2012

Genetic Improvement of Yield and Yield Contributing Characters of Chickpea (Cicer arietinum L.) through Mutation Breeding

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Genetic Improvement of Yield and Yield Contributing Characters of Chickpea (*Cicer arietinum* L.) through Mutation Breeding

A Thesis

Submitted to the University of Rajshahi in fulfilment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

by

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DECEMBER, 2012
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DEDICATED

TO

MY LATE FATHER
AND
BELOVED MOTHER

DECLARATION

I hereby declare that the entire work submitted as a thesis towards the fulfilment for the degree of doctor of philosophy for the University of Rajshahi, Rajshahi, Bangladesh is the results of my own investigation.

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The undersigned certify that the research work embodied in this thesis was done by the author and that as to the style and contents, the thesis suitable for submission. The undersigned also certify that this thesis has not already been submitted in substance for any degree and has not concurrently been submitted in candidature for any degree.

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ACKNOWLEDGEMENTS

I express my heartfelt appreciation to the almighty God without whose kindness this dissertation would not be possible to complete.

It is a great pleasure and privilege to express my deepest sense of gratitude, sincere regard and indebtedness to my respected supervisor Dr. M. A. Khaleque, Professor, Department of Botany, University of Rajshahi, for his scholastic guidance, supervision, suggestion, advice, constant inspiration, encouragement and sympathetic cooperation during the whole period of research work and preparing the manuscript.

I express my deepest sense of gratitude, sincere regard and indebtedness to my respected co-supervisor Dr. Anil Chandra Deb, Professor and Chairman of the Department of Genetic Engineering and Biotechnology, University of Rajshahi, for his scholastic guidance, supervision, suggestion, advice, constant inspiration, encouragement and sympathetic cooperation during the whole period of research work.

I am deeply indebted to the most senior and respected teacher Professor O. I. Joarder, the founder chairman of the Department of Genetic Engineering and Biotechnology, University of Rajshahi for his help and encouragement. Besides, I must express my sincere thanks to the rest of the teachers of the above department.

Special thank is due to F. M. Ali Hayder, Assistant Professor, Department of Botany, University of Rajshahi of Biometrical Genetic Lab. for his kind cooperation, encouragement in many times during my research work.

Sincere thanks are due to the research students of Biometrical Genetics Lab., Department of Botany, University of Rajshahi, namely Md. Abul Kalam Azad, Md. Rahimul Alam, Md. Abdus Samad, Dr. Rumman Ara, Anuradha Roy Chowdhury, Hosne Ara Banu, Md. Shahidul Islam for their cooperation in different ways during the whole period of my study.

I am very much indebted to my mother without whose blessings, sacrifice in many ways I did not complete this work successfully.

Finally, I am deeply indebted to my husband Dr. Jugol Kumar Sarker, Associate Professor, Department of Crop Science and Technology, University of Rajshahi, for his continuous encouragement, inspiration, valuable suggestions and patience for successfully completing this research work.

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ABSTRACT

The whole work of the present investigation was carried out in three separate heads, such as study of genetic control, study of genotype-environment interaction and study of variability, correlation, path-coefficients and selection index. Eight chickpea lines were studied for eleven yield and yield contributing characters viz. days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD), number of pods per plant (NPPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and seed weight per plant (SWPP).

In part I, in the study of genetic control five single crosses were used. In the analysis using generation means, the additive-dominance model, gene effects, degree of dominance, heritability, genetic advance, effective factors, heterosis and inbreeding depression were evaluated. The findings of this part I was first for the development of pure lines and the second for utilization of hybrid vigour commercially. It has been found from the analyses that the additive dominance model was found to be adequate as the χ^2 values were non-significant supported by ABC scaling test for the characters viz, NSBMF, PHMF, NPPP and PdWPP in cross I (1A × 3A); DMF, PHMF, NPPP and NSPP in cross II (2C × 4C); NSBMF, PHMF, NPPP and NSPP in cross III (4C × 3C); DMF and NPBMF in cross IV (4A × 7B). These crosses for those characters also indicated high narrow sense heritability and high genetic advance. Therefore these crosses for those characters would likely be good materials for the development of prospective pure lines for further breeding works.

The second line of fruitful research would likely be with the crosses for the exploitation of hybrid vigour commercially. In this regard, the characters viz, NSPP and SWPP in cross I (1A × 3A); NPBMF, 1000-SW and SWPP in cross II (2C × 4C); DMF and PdWPP in cross III (4C × 3C); RWFD and 1000-SW in cross

IV (4A × 7B) and NSBMF in cross V (5A × 6A) showing high heterosis both for mid parent and better parent and also showing overwhelming dominance and duplicate type of epistasis suggesting that these crosses for those characters be utilized for the commercial utilization of hybrid vigour.

In part II, investigation on genotypic × environment interaction was done. The same eleven quantitative characters as in part I eight lines were studied. In this part four irradiation doses namely no irradiation (D_0), 20Kr (D_A), 30Kr (D_B) and 40Kr (D_C) and three consecutive years (2007-08, 2008-09 and 2009-10) were considered as the twelve environments in this investigation. The range of variation was wide and pronounced in the genotypic means for all the characters indicated that genotypic differences among the chickpea lines. Here environmental means also indicated that different environments had different effects on all the traits. Joint regression analysis revealed that genotypic × environment interaction accounted for by both linear and non-linear functions of environment. A non-significant greater portion was accounted for by the linear function of environments. From the estimation of stability parameters the genotypes, like line-2, line-4, line-6 and line-8 for DMF; line-1, line-4, line-7 and line-8 for NPBMF; line-1, line-2, line-5 and line-7 for NSBMF; line-2, line-3, line-4, line-5, line-6 and line-7 for PHMF; line-1 for PWFD; line-3 and line-6 for RWFD; line-4 for PdWPP; line-2 for NSPP and line-4 for SWPP were predicted to show the stable performances i.e., adaptable to all environments and could be used for further breeding research. Besides, line-3 and line-5 for NPBMF; line-4 for NSBMF; line-1 for PHMF; line-1, line-7 and line-8 for RWFD; line-2 and line-6 for PdWPP, line-4 for 1000-SW and line-2 and line-6 for SWPP were adaptable for favourable environment. On the other hand, line-5 and line-6 for DMF; line-2 and line-6 for NPBMF; line-3, line-6 and line-8 for NSBMF; line-8 for PHMF; line-2, line-4 and line-5 for RWFD; line-1 and line-8 for PdWPP; line-1, line-3 and line-8 for SWPP showed stable performances for unfavourable environments.

In part III, variability, correlation, path-coefficients and selection index were studied at four irradiation doses and in two consecutive years (2008-09 and 1009-10).. The lines were genetically well differentiated as indicated by the analysis of variance. The characters NSPP, NPPP, PWFD and 1000-SW showed the higher value for σ^2_p, σ^2_g, PCV and GCV which indicated a wide scope of improvement of these traits through selection. On overall basis broad sense heritability (h^2_b) estimates was found to be low. The highest value of h^2_b was found for 1000-SW followed by NPBMF and RWFD. Genetic advance (GA) and genetic advance as percentage of mean (GA%) were high for 1000-SW and NSPP. In the present investigation the characters NPPP, PdWPP and NSPP showed positive and highly significant correlation with SWPP both at phenotypic and genotypic levels .Path coefficient analysis revealed that at genotypic level the highest positive direct effect was observed for NSPP followed by PdWPP and 1000-SW and at phenotypic level the highest positive direct effect was found for NSPP followed by 1000-SW and NSBMF on SWPP. In the discriminant function analysis, the highest expected genetic gain of 638.460 % was observed for characters combination viz, NPBMF + NSBMF followed by 636.932 % for NPBMF + RWFD and 571.392 % for NPBMF + SWPP. It may be concluded that NPBMF is the most important for selection because with yield it gave the highest expected genetic gain and it also showed moderate heritability, significant positive correlation and positive direct effect with SWPP both at phenotypic genotypic levels. To make the selection breeding programme effective with NPBMF emphasis should be given on other yield contributing characters, like PdWPP and NSPP as they showed highly significant positive correlation and high positive direct effect on yield.

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GENERAL INTRODUCTION

Pulses are important crops for food security worldwide. These are known to be among the earliest food crops to be cultivated by man. Currently, these are very important to the livelihoods of millions of people, especially in developing countries, where, from its production, households derive food, animal feed and income. In Bangladesh it occupies an area about 593384 acre of land producing 220786 metric tons (BBS, 2009-2010).

Pulses are defined as dry edible seeds of leguminous plant and are important foodstuffs especially in tropical and subtropical regions, where they are second in importance only after cereals as a source of protein. In Bangladesh it is the most essential item for rice based diet. The major pulses grown in Bangladesh are lentil, chickpea, blackgram, mungbean, khesary and fieldpea. Among these, lentil, chickpea, khesary and fieldpea are grown during the winter season (November-March) and contribute about 82% of the total pulses. Blackgram is grown in late summer (August-December). Mungbean is grown both in early summer (February-April) and late summer.

Pulses are a good source of protein, minerals and energy in human diet. These are complementary to cereals in terms of pattern and profile of amino acids. That would probably explain the adoption to dhal-roti or dhal-bhat as the staple food in the daily diet of the people of our country. Pulses may play an important role in meeting the quantitative and qualitative protein requirements of a large part of human lives, especially in the developing countries of Asia, Africa and Latin America, where the major sources of protein and energy are non-animal product. Protein is the chief ingredient of life. The importance of protein in the nutrition needs no elaboration. For balanced diet optimum protein content is very much

essential in our daily diet with other components. It is the main component of different organ of our body viz. brain, blood, bones muscles and skins. Deficiency of protein in our daily diet is obvious. 50% of the present population of Bangladesh is severely under nourished. Malnutrition and protein deficiency is the root causes of ill health of the population of this sub-continent. To minimize this situation more pulse crops are to be grown and more pulses are to be taken in the daily diets.

Among legumes, pulses play an important role mainly for its food value and for nitrogen fixation into the soil. Leguminous crops not only can fix the atmospheric nitrogen towards the benefit of crops but also save nitrate leaching during precipitation (Jones, 1939). The production of pulse was 220786 metric tons in the year 2009-2010 and 257505 metric tons in the year 2006-07 which indicated that pulse production gradually decreased. The future of pulse crop in Bangladesh lies in their capacity to fit in the tight cropping patterns and as intercrops with various other crops. It is expected that adequate research attention would be given to this aspect of pulse cultivation. Table-1 showed the area and production of various crops in Bangladesh.

Table 1: Area and production of major crops in Bangladesh from 2006-07 to 2009-10.

(Area in acres and production in metric tons)

Crops	2006-07		2007-08		2008-09		2009-10	
	Area	Prod.	Area	Prod.	Area	Prod.	Area	Prod.
Rice	26142208	27318250	26129740	28930824	27871907	31316777	28055715	31975251
Wheat	987960	736893	958347	844145	975125	849046	929766	901490
Potato	852325	5166672	993005	6647778	977540	5268327	1073846	7930240
Oil seed	841071	683460	875069	701476	1200034	661312	736002	716171
Pulses	**769040**	**257505**	**557508**	**203535**	**559416**	**196071**	**593384**	**220786**
Sugarcane	383587	6355146	329026	5540249	319686	5800635	296239	5083978

Source: Online Year Book of Agricultural Statistics of Bangladesh, 2010.

In accordance to the availability of statistics, the total area and production of different pulses in Bangladesh are presented in the following table 2.

Table 2: Area and production of pulses in Bangladesh from 2005-06 to 2009-10.

(Area in acres and production in metric tons)

Name of pulses	2005-06		2006-07		2007-08		2008-09		2009-10	
	Area	Prod.	Area	Prod.	Area	Prod.	Area	Prod.	Area	Prod.
Gram	**31450**	**9760**	**31100**	**9810**	**23101**	**7168**	**20206**	**6551**	**17850**	**5744**
Arhar	4320	1015	3715	1445	2998	1140	2244	841	2003	772
Masur	332695	115370	339905	116810	179354	71535	175328	60534	190982	71100
Motor	23475	7780	19945	6645	18360	6093	17780	6510	15648	5567
Mung	55325	16870	60290	18675	59717	20628	53557	17890	57462	20177
Mashkalai	57675	17400	57505	18190	58918	20557	61303	21837	79287	28356
Kheshari	314740	107250	245630	82735	201426	71597	212210	75832	212313	81705
Gari Kalai	-	-	-	-	677	254	518	177	535	185
Other pulses	13620	3975	10950	3195	12957	4563	16270	5896	17304	7180
Total	**833300**	**279420**	**769040**	**257505**	**557508**	**203535**	**559416**	**196071**	**593384**	**220786**

Source: Online Year Book of Agricultural Statistics of Bangladesh, 2010.

Among pulses, chickpea is the fourth largest grain legume crop in the world, with a total production of 10.89 million tons from an area of 11.98 million ha and productivity of 0.91 tons ha^{-1} (FAOSTAT-2010). Chickpea is excellent sources of protein, but this is treated as minor crop and receives little attention from farmers and policymakers. The area of chickpea production has decreased continuously for the past 10 years. Cultivation of chickpea mainly concentrated within the Ganges floodplain areas of the northern districts and in some southern districts of the country. In Bangladesh about 85% of the chickpea crops are grown in the five greater districts at Foridpur, Jessore, Kustia, Pabna and Rajshahi. The average annual yield of the different pulses ranges from 700 to 800 kg per hectare.

Table 3: Area and production of gram by region, 2005-2006 to 2009-2010.

(Area in acres and production in metric tons)

Region	2005-06		2006-07		2007-08		2008-09		2009-10	
	Area	Prod.	Area	Prod.	Area	Prod.	Area	Prod.	Area	Prod.
Bandarban	-	-	-	-	-	-	-	-	-	-
Chittagong	130	40	135	45	128	40	123	36	110	33
Comilla	20	05	20	05	04	03	04	03	04	03
Khagrachhari	-	-	-	-	-	-	-	-	-	-
Noakhali	335	95	340	95	320	87	318	108	268	96
Rangamati	-	-	-	-	-	-	-	-	-	-
Sylhet	-	-	-	-	-	-	-	-	-	-
Dhaka	365	115	340	105	218	72	191	62	168	54
Faridpur	6455	1960	6210	1770	4242	1264	3778	1183	3861	1242
Jamalpur	90	30	90	30	68	19	68	20	69	20
Kishoreganj	175	80	165	75	53	17	53	18	54	18
Mymensingh	400	175	375	160	328	162	257	111	219	100
Tangail	70	20	65	20	50	17	20	06	21	06
Barisal	1470	405	1395	395	1492	353	1242	338	1282	427
Jessore	8100	2845	8555	3180	6425	2286	5083	1886	4665	1733
Khulna	330	85	295	75	261	81	188	63	193	62
Kushtia	3525	1090	3225	1060	1156	427	921	290	816	266
Patuakhali	3660	780	3585	740	3171	771	3182	882	2935	603
Bogra	75	25	80	30	66	24	69	27	73	28
Dinajpur	1400	540	1360	530	841	263	641	178	579	170
Pabna	700	250	690	240	367	134	323	111	300	114
Rajshahi	3575	1035	3615	1075	3342	989	3323	1078	5388	1957
Rangpur	570	185	560	180	469	159	431	151	4101	145
Total	**31450**	**9760**	**31100**	**9810**	**23101**	**7168**	**20206**	**6551**	**17850**	**5744**

Source: Online Year Book of Agricultural Statistics of Bangladesh, 2010.

Chickpea is commonly known as "gram" in our country. It belongs to the sub-family Papilionaceae under the family Leguminosae (Fabacae). The plant is small, much branched and annual herb. Leaves are an even-pinnate, alternate, stipulate, leaflet elliptic-ovate, dentate. Flowers are solitary auxiliary, small, bluish purple, on slender peduncle. Inflorescence is raceme with one or two flowers. Fruit is pod. The pods are large, elongated, slender, turgid sessile and two seeded. Seeds are obviated or subglobose, beaked.

Like other pulses, chickpea is also highly nutritious. splitted chickpea seeds are `used for the production of flavoured soups. In Bangladesh and some other countries of this sub-continent the splitted chickpea are used as "dahl". The percentage recovery of dahl is 66-80%. Chickpea powder obtained by grinding the seeds is called "beson" and used in food preparation, another powder form of the perched seed is called "chattu" is popular in our rural areas. Seed of the gram soaked in water is given to the player to make them strong. Chickpea seeds also used as boiled. It is a good food for invalids and infants. Its young pods are used as vegetables. Chickpea seeds contain essential amino acids like isoleucine, leucine, lysine, phenylalanine and valine (Karim and Fattah, 2006). The protein in chickpea is highly digestible (70-90%) (Williams and Singh, 1987). It's dried stem and husks are good source of animal foods (Rahman and Patrh, 1988).

Table 4: Nutritional components of chickpeas, mature seeds, cooked without salt
Nutritional value per 100 gm.

Energy	164 kcal	Pantothenic acid (Vit. B_5)	0.286 mg
Carbohydrates	27.42 gm	Vitamin B_6	0.139 mg
-Sugars	4.8 gm	Folate	172 µg
-Dietary fiber	7.6 gm	Vitamin B_{12}	0.0 µg
Fat	2.59 gm	Vitamin C	1.3 mg
-saturated	0.269 gm	Vitamin E	0.35 mg
-monounsaturated	0.583 gm	Vitamin K	4 µg
-polyunsaturated	1.1156 gm	Calcium	49 mg
Protein	8.86 gm	Iron	2.89 mg
Water	60.21 gm	Magnesium	48 mg
Vitamin A	1 µg	Phosphorus	168 mg
Thiamine (Vit. B_1)	0.116 mg	Potassium	291 mg
Riboflavin (Vit. B_2)	0.063 mg	Sodium	7 mg
Niacim (Vit. B_3)	0.526 mg	Zinc	1.53 mg

Source: USDA Nutrient Database

Chickpea is the most important leguminous plant and it is important as replenishes the soil nitrogen. It develops nodule on their roots in which nodule colonies (*Rhizobium sp.*) live in symbiosis with the plants. These bacteria have the capacity to fix atmospheric nitrogen into nitrates in soil and thus soil fertility is improved.

Such important crops are neglected and very few works have been done for the improvement of this crop in early days in our country. It is generally cultivated in Bangladesh as a low yielding rainfed rabi crop with poor filed management condition, whereas it has been cultivated extensively in Western Asia, Middle East and India. It has also achieved cosmopolitan distribution in Africa, Europe and America. At present some work to develop advanced lines of pulses has concentrated by the Bangladesh pulse research institute at Ishurdi in Pabana. Therefore, extensive research efforts are necessary for the improvement of chickpea in our country.

The necessity of self-sufficiency in food and foodstuff is vital for the economic wellbeing of a country. One way, this need could be satisfied by performing the extensive research work for the improvement of economically important plants that exist in the country. Bangladesh is agriculture based densely populated country; therefore, its economic and social progress depends on the development of the agriculture. In this regard grain legume research is very much important because it constitutes an important component in the farming system of the country and related directly with human and animal food nutrition. Among pulses chickpea has occupied a significant position in farming system of the northern zone of the country because of its various use in different human foodstuffs, in industry and also as animal feed.

The major aim of the national agriculture system is to increase the productivity and total production of major food crops including pulses. Plant breeders have been working incessantly to breed improved cultivars of various pulses. However not much success could be achieved in increasing the production

of different grain legumes in our country due to various technical reasons. Plant breeders are constantly seeking new sources of allelic variation to promote yields and improve its stability. For this in crop improvement programme improved methodologies for mutation induction and utilization of induced mutation are developed. These mutant varieties have contributed immensely in increasing the pulse production.

As all cultivated plants, the main objective of chickpea is to grow high yield and high quality crops. Improvement of yield is important in any breeding programme. Yield by itself is probably not an adequate criterion of economic value, because yield is quantitative in nature and is associated with other component characters. So the objectives of the present investigation are as follows:

1. To create heritable variation by means of irradiation, i.e mutational breeding and crossing so that selection criterion may be applied to choose well adapted lines
2. To test suitability of additive-dominance model
3. To estimate and compare genetic parameters such as gene effects and heritability and also heterosis for some traits in chickpea
4. To get better progeny lines by the application of G × E interaction model
5. To study variability, genotypic and phenotypic correlations, together with path-coefficient and to determine the discriminant function for the construction of a suitable selection index.

For detail investigation with the above objectives the whole work has been divided into following three parts:

Part I: Deals with the study of genetic control

Part II: Deals with the study of genotype-environment interaction

Part I: Deals with the study of variability, correlation, path-coefficients and selection index

PART I

GENETIC CONTROL

INTRODUCTION

At present, an understanding of genetic characteristics, determination of agronomic characters is a primary step for breeding studies. However, as for all cultivated plants so also for chickpea the main objective is to grow high yield and high quality crops. Since genotypic and environmental factors are components determining yield and quality in plants, the primary aim should be the determination of effects of genetic architecture in selection. The different types of gene actions are important in different crosses. The breeding strategy should therefore, be based on the gene action involved in that particular cross to get a desirable genotype.

The yield and yield contributing characters of chickpea and other crops are controlled by polygenes which have small effects and the task become difficult for the breeder. Here both the additive and non-additive gene action and interactions are found to be operative. In case of additive effect, parents do transmit their characters to their offspring and in non-additive, they do not. Crossing with additive genetic effect is beneficial. Most characters have additive effects. The other factor is the environmental effects. A variety may give more yields in a good year but less in another. While selecting a variety, it is important to minimize the environmental effects and maximize the genetic effects.

The development of high yielding chickpea cultivars is the major objective of this breeding programme. Knowledge of the genetic nature, magnitude of gene effects and their contribution to the control of quantitative traits is important in formulating an efficient breeding programme for chickpea genetic improvements.

Gene action is the magnitude of gene expression, causing heritable and non-heritable differences among individuals or populations. Fisher (1918) conceived that genetic variation in case of quantitative segregation may arise from three types of gene action, viz. (i) an additive (d) components describing the differences between two homozygous at any single locus, (ii) a dominance (h) component

arising from interaction of alleles of the same genes and (iii) an epistatic gene action between different genes. Based on some genetic and statistic assumptions he separated the genetic components of total variation and then partitioned it into three sub-components.

Mather (1949) and Hayman and Mather (1955) developed the scaling test and three-parameter model for estimation of the components of generation means. In model fitting, adequacy of scale must satisfy that genes are independent in action (no-non allelic interaction) and independent in distribution (no linkage) and also independence of heritable components from non-heritable ones. Hayman (1958) and Jinks and Jones (1958) gave six-parameter model for estimation of various genetic components including non-allelic interactions, viz. additive-additive, additive-dominance, dominance-additive and dominance-dominance.

The partitioning of genetic variance in intercrossed population would provide estimates of additive, dominance and epistatic effects. Since, Fisher's (1918) papers, many genetic models, which assume certain basic requirements, have been proposed for the estimation of gene effects. Most of the genetic models (Comstock and Robinson, 1948 and 1952; Hayman, 1954; Jinks, 1954; Mather, 1949) were developed to estimate the relative importance of additive and dominance gene effects. Epistatic gene effects were assumed to be negligible. Reports of Anderson and Kempthorne (1954), Gamble (1957), Hayman (1958) and Jinks (1954) indicated that epistatic gene effects are present in sufficient magnitude in quantitative characters preclude the assumption of negligible epistatic gene effects.

In chickpea, genetical work is a great problem. It is due to chickpea is a highly self pollinated crops. Works reported on the scaling test in various crops are scanty. Uddin (1983) and Shahid (1996) have done the scaling test in wheat. Khaleque (1975), Islam (1980) and Rahman (1984) have done the scaling test in rice, egg plant and eri silkworm, respectively. Yingxin and Xiangning (1998) and Abdallah *et al.*, (1999) reported the presence of both additive and non-additive genetic effect for yield of seed cotton. Using Griffing (1956) technique Subhan *et al.*, (2001) observed significant differences among hybrids and their parents for

yield of seed cotton per plant. In lentil Khodambashi *et al.* (2012) observed generation mean analysis using A, B, C and joint scaling tests indicated that additive, dominance and at least one of the epistatic effect were involved in the inheritance of the studied traits. Samad *et al.*, (2009) studied A, B and C scaling test and joint scaling test in blackgram. In pigeonpea Hooda *et al.* (2000) observed significant additive gene effect for plant height and 100-seed weight.

Heritability estimates along with the genetic advance are important selection parameters and normally more helpful in predicting the gain under selection than heritability estimates alone. However, heritability estimates are influenced by the type of genetic material, sample size, method of sampling, conduct of experiment, method of calculation and effect of linkage. Genetic advance which refers to the improvement in the mean genotypic value of selected individuals over the parental population is influenced by the genetic variability, heritability and selection intensity (Alza and Martinez, 1997; Sharma, 2003). High heritability was pointed by several researchers such as Aich *et al.* (2007), Esparza and Foster (1998), Ketata *et al.* (1976a) and Novoselovic *et al.* (2004) and Alam *et al.* (2004).

In fact the development of any plant breeding programme is dependant upon the existence of genetic variability. The efficiency of selection and expression of heterosis also largely depend upon the magnitude of genetic variability present in the plant population (Singh and Narayanan, 1993; Singh and Chaudhary, 1999). Heterosis or hybrid vigour is manifested as improved performance for F_1 hybrids generated by crossing two inbred parents. Inbreeding depression is usually defined as the lowered fitness or vigour of inbred individuals compared with their non-inbred counter parts.

Keeping this view in mind, the present investigation was undertaken to study the scaling test, estimation of gene effects, components of genetic variations, heritability, genetic advance, degree of dominance, number of effective factors, heterosis and inbreeding depression of yield and yield components in chickpea (*Cicer arietinum* L.)

REVIEW OF LITERATURE

Literatures in respect of genetic study of agronomical characters through single cross analysis in chickpea (*Cicer arietinum* L.) are scarce. In fact reports on chickpea are few and scattered. A few numbers of papers have been published dealing with the problem of genetic content of different quantitative characters on various leguminous crop plants. Therefore, review of literature was made on the problem of this crop as well as on the other crops also and described below:

East (1915) reported that the continuous variation in the segregating generation for a quantitative character is due to the both genetic and environmental effects.

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

The work of Fisher *et al.* (1932) influenced several investigators, such as Yates (1947), Comstock and Robinson (1948 and 1952), Mather (1949), Cavalli (1952), Anderson (1953), Burton (1951), Kempthorne (1954), Jinks (1954), Jinks and Jones (1958) and Peter and Frey (1966) to work on gene action and interactions in continuous variation and thus, most of the genetic models to study the continuous variation came into existence. Anderson and Kempthorne (1954) provided all the information about additive, dominance and digenic epistatic varition through six-parameter model.

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.

Hayman (1958) successfully separated additive and dominance effects from epistasis by using three and six-parameter models. He suggested that means of generation were influenced by epistasis, which might present in the form of

interaction with additive effect, with dominant effect or with both additive and dominant effects.

Johanson *et al.* (1966) studied F_1s, back crosses and segregating generations of a cross between short varieties. They found that earliness and kernel weight was controlled by a few genes. Heritability estimates for ear length, maturity period and kernel weight were high indicating that selection for this characters in the F_3 generation could be effective.

Ketata *et al.* (1976b) studied the inheritance of eight agronomic characters in a winter wheat cross. Narrow sense heritability estimates were found to be very high for heading date, moderately high for kernel weight and plant height and moderate for number of tillers per plant and low for spikelet per ear, kernel per spikelet and grain yield, duplicate epistatis was detected for heading date and grain yield suggesting that difficulty would be uncounted in selecting for earlier maturity or higher yield in the cross.

Sharma and Singh (1976) reported that both additive and non-additive components of genetic variances were highly significant for plant height and ear length in all the populations of F_1 generations of wheat. Magnitude of additive components was higher than that of non-additive component.

Gutierrez and Singh (1985) studied the heterosis and inbreeding depression in 13 crosses involving 10 dry bush bean (*Phaseolus vulgaris* L.) lines and varieties for days to maturity, pods per plant, 100-seed weight, seeds per pod, and bean yield. Six crosses showed positive heterosis (27.8 - 47.3%) over the mid-parent value for bean yield. Parents in each of these heterotic crosses differed for growth habit, seed size and geographical origin. But none of the F_1 hybrids yield significantly better than the highest yielding parental line. None of the crosses showed heterosis for pods per plant. All significant heterotic values for seeds per pod were negative. For 100-seed weight three crosses, both parents of which had small seeds, showed positive heterosis but one cross which had a significant

negative value had one parent with small seeds and the one with large seeds. One heterotic cross each for bean yield and 100-seed weight showed subsequent inbreeding depression. But five crosses for bean yield, and one cross for 100-seed weight showing positive heterosis did not exhibit reduction due to inbreeding. Also, some crosses which either had non-significant or negative heterotic values for bean yield and yield components showed positive effects of inbreeding, i.e. the F_2 outperformed the corresponding F_1 hybrids. Possible causes for these phenomena are discussed.

Kidambi *et al.* (1988) conducted a study to investigate the genetic inheritance of morpho-physiological leaf traits in chickpea (*Cicer arietinum* L.). The experimental materials comprised six generations, viz., two inbred parents, 'T88' and 'Bold Seeded', having contrasting leaf traits, and their derived F_1, F_2 and backcross of F_1 to either parent (B_1 and B_2). The experiment was following randomized complete block design with three replications. Genetic parameters were estimated by generation mean analysis using all the six generations. Data were collected on individual plants within each family just before flowering on leaflet area (LA), number of leaflets per leaf (LL), rachis length (RL), and leaflet density (LD), which was calculated as number of leaflets per unit length of rachis. A simple additive-dominance model was found to be adequate to describe the inheritance of LL and LA, while dominance × dominance (i.e. [l]) and additive × dominance (i.e. [i]) interactions were also significant for RL and LD, respectively. Improvement or seed yield per plant may result from selection for LA by improving both RL and LL. Leaflet area may be included in the ongoing selection schemes, as a supplementary trait to increase the speed of improvement in seed yield per plant. Lanceolate leaflet shape was observed to be monogenically dominant over obovate leaflet shape, and segregated independently from purple/white flower color.

Cheema *et al.* (1990) studied heterosis and inbreeding depression for yield components in six hybrids of four parents. Significant heterosis and inbreeding depression were estimated for trait studied. The maximum heterosis of 111.6%

was observed for yield in hybrid DM16-5-1 × Kashmer Basmati. Crosses combination of Basmati 370 × DM 16-5-1 and DM16-5-1 × DM107-4 showed highly significant heterosis with a non-significant inbreeding depression. The traits of other hybrids were also discussed.

Singh *et al.* (1993) studied P_1, P_2, F_1, F_2, BC_1 and BC_2 of six intervarietal crosses of chickpea. They recorded both additive and non-additive gene effects for days to flower, plant height, primary branches per plant, secondary branches per plant, pods per plant, seeds per plant, 100-seed weight and yield per plant.

Kumar and Singh (1995) studied the inheritance of seed size in chickpea (*Cicer arietinum* L.) in two desi × desi crosses, ICCV 10 × ICC 4958 and ICCV × K850, using generation means of parents, F_1, F_2 and both the backcrosses. Small seed size was partially dominant over large seed size. Generation mean analysis showed that the major contribution to genetic variation in these crosses came from additive gene effects, indicating that selection for seed size in early generation should be effective. However, non-additive gene action (dominance and additive × dominance interaction) also affected to a small extent the expression of this character. The estimates of narrow-sense heritability and the expected genetic gain were high. The minimum number of effective factors controlling the seed size varied from 1.33 to 2.19.

Shahid (1996) studied gene action with some quantitative characters in wheat. He did the scaling test and observed that epistasis was operative in almost all the cases and indicated the inadequacy of additive-dominance model. Additive dominance model was found to be adequate to explain the gene action for spikelet per ear, grains per ear and fertile tillers per plants only in C_1. Heritability both in broad and narrow senses were low to moderate in most of the cases, but high narrow sense heritabilities were observed in C_1, C_5 and C_6 for DH in C_1, C_5 C_6 and C_7 to GY in C_5 C_6 and C_7 for FT and SE. Significant heterotic performances in most of the traits in all crosses indicated good prospect of hybrid wheat. Significant positive better parent heterotic performances were observed for PH in

all the crosses except C_2, for DH in C_1, C_2, C_3 and C_6 for FT in C_5 and C_6, for S/E in C_2 and C_5 and for G/E ear in C_5.

Rahman and Saad (2000) investigated inheritance of yield and yield contributing characters by using generation mean analysis, utilizing the mean of six basic populations viz, P_1, P_2, F_1, F_2, BC_1 and BC_2 in four crosses of *Vigna sesquipedalis*. The analysis reiterated that the importance of dominance (h) gene effects for pod yield per plant and pods per plant as compared to additive (d) gene effects. However, significant and positive additive effects were noticed for pod yield per plant, pods per plant, pod weight and seed weight in different crosses. The three types of gene interactions (additive, dominance and epistasis) were significantly involved for pods per plant in cross KU7 × KU8. Among the digenic epistatic interactions, both additive × additive (i) and dominance × dominance (l) contributed more for pod yield per plant and pods per plant, however, it varied among crosses. Populations having earliness can be developed as indicated by reducing dominance effects. pedigree selection and heterosis breeding is suggested to exploit the fixable and non-fixable components of variation respectively in *Vigna sesquipedalis*.

Abdullah *et al.* (2002) carried out an experiment on 'Heterosis study of certain important traits in wheat'. They studied heterosis in ten crosses of bread wheat involving three varieties, Chawal-86, PAK-81 and M. H. 97 and two lines 9068 and 243-1 and found that highly significant genetic variability was present in the experimental material for the trait under study except number of tillers per plant and spike length. Most of the crosses showed significant heterosis over mid and better parents for various characters. The crosses 9068 × 243-1, Chakwal-86 × 243-1 and PAK-81 × 243-1 may be considered for selection as hybrid or pure line wheat varieties after achieving desired homozygosity.

Gayen *et al.* (2002) studied the genetic variability and analysis of yield components in mungbean. They observed that high heritability and high or moderate genetic advance for all the characters that he studied except number of

seed per pod. Seed yield was significantly and positively related with cluster per plant, number of pods per plant and pod length.

Hasib *el al.* (2002) studied the gene effects for grain yield and its components including grain characters using parental, F_1, F_2, BC_1 and BC_2 generations in five crosses of aromatic rice involving induced mutants and 'basmati' varieties. Epistasis was noticed in the majority of characters for all crosses. Additive and dominance effects had major role in most of the crosses for the expression of plant height, days of flowering, panicle number per plant, panicle length, spikelet fertility per plant, grain length, grain length/breadth ratio, test weight and grain yield per plant. Among interactions, additive × additive and dominance × dominance effects were almost equally important, while additive × dominance was less important than the other genetic effects for the inheritance of traits. Duplicate type of epistasis was observed in most of the traits studied. In general, both additive and non-additive gene actions were important for the expression of almost all the characters studied. Biparental mating, recurrent selection and diallel selective mating system could be used to obtain desirable recombination like reduced height high yielding aromatic plants with long slender grains similar to 'basmati' type.

Iqbal and Nadeem (2003) performed an experiment on generation mean analysis for seed cotton yield and number of sympodial branches per plant in cotton (*Gossypium hirsutum* L.). Genic effect for yield seed cotton and number of sympodial branches per plant were estimated from two upland cotton crosses through generation mean analysis from six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2). They found that five crosses over mid and four crosses over better parent showed significant heterosis for number of sympodial branches per plant, whereas only four crosses exhibited inbreeding depression for this character. The generation mean analysis advocates the presence of additive gene action in crosses i. e., S-12 × S-14, S-12 × Albacala (69)11, LRA-5166 × S-12 and LRA-5166 × S-14 for number of sympodial branches per plant. All the crosses exhibited heterosis in desire direction over mid and better parents except Albacala (69)11 × S-12 for

yield of seed cotton per plant. Significant marked inbreeding depression from F_1 and F_2 generations were observed in all the crosses except S-14 × LRA-5166 for yield of seed cotton per plant. Maximum degree of dominance was associated with S-14 × S12. It reflected the presence of maximum number of dominance genes, which need to be the cause of significant heterosis in this combination. Most recessive allels for seed cotton yield accumulated Albacala (69)11 × S-12, which expressed least positive degree of dominance. The scaling test revealed involvement of epistasis in all the crosses, except S-14 × LRA-5166 for yield seed cotton per plant. The rest of all the crosses were predominantly under non-additive genetic control except S-14 × LRA5166 for yield of seed cotton per plant, hence delayed selection will be fruitful in these crosses.

The genetic basis of heterosis was studied by Alam *et al.* (2004) through mid-parent, standard variety and better parent for 11 quantitative traits in 17 parental lines and their 10 selected hybrids in rice (*Oryza sativa* L.). The characters were plant height, days to flag leaf initiation, days to first panicle initiation, days to 100% flowering, panicle length, flag leaf length, days to maturity, number of fertile spikelet/panicle, number of effective tillers/hill, grain yield/10-hill, and 1000-grain weight. In general the hybrids performed significantly better than the respective parents. Significant heterosis was observed for most of the studied characters. Among the 10 hybrids, four hybrids viz., 17A×45R, 25A×37R, 27A×39R, 31A×47R, and 35A×47R showed highest heterosis in 10-hill grain yield/10-hill. Inbreeding depression of F_2 progeny was also studied for 11 characters of 10 hybrids. Both positive and negative inbreeding depressions were found in many crosses for the studied characters, but none was found significant. Selection of good parents was found to be the most important for developing high yielding hybrid rice varieties.

Khattak *et al.* (2004b) assessed the nature of gene action for days to flowering, plant height at different growth stages, synchrony in pod maturity and indeterminate plant growth habit in two sets of crosses involving four parents through generation mean analysis in mungbean. The mean data of six populations

(both parents, F_1, BC_1, BC_2 and F_2) were subjected to joint scaling test. They used six-parameter model in the presence of epistasis to detect all types of gene effects. They observed from their analysis that most of the traits appeared to be complex in the expression of gene effects in both the crosses. Both additive (d) and dominant (h) gene effects were important in both the crosses for all the traits examined except days to first flower and first pod maturity in ML-5 × NM 54, where dominant gene effects were non-significant. The days to 90% pods maturity and plant height at first flower in case of 6601 × NM 92, and days to first pod maturity and plant height at first flower in ML-5 × NM 54 cross had showed no digenic interactions. The digenic interactions i.e., additive x additive (i), additive x dominance (j), and dominance x dominance (l) played an important role in the expression of all those traits which showed complex gene effects for their inheritance. The biparental approach is suggested for the exploitation of the complex inherited traits particularly for improved synchrony in pod maturity and determinate growth habit in mungbean.

