower (LAMF) and plant height at maximum flower (PHMF). In this study the range of variation was wide and pronounced for all the characters, indicating that there were genotypic differences among the varieties. For the analysis of stability, under three models, namely Eberhart and Russell (1966), Perkins and Jinks (1968) and Freeman and Perkins (1971) were compared to select the stable genotypes. Following all the three models varieties abrevaitum for PHMF, acuminatum for NPBFF, abbreviatum, annuum and cerasiformis for PHFF were found to be stable having unit regression co-efficient (b_i), non-significant deviation from regression ($S_{d_i}^{-2}$) and high mean performances. Following Eberhart and Russell's (1966) model, the linear component in the joint regression analysis was found to be important. In Perkins and Jinks (1968) model both linear and non linear components were found to be important. But in Freeman and Perkins (1971) model, only non-linear component was significant.

3. MATERIALS AND MATHODS

3.1 MATERIALS

The materials for the present investigation comprised seventeen (17) genotypes of chickpea (*Cicer arietinum L.*). The materials were received from the Biometrical Genetics Laboratory, Department of Genetics and Breeding, University of Rajshahi. The seventeen genotypes of chickpea used for the present work are tabulated below.

Table – 4 : List of seventeen genotypes of chickpea

Sl. No.	Stock No.
1	V – 3
2	V – 6
3	V – 9
4	V –18
5	V – 22
6	V – 30
7	V – 31
8	V – 32
9	V – 33
10	V – 35
11	V – 36
12	V – 38
13	V – 40
14	V – 41
15	V – 42
16	V – 45
17	V – 49

Ten morphological characters were selected for the study of phenotype expression of chickpea genotype under different environmental conditions in 1999-2000, 2000-2001 and 2001-2002.

The characters studied are as follow :-

1. Days to first flowering (DFF)
2. Number of primary branches at first flowering (NPBFF)
3. Plant height at first flowering (PHFF)
4. Plant height at maximum flowering (PHMF)
5. Number of primary branches at maximum flowering (NPBMF)
6. Number of secondary branches at maximum flowering (NSBMF)
7. Pod weight per plant (PdWPP)
8. Number of pod per plant (NPdPP)
9. Number of seed per plant (NSPP)
10. Seeds yield per plant (SYPP)

3.2 METHODS

Methods followed to conduct the experiment and analysis of data are divided into the following sub-heads :

1. Preparation of experimental field
2. Design and size of the experimental field
3. Sowing of seeds and raising of seedlings
4. Maintenance of experimental field
5. Collection of data

6. Techniques of analysis of data

3.2.1 Preparation of the experimental field :

Before sowing the seeds the experimental field ploughed thoroughly for several times. By repeated ploughing, laundering and hammering, the surface layer of the soil was well pulverized. No chemical fertilizers were used for the experiment. Only cowdung manure was mixed with the soil through ploughing and weeds were removed from the field completely. No irrigation was supplied after sowing the seeds.

3.2.2 Design and size of the experimental field :

Seventeen genotypes of chickpea were grown in randomized block design with three replications at the research field of the Department of Botany, University of Rajshahi during the rabi season of 1999-2000, 2000-2001 and 2001-2002. The field size for the experiment was 1080 cm × 1294 cm. Each replication consisted of two blocks. The size of each block was 164 cm. × 1080 cm. The whole experimental field was comprised of 54 plots. Hence each replication contained seventeen plots in two blocks. As a result one block got 9 plots. One plot contained 3 rows, 40 cm apart form one another

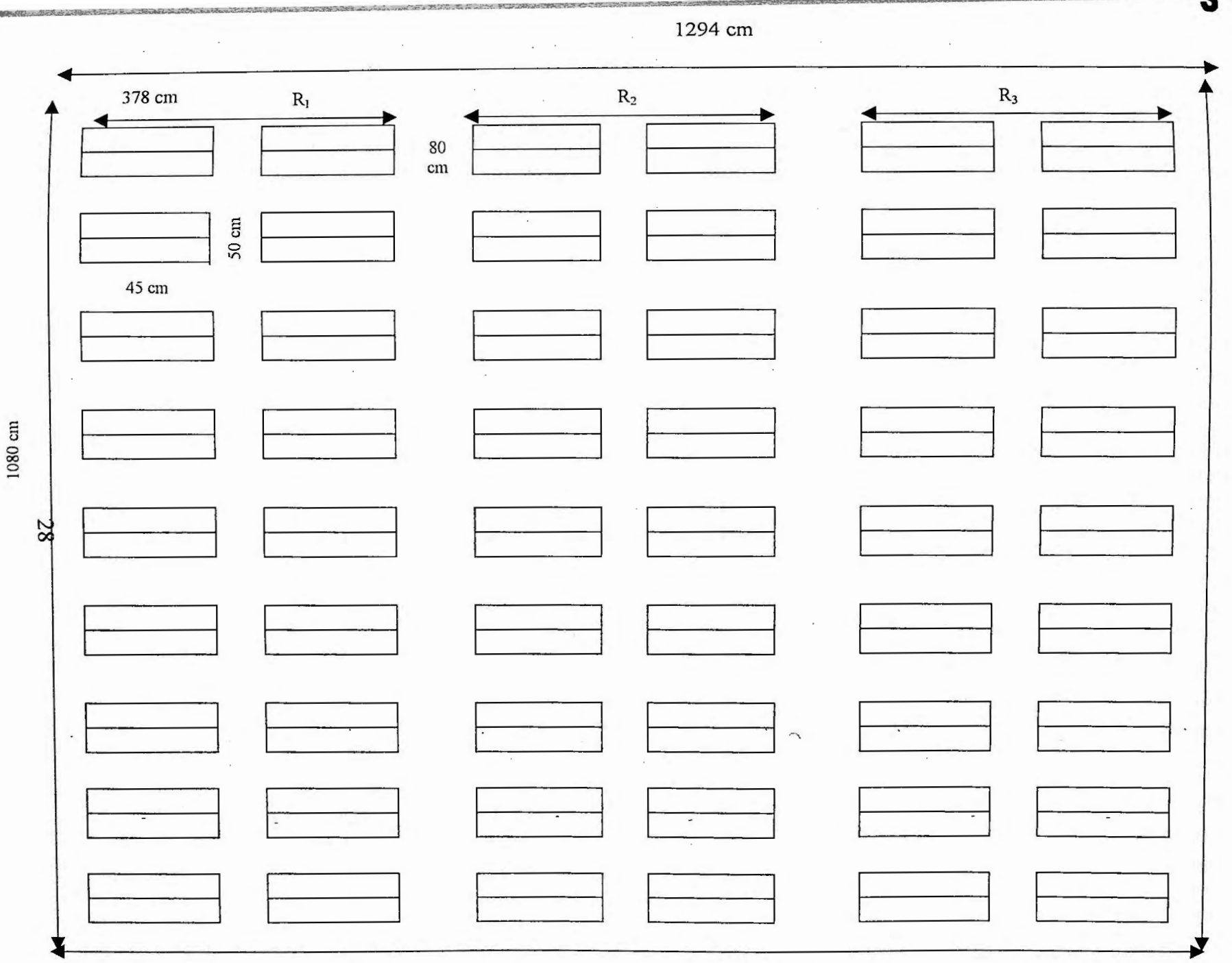


Figure-3 : Design of layout of the Experimental field.

and in one row there were 5 hills. Thus, altogether one plot had 15 plants. In the row plant-to-plant distance was 41 centimeters. One replication had 17 plots. The genotypes were randomly assigned to rows in block per replication. There was 45cm wide space between two plots. The space between replication and block was 50 centimeters and there was a foot path of 80 centimeters wide all around the experimental field. The space between plots were 45 centimeters.

3.2.3 Sowing of seeds and raising of seedlings :

The seeds of 17 genotypes were randomly assigned to the inner seventeen rows in each replication. Along each row 2 inches deep line was made by hand plough and seeds were sown in the line at a regular interval two seeds were placed at each site in row 41 centimeters in the first year (1999-2000) and the second year (2000-2001) and third year 2001-2002. After sowing the seeds were covered with the soil.

Table :

Sowing date	Year	Symbol
7th November	1999	S-1
13th November	2000	S-2
1st December	2001	S-3

3.2.4 Maintenance of the experimental field :

Regular weeding and hoeing was done. When the seedlings were 19 or 20 cm. in height, the excess seedling were removed by thinning from the experimental field.

3.2.5 Collection of data :

Data on different quantitative characters were collected on individual plant basis from nine plants randomly selected in each plot. All the measurement was taken in C.G.S. system. Data were collected on the following characters.

(I) **Days to first flowering (DFF) :** Total number of days at first flowering stage per selected plants was counted.

(II) **Number of primary branches at first flowering (NPBFF) :** Number of main branches from the stem was counted as the number of primary branches per plant. Data were taken at the time of first flowering .

(III) **Plant height at first flowering (PHFF) :** Height of the selected plants was measured in centimeters and recorded on the day of first flowering .

(IV) **Plant height at maximum flowering (PHMF) :** Plant height of the individual plants was recorded from the base of the stem to the top at the time of maximum flowering stage.

(V) **Number of primary branches at maximum flowering (NPBMF) :** Total number of developed primary branches was

counted and recorded. Data was taken at the time of maximum flowering .

(VI) Number of secondary branches at maximum flowering (NSBMF) : Total number of secondary branches developed on the primary branches per plant was counted and recorded. Data was taken at the time of maximum flowering .

(VII) Number of pods per plant (NPdPP) : The total number of pods per selected plant was counted at the time of harvesting.

(VIII) Pod weight per plant (PdWPP) : The pods from the selected plants were weighted and recorded.

(IX) Number of seeds per plant (NSPP) : All pods of the plant were threshed, seeds were taken out from the pods and cleaned, then the total number of seeds were counted and recorded.

(X) Seed yield per plant (SYPP) : After threshing the pods, seeds were cleaned and total weight of the seeds for individual plant was recorded in gram.

3.2.6 Techniques of analysis of data :

The collected data were analysis following standard biometrical technique.

The techniques used are described under the following sub-heads :

3.2.6 (a) Mean $(\overline{X})$:-

Data on individual plant were added together then divided by the total number of observation and the mean was obtained as follows :

$$\overline{X} = \frac{\sum_{i=1}^{n} X_i}{n}$$

Here,

X_i = The individual reading recorded on each of the plant.

$\overline{X}$ = The mean of the readings.

$\sum$ = Summation

n = Number of observation

i = 1, 2, 3, 4, 5 ..... n .

3.2.6 (b) Standard deviation (Sd) :

Standard deviation is average deviation of the individual observation from the mean. It was calculated as the square root of the variance as follows :

$$Sd = \sqrt{\delta^2}$$

Where

δ^2 = Variance

Sd = Standard deviation

3.2.6 (c) Standard error of mean (SE) :

If, instead of taking one sample, several sample are considered, it will be found that standard deviation of different samples will also vary. This variation is measured by the standard error, which was calculated as follows :

$$SE = \frac{Sd}{\sqrt{n}}$$

where

SE = Standard error of mean

Sd = Standard deviation

n = Total number of individuals

Standard error of mean gives an idea as to how any mean obtained from a sample may differ from the true hypothetical mean of the population.

3.2.6 (d) Co-efficient of variability in percentage (CV%) :

Co-efficient of variability in percentage (CV%) was calculated according to the following formula :

$$CV\% = \frac{Sd}{\overline{X}} \times 100$$

Where

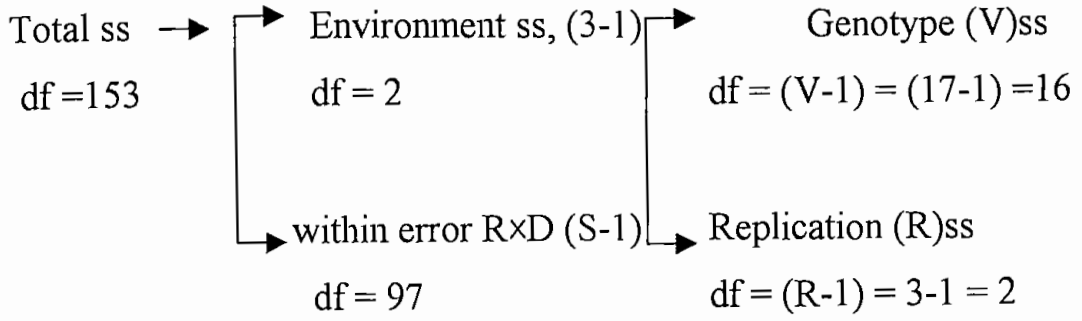
Sd = Standard deviation

$\overline{X}$ = Line mean

3.2.6 (e) Analysis of variance :

Variance is a measure of dispersion of a population. So, the analysis of variance was done for testing the significance of difference among the population. Variance analysis for each character was carried out separately using mean value of nine plants in a plot.

The variance due to different sources such as genotype (V), replication (R), environment (E) and genotype × environment interaction (V × E) and within error of a population were calculated as per following skeleton of Analysis.



Expectation mean squares (MS) used in the analysis of variance is as follows :-

Item	df	SS	MS	F Value
Genotype (V)	16	SS (V)	$\frac{VSS}{df}$	$\frac{VMS}{EMS}$
Replication (R) in environment	6	SS (R)	$\frac{RSS}{df}$	$\frac{RMS}{EMS}$
Year (Y) (Environment) (E)	2	SS (Y)	$\frac{YSS}{df}$	$\frac{YMS}{EMS}$
V × Y	32	SS (I)	$\frac{ISS}{df}$	$\frac{IMS}{EMS}$
Error	97	SS (E)	$\frac{ESS}{df}$	

3.2.6 (f) Test of significant :-

Analysis of variance provides the basis for test of significance. Significance of different among the population were worked out by test (variance ratio) as follow :

$$\text{'F' test} = \frac{MS}{EMS}$$

Where

MS = Mean square

EMS = Error mean square

3.2.6 (g) Techniques of analysis of data for stability :-

The collected data were analyzed following biometrical technique of analysis as developed and used by Eberhart and Russell (1966) in maize based on the mathematical methods of Fisher *et al.* (1932).

The techniques used are described under the following sub-heads:

Mean, (Similar formula followed for treatment).

Variance analysis was made on mean value .

Analysis of variance :

Pooled analysis of variance for stability analysis was done according to Singh and Chaudhaury (1979). Expectation of mean square (MS) used in the analysis of variance is as follows :

Item	df	SS	MS	F Value
Genotype (V)	16	SS (V)	$\frac{VSS}{df}$	$\frac{VMS}{EMS}$
Replication (R) in environment	6	SS (R)	$\frac{RSS}{df}$	$\frac{RMS}{EMS}$
Year (Y) (Environment) (E)	2	SS (Y)	$\frac{YSS}{df}$	$\frac{YMS}{EMS}$
V × Y	32	SS (I)	$\frac{ISS}{df}$	$\frac{IMS}{EMS}$
Error	97	SS (E)	$\frac{ESS}{df}$	

Analysis of variance :

Collected data were analyzed following standard method of analysis of variance. Genotype x environment interaction was analyzed following statistical techniqus developed and used by Mather and Jones (1958).

Table :

Source	df	SS	MS	F Value
Genotype (V)	16	SS (V)	$\frac{VSS}{df}$	$\frac{VMS}{EMS}$
Replication (R)	2	SS (R)	$\frac{RSS}{df}$	$\frac{RMS}{EMS}$
Error (E)	32	SS (E)	$\frac{ESS}{df}$	
Total	50			

Table :

Item	df	SS	MS	F
Genotype (V)	16	SS (V)	$\frac{VSS}{df}$	$\frac{VMS}{EMS}$
Year (Y)	2	SS (Y)	$\frac{YSS}{df}$	$\frac{YMS}{EMS}$
Error	32	SS (E)	$\frac{ESS}{df}$	
Total	50			

Table :- Analysis of variance (Pooled data)

Source of genotype	df	SS	MS	F
Total	St-1	SS (Total)		
Genotype	t-1	SS (genotype)	MS (var)	F= $\frac{MS(Var)}{MS(Pool)}$
Env+ (genotypes × Env)	t(s-1)	SS (E +V)		
Environment (Linear)	1	SS (E)		
Genotype × Environment (linear)	t-1	SS (V×E)	MS (V×E)	F = $\frac{MS(V \times E)}{MS(Pool)}$
Pooled deviation	t (3-2)	SS (Pool)	MS (Pool)	
Genotype – 1	s – 2			
Genotype – 2	s – 2			
Genotype – 3	s – 2			
Genotype – 4	s – 2			
Genotype – 5	s – 2			
Genotype – 6	s – 2			
Genotype – 7	s – 2			
Genotype – 8	s – 2			
Genotype – 9	s – 2			
Genotype – 10	s – 2			
Genotype – 11	s – 2			
Genotype – 12	s – 2			
Genotype – 13	s – 2			
Genotype – 14	s – 2			
Genotype – 15	s – 2			
Genotype – 16	s – 2			
Genotype – 17	s – 2			
Pooled error	st(n-1)	SS (error)		

3.2.6 (h) Estimation of variance :

Variance is a measure of variability in a population in accordance with components. So the analysis of variance was done for testing the significance of difference among populations. Variance analysis for each character of 17 verities was carried out separately on means plot values.

The expectation of mean squares (MS) are derived as follows.:-

Iem	MS	Expectation of MS
Genotypes (V)	M_{V17}	$\delta^2_{e17} + V\delta^2_{r17} + \delta^2_{v17}$
Replication (r)	M_{r17}	$\delta^2_{e17} + V\delta^2_{r17}$
Error (e)	M_{e17}	δ^2_{e17}

Where

M_{V17} = Mean square of 17 genotypes

M_{r17} = Mean square of replication

M_{e17} = Mean square of error

δ^2_{e17} = Environment variance

δ^2_{r17} = Variance due to replication

δ^2_{v17} = Variance due to genotype (genetically variance)

A. Estimation of phenotypic (δ^2_p), Genotypic (δ^2_g) and environmental (δ^2_e) components of variability in chickpea genotypes.

$$\delta^2_{e17} = \frac{M_{v17} - M_{e17}}{r}, \quad \delta^2_{p17} = \delta^2_{e17} + \delta_{g17}$$

Here $\delta^2_{g17} = \delta^2_{v17}$, $\delta^2_e = M_{e17}$

3.2.6 (i) Co-efficient of variability (CV) :

Deviation is also expressed by the Co-efficient of variation given by the formula of Burton and Devane (1953) as follows :

$$\text{Co-efficient of variability (CV)} = \frac{S^2}{\overline{X}} \times 100$$

Co-efficient of variability at different levels were calculated as follows :

1. Phenotypic Co-efficient of variability (PCV) = $\frac{\delta_p^2}{\overline{X}} \times 100$
2. Genotypic Co-efficient of variability (GCV) = $\frac{\delta_g^2}{\overline{X}} \times 100$
3. Environment Co-efficient of variability (ECV) = $\frac{\delta_e^2}{\overline{X}} \times 100$

Where

$\overline{X}$ = Grand mean

δ_p^2 = Phenotypic variance

δ_g^2 = Genotypic variance

δ_e^2 = Environment variance

3.2.6 (j) Habitability in broad sense (h_b^2) :

Habitability (inbroad sense) was calculated by dividing the genotypic variance by the phenotypic variance and then multiplying by 100 as suggested by Warner (1952).

$$h_b^2 = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where δ_g^2 = Genotypic variance

δ_p^2 = phenotypic variance

3.2.6 (k) Genetic advance (GA) :

Genetic advance was calculated by the following formula as suggested by Lush (1949).

$$GA = K\delta_p\left(\delta_g^2 / \delta_p^2\right)$$

Where

K = The selection differential in standard units for the present study it is 2.06 at 5% level of selection (Lush, 1949).

δ_p^2 = phenotypic variance

δ_g^2 = Genotypic variance

δ_p = square root of the phenotypic variance

3.2.6 (l) Genetic advance as percentage of mean (GA%) :

This was calculated by the following formula.

$$\text{GA \% of mean} = \frac{GA}{\bar{X}} \times 100$$

Where, $\overline{X}$ = Grand mean for a particular character.

3.2.6 (m) Stability parameters (according to Eberhart and Russell's model) :

In this approach, the regression co-efficient and the deviation from regression are used as parameters of stability. As the regression of d_I on e_j is one and regression of g_{ij} on e_j is B_i, therefore the b_i value of Eberhart and Russell's model is $b_i = 1 + B_i$ and $B_i = b_i - 1$`

Eberhart and Russell (1966) used the following model to study stability of genotypes under different environments :

$$Y_{ij} = m + \beta_i I_i + \delta_{ij} \qquad (i = 1,2,..... t \text{ and } j = 1,2.....s)$$

Where

Y_{ij} = Mean of the ith genotypes in jth environment

m = Mean of all genotypes overall the environments

β_i =The regression coefficient of the ith genotype on the environmental index which measures the response of this genotype to varying environments.

I_j = the environmental index which is defined as the deviation of the mean of all the genotypes at a given year from the overall mean.

$$= \frac{\sum_i Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{ts}$$

With $\sum_j I_j = 0$

and δ_{ij} = The deviation from the regression of ith lines at jth environment.

3.2.6 (n) Computation of environment index (I_j) :-

It was calculated as follows :

$$I_j = \frac{\sum_i Y_{ij}}{t} - \frac{\sum_i \sum_j Y_{ij}}{ts}$$

$$= \frac{\text{Total of all the varieties at jth environment}}{\text{Number of varieties}} - \frac{\text{Grand total}}{\text{total number of observation}}$$

3.2.6 (o) Computation of regression co-efficient (b_i) for each line :

$$b_i = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

Where,

$\sum_j I_j^2$ is the sum of square of environments, $\sum_j Y_{ij} I_j$ for each of the genotype is the sum of products of environmental index (I_j) with the corresponding mean $(\overline{X})$ of that genotype at each year. There values may be obtained in following manner :

$$[\overline{X}][I_j] = \left[\sum_j Y_{ij} I_j\right] = [S]$$

Where,

$[\overline{X}]$ = Matrix of means

$[I_j]$ = Vector for environmental index and

$[S]$ = Vector for sum of product, i.e. $\sum_j Y_{ij} I_j$

3.2.6 (p) Computation of stability ($\overline{S}^2_{di}$) :

In general, it is obtained by subtracting the variance due to regression from δ_Y^2. It is calculated as follows :

$$\overline{S}^2_{di} = \left[\sum_j \delta^2_{ij} \Big/ (IY-2) \right] - \left(S^2_e / r \right)$$

Where, $$\sum_j \delta^2_{ij} = \left[\sum_j Y^2_{ij} - \frac{Y^2_i}{t} \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I^2_j}$$

$\sum_j Y_{ij} - Y^2_i / t$ = The variance due to dependent variable (SSy)

$\sum_j \delta^2_{ij}$ = The variance due to deviation from regression i.e remainder of sum of square.

$\left(\sum_j Y_{ij} I_j \right)^2 \Big/ \sum_j I^2_j$ = The variance due to regression (Reg. SS).

S^2_e = The estimate of pooled error.

r = The number of replications.

3.2.6 (q) Computation of standard error of regression co-efficient (Sb_i) :

It was calculated as follows :

$$\pm Sb_i = \sqrt{\frac{remainder \ \ SS}{SS(X)}}$$

To test the stability of genotype on the basis of its $\overline{S}^2_{di}$ value, $\pm \overline{S}_{di}$ is calculated. The $\pm \overline{S}_{di} \times 2$ and compared with $\overline{S}^2_{di}$. If $\pm S_{di} \times 2$ value is greater than $\overline{S}^2_{di}$ value of a genotype then it is said non significant and vice versa as shown below. Non-significant $\overline{S}^2_{di}$ value indicated that the genotype was stable

over a range of environments and significant $\overline{S}^2_{di}$ value indicates the genotype was non-stable over a range of environment for the respective character.

$$\pm \overline{S}_{di} = \sqrt{\frac{remainderSS}{r}}$$

$\pm \overline{S}_{di} \times 2 > \overline{S}^2_{di}$ = Non-significant (Stable)

$\pm \overline{S}_{di} \times 2 < \overline{S}^2_{di}$ = Significant (Non stable)

where,

r = Replication

CHAPTER- 4

RESULT

4. RERULTS

The present investigation deals with variability, heritability, genetic advance and genetic advance percentage of mean, analysis of variance, joint regression analysis, deviation from their regression and stability of some yield contributing character in chickpea. Ten quantitative characters such as days to first flowering (DFF), number of primary branches at first flowering (NPBFF), plant height at first flowering (PHFF), plant height at maximum flowering (PHMF), number of secondary branches at maximum flowering (NSBMF), pod weight per plant, number of pod per plant (NPdPP), number of seed per plant (NSPP), seed yield per plant (SYPP) were studied in this investigations. The results obtained are presented under the following sub-heads :

4.1 Study of variability

The values of range, mean with standard error and co-efficient of variability in percentage were calculated for the data under three environments viz S_1, S_2 and S_3 and showed in Table -5 (A-J).

4.1.1 Range :

The values of the range of ten quantitative characters were different, which are described as follows :-

DFF :- Days to first flowering showed the highest range of 7.5 – 18.8 in the genotypeV_3 while the lowest range was recorded 18.8 – 23.75 in the genotype V_{42} .

NPBFF : The highest range for member of primary branches at first flower was recorded as 2.25 – 4.88 in the genotype V_6 while the lowest was recorded in the genotype V_{18} with the values of 2.00 – 3.53.

PHFF : The highest range of plant height at first flower was recorded in the genotype V_{49} with the value of 27.25 – 38.2cm. While the lowest was recorded in the genotype V_6 with the value of 30.88 – 32.80cm.

PHMF : For character, plant height at maximum flower, the highest range was recorded for V_6 (39-49.87 cm) and the lowest range performance was found for V_{31} genotype with value of 41.5 – 43.66cm.

NPBMF : For character, number of primary branches at maximum flower, on an average the highest and lowest range performance were recorded for genotype V_{32} (2.89 – 6.33) and V_{36} (4.52 – 5.79), respectively.

NSBMF : For this character, on an average the highest range was recorded in the genotype V_{42} with the value of 14.28 – 35.88 while the lowest value of 32.00 – 38.2 was found in the genotype V_{36}.

NPdPP : The highest range of number of pod per plant noted in the genotypeV_3 with the value of 33.77 – 124.33 and the lowest range was noted in the genotype no- V_{45} with the value of 44.22 – 59.16.

NSPP : For character number of seeds per plant, on an average the highest and lowest range were V_{36} (62.00 – 214.30) and V_{49} (50 – 63.37) respectively.

SYPP : The highest range of seed yield per plant was noted in the genotype V_{18} with the value of 7.28 – 20.55 gm. and the lowest range was noted in the genotype V_{49} with the value of 5.56 – 7.41 gm.

4.1.2 Mean with standard error :

Mean with the standard error in different environments of each genotypefor ten quantitative characters were different Table -5(A-J) . For each characters the value of mean as calculated showed variation form environment to environment in each genotype.

DFF : The highest mean with standard error of days to first flowering was noted in the genotype V_{22} with the value of 21.523 ± 0.608 and the lowest was noted in the genotype V_3 with the value of 15.271 ± 0.862.

NPBFF : For character number of primary branches at first flower, on an average the highest and lowest mean with standard error were recorded for genotype V_6 (3.754 ± 0.127) and genotype V_{35} (2.669 ± 0.126), respectively.

PHFF : For character, plant height at first flower, genotypeV_{45} (37.804 ± 0.855 cm) gave the highest value and genotypeV_9 (30.938 ± 1.049 cm) gave the lowest value.

PHMF : For this character, the highest mean with standard error was noted V_{42} with the value of 43.448 ± 0.583 cm and the lowest value was noted 37.58 ± 0.251 cm in the genotype. V_{30}.

NPBMF : For this character, on an average the highest and lowest values were recorded for V_{33} (5.71 ± 0.203) and V_9 (3.962 ± 0.113), respectively.

NSBMF : For this character, on an average the highest mean was recorded in the genotype V_{22} with the value of 35.545 ± 0.955 while the lowest was recorded in the genotype V_9 with the value of 24.276 ± 1.296 .

PdWPP : For this character, on an average the highest and lowest values were recorded for V_{36} and V_{40} with the values of 20.277 ± 1.178 and 10.293 ± 0.317, respectively.

NPdPP : In this character the highest mean was noted in the genotype V_{36} with the value of 92.938 ± 5.34 while the lowest was noted in the genotype V_{49} with the value of 42.952 ± 1.351.

NSPP : For character number of seed per plant, on an average the highest and lowest values were recorded for V_{36} (131.371 ± 10.886) and V_{40} (58.116 ± 1.489) .

SYPP : For this character, the highest mean with standard error was recorded in the genotype V_{36} with the value of 15.528 ± 0.992 and the lowest was recorded in the genotype V_{40} with the value of 6.54 ± 0.285.

4.1.3 Co-efficient of variability in percentage (CV%) :

The result of CV% in different environment (year) in each genotypeshowed a remarkable difference for different characters. The results are shown in Table -5 (A-J) .

DFF : For this character the highest CV% war recorded in the genotype V_3 with a value of 23.284 while the lowest was recorded in the genotype V_{31} with a value of 6.291 on an average three years.

NPBFF : In this character the highest CV% was noted in the genotype V_6 with a value of 22.138 and the lowest was 6.959 in the genotype V_9 for average three years.

PHFF : For this character the highest CV% was noted in the genotype. V_9 with the value of 13.984 cm while the lowest was 1.940 cm in the verity of V_{22} for different three environments.

PHMF : For this character, the highest CV% was observed in V_9 and lowest value was 1.650 for V_{31} on an average three years.

NPBMF : For character number of primary branches at maximum flower, on an average the highest CV% was recorded for V_{32} (21.257) and the lowest CV% was found for V_{22} (6.865).

NSBMF : For character, number of secondary branches at maximum flower, the highest CV% was noted in the genotype V_{42} with the value of 30.61 and the lowest was 4.277 in the genotype V_{18} on an average three years.

PdWPP : For character, pod weight per plant, genotype V_6 (38.610) showed the highest CV% and the genotype V_{45} (6.61) showed the lowest CV% for average three years.

NPdPP : For this character, the highest and lowest values were recorded for V_3 (36.061) and V_{45} (8.639).

NSPP : For this character, the highest CV% was noted in the genotype V_3 (35.879) while the lowest CV% was noted V_{49} (5.205) on an average three years.

SYPP : In this character, on an average three years, the highest CV% noted in the genotype V_3 with the value of 36.704 and the lowest was noted in the genotype V_{49} with the value of 8.766.

Table -5 (A-J) : The values of range of means, mean with standard error and co-efficient of variability in percentage for ten characters of 17 chickpea genotypes in 3 years.

Table - A : Days to first flowering (DFF)

Genotypes	Range of means	Mean with Standard Error	CV%
V-3	7.500 - 18.800	15.271 ± 0.862	23.284
V-6	12.420 - 20.400	16.176 ± 0.615	15.671
V-9	15.080 - 21.575	19.193 ± 0.505	10.858
V-18	13.530 - 21.800	18.160 ± 0.556	12.628
V-22	18.770 - 26.700	21.523 ± 0.608	11.647
V-30	14.900 - 19.400	16.900 ± 0.347	8.463
V-31	16.800 - 20.636	19.067 ± 0.291	6.291
V-32	15.200 - 18.672	17.059 ± 0.279	6.733
V-33	14.370 - 23.400	18.752 ± 0.749	16.468
V-35	10.500 - 26.000	17.105 ± 1.244	29.991
V-36	10.800 - 21.500	15.786 ± 0.813	21.246
V-38	11.500 - 19.200	15.351 ± 0.581	15.613
V-40	17.000 - 23.400	20.015 ± 0.504	10.389
V-41	16.300 - 23.000	19.967 ± 0.587	12.111
V-42	18.800 - 23.750	21.617 ± 0.394	7.507
V-45	14.330 - 26.300	20.607 ± 1.052	21.042
V-49	15.850 - 23.200	19.206 ± 0.605	12.993

Table -B : Number of primary branches at first flowering (NPBFF)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	2.330 - 3.717	3.049 ± 0.127	17.185
V-6	2.250 - 4.880	3.754 ± 0.202	22.138
V-9	2.500 - 3.122	2.799 ± 0.047	6.959
V-18	2.000 - 3.529	2.970 ± 0.134	18.535
V-22	2.330 - 4.104	3.073 ± 0.128	17.216
V-30	2.110 - 3.342	2.816 ± 0.101	14.838
V-31	3.110 - 3.894	3.356 ± 0.069	8.444
V-32	2.130 - 4.000	3.284 ± 0.160	20.093
V-33	2.570 - 4.270	3.673 ± 0.155	17.453
V-35	2.160 - 3.574	2.669 ± 0.126	19.478
V-36	2.550 - 3.424	3.021 ± 0.073	9.973
V-38	2.670 - 3.918	3.123 ± 0.111	14.623
V-40	2.800 - 3.994	3.356 ± 0.101	12.390
V-41	2.330 - 3.492	2.951 ± 0.121	16.929
V-42	3.110 - 3.886	3.357 ± 0.071	8.674
V-45	2.440 - 3.889	3.152 ± 0.126	16.419
V-49	2.000 - 3.528	2.692 ± 0.131	20.074

Table -C : Plant height at first flowering (PHFF)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	30.330 - 36.880	33.389 ± 0.445	5.497
V-6	32.630 - 40.500	35.253 ± 0.655	7.665
V-9	25.000 - 39.330	30.938 ± 1.049	13.984
V-18	30.440 - 35.250	32.956 ± 0.380	4.753
V-22	32.320 - 34.536	33.475 ± 0.157	1.936
V-30	30.880 - 32.800	31.818 ± 0.166	2.157
V-31	31.700 - 36.024	34.030 ± 0.354	4.292
V-32	28.400 - 33.400	30.724 ± 0.364	4.887
V-33	29.500 - 33.830	31.507 ± 0.299	3.907
V-35	30.500 - 36.250	33.254 ± 0.395	4.897
V-36	31.710 - 36.890	34.495 ± 0.430	5.138
V-38	32.410 - 36.880	34.434 ± 0.363	4.350
V-40	28.420 - 34.600	32.332 ± 0.516	6.583
V-41	28.330 - 36.330	32.901 ± 0.578	7.242
V-42	33.710 - 39.330	36.749 ± 0.381	4.277
V-45	33.600 - 43.000	37.804 ± 0.855	9.330
V-49	27.250 - 38.200	34.710 ± 0.879	10.443

Table -D : Plant height at maximum flowering (PHMF)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	37.780 - 43.220	40.129 ± 0.408	4.191
V-6	39.000 - 49.870	42.616 ± 0.871	8.422
V-9	33.700 - 46.400	37.855 ± 1.038	11.304
V-18	38.200 - 42.370	40.358 ± 0.331	3.379
V-22	40.000 - 42.360	41.186 ± 0.184	1.841
V-30	36.300 - 39.500	37.580 ± 0.251	2.754
V-31	41.500 - 43.660	42.626 ± 0.171	1.650
V-32	34.720 - 44.400	38.358 ± 0.772	8.301
V-33	37.210 - 42.420	39.782 ± 0.455	4.719
V-35	38.300 - 45.500	41.069 ± 0.535	5.376
V-36	40.330 - 44.850	42.616 ± 0.409	3.957
V-38	41.240 - 46.110	43.113 ± 0.380	3.635
V-40	36.420 - 44.100	40.843 ± 0.588	5.936
V-41	34.170 - 43.200	39.858 ± 0.667	6.902
V-42	40.280 - 48.300	43.448 ± 0.583	5.529
V-45	33.000 - 48.250	41.461 ± 1.059	10.529
V-49	32.870 - 46.300	42.299 ± 1.112	10.838

Table -E : Number of primary branches at maximum flowering (NPBMF)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	3.780 - 5.100	4.541 ± 0.117	10.580
V-6	4.620 - 6.750	5.605 ± 0.161	11.842
V-9	3.120 - 4.660	3.962 ± 0.113	11.773
V-18	3.250 - 4.832	4.108 ± 0.151	15.122
V-22	4.670 - 5.679	5.251 ± 0.087	6.865
V-30	3.500 - 5.082	4.309 ± 0.140	13.417
V-31	4.300 - 5.479	4.709 ± 0.106	9.292
V-32	2.890 - 6.332	5.230 ± 0.270	21.257
V-33	4.710 - 7.100	5.710 ± 0.203	14.673
V-35	3.200 - 5.355	4.345 ± 0.162	15.414
V-36	4.520 - 5.790	5.149 ± 0.121	9.724
V-38	4.330 - 6.250	5.368 ± 0.172	13.220
V-40	4.400 - 5.903	5.256 ± 0.137	10.781
V-41	3.440 - 5.210	4.440 ± 0.134	12.434
V-42	3.110 - 5.019	4.155 ± 0.140	13.894
V-45	4.370 - 6.187	5.200 ± 0.122	9.664
V-49	2.870 - 5.250	4.473 ± 0.184	16.995