Novoselovic *et al.* (2004) estimated genetic effect and genetic variability for some quantitative traits of two winter wheat crosses (Soissons/Zitarka and Soissons/Sana) by generation mean analysis. In most cases a diagenic epistatic model was sufficient to explain variation in generation means. The additive-dominance model was adequate for plant height and grain weight per spike of the longest clum. In two cases (grain yield per plant and single grain weight) these models failed to explain variation in generation means. The estimated value of narrow sense heritability (h^2_n) varied for plant height (54 – 81%), number of heads per plant (9 - 76 %), number of grains per spike (11 – 98%), grain weight per spike (23 – 73%), grain yield per plant (21 – 78%) and single grain weight (49.7 – 72%).

Veeramani *et al.* (2005) worked on genetic variability, heritability and genetic advance analysis in segregating generation of blackgram (*Vigna mungo* L. Hppper). Here from the heritability estimation high heritability coupled with high genetic advance as percentage of mean were conserved for plant height, number of branches per plant, number of clusters per plant and number of pods per plant.

Number of pods per cluster recorded high heritability and high genetic advance in LBG/LBG 20, whereas high heritability with high genetic advance was observed for length in LBG 645/LBG20.

Aliyu (2006) conducted generation mean analysis between a cowpea variety IT82D-716 and two accessions of *Vigna rhomboidea* to investigate the gene effects and heritability for incorporating pubescence into cultivated cowpea from *V. rhomboidea*. The additive-dominance model that was adopted in the analysis was observed to sufficiently explain the mode of inheritance of leaf and stem pubescence with the additive effect being more important than the dominance effect. A six-parameter model with epistatic gene interactions was adequate for explaining the inheritance of pod pubescence. Heritability estimates, in the narrow sense were high for pubescence density and pubescence length. Inheritance of pubescence in crosses between cowpea and *V. rhomboidea* was governed by one and two groups of genes. Significant and higher additive gene effects and high heritability suggest that backcross selection schemes should be responsive in the development of pubescent cowpea lines.

Adeniji *et al.* (2007) carried out a work on Genetic studies on seed yield of West African okra [*Abelmoschus caillei* (A. Chev.) Stevels]. They considered F_1 hybrids of eight accessions of West African okra to produce F_2 seeds and backcross generations. Field evaluation of six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) from five crosses was carried out in a randomized complete block design with three replications. The A, B, and C scaling tests were not significant for 100 seed weight, while significant A, B, or C scaling test for seed yield per plant was recorded. Additive gene effects [d] appeared to have contributed immensely to the inheritance of both characters. However, a non-significant interaction (i, j, l) for 100 seed weight corroborates with the results of individual A, B, and C scaling tests. A duplicate epitasis (Acc5 × Acc4) implied difficulty in evolving improved varieties. Estimates of genetic effects confirmed the preponderance of additive gene effects for 100 seed weight and seed yield per plant. High narrow sense

heritability and genetic advance indicate the possibility of substantial improvement in seed yield.

Bhardwaj and Sandhu (2007) estimated the gene action operating in the inheritance of yield and its components by using generation mean analysis in two chickpea crosses. Six basic generations viz., P_1, P_2, F_1, BC_1, BC_2 and F_2 of two crosses, namely GNG 469 x ICCV 93929 (C1) and PBG 5 x ICCV 93929 (C2) were studied. Scaling tests A, B, C and Joint Scaling Test were applied to test the adequacy of additive-dominance model for eleven agronomic traits. Significant C2 values indicated higher order of interactions for all traits except grain yield/plant for C2. Generally, the dominance component was higher in magnitude than additive component except for days to maturity (C1), pods/plant (both crosses), grain yield/plant (C2). Duplicate type of epistasis was present in most of the cases. From their investigation they concluded that additive, dominance and epistatic gene effects contribute significantly to the inheritance of various component characters in chickpea and the improvement can be sought by bulk method followed by modified pedigree method.

Toklu and Yagbasanlar (2007) studied on genetic analysis of kernel size and kernel weight in bread wheat (*T. aestivum* L.). They set the experiment with reciprocal crosses in six combinations to estimate genetic parameters, heterosis and heritability for the kernel size and kernel weight of three bread wheat genotypes 84 CZT 04 (large-kerneled), Panda (medium kerneled) and Bow S/CrowS (small-kerneled). Means of the six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) were used to estimate genetic parameters. Generation mean analyses of genetic effects indicated that large kernel ratio is dominant over thin kernel and high kernel weight is dominant over low. Heterosis ranged from 0.03 to 45.53% and 0.63 to 15.12% for large kernel ratio and kernel weight, respectively. Higher heterosis were detected in the crosses where large-kerneled parent used as female. Narrow-sense heritability estimates ranged from 60 to 99% for large kernel ratio and 23 to 100% for kernel weight. Additive (d) and dominance (h) effects were

more consistent and important in determining large kernel ratio and also epistatic gene action is effective for kernel weight.

Farshadfar *et al.* (2008) studied the inheritance and genetic analysis of drought tolerance indicators with six generations of F_1, F_2, BC_1 and BC_2 of the cross Hashem cultivar × ICCV96029 using generation mean analysis in chickpea. Genetic variation was found for grain yield, biological yield, no. of pod per plant, no. of seed per plant, earliness and proline content. High heterosis was observed in the F_1 hybrid for grain yield, biological yield, harvest index, no. of pod per plant and no. of seed per plant. Genetic analysis indicated dominance in the inheritance of grain yield, biological yield, harvest index, seed weight and no. of seed per plant, while over dominance gene action for no. of pod per plant, earliness and proline content. Moderate narrow-sense heritability estimates were observed for biological yield, harvest index, seed weight, no. of seed per plant and proline content. Moderate genetic advance for grain yield and proline content indicated that direct and indirect selection through correlated response could be effective. The joint scaling test revealed additive × dominance = [j] for grain yield, biological yield and proline content, while duplicate epistasis (additive × dominance = [j] and dominance × dominance = [l]) were shown for no. of pod per plant and no. of seed per plant. Since several important characters are influenced by dominance and non-allelic gene interaction, it is advisable to delay selection to later generation with increased homozygosity.

Deb and Khaleque (2009) studied nine agronomic characters such as days of first flower (DFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), plant height at maximum flower (PHMF), plant weight just after harvest (PWH), number of pods per plant (NPd/P), pod weight per plant (PdW/P), number of seeds per plant (NS/P) and seed weight per plant (SW/P) of P_1, P_2, F_1, F_2 and F_3 generations of chickpea (*Cicer arietinum* L.). In their study, scaling test revealed that in cross 1 for NPBFF, PWH, NPd/P, PdW/P, NS/P, in cross 2 for NPBFF, PWH, and PdW/P and in cross 3 for PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P additive-dominance model was found to be

adequate. Analysis of components of variation revealed that dominance component (H) expressed positive values in 11 cases and negative in 16 cases, whereas additive component (D) exhibited positive values in 17 cases and negative in 10 cases. Genetic advance (GA) and genetic advance expressed as percentage of mean (GA%) were low in majority of the characters and crosses. Heritabiliy both in broad (h^2_b) and narrow (h^2_n) senses were found to be low in majority cases. But in some cases these value were high.

Naveed *et al.* (2009) carried out the field experiments to assess the genetic potential of okra genotypes for drought tolerance through breeding and selection in 6 generations of 4 crosses between pairs of genotypes with a degree of tolerance to drought. They observed that narrow sense heritability and genetic advance varied across crosses, traits and stress conditions. For fruit yield, narrow sense heritability and genetic advance were high under non-stress condition as compared to drought, which indicated that direct selection of fruit yield would only be feasible under non-stress conditions. They found among the agronomic traits, although number of pods per plant had shown good narrow sense heritability and genetic advance under drought, yet leaf water potential appeared to be better indicator for selection criteria owning to higher heritability under drought. Among the crosses, Sanam × Arka Anamika appeared elite in terms of narrow sense heritability and genetic gain compared with other crosses, with highest fruit yield and pod number per plant under both conditions. They thought that there has a chance to find stress tolerant breeding material in segregating populations of this cross would be promising.

The genetic control of soluble protein in root nodules and seeds per plant in four lines of blackgram (*Vigna mungo* (L.) Hepper) in two different crosses (cross I: 5×21 & cross II: 17×20) were studied by Samad *et al.* (2009) separately. They found that additive-dominance relationships for soluble protein in root nodules in cross II and also for soluble protein in seeds in both of the crosses were non-significant. Potence values were significant in all the cases except for soluble protein in seeds in cross I. Components of variation, D and H for both of the characters and crosses expressed positive and negative values. Negative sign was

due to large sampling variation and genotype-environmental interaction. Dominance ratio showed complete to over dominance in negative direction, which indicated dominance towards decreasing parent. The narrow sense heritability, being high mostly, indicated that selection might be fruitful for soluble protein in nodules in cross I and for soluble protein in seeds in cross II. Genetic advance (GA) was negative in most of the cases, but in some cases it showed positive genetic advance. Positive genetic advance in narrow sense for the characters root nodules in cross I and for the same in seeds in cross II accompanied by high narrow sense heritability was obtained. This indicated that selection of soluble protein in nodules and seeds in these crosses would likely be fruitful in an advance generations.

Bnejdi and El-Gazzah (2010) studied the epistasis and genetype-environment interaction of grain yield content in durum wheat and evaluated parental, F_1, F_2, BC_1 and BC_2 generations of four crosses including four cultivars of durum wheat at two site of Tunisia. A three-parameter model was found inadequate in all cases except crosses chili × cocorit 71 at site Sidi Thabet and inrat 69 × karim at both sites. In most cases a digenic epistatic model was sufficient to explain variation in generation means. Dominance effects (h) and additive × additive epistasis (i) (when significant) were more important than additive (d) effects and other epistatic components. Considering the genotype-environment interaction, the non-interactive model (m, d, h, e) was found adequate. Additive variance was higher than environmental variance in three crosses at both sites. The estimated values of narrow-sense heritability were dependant upon the cross and the sites and were 0 %-85 %. The result indicated that appropriate choice of environment and selection in later generations would increase grain protein content in durum wheat.

Eshghi and Akhundova (2010) estimated the gene effects for important quantitative traits of two hulless barley crosses (ICNBF93-369 × ICNBF-582 and SB91925 × ICB-102607) by generation mean and variance analysis. Three-parameter model [m, d, j] provided the best fit for plant height and yield per plant in cross SB91925 × ICB-102607 and number of tillers and days to maturity in both

crosses. Five-parameter model [m, d, h, j, l] was observed for plant height and grain yield per plant in cross ICNBF93-369 × ICNBF-582 and number of grain per spike in cross SB91925 × ICB-102607 and five parameter model was adequate for number of grain per spike in cross ICNBF93-369 × ICNBF-582. Genetic variation analysis showed that additive gene action in inheritance of plant height, number of tillers and days to maturity. Although in cross ICNBF93-369 × ICNBF-582 the dominance effects had a greater share. In cross SB91925 × ICB-102607 the additive effects played major role in the inheritance of grain yield per plant, since narrow sense heritability of this trait was low.

Nahar *et al.* (2010) carried out the genetic study of six agronomic characters namely shoot weight (SHW), root weight (RW), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP) and seed weight per plant (SWPP) in two crosses viz. cross I (line-21×line-17) and cross II (line-21×line-20) between three lines of blackgram. They found that in Mather's scaling test, A, B and C were non-significant in most of the cases. The potence values were observed non-significant for all the characters, except for NPdPP in cross II where it was significant. In the Joint scaling test, the non-significant χ^2 values were found in cross I for SHW, PdWPP and SWPP. They also found non-significant χ^2 in RW in both of the crosses. Non-significant χ^2 values indicated that the presence of only additive-dominance relationship in these characters. For estimates of the components of variation, D and H for all the characters in both of the crosses expressed negative values, except for NPdPP and NSPP where D were positive. In almost all the cases over dominance was found in negative direction. In these materials due to the low and negative genetic components of variation, heritability and genetic advance were found to be low and negative. However, high and moderate heritability with 77% and 35% for NPdPP and NSPP, respectively were found in cross II. Selection practices may be fruitful with these characters and crosses as they also showed positive and moderate genetic advance.

Samineni *et al.* (2011) studied on estimation of genetic components of variation for salt tolerance in chickpea using the generation mean analysis. They inter-crossed two chickpea land races, ICC 6263 (salt sensitive) and ICC 1431 (salt tolerant) and studied gene action involved in different agronomic traits under saline and control conditions. The generation mean analysis in six populations, viz. P_1, P_2, F_1, F_2, BC_1 and BC_2, revealed significant gene interactions for days to flowering, days to maturity, and stem Na^+ and K^+ concentrations in control and saline treatments, as well as for 100-seed weight under salinity. Seed yield, pods per plant, seeds per plant, and stem Cl^- concentration were controlled by additive effects under saline conditions. Broad-sense heritability values (>0.5) for most traits were generally higher in saline than in control conditions, whereas the narrow-sense heritability values for yield traits, and stem in Na and K concentrations, were lower in saline than control conditions. The influence of the sensitive parent was higher on the expression of different traits; the additive and dominant genes acted in opposite directions which led to lower heritability estimates in early generations. These results indicate that selection for yield under salinity would be more effective in later filial generations after gene fixation.

Thangavel and Thirugnanakumar (2011) studied six families P_1, P_2, F_1, F_2, B_1 and B_2 of six crosses for five metric traits. The results suggested the presence of additive and dominance gene effects along with epistatic interaction in almost all the crosses indicated the importance of both additive and non-additive gene action in the expression of all the five characters of interest. Duplicate dominant epistasis was prevalent in most of the cases.

Khodambashi *et al.* (2012) studied generation mean analysis for grain yield and its related traits in lentil. In order to estimate heritability and gene action for grain yield and its related traits in lentil. They evaluated six basic generations in a randomized complete block design with three replications in a field experiment. Besides, seed yield per plant, plant height, pod length, and 100-seed weight, the number of pods per plant, primary branches, clusters per plant, nodes per main stem, secondary branches, and the number of seeds per pod were recorded.

Generation mean analysis using A, B, C and joint scaling tests indicated that additive [a], dominance [d] and at least one of the epistatic effect (additive × additive [aa], additive × dominance [ad] and dominance × dominance [dd]) were involved in the inheritance of the studied traits. However, simple additive-dominance model was sufficient only for pod length. Significant dominance [d] and dominance × dominance [dd] interactions with opposite sign indicated duplicate epistasis for all traits except pod length. Narrow-sense heritability was low for seed yield per plant, pod length, number of seeds per pod and 100-seed weight and moderate for other traits. Average dominance ratio was more than unity for seed yield per plant, number of primary and secondary branches, pod length, and 100-seed weight, which showed the high importance of dominance gene effect in control of these traits. Due to the presence of greater non-additive gene effects combined with low narrow-sense heritability, selection for almost all of the studied traits in this cross, especially in early generations, would be complex in conventional methods.

MATERIALS AND MATHODS

A. MATERIALS

For this experiment chickpea (*Cicer arietinum* L.) was taken as materials. The seeds of eight varieties BARI Chola seeds were collected from BARI, Regional Agriculture Station, Ishurdi, Pabna.

Selected lines of chickpea were irradiated with irradiation source Co^{60} at the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, on November 8, 2007. The radiation doses are A-20Kr (D_A), B-30Kr (D_B), C-40Kr (D_C) and control D_0

Table 5: Eight chickpea lines with four doses.

Serial No.	Line with Doses	Serial No.	Line with Doses
1	1A-20Kr 1B-30Kr 1C-40Kr 1D-control	5	5A-20Kr 5B-30Kr 5C-40Kr 5D-control
2	2A-20Kr 2B-30Kr 2C-40Kr 2D-control	6	6A-20Kr 6B-30Kr 6C-40Kr 6D-control
3	3A-20Kr 3B-30Kr 3C-40Kr 3D-control	7	7A-20Kr 7B-30Kr 7C-40Kr 7D-control
4	3A-20Kr 3B-30Kr 3C-40Kr 3D-control	8	8A-20Kr 8B-30Kr 8C-40Kr 8D-control

Eight lines of chickpea irradiated with four doses were taken for cross programme. Finally, five single crosses obtained in this way were considered for analysis between the selected parents. The selected five crosses are given in table 6.

Table 6: Five single crosses of chickpea.

Serial No.	P_1 ♀	P_2 ♂	F_1	F_2	B_1	B_2
1.	1A	3A	1A × 3A	1A × 3A	1A × (1A × 3A)	3A × (1A × 3A)
2.	2C	4C	2C × 4C	2C × 4C	2C × (2C × 4C)	4C × (2C × 4C)
3	4C	3C	4C × 3C	4C × 3C	4C × (4C × 3C)	3C × (4C × 3C)
4.	4A	7B	4A × 7B	4A × 7B	4A × (4A × 7B)	7B × (4A × 7B)
5.	5A	6A	5A × 6A	5A × 6A	5A × (5A × 6A)	6A × (5A × 6A)

B. METHODS

For the ease of experiment and analyses of the data the present work are divided into the following sub heads:

1. Collection and Irradiation of the Experimental Seeds;
2. Preparation of the Experimental Seeds;
3. Preparation of the Experimental Field;
4. Design of the Experimental Field;
5. Sowing of Seeds and Raising of the Seedlings;
6. Maintenance of the Experimental Field;
7. Collection of Data and
8. Techniques of Analyses.

1. Collection and Irradiation of the Experimental Seeds

Eight lines of BARI chola seeds were collected from Regional Agriculture Research Station, Ishurdi, Pabna, Bangladesh. Selected lines of chickpea were irradiated with irradiation source of Co^{60} at the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, on November 8, 2007. The radiation doses are A-20Kr, B-30Kr, C-40Kr and D_0.

2. Preparation of the Experimental Seeds

Irradiated seeds were sown in the field and plants were raised. At flowering stage, hybridization (to raise F_1 seeds) was done. Hybridization is the process of intercrossing between individuals of different lines or genetically divergent individuals from the same species. Offspring produced by hybridization may be fertile, partially fertile, or sterile. The hybridization consists of emasculation and artificial pollination. The process of emasculation and crossing in Chickpea is narrated below:

Materials required: Fine pointed scissors (straight and curved), pointed forceps (straight and curved), hand lens, needles (pointed and curved), camel hair brush, watch glass, scalpels, sticks, threads, pins, jems clips, labels, a small stopper bottle with 95% alcohol , cotton, transparent paper bags and a field note book.

Selection of buds for emasculation: Buds that are likely to be in anthesis after one or two days are selected for emasculation. In such a bud (hooded bud), the anthers are not yellow.

Method of emasculation: The bud to be emasculated should be held gently at the base with the thumb and fore finger. The frontal sepal was snipped off and the keel petal was pushed downwards by slitting it with a fine-pointed forceps to expose the anthers. The anthers were then removed and counted. Then it was checked with the help of a lens to ensure that no anthers were left in the flower. The pedicel, style, and stigma are fragile. Therefore, care must be taken not to damage these parts during emasculation. A coloured cotton thread was tied loosely around the pedicel of the emasculated flower for identification. The emasculated flowers were usually covered with a setting bag to prevent cross-pollination.

Pollination: Singh and Auckland (1975) reported that at ICRISAT Asia Center, Patancheru, India, pollination can be done at any time between 0800 and 1700 h. In this experiment pollination time is in between 10.00 to 11.30 (A.M.). Collected pollen from matured anther dusted on the stigma of emasculated flowers. After

pollination, the transparent paper bag was put on the pollinated flower. The date of pollination was noted on the label already given to the emasculated flower. The cross number and other particulars were also noted on a field notebook. After 2 to 3 days of pollination, the bag was removed and the plant was kept under careful observation. The pod with the label was collected when it was fully matured.

3. Preparation of the Experimental Field

The experimental field was on the north-western side of the third Science Building of the University of Rajshahi. The experiment was conducted during the Rabi crop season of 2009-2010. The experimental field was ploughed six times repeatedly. Weeds were removed completely before layout of the field and sowing of the seeds. The field was pulverized and leveled properly. No chemical fertilizer was used before or after sowing of seeds. As the experimental field was sufficiently moist, no irrigation was given before sowing of the seeds. Thus prepared, the experimental field was ready for sowing of the seeds.

4. Design of the Experimental Field

Layout of the experimental field and trial of the P_1, P_2, F_1, F_2, B_1 and B_2 generations was conducted under randomized complete block design.

5. Sowing of Seeds and Raising of the Seedlings

The seeds of F_1, F_2, B_1 and B_2 along with their parents were sown on the 9th November 2009. Different rows with five hills were considered for both individual lines and generations. Seeds of the parents and different generations derived from them were sown randomly in different small plots. The seeds were germinated and seedlings came out from the soil within 5-7 days. Fungicides were sprayed at an interval of one week to keep the normal growth of the plants.

6. Maintenance of the Experimental Field

At the seedling stage, the weeds were removed from the field. The insecticides were sprayed whenever it was necessary. The excess seedlings were removed from the field when the seedlings were 8-9 inches in height.

7. Collection of Data

The data of eleven quantitative characters were collected on individual plant basis. The measurement of a character was done following C.G.S system. The eleven characters measured, are as follows:

a.) Days to maximum flower (DMF);

b.) Number of primary branches at maximum flower (NPBMF);

c.) Number of secondary branches at maximum flower (NSBMF);

d.) Plant height at maximum flower (PHMF);

e.) Plant weight after fully dry (PWFD);

f.) Root weight after fully dry (RWFD);

g.) Number of pods per plant (NPPP);

h.) Pod weight per plant (PdWPP);

i.) Number of seeds per plant (NSPP);

j.) 1000- seed weight (1000-SW) and

k.) Seed weight per plant (SWPP)

8. Techniques of analyses of data

The colleted data were analyzed following biometrical technique as suggested by Mather (1949) based on the mathematical model of Fisher *et al.* (1932) and those of Lush (1949), Cavalli (1952), Warner (1952), Hayman and Mather (1955), Mather and Jinks (1971). The techniques that have been used are described in the following sub-heads:

a) Mean

The arithmetic mean is the "standard" average, often simply called the "mean". The mean is the arithmetic average of a set of values, or distribution. In case of this study, the mean was calculated as follows:

$$\text{Mean } (\overline{X}) = \sum_{i=1}^{n} X/n$$

Where, X = Value of individual observation and

n = Total no. of observations per generation.

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

$\sum$ = Summation

b) Standard deviation

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

$$S = \sqrt{S^2}$$

Where,

S = Standard deviation

S^2 = Variance

c) Standard error of mean

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. The standard error of mean could be determined as follows:

I. $S_{\bar{x}} = \frac{S}{\sqrt{n}}$ Where, $S_{\bar{x}}$ = Standard error of mean

II. $S_{\bar{x}} = \sqrt{S^2/n}$ S = Standard deviation

n = Total number of individuals.

S^2 = Variance

d) Variance

Analysis of Variance (ANOVA) is an important method of statistics. Variance is a measure of dispersion of a population or sample. So, the analysis of variance is done for testing the significant differences among the population or sample. Variances for the six generations *i e*, P_1, P_2, F_1, F_2, B_1 and B_2 carried out for the eleven characters in five crosses of chickpea.

I. Variance $(S^2) = \frac{\sum x_i^2 - (\sum x_i)^2/n}{n-1}$

II. Variance of mean = S^2/n

Where,

x_i = the individual reading recorded on each of the plants

n = the total number of observations

$\sum$ = Summation

n-1 = degrees of freedom

i = 1, 2, 3... n

The variances between sources such as replicates (r) and within (w) were analyzed in the present study. They are shown in table 7.

Structures of ANOVA for the estimation and significant test of two items in P_1, P_2, F_1, F_2, B_1 and B_2.

Item	Degrees of freedom (df)	Sum of square (SS)	Mean sum of square (MS)	Variance Ratio (VR)
Replicates	(r-1)	SS_r	$\frac{SS_r}{(r-1)} = MS_r$	MS_r / MS_{wi}
Within	2(s-1)	SS_{wi}	$\frac{SS_w}{2(s-1)} = MS_w$	

Where,

s = number of plants per row

r = number of replications

Variance analysis is a measure of dispersion of a population. In this study variance and variance of mean were done over the observation numbers of P_1, P_2, F_1, F_2, B_1 and B_2 generations.

e) Analysis of components of mean

i) Mather's scaling test:

Adequacy of scale must satisfy two conditions namely, additively of gene effects and independence of heritable components from non-heritable ones. The test of first condition provides information regarding absence or presence of gene interactions. The test of adequacy of scales is important because in most of the cases the estimation of additive and dominance components of variances is made assuming the gene interaction. Mather (1949) and Hayman and Mather (1955) gave following four tests for scale effects:

$$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1$$

$$B = 2\bar{B}_2 - \bar{P}_1 - \bar{F}_1$$

$$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

Significance of any of these scales indicated the presence of epistasis. When the scale is adequate, the values of A, B and C should be zero within the limits of their respective standard errors. The test of significance was done with the use of respective standard errors of the scales. The computation of standard error is given below:

$$V_A = 4V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)$$

$$V_B = 4V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)$$

$$V_C = 16\,V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$$

Where,

VP_1, VP_2, VF_1, VF_2, VB_1 and VB_2 are the variances of $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$, $\bar{B}_1$ and $\bar{B}_2$ populations, respectively.

$$S.E._{(A)} = (V_A)^{1/2}$$

$$S.E._{(B)} = (V_B)^{1/2}$$

$$S.E._{(C)} = (V_C)^{1/2}$$

't'(C) values are calculated as follows:

$$t_A(C) = \frac{\text{Estimated value of A}}{S.E._{(A)}}$$

$$t_B(C) = \frac{\text{Estimated value of B}}{\text{S. E.}_{(B)}}$$

$$t_C(C) = \frac{\text{Estimated value of C}}{\text{S.E.}_{(C)}}$$

ii) Test of potence:

It could be done by comparing F_1 and F_2 means and is calculated by the following formula:

$$\begin{aligned} \overline{F_1} &= m + [h] \\ -\overline{F_2} &= -m + -\tfrac{1}{2}[h] \\ \hline \overline{F_1} - \overline{F_2} &= \tfrac{1}{2}[h] \end{aligned}$$

Test of significance by "t" test (t) = $\frac{\text{Estimated value of potence}}{\text{Standard error of mean}}$

Non-significance of this test will indicate no difference between F_1 and F_2 and there will be no potence.

iii) Joint scaling test:

Cavalli (1952) proposed a unique technique known as joint scaling test. The three important features of this test are:

a) It can combine any combination of families at the same time,

b) It also estimates the parameters of the model viz. m, [d] and [h],

c) It tests the goodness of fit of the model and only if more than 3 families available. Since to estimate 3-parameters, m, [d] and [h], minimum of 3 families are required, in that case no degrees of freedom is left for testing the goodness of fit of this model.

In the present study, joint scaling test was done based on 3-parameter model for six generations as shown in table below. For testing the adequacy of additive-dominance model following weighted least square technique was done as proposed by Cavalli (1952).

Generation means, weight and co-efficient of 3-parameter model.

Generation	Mean	Weight	Co-efficient of parameter		
			m	[d]	[h]
$\bar{P}_1$			1	1	0
$\bar{P}_2$			1	-1	0
$\bar{F}_1$			1	0	1
$\bar{F}_2$			1	0	0.5
$\bar{B}_1$			1	-0.5	0.5
$\bar{B}_2$			1	0.5	0.5

After getting the values of the three parameters, m, [d] and [h] the significance of these parameters are tested against their standard errors as:

t = Estimate of the parameter / standard error of the parameter

Here, 'm' measures the mean of the base population, [d] measures the additive gene effects and [h] measures the dominance gene effects. Testing the goodness of fit of the 3-parameter model for six generations following two steps are involved:

i) Computation the expected means of these six families using estimates of m, [d] and [h] in a manner given below:

$$\bar{P}_1 = m + [d]$$

$$\bar{P}_2 = m - [d]$$

$$\bar{F}_1 = m + [h]$$

$$\bar{F}_2 = m + \frac{1}{2}[h]$$

$$\bar{B}_1 = m - \frac{1}{2}[d] + \frac{1}{2}[h]$$

$$\bar{B}_2 = m + \frac{1}{2}[d] + \frac{1}{2}[h]$$

Where 'm' measures base population mean, [d] measures the additive gene effects and [h] measures the dominance gene effects.

(ii) Calculation of the squared deviation of the observed mean from the expected mean for each family and calculation of the χ^2 values where done as shown below:

Generation	Observed (O)	Expected (E)	(O-E)	$(O-E)^2$	$\chi^2 = (O-E)^2 \times$ Weight
$\bar{P}_1$					
$\bar{P}_2$					
$\bar{F}_1$					
$\bar{F}_2$					
$\vec{B}_1$					
$\bar{B}_2$					$\sum\chi^2 =$

If the $\chi 2$ value is significant, it indicates that the additive-dominance model is inadequate and the estimates of the 3-parameter and 2-parameter are biased to an unknown extent by the effects not attributable to the additive and dominance actions of the genes.

iv) Six-parameter model:

Jinks and Jones (1958) gave six-parameter model for estimation of various genetic components:

$$m = \tfrac{1}{2}\bar{P}_1 + \tfrac{1}{2}\bar{P}_2 + 4\bar{F}_2 - 2\vec{B}_1 - 2\bar{B}_2$$

$$[d] = \tfrac{1}{2}(\bar{P}_1 - \bar{P}_2)$$

$$[h] = 6\vec{B}_1 + 6\bar{B}_2 - 8\bar{F}_2 - \bar{F}_1 - 3/2\bar{P}_1 - 3/2\bar{P}_2$$

$$[i] = 2\vec{B}_1 + 2\bar{B}_2 - 4\bar{F}_2$$

$$[j] = 2\vec{B}_1 - \bar{P}_1 - 2\bar{B}_2 + \bar{P}_2$$

$$[l] = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\vec{B}_1 - 4\bar{B}_2$$

The estimated values were tested for significance by C-test.

f) Analysis of the components of variation

The techniques of Mather (1949) were followed to estimate components of variation according to the formulae:

$V(F_2) = 1/2D + 1/4H + E$ ..... (i)

$V(B_1) + V(B_2) = ½ D + ½ H + 2 E$ .....(ii)

$\{V(P_1) + V(P_2) + V(F_1)\} / 3 = E$ ..... (iii)

Where,

$V(F_1)$ = Variance of F_1

$V(F_2)$ = Variance of F_2

$V(P_1)$ = Variance of P_1

$V(P_2)$ = Variance of P_2

$V(B_1)$ = Variance of B_1

$V(B_2)$ = Variance of B_2

Here,

D = Additive component of variation

H = Dominance component of variation and

E = Environmental variation.

There were three equations and two unknowns (D and H); by solving the algebraic equations the values of D and H are calculated as follows:

Multiplying the equation (i) by 2 and then subtracting the equation (ii) from the multiplied equation (i), it becomes,

$$D + 1/2H + 2E = 2V(F_2)$$

$$\underline{-\ 1/2D \pm 1/2H \pm 2E = V(B_1) \pm V(B_2)}$$

$$1/2D = 2V(F_2) - \{V(B_1) + V(B_2)\}$$

$$D = 2[2V(F_2) - \{V(B_1) + V(B_2)\}]$$

When the values of D and E are known, the value of H is determined by putting the value of D and E in either of the equations (i) or (ii) as follows:

$1/4H = V(F_2) - (1/2D + E)$

$H = 4\{V(F_2) - (1/2D + E)\}$

g) Degree of dominance

The average degree of dominance over all loci was determined by the square root of the ratio between H and D (Mather, 1949).

$$\text{Degree of dominance} = \sqrt{\frac{H}{D}}$$

Here, D = Additive component of variation

H = Dominance component of variation

Where, $(H/D)^{1/2} = 0$, denotes no dominance

$(H/D)^{1/2} = 1$, denotes complete dominance

$(H/D)^{1/2} < 1$, denotes partial dominance

$(H/D)^{1/2} > 1$, denotes over dominance

h) Heritability

Heritability was calculated in two different ways following Mather (1949) as follows:

i) Broad sense heritability (h^2_b)

It is expressed as the ratio of the genetic variance over the (expected) phenotypic variance of F_2 generation as follows:

$$h^2_b = (\frac{1}{2}D + \frac{1}{4}H) / (\frac{1}{2}D + \frac{1}{4}H + E_1)$$

ii) Narrow sense heritability (h^2_n):

It is expressed as the ratio of fixable heritable variation (D) over the (expected) phenotypic variance of the F_2 generations as follows:

$$h^2_n = \frac{1}{2}D / (\frac{1}{2}D + \frac{1}{4}H + E_1)$$

Here, *D*, *H* and *E* are the estimates of components of variation. It is noticed that heritability is always expressed as percentage (%) as suggested by Warner (1952).

i) Genetic advance:

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

$$GA = K \times \sigma_P \times h^2_b \text{ or } h^2_n$$

Where,

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

σ_P = Standard deviation of the phenotypic variance of F_2

h^2_b = Heritability in broad sense

h^2_n = Heritability in narrow sense

j) Genetic advance as percentage of mean (GA %)

It was measured by the following formula:

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

Where, $\bar{X}$ = Grand mean for a respective character.

k) Number of effective factors

The numbers of effective factors were estimated by the following formula (Mather, 1949).

$$K_1 = \frac{\frac{1}{4}(\bar{P}_1 - \bar{P}_2)^2}{D}$$

Where, D = Least square estimate of component of genetic variation.

l) Heterosis and inbreeding depression

Heterosis was expressed as increase of F_1 hybrid over the average of the parent (mid-parent) or over better-parent, while inbreeding depression was the reduction of F_2 below the F_1 performance. They were measured as follows:

$$\text{Heterosis over mid-parent} = \frac{\bar{F}_1 - MP}{MP}$$

$$\text{Heterosis over better-parent} = \frac{\bar{F}_1 - BP}{BP}$$

$$\text{Inbreeding Depression} = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1}$$

In order to test each of the values standard errors were calculated from the error variance of appropriate variance analysis and "t" test was done to test the significant difference from zero.

RESULTS

Quantitative characters viz. days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD), number of pods per plant (NPPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and seed weight per plant (SWPP) showed continuous variation indicating polygenic control. Therefore, biometrical techniques were applied to determine the nature of gene action in the expression of these characters. The results are described under following sub-heads

A. Analysis of component of means

1. Mather's scaling test

Mean and variance of six generations viz. P_1, P_2, F_1, F_2, B_1 and B_2 were calculated separately for eleven quantitative characters viz. DMF NPBMF, NSBMF PHMF, PWFD, RWFD, NPPP, PdWFD, NSPP, 1000-SW and SWPP in each of the five crosses. In the analysis of the components of mean viz. m, [d] and [h] first Mather scaling test was done to see whether additive-dominance model was adequate or not and the results for all the characters for five different crosses are presented separately in table 7.

For the character DMF, NPBMF, NSBMF, PHMF, RWFD, NPPP and PdWPP in cross I (1A×3A) all the parameters A, B and C were non-significant. While, for the character PWFD A was significant and for NSPP C was significant. In this cross for 1000-SW and SWPP A, B and C were significant.

In cross II (2C×4C) for the characters DMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP and SWPP all the parameters A, B and C were non-significant. For the character NPBMF A and B were significant and C was non-significant whereas for 1000-SW all the parameters were significant. In cross III

(4C×3C) for the characters NPBMF, NSBMF, PHMF, NPPP, NSPP and SWPP A, B and C were non-significant. While for DMF A, B was non-significant and C was significant. For PWFD A was significant whereas B and C were non-significant. For RWFD only C was significant. In this cross for the character PdWPP A and C were non-significant and B was significant. For 1000-SW only the parameter C was non- significant.

In cross IV (4A×7B) the characters DMF, NPBMF, NSBMF and PdWPP all the parameters A, B and C were non-significant. For PHMF only A was non-significant. Whereas for PWFD, RWFD and NPPP only A was significant. For NSPP A and C were non-significant and B was significant. All the parameters were significant for the trait 1000-SW. For SWPP only B parameter was significant. In crass V (5A×6A) NPBMF, PHMF, NPPP and NSPP were non-significant for all the parameters. For DMF in this cross A and B were non-significant and C was significant. For NSBMF only scale B was significant. The characters, PWFD and RWFD showed similar results where A was non-significant and, B and C were significant. While PdWPP showed significant result only for C. 1000-SW trait showed significant result for all the parameters. Whereas for SWPP A, B were non-significant and C was significant.

2. Test of potence

The test of potence was done in five different crosses for all the eleven characters and the results were given in table 7. From the table it was showed that in cross I (1A×3A) potence was significant for all the characters except 1000-SW which showed non-significant result.

In cross II (2C×4C) potence was significant for all the characters except DMF, NSBMF and PWFD in which it was non-significant. While only three characters such as PWFD, 1000-SW and SWPP exhibited non-significant potence and the rest of the characters indicated significant potence in cross III (4C×3C). From cross IV (4A×7B) it was observed that potence was significant for all the characters. While,

in cross V (5A×6A), it showed non-significant potence only for NSPP and SWPP and the rest of the characters showed significant results.

3. Joint scaling test

In the presence of epistasis the data fit with the 2 parameters model and when epistasis was absence the data fit with the 3-parameter model in which m measures a constant (base population mean), [d] and [h] estimate the algebraic sum of the additive and dominance effects, respectively. The values of m, [d] and [h] were calculated in terms of 3 and 2 parameters model. The χ^2 test was done to test the goodness of fit of the observed generation means with that of the expected means based on the 3 and 2 parameters estimate. The χ^2 value obtained for each of the characters are shown in table 8.

In cross I (1A×3A) the characters NSBMF, PHMF, PWFD, RWFD, NPPP and PdWPP had non-significant χ^2 values, while DMF, NPBMF, NSPP, 1000-SW and SWPP had significant χ^2 values. In case of cross II (2C×4C) it was observed that the characters like NPBMF, NSBMF, PWFD, PdWPP, 1000-SW and SWPP had significant and characters like DMF, PHMF, RWFD, NPPP and NSPP had non-significant χ^2 values. From table 8 it was observed that NSBMF, PHMF, RWFD, NPPP, NSPP and SWPP had non-significant χ^2 values while characters like DMF, NPBMF, PWFD, PdWPP and 1000-SW had significant χ^2 values in cross III (4C×3C). However, in cross IV (4A×7B) most of the characters like, DMF, NPBMF, NSBMF, PHMF, PWFD, NPPP and NSPP had non-significant χ^2 except RWFD, PdWPP, 1000-SW and SWPP, these had significant χ^2 values. In cross V (5A×6A) table 8 showed that most of the characters exhibited significant χ^2 values except NPBMF, NPPP and NSPP which indicated non-significant χ^2 values.