Table -F: Number of secondary branches at maximum flowering (NSBMF)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	21.370 - 34.800	27.111 ± 1.010	15.362
V-6	24.870 - 36.000	29.111 ± 0.861	12.188
V-9	16.000 - 33.600	24.276 ± 1.296	22.015
V-18	25.120 - 29.068	27.447 ± 0.285	4.277
V-22	29.300 - 42.160	35.545 ± 0.955	11.074
V-30	17.780 - 31.000	24.140 ± 0.927	15.831
V-31	28.700 - 40.700	34.027 ± 0.840	10.183
V-32	25.500 - 38.600	31.307 ± 0.913	12.025
V-33	24.600 - 34.000	29.868 ± 0.772	10.660
V-35	19.800 - 30.919	27.044 ± 0.875	13.338
V-36	32.000 - 38.200	35.079 ± 0.438	5.150
V-38	29.670 - 39.220	35.312 ± 0.690	8.060
V-40	24.000 - 35.220	31.650 ± 0.871	11.353
V-41	29.680 - 34.440	31.709 ± 0.379	4.932
V-42	14.280 - 35.880	25.484 ± 1.892	30.610
V-45	21.300 - 28.000	25.001 ± 0.451	7.439
V-49	28.000 - 35.800	31.914 ± 0.705	9.115

Table - G : Pod weight (gm) per plant (PdWPP)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	7.880 - 27.110	18.367 ± 1.490	33.460
V-6	6.800 - 21.870	13.349 ± 1.250	38.610
V-9	10.200 - 15.900	14.152 ± 0.430	12.517
V-18	11.000 - 26.050	17.507 ± 1.354	31.897
V-22	9.340 - 14.227	12.302 ± 0.381	12.779
V-30	8.950 - 12.450	10.555 ± 0.282	11.005
V-31	6.600 - 19.080	13.724 ± 0.950	28.529
V-32	10.730 - 13.800	12.656 ± 0.230	7.504
V-33	10.880 - 14.670	12.787 ± 0.296	9.548
V-35	10.100 - 17.500	13.061 ± 0.604	19.062
V-36	10.070 - 24.620	20.277 ± 1.178	23.955
V-38	9.670 - 19.200	14.954 ± 0.811	22.364
V-40	8.250 - 12.023	10.293 ± 0.317	12.706
V-41	7.960 - 13.160	10.660 ± 0.422	16.321
V-42	6.780 - 17.580	11.214 ± 0.842	30.962
V-45	9.840 - 12.088	11.314 ± 0.181	6.610
V-49	6.600 - 11.630	10.228 ± 0.402	16.218

Table -H : Number of pod per plant (NPdPP)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	33.770 - 124.330	77.138 ± 6.747	36.061
V-6	37.250 - 81.800	53.434 ± 3.661	28.251
V-9	51.000 - 75.600	67.536 ± 1.851	11.300
V-18	51.890 - 103.000	70.888 ± 4.243	24.678
V-22	38.200 - 63.140	53.611 ± 1.915	14.727
V-30	38.000 - 54.300	46.544 ± 1.552	13.747
V-31	32.110 - 110.000	68.025 ± 5.813	35.232
V-32	47.300 - 63.110	52.002 ± 1.293	10.252
V-33	46.600 - 78.500	61.975 ± 2.394	15.925
V-35	42.100 - 90.620	66.763 ± 3.712	22.923
V-36	49.440 - 118.000	92.938 ± 5.340	23.692
V-38	47.110 - 90.400	67.863 ± 4.181	25.401
V-40	38.200 - 53.300	48.349 ± 1.206	10.282
V-41	41.890 - 57.800	49.145 ± 1.477	12.394
V-42	40.500 - 69.570	50.013 ± 2.354	19.405
V-45	44.220 - 59.160	51.841 ± 1.086	8.639
V-49	32.110 - 52.300	42.952 ± 1.351	12.964

Table -I : Number of seed per plant (NSPP)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	52.110 - 150.000	88.709 ± 7.719	35.879
V-6	49.250 - 118.000	73.885 ± 5.586	31.175
V-9	53.330 - 95.830	79.639 ± 3.072	15.907
V-18	57.000 - 145.000	89.459 ± 6.774	31.220
V-22	46.330 - 88.000	70.230 ± 3.401	19.966
V-30	43.220 - 82.000	61.004 ± 3.144	21.249
V-31	50.000 - 147.000	93.686 ± 7.419	32.650
V-32	58.670 - 70.880	65.582 ± 0.828	5.205
V-33	59.500 - 93.200	75.710 ± 2.507	13.652
V-35	56.200 - 103.200	82.337 ± 3.452	17.287
V-36	62.000 - 214.300	131.371 ± 10.886	34.165
V-38	63.330 - 129.800	93.699 ± 6.047	26.610
V-40	46.350 - 65.160	58.116 ± 1.489	10.561
V-41	49.830 - 84.330	62.453 ± 2.775	18.319
V-42	59.830 - 155.000	92.652 ± 7.278	32.387
V-45	55.400 - 85.000	69.476 ± 2.509	14.887
V-49	50.000 - 63.370	59.513 ± 1.063	7.363

Table -J : Seed yield per plant (SYPP)

Genotypes	Range of means	Mean ± Standard Error	CV%
V-3	5.800 - 21.560	13.483 ± 1.200	36.704
V-6	5.570 - 12.370	8.536 ± 0.512	24.720
V-9	6.050 - 11.970	9.585 ± 0.417	17.936
V-18	7.280 - 20.550	12.689 ± 1.125	36.541
V-22	4.390 - 9.442	7.640 ± 0.375	20.212
V-30	3.970 - 9.500	6.852 ± 0.481	28.963
V-31	6.520 - 16.160	11.192 ± 0.719	26.492
V-32	5.850 - 9.830	7.536 ± 0.300	16.427
V-33	6.780 - 12.410	9.994 ± 0.415	17.120
V-35	5.900 - 13.820	10.145 ± 0.533	21.682
V-36	7.800 - 20.500	15.528 ± 0.992	26.334
V-38	7.250 - 12.900	10.503 ± 0.485	19.020
V-40	4.390 - 8.123	6.540 ± 0.285	17.968
V-41	6.270 - 13.600	8.464 ± 0.608	29.608
V-42	6.220 - 10.700	8.100 ± 0.385	19.583
V-45	5.060 - 10.480	8.272 ± 0.433	21.565
V-49	5.560 - 7.405	6.485 ± 0.138	8.766

4.2 Analysis of variance :

The results of analysis of variance for all the ten characters were done separately and which shown in Tables 7 (A-J). For testing main item and their interaction effects, a mixed model as shown in Table 6 (A-J) was followed.

The item genotype (V) was highly significant for selected ten characters, indicating that a real differences existed among the genotypes for the studied characters. The item replication was non significant for most of the quantitative characters except DFF, PHFF, PHMF and NSBMF. The interaction between genotypes × environment (year) was significant for all the characters except NPBFF, PHMF and NSPP.

Table -6 (A-J) : Analysis of variance of 10 characters in 17 chickpea genotypes under three environments.

Table A : Analysis of variance for DFF

Source	df	SS	MS	F
Genotype (V)	16	616.25	38.51	10.466 *
Environment (E)	2	156.71	78.35	21.293 *
Replication in environment	6	46.08	7.68	2.087 **
Genotype X environment (V x E)	32	529.74	16.55	4.498 *
Error	97	357.02	3.68	
Total	153	1705.83		

Table B : Analysis of variance for NPBFF

Source	df	SS	MS	F
Genotype (V)	16	13.97	0.87	5.86 *
Environment (E)	2	12.63	6.31	42.66 *
Replication in environment	6	0.06	0.01	.0705 ns
Genotype X environment (V x E)	32	7.51	0.23	1.576 ns
Error	97	14.44	0.14	
Total	153	48.62		

Table C : Analysis of variance for PHFF

Source	df	SS	MS	F
Genotype (V)	16	529.49	33.09	7.987 *
Environment (E)	2	63.05	31.52	7.60 *
Replication in environment		128.49	21.41	5.185 *
Genotype X environment (V x E)		214.43	6.70	1.617 **
Error	97	401.94	4.14	
Total	153	1337.42652		

Table D : Analysis of variance for PHMF

Source	df	SS	MS	F
Genotype (V)	16	473.62	29.60	4.534 *
Environment (E)	2	70.06	35.03	5.373 *
Replication in environment		319.73	53.28	8.78 *
Genotype X environment (V x E)		265.78	8.30	1.273 ns
Error	97	633.29	6.52	
Total	153	1762.50		

Table E : Analysis of variance for NPBMF

Source	df	SS	MS	F
Genotype (V)	16	45.25	2.82	13.032 *
Environment (E)	2	15.73	7.86	36.253 *
Replication in environment		0.79	0.13	0.6155 ns
Genotype X environment (V x E)		18.11	0.56	2.61 *
Error	97	21.03	0.21	
Total	153	100.94		

Table F : Analysis of variance for NSBMF

Source	df	SS	MS	F
Genotype (V)	16	2231.62	139.47	13.75 *
Environment (E)	2	58.34	29.17	2.875 ns
Replication in environment		280.63	46.77	4.609 *
Genotype X environment (V x E)		867.57	27.11	2.672 *
Error	97	984.35	10.14	
Total	153	4422.53		

Table G : Analysis of variance for PdWPP

Source	df	SS	MS	F
Genotype (V)	16	1247.41	77.96	16.32 *
Environment (E)	2	283.77	141.88	29.75 *
Replication in environment		43.65	7.27	1.525 ns
Genotype X environment (V x E)		703.14	21.97	4.606 *
Error	97	463.28	4.77	
Total	153	2741.27		

Table H : Analysis of variance for NPdPP

Source	df	SS	MS	F
Genotype (V)	16	24922.48	1557.65	11.94 *
Environment (E)	2	4732.61	2366.30	18.13 *
Replication in environment		1293.54	215.59	1.65 ns
Genotype X environment (V x E)		9754.48	304.82	2.43 *
Error	97	12654.04	130.45	
Total	153	53357.17		

Table I : Analysis of variance for NSPP

Source	df	SS	MS	F
Genotype (V)	16	48356.36	3022.27	8.06 *
Environment (E)	2	12396.50	6198.25	16.54 *
Replication in environment		3960.42	660.07	1.75 ns
Genotype X environment (V x E)		14748.04	460.87	1.22 ns
Error	97	36349.59	374.73	
Total	153	115810.93		

Table J : Analysis of variance for SYPP

Source	df	SS	MS	F
Genotype (V)	16	941.06	58.81	16.66 *
Environment (E)	2	183.94	91.97	26.05 *
Replication in environment		26.11	4.35	1.23 ns
Genotype X environment (V x E)		371.25	11.60	3.28 *
Error	97	342.48	3.53	
Total	153	1864.86		

* Significant at 1% level

** Significant at 5% level

ns = non significant.

Table -7 (A-J) : Analysis of variance for different characters in 17 chickpea genotypes in 3 years.

Table A : Analysis of variance for DFF

Source of Variation	df	SS	MS	F
Genotype (V)	16	1870.43	116.90	2.35**
Year (E)	2	478.62	239.31	4.81**
Error	32	1590.68	49.70	
Total	**50**	**3939.74**		

Table B : Analysis of variance for PHBFF

Source of Variation	df	SS	MS	F
Genotype (V)	16	1601.54	100.09	4.98*
Year (E)	2	195.74	97.87	4.87**
Error	32	642.87	20.08	
Total	**50**	**2440.16**		

Table C : Analysis of variance for NPBMF

Source of Variation	df	SS	MS	F
Genotype (V)	16	137.93	8.62	5.01*
Year (E)	2	48.10	24.05	13.98*
Error	32	55.05	20.08	
Total	**50**	**241.09**		

Table D : Analysis of variance for PdWPP

Source of Variation	df	SS	MS	F
Genotype (V)	16	3751.87	234.49	3.556744*
Year (E)	2	852.23	426.11	6.46327*
Error	32	2109.72	65.92	
Total	**50**	**6713.82**		

Table E : Analysis of variance for NSPP

Source of Variation	df	SS	MS	F
Genotype (V)	16	145691.8	9105.74	6.58*
Year (E)	2	37191.87	18595.94	13.45*
Error	32	44242.74	1382.58	
Total	**50**	**227126.5**		

Table F : Analysis of variance for NPBFF

Source of Variation	df	SS	MS	F
Genotype (V)	16	47.65	2.97	4.34*
Year (E)	2	32.51	16.25	23.70**
Error	32	21.94	0.68	
Total	**50**	**102.11**		

Table G : Analysis of variance for PHMF

Source of Variation	df	SS	MS	F
Genotype (V)	16	1400.84	87.55	3.51*
Year (E)	2	211.51	105.75	4.24**
Error	32	797.21	24.91	
Total	**50**	**2409.56**		

Table H : Analysis of variance for NSBMF

Source of Variation	df	SS	MS	F
Genotype (V)	16	6657.01	416.06	5.11*
Year (E)	2	175.17	87.58	1.07 ns
Error	32	2601.30	81.29	
Total	50	9433.48		

Table I : Analysis of variance for NPdPP

Source of Variation	df	SS	MS	F
Genotype (V)	16	74668.11	4666.75	5.10*
Year (E)	2	14202.6	7101.29	7.76*
Error	32	29262.55	914.45	
Total	50	118133.3		

Table J : Analysis of variance for SYPP

Source of Variation	df	SS	MS	F
Genotype (V)	16	2784.96	174.06	5.01*
Year (E)	2	542.86	271.43	7.80*
Error	32	1113.22	34.78	
Total	50	4441.06		

* Significant at 1% level

** Significant at 5% level

ns = Non significant

4.3 Components of Variation

The calculation of phenotypic variation (δ_p^2), genotypic Variation (δ_g^2), Environment variation (δ_e^2), were calculated separately for all the ten characters and the results are shown in the Table - 8.

Table - 8 : Component of phenotypic variation (δ_p^2), genotypic variation(δ_g^2), environment variation (δ_e^2) for ten characters of seventeen chickpea genotypes in 3 years.

Character	δ_p^2	δ_g^2	δ_e^2
DFF	15.293	11.612	3.681
NPBFF	0.390	0.241	0.149
PHFF	13.794	9.650	4.144
PHMF	14.220	7.691	6.529
NPBMF	1.087	0.870	0.217
NSBMF	53.257	43.109	10.148
PdWPP	29.172	24.396	4.776
NPdPP	606.18	476.734	130.454
NSPP	1257.25	882.512	374.738
SYPP	21.96	18.43	3.531

Phenotypic variation (δ_p^2) : For all the character δ_p^2 was always greater than those of other component variation as expected. Table shows that greater portion of the total δ_p^2 appeared mostly due to the within error variation for all the characters. The highest value δ_p^2 was observed for the character NSPP with a value 1257.25 and the lowest value was 0.390 for the character NPBFF. The

remaining characters followed with their lower to higher values were as NPBMF, PHFF, PHMF, DFF, SYPP, PdWPP, NSBMP and NPdPP.

Genotypic variation (δ_g^2) : The highest genotypic variation was found for the character NSPP with a value of 882.512 while the lowest value was 0.241 for the character NPBFF. The other characters according to lower to higher values were as NPBMF, PHFF, PHMF, DFF, SYPP, PdWPP, NSBMF and NPdPP.

Environmental variation (δ_e^2) : The highest environment variation was 374.738 for the character NSPP, while the lowest value was 0.149 for NPBFF. The maximum δ_e^2 was observed from DFF, PHFF, PdWPP and SYPP.

4.4 Co-efficient of Variability

The calculation of phenotypic co-efficient of variability (PCV), genotypic co-efficient of variability (GCV) and environmental co-efficient of variability (ECV) were done separately and the result are shown in the Table 9.

PCV : The phenotypic co-efficient of variability was the highest for the character SYPP with the value of 49.313 while the lowest was 9.221 for PHMF. The remaining characters followed with their lower to higher values like PHFF, NPBFF, DFF, NSBMF, PdWPP, NPdPP and NSPP.

GCV : For the character SYPP, the highest GCV was found, while the lowest was in the PHMF with the values of 45.175 and 6.782, respectively. The maximum GCV was observed from NSBMF, PdWPP, NPdPP and NSPP.

ECV : The value of 24.422 was the highest error co-efficient of variability for the character NSPP, while the lowest was for character pHFF and pHMF with the values of 6.063 and 6.24 respectively. The other characters accordingly lower to higher values were as PHMF, NPBMF, NSBMF, DFF, PdWPP, NPdPP and SYPP.

Table -9 : Co-efficient of phenotypic variability (PCV), Co-efficient of genotypic variability (GCV), Co-efficient of environmental variability (ECV) for ten character of seventeen chickpea genotypes in 3 years.

Characters	PCV	GCV	ECV
DFF	21.324	18.528	10.462
NPBFF	20.006	15.733	12.357
PHFF	11.062	9.252	6.063
PHMF	9.221	6.782	6.248
NPBMF	21.668	19.387	9.677
NSBMF	24.517	22.038	10.702
PdWPP	40.378	36.925	16.338
NPdPP	40.994	36.316	19.017
NSPP	44.733	37.478	24.422
SYPP	49.313	45.175	19.774

4.5 Heritability (h_b^2), Genetic advance (GA) and GA% :-

Table -10 : Heritability (h_b^2), Genetic advance (GA) and GA% for ten characters of seventeen chickpea genotypes in 3 years.

Characters	(h_b^2)	GA	GA%
DFF	87.139	6.117	33.355
NPBFF	78.642	0.796	25.487
PHFF	83.642	5.352	15.942
PHMF	73.543	4.201	10.274
NPBMF	89.473	1.720	35.733
NSBMF	89.970	12.169	40.882
PdWPP	91.448	9.305	69.560
NPdPP	88.589	39.804	66.274
NSPP	83.782	51.272	84.683
SYPP	91.609	8.101	85.252

The heribility in broad sense (h_b^2), genetic advance (GA) and genetic advance expressed as percentage of mean GA% were calculated separately and presented in the Table - .

Heritability (h_b^2) : In the present investigation the highest (h_b^2) was 91.609 for SYPP and the 2nd highest (h_b^2) was 91.45 for Pdwpp while the lowest was 73.543 for PHMF. Result denote that the maximum h_b^2 was observed from PdWPP, NPBMF, NSBMF, NPdPP and NSPP.

Genetic advance (GA) : The highest value of Genetic advance was for NSPP with a value of 51.272, while the lowest was 0.796 for NPBFF. The 2nd highest GA was NPdPP.

Genetic advance as percentage of mean (GA%) : The highest genetic advance (GA%) of mean in the character SYPP, while the lowest was for PHMF with a value of 85.252 and 10.274 respectively. The maximum GA% was observed NSBMF, PdWPP, NPdPP and NSPP. The highest GA% had a wide possibility for improvement.

4.6 Table -11 (A-J) :- Deviation from their regression analysis (according to Eberhart and Russell's Model) for ten characters of seventeen chickpea genotypes (*Cicer arietinum* L.) in 3 years.

Table A : Deviation from their regression analysis (according to Eberhart and Russell's model) for DFF of seventeen chickpea genotypes in 3 years.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	7.7939	-1.4799	-4.5476	6.7299	1.0640
V-6	10.7086	1.8570	5.7064	10.5967	0.1120
V-9	4.4693	1.2060	3.7059	4.4693	0.0000
V-18	4.7035	1.2326	3.7878	4.6690	0.0345
V-22	8.3293	1.6302	5.0093	8.1660	0.1634
V-30	3.7052	1.0923	3.3565	3.6662	0.0389
V-31	0.7032	0.4145	1.2736	0.5278	0.1754
V-32	0.3965	-0.2242	-0.6888	0.1544	0.2421
V-33	23.3745	2.7272	8.3804	22.8549	0.5196
V-35	53.7565	4.1221	12.6670	52.2148	1.5417
V-36	19.7172	-2.4302	-7.4677	18.1479	1.5692
V-38	4.2479	1.1755	3.6123	4.2464	0.0016
V-40	8.5462	1.6670	5.1226	8.5394	0.0068
V-41	14.4319	-2.0557	-6.3171	12.9862	1.4458
V-42	0.2800	-0.0482	-0.1480	0.0071	0.2729
V-45	48.5461	3.9180	12.0396	47.1706	1.3754
V-49	15.1110	2.1958	6.7476	14.8165	0.2945
TOTAL	228.8209	17.0000	52.2397	219.9631	8.8578

Table B : Deviation from their regression analysis for NPBFF

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	0.6991	1.6229	0.4019	0.6523	0.0468
V-6	0.2168	0.7848	0.1944	0.1525	0.0642
V-9	0.0442	0.1985	0.0492	0.0098	0.0344
V-18	0.7334	1.5915	0.3942	0.6273	0.1061
V-22	0.3389	1.1369	0.2816	0.3201	0.0188
V-30	0.3017	1.0612	0.2628	0.2789	0.0229
V-31	0.1335	0.6927	0.1715	0.1188	0.0147
V-32	0.4192	-0.0578	-0.0143	0.0008	0.4184
V-33	0.9179	1.5852	0.3926	0.6223	0.2956
V-35	0.1725	0.7921	0.1962	0.1554	0.0171
V-36	0.2191	0.9332	0.2311	0.2157	0.0034
V-38	0.2976	1.0946	0.2711	0.2967	0.0009
V-40	0.4192	1.2647	0.3132	0.3961	0.0231
V-41	0.5993	1.5133	0.3748	0.5671	0.0322
V-42	0.1966	0.6881	0.1704	0.1173	0.0794
V-45	0.6632	1.6027	0.3969	0.6362	0.0270
V-49	0.3418	0.4955	0.1227	0.0608	0.2810
TOTAL	6.7141	17.0000	4.2103	5.2282	1.4859

Table C : Deviation from their regression analysis for PHFF.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	0.1187	0.3077	0.3804	0.1170	0.0017
V-6	4.3761	1.8675	2.3090	4.3121	0.0640
V-9	3.9668	1.7821	2.2033	3.9266	0.0403
V-18	1.2258	-0.8705	-1.0763	0.9369	0.2889
V-22	0.2330	0.4035	0.4989	0.2013	0.0316
V-30	0.5918	-0.4906	-0.6065	0.2976	0.2942
V-31	0.1455	0.0681	0.0842	0.0057	0.1398
V-32	3.4093	1.6516	2.0420	3.3724	0.0369
V-33	0.2529	0.4233	0.5234	0.2215	0.0314
V-35	4.4522	1.8539	2.2922	4.2496	0.2026
V-36	7.7564	2.4570	3.0378	7.4637	0.2927
V-38	4.4968	1.8906	2.3376	4.4195	0.0773
V-40	10.4640	2.8890	3.5719	10.3190	0.1450
V-41	0.4897	-0.4431	-0.5479	0.2428	0.2469
V-42	3.1182	1.5875	1.9628	3.1159	0.0024
V-45	31.8253	4.9188	6.0815	29.9133	1.9120
V-49	15.5742	-3.2964	-4.0756	13.4345	2.1397
TOTAL	92.4968	17.0000	21.0186	86.5494	5.9474

Table D: Deviation from their regression analysis for PHMF.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	1.1696	0.8923	1.2259	1.0939	0.0757
V-6	7.3903	2.2354	3.0712	6.8654	0.5249
V-9	18.4958	3.5513	4.8791	17.3272	1.1686
V-18	1.7308	-0.7515	-1.0325	0.7760	0.9549
V-22	0.9885	0.8281	1.1378	0.9422	0.0463
V-30	1.4958	1.0214	1.4033	1.4333	0.0625
V-31	0.4980	0.5966	0.8197	0.4891	0.0089
V-32	9.7599	2.6218	3.6020	9.4437	0.3162
V-33	8.8402	2.4919	3.4237	8.5316	0.3086
V-35	1.8516	1.1471	1.5761	1.8080	0.0437
V-36	7.3575	2.2331	3.0680	6.8512	0.5063
V-38	2.3738	1.2986	1.7841	2.3167	0.0571
V-40	13.1958	3.0068	4.1311	12.4215	0.7743
V-41	2.3241	-1.1157	-1.5329	1.7103	0.6137
V-42	3.9991	1.6901	2.3221	3.9246	0.0745
V-45	1.0513	-0.5896	-0.8101	0.4777	0.5737
V-49	29.4281	-4.1577	-5.7123	23.7500	5.6781
TOTAL	111.9503	17.0000	23.3562	100.1623	11.7880

Table E : Deviation from their regression analysis for NPBMF.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	0.5421	1.1747	0.3624	0.4257	0.1164
V-6	0.0932	0.0148	0.0046	0.0001	0.0931
V-9	0.0863	0.3247	0.1002	0.0325	0.0538
V-18	0.8900	1.4976	0.4620	0.6919	0.1981
V-22	0.2031	0.7978	0.2461	0.1964	0.0068
V-30	0.5136	0.1678	0.0518	0.0087	0.5049
V-31	0.3097	0.6557	0.2023	0.1326	0.1771
V-32	1.5693	-0.8312	-0.2564	0.2132	1.3562
V-33	1.4789	1.9000	0.5862	1.1137	0.3652
V-35	0.7342	1.5250	0.4705	0.7175	0.0168
V-36	0.5660	1.2466	0.3846	0.4794	0.0866
V-38	1.1457	1.7783	0.5486	0.9757	0.1701
V-40	0.7922	1.5615	0.4817	0.7522	0.0400
V-41	0.4909	1.1434	0.3527	0.4033	0.0875
V-42	0.5013	1.2486	0.3852	0.4810	0.0204
V-45	0.3623	1.0833	0.3342	0.3621	0.0003
V-49	1.0055	1.7113	0.5280	0.9035	0.1019
TOTAL	11.2844	17.0000	5.2447	7.8895	3.3950

Table F : Deviation from their regression analysis for **NSBMF.**

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	3.7291	-1.2453	-1.4247	1.7742	1.9548
V-6	4.8306	2.0093	2.2987	4.6187	0.2118
V-9	0.9398	0.9013	1.0312	0.9294	0.0104
V-18	0.7841	-0.4542	-0.5197	0.2361	0.5481
V-22	22.2283	4.1593	4.7583	19.7911	2.4372
V-30	27.3118	-4.3282	-4.9516	21.4315	5.8803
V-31	18.3094	3.8241	4.3748	16.7296	1.5798
V-32	21.8528	-3.8181	-4.3680	16.6774	5.1754
V-33	24.8720	4.4190	5.0555	22.3404	2.5316
V-35	7.5884	-2.0585	-2.3549	4.8475	2.7408
V-36	0.3017	0.4320	0.4943	0.2135	0.0881
V-38	1.1332	-0.6346	-0.7260	0.4607	0.6725
V-40	18.1349	3.7507	4.2909	16.0936	2.0413
V-41	0.7541	0.8077	0.9241	0.7464	0.0076
V-42	152.5379	10.7012	12.2425	131.0098	21.5282
V-45	3.0940	-1.4380	-1.6451	2.3656	0.7285
V-49	0.2392	-0.0277	-0.0317	0.0009	0.2383
TOTAL	308.6413	17.0000	19.4486	260.2665	48.3748

Table G : Deviation from their regression analysis for **PdWPP.**

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	71.6520	3.5543	19.7766	70.2918	1.3602
V-6	62.9327	3.3448	18.6108	62.2492	0.6834
V-9	1.8985	0.5776	3.2138	1.8563	0.0422
V-18	78.6527	3.7168	20.6807	76.8658	1.7868
V-22	0.4607	0.2203	1.2258	0.2700	0.1907
V-30	0.4965	-0.1709	-0.9509	0.1625	0.3340
V-31	23.7635	2.0624	11.4758	23.6682	0.0953
V-32	1.4327	0.5022	2.7942	1.4031	0.0296
V-33	2.3362	-0.5778	-3.2147	1.8573	0.4789
V-35	1.8741	-0.5109	-2.8427	1.4523	0.4218
V-36	26.8835	2.1972	12.2253	26.8610	0.0225
V-38	26.4736	2.1735	12.0936	26.2852	0.1884
V-40	0.2349	-0.1205	-0.6705	0.0808	0.1541
V-41	7.0090	1.1139	6.1976	6.9033	0.1058
V-42	20.5219	-1.8599	-10.3488	19.2478	1.2742
V-45	0.2314	0.1601	0.8906	0.1425	0.0889
V-49	2.1184	0.6170	3.4332	2.1184	0.0000
TOTAL	328.9724	17.0000	94.5904	321.7157	7.2568

Table H : Deviation from their regression analysis for NPDPP .

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	1014.1896	3.3052	306.7099	1013.7361	0.4535
V-6	454.5826	2.2125	205.3121	454.2536	0.3290
V-9	58.4317	0.7935	73.6352	58.4306	0.0011
V-18	641.0090	2.6266	243.7384	640.2020	0.8070
V-22	16.1928	0.4176	38.7542	16.1847	0.0080
V-30	0.2367	0.0415	3.8545	0.1601	0.0766
V-31	781.9606	2.9015	269.2468	781.2145	0.7460
V-32	23.3939	-0.4971	-46.1310	22.9327	0.4612
V-33	161.0968	-1.3120	-121.7503	159.7383	1.3585
V-35	0.3831	0.0273	2.5308	0.0690	0.3141
V-36	573.4389	2.4853	230.6273	573.1794	0.2595
V-38	785.1695	2.9082	269.8736	784.8563	0.3132
V-40	34.1994	0.6070	56.3313	34.1955	0.0039
V-41	95.2000	1.0129	93.9896	95.1983	0.0017
V-42	156.3193	-1.2961	-120.2721	155.8831	0.4362
V-45	4.3277	0.2080	19.3002	4.0141	0.3135
V-49	28.9018	0.5581	51.7869	28.9007	0.0011
TOTAL	4829.0334	17.0000	1577.5374	4823.1493	5.8841

Table I : Deviation from their regression analysis for NSPP.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	1723.2342	2.6622	647.0943	1722.6851	0.5491
V-6	1034.4348	2.0629	501.4317	1034.4137	0.0211
V-9	236.5896	0.9865	239.7963	236.5678	0.0218
V-18	1380.4724	2.3831	579.2558	1380.4211	0.0513
V-22	16.5893	0.2599	63.1841	16.4243	0.1650
V-30	63.5626	0.5113	124.2809	63.5447	0.0179
V-31	1737.5733	2.6730	649.7309	1736.7521	0.8212
V-32	0.9807	0.0541	13.1619	0.7127	0.2680
V-33	140.7319	-0.7603	-184.8027	140.5036	0.2283
V-35	12.1769	0.2225	54.0768	12.0307	0.1462
V-36	94.9453	-0.6241	-151.7063	94.6843	0.2610
V-38	1592.7352	2.5596	622.1641	1592.5047	0.2305
V-40	27.0023	0.3333	81.0131	27.0011	0.0012
V-41	258.9407	1.0321	250.8792	258.9406	0.0001
V-42	443.9795	1.3514	328.4928	443.9380	0.0415
V-45	270.3059	1.0545	256.3250	270.3042	0.0017
V-49	13.9294	0.2378	57.7917	13.7405	0.1889
TOTAL	9048.1841	17.0000	4132.1697	9045.1694	3.0147

Table J : Deviation from their regression analysis (according to Eberhart and Russell's model) for SYPP of seventeen chickpea genotypes in 3 years.

Genotypes	$\delta^2 V_i$	b_i	$\Sigma Y_{ij} I_j$	$b_i \Sigma Y_{ij} I_j$	$\Sigma \delta^2_{ij}$ (remainder ss)
V-3	43.6114	3.4227	12.3447	42.2519	1.3595
V-6	9.3772	1.5832	5.7101	9.0400	0.3372
V-9	0.5706	0.3164	1.1411	0.3610	0.2095
V-18	49.0237	3.6250	13.0742	47.3933	1.6304
V-22	1.4127	0.6070	2.1894	1.3291	0.0837
V-30	0.4454	-0.0228	-0.0823	0.0019	0.4435
V-31	15.9498	2.0817	7.5080	15.6292	0.3206
V-32	2.4439	-0.6944	-2.5044	1.7390	0.7049
V-33	3.6843	-0.9017	-3.2523	2.9327	0.7516
V-35	0.2817	0.1181	0.4259	0.0503	0.2314
V-36	26.8654	2.6863	9.6888	26.0274	0.8380
V-38	9.7898	1.6465	5.9386	9.7783	0.0115
V-40	0.5322	0.3733	1.3463	0.5025	0.0297
V-41	8.3912	1.5148	5.4634	8.2760	0.1152
V-42	5.1511	-1.0198	-3.6782	3.7510	1.4001
V-45	7.2216	1.4072	5.0754	7.1420	0.0796
V-49	0.3148	0.2566	0.9255	0.2375	0.0773
TOTAL	185.0668	17.0000	61.3142	176.4431	8.6237

4.7 Stability Performance

Stability performance is one of the most desirable properties of genotype to be released as a genotype for wide adaptation. A number of statistical methods are now known for estimation of phenotypic stability. For this purpose the multi treatment traits over a number of years were conducted and seventeen genotypes were tested under three environments. For this investigation Eberhart and Russell's model has been used to study the stability of genotypes under three environments.

4.7.1 Stability Parameter

According to Eberhart and Russell's Model two parameters of stability are calculated (a) The regression co-efficient which is the regression of the performance of each genotypes under different environments on the environmental mean overall the genotypes and (b) Mean square deviations from liner regression. The results of two parameters are shown in the Tables (12 and 13) and are described separately as bellow :-

(a) Regression co-efficient (b_i) and

(b) Mean square deviation $\left(\overline{S}^2_{di}\right)$

4.7.1(a) Regression co-efficient (b_i) : To detect the response of individual genotypes in three environments i.e. Year-1 (1999 – 2000), Year- 2 (2000 - 2001) and Year –3 (2001 – 2002), regression co-efficient with standard error were calculated, the regression co-efficient (b_i) are given Table

(12 and 13). Regression Co-efficient (b_i) in present investigation were $b_i > 1.00$ and $b_i < 1.00$ indicated an above average and below average response, respectively by genotypes.

DFF (Days to First Flowering) :

For this character the regression co-efficient (b_i) and (Sb_i) are – 1.480 ± 0.596 in genotype-3 (V_3) and 1.857 ± 0.193 in the genotype-6 (V_6), 1.206 ± 0.001 in V_9 , 1.233 ± 0.107 in the V_{18} , 1.092 ± 0.114 in the V_{30} , 0.414 ± 0.242 in the V_{31}- o.224 ± 0.284 in the V_{32} , 2.727 ± 0.416 in the genotype33 4.122 ± 0.717 in the V_{35}, - 2.430 ± 0.723 in the V_{36}, 1.176 ± 0.023 in the V_{38} , 1.667 ± 0.048 in the V_{40} , - 2.056 ± 0.694 in the V_{41} , - 0.048 ± 0.302 in the V_{42} , 3.918 ± 0.677 in the V_{45} , 2.196 ± 0.313 in the genotype-49 . For the character genotypes- 6, 22, 35, 36, 40, 45, 49 exhibited the above average response ($b_i > 1$) while the other genotypes were below average response having less than one ($b_i < 1$) values except 30, 9, 18, 38 which are nearer to average response.

NPBFF (Number of Primary Branches at First Flowering) :-

The value of regression co-efficient (b_i) and Sb_i were 1.623 ± 0.125, 0.785 ± 0.146, 0.198 ± 0.107 , 1.592 ± 0.188 ± 0.079, 1.061 ± 0.087, 0.693 ± 0.070, - 0.058 ± 0.373 , 1.583 ± 0.314, 0.792 ± 0.075, 0.933 ± 0.034 , 1.095 ± 0.17, 1.265 ± 0.088, 1.513 ± 0.104 , 0.668 ± 0.163 , 1.603 ± 0.095 , 0.496 ± 0.306 in the genotypes 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49. For this character all the genotypes showed below average response except genotypes 3, 18, 41, 42, 45 they were greater than one, there for showed above average response.

PHFF (Plant Height at First Flowering) :

With respect of this character, the regression co-efficient (b_i) and Sb_i were 0.308 ± 0.024 for V_3, 1.868 ± 0.146 for V_6 , 1.782 ± 0.116 for V_9 , 0.870±0.310 for V_{18} , 0.404 ± 0.103 for V_{22} – 0.491 ± 0.313 for V_{30}, 0.068 ± 0.216 for V_{31} , 1.652 ± 0.111 for V_{32} , 0.423 ± 0.102 for V_{33} , 1.854 ± 0.260 for V_{35} , 2.457 ± 0.312 for V_{36} , 1.891 ± 0.160 for V_{38} , 2.889 ± 0.220 for V_{40} , - 0.443 ± 0.287 for V_{41} , 1.587 ± 0.028 for V_{42} , 4.919 ± 0.798 for V_{45} , - 3.269± 0.845 for V_{49} . For this character the genotypes such as V_6 , V_9, V_{32}, V_{35}, V_{38} , V_{40} , V_{42} and V_{45} showed above average response while the rest of verities indicated less than one there for, showed below average response.