4. Six-parameter model

Estimation of the six-parameter model with mean, additive, dominance, additive × additive, dominance × dominance and additive × dominance interaction terms are shown in table 9.

From the five crosses it was observed that mean values were significant. In case of additive effect the characters DMF and 1000-SW in cross I (1A × 3A); PdWPP, 1000-SW and SWPP in cross II (2C × 4C); DMF and NPBMF in cross III (4C × 3C); 1000-SW in cross IV (4A × 7B) and DMF, NSBMF, PHMF, PWFD, RWFD and 1000-SW in cross V (5A × 6A) showed significant performances. The analysis indicated the presence of the individual type of digenic epistatic effects. The additive × additive interaction effect was positive and statistically significant for DMF, NPBMF and NSPP in cross I (1A × 3A); for PWFD, 1000-SW and SWPP in cross II (2C × 4C); for DMF, NPBMF and NSPP in cross III (4C × 3C); for DMF, NSBMF, 1000-SW and SWPP in cross V (5A × 6A) and negative for 1000-SW and SWPP in cross I (1A × 3A); for NPBMF in cross II (2C × 4C); for PWFD and 1000-SW in cross III (4C × 3C); for RWFD and NSPP in cross IV (4A × 7B). The additive × dominance gene effect was positive and significant for 1000-SW in cross I (1A × 3A); for 1000-SW in cross IV (4A × 7B) and for PWFD and 1000-SW in cross V (5A × 6A) and negative for PWFD in cross I (1A × 3A); for RWFD in cross IV (4A × 7B) and for NSBMF in cross V (5A × 6A). The dominance × dominance interaction effect was positive and significant for 1000-SW and SWPP in cross I (1A × 3A); for NPBMF in cross II (2C × 4C); for PWFD, PdWPP and 1000-SW in cross III (4C × 3C); for PHMF, RWFD, NPPP, NSPP, 1000-SW and SWPP in cross IV (4A × 7B) and for 1000-SW in cross V (5A × 6A) while, it was negatively significant for NSPP in cross I (1A × 3A); for 1000-SW and SWPP in cross II (2C × 4C); for DMF for cross III (4C × 3C); and for DMF and NSBMF in cross V (5A × 6A).

In this analysis, epistasis may be classified into two types only. Those in which [h] and [l] have the same sign it will refer to as complementary type and those in which [h] and [l] have opposite sign it will refer to as duplicate type. From table 9 duplicate type of epistasis was observed for NSPP, 1000-SW and SWPP in cross I (1A × 3A); for NPBMF, 1000-SW and SWPP in cross II (2C × 4C); for DMF, PWFD, PdWPP and 1000-SW in cross III (4C × 3C); for RWFD and 1000-SW in cross IV (4A × 7B) and for DMF, NSBMF and 1000-SW in cross V (5A × 6A).

From this estimation of gene effect it was observed that when none of [i], [j] and [l] interactions are significant and also [h] is non-significant it revealed the absence of non-allelic gene interaction. So it was a perfect fit to the model (m) and [d].

B. Analysis of the components of variation

The estimates of variance components D, H and E are given in table 10. The environmental variation E was calculated from the average of the means of P_1, P_2, and F_1 variance. The additive variation D was estimated from F_2, B_1 and B_2 variance, while dominance variation it was found out from total F_2 variance after subtraction of additive variation D and Environmental variation E.

From the table 10 it showed that dominance (H) expressed negative value in all the five crosses for eleven quantitative characters. On the other hand, additive component (D) expressed positive value in all crosses for all the characters. Exceptional results have been made in the recent study is that additive components expressed negative value for SWPP in cross V (5A×6A).

C. Degree of dominance

The dominance ratio ($\sqrt{H/D}$) as measured from the estimate of components of variation are shown in table 10. Here all the eleven characters in five crosses showed over dominance performances. The highest value, 14.057 of dominance ratio was found in cross V (5A×6A) in the character SWPP. In case of dominance ratio the negative signs in all the cases indicated that dominance towards decreasing parent.

D. Heritability

For eleven quantitative characters heritability estimates, both in broad sense (h^2_b) and narrow sense (h^2_n) based on components of variation are shown in table 11. Study of heritability showed that broad sense heritability was the highest but negative with a value of -355.512 for NSPP in cross V (5A×6A) followed by -345.664 for SWPP in cross V (5A×6A) and -205. 640 for PHMF in cross II (2C ×

4C). On the other hand, broad heritability with a value of -1.207 was found to be the lowest for NSPP in cross IV (4A×7B) followed by -1.356 for PHMF in cross V (5A×6A) and -3.527 for NPPP in cross IV (4A×7B). Here in broad sense heritability the values were negative except 1000-SW (45.051) in cross I (1A×3A) and DMF (6.082) in cross IV (4A×7B).

In case of narrow sense heritability it showed that the highest and positive with a value of 348.210 for NPBMF in cross IV (4A×7B) followed by 328.079 for 1000-SW in cross II (2C×4C) and 279.303 for PHMF in cross III (4C×3C). On the other hand, in narrow sense heritability the value -3.464 was found to be the lowest but negative for SWPP in cross V (5A× 6A) followed by 7.803 for NSPP and 14.672 for NPPP in same cross.

E. Genetic advance (GA)

Genetic advance was calculated both for broad sense and narrow sense for all the characters are shown in table 11. The highest genetic advance in broad sense was observed for NPPP (-24.500) in cross V (5A×6A) followed by PWFD (-20.221) in cross III (4C×3C) and 1000-SW (-12.468) in cross II (2C×4C). On the other hand, the lowest genetic advance in broad sense was observed for DMF (0.084) in cross IV (4A×7B) followed by NSPP and SWPP in the same cross.

Here in narrow sense genetic advance, the highest value was observed for NSPP (41.107) in cross III (4C×3C) followed by 1000-SW (34.531) in cross I (1A×3A) and PWFD (31.992) in cross III (4C×3C). While the lowest value was observed for SWPP (-0.043) in cross V (5A×6A) followed by NPBMF (0.279) in the same cross and RWFD (0.381) in cross II (2C×4C).

F. Genetic advance as percentage of mean (GA%)

Genetic advance as percentage of mean was calculated in different crosses for all the characters are presented in table 11. In the present study, the highest GA% in broad sense was observed for SWPP (-44.109) in cross V (5A×6A) followed by PdWPP (-41.496) and NSPP (-40.833) in the same cross. Here the lowest GA%

value was recorded for PHMF (-0.039) in cross V (5A×6A) followed by DMF (0.091) and NSPP (-0.296) in cross IV (4A×7B).

The highest GA% in narrow sense was observed for SWPP (66.743) in cross II (4C×3C) followed by PdWPP (63.502) and NSPP (59.252) in the same cross. On the other hand, the lowest GA% in narrow sense was recorded for SWPP (-0.442) in cross V (5A×6A) followed by NSPP in the same cross and DMF in cross I (1A×3A).

G. Number of effective factors

Effective factors were calculated according to Mather's formula (1949) and the numbers of effective factors are presented in table 12. From the table it was found that the values for number of effective factors, K_1 was always less than one for all the characters in five crosses.

H. Heterosis and inbreeding depresssion

1. Heterosis

In table 12 the calculated value for mid-parent (MP) and better-parent (BP) heterosis for all the characters in all the crosses are presented. From the table it was observed that in cross I (1A×3A) both mid-parent and better-parent heterosis were significant for all the characters except DMF was non-significant in case of better-parent heterosis while 1000-SW was non-significant in both the cases. In cross II (2C×4C) both mid-parent and better-parent heterosis values were positive and significant except in case of mid-parent heterosis for DMF where it was non-significant, however in case of better-parent heterosis the characters DMF and PWFD were non-significant and positive.

In case of cross III (4C×3C) both mid-parent and better-parent heterosis were significant for all the characters except PWFD and 1000-SW where it was non-significant in both the cases. Here for mid-parent heterosis the character like 1000-SW showed negative performances and in case of better-parent heterosis the characters NPBMF and 1000-SW showed negative values. On the other hand in

cross IV (4A×7B) the mid-parent and better-parent heterosis values for all the characters were significant and positive, significant values except only for 1000-SW it was negative.

In case of cross V (5A×6A) most of the characters showed positive and significant mid-parent heterosis except DMF, PdWPP, NSPP and 1000-SW, where the value were non-significant. While for better-parent heterosis the characters NPPP and NSPP showed non-significant performances.

2. Inbreeding Depression

Inbreeding depression was calculated and presented in table 12. In cross I (1A×3A) the inbreeding depression values were non-significant and positive for all the characters. Cross II (2C×4C) showed positive and non-significant inbreeding depression values for all the characters except 1000-SW, where it was non-significant and negative. Same results were observed in cross III (4C×3C). In cross IV (4A×7B) all the characters expressed positive and non-significant inbreeding depression. Again in cross V (5A×6A) all the characters showed positive and non-significant inbreeding depression except RWFD where it was highly significant. While in the same cases NSPP showed negative performances.

Table 7: Mather's scaling test and test of potence for eleven characters in five crosses of chickpea.

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 1A×3A	A	0.033^{NS}	0.011^{NS}	-0.506^{NS}	0.193^{NS}	-2.216**	-0.099^{NS}	0.078^{NS}	-0.103^{NS}	1.267^{NS}	-30.818**	-0.935**
	B	0.250^{NS}	0.006^{NS}	-0.126^{NS}	0.849^{NS}	-0.122^{NS}	-0.081^{NS}	1.256^{NS}	-0.721^{NS}	0.994^{NS}	-42.826**	-1.461**
	C	-0.693^{NS}	-0.300^{NS}	0.100^{NS}	0.644^{NS}	-2.364^{NS}	-0.122^{NS}	-1.507^{NS}	-0.821^{NS}	-9.057*	-7.174**	-1.541**
	Potence	0.411**	0.150**	0.875**	0.873**	1.929**	0.104*	3.064*	0.379*	3.639**	1.030^{NS}	0.488**
Cross 2C × 4C	A	0.072^{NS}	-0.594**	0.678^{NS}	-0.064^{NS}	0.243^{NS}	-0.066^{NS}	0.578^{NS}	0.225^{NS}	-1.378^{NS}	10.024**	0.337^{NS}
	B	0.950^{NS}	-0.579**	-0.109^{NS}	0.018^{NS}	-0.055^{NS}	0.052^{NS}	0.221^{NS}	0.190^{NS}	-0.735^{NS}	9.128**	0.416^{NS}
	C	0.229^{NS}	-0.129^{NS}	-0.650^{NS}	-0.491^{NS}	-3.391^{NS}	-0.070^{NS}	0.121^{NS}	0.001^{NS}	-3.100^{NS}	5.380**	-0.140^{NS}
	Potence	-0.007^{NS}	0.182*	0.675^{NS}	1.562**	1.518^{NS}	0.261**	2.257**	0.511**	3.625**	3.214**	0.644**
Cross 4C × 3C	A	-0.111^{NS}	-0.017^{NS}	-0.800^{NS}	-0.122^{NS}	-9.017*	-0.194^{NS}	-0.239^{NS}	-1.464^{NS}	-0.156^{NS}	-12.049**	-1.281^{NS}
	B	-0.674^{NS}	0.116^{NS}	-0.944^{NS}	-0.675^{NS}	-6.947^{NS}	-0.007^{NS}	0.641^{NS}	-2.080**	0.524^{NS}	-11.815**	-0.733^{NS}
	C	-5.636**	-0.242^{NS}	-1.450^{NS}	-0.074^{NS}	-1.961^{NS}	-0.344*	-5.579^{NS}	-1.848^{NS}	-11.757^{NS}	4.051^{NS}	-0.915^{NS}
	Potence	2.446**	0.024**	0.900**	0.896**	1.257^{NS}	0.239**	4.932*	1.126*	7.614*	-3.507^{NS}	0.681^{NS}

continued

Table 7 continued

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 4A×7B	A	0.039 NS	-0.144 NS	-0.589 NS	-0.744 NS	1.829*	-0.331*	-5.183*	-0.823 NS	-4.994 NS	-6.116**	-0.648 NS
	B	-0.094 NS	-0.097 NS	-0.253 NS	-1.086*	-0.176 NS	-0.128 NS	-4.885 NS	-0.856 NS	-6.835*	-19.281**	-1.127**
	C	0.707 NS	0.021 NS	-0.814 NS	-1.463*	-0.289 NS	0.028 NS	-6.143 NS	-1.402 NS	-3.793 NS	-24.466**	-1.130 NS
	Potence	0.461*	0.182**	1.079**	1.468**	2.242**	0.104**	9.361**	1.587**	10.786**	2.618*	1.241*
Cross 5A ×6A	A	0.656 NS	0.033 NS	-0.178 NS	0.134 NS	1.522 NS	-0.127 NS	-3.044 NS	-0.997 NS	3.983 NS	-18.995**	-0.069 NS
	B	0.191 NS	-0.015 NS	1.265**	-0.332 NS	-4.867**	-0.240**	0.588 NS	-1.040 NS	5.374 NS	-24.129**	-0.383 NS
	C	-2.936**	-0.193 NS	0.100 NS	-0.325 NS	-6.091**	-0.418**	-8.743 NS	-3.247**	4.271 NS	-55.035**	-2.589**
	Potence	0.896**	0.161**	0.525**	0.950**	2.094**	0.278**	3.511*	0.799*	-1.968 NS	12.178**	0.441 NS

Table 8: Joint scaling test based on two parameters (due to non-significant potence) and three parameters model for eleven characters in five crosses of chickpea.

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 1A×3A	m	95.249±0.087	3.223±0.027	19.168±0.187	48.209±0.189	56.508±0.284	2.046±0.026	41.500±0.776	7.198±0.124	42.556±0.781	125..293±0.373	5.533±0.107
	d	-0.219±0.079	0.046±0.024	-0.146±0.162	-0.103±0.168	0.007±0.257	0.035±0.024	-0.608±0.691	-0.187±0.118	-0.206±0.724	-4.962±0.610	-0.296±0.102
	h	0.423±0.168	0.140±0.050	1.745±0.364	2.105±0.354	2.564±0.532	0.129±0.051	5.257±1.494	0.365±0.229	2.539±1.465		0.252±0.195
	χ^2	34.578**	20.985**	4.892 NS	3.973 NS	7.668 NS	6.246 NS	3.796 NS	6.502 NS	17.790**	706.059**	38.456**
Cross 2C × 4C	m	94.157±0.056	2.814±0.044	22.496±0.074	57.024±0.180	57.071±0.196	2.307±0.037	49.640±0.401	7.724±0.0730	52.719±0.440	124.519±0.563	6.588±0.067
	d	0.133±0.130	-0.019±0.039	-0.260±0.170	-0.151±0.154	-0.466±0.377	-0.015±0.029	0.443±0.347	0.177±0.066	-0.196±0.397	4.054±0.583	0.163±0.061
	h		0.230±0.085		2.853±0.345		0.482±0.071	4.647±0.775	1.051±0.140	5.311±0.852	9.666±1.064	1.249±0.128
	χ^2	5.123 NS	56.561**	12.792*	2.752 NS	9.449*	2.860 NS	4.567 NS	21.650**	3.212 NS	205.542**	30.168**
Cross 4C × 3C	m	96.190±0.150	3.099±0.035	17.092±0.188	50.543±0.182	81.646±0.547	2.040±0.033	54.564±1.274	10.912±0.266	65.457±1.549	138.762±0.361	9.601±0.097
	d	-0.849±0.125	-0.320±0.034	-0.112±0.160	-0.271±0.164	0.924±1.208	0.002±0.030	-1.436±1.079	-0.307±0.220	-1.198±1.321	-1.296±0.732	-0.160±0.192
	h	1.688±0.291	0.265±0.068	0.860±0.364	1.676±0.359		0.263±0.067	6.769±2.475	0.830±0.526	8.452±3.062		
	χ^2	193.114**	265.077**	4.613 NS	6.385 NS	10.910*	5.896 NS	5.589 NS	11.082**	6.243 NS	102.377**	9.204 NS

Continued

Table 8 continued

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 4A×7B	m	91.292±0.089	2.578±0.033	19.035±0.129	49.312±0.135	51.510±0.288	1.934±0.024	26.064±0.536	4.428±0.100	30.037±0.686	112.789±0.742	3.489±0.084
	d	-0.035±0.083	-0.002±0.027	0.082±0.121	-0.189±0.121	-0.113±0.261	0.039±0.022	0.429±0.493	-0.102±0.091	0.064±0.629	-6.434±0.705	-0.130±0.077
	h	1.340±0.180	0.349±0.060	1.655±0.247	1.951±0.263	4.276±0.543	0.220±0.046	12.605±1.200	1.914±0.218	16.958±1.537	-5.636±1.321	1.448±0.182
	χ^2	3.373 NS	6.708 NS	3.986 NS	12.439 NS	5.678 NS	38.207**	7.327 NS	8.596*	7.181 NS	206.465**	15.150**
Cross 5A ×6A	m	77.444±0.132	3.008±0.030	13.014±0.086	54.634±0.117	29.688±0.367	1.690±0.028	58.709±1.044	11.227±0.210	68.515±0.404	149.018±0.618	9.552±0.064
	d	1.043±0.126	-0.032±0.028	0.472±0.084	1.207±0.111	1.839±0.317	0.199±0.025	0.363±0.943	-0.181±0.186	0.494±1.019	-3.727±0.513	-0.066±0.164
	h	0.233±0.248	0.212±0.058	1.361±0.169	1.689±0.239	0.852.±0.739	0.327±0.051	2.631±1.998	-0.319±0.403		-19.838±1.254	
	χ^2	246.610**	7.128 NS	111.956**	410.348**	177.013**	173.719**	6.448 NS	15.080**	3.567 NS	308.641**	21.531**

Table 9: Estimates of gene effects using the six-parameter model of parents, F_1, F_2, B_1 and B_2 for eleven characters.

Characters	Cross I (1A × 3A)					
	m	[d]	[h]	[i]	[j]	[l]
DMF	94.30*±0.34	0.27*±0.10	2.71*±0.93	0.98*±0.33	-0.22^{NS}±0.32	-1.26^{NS}±0.64
NPBMF	2.93*±0.10	-0.05^{NS}±0.03	0.80*±0.27	0.32*±0.09	0.01^{NS}±0.10	-0.33^{NS}±0.18
NSBMF	19.93*±0.72	0.25^{NS}±0.22	-0.30^{NS}±1.89	-0.73^{NS}±0.68	-0.38^{NS}±0.65	1.36^{NS}±1.33
PHMF	47.66*±0.75	0.25^{NS}±0.23	3.91*±1.95	0.40^{NS}±0.71	-0.66^{NS}±0.68	-1.44^{NS}±1.32
PWFD	56.90*±1.13	0.48^{NS}±0.35	0.39^{NS}±2.96	0.03^{NS}±1.07	-2.09*±1.03	2.31^{NS}±2.01
RWFD	2.13*±0.11	-0.03^{NS}±0.03	-0.15^{NS}±0.29	-0.06^{NS}±0.11	-0.02^{NS}±0.10	0.24^{NS}±0.20
NPPP	38.63*±2.96	0.88^{NS}±0.94	12.39^{NS}±7.88	2.84^{NS}±2.80	-1.18^{NS}±2.79	-4.17^{NS}±5.50
PdWPP	7.38*±0.52	0.03^{NS}±0.16	-0.48^{NS}±1.39	0.004^{NS}±0.50	0.62^{NS}±0.49	0.83^{NS}±0.93
NSPP	31.98*±3.02	0.05^{NS}±1.01	27.65*±8.12	11.32*±2.85	0.27^{NS}±2.95	-13.58*±5.56
1000-SW	202.83*±5.05	2.05*±0.77	-208.11*±11.25	-66.47*±4.99	12.01*±2.53	140.12*±6.69
SWPP	6.80*±0.44	0.10^{NS}±0.14	-3.9*±1.16	-0.86*±0.41	0.53^{NS}±0.41	3.25*±0.77

continued

Table 9 continued

Characters	Cross II (2C × 4C)					
	m	[d]	[h]	[i]	[j]	[l]
DMF	93.21*±0.54	0.05 NS ±0.17	2.71 NS ± 1.46	0.79 NS ±0.51	-0.88 NS ±0.53	-1.82 NS ± 1.02
NPBMF	3.95*±0.16	0.05 NS ±0.05	-2.96* ± 0.44	-1.05*±0.15	-0.02 NS ±0.16	2.22*±0.31
NSBMF	20.81*±0.69	0.02 NS ±0.25	4.03* ± 1.85	1.22 NS ±0.64	0.79 NS ±0.69	-1.79 NS ± 1.34
PHMF	56.63*±0.61	0.16 NS ±0.22	3.72* ± 1.66	0.44 NS ±0.57	-0.08 NS ±0.62	-0.40 NS ± 1.17
PWFD	53.16*±1.86	0.41 NS ±0.48	8.69 NS ± 4.79	3.58*±1.80	0.30 NS ± 1.55	-3.77 NS ± 3.29
RWFD	2.25*±0.12	0.05 NS ±0.05	0.59 NS ±0.32	0.06 NS ±0.11	-0.12 NS ±0.12	-0.04 NS ±0.23
NPPP	48.90*±1.59	-0.52 NS ±0.47	6.73 NS ± 4.12	0.68 NS ± 1.52	0.36 NS ± 1.39	-1.48 NS ± 2.84
PdWPP	7.28*±0.30	-0.19*±0.09	2.27* ± 0.78	0.41 NS ±0.28	0.04 NS ±0.27	-0.83 NS ± 0.54
NSPP	52.06*±1.89	0.30 NS ± 0.52	5.56 NS ± 4.92	0.99 NS ± 1.82	-0.64 NS ± 1.63	1.13 NS ± 3.37
1000-SW	109.31*±2.40	-4.23*±0.72	55.81* ± 6.89	13.77*±2.29	0.90 NS ± 2.51	-32.92*±4.75
SWPP	5.66*±0.28	-0.17*±0.08	3.75* ± 0.74	0.89*±0.27	-0.08 NS ± 0.25	-1.64*±0.51

continued

Table 9 continued

Characters	Cross III (4C × 3C)					
	m	[d]	[h]	[i]	[j]	[l]
DMF	91.82*±0.53	0.58*±0.18	10.99*± 1.41	4.85*±0.50	0.56 NS ± 0.50	-4.07* ± 1.00
NPBMF	2.77*±0.15	0.34*±0.04	1.07*±0.41	0.34*±0.14	-0.13 NS ± 0.14	-0.44 NS ± 0.28
NSBMF	17.62*±0.71	0.07 NS ±0.22	-1.26 NS ± 1.84	-0.29 NS ±0.67	0.14 NS ± 0.64	2.04 NS ± 1.29
PHMF	51.3*±0.76	0.2 NS ±0.21	-0.49 NS ± 2.03	-0.72 NS ±0.73	0.55 NS ± 0.69	1.52 NS ± 1.42
PWFD	96.92*±5.09	0.21 NS ±1.82	-42.44*± 13.54	-14.00*±4.75	-2.07 NS ± 4.95	29.97*± 9.89
RWFD	1.94*±0.13	0.04 NS ±0.04	0.39 NS ±0.36	0.14 NS ±0.13	-0.19 NS ± 0.12	0.06 NS ± 0.26
NPPP	48.89*±5.01	1.53 NS ±1.50	19.44 NS ± 12.9	5.98 NS ±4.78	-0.88 NS ± 4.36	-6.38 NS ± 8.94
PdWPP	12.95*± 1.06	0.26 NS ±0.31	-5.61*±2.69	-1.70 NS ±1.01	0.62 NS ± 0.89	5.24*± 1.88
NSPP	53.92*±6.26	1.15 NS ±1.78	33.97*± 16.15	12.13*±6.00	-0.68 NS ± 5.36	-12.49 NS ± 11.33
1000-SW	171.39*±3.40	1.04 NS ±1.01	-84.68*± 8.83	-27.92*±3.25	-0.23 NS ± 2.95	51.78*± 6.50
SWPP	10.63*±0.94	0.33 NS ±0.28	-3.31 NS ± 2.38	-1.10 NS ±0.90	-0.55 NS ± 0.79	3.11 NS ± 1.67

continued

Table 9 continued

Characters	Cross IV (4A × 7B)					
	m	[d]	[h]	[i]	[j]	[l]
DMF	92.04*±0.48	0.03 NS±0.10	-0.30 NS±1.21	-0.76 NS±0.47	0.13 NS ± 0.37	0.82 NS ± 0.82
NPBMF	2.66*±0.12	0.08 NS±0.04	0.14 NS±0.31	-0.09 NS±0.11	-0.22 NS ± 0.11	0.15 NS ± 0.21
NSBMF	19.18*±0.56	0.15 NS±0.15	0.85 NS±1.51	-0.03 NS±0.54	-0.34 NS ± 0.52	0.87 NS ± 1.05
PHMF	49.88*±0.58	0.12 NS±0.16	-0.36 NS±1.51	-0.37 NS±0.56	0.34 NS ± 0.50	2.20* ± 1.05
PWFD	49.43*±1.08	-0.32 NS±0.36	9.87*±2.92	1.94 NS±1.02	2.01 NS ± 1.05	-3.59 NS ± 2.01
RWFD	2.45*±0.09	0.02 NS±0.03	-1.21*±0.26	-0.49*±0.09	-0.20* ± 0.09	0.95*±0.18
NPPP	30.23*±2.88	-0.40 NS±0.56	-2.27 NS±7.84	-3.93 NS±2.82	-0.30 NS ± 2.42	13.99* ± 6.21
PdWPP	4.76*±0.50	0.10 NS±0.10	0.24 NS±1.36	-0.28 NS±0.49	0.03 NS ± 0.43	1.96 NS ± 1.07
NSPP	38.36*±3.65	-0.28 NS±0.72	-8.23 NS±9.86	-8.04*±3.58	1.84 NS ± 3.02	19.87* ± 7.78
1000-SW	119.26*±3.04	2.68*±0.98	-34.26*±8.00	-0.93 NS±2.88	13.17* ± 2.85	26.33* ± 5.31
SWPP	4.20*±0.42	0.07 NS±0.09	-1.15 NS±1.15	-0.65 NS±0.41	0.48 NS ± 0.36	2.42* ± 0.88

continued

Table 9 continued

Characters	Cross V (5A × 6A)					
	m	[d]	[h]	[i]	[j]	[l]
DMF	73.84*±0.60	-1.18*±0.16	8.74*±1.58	3.78*±0.58	0.46 NS ±0.53	-4.63*± 1.07
NPBMF	2.81*±0.12	0.02 NS ±0.04	0.67*±0.32	0.21 NS ±0.11	0.05 NS ±0.11	-0.23 NS ± 0.23
NSBMF	12.06*±0.45	-0.30*±0.10	4.16*±1.19	0.99*±0.44	-1.44*±0.38	-2.07*±0.81
PHMF	54.54*±0.66	-1.26*±0.12	1.79 NS ±1.76	0.13 NS ±0.65	0.47 NS ±0.55	0.07 NS ± 1.22
PWFD	27.77*± 1.50	-3.28*±0.42	3.29 NS ±3.91	2.75 NS ±1.44	6.39*± 1.30	0.60 NS ± 2.83
RWFD	1.71*±0.11	-0.22*±0.03	0.08 NS ±0.29	0.05 NS ±0.10	0.11 NS ±0.10	0.32 NS ± 0.19
NPPP	53.91*±3.60	1.05 NS ± 1.35	12.77 NS ±10.12	6.29 NS ±3.34	-3.63 NS ±3.88	-3.83 NS ± 7.21
PdWPP	10.50*±0.31	0.31 NS ±0.27	0.36 NS ±1.98	1.21 NS ±0.65	0.04 NS ±0.76	0.83 NS ± 1.42
NSPP	62.29*±4.06	0.68 NS ± 1.53	19.90 NS ±11.49	5.09 NS ±3.76	-2.84 NS ±4.41	-15.89 NS ±8.36
1000-SW	139.78*±2.44	3.60*±0.71	-22.46*±6.39	11.91*±2.34	5.13*±2.09	31.21*±4.97
SWPP	8.02*±0.65	0.23 NS ±0.24	3.41 NS ±1.82	2.14*±0.60	0.31 NS ±0.69	-1.68 NS ± 1.32

Table 10: Estimation of components of genetic variation (D, H and E) and degree of dominance ($\sqrt{H/D}$) of eleven characters in five crosses of chickpea.

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 1A×3A	D	0.449	0.046	3.951	4.498	7.701	0.096	47.138	1.353	42.017	286.022	0.951
	H	-1.617	-0.179	-10.858	-12.354	-23.114	-0.242	-155.650	-4.329	-160.978	-440.742	-3.308
	E	0.342	0.035	1.543	1.770	3.935	0.033	27.987	0.798	31.431	40.037	0.623
	$\sqrt{H/D}$	-1.898	-1.975	-1.658	-1.657	-1.733	-1.585	-1.817	-1.789	-1.957	-1.241	-1.865
Cross 2C × 4C	D	1.649	0.171	2.128	2.540	25.391	0.054	17.702	0.661	30.384	23.231	0.583
	H	-5.535	-0.540	-9.119	-9.042	-59.153	-0.271	-47.372	-1.750	-73.060	-91.964	-1.533
	E	0.910	0.085	1.867	1.472	8.210	0.062	7.441	0.242	9.076	14.992	0.205
	$\sqrt{H/D}$	-1.832	-1.778	-2.070	-1.887	-1.526	-2.236	-1.636	-1.628	-1.551	-1.990	-1.621
Cross 4C × 3C	D	2.104	0.123	2.915	4.484	196.053	0.111	217.024	10.278	333.577	65.880	8.228
	H	-6.422	-0.368	-8.939	-11.560	-639.943	-0.314	-553.871	-25.116	-819.010	-185.495	-20.081
	E	1.000	0.056	1.612	1.451	101.802	0.048	74.875	3.287	107.827	34.195	2.630
	$\sqrt{H/D}$	-1.747	-1.733	-1.751	-1.606	-1.807	-1.680	-1.598	-1.563	-1.567	-1.678	-1.562

Continued

Table 10 continued

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 4A×7B	D	1.876	0.134	0.359	2.651	4.517	0.054	57.301	1.607	86.299	61.203	1.102
	H	-3.643	-0.404	-2.131	-6.440	-18.472	-0.169	-116.271	-3.465	-173.568	-187.582	-2.365
	E	0.424	0.054	0.736	0.826	3.942	0.025	12.234	0.399	20.336	30.293	0.289
	$\sqrt{H/D}$	-1.393	-1.740	-2.437	-1.559	-2.022	-1.765	-1.425	-1.468	-1.418	-1.751	-1.465
Cross 5A × 6A	D	2.424	0.035	0.894	2.359	16.957	0.067	3.424	0.466	2.276	29.093	-0.025
	H	-6.051	-0.165	-2.090	-4.752	-42.618	-0.211	-169.345	-7.246	-211.950	-82.366	-4.984
	E	0.835	0.040	0.364	0.616	5.955	0.038	52.292	2.063	66.434	16.890	1.623
	$\sqrt{H/D}$	-1.580	-2.163	-1.529	-1.419	-1.583	-1.780	-7.033	-3.944	-9.650	-1.683	14.057

Table 11. Estimation of heritability in percentage (h^2_b and h^2_n), genetic advance (GA) and genetic advance as percentage of mean (GA%) of eleven characters in five crosses of chickpea.

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 1A×3A	h^2_b (%)	-110.595	-159.952	-91.893	-90.238	-96.090	-60.386	-121.352	-103.262	-157.733	45.051	-129.535
	h^2_n (%)	138.026	168.264	245.605	241.674	191.874	235.405	186.413	172.218	172.271	196.276	175.062
	$GA_{(b)}$	-0.919	-0.385	-1.698	-1.793	-2.804	-0.178	-8.889	-1.333	-11.347	7.922	-1.390
	$GA_{(n)}$	1.147	0.405	4.538	4.802	5.599	0.694	13.655	2.224	12.393	34.531	1.879
	$GA\%_{(b)}$	-0.962	-11.668	-8.509	-3.650	-4.858	-8.448	-20.254	-18.041	-25.754	6.177	-24.429
	$GA\%_{(n)}$	1.201	12.274	22.742	9.775	9.701	32.933	31.113	30.088	28.128	26.910	33.015
Cross 2C × 4C	h^2_b (%)	-159.343	-141.714	-186.778	-205.640	-34.212	-189.205	-67.256	-78.877	-51.186	-321.790	-80.772
	h^2_n (%)	235.006	244.228	163.495	263.768	207.534	126.102	198.957	244.071	253.053	328.079	257.548
	$GA_{(b)}$	-1.944	-0.546	-3.104	-2.940	-1.743	-0.572	-2.922	-0.598	-2.584	-12.468	-0.560
	$GA_{(n)}$	2.868	0.941	2.717	3.771	10.574	0.381	8.645	1.851	12.773	12.712	1.786
	$GA\%_{(b)}$	-2.065	-18.731	-13.803	-5.041	-3.052	-22.665	-5.652	-7.301	-4.684	-9.640	-7.828
	$GA\%_{(n)}$	3.046	32.280	12.082	6.465	18.516	15.106	16.721	22.592	23.155	9.829	24.962
Cross 4C × 3C	h^2_b (%)	-123.939	-122.931	-93.088	-80.754	-155.511	-89.809	-66.687	-53.100	-54.342	-64.703	-52.547
	h^2_n (%)	235.719	245.432	174.555	279.303	246.035	218.201	241.570	239.356	238.739	158.657	238.643
	$GA_{(b)}$	-1.706	-0.400	-1.752	-1.490	-20.221	-0.295	-9.207	1.603	-9.357	-6.073	-1.421
	$GA_{(n)}$	3.244	0.799	3.286	5.155	31.992	0.717	33.352	7.225	41.107	14.892	6.458
	$GA\%_{(b)}$	-1.757	-12.357	-9.995	-2.906	-24.674	-13.598	-15.969	-14.087	-13.487	-4.360	-14.696
	$GA\%_{(n)}$	3.341	24.670	18.742	10.052	39.037	33.037	57.847	63.502	59.252	10.690	66.743

Continued

Table 11 continued

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000S-W	SWPP
Cross 4A×7B	h^2_b (%)	6.082	-179.004	-92.325	-55.647	-149.083	-151.808	-3.529	-18.643	-1.207	-116.390	-16.133
	h^2_n (%)	208.458	348.210	46.857	244.986	142.678	271.892	242.463	238.682	214.740	218.594	221.385
	$GA_{(b)}$	0.084	-0.511	-1.177	-0.798	-3.864	-0.312	-0.249	-0.223	-0.111	-8.971	-0.166
	$GA_{(n)}$	2.881	0.993	0.597	3.712	3.698	0.559	17.169	2.853	19.829	16.848	2.275
	$GA\%_{(b)}$	0.091	-18.762	-5.946	-1.588	-7.229	-15.425	-0.784	-4.182	-0.296	-8.080	-3.990
	$GA\%_{(n)}$	3.135	36.497	3.018	7.392	6.919	27.626	53.872	53.547	52.585	15.175	54.663
Cross 5A ×6A	h^2_b (%)	-56.327	-139.971	-26.120	-1.356	-56.658	-102.887	-348.178	-326.292	-355.512	-55.737	-345.664
	h^2_n (%)	226.869	104.572	154.856	194.052	223.041	176.057	14.672	48.130	7.803	134.132	-3.464
	$GA_{(b)}$	-0.848	-0.374	-0.289	-0.022	-2.276	-0.291	-24.500	-4.675	-27.968	-3.781	-4.297
	$GA_{(n)}$	3.416	0.279	1.714	3.117	8.958	0.498	1.032	0.690	0.614	9.099	-0.043
	$GA\%_{(b)}$	-1.093	-12.016	-2.119	-0.039	-7.522	-15.780	-40.503	-41.496	-40.833	-2.661	-44.109
	$GA\%_{(n)}$	4.400	8.977	12.562	5.627	29.610	27.003	1.707	6.121	0.896	6.403	-0.442

Table 12: Estimation of number of effective factors (K_1), mid-parent heterosis (MPH), better-parent heterosis (BPH) and inbreeding depression (ID) for eleven characters in five crosses of chickpea.