PHMF (Plant Height at Maximum Flowering) :-

For this character the genotypes 6, 9, 32, 33, 36, 40 and 42 indicated above average response and the genotypes 3, 18, 22, 31, 41, 45, 49 indicated below average response and the genotypes 30, 35, 38 showed nearly average response. The value of regression co-efficient (b_i) and Sb_i were 0.892 ± 0.159 for V_3 , 2.235 ± 0.418 for V_6 , 3,551 ± 0.624 for V_9 , - 0.752 ± 0.564 for V_{18} , 0.828 ± 0.124 for V_{22} , 1.021 ± 0.144 for V_{30} , 0.597 ± 0.055 for V_{31} , 2.622 ± 0.325 for V_{32} , 2,492 ± 0.321 for V_{33} , 1.147 ± 0.121 for V_{35} , 2.233 ± 0.411 for V_{36} , 1.299 ± 0.138 for V_{38} , 3.007 ± 0.508 for V_{40} , - 1.116 ± 0.452 for V_{41} , 1.690 ± 0.158 for V_{42} , - 0.590 ± 0.437 for V_{45} , - 4.158 ± 1.376 for V_{49} .

NPBMF (Number of Primary Branches at Maximum flowering):-

For this character the genotypes 18, 33, 35, 40, 42 and 49 showed above average response while genotypes 6, 9, 22, 30, 31 and 32 showed below average response but the genotypes 3, 36, 41 and 45 were nearly average response.

The value of regression co-efficient (b_i) and Sb_i were 1.175 ± 0.197 , 0.015 ± 0.176 , 0.325 ± 0.134 , 1.498 ± 0.257, 0.798 ± 0.047, 0.168 ± 0.410 , 0.656 ± 0.243, - 0.831 ± 0.672, 1.900 ± 0.349, 1.525 ± 0.075, 1.247 ± 0.170, 1.778 ± 0.238 , 1.561 ± 0.115, 1.143 ± 0.171, 1.249 ± 0.042, 1.083 ± 0.009, 1.711 ± 0.184, respectively in the genotypes 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49.

NSBMF (Number of Secondary Branches at Maximum Flowering) :

For this character the genotypes 42, 40, 31, 22 and 33 showed much above average response while rest of the genotypes showed below average response. The b_i and Sb_i were – 1.245 ± 0.807, 2.009 ± 0.266 , 0.901 ± 0.059, - 0.454 ± 0.427 , 4.159 ± 0.90 , - 4.328 ± 1.400 , 3.824 ± 0.726 , - 3.818 ± 1.313 , 4.419 ± 0.919 , - 2.058 ± 0.956 , 0.432 ± 0.171 , - 0.635 ± 0.473 , 3.751 ± 0.825 , 0.808 ± 0.050 , 10.701 ±2.679 , - 1.438 ± 0.493 , - 0.028 ± 0.282 for genotypes 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49 respectively.

PdWPP (Pod Weight Per Plant) :

For this character the genotypes 3, 6, 18, 31, 36 and 38 exhibited above average response and the genotypes 9, 22, 30, 33, 35, 40, 42 and 45 indicated much below average response while 32, 41 and 49 showed below average response.

NPdPP (Number of Pod Per Plant) :

For this character the genotypes 3, 6, 18, 31, 35 and 36 showed above average response because these values are grater than one ($b_i > 1$) while 9, 22, 41 below average response. But the genotypes - 30, 32, 42 and 45 indicated much below average response having less than one ($b_i < 1$) values.

NSPP (Number of Seed Per Plant) :

For this character the value regression co-efficient (b_i) and Sb_i were 2.666 ± 0.428 , 2.063 ± 0.084, 0.987 ± 0.085 , 2.383 ± 0.131, 0.260 ± 0.235, 0.511 ± 0.077, 2.673 ± 523 , 0.054 ± 0.299, - 0.760 ± 0.276 , 0.222 ± 0.221 , - 0.624 ± 0.295, 2.560 ± 0.776, 0.333 ± 0.020 , 1.351 ± 0.118 , 1.055 ± 0.023, 0.238 ± 0.251 respectively in the genotypes 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49.

For this character the genotypes 3, 6, 18, 31 and 38 showed above average response while the genotypes 32, 30, 33, 35, 36 and 49 showed below average response. But the genotypes 41, 42 and 45 showed average response.

SYPP (Seed Yield Per Plant) :

For this character all the genotypes showed bellow average response except genotypes 3, 18, 36, 38 and 41 they were greater than one, there for showed above average response. The value of regression co-efficient (b_i) and Sb_i were 3.42 ± 0.673 , 1.583 ± 0.335, 0.316 ± 0.264 , 3.625 ± 0.737, 0.607 ± 0.167, - 0.023 ± 0.384 , 2.082 ± 0.327 , - 0.694 ± 0.485 , - 0.902 ± 0.501, 0.118 ± 0.278 , 2.686 ± 0.529, 1.647 ± 0.062, 0.373 ± 0.099, 1.515 ± 0.196, - 1.020 ± 0.683 , 1.407 ± 0.163 , 0.257 ± 0.167 in the verity no- 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49 respectively. On the other hand, genotypes 30, 32, 33, 40 and 42 showed much below average response.

Table -12 (A-J) :- Analysis of variance for regression analysis of (joint regression analysis) ten quantitative characters of seventeen verities of chickpea (*Cicer arietinum* L.) according to Eberhart and Russell's model.

Table - A : Analysis of variance for days to first flowering (DFF).

Source	df	SS	MS	F
Total	50	434.240	8.685	
Genotype	16	205.420	12.839	30.35 **
Env+(GenotypeXEnvironment)	32	228.821	7.151	16.905 *
Environment(liner)	1	52.240	52.240	123.498 **
GenotypeXEnvironment(liner)	16	167.723	10.483	24.78 **
Pooled devation	17	7.188	0.423	
Genotype3	1	1.064		
Genotype6	1	0.112		
Genotype9	1	0.000		
Genotype18	1	0.034		
Genotype22	1	0.163		
Genotype30	1	0.039		
Genotype31	1	0.175		
Genotype32	1	0.242		
Genotype33	1	0.520		
Genotype35	1	1.542		
Genotype36	1	1.569		
Genotype38	1	0.002		
Genotype40	1	0.007		
Genotype41	1	1.446		
Genotype42	1	0.273		
Genotype45	1	1.375		
Genotype49	1	0.295		
Pooled error	102	399.204	3.914	

Table - B : Analysis of variance for number of primary branches at first flowering. (NPBFF)

Source	df	SS	MS	F
Total	50	11.372	0.227	
Genotype	16	4.657	0.291	4.23 *
Env+(GenotypeXEnvironment)	32	6.714	0.210	3.043 *
Environment(liner)	1	4.210	4.210	61.014^{ns}
GenotypeXEnvironment(liner)	16	1.018	0.064	0.93^{ns}
Pooled devation	17	1.178	0.069	
Genotype3	1	0.047		
Genotype6	1	0.064		
Genotype9	1	0.034		
Genotype18	1	0.106		
Genotype22	1	0.019		
Genotype30	1	0.023		
Genotype31	1	0.015		
Genotype32	1	0.418		
Genotype33	1	0.296		
Genotype35	1	0.017		
Genotype36	1	0.003		
Genotype38	1	0.001		
Genotype40	1	0.023		
Genotype41	1	0.032		
Genotype42	1	0.079		
Genotype45	1	0.027		
Genotype49	1	0.281		
Pooled error	102	14.371	0.141	

Table - C : Analysis of variance for plant height at first flowering (PHFF).

Source	df	SS	MS	F
Total	50	268.997	5.380	
Genotype	16	176.500	11.031	98.49 **
Env+(GenotypeXEnvironment)	32	92.497	2.891	25.81 *
Environment(liner)	1	21.019	21.019	187.60 *
GenotypeXEnvironment(liner)	16	65.531	4.096	36.57 **
Pooled devation	17	1.896	0.112	
Genotype3	1	0.002		
Genotype6	1	0.064		
Genotype9	1	0.040		
Genotype18	1	0.289		
Genotype22	1	0.032		
Genotype30	1	0.294		
Genotype31	1	0.140		
Genotype32	1	0.037		
Genotype33	1	0.031		
Genotype35	1	0.203		
Genotype36	1	0.293		
Genotype38	1	0.077		
Genotype40	1	0.145		
Genotype41	1	0.247		
Genotype42	1	0.002		
Genotype45	1	1.912		
Genotype49	1	2.140		
Pooled error	102	525.287	5.150	

Table - D :Analysis of variance for plant height at maximum flowering (PHMF).

Source	df	SS	MS	F
Total	50	269.824	5.396	
Genotype	16	157.874	9.867	29.87 **
Env+(GenotypeXEnvironment)	32	111.950	3.498	10.30 *
Environment(liner)	1	23.356	23.356	69.34^{ns}
GenotypeXEnvironment(liner)	16	76.806	4.800	14.54 **
Pooled devation	17	5.536	0.326	
Genotype3	1	0.076		
Genotype6	1	0.525		
Genotype9	1	1.169		
Genotype18	1	0.955		
Genotype22	1	0.046		
Genotype30	1	0.063		
Genotype31	1	0.009		
Genotype32	1	0.316		
Genotype33	1	0.309		
Genotype35	1	0.044		
Genotype36	1	0.506		
Genotype38	1	0.057		
Genotype40	1	0.774		
Genotype41	1	0.614		
Genotype42	1	0.074		
Genotype45	1	0.574		
Genotype49	1	5.678		
Pooled error	102	943.781	9.253	

Table - E : Analysis of variance for number of primary branches at maximum flowering (NPBMF).

Source	df	SS	MS	F
Total	50	26.368	0.527	
Genotype	16	15.084	0.943	4.86 *
Env+(GenotypeXEnvironment)	32	11.284	0.353	1.819^{ns}
Environment(liner)	1	5.245	5.245	27.03
GenotypeXEnvironment(liner)	16	2.645	0.165	0.850^{ns}
Pooled devation	17	3.293	0.194	
Genotype3	1	0.116		
Genotype6	1	0.093		
Genotype9	1	0.054		
Genotype18	1	0.198		
Genotype22	1	0.007		
Genotype30	1	0.505		
Genotype31	1	0.177		
Genotype32	1	1.356		
Genotype33	1	0.365		
Genotype35	1	0.017		
Genotype36	1	0.087		
Genotype38	1	0.170		
Genotype40	1	0.040		
Genotype41	1	0.088		
Genotype42	1	0.020		
Genotype45	1	0.000		
Genotype49	1	0.102		
Pooled error	102	21.623	0.212	

Table - F : Analysis of variance for number of secondary branches at maximum flower (NSBMF).

Source	df	SS	MS	F
Total	50	1052.515	21.050	
Genotype	16	743.874	46.492	16.67 **
Env+(GenotypeXEnvironment)	32	308.641	9.645	3.46 *
Environment(liner)	1	19.449	19.449	6.973
GenotypeXEnvironment(liner)	16	240.818	15.051	5.396 *
Pooled devation	17	47.408	2.789	
Genotype3	1	1.955		
Genotype6	1	0.212		
Genotype9	1	0.010		
Genotype18	1	0.548		
Genotype22	1	2.437		
Genotype30	1	5.880		
Genotype31	1	1.580		
Genotype32	1	5.175		
Genotype33	1	2.532		
Genotype35	1	2.741		
Genotype36	1	0.088		
Genotype38	1	0.673		
Genotype40	1	2.041		
Genotype41	1	0.008		
Genotype42	1	21.528		
Genotype45	1	0.728		
Genotype49	1	0.238		
Pooled error	102	1252.709	12.281	

Table - G : Analysis of variance for Pod weight per plant (PdWPP) .

Source	df	SS	MS	F
Total	50	744.777	14.896	
Genotype	16	415.805	25.988	61.41 **
Env+(GenotypeXEnvironment)	32	328.972	10.280	23.30 *
Environment(liner)	1	94.590	94.590	214.77 *
GenotypeXEnvironment(liner)	16	227.125	14.195	33.63 **
Pooled devation	17	7.168	0.422	
Genotype3	1	1.360		
Genotype6	1	0.683		
Genotype9	1	0.042		
Genotype18	1	1.787		
Genotype22	1	0.191		
Genotype30	1	0.334		
Genotype31	1	0.095		
Genotype32	1	0.030		
Genotype33	1	0.479		
Genotype35	1	0.422		
Genotype36	1	0.023		
Genotype38	1	0.188		
Genotype40	1	0.154		
Genotype41	1	0.106		
Genotype42	1	1.274		
Genotype45	1	0.089		
Genotype49	1	0.000		
Pooled error	102	502.022	4.922	

Table- H : Analysis of variance for number of pod per plant (NPdPP).

Source	df	SS	MS	F
Total	50	13136.529	262.731	
Genotype	16	8307.495	519.218	1578.14 *
Env+(GenotypeXEnvironment)	32	4829.033	150.907	460.06 *
Environment(liner)	1	1577.537	1577.537	4793.32 *
GenotypeXEnvironment(liner)	16	3245.612	202.851	618.45 *
Pooled devation	17	5.570	0.328	
Genotype3	1	0.454		
Genotype6	1	0.329		
Genotype9	1	0.001		
Genotype18	1	0.807		
Genotype22	1	0.008		
Genotype30	1	0.077		
Genotype31	1	0.746		
Genotype32	1	0.461		
Genotype33	1	1.359		
Genotype35	1	0.314		
Genotype36	1	0.259		
Genotype38	1	0.313		
Genotype40	1	0.004		
Genotype41	1	0.002		
Genotype42	1	0.436		
Genotype45	1	0.314		
Genotype49	1	0.001		
Pooled error	102	13812.175	135.413	

Table - I : Analysis of variance for number of seed per plant (NSPP).

Source	df	SS	MS	F
Total	50	25166.972	503.339	
Genotype	16	16118.787	1007.424	6068.67 **
Env+(GenotypeXEnvironment)	32	9048.184	282.756	1703.31 **
Environment(liner)	1	4132.170	4132.170	24891.56 **
GenotypeXEnvironment(liner)	16	4913.000	307.062	1849.75 **
Pooled devation	17	2.824	0.166	
Genotype3	1	0.549		
Genotype6	1	0.021		
Genotype9	1	0.022		
Genotype18	1	0.051		
Genotype22	1	0.165		
Genotype30	1	0.018		
Genotype31	1	0.821		
Genotype32	1	0.268		
Genotype33	1	0.228		
Genotype35	1	0.146		
Genotype36	1	0.261		
Genotype38	1	0.230		
Genotype40	1	0.001		
Genotype41	1	0.000		
Genotype42	1	0.041		
Genotype45	1	0.002		
Genotype49	1	0.189		
Pooled error	102	39918.660	391.359	

Table- J : Analysis of variance for seed yield per plant (SYPP).

Source	df	SS	MS	F
Total	50	498.756	9.975	
Genotype	16	313.689	19.606	39.35 **
Env+(GenotypeXEnvironment)	32	185.067	5.783	11.60 *
Environment(liner)	1	61.314	61.314	127.70
GenotypeXEnvironment(liner)	16	115.129	7.196	14.437 **
Pooled devation	17	8.467	0.498	
Genotype3	1	1.359		
Genotype6	1	0.337		
Genotype9	1	0.210		
Genotype18	1	1.630		
Genotype22	1	0.084		
Genotype30	1	0.444		
Genotype31	1	0.321		
Genotype32	1	0.705		
Genotype33	1	0.752		
Genotype35	1	0.231		
Genotype36	1	0.838		
Genotype38	1	0.012		
Genotype40	1	0.030		
Genotype41	1	0.115		
Genotype42	1	1.400		
Genotype45	1	0.080		
Genotype49	1	0.077		
Pooled error	102	365.021	3.579	

Indicates 1% and 5% level of probability
* Significant
** Highly significant
^{ns} = Non significant

Table –13 (A-J) :- Stability test of ten quantitative characters of seventeen genotypes of chickpea (*Cicer aerietinum* L.) according to Eberhart and Russell's model.

Table -(A) : Days to first flowering (DFF)

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	15.271	-1.480	0.596	-0.016	1.191^{ns}
V-6	16.176	1.857	0.193	-0.968	0.386*
V-9	19.193	1.206	0.001	-1.080	0.002*
V-18	18.160	1.233	0.107	-1.045	0.214*
V-22	21.523	1.630	0.233	-0.916	0.467*
V-30	16.900	1.092	0.114	-1.041	0.228*
V-31	19.067	0.414	0.242	-0.904	0.484*
V-32	17.059	-0.224	0.284	-0.838	0.568*
V-33	18.752	2.727	0.416	-0.560	0.832^{ns}
V-35	17.105	4.122	0.717	0.462	1.434^{ns}
V-36	15.786	-2.430	0.723	0.490	1.446^{ns}
V-38	15.351	1.176	0.023	-1.078	0.046*
V-40	20.015	1.667	0.048	-1.073	0.095*
V-41	19.967	-2.056	0.694	0.366	1.388^{ns}
V-42	21.617	-0.048	0.302	-0.807	0.603*
V-45	20.607	3.918	0.677	0.296	1.354^{ns}
V-49	19.206	2.196	0.313	-0.785	0.627*

Table -(B) : Number of primary branches at first flowering (NPBFF).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	3.049	1.623	0.125	-0.003	0.250
V-6	3.754	0.785	0.146	0.014	0.293
V-9	2.799	0.198	0.107	-0.016	0.214
V-18	2.970	1.592	0.188	0.056	0.376
V-22	3.073	1.137	0.079	-0.031	0.158
V-30	2.816	1.061	0.087	-0.027	0.175
V-31	3.356	0.693	0.070	-0.035	0.140
V-32	3.284	-0.058	0.373	0.368	0.747
V-33	3.673	1.585	0.314	0.246	0.628
V-35	2.669	0.792	0.075	-0.033	0.151
V-36	3.021	0.933	0.034	-0.047	0.067
V-38	3.123	1.095	0.017	-0.049	0.034*
V-40	3.356	1.265	0.088	-0.027	0.175
V-41	2.951	1.513	0.104	-0.018	0.207
V-42	3.357	0.688	0.163	0.029	0.325
V-45	3.152	1.603	0.095	-0.023	0.190
V-49	2.692	0.496	0.306	0.231	0.612

N.B. : All values are non significant except V-38.

Table -(C) : Plant height at first flowering (PHFF).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	33.389	0.308	0.024	-0.948	0.048*
V-6	35.253	1.868	0.146	-0.885	0.292*
V-9	30.938	1.782	0.116	-0.909	0.232*
V-18	32.956	-0.870	0.310	-0.661	0.621*
V-22	33.475	0.404	0.103	-0.918	0.205*
V-30	31.818	-0.491	0.313	-0.655	0.626*
V-31	34.030	0.068	0.216	-0.810	0.432*
V-32	30.724	1.652	0.111	-0.913	0.222*
V-33	31.507	0.423	0.102	-0.918	0.205*
V-35	33.254	1.854	0.260	-0.747	0.520*
V-36	34.495	2.457	0.312	-0.657	0.625*
V-38	34.434	1.891	0.160	-0.872	0.321*
V-40	32.332	2.889	0.220	-0.805	0.440*
V-41	32.901	-0.443	0.287	-0.703	0.574*
V-42	36.749	1.587	0.028	-0.947	0.056*
V-45	37.804	4.919	0.798	0.962	1.59^{ns}
V-49	34.710	-3.296	0.845	1.190	1.68^{ns}

Table -(D) : Plant height at maximum flowering (PHMF).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	40.129	0.892	0.159	-1.013	0.318*
V-6	42.616	2.235	0.418	-0.564	0.837^{ns}
V-9	37.855	3.551	0.624	0.080	1.24 ^{ns}
V-18	40.358	-0.752	0.564	-0.134	1.12 ^{ns}
V-22	41.186	0.828	0.124	-1.042	0.248*
V-30	37.580	1.021	0.144	-1.026	0.289*
V-31	42.626	0.597	0.055	-1.080	0.109*
V-32	38.358	2.622	0.325	-0.773	0.649*
V-33	39.782	2.492	0.321	-0.780	0.641*
V-35	41.069	1.147	0.121	-1.045	0.241*
V-36	42.616	2.233	0.411	-0.582	0.82 ^{ns}
V-38	43.113	1.299	0.138	-1.032	0.276*
V-40	40.843	3.007	0.508	-0.314	1.01 ^{ns}
V-41	39.858	-1.116	0.452	-0.475	0.90 ^{ns}
V-42	43.448	1.690	0.158	-1.014	0.315*
V-45	41.461	-0.590	0.437	-0.515	0.87 ^{ns}
V-49	42.299	-4.158	1.376	4.589	2.752*

Table -(E) : Number of primary branches at maximum flowering (NPBMF).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	4.541	1.175	0.197	0.046	0.39
V-6	5.605	0.015	0.176	0.023	0.352
V-9	3.962	0.325	0.134	-0.016	0.268
V-18	4.108	1.498	0.257	0.128	0.514
V-22	5.251	0.798	0.047	-0.064	0.095
V-30	4.309	0.168	0.410	0.435	0.820
V-31	4.709	0.656	0.243	0.107	0.486
V-32	5.230	-0.831	0.672	1.286	1.345
V-33	5.710	1.900	0.349	0.295	0.698
V-35	4.345	1.525	0.075	-0.053	0.150
V-36	5.149	1.247	0.170	0.016	0.340
V-38	5.368	1.778	0.238	0.100	0.476
V-40	5.256	1.561	0.115	-0.030	0.231
V-41	4.440	1.143	0.171	0.017	0.342
V-42	4.155	1.249	0.082	-0.050	0.165
V-45	5.200	1.083	0.009	-0.070	0.018
V-49	4.473	1.711	0.184	0.032	0.369

N.B. All "F" values are non significant for NPBMF.

Table -(F) : Number of secondary branches at maximum flowering (NSBMF).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	27.111	-1.245	0.807	-0.489	1.61 ns
V-6	29.111	2.009	0.266	-2.232	0.531*
V-9	24.276	0.901	0.059	-2.433	0.118*
V-18	27.447	-0.454	0.427	-1.895	0.855*
V-22	35.545	4.159	0.901	-0.006	1.80 ns
V-30	24.140	-4.328	1.400	3.437	2.800*
V-31	34.027	3.824	0.726	-0.864	1.45 ns
V-32	31.307	-3.818	1.313	2.732	2.627*
V-33	29.868	4.419	0.919	0.088	1.83 ns
V-35	27.044	-2.058	0.956	0.297	1.91 ns
V-36	35.079	0.432	0.171	-2.355	0.343*
V-38	35.312	-0.635	0.473	-1.771	0.947*
V-40	31.650	3.751	0.825	-0.402	1.65 ns
V-41	31.709	0.808	0.050	-2.436	0.101*
V-42	25.484	10.701	2.679	19.085	5.358**
V-45	25.001	-1.438	0.493	-1.715	0.986*
V-49	31.914	-0.028	0.282	-2.205	0.564*

Table -(G) : Pod weight per plant (PdWPP).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	18.367	3.554	0.673	-0.097	1.34 ns
V-6	13.349	3.345	0.477	-0.774	0.95 ns
V-9	14.152	0.578	0.119	-1.415	0.237*
V-18	17.507	3.717	0.772	0.330	1.54 ns
V-22	12.302	0.220	0.252	-1.266	0.504*
V-30	10.555	-0.171	0.334	-1.123	0.667*
V-31	13.724	2.062	0.178	-1.362	0.357*
V-32	12.656	0.502	0.099	-1.427	0.199*
V-33	12.787	-0.578	0.400	-0.978	0.799*
V-35	13.061	-0.511	0.375	-1.035	0.750*
V-36	20.277	2.197	0.087	-1.435	0.173*
V-38	14.954	2.173	0.251	-1.269	0.501*
V-40	10.293	-0.120	0.227	-1.303	0.453*
V-41	10.660	1.114	0.188	-1.351	0.376*
V-42	11.214	-1.860	0.652	-0.183	1.30 ns
V-45	11.314	0.160	0.172	-1.368	0.344*
V-49	10.228	0.617	0.003	-1.457	0.006*

Table-(H) : Number of pod per plant (NPdPP).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	77.138	3.305	0.389	-38.993	0.778*
V-6	53.434	2.213	0.331	-39.117	0.662*
V-9	67.536	0.794	0.019	-39.445	0.038*
V-18	70.888	2.627	0.519	-38.639	1.037*
V-22	53.611	0.418	0.052	-39.438	0.103*
V-30	46.544	0.042	0.160	-39.370	0.320*
V-31	68.025	2.901	0.499	-38.700	0.997*
V-32	52.002	-0.497	0.392	-38.985	0.784*
V-33	61.975	-1.312	0.673	-38.088	1.346*
V-35	66.763	0.027	0.324	-39.132	0.646*
V-36	92.938	2.485	0.294	-39.187	0.588*
V-38	67.863	2.908	0.323	-39.133	0.646*
V-40	48.349	0.607	0.036	-39.442	0.072*
V-41	49.145	1.013	0.024	-39.444	0.048*
V-42	50.013	-1.296	0.381	-39.010	0.763*
V-45	51.841	0.208	0.323	-39.133	0.647*
V-49	42.952	0.558	0.019	-39.445	0.038*

Table -(I) : Number of seed per plant (NSPP).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	88.709	2.662	0.428	-111.913	0.856*
V-6	73.885	2.063	0.084	-112.441	0.168*
V-9	79.639	0.987	0.085	-112.441	0.170*
V-18	89.459	2.383	0.131	-112.411	0.261*
V-22	70.230	0.260	0.235	-112.297	0.469*
V-30	61.004	0.511	0.077	-112.445	0.154*
V-31	93.686	2.673	0.523	-111.641	1.046*
V-32	65.582	0.054	0.299	-112.194	0.598*
V-33	75.710	-0.760	0.276	-112.234	0.552*
V-35	82.337	0.222	0.221	-112.316	0.441*
V-36	131.371	-0.624	0.295	-112.201	0.590*
V-38	93.699	2.560	0.277	-112.232	0.554*
V-40	58.116	0.333	0.020	-112.461	0.041*
V-41	62.453	1.032	0.005	-112.462	0.009*
V-42	92.652	1.351	0.118	-112.421	0.235*
V-45	69.476	1.055	0.023	-112.461	0.047*
V-49	59.513	0.238	0.251	-112.274	0.502*

Table-(J) : Seed yield per plant (SYPP).

Genotypes	Mean	b_i	Sb_i	$\overline{S}^2_{d_i}$	Test value
V-3	13.483	3.423	0.673	0.261	1.346^{ns}
V-6	8.536	1.583	0.335	-0.761	0.670*
V-9	9.585	0.316	0.264	-0.889	0.529*
V-18	12.689	3.625	0.737	0.532	1.474^{ns}
V-22	7.640	0.607	0.167	-1.015	0.334*
V-30	6.852	-0.023	0.384	-0.655	0.769^{ns}
V-31	11.192	2.082	0.327	-0.778	0.654*
V-32	7.536	-0.694	0.485	-0.394	0.969^{ns}
V-33	9.994	-0.902	0.501	-0.347	1.001^{ns}
V-35	10.145	0.118	0.278	-0.867	0.556*
V-36	15.528	2.686	0.529	-0.260	1.057^{ns}
V-38	10.503	1.647	0.062	-1.087	0.124*
V-40	6.540	0.373	0.099	-1.069	0.199*
V-41	8.464	1.515	0.196	-0.983	0.392*
V-42	8.100	-1.020	0.683	0.302	1.366^{ns}
V-45	8.272	1.407	0.163	-1.019	0.326*
V-49	6.485	0.257	0.161	-1.021	0.321*

* Significant
^{ns} = Non significant.

4.7.1 (b) Deviation mean square $\left(\overline{S}^2_{di}\right)$:

Deviation mean square $\left(\overline{S}^2_{di}\right)$ measure the unpredicTable irregulars in response to the environment. Non-significant $\overline{S}^2_{di} = 0$ values mean that the genotype responded alike in all the environments, indicating that the genotype is stable . The genotype is considered non stable for their significant $\overline{S}^2_{di}$ value. $\overline{S}^2_{di}$ is not equal to zero, this value suggests poor stability to environments.

DFF (Days to First Flowering) :

Genotypes V_3, V_{33}, V_{35}, V_{36}, V_{36}, V_{41} and 45 were stable over all the environment (year was considered as environment) having non-significant $\overline{S}^2_{di}$ value. But its higher value suggests poor stability to environments. While nest of the genotype of the present study were non stable for their significant $\overline{S}^2_{di}$ values, indicting that their response were different over the environments.

NPBFF (Number of Primary Branches at First Flowering) :

Genotypes V_3, V_6, V_9, V_{18}, V_{22}, V_{30}, V_{31}, V_{32}, V_{33}, V_{35}, V_{36}, V_{40}, V_{42}, V_{45} and V_{49} were stable over all the environments having non significant and $\left(\overline{S}^2_{di} \approx 0\right)$ value. These genotypes showed alike response over all the environments for this character while rest of V_{38} genotype was non-stable for its significant $\overline{S}^2_{di}$ values indicating that her response was different over the environment.

PHFF (Plant Height at First Flowering) :

GenotypeV_{45} and V_{45} were stable over all the environments having non-significant and $\overline{S}^2_{di}$ values. These genotypes showed alike response over all the

environments for this character. While rest of the genotypes were non stable for their significant $\overline{S}^2_{di}$ values.

PHMF (Plant Height at Maximum Flowering) :

For this character V_6, V_9, V_{18}, V_{40}, V_{41} and 45 were stable over all the environment having non significant and $\overline{S}^2_{di}$ values, this performance may be predictable. This predictable performance of a genotype is called to be stable. While rest of the genotypes were non stable for their significant $\left(\overline{S}^2_{di}\right)$ values indicating that their response were different over the environments.

NPBMF(Number of Primary Branches at Maximum Flowering):

All the seventeen genotypes of the present study were stable over all the environments having non significant and $\overline{S}^2_{di} \approx 0$ value. These genotypes showed alike response over all the environments for this character.

NSBMF(Number of Secondary Branches Maximum Flowering) :

Genotypes V_3, V_{22}, V_{31}, V_{33} , V_{35} and V_{40} were stable over all the environment having non significant and $\overline{S}^2_{di}$ values. These genotypes showed alike response over all the environments for this character. But genotypeV_{42} had higher $\overline{S}^2_{di}$ values suggests poor stability to environment. While rest of the genotypes of the present study were non stable for their significant $\overline{S}^2_{di}$ values.

PdWPP (Pod Weight Per Plant) :

Genotypes V_3 , V_6 , V_{22} deviation mean square $\left(\overline{S}^2_{di}\right)$ is non significant, the performance may be predictable . This predictable performance of a genotype is said to be stable. While rest of the genotypes of the present study

were non stable for their significant $\overline{S}^2_{di}$ values indicating that their response were different over the environment.

NPdPP (Number of Pod Per Plant) :

All the seventeen genotypes of the present study were non stable for their significant $\overline{S}^2_{di}$ values indicating that their response were different over the environments for this character.

NSPP (Number of Seed Per Plant) :

All the 17 genotypes of the present study were non stable for their significant $\overline{S}^2_{di}$ values, indicating that their response were different over the environment for this character.

SYPP (Seed Yield Per Plant) :

Genotypes V_3, V_9, V_{30}, V_{32} , V_{33} , V_{36} and V_{42} were stable over of all the environment having non significant and $\overline{S}^2_{di} \approx 0$ value. These genotypes showed alike response over all the environments for this character. While rest of the genotype were non stable for their significant $\overline{S}^2_{di} \approx 0$ value indicating that their response were different over the environments.

Different figures for average performance of 10 characters of 17 chickpea (*Cicer arietinum* L.) genotypes in different environments.

Fig-4. Showing plant height at 17 genotypes first flowering stage as influenced by different environments.

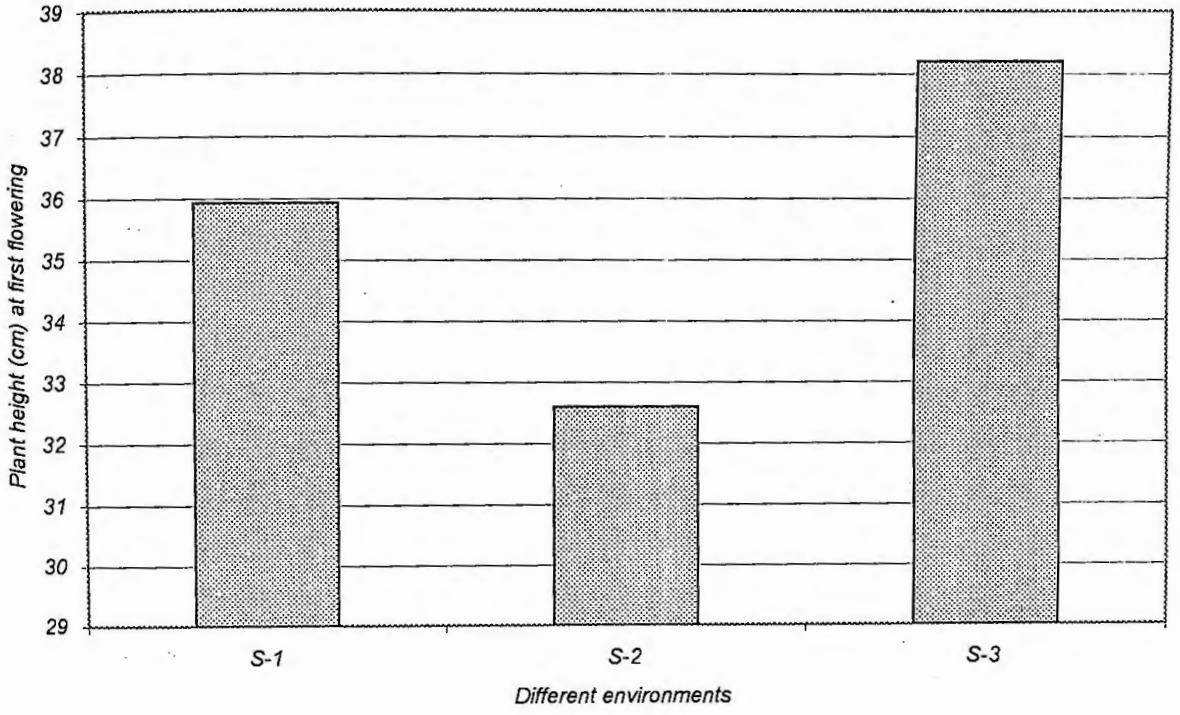


Fig-5. Showing plant height at maximum flowering stage as influenced by different environments.

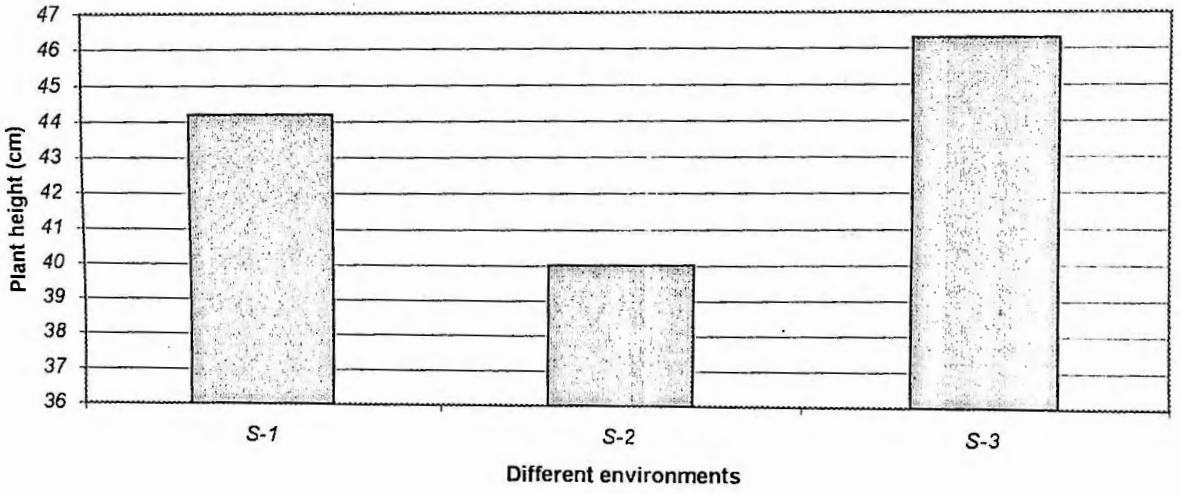


Fig-6. Showing number of secondary branches during the maximum flowering stage as influenced by different environments .