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 1A×3A	K_1	0.168	0.055	0.016	0.014	0.031	0.008	0.0162	0.001	0.00006	0.015	0.011
	MPH	0.499**	4.615**	9.375**	4.302**	4.699**	7.134**	12.960**	4.713**	6.351**	-1.120 ^{NS}	3.451**
	BPH	0.209 ^{NS}	3.030**	7.969**	3.767**	3.815**	5.728**	10.626**	4.324**	6.228**	-2.585 ^{NS}	1.738**
	ID	0.004 ^{NS}	0.044 ^{NS}	0.042 ^{NS}	0.017 ^{NS}	0.032 ^{NS}	0.047 ^{NS}	0.065 ^{NS}	0.049 ^{NS}	0.079 ^{NS}	0.008 ^{NS}	0.079 ^{NS}
Cross 2C × 4C	K_1	0.002	0.015	0.0003	0.010	0.007	0.046	0.016	0.056	0.003	0.772	0.049
	MPH	0.106 ^{NS}	10.345**	4.654**	5.044**	2.366**	21.212**	9.2284**	13.284**	10.745**	7.408**	18.594**
	BPH	0.053 ^{NS}	8.475**	4.535**	4.749**	1.636 ^{NS}	18.644**	8.084**	10.520**	10.122**	3.837**	15.603**
	ID	0.00007 ^{NS}	0.057 ^{NS}	0.029 ^{NS}	0.026 ^{NS}	0.026 ^{NS}	0.094 ^{NS}	0.042 ^{NS}	0.059 ^{NS}	0.082 ^{NS}	-0.024 ^{NS}	0.083 ^{NS}
Cross 4C × 3C	K_1	0.157	0.922	0.002	0.008	0.0002	0.014	0.011	0.007	0.004	0.016	0.013
	MPH	2.146**	9.188**	6.205**	3.470**	1.849 ^{NS}	14.664**	12.893**	11.800**	14.156**	-3.478 ^{NS}	9.501**
	BPH	1.542**	-1.449**	5.747**	3.073**	1.589 ^{NS}	12.500**	9.840**	9.252**	12.203**	-4.170 ^{NS}	5.877**
	ID	0.025 ^{NS}	0.060 ^{NS}	0.049 ^{NS}	0.017 ^{NS}	0.015 ^{NS}	0.100 ^{NS}	0.080 ^{NS}	0.090 ^{NS}	0.101 ^{NS}	-0.025 ^{NS}	0.065 ^{NS}

Continued

Table 12 continued

		Characters										
		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPPP	PdWPP	NSPP	1000-SW	SWPP
Cross 4A×7B	K_1	0.0003	0.042	0.063	0.005	0.023	0.006	0.003	0.006	0.0009	0.117	0.005
	MPH	1.397**	14.563**	9.138**	4.453**	8.449**	11.309**	59.506**	55.098**	64.881**	-5.914**	53.900**
	BPH	1.369**	11.321**	8.290**	4.201**	7.777**	10.327**	57.116**	51.799**	63.399**	-7.994**	50.764**
	ID	0.005 ^{NS}	0.062 ^{NS}	0.052 ^{NS}	0.028 ^{NS}	0.040 ^{NS}	0.048 ^{NS}	0.223 ^{NS}	0.228 ^{NS}	0.216 ^{NS}	0.024 ^{NS}	0.227 ^{NS}
Cross 5A ×6A	K_1	0.570	0.018	0.101	0.670	0.633	0.720	0.322	0.203	0.001	0.446	-2.065
	MPH	0.419 ^{NS}	7.438**	8.429**	3.179**	3.744**	19.755**	4.402*	-0.213 ^{NS}	-2.643 ^{NS}	-2.085 ^{NS}	-4.057**
	BPH	-1.079**	6.557**	5.993**	0.858*	-6.318**	6.501**	2.612 ^{NS}	-2.766**	-2.715 ^{NS}	-4.356*	-6.165**
	ID	0.012 ^{NS}	0.049 ^{NS}	0.037 ^{NS}	0.017 ^{NS}	0.066 ^{NS}	0.132**	0.056 ^{NS}	0.068 ^{NS}	-0.030 ^{NS}	0.082 ^{NS}	0.045 ^{NS}

DISCUSSION

Quantitative characters showed a continuous variation which are controlled by polygenes and it is not possible to classify them into distinct classes. Information about the genetic components of variation helps the breeder in the selection of desirable parents for crossing programmes and also in deciding a suitable breeding procedure for the genetic improvement of various quantitative traits (Singh and Narayanan, 1993).

The inheritance studies of quantitative characters have to imply through biometrical genetics by construction of special models and procedures. Genetic information regarding the nature, relative magnitude and type of gene action following a proper genetic model is very important in a crop for successful breeding research. Plant breeders need to quantify additive and non-additive components of genetic variation in order to determine appropriate selection methods to improve quantitative characteristics. In this part eleven quantitative characters are studied under five consecutive crosses.

This study was undertaken to investigate genetical architecture of yield and yield contributing characters. In this situation estimation of genetic parameters and information on type of gene action; generation mean and the joint scaling test (based on two and three parameters model) and thereby computation of the additive and dominance effects were useful to evaluate genetical mechanism of some plant characters. Therefore in this regard many researchers used this method for inheritance studies (Esparza and Foster, 1998; Zhang *et al.*, 1999; Przulj and Maldenov, 1999; Malik *et al.*, 1999; Sharma *et al.*, 2002; Akhtar and chowdhury, 2006).

The result of Mather's test indicated that adequacy of additive-dominance model for the characters DMF, NPBMF, NSBMF, PHMF, RWFD, NPPP and PdWPP in cross I (1A × 3A); for the characters DMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP and SWPP in cross II (2C × 4C); for the characters

NPBMF, NSBMF, PHMF, NPPP, NSPP and SWPP in cross III (4C × 3C); for the characters DMF, NPBMF, NSBMF and PdWPP in cross IV (4A ×7B) and also the characters NPBMF, PHMF, NPPP and NSPP in cross V (5A ×6A). But in the rest of the characters in these five crosses, scaling test A, B and C showed that simple additive-dominance model was not suitable, i.e., model was inadequate.

Khodambashi *et al.* (2012) studied lentil and found that only the trait pod length was suitable for simple additive-dominance model. In A, B, C scaling test due to the significant and negative results for seed yield per plant, plant height, 100-seed weight, number of pods per plant, nodes per main stem and the number of secondary branches Kearsey and Pooni (1996) indicated the importance of epistatic effects in the control of these traits. Aliyu (2007) found in cowpea that in the A, B, C scaling test C scale was not significant different from zero for leaf pubescence density, leaf pubescence length, stem pubescence density and stem pubescence length for the two crosses. However, the C scale was not adequate for pod pubescence density and length. In chickpea Kidambi *et al.* (1988) observed that a simple additive model was adequate to the inheritance of LL and LA traits. In wheat Shahid (1996) found that additive–dominance model was adequate to explain the gene action for spikelet per ear, grains per ear and fertile tillers per plant.

Adeniji *et al.* (2007) in West African okra observed that the A, B and C scaling test were non-significant for 100-seed weight, while it was significant for seed yield per plant. Hasib *et al.* (2002) in aromatic rice observed that individual scaling test and combined scaling test were non-significant for days to flowering and test weight in 88-8-3/ Basmati 370, spikelet fertility percent in 88-8-3/ Pakistan Basmati and 124-17-4/ Basmati 370, plant height and grain number per penicle in 33-9-15/ pusa Basmati-I and days to flowering, spikelet fertility percent, test weight and grain yield per plant in 124-17-4/ pusa Basmati-I, indicating the absence of epistatic interaction. Iqbal and Nadeem (2003) found significant difference for yield of seed cotton per plant in one or the other tests in all the crosses except S-14 × LRA5166. These significant tests were indicating inadequacy of simple additive-dominance model. While for number of sympodial

branches per plant, scaling test divulged the absence of non-alleic interaction in most of the crosses except S-12 × S-14, S-14 × LRA5166, LRA5166 × S-12 and LRA5166 × S-14. These findings partially agreed with the results of Azhar *et al.* (1994).

Novoselovic *et al.* (2004) estimated genetic effect of two winter wheat crosses and found that the additive-dominance model was adequate for plant height and grain weight per spike of the longest clum. In scaling test, Deb and Khaleque (2009) found that in cross I for MPBFF, PWH, NPD/P, PdW/P, NS/P; in cross II for NPBFF, PWH and PdW/P and in cross III for PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P additive-dominance model was found to be adequate in chickpea crosses. Samad *et al.* (2009) in blackgram found that additive-dominance relationship for soluble protein in root nodules in cross II and also for soluble protein in seeds in both of the crosses were non-significant i.e., additive-dominance models were adequate for these traits. In blackgram Nahar *et al.* (2010) also found that simple additive-dominance model were adequate in most of the cases.

In the Cavalli's (1952) joint scaling test the χ^2-values were found to be non-significant for NSBMF, PHMF, PWFD, RWFD, NPPP and PdWPP in cross I (1A × 3A); for DMF, PHMF, RWFD, NPPP and NSPP in cross II (2C × 4C); for NSBMF, PHMF, RWFD, NPPP, NSPP and SWPP in cross III (4C × 3C); for DMF, NPBMF, NSBMF, PHMF, PWFD, NPPP and NSPP in cross IV (4A × 7B) and for NPBMF, NPPP and NSPP in cross V (5A × 6A). Thus it exhibited the presence of only additive-dominance effects in the inheritance of these characters and crosses. This result of the present investigation indicated that due to the presence of only the additive-dominance relationship for those characters and crosses these materials would likely be helpful in doing successful breeding plan for the development of potential lines in chickpea.

Shahid (1996) observed that almost all the characters in all the crosses except Aghrani × FM-32 (4) for harvest index, fertile tillers/plant, spikelets/ear and grains/ear, where 3-parameters model was satisfactory to explain the genetic

differences. Similar results were obtained by different workers such as Islam (1980) in egg plant for different characters and crosses viz. YP and HT in cross 1; PS in cross 2; FW, TF, and YT in cross 3; PS and PB in cross 4 and PB, FW and TF in cross 5 and Uddin (1983) in wheat for EL in cross 1, 3, 5, 7and 8; for FEN/P in cross 1, 2, 3, 4, 5, 7and 8; for SN/E in cross 1, 2, 5 and 6; for KN/E in cross 3 and 4 and for Y/P in cross 1, 2, 3, 4 and 5. Rahman (1984) also observed that additive-dominance model was adequate for LL4, LLS, LW5, LV4 CW, PW and PV in *Philosamia ricini*. Novoselovic *et al.* (2004) observed both non-significant and significant χ^2-values when studied six quantitative traits of wheat plant in two crosses at two site. Same results observed by Hasib (2002) in aromatic rice. The χ^2-values were found to be non-significant for soluble protein by Samad *et al.* (2009) in both of the characters and crosses in blackgram. Eshghi and Akhundova (2010) observed two hulless barley crosses; here the joint scaling test revealed that the additive-dominance was adequate in three cases. Nahar *et al.* (2010) found similar result in some traits in two crosses of blackgram. Khodambashi (2012) observed that the simple additive-dominance model fitted only in case of pod length, hence epistatic interactions are involved in genetic control of the other studied traits in lentil. Using joint scaling tests, Mittal and Bhardwaj (2008) observed the presence of epistasis for pods per plant, pods per cluster, 100-seed weight and seed yield per plant in cowpea. The χ^2-values of the joint scaling test in the rest of the characters such as DMF, NPBNF, NSPP, 1000-SW and SWPP in cross I(1A × 3A); for NPBMF, NSBMF, PWFD, PdWPP, 1000-SW and SWPP in cross II (2C × 4C); for DMF, NPBMF, PWFD, PdWPP and 1000-SW in cross III (4C × 3C); for RWFD, PdWPP, 1000-SW and SWPP in cross IV (4A × 7B) and for DMF, NSBMF, PHMF, PWFD, RWFD PdWPP 1000-SW and SWPP in cross V (5A × 6A) were significant, i.e., inadequacy of the additive-dominance model. Inadequacy of the model showed that in the inheritance of these characters with the additive-dominance gene effects, non-allelic interaction and linkage may play a part. Toklu and Yagbasanlar (2007) studied two traits and observed that significant additive-dominance gene effect detected in all the crosses according to joint scaling test for 1000-kernel weight.

Deb and Khaleque (2009) observed non-significant χ^2 values for NPBFF, PHMF, PWH, PdW/P and NS/P in cross 1, for NPBFF, PWH and PdW/P in cross 2 and PHMF, PWH, NPD/P, PdW/P, NS/P and SW/P in cross 3 which indicated the presence of only additive-dominance relationship. Aliyu (2006) in cowpea for testing the adequacy of the model the chi-square (χ^2) value found to be significant for PPD and PPZ in cross IT82D-716 × TVnu515 and also for LPD, PPD and PPL of the cross IT82D-716 × RVnu1473. Significant χ^2-values were noted by Joarder *et al.* (1980) in rice and Uddin (1983) in wheat, Islam (1980) in egg plant, Rahman (1984) in *Philosamia ricini*, Eshghi and Akhundova (2002) in hulless barley and Nahar *et al.* (2010) in blackgram.

The results of the six parameters model indicated the presence of the individual type of digenic epistatic effects. From table 9 it was observed that both significant and non-significant values of m, [d], [h], [i], [j] and [l] were obtained from the five respective crosses for eleven quantitative characters. In the analysis it was observed that duplicate types of epistasis were present in different characters and crosses. Many researchers worked on six parameters model, such that Adeniji *et al.* (2007) worked with this model on earliness in West African Okra among five crosses he found a non-significant [i], [j], [l] interaction effect on one cross and in others a duplicate type of epistasis were present. Here the additive and the additive × dominance gene effect was positive and significant for some crosses. Toklu and Yagbasanlar (2007) in wheat reported that for the large kernel ratio, additive gene effect was significant in all crosses, while dominance gene effect was significant only in two crosses. Significant additive × additive and dominance × dominance epistatic gene action was detected in Bow "S"/Crow "S" × Panda cross for the large kernel ratio. Eshghi and Akhundova (2007) in two crosses of hulless barley detected significant additive × additive, additive × dominance and dominance × dominance gene effect for some traits. Here duplicate type of epistasis was found for plant height and grain yield per plant in cross ICNBF93-369 × ICNBF-582 and for number of grains per spike in both crosses. Thangavel and Thirugnanakumar (2011) in green gram studied six-parameter model for five metric traits. From this result he suggested the presence of additive and dominance gene effects along with

epistatic interaction in almost all the crosses indicating the importance of both additive and non-additive gene action in the expression of all the five characters, however, a duplicate dominant epistatic was prevalent in most of the case. Khodambashi (2012) in lentil also found duplicate epistasis for all traits except pod length in the cross L3685 × Lc74-1-5-1. Iqbal and Nadeem (2003) in cotton also found that additive × additive interaction was significant in all the crosses except S-14 × LRA 5166. The additive × dominance epistasis was significant in two crosses i.e., Albacala (69)11 × S-12 and LRA 5166 × S-12 and the dominance × dominance was significant in all the crosses except S-12 × Albacala (69)11 and S-14 × LRA 5166. These findings collaborated with the work of Saudhu and Nittal (1988). Bnejdi and El-Gazzah (2010) in durum wheat found that in most cases a digenic epistatic model explained variation in generation means. Dominance effects and dominance × dominance epistasis were more important than additive effects and other epistatic components. Similar observation were made by Khattak *el al.* (2004a and 2004b) in mungbean; Aliyu (2006) in cowpea; Bnejdi and El-Gazzah (2010) in wheat on epistasis and six-parameter model. Novoselovic (2004) in wheat reported that dominance effects and additive × additive epistasis were more important than additive effects and other epistatic components. Duplicate type of epistasis were also obtained by Farshadfar *et al.* (2008) in chickpea; Singh *et al.* (2007) in mungbean; Ketata *et al.* (1976a and 1976b) in wheat; Perera *et al.* (1986); Hasib *et al.* (1976); Buu and Tao (1992) in rice.

Components of variation were computed on the basis of additive-dominance model. Three equations of three parameters viz, D, H and E, a perfect fit solution to them was obtained. The estimation of additive (D) component expressed positive value in all the crosses for all the characters except SWPP in cross V (5A × 6A) where it was negative. Considerable amount of positive D values indicated that additive component of variation was important in the present investigation. Similar results were reported by Paul *et al.* (1976) and Samad (1991) in rapseed, Joarder (1982) in mustard, Hogarth and Kingsfon (1984), Wu *et al.* (1980) and Nahar (1997) in sugarcane and Husain (1997) in chilli, Benjdi and El-Gazzah (2010) in durum wheat, Adeniji *et al.* (2007) in West African okra, Samad *et al.*

(2009) in blackgram, Deb and Khaleque (2009) in chickpea and Farshadfar *et al.* (2008) in chicpea.

The estimation of H component was negative in all the five crosses for eleven quantitative characters. The negative dominance (H) component is also supported by Moll *et al.* (1960), Lindsey *et al.* (1962) and Willium *et al.* (1965) in maize, Joarder *et al.* (1977) in mustard, Samad (1991) in rapeseed, Nahar *et al.* (2000) in sugarcane, Benjdi and El-Gazzah (2010) in durum wheat, Adeniji *et al.* (2007) in West African okra, Samad *et al.* (2009) in blackgram, Nahar *et al.* (2010) in blackgram. On the other hand, D and H components were found to be negative only for SWPP in cross V (5A × 6A).

Negative estimation of components of variation, however might arise from sampling errors (Mather, 1949) and genotype-Environment interaction (Hill, 1996). Similar results were obtained by Novoselovic *et al.* (2004) in wheat plant that in all the traits additive (D) component was positive and dominance (H) was negative except in grain yield per plant where dominance and additive components were negative at soissons/zitarka cross at Nova Gradiska site. Iqbal and Nadeem (2003) in cotton also found negative value in both D and H components. Khaleque *et al.* (1978) in rice, Paul *et al.* (1978) in Indian mustard, Joarder *et al.* (1980) in rice, Walton (1972) and Rahman (1982) in wheat also found similar results.

The degree of dominance as measured by the ratio of $\sqrt{H/D}$ showed over dominance in five crosses for all the eleven quantitative characters. Eunus (1964) observed over dominance in three different crosses viz, Atsel × Tulate, Frontier × Bonneville and Montclam × Beecher. In Hulless Barley Eshghi and Akhundova (2010) observed over dominance gene action for number of grains/ spike and grain yield/ plant of ICNBF93 × ICNBF-582. Degree of dominance for most of the characters (except grain yield and biological yield) showed over dominance which was observed by Farshadfar *et al.* (2008) in chickpea. Khodambashi *et al.* (2012) found that the average dominance ratio was more than unity (over dominance) for seed yield per plant, number of primary branches, number of secondary branches, pod length and 100-seed weight which showed the importance of the dominance

gene effects. Nahar *et al.* (2010) in blackgram also found that all the characters in both the crosses showed over dominance. Similar results were also obtained by Uddin (1983) in wheat, by Deb and Khaleque (2009) in chickpea and by Samad *et al.* (2009) in blackgram.

Heritability estimation both in broad sense and narrow sense were found to be high in majority cases. Toklu and Yagbasanlar (2007) reported higher narrow sense heritability calculated in Panda × 84CZT04 and Panda × Bow "S"/Crow "S" crosses were 99.0% and 60.0%, respectively. Adeniji *et al.* (2007) estimated high broad sense heritability as found in his study and suggested that the earliness among the generations was highly heritable. Bnejdi and El-Gazzah (2010) studied grain protein content in durum wheat in four crosses at two sites and found that values of narrow sense heritability were moderate to high (48% - 85%). Novoselovic *et al.* (2004) in wheat estimated narrow sense heritability for plant height, number of heads per plant, number of grain per spike of the longest clum, grain yield per plant and single grain weight and found high narrow sense heritability in maximum cases and these heritabiliy values are in accordance with Sidwell (1978), Baric (1996) and Drezner (1996). Narrow sense heritability estimates were found to be very high for heading date, moderately high for kernel weight and plant height and moderate for number of tillers per plant and low for spikelet per ear, kernel per spikelet and grain yield in winter wheat cross when studied by Ketata *et al.* (1976a and 1976b). Aliyu (2006) observed high narrow sense heritability for pubescence density and pubescence length. Toklu and Yagbasanlar (2007) also estimate narrow sense heritability ranged from 60% to 99% for large kernel ratio and 23% to 100% for kernel weight.

Khodambashi *et al.* (2012) estimated high value of narrow sense heritability for pod per plant, seeds per plant and seeds per pod indicated that selection for these three yield components is likely to be successful. Here they also found low narrow sense heritability for pod length and 100-seed weight, therefore, it is apparent that selection for these traits would likely be difficult and high environmental influence may be a problem. In studies by Gangele and Rao (2005) in lentil and Arshad *et al.* (2002) in cow pea, the low heritability was reported for pod length and seed yield

per plant. Similar results with high heritability for plant height, 100-seed weight, number of seeds per pod and seed yield per plant were reported by Bicer and Sarker (2004), Singh and Singh (2004) and Khan *et al.* (2006) in lentil, Saleem *et al.* (2002) in chickpea and Salgotra and Gupta (2005) in common bean. Eshghi and Akhundova (2010) estimated broad and narrow sense heritability for five characters in two crosses and found both high and low heritability. Low broad sense and narrow sense heritability was also observed by Alam *et al.* (2009) in sugarcane, Husain *et al.* (2000) in chilli, Deb and Khaleque (2009) in chickpea, Samad *et al.* (2009) and Nahar *et al.* (2010) in blackgram.

In the present investigation, the genetic advance (GA) was lower in all of the characters in all crosses. Nahar (1997) in sugarcane recorded lower values of genetic advance for CH, CD, TC, MCC, FB, RSP and CYC. Veeramani *et al.* (2005) reported high heritability with high genetic advance and high genetic advance as percentage of mean for some studied traits. Farshadfar *et al.* (2008) estimated moderate narrow sense heritability for grain yield with moderate genetic advance for grain yield and protein content. Genetic advance as percentage of mean (GA%) values in the present study showed low values in broad sense while in narrow sense it showed moderate high values. It showed high values for NPPP, PdWPP and NSPP in cross III and for NPPP, PdWPP, NSPP and SWPP in cross IV. Majid *et al.* (1982) studied blakcgram and found the highest GA and GA% for the number of pods per plant. Nahar (1997) also obtained the highest GA with GA% for leaf area in sugarcane suggesting that the direct selection for the characters would be effective for the improvement of yield.

According to Mather (1949), the effective factor is the smallest unit of hereditary materials that is capable of being recognized by the method of biometrical genetics. Either it may be a closely linked gene, or at the lower unit a single gene. K_1 was estimated on the basis of the following assumptions: (i) considering equal importance of all genes, (ii) all the minus genes consisting in one parent and the other parent consists of all the plus genes, (iii) no linkage between parental genes, (iv) additive effects of gene, (v) similar degree of dominance due to all the plus genes and (vi) no non-allelic interaction. With these

conditions, failure of any one to fulfill in the parents will underestimate the number of effective factors. In the present investigation, the values of K_1 (Table 12) were very low for all the characters and crosses. The present findings agree with the reports of different workers in different crops viz. Eunus (1964) in barley; Goto (1964), Lal *et. al.* (1971), Joarder *et al.* (1980) in rice and Islam (1980) in eggplant; Uddin (1983) in wheat and Rahman (1984) in eri silkworm, Kumar and Singh (1995) and Deb (2002) in chickpea.

Heterosis as a measure of the superior performance of hybrid relative to the average of the parents is a means of identifying superior genotypes. From table 12 it was observed that most of the characters in five crosses both mid parent and better parent heterosis were significant. Shahid (1996) reported significant heterotic performances in most of the traits in all crosses indicated good prospect of hybrid wheat. Iqbal and Nadeem (2003) observed that mid parent heterosis were significant for all the crosses except Albacala (69) × S-12 and these results are in accordance with the findings of Subhan *et al.* (2001). Abdullah *et al.* (2002) observed that most of the crosses showed significant heterosis over mid-parent and better-parent for various characters. Cheema *et al.* (1990) found cross combination of Basmati 370 × DM16-5-1 and DM 16-5-1 × DM 107-4 showed highly significant heterosis. Islam (1980) obtained non-significant heterosis both over MP and BP levels in eggplant for different characters and crosses. Husain (1997) also noted non-significant BPH for DFR in chilli. Alam *et al.* (2004) in rice observed significant heterosis for most of the traits and among the 10 hybrids, four hybrids viz, 17A × 45R, 25A × 37R, 31A × 47R and 35A × 47R showed the highest heterosis. Adenij *et al.* (2007) observed high (0.85-1.13%) MPH in crosses Ace4 × Ace5 and Ace1 × Ace2 in West African okra. Similarly, Toklu and Yagbasanlar (2007) in bread wheat and Farshadfar *et al.* (2008) in chickpea where they also observed higher mid-parent heterosis for most of the characters.

In the present investigation the inbreeding depression showed non-significant values in all the eleven quantitative characters in all the crosses except only RWFD in cross V (5A × 6A) where it was highly significant. Cheema *et al.* (1990) observed non-significant inbreeding depression in two cross combinations in rice.

Non-significant inbreeding depression was also observed by Cheema *et al.* (1990) in two cross combinations in rice and Husain (1997) in BPH for DFR in chilli. Alam *et al.* (2004) in rice found non-significant and both positive and negative inbreeding depression in many crosses for the studied characters.

The present investigation showed that further breeding experiment could be done considering two lines of researchers with these materials; first for the development of pure lines and second for the utilization of hybrid vigour commercially. It has been found from the analysis that the characters viz, NSBMF, PHMF, NPPP and PdWPP in cross I (1A × 3A); DMF, PHMF, NPPP and NSPP in cross II (2C × 4C); NSBMF, PHMF, NPPP and NSPP in cross III (4C × 3C); DMF and NPBMF in cross IV (4A × 7B) additive-dominance model was found to be adequate as the χ^2 values were non-significant which was supported by ABC scaling test. These crosses for those characters also indicated high narrow sense heritability and high genetic advance. The high heritability and high genetic gain are the indication of additive gene effect (Panse, 1957). Therefore these crosses for those characters would likely be good materials for the development of prospective pure lines for further breeding works.

The second line of fruitful research would likely be with the crosses for the characters viz, NSPP and SWPP in cross I (1A × 3A); NPBMF, 1000-SW and SWPP in cross II (2C × 4C); DMF and PdWPP in cross III (4C × 3C); RWFD and 1000-SW in cross IV (4A × 7B) and NSBMF in cross V (5A × 6A) showing high heterosis both for mid-parent and better-parent and also showing over whelming dominance and duplicate type of epistasis suggesting that these crosses for those characters be utilized for the commercial exploitation of hybrid vigour.

SUMMARY

In the present genetic study, eleven quantitative characters are investigated with five single crosses of chickpea (*Cicer arietinum* L.) using six generations (P_1, P_2, F_1, F_2, B_1 and B_2). The objective of the present investigation was the genetic analysis of quantitative characters in chickpea using generation means, where additive-dominance model, gene effects, heritability, genetic advance, effective factors, heterosis and inbreeding depression were evaluated.

Mather's (1949) scaling test were done for testing the adequacy of additive-dominance model and joint scaling test was applied for testing the goodness of fit of the model by compared observed generation means with that of the expected means.

From the Mather's scaling test it was revealed that the additive-dominance model was adequate for the characters DMF, NPBMF, NSBMF, PHMF, RWFD, NPPP and PdWPP in cross I (1A × 3A); for the characters DMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP and SWPP in cross II (2C × 4C); for the characters NPBMF, NSBMF, PHMF, NPPP, NSPP and SWPP in cross III (4C × 3C); for the characters DMF, NPBMF, NSBMF and PdWPP in cross IV (4A × 7B) and also the characters NPBMF, PHMF, NPPP and NSPP in cross V (5A × 6A).

From joint scaling test the χ^2-values were found to be non-significant for NSBMF, PHMF, PWFD, RWFD, NPPP and PdWPP in cross I (1A × 3A); for DMF, PHMF, RWFD, NPPP and NSPP in cross II (2C × 4C); for NSBMF, PHMF, RWFD, NPPP, NSPP and SWPP in cross III (4C × 3C); for DMF, NPBMF, NSBMF, PHMF, PWFD, NPPP and NSPP in cross IV (4A × 7B) and for NPBMF, NPPP and NSPP in cross V (5A × 6A), which showed the presence of only additive-dominance effects in these characters and crosses.

From the six-parameters model (Jinks and Jones, 1958) it appears that the parameters and their gene interactions ([i], [j], [l]) were operative in all the crosses.

The presence of duplicate type of epistasis was detected for some characters in all the crosses.

Components of variation were computed on the basis of additive-dominance model. The estimation of additive (D) component expressed positive value in all the crosses for all the characters except SWPP in cross V (5A × 6A) and the H component was negative in all the five crosses. The degree of dominance indicated over dominance in five crosses for all the eleven quantitative characters.

Heritability both in broad and narrow sense were found to be high in majority of the cases. Genetic advance (GA) and genetic advance as percentage of mean (GA%) were moderate to high in both broad and narrow sense.

In the present study the values for number of effective factors (K_1) were very low for all the characters and crosses indicated the presence of one group of polygenes. Both mid and better parent heterosis was significant for most of the characters in five crosses. In case of inbreeding depression all the characters in five crosses showed non-significant inbreeding depression except RWFD in cross V (5A × 6A).

In cross I (1A × 3A) NSBMF, PHMF, NPPP and PdWPP; in cross II (2C × 4C) DMF, PHMF, NPPP and NSPP; in cross III (4C × 3C) NSBMF, PHMF, NPPP and NSPP; in cross IV (4A × 7B) DMF and NPBMF, these crosses for those characters might be used for the development of pure line in further breeding research because of their adequacy of the additive-dominance model and high narrow sense heritability with high genetic advance.

The characters viz., NSPP and SWPP in cross I (1A × 3A); NPBMF, 1000-SW and SWPP in cross II (2C × 4C); DMF and PdWPP in cross III (4C × 3C); RWFD and 1000-SW in cross IV (4A × 7B) and NSBMF in cross V (5A × 6A) would be utilized for commercial utilization of hybrid vigour because of the presence of high heterosis, overwhelming dominance and duplicate type of epistasis.

PART II

GENETYPE-ENVIRONMENT INTERACTION

INTRODUCTION

Chickpea, like many other legumes, received very little attention in the past from the genetic improvement point of view. This had been mainly due to the scarcity of genetic variability in the world stock of germplasm. Chickpea has faced tough competition in recent years with cereal crops, where high yielding and inputs responsive varieties are available.

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 genotype-environment interaction in a biometrical analysis, have long been recognized as an important source of phenotypic variation (Immer *et al.* 1934: Yates and Cochran, 1938 and Mather, 1949).

Environmental involvement in the expression of phenotype of an individual was first recognized by Johannsen (1909) while working with dwarf bean (*Phaseolus vulgaries*). He reported that heritable and non-heritable differences were jointly responsible for the variation in seed weight of beans and were of the same order of magnitude in effect. The different analysis of continuous variation over a number of years on many plant and animal species revealed the combination of heritable and non-heritable agencies in the determination of continuous variation.

In the recent past, two main approaches have been made under regression for detecting and estimating the interaction between genotypes and environments. The first is purely statistical methods originally proposed by Yates and Cochran (1938), which was later on modified by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). Finlay and Wilkinson (1963) used this method to detect and measure the magnitude of G × E interactions in barley and considered linear regression slopes as a measure of stability. Eberhart and Russel (1966) emphasized the need of

considering both the linear (b_i) and non-linear ($\bar{S}^2_{di}$) components G ×E interaction in judging the phenotypic stability of a genotype. A cultivar with a high mean with unit regression coefficient (b =1.0) and a deviation of zero ($\bar{S}^2_{di} = 0$) from regression is referred as stable genotype.

The second approach involves the fitting of models, which specify the contribution of genetic and environmental actions and genotype-environment interactions to the generation means and variances. It also determines the contribution of additive, dominance and non-allelic gene action to the total genotype-environment interaction components. This approach had been used by Mather (1949), Jinks (1954), and Jinks and Mather (1955) in *Nicotiana rustica* L. followed by Bucio Alanis (1966), Bucio Alanis and Hill (1969), and Perkins and Jinks (1968).

Perkins and Jinks (1968) formed a bridge over the gap between two alternative analyses. Breese (1969) and Paroda and Hayes (1971) advocated that the linear regression (b_i) could simply be regarded as measure of response of a popular genotype, whereas the deviations around the regression lines ($\bar{S}^2_{di}$) were considered as better measure of stability; genotypes with their lowest deviations being the most stable and vice versa. Using the above definition of the term stability, it was possible to judge the phenotypic stability and due consideration was also given to the mean performance and linear response of the individual genotype.

The joint regression analysis, a form of the analysis of variance, has been widely used in the study of G ×E interaction. Its procedures and applications were reviewed by Freeman (1973) and Hill (1975). The effectiveness of the analysis in resolving the differences in genotypic response is related to the degree of linearity of response. On the other hand, successful application necessitates that a high portion of G × E interaction sum of square is attributed to the linear regression.

The performance of crop plants varies in different environments which indicate their adaptability to specific region or over wide areas (Khan *et al.*, 2002). With the help of statistical techniques developed to estimate stability parameters, it is possible to determine genotypic response for wider adaptability. Eberhart & Russell (1966) model had been widely used to study stability parameters. With the advancement of statistical techniques, methods are available for analysis of G x E interactions which consists of complementary procedures of classification and grouping the genotypes according to their response in different environments (Tuteja, 2006). Berger *et al.*, (2007) listed 30 publications that reported highly significant G x E interaction for yield, which suggested that the issue was important in chickpea.

At present, it has become a challenge to breeders to understand fully the control of genetic variation due to the occurrence of genotype- environment interaction. When a set of plant genotype is grown over a range of environments the genotypes do not behave in the same relative way in all environments and it is due to the interaction of different genotypes with different environments differently. This situation leads the breeder to face serious problems in the realization of the breeding objective for any economic crop.

Genotype × environment interaction (G × E) is increasingly important, because breeding programmes tend to be more internationally oriented. During recent decades, new improvements have been accomplished in plant physiology, agronomy and statistics and some incorporated approaches emerged for G × E interactions evaluation (Brancourt, 1999).

The genotype × environment interaction was studied by different researchers in various crops (Singh *et al.*, 1987; Jain and Pandya 1988; Rao and Suryawanshi 1988; Ashraf *et al.*, 2001; Zubair and Ghafoor, 2001). The stability parameters have also been studied in grain legumes for measuring phenotypic stability (Khan *et al.*, 1987; Khan *et al.*, 1988; Bakhsh *et al.*, 1995, Sharif *et al.*, 1998, Qureshi, 2001).

Breeding experiment needs wide variation of the selected lines and crossing between them, then in final selection of the progenies to be established as fortuitous varieties. In this respect of course G × E interaction is very important, by applying the treatment causing variation among the population and their interaction with the treatments i. e., the environments provide us the information about the varieties which could be adaptable to wide range of environment give us the opportunities of doing appropriate breeding experiment and through which characters of interest would likely be improved in consideration of the environment as limiting factor.

The major goal of this work to study the genotype-environment interaction and some genetic parameter for these selected lines. Moreover, selection of the favourite promising lines which had a stable genotypes under different climatic conditions in Bangladesh.

REVIEW OF LITERATURE

The relationship between genotype and environment was realized in the last century while the fundamental nature of gene action and interaction involved in the inheritance of quantitative characters were not understood. The development of genetics began with the rediscovery of Mendel's work in 1900. Johannsen (1909) for the first time put forward the idea of the relationship between heritable and non heritable (environmental) effects and that the variation in a pure line was due to environment. Many papers have already been published in various crops and a few in chickpea concerning with the problem of genotype-environment interactions at different times and some of these papers are reviewed below.

East (1915) showed that the continuous variation in the segregating generation was due to both genotype and environmental effects.

At first Mather (1949) introduced the biometrical technique based on mathematical models of Fisher *et al.*, (1932) for measurement of the continuous variation from two distinct lines developed with the development of first (mean) and second (variance and covariance) degree statistics. Also then, Mather and Jones (1958) and Jinks and Stevens (1959) were combindly formulated the techniques to measure the genotype–environment interaction based on the mathematical models of Fisher *et al.*, (1932). This technique provided the partitioning of total variation into genetic and environmental components while studying the genetic variance in relation to the environmental effects.

Finlay and Wilkinson (1963) developed statistical technique to compare the yield performance of a set of cereal varieties grown at several locations for several seasons. The regression of yield on mean yield of all varieties for each site and season when tested for varieties and sites had a high degree of linearity and has been used as a

measure of adaptability of the varieties. Yates and Cochran (1938) also developed similar techniques.

Eberhart and Russell (1966) recommended that a genotype with a regression coefficient (b) about 1.0 showed average stability over all environments tested when b>1.0 there is evidence of good yielding capacity for favorable environments and when b<1.0 there is deficiency in yielding ability under these condition. They again proposed that a variety with mean > grand mean, unit regression coefficient (b=1.0) and least deviation from regression ($\bar{S}^2_{di}$=0) is considered as a stable genotype.

Khaleque (1975) worked on 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 of *Brassica campestries* L. All of them showed that genotype-environment 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.

Joarder *et. el.* (1978) studied G × E interaction of some quantitative characters of four varieties of *Brassica campestries* L. They reported that G × E interaction item was highly significant for all the characters they studied and in all the six generations. The joint regression analysis showed that all the items were significant at 1% level except environment residuals for seed/siliqua and yield/plant. Both the linear and non-linear items were significant for all the characters and generations. Mean performance was significantly correlated with S^2_{di} but bi was independent of Xi. Correlation between bi and S^2_{di} was highly significant but is negative in case of seeds/ siliqua and yield/plant.

Samad (1991) worked on G × E interaction of six agronomical characters in fifteen rapeseed (*Brassica campestris* L.) cultivars in six consecutive years. He

observed that genotype-environment interactions were significantly operative in the experiment. He also observed all the genotypes for plant height and number of pods per plant failed to show the stable performance, while some of the genotypes like Polar, Tori-9, Tori-7 and Sampad were predicted to show the stable performances in regard to the agronomical characters such as number of secondary branches, number of seeds/pod and yield/plant.

Deb (1994) studied G × E interaction on 7 chili varieties using 5 quantitative characters under 4 consecutive years. He reported in his study that the performances of different characters in 7 chili varieties where b was significant due to response in different years. Joint regression analysis indicated that both linear and non-linear relationship exist with environment. He also reported that none of the genotype fulfilled the criteria of stable genotype for a particular character. However, var-6 for NLIF, var-2 for NLMF, var-6 for NPBIF and var-3 and var-6 for 100-fruit weight/plant showed stable performances.

Kumar *et. al.* (1996) conducted multilocation trials of 16 genotypes of desi and kabuli chickpea in a number of countries in three seasons at 17 (1981-'82), 31(1982-'83) and 22 (1983-'84) locations between 10°-52° latitudes. Combined analysis of variance for seed yield was done to study the genotype × environment interactions and stability of genotypes. Mean squares for locations, genotypes and genotypes × location interactions were significant. Locations and genotype × location interaction variances were much higher than those for genotypes. Genotypes exhibited relatively more interaction with winter-sown locations than with spring-sown locations. Desi types showed more variation than the kabuli types. They observed that seed size did not appear to influence yield performance and stability.

Hoque (1997) studied genotype – environment interaction of some morphological characters under soil moisture stress condition in chickpea (*Cicer arietinum* L.). He observed genotype and environmental items were significant for all the characters.

Joint regression analysis indicated that the linear portion of G × E interaction were 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 PHFF, ICCL-83105 for PHMF in 1993-'94 and all the genotypes for NSBFF 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 conditions.