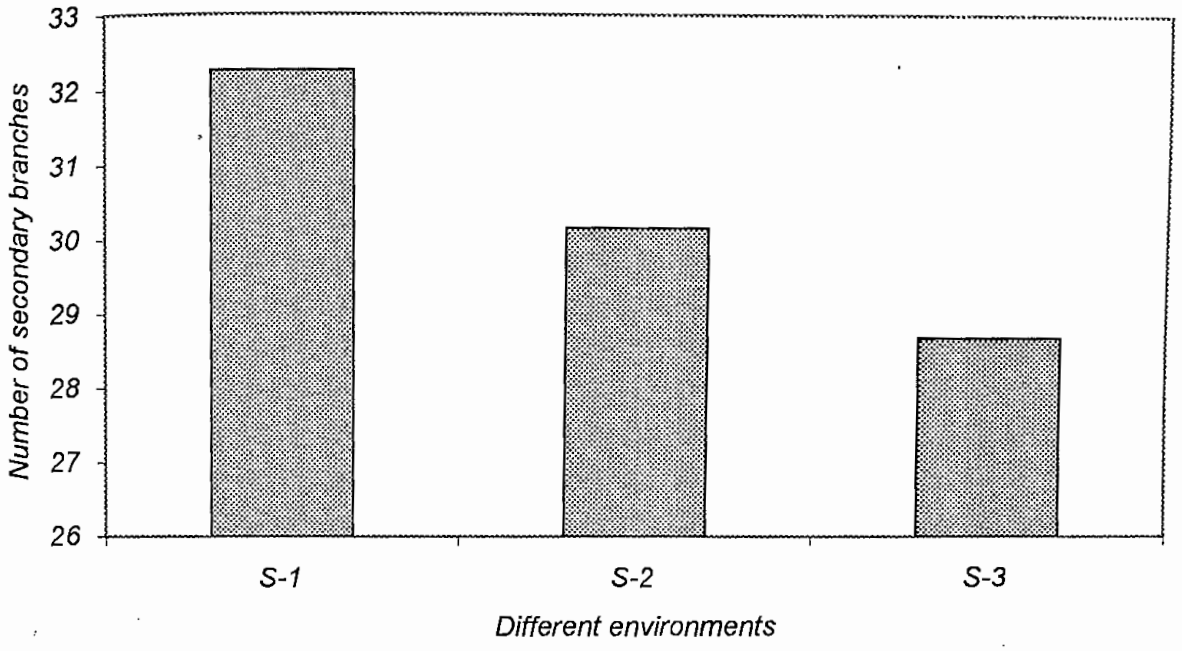


Fig-7. Showing number of pod per plant of 17 genotypes as influenced by different environments

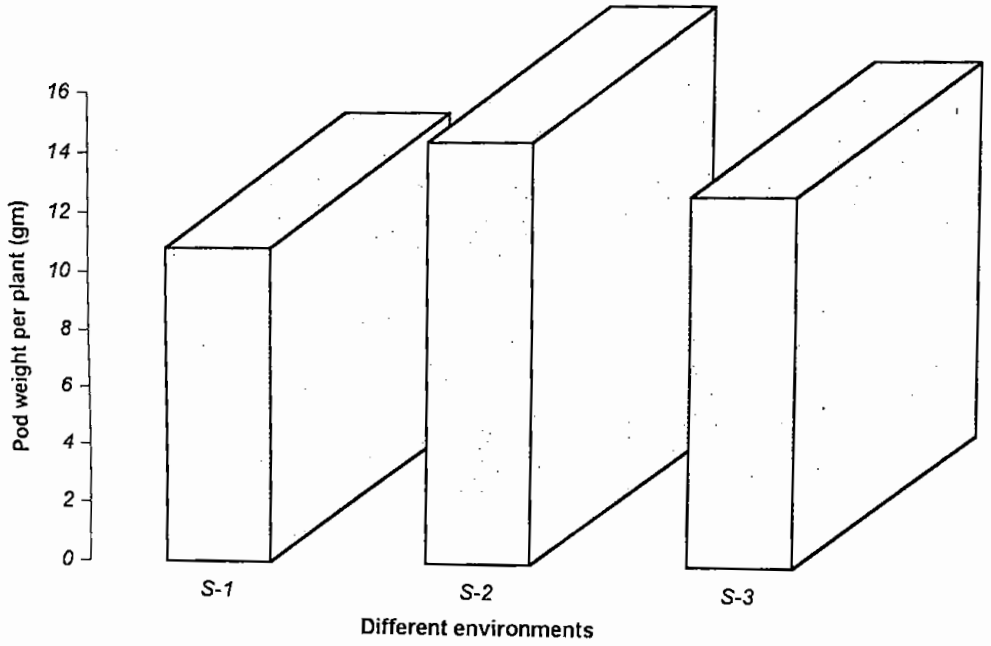
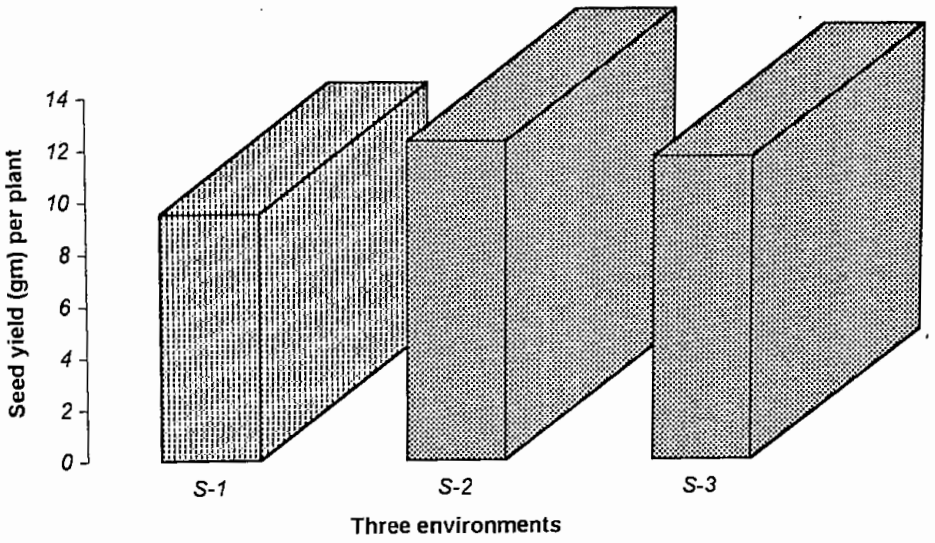


Fig 8. Showing seed yield per plant of 17 genotypes as influenced by three environments.



N.B. : S-1 = Year-1, S-2 = Year- 2, S-3 = Year-3.

Years indicate environments.

Fig-9. Showing plant height of chickpea at first floweing period average of 3 environments.

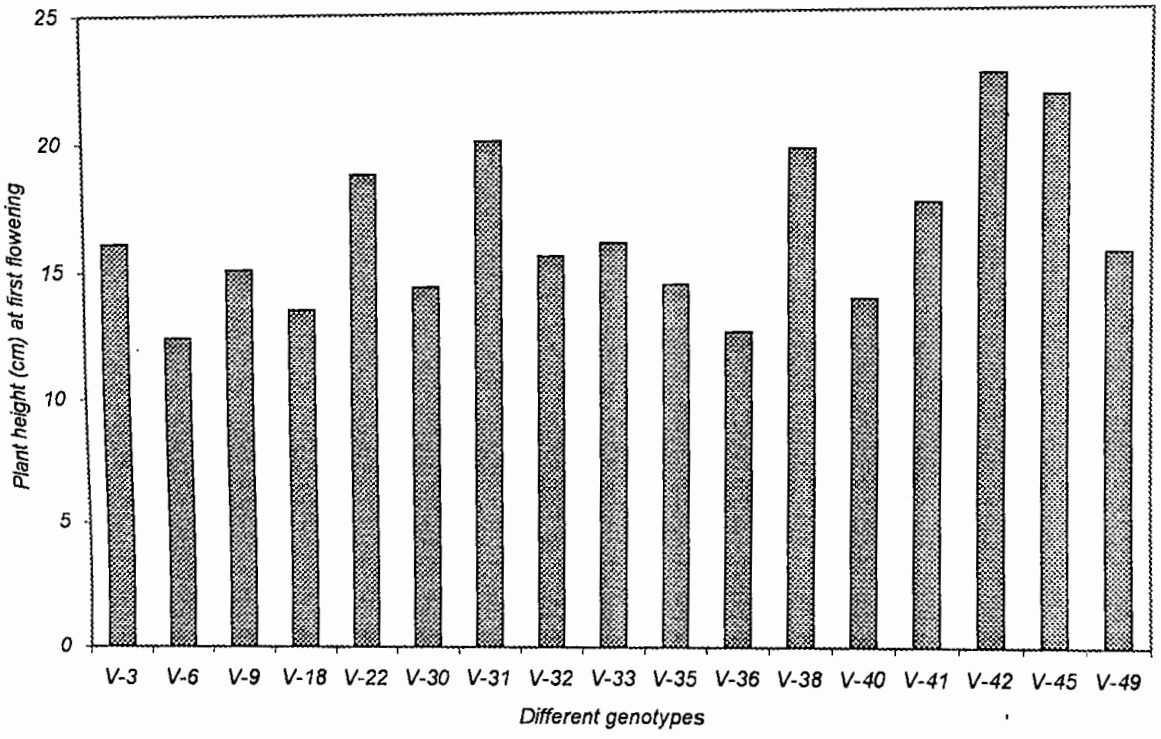


Fig-10. Showing number of primary branches of chickpea at first flowering priod of different genotypes

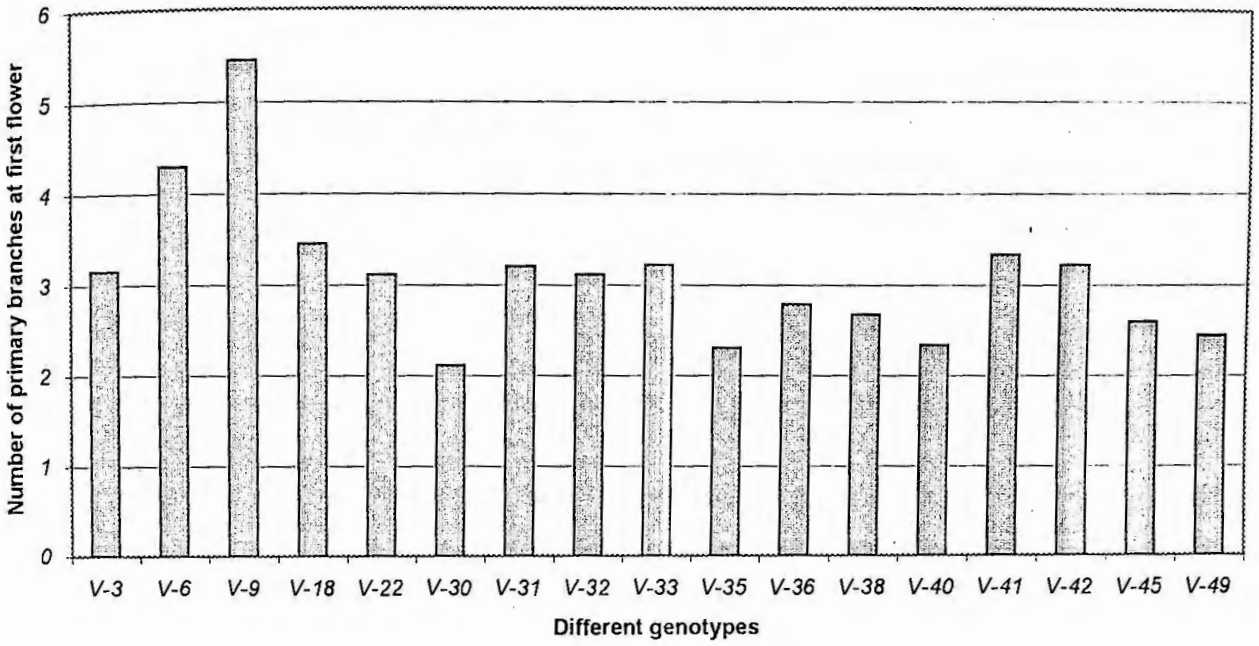


Fig-11. Showing plant height at maximum flowering stage exhibited by different genotypes

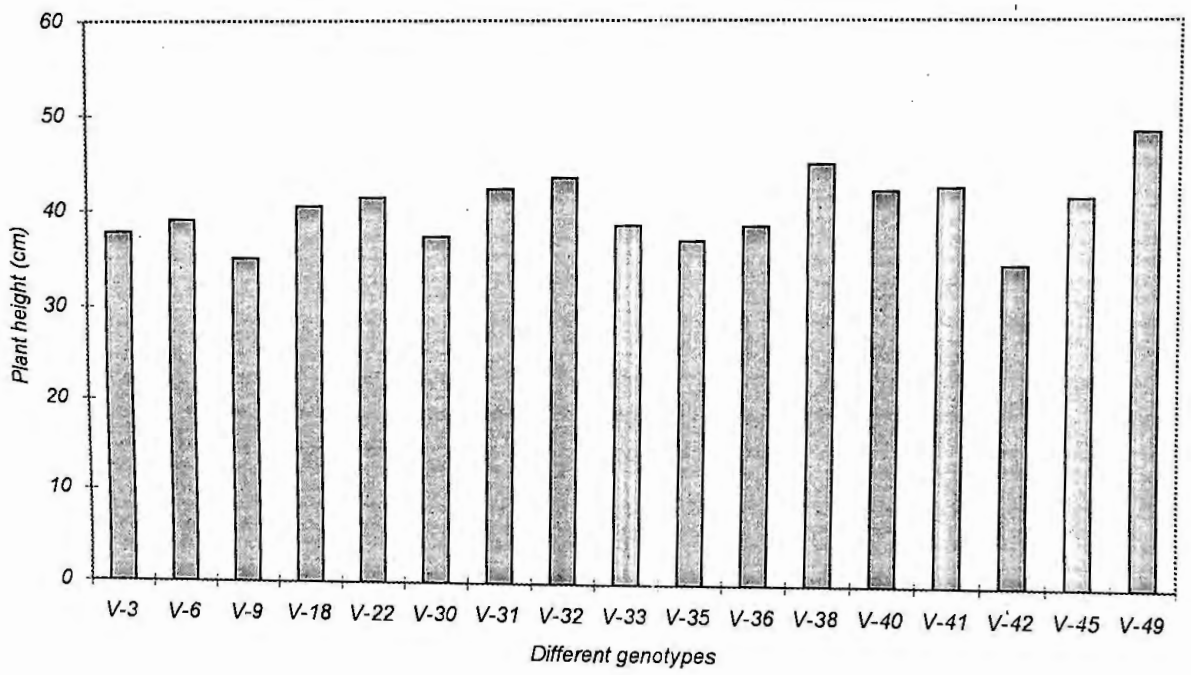


Fig-12. Response of different genotypes on number of seeds per plant of chickpea as influenced by different environments.

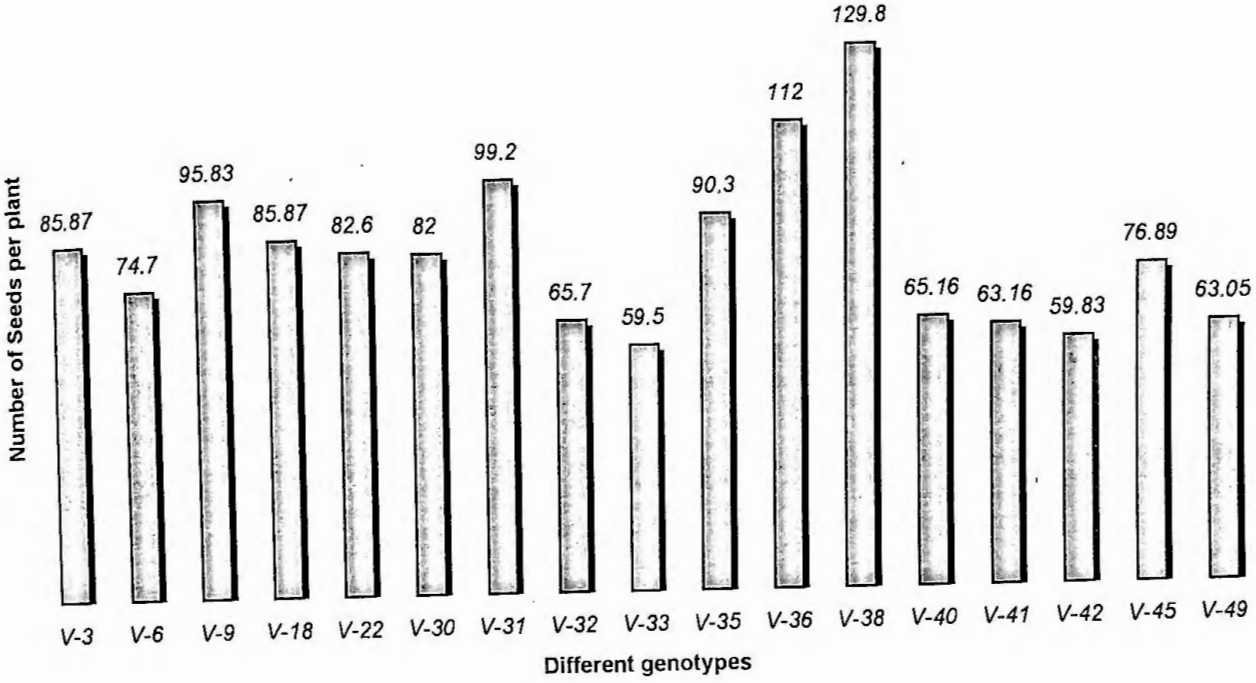
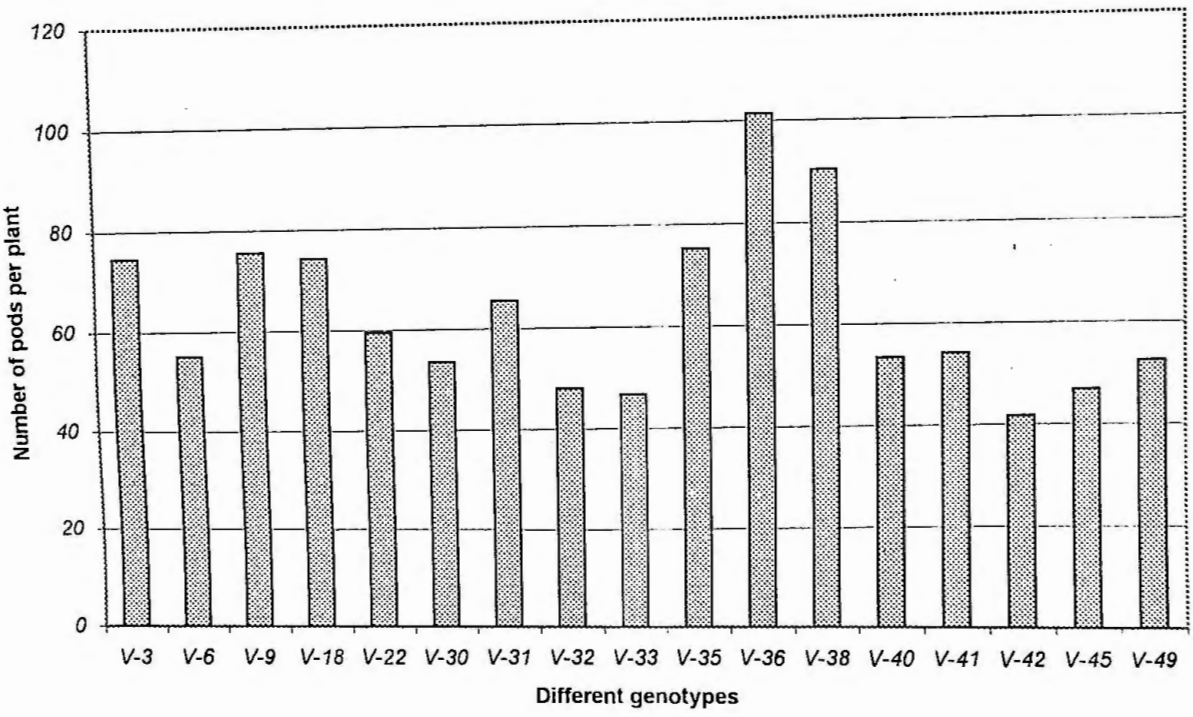


Fig-13. Showing number of pods per plant average of 3 environments exhibited by different genotypes.