Nahar (1997) worked on genotype × environment interaction of ten sugarcane clone for eight quantitative characters at two different locations under two consecutive years (1992-'93 and 1993-'94). She observed that genotype-environment interaction were operative. A significantly greater portion was accounted for by linear function of the environmental mean and some portions of interactions were non-linear and independent of the linear function. She also observed that both linear and non-linear components of genotype × environment interactions were under the control of different gene systems. In her investigation, she recorded stability performances of different clones were different for different characters. The genotypes Isd 2- 54 and Isd 20 for CH and RSP; L Jaba C for CH, MCC, FB and RSP; B 34-231 for TC; Isd 16 for CD and RSP; were predicted to show the stable performance; *i.e.* adaptable to all environments. The clones which were adaptable for favourable environments are Isd 2- 54 for LA and MCC; Isd 16 for CH, LA and FB; Isd 18 for CH, MCC, FB,RSP and CYC; Isd 20 for FB; I525-85 for CH,MCC and RSP;B34-231 for MCCand BC_1 for CYC. The poorly adaptable varieties for all environments were Isd 2-54 for CYC, Isd 16 for TC, B34-231 for CH and RSP; and CP 55-30 for RSP.

Islam *et al.* (2000) studied eighteen chickpea (*Cicer arietinum* L.) lines for germination test of length of radicle (RL) and 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 environment (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 coefficient were largely significant for all the genotypes. The differences between the genotypes both for pulmule and radicle length 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 environments.

Hasan (2001) worked on stability parameters regarding irrigation treatments on six yield component of six chickpea (*Cicer arietinum* L.) lines. In regression analysis, he observed that, genotype was highly significant for all the characters and the $\bar{S}^2_{di}$ value was also found to be non-significant for all the characters. Some of the lines (genotypes) having non-significant $\bar{S}^2_{di}$ values and average regression coefficient values with less standard error indicated that they would likely to show stable performance in different environmental conditions. Besides, some of the lines exhibited above average regression coefficient values, which indicated that these lines would likely to perform well in better environment only.

Islam *et al.* (2002) worked on genotype- environment interaction on yield and some of the yield components in lentil (*Lens culinaris* Medic.). They carried out investigation for NPBFF, NSBMF, DWPP, PdWPP, NPdPP, NSPP and SWPP in twelve genotypes at eight environments. The item G was highly significant for all the characters, indicating that genotypes were genetically different. On the other hand, environment item was significant for all the characters except NSPP. Significant G × E item indicated that the genotypes interacted with the environments differently for most of the characters under study. In the joint regression analysis, major part of G × E interaction was not due to heterogeneity however, remainder item was found to be highly significant for all the characters. The regression coefficient (b_i) exhibited above average responses for significance of regression values in different genotypes for all the characters except NSBMF, NPdPP and NSPP. The high and significant $\bar{S}^2_{di}$ values indicated the unstable performance for all the genotypes and characters under study.

Arshad *et al.* (2003a) studied 25 genotypes of chickpea for stability of grain yield under 12 diverse environments. The interaction between the genotypes and environments (G × E interaction) was used as an index to determine the yield stability of genotypes under all the environments. The G × E interaction was highly significant and both linear as well as non-linear components were equally important for determining the yield stability. Since the regressions (b_i) were not significantly different from linearity, therefore, stable performance of the varieties could not be predicted on 'b_i' alone. In this case, deviations from regression and the cultivars yield were used to judge the superior genotypes. The genotypes; '96051', '90280', 'C44', '91A039', 'NCS95004', 'NCS950010', 'NCS950180', '99101', 'A-16', '91A001', 'NCS950012' and '93009' produced above average yield. The genotypes '96051' and '98280' gave highest grain yield but their high deviation from regression showed fluctuation in the performance under different environments. The genotypes 'C44', 'NCS950183' and '93009' had also above average yield but their low deviation from regression revealed more stable performance compared to others.

Asif *et al.* (2003) studied nine genotypes of wheat developed for rainfed areas viz., DN-18, NRL- 9822, NR-200, V-99166, 98CO13, V-3, PR-72, NR-181 and SN - 7 and were evaluated for stability of grain yield under seventeen diverse rainfed environments. The interaction between the genotypes and environments (G × E interaction) was used as an index to determine the yield stability of genotypes under all the environments during 2001-02. Both predictable (linear) and unpredictable (non-linear) portions of variation were found to be significant indicating equal importance in determining the stability of grain yield. The genotype V-99166 was the most adopted showing good performance in the entire set of environments under study.

Jeanne and Consorcia (2004) investigated genotype × environment interaction (GE) in transplanted rice using yield data in 2002 wet season at 18 locations. Significant heterogeneity of variances among the 18 locations were revealed by the

Bartlett's Chi-Square test (p=1.000). A subset consisting of 5 locations whose Error Mean Square (MSEs) were more or less homogeneous (p=0.06) were pooled in the combined analysis of variance to have a valid test for the significance of the G × E interactions. Highly adapted genotypes were identified namely *Matatag5*, *Matatag6*, *Matatag3* and PSB Rc28 as forming a convex hull in the AMMI1 biplot. IR65 and IR72 showed specific adaptability while, PR31563-AR32-19-3-4, PR30244-AC-9-1 and PR27445-3B-12-1 showed general adaptability to all environments.

Dethe and Dumbre (2005) studied on eighteen genotypes of French bean comprising the newly developed lines and certain existing varieties under three distinct environments for nine quantitative traits including seed yield. The significant value of the G x E interactions revealed differential response of the genotypes to varying environmental conditions. Stability parameters revealed that the genotypes viz., Red Cloud, ACPR-94038, ACPR-94039, Contender and HPR-35 possessed stability for seed yield. Most of the high yielding genotypes were relatively stable. Genotypes possessing stability indicated their suitability for general cultivation and also to use as donor parents in breeding program.

Bakhsh *et. al.* (2006) studied on the effect of genotype x environment interaction on relationship between yield and three yield components in 20 genotypes of chickpea. Significant differences were found between genotypes for the three yield components at all the locations. It was found that the pattern and strength of correlation between number of seeds pod-1 and yield, between number of seeds pod-1 and number of pods plant-1 and number of seeds pod-1 and number of branches plant-1 differed from location to location. The relationship of fruit bearing branches and number of pods plant-1 with grain yield remained positive at all the locations, though the strength of their correlation with grain yield was affected by environments. On the basis of this study it is proposed that importance should be placed on number of pods and number of fruit bearing branches while making selection from segregating populations for yield improvement.

Khatod *et al.* (2006) studied on G × E interaction and stability of 10 sugarcane genotypes. In their results genotype, environment and its interaction at linear and non-linear level were found significant for the characters cane yield, CCS yield, single cane yield and NMC '000'/ha, while G × E interaction at linear and non-linear were non- significant for number of tiller and juice extraction%.

Hammed and Al-Badrany (2007) studied on Stability of chickpea (*Cicer arietinum L.)* varieties under rainfall conditions in northern Iraq and evaluated the stability of seed yield, iis components and protein content. They grown twenty-two chickpea genotypes (lines and cultivars) in five different environments under rainfed conditions in the area of northern of Iraq and found the combined analysis had a significant difference at 1% level for genotype, environments and their interactions for all characters. Local variety exhibited the highest order for stability in the no. of days to 50% flowering and 90% maturation with four stability techniques. Dijla variety showed the highest rank for plant height and protein content. Rafidain gave the highest order for no. of pods per plant and seed yield (kg / ha) in more stability techniques.

Asad *et al.* (2009) worked to determine the possible effects of environments and genotypic differences for yield in 7 advanced mutants of non-aromatic rice along with parent variety IR6 and 2 checks were tested at 8 different sites in Sindh during 2004 and 2005 rice cropping season. Genotypes, locations, genotype × environment interactions were highly significant ($P< 0.01$) indicating genetic variability between genotypes by changing environments. Stability analysis showed that mutants IR6-15/A and IR6-15/E had the mean paddy yield with regression coefficient (b) less than or close to unity (1.10 and 0.85) and the lowest deviation from regression (S^2d) (0.03 and 0.17) suggesting above average stability and adaptability over environments. IR6-15-18 produced low mean yields with the highest regression coefficient (b) and highest deviation from regression coefficient (S^2d) had below average stability and is specifically adapted to favorable environments.

Atta *et al.* (2009) developed elite chickpea genotypes through mutation breeding at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad and evaluated for stability of grain yield at four diverse locations in the Punjab province during 2003-04, 2004-05 and 2005-06. They used the genotype yield, regression coefficient (bi), deviations from regression (S^2_{di}) with sustainability index to identify the stable genotypes. The analysis of variance for seed yield at individual locations showed significant to highly significant differences between genotypes. Pooled analysis of variance over locations displayed highly significant differences between genotypes, locations and genotype x location interaction. Among 14 genotypes, the maximum mean seed yield over the locations was produced by the CC119/00 (1.229 t ha^{-1}) and the highest mean seed yield producing location was NIAB (1.412 t ha^{-1}). The analysis of stability based on mean grain yield, regression coefficient and deviation from regression revealed that the genotypes; CC119/00, CC117/00 (Colchicine mutants), CM256/99, CH38/00 and K-70022 were most stable and adapted to the diverse environmental conditions of Punjab.

Dar *et al.* (2009) studied on eleven promising genotypes of Chickpea (*Cicer arietinum* L.) in three environments for seed yield and observed significant differences among the genotypes which revealed the presence of variability for the trait under investigation. Significant variance due to G x E over environments indicating that the yield performance of the genotypes showed a differential reaction in different years. G x E (linear) effect was not significant which indicated that the yield performance of the genotypes could not be predicated over environments. Significant pooled deviations showed that the variation in the seed yield of the genotypes was influenced by some unpredictable factors. Three genotypes SKUA-C 23311, SKUA-C 23109, and SKUA-C 23320 were most stable coupled with high mean performance for seed yield over the environments with least deviation from

regression co-efficient ($\bar{S}^2_{di}$). These genotypes can be incorporated in the breeding programs for getting high yielding and stable segregants in chickpea.

Mosisa and Zelleke (2009) worked on the nature and magnitude of genotype x environment (G × E) interaction and phenotypic yield stability of twenty maize cultivars at nine locations with three replications for two years. Variances due to genotypes, years, locations, genotype × year, genotype × location and genotype × year × location interaction were significant ($P<0.01$). Most of the cultivars had significant deviation mean squares ($\bar{S}^2_{di}$), implying that these cultivars had unstable performance across the testing environments.

Shah *et al.* (2009) studied on genotype-environment interactions and stability analysis of yield and yield attributes of ten contemporary wheat varieties of Pakistan for testing of wheat varieties in different agro-ecological zone that is essential for evaluation of stability of performance and range of adaptations. They determined variety-environment interaction, stability and adaptability of various characters and effect of different environments relationship of characters with grain yield and grain protein percentage in spring wheat (*Triticum aestivum* L.). Ten varieties viz. Kiran-95, Mehran-89, Tandojam-83, Abadgar-93, Anmol-91, Punjab-96, Chakwal 86, Shahkar-87, Parwaz-94 and Pirsabak-85 were evaluated at nine different locations for three years during the 1999-2000, 2000-2001 and 2001-2002, respectively. They recorded data on various plant characters viz. plant height, peduncle length, flag leaf area, productive tillers per meter, spike length, number of spikelets per spike, rachis segment length, number of grains per spike, 1000-grain weight, grain protein percentage, number of maturity days and grain yield (t/h). Variety-location (σVL) variety-year (σVY) and variety-location-year (σVLY) interactions were highly significant for all the characters. They concluded that the relative magnitude of interaction variance components indicate the relative performance of varieties for plant height, peduncle length, flag leaf area, productive tillers parameter, rachis

segment length, 1000-grain weight, grain protein percentage and grain yield were more inconsistent across locations than years. The opposite was true for spike length spikelets per spike, grain per spike and maturity days. The stability parameters (within variety mean square (Si^2), variety coefficient of variation (CVi %), ecovalence (Wi^2), variety interaction variance (σi^2), regression coefficient (bi), deviation from regression mean square (σi^2) and coefficient of determination (Ri^2)), revealed a range of stability for all the characters.

Kan *et. al.* (2010) carried out a study to identify stability and adaptability of 19 chickpea (*Cicer arietinum* L.) cultivars grown in arid and semi arid conditions at three locations (Field Crops Central Research Institute in Ankara, Bahri Dagdas International Agricultural Research Institute in Konya and Research Farms of Agriculture Faculty of Suleyman Demirel University in Isparta) for two years (2005 and 2006 years). Experiments was set up as randomized complate block design with three replications. Studied parameters were plant height, first pod height, 100 - grain weight and grain yield and stability parameters were calculated according to Finlay-Wilkinson and Ketata methods. Results showed (confirmed) that Menemen 92 (4) and Izmir 92 (6) were the highest yielding and stable cultivars at three locations during the study period in terms of plant height, first pod height and grain yield. For the 100 grain weight, Cagatay (2), Akcin 91 (9) and Er 99 (13) cultivars performed better than other cultivars.

Taghouti *et al.* (2010) studied on genotype × environment interaction of twelve Moroccan durum wheat cultivars representing a range of agronomic adaptation were tested in five locations representing a range of environments in three growing seasons. The results indicated significant effects of genotype, environment and G × E for all the quality traits. The component of variation due to genotype was larger than due to the environment, indicating the greater influence of genotypes on these traits. However, for vitreousness and protein content, the effect of environment was higher than the effect due to genotypes. Thus, these traits are controlled greatly by

environments than genes. The variation due to G × E was higher than that of genotype for vitreousness and test weight indicating high G × E interaction effect and less genotypic stability for these traits. For protein content, where the environmental effect was greater than that of genotype and G × E effect, multiple environmental trials are necessary in order to determine protein content of a cultivar.

Hamayoon *et al.* (2011) made a study on seed yield of 20 genotypes of chickpea under two different environmental conditions of Pakistan during 2007 to 2008. They carried out their experiment in randomized complete block design with three replications in each environment. Within environment, genotype main effect was significant. Similarly, genotype by environmental interaction was also significant. Genotypes at Karak produced significantly greater seed yield than at Peshawar. Cluster analysis of chickpea genotypes based on seed yield resulted in two main clusters. These two clusters were again subdivided into three and two sub-clusters indicating considerable diversity for grain yield among the chickpea genotypes. GGE biplot analysis ranked genotypes on above average seed yield across environments as Lo-3, Lo-2, Pk-2, Lo-4 and Pk-3 as top five genotypes, while the bottom five genotypes were identified as Sy-7, Pk-1, Sy- 4, Sy-5 and Pk-5. For stability of performance across environments, Pk-4, In and Pk-3 were identified as most stable genotypes followed by Lo-2, Pk-2, Pk-3 and Lo-3. On the basis of both stable performance and mean seed yield across environment, the GGE biplot ranked genotypes Lo-3 as the best among all, followed by Lo-2, Pk-2, Pk-3 and Lo-4, while the rest of the genotypes were identified as inferior. Karak was identified as representative environment as compared to Peshawar.

A study accomplished by Duzdemir (2011) on the influence of genotype × environment interactions on phenological characteristics of chickpea. Field experiments were carried out on four different locations, in semi-arid conditions, in complete randomized block design with four replications from 2001 to 2002. Eleven certified and 3 indigenous varieties were used. Emergency date, first flowering period,

flowering period and vegetation period were examined as phonological characteristics. For all the characteristics, important changes, source of genotype x environment interactions, were determined at $P<0.01$. Stability analysis was carried out for all the characteristics according to Finlay-Wilkinson and Eberhart-Russel models. Stable genotypes for each characteristic were found for two parameters.

Tiawari *et al.* (2011) were evaluated sixteen early maturing and elite genotypes of sugarcane at different environmental condition for identifying the stable cultivars. The stability of genotypes was estimated by using the method of Eberhart and Russell. In this analysis sum of square due to G × E were partitioned into individual genotypes (X-i), regression of environmental means (bi) and deviation from regression (S^2d). The regression coefficients (bi) and mean square deviation from regression (S^2di) were used to define genotype stability. Significantly mean square differences among Genotypes × Environment for all the characters were observed, this is an indication of significant variability among the experimentation. The stability parameters for NMC, cane yield, sucrose % and CCS% shown by the genotype CoJ64 compared to UP05233, CoS05266, CoS05260, CoS05276 and CoS05263 indicated better adoption and less sensitive to environmental changes. They concluded that for cane yield and sucrose % in juice the genotypes UP05233 and CoS05263 performance better than rest of elite genotypes studied having high mean values of genotypes over all three environments. Therefore, these genotypes may be commercially cultivated over a wide range of environments.

MATERIALS AND METHODS

A. MATERIALS

The materials used in this part were same as the materials used in part-I.

B. METHODS

The methods used in this study are described under the following sub-heads:

1. Collection and Irradiation of the Experimental Seeds.
2. Preparation of the Experimental Field.
3. Design and Size of the Experimental Field
4. Sowing of Seeds and Raising of the Seedlings.
5. Maintenance of the Experimental Field.
6. Collection of Data and
7. Techniques of Analyses.

The methods from 1 to 6 are the same as those described under the methods of PART-I except design of the experimental field. Layout of the experimental field and trial of the irradiated lines was conducted under randomized complete block design with 4 replications. Each replication having 4 blocks and each block having 8 plots. Each plot contains 3 rows and per row there are 5 hills. In each hill, one plant was maintained for data. Gap between block and that between plots were 50 cm. The same between rows and that between plants were 70 cm and 25 cm, respectively. The four irradiation doses considered as environment were (i) no irradiation (D_0) (ii) 20Kr (D_A) (iii) 30Kr (D_B) and (iv) 40Kr (D_C) conducted in the experiment in three consecutive years namely 2007-2008 (Y1), 2008-2009 (Y2) and 2009-2010 (Y3). For the study of genotype × environment interaction the 12 environments were as: Env.1- $Y1D_0$, Env.2-$Y1D_A$, Env.3-$Y1D_B$, Env.4-$Y1D_C$, Env.5- $Y2D_0$, Env.6-$Y2D_A$, Env.7-$Y2D_B$, Env.8-$Y2D_C$, Env. 9-$Y3D_0$, Env. 10-$Y3D_A$, Env. 11-$Y3D_B$ and Env. 12-$Y3D_C$.

7. Techniques of the Analysis of Data

To study the genotype × environment interaction, the data were analysed following the techniques of analysis as developed and used by Finlay and Wilkinson (1963) in barley; Eberhart and Russell (1966) in maize; Bucio Alanis (1966), Perkins and Jinks (1968) in *Nicotiana rustica* and Breese (1969) in grasses. In the study the following analyses were computed:

a) Mean: Data on individual plant basis were added together then divided by the total number of observations and the mean was obtained as follows:

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

Where,

X_i = The individual reading recorded on each plant

$\bar{X}$ = The mean of all the readings

$\sum$ = Summation

n = Number of observations

i = 1, 2, 3, - - - - n

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

$$S_{\bar{x}} = \frac{S}{\sqrt{N}}$$

Where,

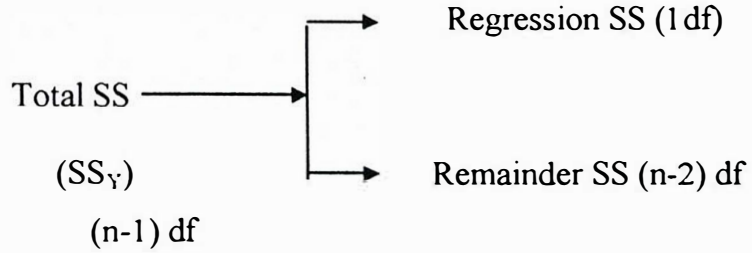
$S_{\bar{x}}$ = Standard error of mean

S = Standard deviation

N = Total number of individuals.

c) Regression analysis: Regression analysis was done following Perkins and Jinks (1968) and Eberhart and Russell's (1966) models.

The primary analysis of regression was done as follows:



Where,

n = number of observation

Regression SS = $(SP_{XY})^2/SS_X$

Remainder SS= Total SS (SS_Y) – Regression SS

Where, $SS_X = \sum X^2 - (\sum X)^2 /n$

$SP_{XY} = \sum XY - \sum X.\sum Y/n$

$SS_Y = \sum Y^2 - (\sum Y)^2 /n$

Regression coefficient ($1+b_i$): The responses of each genotype under different environments on the environmental means over all the genotypes are measured by regression coefficient. This was estimated as follows:

$$b_i = \frac{SP_{XY}}{SS_X}$$

Perkins and Jink's model (Joint regression analysis)

The analysis of genotype × environment interaction was followed as the specification given by Mather and Jones (1958). A practical application of these specifications in inbred lines as well as in segregating generation was given by Bucio Alanis (1966) and Bucio Alanis *et al.* (1969). Finally, the approach extended to any number of lines using the joint regression analysis by Yates and Cochran (1938) and put into a biometrical genetical context by Perkins and Jinks (1968), was followed.

The application is as follows:

In general, the Y_{ij} of the r replicates of the ith genotype in the jth environment is expected to be the sum of four components.

$$Y_{ij} = \mu + d_i + e_i + g_{ij}$$

With i varies from 1 to L, the number of genotypes and j varies from 1 to D, the number of environments.

μ, the over all means which is estimated as

$$Y../ LD = \sum_{i=1}^{L} \sum_{j=1}^{D} Y_{ij} / LD$$

d_i is the genetical deviation of the ith genotypes and as estimated as

$$(Y_{i}./ D) - \mu = \left(\sum_{j=1}^{D} Yij / D \right) - \mu$$

ej is the additive environmental deviation of the jth environment and is estimated as

$$\left(Y_{.j} / L\right) - \mu = \left(\sum_{i=1}^{L} Y_{ij} / L \right) - \mu$$

Finally, g_{ij} the genotype × environment interaction of the ith genotype and the jth environment is estimated as

$$Y_{ij} - \mu - d_i - e_j$$

Besides, the data was subjected to a standard two way analysis of variance to test the significance of the items which necessitates the inclusion of genotype × environment interaction model where environmental effects in each genotype are linear function of the additive environmental variance i.e.

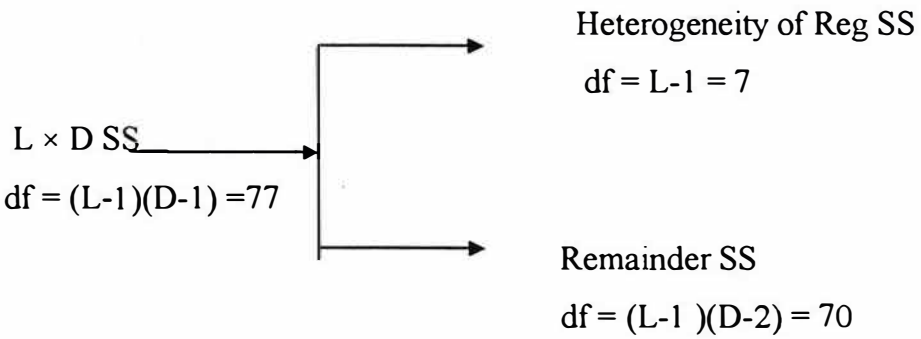
$$g_{ij} = b_i e_j$$

Whether these linear function differ among the genotypes is tested by the adequacy of the models

$$Y_{ij} = \mu + d_i + (1+b_i) e_j$$

by a joint regression analysis in which the sum of squares for genotype × environment interactions are partitioned into linear and non-linear portions following Perkins and

Jinks (1968). In the joint regression analysis the L × D SS is partitioned into heterogeneity of regression SS and non-linear (remainder SS) portion, as follows:



The whole joint regression analysis is shown in the following table:

Item	Df	SS	MS	F
Line (L)	L-1		MS_1	MS_1/MS_6
Environments (D)	D-1		MS_2	MS_2/MS_6
L × D	(L-1)(D-1)		MS_3	MS_3/MS_6
Heterogeneity of Reg.	L-1		MS_4	MS_4/MS_6
Remainder	(L-1)(D-2)		MS_5	MS_5/MS_6
Within error	LD(r-1)		MS_6	

Stability parameter

In this approach, the regression coefficient and the deviation from regression are used as the parameters of stability. As the regression of e_j on e_j is one, and regression of g_{ij} on e_j is β, therefore, the b_i value of Eberhart and Russell's (1966) model is

$$b_i = 1 + \beta_i$$

$$\beta_i = b_i - 1$$

Eberhart and Russell's model

The stability parameters following Eberhart and Russell's (1966) model are calculated as follows:

$$Y_{ij} = m + \beta_i I_j + \sigma_{ij}$$

Where,

i varies from 1 to L, the number of Lines and

j varies from 1 to D, the number of environments (doses)

Y_{ij} = Mean of ith lines in jth environments,

m = Mean of all the lines over all the environments.

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

I_j = The environmental index which is defined as the deviation of the mean of all the genotypes at a given environment from the over all mean.

$$= \frac{\sum_i Y_{ij}}{L} - \frac{\sum_i \sum_j Y_{ij}}{LD} \qquad \text{with } \sum_j I_j = 0$$

and σ_{ij} = The deviation from regression of the i th genotypes at j th environment.

Two parameters of stability are calculated:

(a) The regression coefficient which is the regression of the performance of each genotype under different environment on the environmental mean over all the genotypes. This is estimated as follows:

$$bi = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

Where,

$\sum_j Y_{ij} I_j$ is the sum of products and

$\sum_j I_j^2$ is the sum of squares.

(b) Mean square deviations, $\bar{S}^2_{di}$ (Stability) from linear regression: It is estimated by the following formula,

$$\bar{S}^2_{di} = \frac{\sum_j \sigma^2_{ij}}{(S-2)} - \frac{S^2_e}{r}$$

Where,

$$\sum_j \sigma^2_{ij} = \left[\sum_j Y_{ij}^2 - \frac{Y_i^2}{L}\right] - \frac{\left(\sum_i Y_{ij} I_j\right)^2}{\sum_j I^2_j}$$

$\sum_j \sigma^2_{ij}$ = The variance due to the deviation from regression, i.e., remainders sum of square.

$\sum_j Y_{ij}^2 - \frac{Y_i^2}{L}$ = The variance due to the dependent variable (SS_Y).

$\frac{\left(\sum_i Y_{ij} I_j\right)^2}{\sum_j I_j^2}$ = The variance due to regression (Reg.SS).

S^2_e = the estimate of the pooled error and

r = the number of replications.

The various computational steps involved in the estimation are as follows:

(i) Computation of environmental index (I_j):

$$I_j = \frac{\sum_j Y_{ij}}{L} - \frac{\sum_i \sum_j Y_{ij}}{LD}$$

$$= \frac{\text{Total of the genotyes at the environment}}{\text{Number of genotypes}} - \frac{\text{Grand total}}{\text{Total number of observations}}$$

(ii) Computation of regression coefficient (b_i) for each genotype:

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

Where,

$\sum_j Y_{ij} I_j$ = each genotype is the sum of products of environmental index (I_j)

with the corresponding mean ($\bar{X}$) of that genotype at each environment.

$\sum_j I_j^2$ = is the sum of squares of environment.

(iii) Computation of $\bar{S}_{di}^2$: In general, it is obtained by subtracting the variance due to regression from σ_y^2. It is calculated as follows:

$$\bar{S}_{di}^2 = \left[\sum \sigma_{ij} / (S-2)\right] - \left(S_e^2/r\right)$$

Standard error of b_i was calculated as follows:

$$S_{bi} = \sqrt{\frac{Rem.ms}{SS_X}}$$

d) Graphical analysis

(i) *Curve*

In the graphical analysis, curves were drawn separately for eleven yield and yield contributing characters of chickpea viz. Days to maximum flower (DMF), Number primary branches at maximum flower (NPBMF), Number of secondary branches at maximum flower (NSBMF), Plant height at maximum flower (PHMF), Plant weight after fully dry (PWFD), Root weight after fully dry (RWFD), Number of pods per plant (NPPP), Pod weight per plant (PdWPP), Number of seeds per plant (NSPP), 1000 seed weight (1000-SW) and Seed weight per plant (SWPP). For this purpose, environmental mean were plotted along the X- axis and the Lines mean along the Y-axis.

(ii) *Regression graph*

The regression graphs were drawn by plotting Y_i, the genotypic values along the vertical axis against X_i, the environmental values which are independent along the horizontal axis. In the figure the straight line drawn in the simple regression of Y on X, sometimes called fitted lines. The equation of regression line is as follows:

$$Y = a + b\,(X_i - \bar{X})$$

Where, Y is the estimated genotypic values given by an amount of X of the environment, and $a = \bar{Y}$, mean of all genotypes, $\bar{X}$ = environmental mean and the b, the regression coefficient is given by

$$b = \frac{SP_{XY}}{SS_X}$$

Where,

SP_{XY} = Sum of product between X and Y

SS_X = Sum of squares of X.

RESULTS

A. GENOTYPIC AND ENVIRONMENTAL MEANS

In this investigation eleven quantitative characters such as DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP, 1000-SW and SWPP of eight chickpea lines studied (as in part I). The results of genotypic and environmental means are described under the following sub-heads:

1. Genotypic mean

The mean performance of 8 lines over 4 replication and 12 environments (4 doses and 3 years) were computed and presented in table 13. From the table it is observed that the means were highly significant in all cases. The table 13 also showed that the different lines performed differently for different characters. For the character DMF the highest mean performance (96.6088±0.9018) was observed for line-5 followed by line-3 (96.2222±1.2261) and line-7 (93.1806±2.7013) and the lowest value (91.5556±1.0996) was found in line-2.

In case of NPBMF the line-5 exhibited the highest (3.3148±0.1001) performance; next highest values were shown in line-3 (3.2662±0.1042) and line-6 (3.2381±0.0822). The lowest value (2.3649±0.0571) was found in line-8 for this character. Regarding the character NSBMF the highest mean value (15.7208±0.4740) revealed by the line-1 followed by line-7 (15.5972±0.4651) and line-5 (15.5394±0.3958) and the lowest value (14.3634±.3320) was found in the line-8. In case of PHMF the line-4 exhibited the highest value (54.9514±0.7485), next highest values were shown by line-7 (53.9297±0.7136) and line-2 (53.3809±0.7065). The lowest value (50.4475±0.6866) was found in line-6 for this trait. Comparatively wide range of variation was observed for the character PWFD, here the line-2 exhibited the maximum value (75.6213±4.2016) followed by line-3 (74.2900±4.1413) and line-1 (68.0731±4.0289) and the line-8 showed the lowest value (61.5396±3.4383). Maximum RWFD mean (2.4449±0.0870) was found in the line-8 followed by line-2

(2.2651±0.0872) and line-3 (2.2375±0.0763) while the lowest value (1.3925±0.0423) was shown by the line-5. In case of NPPP, the mean data showed wide range of variation. Here the highest mean performance (61.0231±4.5340) was observed in line-5 followed by line-6 (53.9144±4.6296) and line-7 (53.2894±4.3584) and the lowest mean performance (26.5046±2.4059) was found in line-8. The line-2 exhibited the maximum value for PdWPP (12.4483±1.0726) followed by line-3 (12.3842±1.0913) and line-5 (12.2388±0.9317) and the lowest value (6.9065±0.6010) exhibited by the line-8. In case of NSPP the line-5 showed the highest value (68.5139±5.0630) followed by line-7 (60.9282±5.0441) and line-2 (58.2569±4.6123). The line-8 exhibited the lowest value (28.3606±2.6295). For 1000-SW the line-8 showed the highest mean value (199.9188±4.2355) followed by line-6 (159.6300±3.5948) and line-3 (158.5687±3.0986) while the lowest value was shown by the line-5 (139.2927±2.1153). In case of SWPP the highest line mean was observed in line-5 (9.5760±0.7422) followed by line-6 (9.3022±0.8050) and line-2 (9.1803±0.7842). For this trait the lowest mean performance was shown by line-8 (5.3940±0.4872).

2. Environmental mean

The environmental mean performances of all the eleven characters (DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP, 1000SW and SWPP) averaged over four replications and eight genotypes were calculated separately and are presented in table 14. It was noted from the table 14 that the mean values were highly significant in comparison to their respective standard errors. From this table it was observed that second year (2008-2009) and third year (2009-2010) environmental mean performances were higher than that of the first year (2007-2008) mean performances for all the characters except NPBMF and 1000-SW. While comparison between second year (2008-2009) and third year (2009-2010) the characters NPPP, PdWPP, NSPP, 1000-SW and SWPP showed higher mean performances in second year and DMF, NPBMF, NSBMF, PHMF and PWFD showed higher environmental mean performances in third year. The characters NPPP, PdWPP, NSPP and SWPP had the highest mean performances in Env.5 (Y_2D_0). On

the other hand the characters DMF, NSBMF and PWFD showed the highest value for the Env.10 (Y_3D_A). While the character NPBMF showed highest mean value in Env.4 (Y_1D_C), PHMF showed the highest value in Env.7 (Y_2D_B), RWFD showed highest mean performance in Env.11 (Y_3D_B) and the characters 1000-SW showed the highest mean performance in Env.2 (Y_1D_A). While the characters PWFD, NPPP, PdWPP, NSPP and SWPP showed the lowest mean performances in Env.2 (Y_1D_A), the characters DMF, NSBMF showed lowest value in Env.1 (Y_1D_0). On the other hand the characters NPBMF and 1000-SW showed the lowest mean values in Env.7 (Y_2D_B) and PHMF in Env.4 (Y_1D_C) and RWFD in Env.3 (Y_1D_B) showed the lowest environmental mean performances.

B. REGRESSION ANALYSIS

To get more useful information on genotype-environment interaction, the data were subjected to regression analysis in Part-II. From this analysis we know the response of individual genotype in different environments. The results of regression analysis for the present investigation were done following different models (Perkins and Jinks, 1968; Eberhart and Russell, 1966) were presented in table 15, 16, 17 and 18 which were illustrated below.

1. Joint regression

Joint regression analysis of eleven quantitative characters were done in eight chickpea line under twelve environment (4 doses and 3 years) are shown in table 15. The environmental effects for each of the eight lines, whether a linear function of the additive environmental values or not were tested by joint regression analysis. The regression analysis of the eight lines was conducted separately (Table 15) before calculating the joint regression analysis. On summing up over all the eight lines sum of squares for regression (Reg SS) and remainder (Rem SS) in table 15, a total sum of squares for regression SS and remainder SS were determined. The heterogeneity of regression was calculated by subtracting total Rem SS from L × D SS (joint regression). An experimental sum of square was made within the replication means of

experiment from each environment and was termed as within error. Table 15 showed that the main item L was highly significant for all the characters except NSBMF which showed significance at 5% level when tested against within error. Another main item environment was highly significant for all the characters. The interaction item L × E was significant only for 1000-SW.

In the joint regression analysis L × E interaction sum of square was partitioned into heterogeneity of regression (linear) and remainder (non-linear) (Table 15). It was observed from the table 15 that the heterogeneity of regression was highly significant only for 1000-SW and the characters NPPP and SWPP were significance at 5% level. The rest of the characters were non-significant when tested against within error. Significant heterogeneity of regression indicated that the major portion of genotype-environment interaction was due to the differences between the slopes of linear regression for these traits. The remainder item was non-significant for all the characters except 1000-SW which was significance at 5% level. Here all the traits showed non-significant heterogeneity indicated that there were deviations from linearity in these lines. The significant remainder item suggested that non-linear type of L × E interaction was existed in the lines.

2. Remainder mean square

To get information about individual line, each of the remainder mean square of individual line was tested against respective individual line error. It was observed from the table 17 that the remainder mean square of all the lines in all the characters were non-significant.

3. Phenotypic regression

The regression technique for studying the genotype-environment interaction is important among the most widely used methods for investigating the response pattern of the individual line. The results of regression coefficient (b_i), (β_i) and standard error of regression coefficient (S_{bi}) for eleven quantitative characters of eight chickpea lines are presented in table 18.

In fact, the regression coefficient measures the responses of increments in an improving environment. As these increments were measured by the mean of all the lines, the average response for any set of lines under consideration must have a regression coefficient of unity. Regression coefficient in the present investigation were $b_i = 1.0$, $b_i > 1.0$ and $b_i < 1.0$ indicated an average, above average and below average response, respectively by the lines. The character wise responses of different lines were as follows:

Days to maximum flower (DMF): It was observed from table 18 that most of the line showed significant regression coefficients in this character except line-1, line-5 and line-7 where regression coefficient was non-significant. In this trait all the lines showed average response to the environment except lin-5 which showed below average response.

Number of primary branches at maximum flower (NPBMF): In respect of this character, all the lines showed non-significant regression coefficient except line-1 which showed significant regression coefficient. The above average responses were observed in line-5. The line-1, line-3, line-4, line-7 and line-8 exhibited average response, on the other hand lin-2 and line-6 expressed below average response.

Number of secondary branches at maximum flower (NSBMF): For this character, line-4, line-6 and line-7 showed significant and line-1, line-2, line-3, line-5 and line-8 showed non-significant regression coefficients. The above average responses were noted for line-4. Line-1, line-2, line-3, line-5 and line-7 showed average response and the line-6 and line-8 exhibited below average responses to the environments.

Plant height at maximum flower (PHMF): Regarding this character, significant regression coefficient was recorded for all the lines except line-5, line-6 and line-8. All the lines exhibited average response, only line-8 showed below average response to the changing environment.

Plant weight after fully dry (PWFD): For this trait all the lines exhibited significant linear responses to the environment except line-5. The average response was observed for all the line except line-4 and line-5 which showed below average responses.

Root weight after fully dry (RWFD): For this character only line-8 showed significant regression coefficient. The above average responses were noted for line-1, line-7 and line-8. The line-3 and line-6 exhibited average responses to the environments and the rest of the lines showed below average responses.

Number of pods per plant (NPPP): For this trait, significant regression coefficient was recorded for all the lines. The average responses to the changing environments were shown by all the lines except line-8 which showed below average response.

Pod weight per plant (PdWPP): In respect of PdWPP, all the lines responded significantly to the changing environment except line-3. The line-2 exhibited above average responses. Average responses to the environments showed by the line-3, line-4, line-5, line-6 and line-7, while line-1 and line-8 showed below average responses.

Number of seeds per plant (NSPP): For this character, all the lines responded significantly to the environment. Here line-1, line-2, line-4, line-5, line-6 and line-7 showed average responses. The remaining lines viz, line-3 and line-8 showed below average responses to the changing environments.

1000-seed weight (1000-SW): In respect to this character all the lines were non-significant regarding b_i values. The line-2, line-4 and line-6 exhibited above average responses, while only line-8 showed average responses. The remaining lines viz, line-1, line-3, line-5 and line-7 showed below average responses to the changing environments.

Seed weight per plant (SWPP): Here all the lines responded significantly to the environment. The above average response was observed for line-2 and line-6. Average responses exhibited line-4, line-5 and line-7. The line-1, line-3 and line-8 exhibited below average response regarding this character.

4. Deviation mean squares ($\bar{S}^2_{di}$)

Stability performance is one of the most important desirable characters of a genotype to be released as a variety for wide adaptation. A number of statistical methods are known for estimation of phenotypic stability. Two parameters of stability such as regression coefficient (b_i) and deviation mean squares ($\bar{S}^2_{di}$) are computed according to Eberhart and Russell's model (1966). The significant deviation mean square measures the unpredictable irregularities in response to the environments. When the deviation mean square is non-significant, performance may be predictable. This predictable performance of a genotype is said to be stable. The individual genotypic $\bar{S}^2_{di}$ were tested by C test. The results of $\bar{S}^2_{di}$ values obtained for all the eleven quantitative characters of eight chickpea genotypes are shown in table 18.

Days to maximum flower (DMF): For this character all the lines except line-1, line-3 and line-7 showed non-significant deviation mean square from regression. This result indicated that most of the lines showed stability for this trait.

Number of primary branches at maximum flower (NPBMF): In this case all the lines showed non-significant deviation mean squares from regression. This result indicated that most of the lines showed stability for this trait.

Number of secondary branches at maximum flower (NSBMF): For this character all the lines also showed non-significant deviation mean squares from regressions, which suggested that all the lines were stable to changing environments for this character.

Plant height at maximum flower (PHMF): Regarding this character all the lines also indicated non-significance deviation mean squares from regression which exhibited their stability.

Plant weight after fully dry (PWFD): In respect of this character, majority of the lines except line-1 showed significant deviation mean squares, thus showing their instability.

Root weight after fully dry (RWFD): For this character all the lines showed non-significant deviation mean square values. This result indicated that the lines were stable for this trait.

Number of pods per plant (NPPP): In this case all the lines except line-2 had high and significant deviation mean squares indicating their in stability to the environment.

Pod weight per plant (PdWPP): For this character the line-1, line-2, line-4, line-6 and line-8 exhibited non-significant deviation mean squares from regressions. This result indicated that these lines showed stability for this trait. On the other hand line-3, line-5 and line-7 showed significant deviation mean squares indicating their instability.

Number of seeds per plant (NSPP): In respect of this character all the genotypes except line-2 exhibited high and significant deviation mean squares indicating their instability to the environment.

1000-seed weight (1000-SW): The line-4 responded non-significantly to deviation mean squares indicating its stability while rest of the lines showed significant deviation mean square values indicated their instability for this trait.

Seed weight per plant (SWPP): For SWPP all the lines except line-7 responded non-significantly to deviation mean squares indicating their stability to the changing environments.

C. GRAPHICAL ANALYSIS

The graphical analyses are described under the following sub-heads:

1. Curve

The performances of different lines in different environments for different characters are shown by curves. For this purposes the mean performance of each of the individual genotypes against the mean performance of each of the environments plotted were presented in Figure 1 to 11 for DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP, 1000SW and SWPP.

Days to maximum flower (DMF): The performances of eight lines against 12 environments for DMF were presented in Figure 1. It was observed from the figure that line-1 in Env.11, line-2 in Env.9, line-3 and line-6 in Env.12, line-4 in Env.5, line-5 in Env.5 and line-7 and line-8 in Env.7 were exhibited the highest performances. On an overall basis line-7 showed the highest performance in Env.7 and line-8 showed the lowest performance in Env.1 in all the twelve environments. The figure also showed that individual curves are intersected at some points among themselves indicating the existence of genotype-environment interactions for this character. It is in agreement with the joint regression analysis.

Number of primary branches at maximum flower (NPBMF): The performances of lines for this character are shown in Figure 2. The highest mean performance for line-1, line-2, line-3, line-4, line-5 and line-7 were observed in Env.2. On the other hand line-6 and line-8 showed the highest mean performances in Env.10 and Env.5 respectively. Among all the lines, line-5 showed the highest performance in Env.2 and line-8 showed the lowest performance in Env.7. The intersection of curves observed for this trait also indicating the existence of G × E interaction which was supported by joint regression analysis.

Number of secondary branches at maximum flower (NSBMF): The line performances for NSBMF are presented in Figure 3. The line-1, line-2 and line-4 in Env.7 and line-5, line-6, line-7 and line-8 in Env.12 and line-3 in Env.10 showed highest mean performances. On an overall basis performances of line-1 in Env.7 had the highest and line-4 in Env.6 had the lowest performances for this trait also.

Plant height at maximum flower (PHMF): The performances of lines for this character were presented in Figure 4. Here Env.7 had the highest increasing influence in line-1, line-4 and line-5. On the other hand line-2 in Env.11, line-3 and line-8 in Env.9, line-6 in Env.5 and line-7 in Env.12 had the highest mean performances, respectively. Figure 4 also showed that line-4 and line-6 exhibited the highest and the lowest mean performances in Env.7 and Env.3. Intercrossing of curves in the graphs indicating the existence of G × E interaction for this trait.

Plant weight after fully dry (PWFD): For the character PWFD most of the lines showed the highest increasing influence in Env.10 and Env.12. Among all the lines, line-3 showed the best performance in Env.12 and line-5 in Env.4 exhibited the worst performance. The Figure 5 also showed that individual lines are intersected at some points with each other which is in agreement with the joint regression analysis.

Root weight after fully dry (RWFD): From Figure 6 it was observed that lines showed slightly increasing tendency to the environment. Here the line-8 in Env.8 showed the highest performance. It was noted that line-5 at all the environments showed decreasing performances.

Number of pods per plant (NPPP): In case of this character (Figure 7) showed that line-1 in Env.8, line-2 in Env.10, line-3 in Env.11 and line-6 in Env.7 showed the highest performances. Rest of the lines showed the highest performances in Env.5. Here line-8 in Env.3 showed the lowest mean performance. Intersecting of the curves in the graph indicating the existence of G × E interaction for this trait.

Pod weight per plant (PdWPP): From Figure 8 it was observed that line-1 in Env.8; line-2, line-3 in Env.6; line-4 in Env.9; line-6 in Env.7 and line-5, line-7 and line-8 in Env.5 exhibited better performances, while line-8 in Env.3 had the lowest performance. Intersecting of curves are prominent for this trait also.

Number of seeds per plant (NSPP): Line mean performances for this trait are presented in Figure 9. Line-4 in Env.9 showed the highest mean performance while line-8 in Env.3 showed the lowest performance. Here also it was observed that line-8 among all the lines showed the lowest performance in all the environments. Prominent intercrossing indicating the existence of genotype-environment interaction.

1000-seed weight (1000-SW): The performances were presented in Figure 10. It was observed that line-1, line-6 and line-8 in Env.4; line-2 in Env.5; line-3 in Env.10; line-4 in Env.2 and line-5 and line-7 in Env.9 exhibited the highest performances, respectively. The lowest mean performance observed in line-5 in Env.2. Here intercrossing of curves among themselves were also observed.

Seed weight per plant (SWPP): The performances of different lines for this character are shown in Figure 11. The figure showed that line-1 in Env.7; line-2 and line-3 in Env.10; line-4 in Env.9; line-5 and line-7 in Env.5 and line-6 and line-8 in Env.10 exhibited the highest mean performances. From this figure it observed that line-8 in Env.3 had the lowest mean performance. In these figures intersecting of the curves among themselves indicating the existence of G × E interaction which is supported by the joint regression analysis.

2. Regression graph

The regression lines for each variety against the corresponding environmental mean are shown in Figs.12 to 22, respectively for DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD, NPPP, PdWPP, NSPP, 1000SW and SWPP. The individual points were not plotted in the figure to avoid confusion. Plotting environmental means on X-axis and genotypic performance on Y-axis, the regression lines were drawn. Intercrossing of regression lines were much prominent in all the characters indicating the presence of genotype – environment interaction for these traits.

Table 13: Line means over replications and environment for different characters in chickpea.

Line	Characters					
	DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD
Line-1	92.6597 ±1.3786	3.1574 ±0.0733	15.7208 ±0.4740	53.2448 ±0.8063	68.0731 ±4.0289	1.8522 ±0.0859
Line-2	91.5556 ±1.0996	3.0972 ±0.0742	15.2037 ±0.4557	53.3809 ±0.7065	75.6213 ±4.2016	2.2651 ±0.0872
Line-3	96.2222 ±1.2261	3.2662 ±0.1042	15.4583 ±0.4402	52.9583 ±0.7378	74.2900 ±4.1413	2.2375 ±0.0763
Line-4	91.7523 ±1.1451	3.0203 ±0.0637	14.6157 ±0.4957	54.9514 ±0.7485	65.7414 ±3.0969	1.9680 ±0.0854
Line-5	96.6088 ±0.9018	3.3148 ±0.1001	15.5394 ±0.3958	52.2556 ±0.6286	64.9303 ±3.7906	1.3925 ±0.0423
Line-6	92.3750 ±1.0595	3.2381 ±0.0822	15.4588 ±0.3482	50.4475 ±0.6866	64.3590 ±4.3736	2.0281 ±0.0741
Line-7	93.1806 ±2.7013	3.2176 ±0.0786	15.5972 ±0.4651	53.9297 ±0.7136	65.2748 ±5.0185	1.9691 ±0.0844
Line-8	91.9745 ±1.2683	2.3649 ±0.0571	14.3634 ±0.3320	52.4923 ±0.7150	61.5396 ±3.4383	2.4449 ±0.0870

continued

Table 13 continued

Line	Characters				
	NPPP	PdWPP	NSPP	1000SW	SWPP
Line-1	47.5046 ±3.5835	9.97194 ±0.7228	55.1296 ±4.2112	144.8175 ±2.1890	7.6516 ±0.5468
Line-2	53.0972 ±4.3077	12.4483 ±1.0726	58.2569 ±4.6123	154.8388 ±2.2722	9.1803 ±0.7842
Line-3	52.375 ±3.9976	12.3842 ±1.0913	54.9914 ±3.956	158.5687 ±3.0986	8.6703 ±0.6602
Line-4	49.6343 ±4.2198	10.5153 ±0.9311	55.6116 ±5.0045	145.0721 ±3.0701	7.7475 ±0.6749
Line-5	61.0231 ±4.5340	12.2388 ±0.9317	68.5139 ±5.063	139.2927 ±2.1153	9.576 ±0.7422
Line-6	53.9144 ±4.6296	11.9792 ±1.0342	57.8681 ±4.9285	159.6300 ±3.5948	9.3022 ±0.805
Line-7	53.2894 ±4.3584	11.5447 ±1.0388	60.9282 ±5.0441	146.8114 ±1.9118	8.8543 ±0.7524
Line-8	26.5046 ±2.4059	6.9065 ±0.6010	28.3603 ±2.6295	199.9188 ±4.2355	5.3940 ±0.4872

Table 14: Environmental means over lines and replications for different characters in chickpea.

Charac-ters	1st year (2007-08)				2nd year (2008-09)			
	D_0	D_A	D_B	D_C	D_0	D_A	D_B	D_C
DMF	82.9444±0.7971	89.7000±0.9828	83.4722±0.9586	85.4936±0.9470	94.7917±1.4869	92.9340±0.8960	98.3333±2.8423	94.5417±2.7359
NPBMF	3.1319±0.0826	3.0590±0.1209	3.1944±0.1143	3.6146±0.1548	3.1389±0.0752	2.9896±0.1030	2.5924±0.0892	2.9343±0.0981
NSBMF	12.4201±0.3187	13.8576±0.4417	13.0278±0.2955	13.9110±0.4102	16.5625±0.3496	14.4549±0.3857	18.0208±0.5391	13.8924±0.4971
PHMF	48.9371±0.4807	49.5035±0.4602	47.9028±0.5279	47.4670±0.5558	55.5677±0.6030	51.2799±0.8685	57.7878±0.7946	53.5587±0.8348
PWFD	56.9698±2.2841	48.4708±2.4290	53.2878±2.3803	56.9587±2.5630	62.4753±2.7805	62.3566±2.3990	75.7253±3.7387	54.7003±1.7446
RWFD	1.9896±0.1045	1.7888±0.1073	1.6936±0.0846	1.7332±0.0743	1.9502±0.1004	2.1237±0.1226	1.9542±0.0908	2.0455±0.0720
NPPP	25.5938±3.0801	22.7292±1.9137	30.0278±2.8249	24.9861±2.0776	73.9688±3.5369	62.7118±3.1699	65.1875±5.4192	64.6181±4.1097
PdWPP	5.6673±0.7731	5.2682±0.4343	6.7295±0.7103	5.7343±0.4789	15.9944±0.8174	14.0275±0.7480	14.2475±1.1887	15.2598±1.0942
NSPP	30.1597±4.8299	26.3681±2.4209	35.4132±3.7252	29.0354±2.5347	79.5174±3.7527	68.4965±3.5926	71.2463±5.8942	72.6424±4.7160
1000SW	152.5225±6.2522	167.5119±5.7018	152.7184±4.5498	160.1008±5.7402	157.6791±3.1460	153.8701±3.2852	148.5942±4.0407	157.5195±4.7006
SWPP	4.2919±0.5666	4.2010±0.3445	5.2058±0.5513	4.3723±0.3657	12.1856±0.5815	10.1529±0.4815	10.2723±0.8560	11.1705±0.7413

continued

Table 14 continued

Characters	3rd year (2009-10)			
	D_0	D_A	D_B	D_C
DMF	98.7257±1.0998	100.8056±0.7482	99.0590±0.7732	98.7014±0.6614
NPBMF	3.1285±0.0745	3.0278±0.1038	2.9375±0.1037	3.2652±0.1010
NSBMF	15.0104±0.3476	18.1778±0.4820	16.5764±0.5066	17.0243±0.3334
PHMF	56.0497±0.5125	56.8448±0.5382	56.0292±0.5985	54.5632±0.8113
PWFD	66.0340±2.7517	112.1010±6.6655	52.9722±2.4308	107.6924±6.1977
RWFD	2.2431±0.1097	2.1666±0.1096	2.3107±0.1457	2.2361±0.1183
NPPP	63.6597±6.3052	25.1979±2.1069	69.1528±3.4034	68.1806±4.7191
PdWPP	13.9412±1.4377	5.5773±0.4841	13.9532±0.9451	15.5832±1.0679
NSPP	72.4803±7.1452	29.0174±2.9343	68.4063±3.8702	76.3472±5.4083
1000SW	152.3108±3.6965	151.9664±5.1559	158.2521±3.5887	162.2993±5.4482
SWPP	11.0155±1.0685	4.2227±0.3578	10.5576±0.6173	11.9161±0.8325

Table 15. Results of joint regression analysis for different characters in chickpea.

Days to maximum flower

Source	df	SS	MS	F
L	7	335.5439	47.9348	3.1525**
E	11	3641.1470	331.0134	21.7695**
L × E	77	1435.5544	18.6436	1.2261^{NS}
Heterogeneity of reg.	7	67.0157	9.5737	0.6296^{NS}
Remainder	70	1368.5388	19.5506	1.2858^{NS}
Within error	288	4379.1454	15.2054	

Number of primary branches at maximum flower

Source	df	SS	MS	F
L	7	7.8582	1.1226	17.0277**
E	11	5.0548	0.4595	6.9702**
L × E	77	5.2988	0.0688	1.0438^{NS}
Heterogeneity of reg.	7	0.5543	0.0792	1.2011^{NS}
Remainder	70	4.7445	0.0678	1.0281^{NS}
Within error	288	18.9871	0.0659	

Number of secondary branches at maximum flower

Source	df	SS	MS	F
L	7	20.4378	2.9197	2.2455*
E	11	336.7227	30.6112	23.5422**
L × E	77	121.3952	1.5766	1.2125^{NS}
Heterogeneity of reg.	7	17.2578	2.4654	1.8961^{NS}
Remainder	70	104.1374	1.4877	1.1441^{NS}
Within error	288	374.4766	1.3003	

Plant height at maximum flower

Source	df	SS	MS	F
L	7	146.3083	20.9012	7.1496**
E	11	1230.3384	111.8489	38.2600**
L × E	77	263.0068	3.4157	1.1684^{NS}
Heterogeneity of reg.	7	29.1978	4.1711	1.4268^{NS}
Remainder	70	233.8090	3.3401	1.1426^{NS}
Within error	288	841.9370	2.9234	

continued

Table 15 continued

Plant weight after fully dry

Source	df	SS	MS	F
L	7	2069.0972	295.5853	2.9110**
E	11	39097.3369	3554.3034	35.0031**
L × E	77	5616.3965	72.9402	0.7183 NS
Heterogeneity of reg.	7	1139.1446	162.7349	1.6026 NS
Remainder	70	4477.2519	63.9607	0.6299 NS
Within error	288	29244.2441	101.5425	

Root weight after fully dry

Source	df	SS	MS	F
L	7	8.5813	1.2259	17.0052**
E	11	3.7333	0.3394	4.7079**
L × E	77	4.5360	0.0589	0.8172 NS
Heterogeneity of reg.	7	0.8771	0.1253	1.7381 NS
Remainder	70	3.6589	0.0523	0.7251 NS
Within error	288	20.7619	0.0721	

Number of pods per plant

Source	df	SS	MS	F
L	7	8644.7464	1234.9638	12.7662**
E	11	40337.2410	3667.0219	37.9070**
L × E	77	6227.3906	80.8752	0.8360 NS
Heterogeneity of reg.	7	1568.5918	224.0845	2.3164*
Remainder	70	4658.7988	66.5543	0.6880 NS
Within error	288	27860.3503	96.7373	

Pod weight per plant

Source	df	SS	MS	F
L	7	298.2228	42.6033	7.0457**
E	11	1902.7364	172.9760	28.6065**
L × E	77	365.0973	4.7415	0.7841 NS
Heterogeneity of reg.	7	75.9963	10.8566	1.7954 NS
Remainder	70	289.1011	4.1300	0.6830 NS
Within error	288	1741.4626	6.0467	

continued

Table 15 continued

Number of seeds per plant

Source	df	SS	MS	F
L	7	11359.8075	1622.8296	11.6544**
E	11	43854.9252	3986.8114	28.6313**
L × E	77	7401.1829	96.1193	0.6903 NS
Heterogeneity of reg.	7	1903.2553	271.8936	1.9526 NS
Remainder	70	5497.9276	78.5418	0.5640 NS
Within error	288	40103.0071	139.2466	

1000-seed weight

Source	df	SS	MS	F
L	7	30694.8101	4384.9729	53.7265**
E	11	2773.1955	252.1087	3.0889**
L × E	77	12058.4981	156.6039	1.9188**
Heterogeneity of reg.	7	1716.8236	245.2605	3.0050**
Remainder	70	10341.6746	147.7382	1.8101**
Within error	288	23505.5838	81.6166	

Seed weight per plant

Source	df	SS	MS	F
L	7	156.2630	22.3233	6.9960**
E	11	1045.5938	95.0540	29.7893**
L × E	77	182.9914	2.3765	0.7448 NS
Heterogeneity of reg.	7	47.6628	6.8090	2.1339*
Remainder	70	135.3286	1.9333	0.6059 NS
Within error	288	918.9733	3.1909	

Table 16: Regression analysis for eight lines in twelve environments for different characters in Chickpea.

Days to maximum flower

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	92.6597	1.0883	495.3526	539.1140	326.7781
Line-2	91.5556	1.0152	462.0702	469.1025	62.4639
Line-3	96.2222	0.9693	441.1887	427.6618	61.8336
Line-4	91.7523	1.0688	486.4647	519.9415	82.9327
Line-5	96.6088	0.7036	320.2476	225.3323	95.4138
Line-6	92.3750	0.8976	408.5163	366.6659	80.8117
Line-7	93.1806	1.0958	498.7640	546.5652	585.3569
Line-8	91.9745	1.1613	528.5429	613.7794	72.9481

Number of primary branches at maximum flower

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	3.1574	1.0281	0.6496	0.6679	0.1089
Line-2	3.0972	0.6236	0.3940	0.2457	0.7458
Line-3	3.2662	1.2369	0.7815	0.9667	0.5155
Line-4	3.0203	0.9149	0.5781	0.5289	0.4593
Line-5	3.3148	1.5803	0.9985	1.5780	0.9704
Line-6	3.2381	0.4360	0.2755	0.1201	1.2701
Line-7	3.2176	1.1035	0.6973	0.7695	0.2087
Line-8	2.3649	1.0766	0.6802	0.7324	0.4659

continued

Table 16 continued

Number of secondary branches at maximum flower

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	15.7208	1.1802	49.6752	58.6269	15.2932
Line-2	15.2037	1.0468	44.0608	46.1234	24.1857
Line-3	15.4583	0.8805	37.0585	32.6281	16.1489
Line-4	14.6157	1.3314	56.0389	74.6100	16.8450
Line-5	15.5394	0.9655	40.6370	39.2338	11.4352
Line-6	15.4588	0.8280	34.8526	28.8595	4.1716
Line-7	15.5972	1.1948	50.2911	60.0898	8.0916
Line-8	14.3634	0.5728	24.1087	13.8091	7.9663

Plant height at maximum flower

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	53.2448	1.2412	190.8803	236.9123	18.9403
Line-2	53.3809	0.9710	149.3368	145.0104	15.9368
Line-3	52.9583	1.0730	165.0195	177.0664	20.3221
Line-4	54.9514	1.1566	177.8709	205.7193	40.4478
Line-5	52.2556	0.9148	140.6832	128.6915	42.3955
Line-6	50.4475	0.9345	143.7146	134.2973	40.9595
Line-7	53.9297	1.0080	155.0221	156.2617	23.9151
Line-8	52.4923	0.7010	107.8110	75.5773	30.8920

continued

Table 16 continued

Plant weight after fully dry

Line	Mean performance ($\mu+d\hat{i}$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	68.0731	1.1299	5521.8474	6238.9516	901.9351
Line-2	75.6213	1.0237	5003.0902	5121.7630	362.2599
Line-3	74.2900	1.1278	5511.6231	6215.8687	638.6904
Line-4	65.7414	0.6635	3242.4356	2151.2234	423.9969
Line-5	64.9303	0.8158	3986.7390	3252.2088	1111.9164
Line-6	64.3590	1.1482	5611.2881	6442.7005	575.6840
Line-7	65.2748	1.1597	5667.5055	6572.4411	102.7386
Line-8	61.5396	0.9316	4552.8081	4241.3246	360.0307

Root weight after fully dry

Line	Mean performance ($\mu+d\hat{i}$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	1.8522	1.3775	0.6428	0.8855	0.4557
Line-2	2.2651	0.4489	0.2095	0.0940	0.8634
Line-3	2.2375	0.9204	0.4295	0.3953	0.4716
Line-4	1.9680	0.8225	0.3838	0.3157	0.7475
Line-5	1.3925	0.2514	0.1173	0.0295	0.1245
Line-6	2.0281	0.9001	0.4200	0.3781	0.2419
Line-7	1.9691	1.5808	0.7377	1.1662	0.4199
Line-8	2.4449	1.6983	0.7926	1.3460	0.3343

continued

Table 16 continued

Number of pods per plant

Line	Mean performance ($\mu+d\hat{i}$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	47.5046	0.9256	4666.8812	4319.5379	505.0236
Line-2	53.0972	1.1267	5680.7627	6400.2524	1182.0293
Line-3	52.3750	0.8576	4324.3094	3708.6626	686.0311
Line-4	49.6343	1.0361	5223.9586	5412.3173	592.8383
Line-5	61.0231	1.1665	5881.8896	6861.4758	439.4359
Line-6	53.9144	1.2256	6179.6999	7573.8825	788.5611
Line-7	53.2894	1.0880	5486.0440	5969.0109	167.2290
Line-8	26.5046	0.5739	2893.6955	1660.6934	297.6505

Pod weight per plant

Line	Mean performance ($\mu+d\hat{i}$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	9.9719	0.8246	196.1137	161.7064	19.5277
Line-2	12.4483	1.2827	305.0878	391.3460	77.6349
Line-3	12.3842	0.9462	225.0401	212.9272	56.5416
Line-4	10.5153	0.9449	224.7306	212.3419	37.9958
Line-5	12.2388	1.0313	245.2913	252.9739	26.6825
Line-6	11.9792	1.2341	293.5134	362.2157	41.3237
Line-7	11.5447	1.1051	262.8451	290.4765	17.4392
Line-8	6.9065	0.6312	150.1145	94.7450	11.9557

continued

Table 16 continued

Number of seeds per plant

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	55.1296	1.0519	5766.5451	6066.0083	712.9243
Line-2	58.2569	1.1666	6395.3459	7461.0455	1197.9793
Line-3	54.9914	0.6960	3815.1722	2655.2163	517.7308
Line-4	55.6116	1.0520	5767.0273	6067.0229	1093.0636
Line-5	68.5139	1.0927	5990.2700	6545.8253	564.4949
Line-6	57.8681	1.1671	6397.9276	7467.0705	852.3479
Line-7	60.9282	1.1691	6409.0451	7493.0437	168.1870
Line-8	28.3603	0.6045	3313.5920	2002.9480	391.1997

1000-seed weight

Line	Mean performance ($\mu+d_i$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	144.8175	0.7990	276.9876	221.3249	914.8804
Line-2	154.8388	1.3651	473.2225	646.0115	993.1265
Line-3	158.5687	0.3821	132.4590	50.6142	765.8283
Line-4	145.0721	1.4619	506.7583	740.8174	1417.7708
Line-5	139.2927	0.4361	151.1701	65.9237	1130.1235
Line-6	159.6300	2.6052	903.0742	2352.6449	2248.4694
Line-7	146.8114	-0.1324	-45.9075	6.0796	293.5939
Line-8	199.9188	1.0830	375.4313	406.6029	2577.8818

continued

Table 16 continued

Line	Seed weight per plant				
	Mean performance ($\mu+d\hat{i}$)	Linear reg. coefficient ($1+\beta_i$)	Sp xy (11df)	Reg. ss (1 df)	Rem.ss (10df)
Line-1	7.6516	0.8385	109.5947	91.8980	13.7208
Line-2	9.1803	1.2620	164.9384	208.1472	31.9272
Line-3	8.6703	0.7588	99.1703	75.2473	16.6775
Line-4	7.7475	0.9300	121.5558	113.0521	17.8530
Line-5	9.5760	1.1533	150.7384	173.8501	11.5245
Line-6	9.3022	1.2591	164.5679	207.2131	32.3083
Line-7	8.8543	1.1181	146.1301	163.3828	4.4208
Line-8	5.3940	0.6802	88.8981	60.4661	6.8966

Table 17: Results of remainder mean squares of eight lines for different characters in chickpea

Line	Characters							
	DMF		NPBMF		NSBMF		PHMF	
	RMS	F	RMS	F	RMS	F	RMS	F
Line-1	40.8473	1.1899 ^{NS}	0.01361	0.0362 ^{NS}	1.9116	0.2172 ^{NS}	2.3675	0.1282 ^{NS}
Line-2	7.8080	0.3114 ^{NS}	0.09322	0.2642 ^{NS}	3.0232	0.3875 ^{NS}	1.9921	0.0992 ^{NS}
Line-3	7.7292	0.1294 ^{NS}	0.06444	0.0833 ^{NS}	2.0186	0.2001 ^{NS}	2.5403	0.1391 ^{NS}
Line-4	10.3666	0.4550 ^{NS}	0.05741	0.2655 ^{NS}	2.1056	0.2682 ^{NS}	5.0560	0.4347 ^{NS}
Line-5	11.9267	0.5188 ^{NS}	0.12130	0.2346 ^{NS}	1.4294	0.2276 ^{NS}	5.2994	0.6144 ^{NS}
Line-6	10.1015	0.3265 ^{NS}	0.15876	0.3928 ^{NS}	0.5214	0.0885 ^{NS}	5.1199	0.3391 ^{NS}
Line-7	73.1696	0.1471 ^{NS}	0.02608	0.0624 ^{NS}	1.0114	0.1127 ^{NS}	2.9894	0.1676 ^{NS}
Line-8	9.1185	0.2481 ^{NS}	0.05824	0.5429 ^{NS}	0.9958	0.1479 ^{NS}	3.8615	0.1274 ^{NS}

continued

Table 17 continued

Line	Characters							
	PWFD		RWFD		NPPP		PdWPP	
	RMS	F	RMS	F	RMS	F	RMS	F
Line-1	112.7419	0.3359 ^{NS}	0.0570	0.0947 ^{NS}	63.1279	0.1566 ^{NS}	2.4410	0.1291 ^{NS}
Line-2	45.2825	0.0607 ^{NS}	0.1079	0.1945 ^{NS}	147.7537	0.3075 ^{NS}	9.7044	0.3238 ^{NS}
Line-3	79.8363	0.1700 ^{NS}	0.0589	0.1463 ^{NS}	85.7539	0.1114 ^{NS}	7.0677	0.1054 ^{NS}
Line-4	52.9996	0.1122 ^{NS}	0.0934	0.1841 ^{NS}	74.1048	0.1101 ^{NS}	4.7495	0.1194 ^{NS}
Line-5	138.9895	0.2230 ^{NS}	0.0156	0.1090 ^{NS}	54.9295	0.0768 ^{NS}	3.3353	0.0953 ^{NS}
Line-6	71.9605	0.1145 ^{NS}	0.0302	0.0732 ^{NS}	98.5701	0.1587 ^{NS}	5.1655	0.1552 ^{NS}
Line-7	12.8423	0.0102 ^{NS}	0.0525	0.1294 ^{NS}	20.9036	0.0274 ^{NS}	2.1799	0.0435 ^{NS}
Line-8	45.0038	0.1307 ^{NS}	0.0418	0.0968 ^{NS}	37.2063	0.1709 ^{NS}	1.4945	0.0924 ^{NS}

continued

Table 17 continued

Line	Characters					
	NSPP		1000-SW		SWPP	
	RMS	F	RMS	F	RMS	F
Line-1	89.1155	0.1659 ^{NS}	114.3600	0.4380 ^{NS}	1.7151	0.1632 ^{NS}
Line-2	149.7474	0.2691 ^{NS}	124.1408	0.5852 ^{NS}	3.9909	0.2242 ^{NS}
Line-3	64.7164	0.0687 ^{NS}	95.7285	0.1249 ^{NS}	2.0847	0.0813 ^{NS}
Line-4	136.6329	0.1177 ^{NS}	177.2213	0.3368 ^{NS}	2.2316	0.1063 ^{NS}
Line-5	70.5619	0.0576 ^{NS}	141.2654	0.6385 ^{NS}	1.4406	0.0690 ^{NS}
Line-6	106.5435	0.1188 ^{NS}	281.0587	0.6275 ^{NS}	4.0385	0.1924 ^{NS}
Line-7	21.0234	0.0189 ^{NS}	36.6992	0.1250 ^{NS}	0.5526	0.0219 ^{NS}
Line-8	48.9000	0.1949 ^{NS}	322.2352	0.2710 ^{NS}	0.8621	0.0778 ^{NS}

Table 18: Mean performance ($\bar{X}_i$), regression coefficients (b_i), (β_i), standard error of b_i (S_{bi}) and stability ($\bar{S}^2_{di}$) of eight lines for different characters in chickpea.

Days to maximum flower

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	92.6597	1.0883	±0.8473	0.0883	24.0958	8.2252
Line-2	91.5556	1.0152	±0.3705	0.0152	-0.0217	-0.0087
Line-3	96.2222	0.9693	±0.3686	-0.0307	-8.7487	-2.2640
Line-4	91.7523	1.0688	±0.4269	0.0688	2.5974	1.0883
Line-5	96.6088	0.7036	±0.4579	-0.2964	3.7937	1.5824
Line-6	92.3750	0.8976	±0.4214	-0.1024	0.3468	0.1247
Line-7	93.1806	1.0958	±1.1341	0.0958	-65.7810	-5.8998
Line-8	91.9745	1.1613	±0.4003	0.1613	-1.8928	-0.6245

Number of primary branches at maximum flower

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	3.1574	1.0281	±0.4151	0.0281	-0.0830	-0.2709
Line-2	3.0972	0.6236	±1.0864	-0.3764	-0.0136	-0.0459
Line-3	3.2662	1.2369	±0.9033	0.2369	-0.1418	-0.3224
Line-4	3.0203	0.9149	±0.8526	-0.0851	-0.0081	-0.0349
Line-5	3.3148	1.5803	±1.2393	0.5803	-0.0322	-0.0896
Line-6	3.2381	0.4360	±1.4178	-0.5640	0.0260	0.0817
Line-7	3.2176	1.1035	±0.5747	0.1035	-0.0837	-0.2588
Line-8	2.3649	1.0766	±0.8587	0.0766	0.0198	0.1207

Number of secondary branches at maximum flower

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	15.7208	1.1802	±0.6028	0.1802	-0.6710	-0.4524
Line-2	15.2037	1.0468	±0.7580	0.0468	0.4681	0.3352
Line-3	15.4583	0.8805	±0.6194	-0.1195	-0.9067	-0.5710
Line-4	14.6157	1.3314	±0.6326	0.3314	-0.2780	-0.1985
Line-5	15.5394	0.9655	±0.5212	-0.0345	-0.4263	-0.3403
Line-6	15.4588	0.8280	±0.3148	-0.1720	-1.0556	-0.8698
Line-7	15.5972	1.1948	±0.4385	0.1948	-1.4337	-0.9573
Line-8	14.3634	0.5728	±0.4350	-0.4272	-0.8863	-0.6832

Continued

Table 18 continued

Plant height at maximum flower

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	53.2448	1.2412	±0.3509	0.2412	-2.7226	-1.2671
Line-2	53.3809	0.9710	±0.3219	-0.0290	-3.4291	-1.5301
Line-3	52.9583	1.0730	±0.3635	0.0730	-2.5340	-1.1859
Line-4	54.9514	1.1566	±0.5128	0.1566	1.1369	0.6667
Line-5	52.2556	0.9148	±0.5250	-0.0852	2.0833	1.4188
Line-6	50.4475	0.9345	±0.5161	-0.0655	0.3213	0.1654
Line-7	53.9297	1.0080	±0.3943	0.0080	-2.0667	-0.9788
Line-8	52.4923	0.7010	±0.4482	-0.2990	-4.4888	-1.6306

Plant weight after fully dry

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	68.0731	1.1299	±0.4296	0.1299	6.2740	0.6849
Line-2	75.6213	1.0237	±0.2723	0.0237	-150.1266	-10.9974
Line-3	74.2900	1.1278	±0.3615	0.1278	-53.5580	-4.9424
Line-4	65.7414	0.6635	±0.2945	-0.3365	-75.6836	-6.9648
Line-5	64.9303	0.8158	±0.4770	-0.1842	-44.6310	-3.5754
Line-6	64.3590	1.1482	±0.3432	0.1482	-99.5246	-7.9406
Line-7	65.2748	1.1597	±0.1450	0.1597	-303.4419	-17.1320
Line-8	61.5396	0.9316	±0.2714	-0.0684	-50.0933	-5.3987

Root weight after fully dry

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	1.8522	1.3775	±0.9882	0.3775	-0.1048	-0.2702
Line-2	2.2651	0.4489	±1.3602	-0.5511	-0.0524	-0.1406
Line-3	2.2375	0.9204	±1.0052	-0.0796	-0.0535	-0.1687
Line-4	1.9680	0.8225	±1.2657	-0.1775	-0.0522	-0.1464
Line-5	1.3925	0.2514	±0.5166	-0.7486	-0.0233	-0.1231
Line-6	2.0281	0.9001	±0.7200	-0.0999	-0.0791	-0.2461
Line-7	1.9691	1.5808	±0.9486	0.5808	-0.0595	-0.1867
Line-8	2.4449	1.6983	±0.8464	0.6983	-0.0745	-0.2268

continued

Table 18 continued

Number of pods per plant

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	47.5046	0.9256	±0.3165	-0.0744	-50.2469	-5.0060
Line-2	53.0972	1.1267	±0.4842	0.1267	-1.9331	-0.1764
Line-3	52.3750	0.8576	±0.3689	-0.1424	-123.8275	-8.9265
Line-4	49.6343	1.0361	±0.3429	0.0361	-108.9676	-8.4008
Line-5	61.0231	1.1665	±0.2952	0.1665	-134.9430	-10.0893
Line-6	53.9144	1.2256	±0.3955	0.2256	-76.3922	-6.1311
Line-7	53.2894	1.0880	±0.1821	0.0880	-173.9926	-12.5990
Line-8	26.5046	0.5739	±0.2430	-0.4261	-24.6651	-3.3432

Pod weight per plant

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	9.9719	0.8246	±0.2865	-0.1754	-2.7735	-1.2758
Line-2	12.4483	1.2827	±0.5713	0.2827	0.2703	0.0987
Line-3	12.3842	0.9462	±0.4876	-0.0538	-11.1052	-2.7127
Line-4	10.5153	0.9449	±0.3997	-0.0551	-6.1451	-1.9486
Line-5	12.2388	1.0313	±0.3349	0.0313	-6.0769	-2.0549
Line-6	11.9792	1.2341	±0.4168	0.2341	-4.1884	-1.4520
Line-7	11.5447	1.1051	±0.2708	0.1051	-10.7855	-3.0470
Line-8	6.9065	0.6312	±0.2242	-0.3688	-2.8466	-1.4159

Number of seeds per plant

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	55.1296	1.0519	±0.3606	0.0519	-62.9978	-5.4363
Line-2	58.2569	1.1666	±0.4675	0.1666	-19.3294	-1.6387
Line-3	54.9914	0.6960	±0.3073	-0.3040	-183.8025	-11.9753
Line-4	55.6116	1.0520	±0.4465	0.0520	-180.9042	-10.6192
Line-5	68.5139	1.0927	±0.3209	0.0927	-249.6865	-14.2705
Line-6	57.8681	1.1671	±0.3943	0.1671	-138.9516	-9.2802
Line-7	60.9282	1.1691	±0.1752	0.1691	-261.8832	-15.6869
Line-8	28.3603	0.6045	±0.2671	-0.3955	-23.6107	-2.9810

continued

Table 18 continued

1000-seed weight

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	144.8175	0.7990	±1.6246	-0.2010	26.2201	3.2455
Line-2	154.8388	1.3651	±1.6926	0.3651	46.2784	6.3548
Line-3	158.5687	0.3821	±1.4863	-0.6179	-115.0347	-8.3102
Line-4	145.0721	1.4619	±2.0224	0.4619	10.2173	0.8908
Line-5	139.2927	0.4361	±1.8056	-0.5639	57.6969	7.7576
Line-6	159.6300	2.6052	±2.5468	1.6052	112.8797	10.6677
Line-7	146.8114	-0.1324	±0.9203	-1.1324	-44.0499	-5.1413
Line-8	199.9188	1.0830	±2.7270	0.0830	-39.4395	-2.2876