It was observed that the S-3 environment gave the tallest plant height (38.2 cm) and S-2 env. produced the smallest plant height (32.6 cm) in both plant height at first flowering and plant height at maximum flowering periods (Fig. 4 and 5). The number of secondary branches at maximum flowering stage gradually decreased with environments S-1, S-2 and S-3, respectively (Fig. 6). The S-2 environment showed the highest and S-1 showed the lowest NPdPP and SYPP with the values of 14 gm. and 10.5 gm. on the Fig. 7 and Fig. 8, respectively. The genotypes V-9 produced more number of primary branches where as genotypes V-30, V-35, V-40 less number of primary branches in the harvesting period after sowing the seeds (Fig-10). It was noticed that different genotypes such as V-35, V-36 and 38 showed more NPdPP and genotypes V-3, V-6, V-9, V-18, V-22 and V-31 showed maximum number of pods per plant (Fig-13).

CHAPTER- 5

DISCUSSION

5. Discussion

In genetic and breeding research quantitative characters are necessary for the preparation of the collective meaningful breeding programme on crop for its improvement. In the present investigation the characters studied are economically important, which are DFF, NPBFF, PHFF, FHMF, NPBMF, NSBMF, PdWPP, NPdPP, NSPP and SYPP. Performance of seventeen genotypes for ten characters in respect of variance and factorial analysis, variability, heritability, genetic advance and stability parameters were statistically analyzed and studied.

In the analysis all the ten characters showed a wide range of variation Table-5 (A-J) indicating that these characters were quantitative in nature and were under polygenic control. The wide range of variation showed that these chickpea (*Cicer arietinum* L.) lines are good breeding materials. Similar result in sugarcane was obtained by Chaudhury *et al.* (1982), Nahar and Khaleque (1996), Paul *et al.* (1976) and Chaudury and Prasad (1968). Joarder and Eunus (1968-1970) also obtained result in mustard. Malhotra *et al.* (1974) and Bhargava *et al.* (1966) also found a wide range of variation in all the characters they studied in lentil.

In the present investigation the degree of co-efficient of variability in percentage (CV%) was indicated by the range of variations. Moderately high co-efficient of variability in percentage (CV%) was found for pod weight per plant (PdWPP) in different environments while comparatively lowest CV%

was shown for plant height at maximum flower (PHMF) in all the characters except V_9, V_{45} and V_{49} on an average 3 years. However, for all the genotypes CV% of a particular character varied from year to year and also genotype to genotype. The Table 5 (A-J) indicated that the genotypes included in the analysis could be worthwhile for further breeding research for the improvement of the characters studied in the present investigation.

The quantitative characters of chickpea also reported by Khaleque et al (1994), Shafiyoul (1997), Islam *et al.* (2000), A.C. Deb (2002). There for, the biometrical techniques developed to study the quantitative characters were found suitable to estimate the genetic system involved in controlling these characters. Fisher (1918) studied the genetic variance in relation to environmental effect and he was the first to provide statistical methods of partitioning the total variation into genetic and environmental components with the development of First (mean) and Second (variance and co-variance) degree two statistical line developed for the measurement of continuous variation.

The phenotypic variance was higher than genotypic and environmental variance for all the characters studied. (Majid *et al.* 1982). Therefore, greater portion of phenotypic variation was genetic in nature. In the present study, the highest phenotypic and genotypic variations were observed in number of seeds per plant (NSPP). So, genetic variation was found for all the characters.

In the analysis of variance Tables (6 and 7) the genotype item for all the characters were found significant, which indicated the genotypes were well differentiated, which might be due to a set of random samples indicated for the

preliminary selection study, as was also recorded by Samad (1991) in some chemical characters of Chilli. The environment item (year item) was significant for all the characters, which indicated that year effects were significantly different. The interaction between environment (year) and genotype (V×E) was significant for all the characters except NPBFF, PHMF and NSPP. Except these three characters the result indicated that environments (years) interacted significntly with the genotypes.

The different components of variation varied differently in different characters. Phenotypic component of variation (δ_p^2) was higher than genotype (δ_g^2) and the interaction items. These results are in conformity with the findings of Samad (1991) and Deb (1994). The difference between phenotypic and genotypic variation were greater in magnitude for NPdPP, NSPP, and NSBMF which indicated that environment, has considerable effect on these characters. In the present materials, high phenotypic values cause high genotypic value. Larger genotypic value for any character is always helpful for effective selection. The highest values for δ_p^2, δ_g^2 and δ_e^2 components of variation indicated better scope for improvement of these character through selection, while low values for δ_p^2, δ_g^2, interactions and δ_e^2 indicating difficulties regarding improvement of these traits through selection. Ramanujam and Thirumalachar (1967) also reported the presence of wide range of phenotypic variation in a number of characters in Chilli.

These result reveal that different components of variation varied differently in various characters and phenotypic components of variation were higher than genotypic components. In a character the greater difference

between PCV and GCV indicated that environment had considerable effect on this character. These results are in agreement with the finding of Samad (1991) in rapeseed, Deb (1994) in Chilli and Singh and Sharma (1984) in Sugarcane.

The highest phenotypic and genotypic co-efficient of variability were observed by seed weight per plant (SYPP). The highest co-efficient of variability for genotype was shown by SYPP which indicated that characters under study were inherited with lower variability within their sibs. Sing and Malhotra (1970) studding cowpea found the highest genotypic co-efficient of variability for NPdPP. Seth *et al.* (1972) found the highest co-efficient of variability for NPdPP in chickpea.

Heritability in broad sense (h^2b), genetic-advance (GA) and genetic advance as a percentage of mean (GA%) were computed and the results are shown in the Table 10.

High genetic advance with high heritability estimates of characters indicated that additive gene effect is probably more important for the characters for selection. The highest genetic advance (51.272) was estimated in number of seed per plant (NSPP) while the lowest value of genetic advance (0.796) was calculated for number of primary branches at first flowering (NPBFF) . The highest heritability (h_b^2) and genetic-advance as a percentage of mean (GA%) with a value of 91.609 and 85.252 respectively, were recorded for seed weight per plant (SYPP). The second highest h_b^2 and GA% were recorded for pod weight per plant (PdWPP) and number of seeds per plant (NSPP) respectively. Therefore, selection might be fruitful in these characters

(SYPP, PdWPP, NSPP) (Panse, 1957). In Pulses regarding some of the characters high heritability estimates were reported by several workers such as Rount and Patel (1975), Patel and Phantis (1977). In their investigation high heritability with high genetic advance was also reported by Goud *et al.* (1977) for pod length and 100 seed weight in black gram.

The heritable portion of variability cannot be judged by genetic co-efficient of variation alone. The heritability together with genotypic co-efficient of variation can give the actual picture of heritable variation. However, heritability does not provides indication of amount of genetic progress would result from selecting the best individuals. Johnson *et al.* (1955), Ramanujam (1967), and Sing *et al.* (1981) suggested that heritability estimates with genetic gain are more useful for effective improvement.

Joint regression analysis of variance Table 12 (A-J) revealed the existence of sufficient variability among the genotypes for all the characters. Joint regression analysis showed that the genotype item was highly significant for all the characters and indicated that the genotypes were different which justifies the inclusion of genotypes as materials in the present study. The item environment + (genotype × environment) i.e., V × E was also significant for all the characters except NPBMF when tested against respective pooled deviation. The genotype × environment (linear) interaction was highly significant for DFF, PHFF, PHMF, NSBMF, PdWPP, NPdPP, NSPP and SYPP while this item was non significant for NPBFF and NPBMF.

The significant V × E (linear) component indicated that the genotypes studied responded differently in different environment i.e., different years. It also showed that as each of genotypes were significantly different as they possessed different in genotypes. The V × E with its linear components is under genetic control. So, the present analysis V × E interactions were operative. These results are in conformity with the finding of Samad (1991) in rapeseed, Tai *et al.* (1982), Ghosh and Singh (1996) and Nahar (1997) in sugarcane, Deb (1994) in chilli.

Genotype-environment interactions are of major consideration to develop improve genotypes. The role of V × E interaction has long been of great importance to the breeders for selection of strain (genotype) under different environmental conditions in fortuitous breeding programme. The stability of a genotype that shows minimum interaction with environment is one of the essential character for a cultivars genotypes capacity to yield well over a range of environments has an importance equal to that of its yield potential (Johnson *et al.* 1968). The information in relation to G × E would enable the breeders to select genotypes with wider adaptation across the environments. Grafius (1956) emphasized that the studies of individual yield components can lead to simplification in genetic explanation to yield stability and hence are valuable to breeders in prediction and determination of the effects of the environments. Finlay and Wilkinson (1963) pointed out that the mean yield of different genotypes for each site and season usually provide a quantitative, grading of the environment and from the analysis of genotypes, especially adapted to good on poor seasons and those showing general adaptable might be identified. The study of genotype × environment interaction

could lead to successful evaluation of stable genotypes which could be used in further breeding programme.

Originally, Finlay and Wilkinson (1963) considered the linear regression slope (b_i) as a measure of stability, but later on Eberhart and Russell (1966) emphasized the need of considering both regression slope and deviation from regression in judging the stability of a genotype, Hence, a desired genotype should be one with high mean performance with regression co-efficient (b_i) should be 1.00 and the deviation from regression (irrespective of sign) as small as possible $\left(\overline{S}^2_{d_i} = 0\right)$. Eberhart and Russell (1966) suggested that both linear (b_i) and non linear $\left(\overline{S}^2_{di}\right)$ components of the genotype – environment interaction should be considered while judging the phenotypic stability of particular genotype.

Further Breese (1969), Paroda *et al.* (1973) and Langer *et al.* (1979) stated that regression co-efficient is a measure of response to varying environments and the means square deviation from linear regression is a true measure of stability and the genotype with the lowest deviation being the most stable and vice-versa.

But Benis and Gupta (1972) stated that the potentiality of a genotype to express greater mean over environments should be the most important criterion, since the other two parameters may not have any particular utility if the genotype is potentially week. From the above discussions it may be stated that –

(1) Lines with high mean performances $(\overline{X})$, average b_i values and non-significant $\overline{S}^2_{di}$ values may be considered as stable genotypes for all environments.

(2) Lines with above average mean performances and regression co-efficient, and non-significant $\overline{S}^2_{di}$ are sensitive to environmental changes may be recommended for favourable environments.

(3) The lines with high mean with the below average response, (b_i) and non-significant $\overline{S}^2_{di}$, may be adapted to poor environment.

(4) A line having less mean performance, regression co-efficient close to 1.00 and non-significant $\overline{S}^2_{di}$ indicating poor adaptability to all environment.

(5) A line having less mean performance, b_i above average and non-significant $\overline{S}^2_{di}$ indicating poor adaptability to fovourable environment.

(6) Lines having less mean performance b_i and non-significant $\overline{S}^2_{di}$ indicate poor adaptation to unfavorable in environment.

On the basis of the above mentioned criteria the genotypes (genotype) which should stable performance i.e., adaptable to all environment were genotypes 6 and 40 for NPBFF, genotypes 3 and 22 for PHMF, genotypes 36 and 45 for NPBMF due to their high mean performance $(\overline{X})$, average b_i values and non-significant $\overline{S}^2_{di}$ values.

Some genotypes such as genotype 45 for DFF, PHFF and NPBFF, genotypes 33 and 40 for NPBFF, genotype 6 for PHMF, genotypes 33, 38 and 40 for NPBMF, genotypes 22 and 31 for NSBMF, genotypes 3 and 18 for PdWPP, genotypes 3, 18 and 31 for SYPP were sensitive to environmental

changes might be recommended for favourable environments, because of their above average mean performance and regression co-efficient (b_i) and non-significant $\overline{S}^2_{di}$ values.

The genotype 6 for NPBFF, genotypes 18 and 45 for PHMF, genotypes 6, 22 and 32 for NPBMF adapted to poor environment, because they had high mean with the below average response (b_i) and non significant $\overline{S}^2_{di}$ values. Several genotypes like 30 and 35 for NPBFF, genotype 42 for NPBMF and genotype 22 for SYPP indicated poor adaptability to all environments having less mean performance, b_i closed to 1.00 and non significant $\overline{S}^2_{di}$ values (Sing and Rai 1989 and Sing *et al.* 1993).

On the other hand genotype 30 and 41 for NPBFF, genotype 9 for PHMF, genotypes 18, 42 and 49 NPBMF, genotypes 40 and 33 for NSBMF showed poor adaptability to favourable environment, due to their low mean performance, b_i above average and non significant $\overline{S}^2_{di}$ values while genotypes 3 and 36 for DFF, genotypes 9, 35 and 49 for NPBFF, genotype 41 for PHMF, genotypes 9 and 30 for NPBMF, genotypes 3, 35 for NSBMF, genotype 42 for PdWPP, genotypes 30, 32, 33 and 42 for SYPP indicated poor adaptation to unfavourable environment, because they had low mean performance, below average response (b_i) and non significant $\overline{S}^2_{di}$ values.

It is therefore, suggested that breeders are likely to select suitable genotypes by growing them under varied environmental conditions, which might lead, be able to increase the yield potential by increasing the performances of yield components in the suitable environments.

CHAPTER- 6

SUMMARY

6. SUMMARY

The Present investigation on the study of phenotypic expression of chickpea (*Cicer arietinum* L.) genotypes under different environmental conditions on some yield components included ten quantitative characters such as days to first floweringing (DFF), number of primary branches at first flowering (NPBFF), plant height of first flowering (PHFF), plant height at maximum flowering (PHMF), number of secondary branches at maximum flowering (NSBMF), pod weight per plant (PdWPP), number of pod per plant (NPdPP), number of seed per plant (NSPP), seed weight per plant (SWPP) for seventeen genotypes . Seeds of seventeen genotypes viz 3, 6, 9, 18, 22, 30, 31, 32, 33, 35, 36, 38, 40, 41, 42, 45 and 49 were supplied from the germ-plasm stock of Biometrical Genetics Laboratory, Department of Genetics & Breeding, University of Rajshahi. The experiment was set up at the research field of the Department of Botany, University of Rajshahi, during the consecutive 3 robi seasons following randomized block design. Data were collected in CGS system and analyzed following standard biometrical process.

In the present investigation, range, mean with standard error and co-efficient of variability in percentage were very much pronounced and varied form genotype to genotype for all the characters which indicated that these characters were under polygenic control and quantitative in nature. Analysis of variance for all the characters for genotype

item was significant, which indicated the presence of diversity in genotypes and hence justified their inclusion as materials in the study. The highest phenotypic and genotypic variations were found for number of seed per plant (NSPP). The second highest GCV and PCV were observed for seed weight per plant (SWPP). The highest heritability (h_b^2) and GA% were found for seed yield per plant (SYPP). The second highest (h_b^2) and GA% were found for pod weight per plant (PdWPP) and number of seed per plant (NSPP) respectively. Therefore, additive gene effects are found in the inheritance of these characters.

The above result indicated that five yield components in NSBMF, PdWPP, NPdPP, NSPP and SWPP may be considered as the primary yield and among these character NPdPP, PdWPP and SWPP are the most important for selection for their high heritability, high genetic advance and GA%. The lower values for DFF, NPBFF, PHFF and PHMF in maximum cases indicated the difficult in improvement of these traits through selection.

Joint regression analysis showed that the genotype item was highly significant for all the characters and indicated that the genotypes were different which justified the inclusion of genotypes as materials in the present study. The item E + (V × E) was also significant for all the characters except NPBMF. The significant E + (V × E) indicated the differential reaction of genotypes with the changes of environment. The V × E (linear) interaction was also highly significant for most of the characters. The significant V × E (linear) variance indicated genetic differences for environmental response. V × E interaction is now recognized as an important source of phenotypic variation,

knowledge about the type of V × E interaction involved in population help the plant breeders to breed and to select better strains.

On the basis of the above mentioned criteria the genotypes (genotype) which should stable performance i.e., adaptable to all environment were genotypes 6 and 40 for NPBFF, genotypes 3 and 22 for PHMF, genotypes 36 and 45 for NPBMF due to their high mean performance $(\overline{X})$, average b_i values and non-significant $\overline{S}^2_{di}$ values.

Some genotypes such as genotype 45 for DFF, PHFF and NPBFF, genotypes 33 and 40 for NPBFF, genotype 6 for PHMF, genotypes 33, 38 and 40 for NPBMF, genotypes 22 and 31 for NSBMF, genotypes 3 and 18 for PdWPP, genotypes 3, 18 and 31 for SYPP were sensitive to environmental changes might be recommended for favourable environments.

Finally, genotype × environment is under genetic control. Breeders would be able to select suitable genotypes in advanced generations by growing them under different environmental conditions. The present study also revealed that yield potential could be increased by increasing the performance of the yield components in suitable environment. Since, those characters are associated with yield.

CHAPTER- 7

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7. REFERENCES

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