Seed weight per plant

Lines	$\bar{X}_i$	b_i	S_{bi}	β_i	$\bar{S}^2_{di}$	C
Line-1	7.6516	0.8385	±0.3240	-0.1615	-1.2545	-0.7741
Line-2	9.1803	1.2620	±0.4942	0.2620	-1.2571	-0.5960
Line-3	8.6703	0.7588	±0.3572	-0.2412	-4.7445	-1.8736
Line-4	7.7475	0.9300	±0.3696	-0.0700	-3.4653	-1.5123
Line-5	9.5760	1.1533	±0.2969	0.1533	-4.0683	-1.7805
Line-6	9.3022	1.2591	±0.4972	0.2591	-2.0166	-0.8803
Line-7	8.8543	1.1181	±0.1839	0.1181	-5.8699	-2.3364
Line-8	5.3940	0.6802	±0.2297	-0.3198	-2.0814	-1.2504

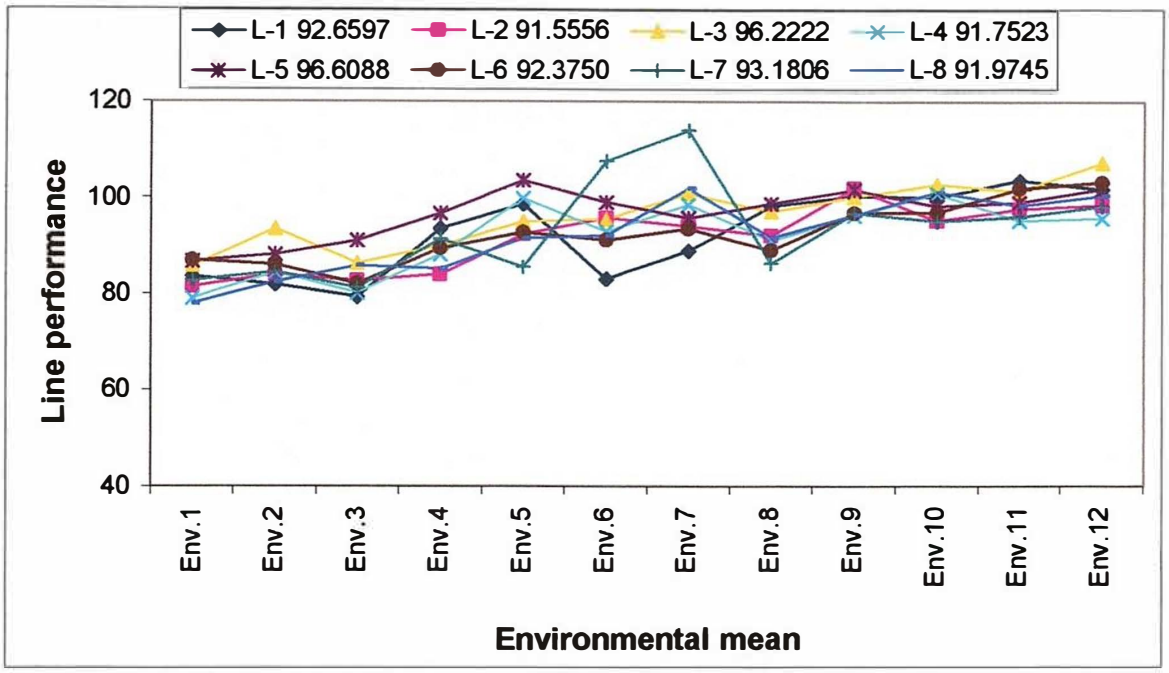


Figure 1: Curves of individual line mean on environmental mean of eight lines for DMF

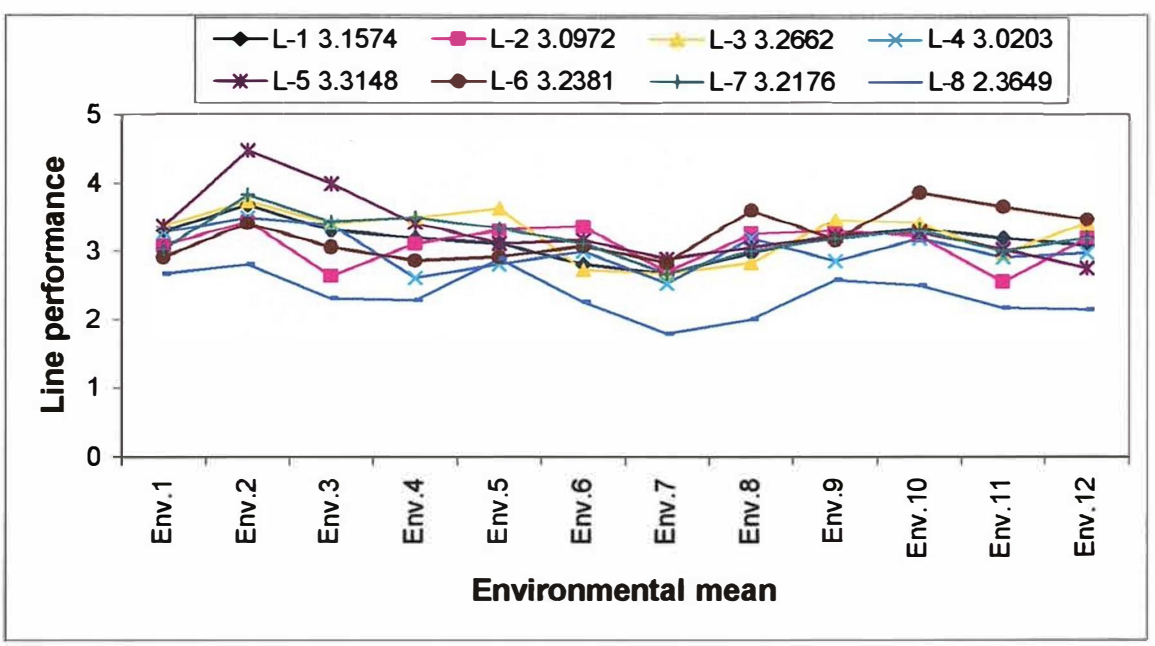


Figure 2: Curves of individual line mean on environmental mean of eight lines for NPBMF

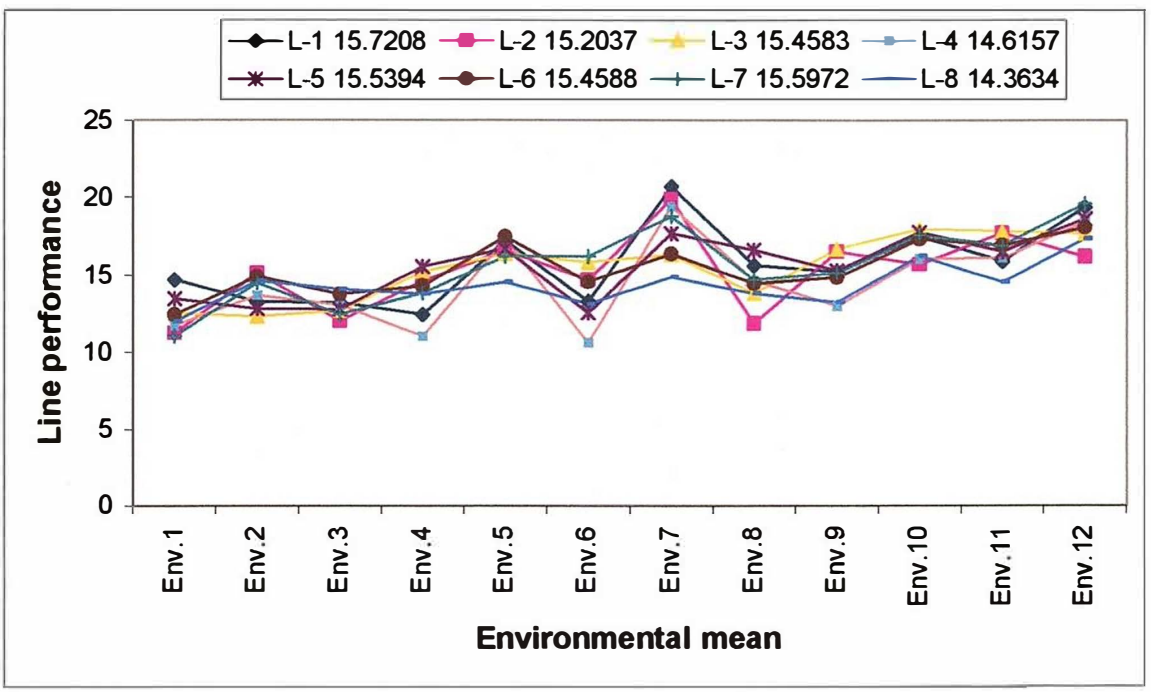


Figure 3: Curves of individual line mean on environmental mean of eight lines for NSBMF

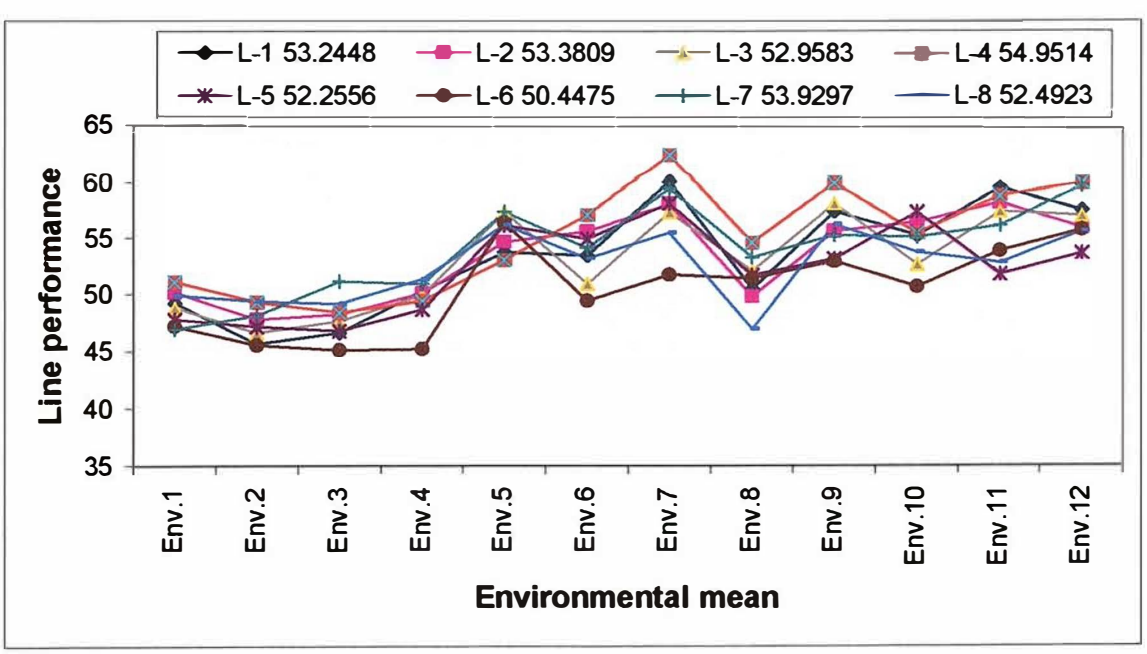


Figure 4: Curves of individual line mean on environmental mean of eight lines for PHMF

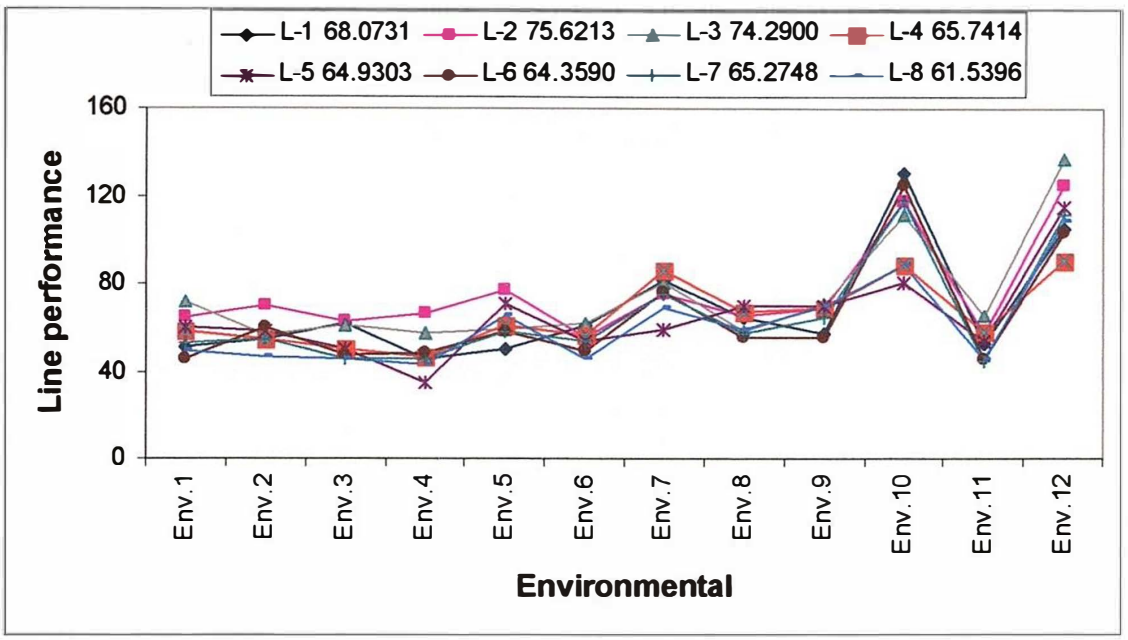


Figure 5: Curves of individual line mean on environmental mean of eight lines for PWFD

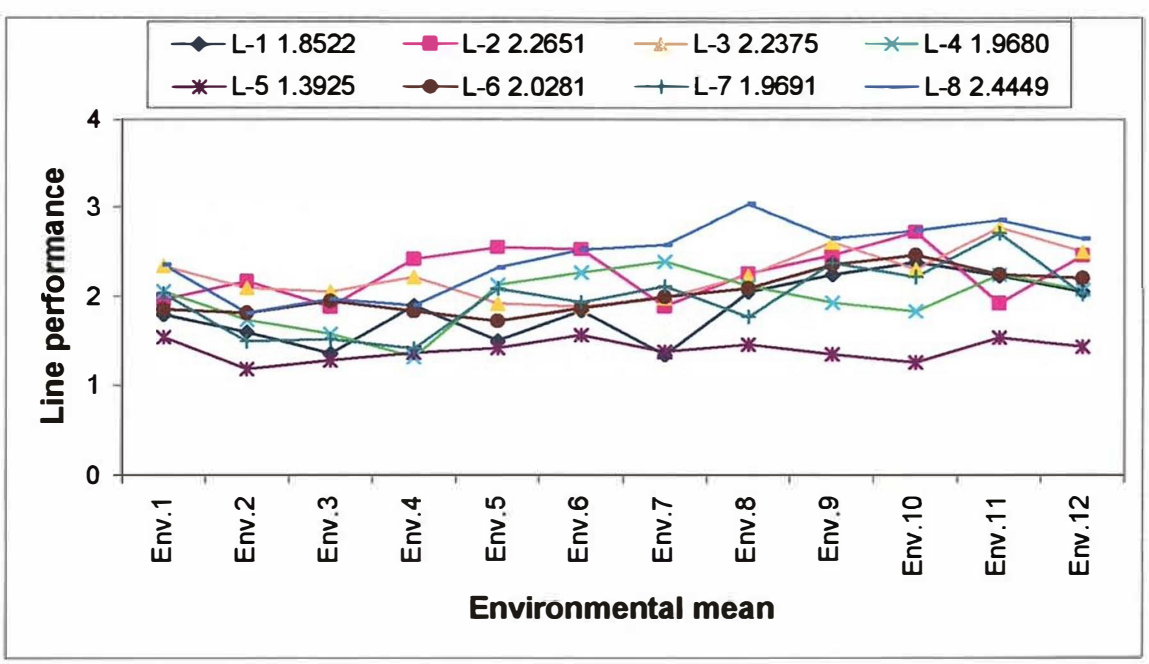


Figure 6: Curves of individual line mean on environmental mean of eight lines for RWFD

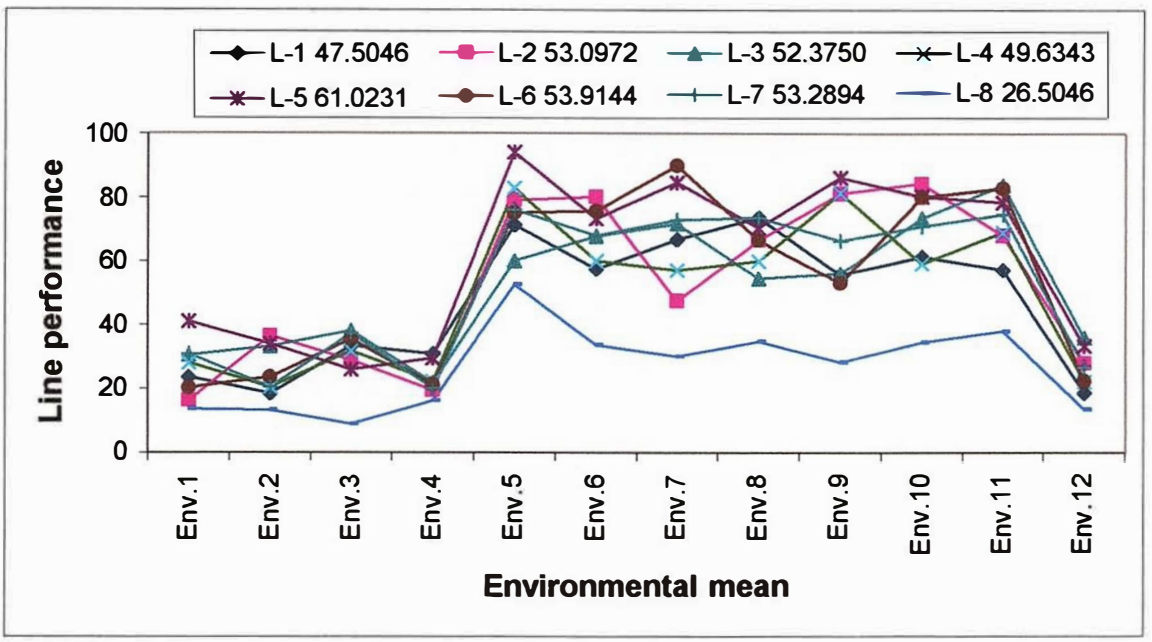


Figure 7: Curves of individual line mean on environmental mean of eight lines for NPPP

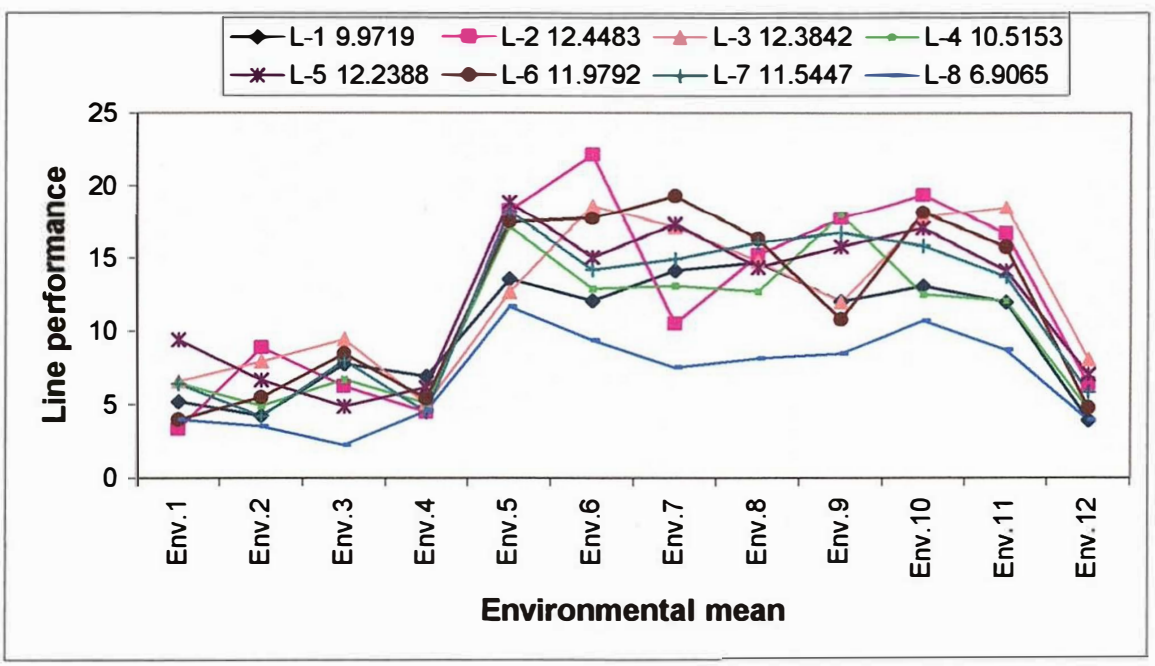


Figure 8: Curves of individual line mean on environmental mean of eight lines for PdWPP

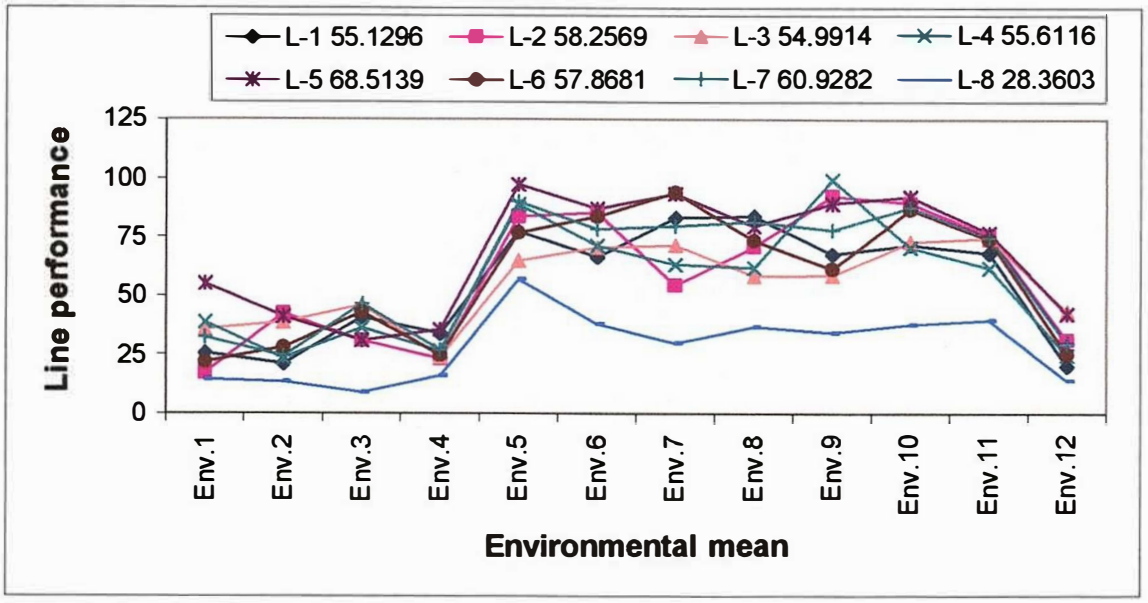


Figure 9: Curves of individual line mean on environmental mean of eight lines for NSPP

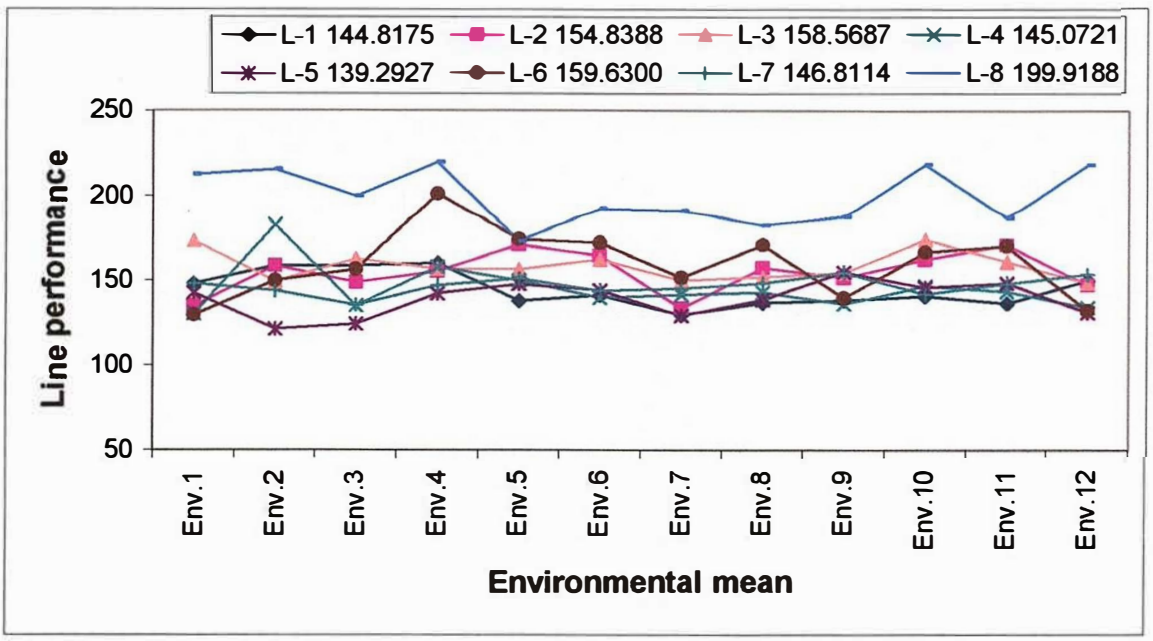


Figure 10: Curves of individual line mean on environmental mean of eight lines for 1000-SW

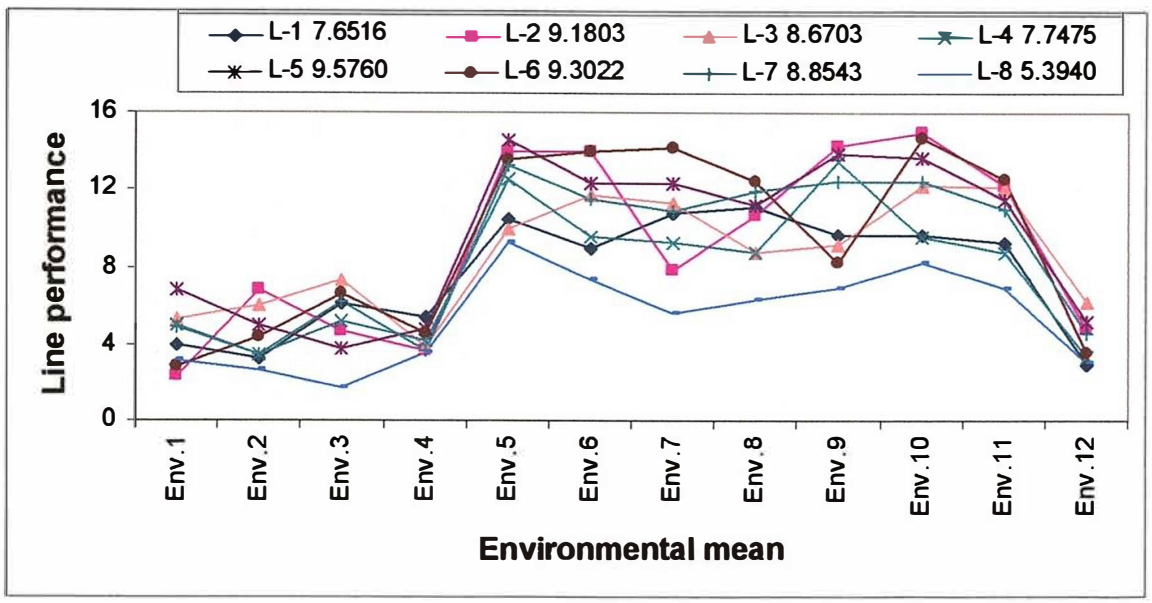


Figure 11: Curves of individual line mean on environmental mean of eight lines for SWPP

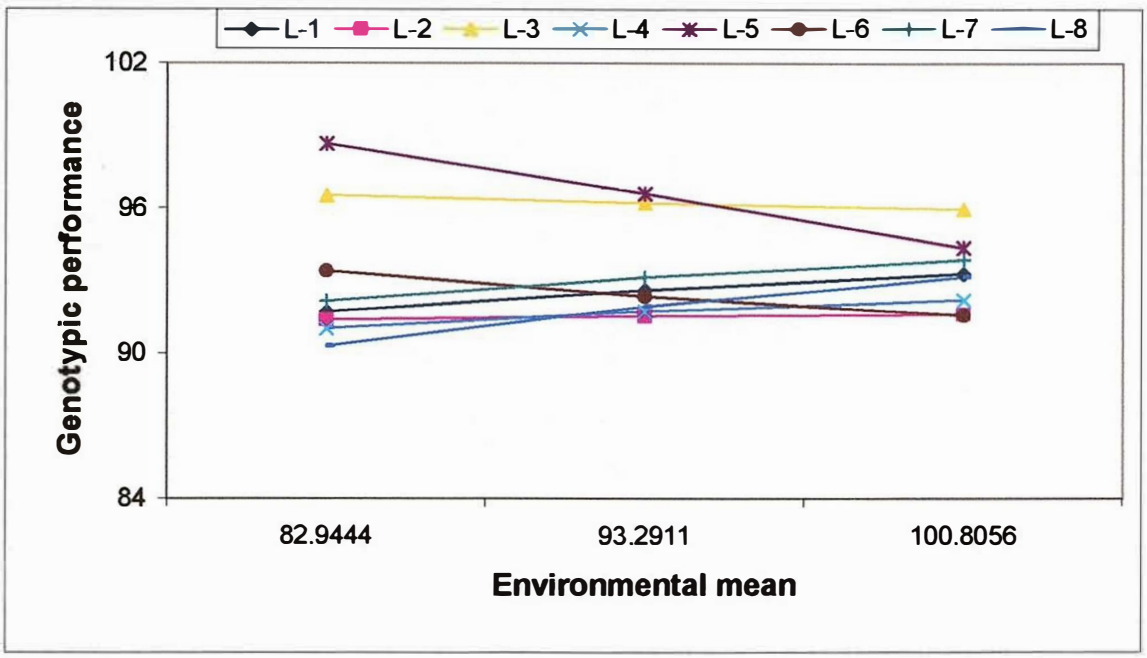


Figure 12: Regression of individual genotypic mean on environmental mean of eight lines for DMF

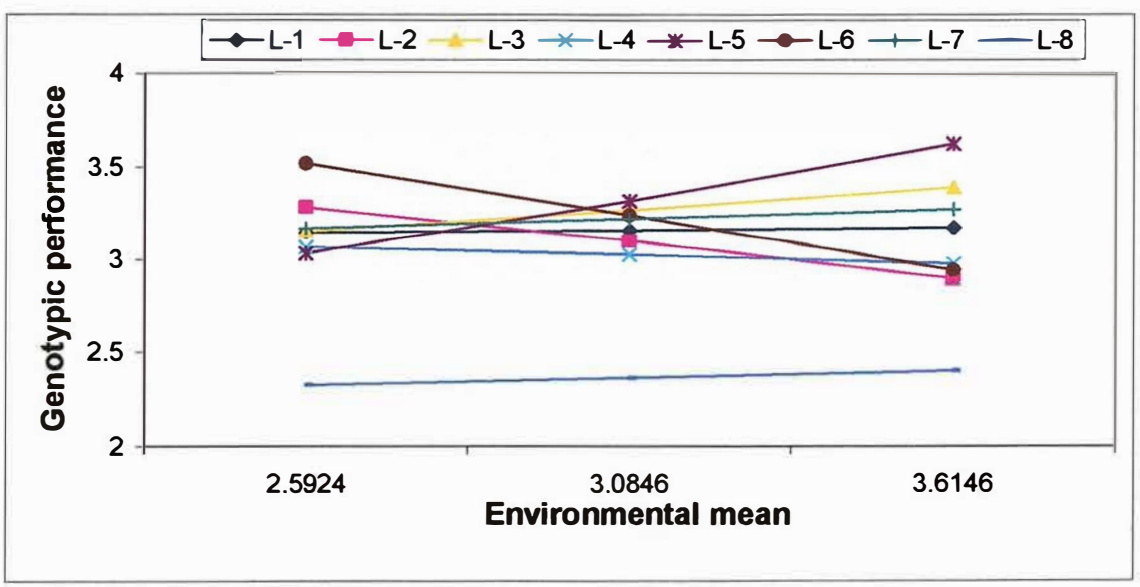


Fig 13: Regression of individual genotypic mean on environmental mean of eight lines for NPBMF

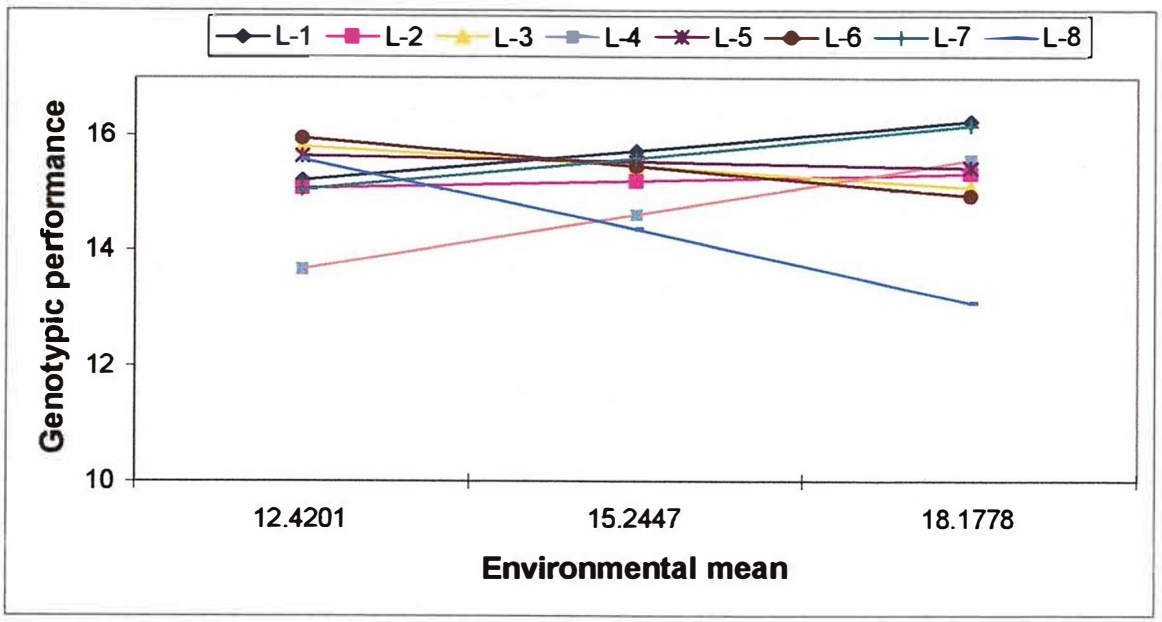


Fig 14: Regression of individual genotypic mean on environmental mean of eight lines for NSBMF

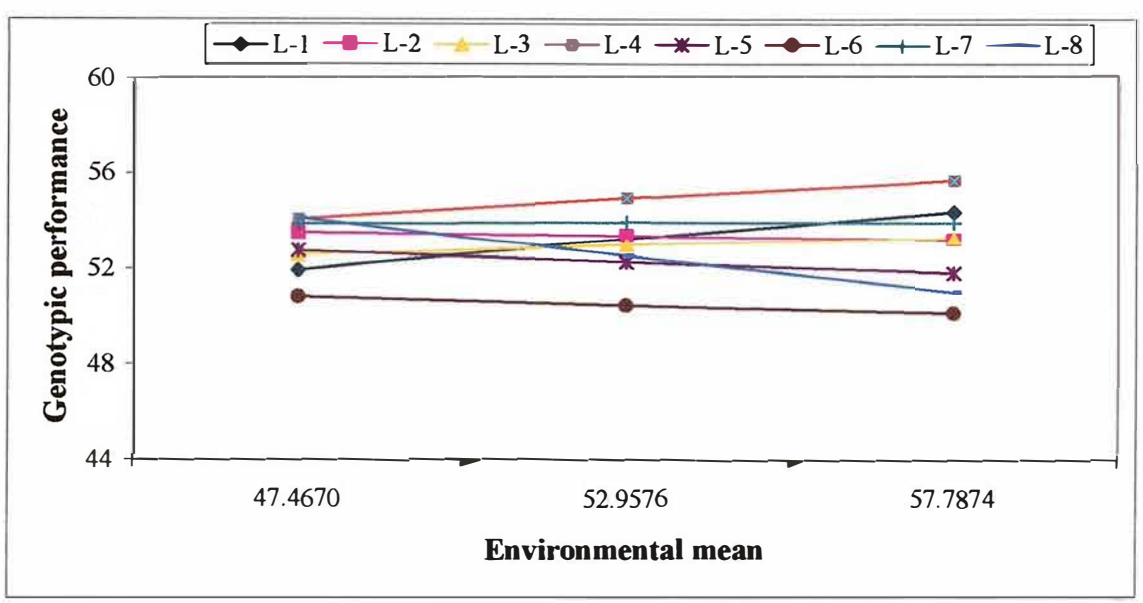


Fig 15: Regression of individual genotypic mean on environmental mean of eight lines for PHMF

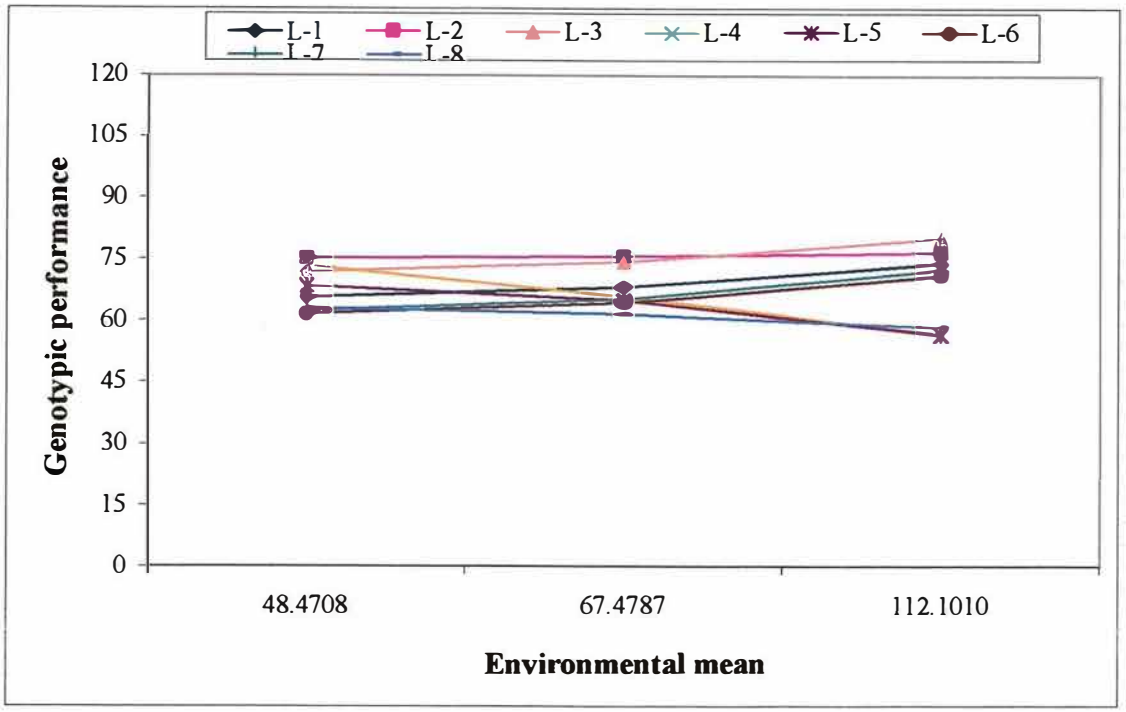


Fig 16: Regression of individual genotypic mean on environmental mean of eight lines for PWFD

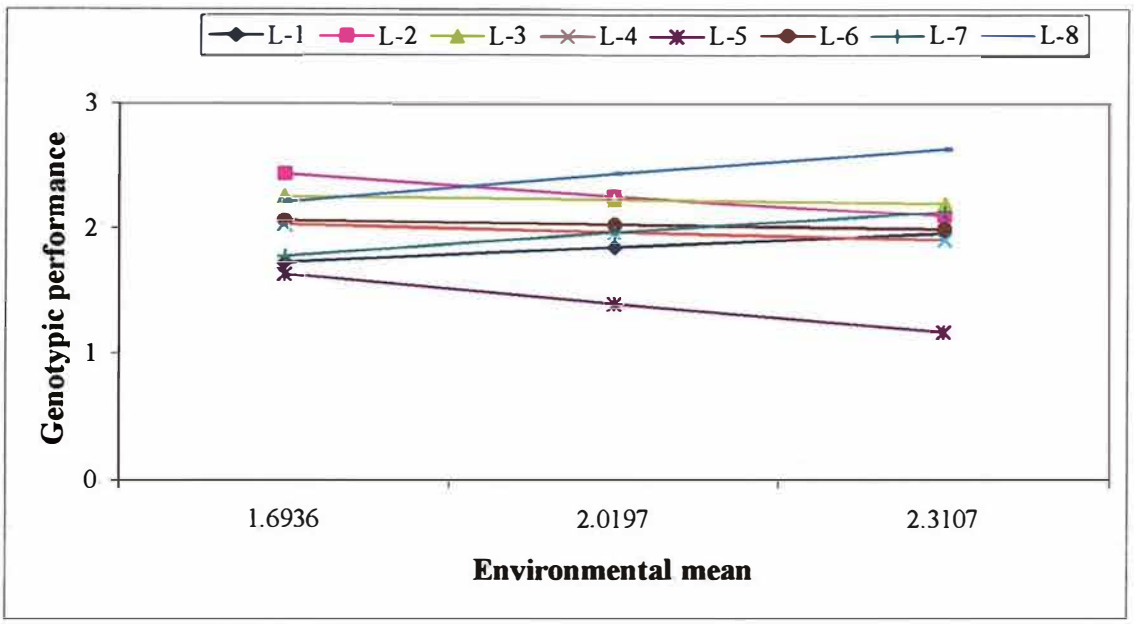


Fig 17: Regression of individual genotypic mean on environmental mean of eight lines for RWFD

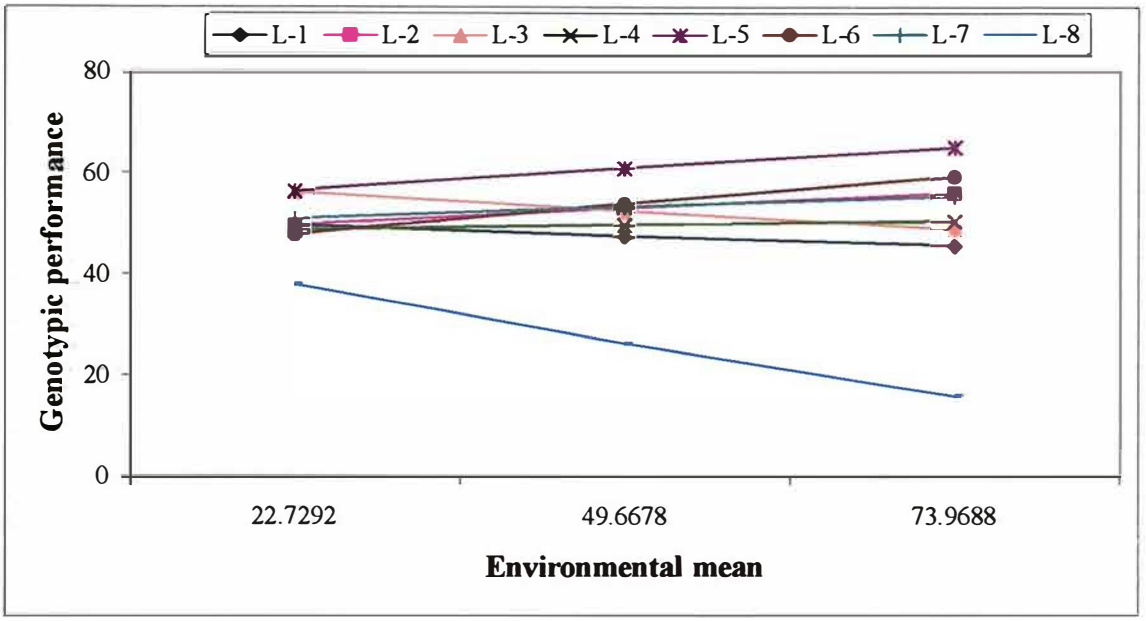


Fig 18: Regression of individual genotypic mean on environmental mean of eight lines for NPPP

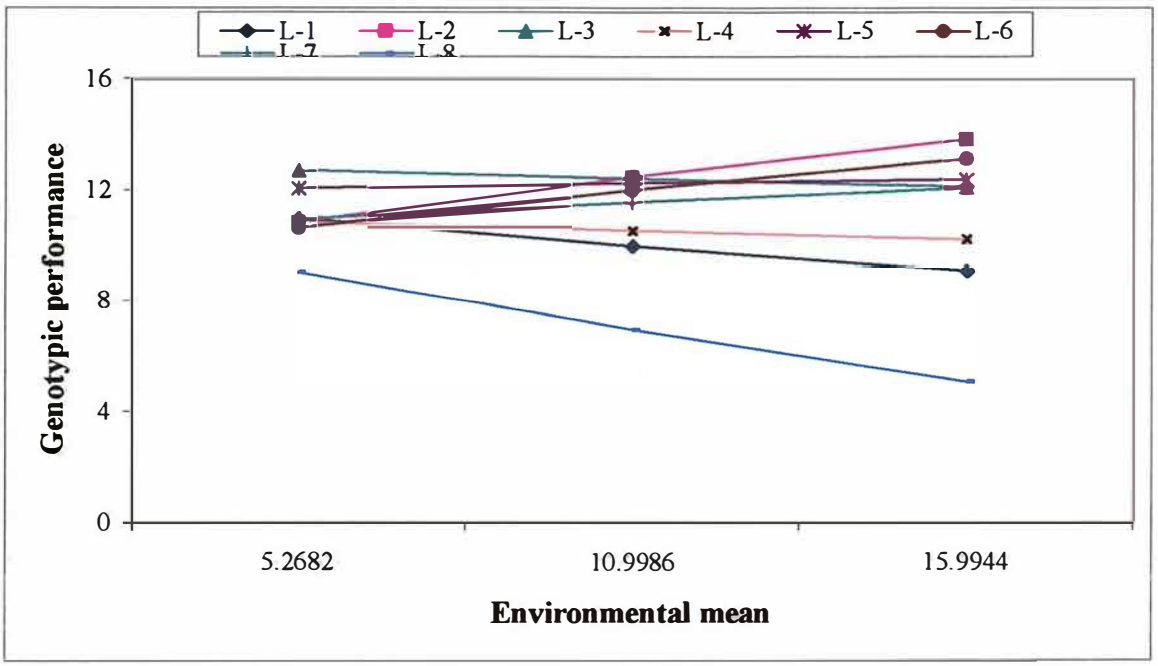


Fig 19: Regression of individual genotypic mean on environmental mean of eight lines for PdWPP

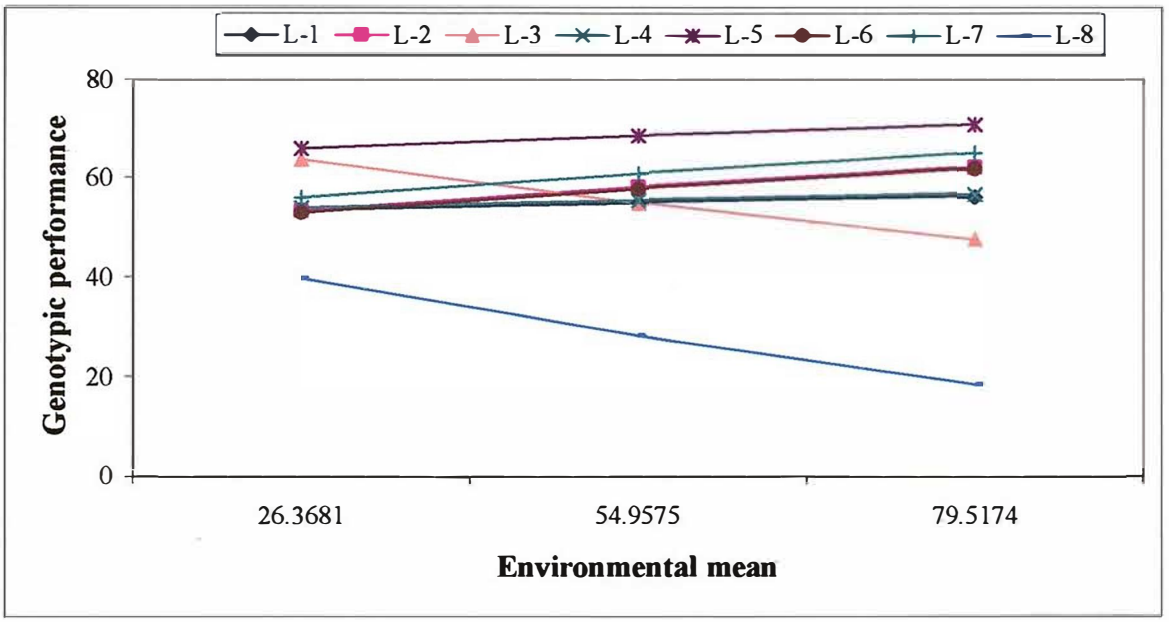


Fig 20: Regression of individual genotypic mean on environmental mean of eight lines for NSPP

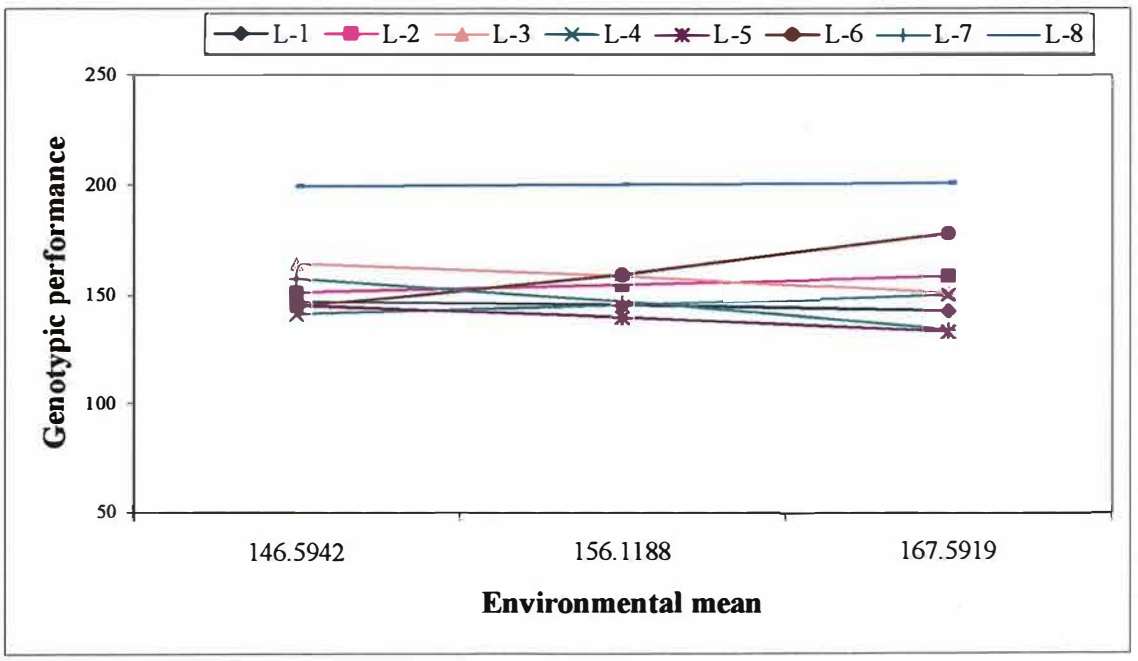


Fig 21: Regression of individual genotypic mean on environmental mean of eight lines for 1000-SW

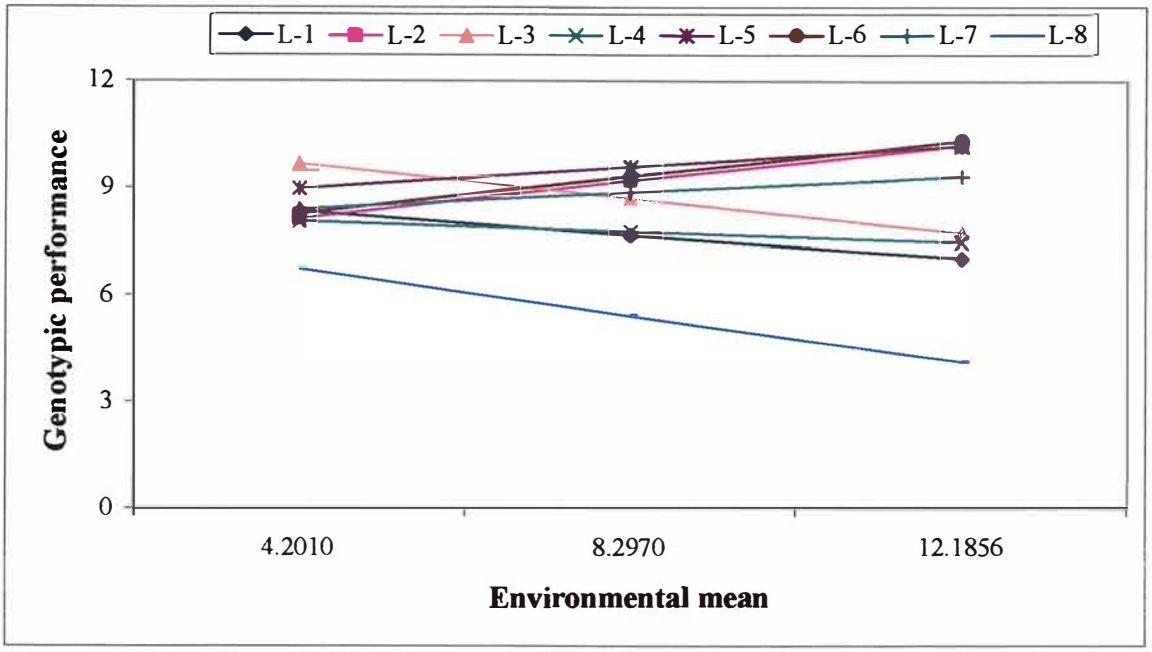


Fig 22: Regression of individual genotypic mean on environmental mean of eight lines for SWPP

DISCUSSION

G × E interaction is increasingly important because breeding programme tend to more internationally oriented. The aim of this research is to investigate the effects of G × E on genetic gain in sib-testing and progeny testing schemes. In crop plant yield and yield contributing characters are quantitative in nature and are highly influenced by environmental variation. The presence of G × E interaction necessitates evaluation of genotypes in a wide range of environments to find out desirable genotypes (Zalil *et al.*, 2008).

In the present investigation, the line means (Table 13) were highly significant for all the characters when compared with their respective standard errors. This result indicated that lines were different regarding these characters. Similar results were obtained by Alam *et al.* (1978) and Mandal *et al.* (1978) in rapeseed, Nahar (1997) in sugarcane, Deb (2002) in chickpea and Azad *et al.* (2008) and Dutta (2008) in lentil.

The significant mean values (Table 14) in different environments indicated that environments were different. The results were supported by the joint regression analysis (Table 15). Many investigators concluded that the year interaction effects are often the most important environmental factors affecting the yield and also major components of G × E interactions (Lin and Binns, 1988, 1989: Yang and Baker, 1991). It was observed from table 14 that the phenotypic mean performances were higher which might be due to favorable environmental condition regarding those characters. These findings are in agreement with the findings of Henry and Dauby (1987) in seasam, Samad (1991) in mustard, Nahar (1997) in sugarcane, Hasan (2001) in chickpea, Azad (2008) in lentil, who got maximum yield in better growing condition.

In the joint regression analysis (Table 15) the main item Line (L) and Environment (E) were highly significant for all the characters when tested against within error.

Which suggested that there were real differences existed between the genotypes and between the effects of different environments on the genotypes. Similar findings were reported by Sagor *et al.* (2007) in wheat and Khatod *et al.* (2006) in sugarcane genotypes. Variability in environments is an important factor and in large part determines the usefulness of b_i values (Pfahler and Linskens, 1979). Statistically significant environmental effects in the present investigation indicated that variability between environments was large enough for the proper estimation of b_i values.

The L × E interaction item were non-significant for all the characters except 1000-SW where it was highly significant. Singh and Bejiga (1990) got non-significant G × E for seed yield and biological yield in chickpea. The non-significant L × E interaction indicated that lines were interacted with the environment smoothly and here the environment worked additively, where L × E interactions were operative. These results are supported by graphical analysis. In graphical analysis intercrossing of curves (Figures 1-11) and regression lines (Figures 12-22) for different characters indicated the existence of L × E interaction. Significant L × E results are in conformity with the findings of Samad (1991) in rapeseed, Golani *et al.*, (2005) in onion, Kumar *et al.* (2007), Dutta (2008) in lentil, Sharma *et al.* (2007) and Alwawi *et al.* (2009) and Rao (2011) in chickpea.

A significant L × E interaction may be either i) a non-crossover L × E interaction, in which case the ranking of genotypes remain constant across environments and the interaction is significant because of changes in the magnitude of response (Baker, 1988; Blum, 1983; Matus *et al.*, 1997) or ii) a crossover L × E interaction, in which case a significant change in rank occurs from one environment to another (Matus *et al.*, 1997).

In the joint regression analysis L × E interaction sum of square was partitioned into heterogeneity of regression sum of square (linear) and remainder sum of square (non-linear). Most of the cases both linear and non-linear regression was accounted

for this L × E interaction. It was observed that the heterogeneity of regression was non-significant for all the characters. The non-significant heterogeneity of regression indicated that the genotype-environment (L × E) interaction was due to the slopes of non-linear relationship which indicated that the yield performance of the genotypes could not be predicted over environments. These results are in partial agreement with Srivastava *et al.* (1999) in sugarcane, Khatod *et al.* (2006) in sugarcane and Dar *et al.* (2009) in chickpea who got non-significant heterogeneity of regression.

The remainder item was non-significant for all the characters except NPPP, 1000-SW and SWPP. The significant remainder item suggested that non-linear type of L × E interaction was existed in the lines. Both linear and non-linear relationships with environments were reported by many investigators in different crops viz, Tiawari *et al.* (2011), Khatod *et al.* (2006), Azad (2008), Asad *et al.* (2009), Hammed and Al-Badrany (2007) Atta *et al.* (2009), Golani *et al.*(2005) and Choudhary and Haque (2010).

In respect of stability measurement there are various views proposed by different workers. Finlay and Wilkinson (1963) considered the linear regression as a measure of stability. In Eberhart and Russells (1966) model, b (regression coefficient) is considered as parameter of response and $\bar{S}^2_{di}$ as the parameter of stability for a given value of independent variable, the value of dependent variable may be estimated using the regression equation, provided $\bar{S}^2_{di}$ is not significantly different from zero. Assuming $\bar{S}^2_{di} = 0$, a high value of bi will mean more change in Y for a unit change in *I*. In other words the variety is more responsive. Such variety may, therefore be recommended only for highly favorable environment. However, relatively lower value of b (1) will mean less responsive to the environmental change and therefore more adaptive. If b is negative the variety may be grown only in poor environment. $\bar{S}^2_{di}$ is significant from zero will invalidate the linear prediction. If $\bar{S}^2_{di}$ is non-

significant, the performance of a genotype for a given environment may be predicted accordingly a variety whose performance can be predicted is said to be stable.

On the basis of above criterion the lines which showed stable performances i. e., adaptable to all environment are line-2, line-4, line-6 and line-8 for DMF; line-1, line-4, line-7 and line-8 for NPBMF; line-1, line-2, line-5 and line-7 for NSBMF; line-2, line-3, line-4, line-5, line-6 and line-7 for PHMF; line-1 for PWFD; line-3 and line-6 for RWFD; line-4 for PdWPP; line-2 for NSPP and line-4 for SWPP. These lines are most stable with the changing environment and could be used for the future breeding programme. The results are in agreement with the findings of Paroda and Hayes (1971), Arain and Siddiqi (1977), Singh and Bejiga (1990), Srivastava *et al.* (1999), Sharma *et al.* (2007), Choudhary and Haque (2010), Atta *et al.* (2009), Karadavut *et al.* (2010), Islam *et al.* (2002), Khatod *et al.* (2006), Dethe and Dumbre (2005), Sial *et al.* (2000), Amin *et al.* (2005), Shindin and Loktera (2000), Akhtar *et al.* (2010), Kanouni *et al.* (2007), Dehghani (2010) in various crops.

Beside these, it was observed that line-3 and line-5 for NPBMF; line-4 for NSBMF; line-1 for PHMF; line-1, line-7 and line-8 for RWFD; line-2 and line-6 for PdWPP; line-4 for 1000-SW and line-2 and line-6 for SWPP were more responsive to changing environment, having non-significant $\bar{S}^2_{di}$ and high values of b_i. It suggested that these lines might be recommended only for favourable environment. Similar results are obtained by Sial *et al.* (2000) in wheat, Akhtar *et al.* (2010) and Khan *et al.* (2010) in mungbean, Karadavut *et al.* (2010) in faba bean, choudhary and Haque (2010) in chickpea.

While line-5 and line-6 for DMF; line-2 and line-6 for NPBMF; line-3, line-6 and line-8 for NSBMF; line-8 for PHMF; line-2, line-4 and line-5 for RWFD; line-1 and line-8 for PdWPP; and line-1, line-3 and line-8 for SWPP were found poor adaptability to all environments. Singh and Rai (1989) and Singh *et al.* (1993) in

sugarcane, Sial *et al.* (2000) and Amin *et al.* (2005) in wheat, Sharma *et al.* (2007) and Choudhary and Haque (2010) in chickpea also obtained similar results.

In this investigation, some varieties were adaptable in favorable and some were adaptable in unfavorable conditions. Rest of the lines was found unpredictable due to their significant $\bar{S}^2_{di}$ values for different characters.

Hence L × E interaction is under genetic control, plant breeders aim to develop new varieties that consistently have high yield in a variety of environments. The adaptability of a variety is usually tested by the degree of its interaction with different environments. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield with low degree of fluctuation in yielding ability grown over diverse climatic conditions.

SUMMARY

Genotype-environment interaction and stability parameters following Perkins and Jinks (1968) model of eight chickpea lines for eleven quantitative characters at 4 irradiation doses viz. no irradiation (D_0), 20kr (D_A), 30kr (D_B) and 40kr (D_C) in 3 consecutive years (2007-2008, 2008-2009 and 2009-2010) were investigated. The eleven characters studied are Days to maximum flower (DMF), Number of primary branches at maximum flower (NPBMF), Number of secondary branches at maximum flower (NSBMF), Plant height at maximum flower (PHMF), Plant weight after fully dry (PWFD), Root weight after fully dry (RWFD), Number of pods per plant (NPPP), Pod weight per plant (PdWPP), Number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and Seed weight per plant (SWPP).

The range of variation was wide and pronounced in the genotypic means for all the characters. This indicated that there existed genotypic differences among the chickpea lines. Environmental means also indicated that different environments had different effects on all the traits. The mean values in second year (2008-2009) and third year (2009-2010) had the greater effect on the phenotypic expression for all the characters than that of first year (2007-2008).

In the joint regression analysis, the genotype-environment interactions were found to be operative in this investigation.

The genotype-environment interaction accounted for by both linear and non-linear functions of the environments. A non-significant greater portion was accounted for by linear function of the environmental mean and some portions of interaction were non-linear and independent of the linear function.

Both linear and non-linear components of genotype-environment interactions were under the control of different gene systems.

Stability performances of different lines were different for different characters. From the estimation of stability parameter it was concluded that line-4 and line-7 for most of the characters showed stable performances with the changing environment and these stable lines could be used for further breeding programme.

The present research work also exhibited that yield potential of a genotype can be increased by increasing the performance of the yield components in a particular environment, since those characters are associated with yield.

PART III

VARIABILITY, CORRELATION, PATH-COEFFICIENT AND SELECTION INDEX

INTRODUCTION

Yield stability is a major objective in any breeding programme. This could be achieved through a better understanding of the components contributing to final yield. Because yield and yield components are quantitative in nature and governed by polygenes and also largely influenced by the environmental factors.

Before yield improvement breeders need to identify the causes of variability in seed yield in any given environment. Information on genetic variability and heritability are useful to formulate selection criteria for improvement of seed yield.

Works on variability and heritability have been done by several investigators like Begum (1995) in chickpea, Nahar and Khaleque (1996) in sugarcane, Husain (1997) in chilli, Deb (2002) in chickpea, Tyagi and Khan, (2010) in lentil, Younis *et al.* (2008) in lentil, Punia *et al.* (2011) in lentil, Bicer and Sarker (2008) in lentil, Hamdi *et al.* (2003) in lentil, Rasheed *et al.* (2008) in lentil, Arshad *et al.* (2004) in chickpea, Yucel *et al.* (2006) in chickpea, Bakhsh *et al.* (1996) in chickpea, Agarwal (1986) in chickpea, Arshad *et al.* (2003b) in chickpea, Kumar *et al.* (2010).in mung bean.

The knowledge of relationship between yield and yield contributing characters is important for planning yield improvement programme in any crop. It gives breeders more precision and accuracy in their works. The correlation co-efficient gives a measure of the relationship between the studied traits and provides reliable and useful information on the nature, extent and direction of relationship.

When more variables are correlated with yield, it is important to identify appropriate traits for selection. In such case, path analysis provides an effective means of finding out direct and indirect contribution of different component traits towards seed yield. Relationship between yield and yield contributing characters studied through phenotypic and genotypic correlation accompanied with path coefficient analysis has been studied by several workers like Uddin (1983) in spring wheat;

Ghafoor *et al.* (1990) in mash; Padi (2003) in pigeonpea; Ulukan *et al.* (2003) in faba bean; Garcia de Moral *et al.* (2005) in wheat; Chauhan and Singh (2001), Yadav *et al.* (2003), Anjam *et al.* (2005), Azizi *et al.* (2010), Karadavut (2009) in lentil; Kumar *et al.* (2004) in mungbean; Yucel and Anlarsal (2010), Ciftci *et al.* (2004), Khan and Qureshi (2001), Singh *et al.* (1990), Talebi *et al.* (2007), Erman *et al.* (1997), Guler *et al.* (2001), Hasanuzzaman *et al.* (2007), Bakhsh *et al.* (2006) in chickpea.

A complete satisfactory criterion based on discriminant function selection would be more desirable when a combination of two or more characters with yield is studied in a selection index. The characters that show high positive genotypic correlation with yield may serve as basis for selection (Punia *et al.*, 1982). The use of selection index technique would serve a two-fold purpose: (1) to bring about the genetic progress simultaneously in several characters and (2) to improve the yield through selection for relatively more heritable auxiliary characters.

The technique of discriminant function analysis first evolved by Fisher (1936) and adopted for plant selection by Smith (1936). Later on, different workers constructed selection indices for different crops, such as Robinson *et al.* (1951) worked in corn; Paroda and Joshi (1970) in wheat; Khaleque *et al.* (1977) in rice; Joarder *et al.* (1978) Samad (1991) in rapeseed, Husain (1997) in chilli , Singh *et al.* (1979) in onion; Nandan and Pandya (1980) in lentil. Deb (2002) in chickpea; Ferdous *et al.* (2010) in wheat; Ara (2010) in onion; Khan (2009) in potato.

Keeping all these facts in view, the present investigation was planned to study variability, heritability and characters association between yield and its components and determination of direct and indirect relationship between yield and certain plant characters by using path analysis and construction of a suitable selection indices using eight lines of chickpea.

REVIEW OF LITERATURE

Grain yield in any crop is a complex character and is final product of many contributory traits and their interaction. The knowledge of these factors and their relationship with each other and with yield, provide the basic information on yield improvement. Therefore, for convenient of study review of literatures on variability, heritability, genetic advance, characters association, path-coefficient and selection index were made not only in chickpea but also in other crops.

Paroda and Joshi (1970) studied five quantitative characters and constructed selection indices for the different generation of wheat. They observed maximum gain (1950) when all the five characters were included in the discriminant function. Individually, except grain yield/plant, all of the component characters showed negative gains. When two or more characters included in a function the expected gains were positive and high when grain yield/plant was also included as an independent character.

Singh and Singh (1974) used the discriminent function technique to construct a selection index for yield in 20 treatments in 3 crosses of Indian mustard. They reported that selection based on the number of primary branches, number of secondary branches, siliqua length and plant weight gave the highest relative efficiency. Selection based on single character, other than yield and number of primary branches was less effective than straight selection. In general, the more number of characters included in a selection index showed better performance.

Khaleque (1975) studied correlation, path-coefficient and selection index in rice and found that yield/plant correlated with most of the yield components, while negative or no correlation with yield was indicated by some of the characters .The discriminant function for selection was found to be superior over straight selection. Inclusion of yield in the function as an independent character is not essential. A

combination of number of primary branches, spikelet number and kernel number may be used as selection index in the selection practices.

Naskar *et al.* (1982) made a selection index analysis with the help of dispersion matrices of 10 cultivars of sunflower. They reported that maximum genetic gain was obtained when all the characters under study were considered together. Selection of component characters was found more profitable than selection for yield alone.

Punia *et al.* (1982) reported that among the various selection indices constructed in a study of 41 genotypes for cane yield in sugarcane on the basis of discriminant function analysis, the index involving the number of tiller/clump + number of millable cane/clump + thickness + cane weight + cane yield/clump was found to give maximum expected genetic gain over straight selection.

Kumar *et al.* (1988) correlation and discriminant function selection in Indian mustard. They reported that heritability estimate was found to be the lowest for yield/plant. siliqua/plant had the highest heritability (84.67) indicated the presence of additive gene action. The value of genotypic correlation was higher than the phenotypic correlation with primary branches, secondary branches and siliqua/plant. Among the yield contributing characters plant height had positive and significant correlation with primary branches and silique/plant, primary branches with secondary branches and silique/plant. The discriminant function selection showed that when two characters, silique/plant and secondary branches were considered, the maximum relative efficiency was obtained over straight selection.

Yadav and Singh (1988) studied the selection indices for seed yield and four physiological traits in two crosses of Indian mustard. They reported that leaf area Duration and leaf area index at productive phase when selected simultaneously, resulted in the highest genetic gain for seed yield. They also noted selection indices

based on leaf area duration and leaf area index exhibited superiority over straight selection in both crosses.

Samad (1991) constructed selection indices using six agronomical characters in rapeseed (*Brassica campestris* L.) and reported that maximum expected gain was obtained when large number of characters were included in the discriminant function. In the discriminant function analysis seed yield per plant alone gave a negative expected gain, but in combination with two or more characters it showed the highest positive expected gain. He concluded that seed yield is not complete character for higher yield rather it depends on other component characters for higher yield.

Nahar *et al.* (2000) undertook an investigation for variability, heritability and genetic advance in ten sugarcane clones for eight quantitative characters. For heritability estimate which was found to be the highest for cane height (87.63 followed by cane diameter 77.80 and leaf area 73.29). The genetic advance as percentage of mean showed maximum value for leaf area (35.50) followed by cane height (27.47) cane yield/clump (14.96), cane diameter (12.93) and millable cane/clump (11.46).

Deb (2002) studied correlation, path-coefficient and selection index in six chickpea (*Cicer arietinum* L.) lines and found that significant correlation between PdW/P and SW/P, NS/P and SW/P. In path-coefficient analysis, he observed NPBFF, NSBFF, PWH, PdW/P and NS/P to be the most important yield component because they exhibited direct positive effect on SW/P both at phenotypic and genotypic levels. In the discriminant function analysis a combination of NPBFF, NSBFF, PHMF, NS/P and SW/P in an index gave the highest genetic gain in percent.

Saleem *et al.* (2002b) carried out an experiment on a set of 20 chickpea elite genotypes including two check varieties. They found that the genotypes showed highly significant differences for all the characters studied. Seed yield per plant was

positively and significantly correlated with days to flowering, total weight of plant, number of pods per plant and 100-seed weight both at the genotypic and phenotypic levels. The correlation of number of secondary branches per plant with seed yield was negative and significant. Number of pods per plant had maximum positive direct effect on seed yield. The other traits in the study also exhibited considerable indirect effect on the seed yield through number of pods per plant. They concluded that number of pods per plant and 100-seed weight could be used as selection criteria to improve the yield.

Ciftci *et al.* (2004) conducted a research work to determine the relationship among yield and some of the yield components using correlation and path coefficient analysis. They used 14 chickpea cultivars designed in Randomized Block with three replications. They found positive and significant relationships among seed yield and plant height, number of braches, number of pods per plant, biological yield, harvest index and number of seeds per plant. Negative and non-significant relationship was determined between seed yield and 1000-seed weight. According to path coefficient analysis, they also found that there were strong direct effects of the biological yield, harvest index and number of seeds per plant on the seed yield, p.c.: 0.783 and p.c.: 0.441, respectively.

Variability, heritability, genetic advance, correlation coefficients and path coefficients for yield and its components were conducted by Arshad *et al.* (2004) in 24 advance lines of chickpea. High heritability with low genetic advance for days to flowering, days to maturity and 100 seed weight indicated the influence of dominant and epistatic genes for these traits. High heritability for secondary branches and biological yield coupled with high genetic advance revealed that additive gene effects are important in determining these characters. Grain yield had positive and significant correlation with plant height, pods per plant, 100-seed weight and biological yield. High direct effects were contributed by biological yield and harvest index although the later had negative association with grain yield. Moreover, it was noticed that high

indirect contribution was via biological yield by most of the yield components and hence these two parameters (biological yield and harvest index) should be given more consideration while deciding about selection criteria of genotypes for rainfed conditions.

Yucel *et al.* (2006) conducted a study to determine variability, heritability and correlations between yield and yield components in 15 kabuli chickpea (Cicer arietinum L.) genotypes for 2 years. Direct and indirect effects of yield components on seed yield per plant were investigated. Genotypic variance was the highest for 1000 seed weight, followed by seed number per plant. Broad sense heritabilities ranged from 5.47% (days to flowering) to 51.66% (seed number per plant). Heritabilities for seed number, 1000 seed weight, and number of full pods were greater than those for the other traits. Positive and significant ($P < 0.05$) relationships were determined between seed yield per plant and plant height, first pod height, secondary branch, total pod, and number of full pods and seeds per plant. The path coefficient analysis based on seed yield per plant, as a dependent variable, revealed that all of the other traits, except days to flowering, first pod height, and total pod number, exhibited high positive direct effects. Number of seeds and full pods showed the highest direct influence with 47.49% and 44.73%, respectively. Therefore, this research suggests that seed and full pod numbers can be good selection criteria for improving seed yield per plant in kabuli winter chickpea.

Talebi *et al.* (2007) carried out an experiment on thirty six genotypes of chickpea for their yield performance. In the examined characteristics, they found positive and statistically significant relationships between 100-seed weight and plant height, between the number of secondary branches and plant height, between day to heading and day to maturity, between day to maturity and number of primary and secondary branches, between seed yield and number of pods plant^{-1} and number of seeds pod^{-1}, between seed yield and biomass and harvest index and also found negative and significant relationships between number of pods plant^{-1} and 100-seed weight,

between seeds pod^{-1} and number of secondary branches. Harvest index had greatest direct effect on seed yield (p.c. = 0.901**). Also, its indirect effect on seed yield more positive through plant height, number of pods plant^{-1}, number of seeds pod^{-1} and biomass, but negative and low through days to heading and maturity, 100-seed weight and number of primary branches. They suggested that selection for high seed yield should be based on biomass (biological yield) and harvest index in kabuli chickpea.

Tuncturk and Ciftci (2007) carried out an experiment to investigate the relationship between yield and some yield components of 16 oilseed rape cultivars (*Brassica napus ssp. oleifera* L.) by using correlation and path coefficient analysis. The results from their study it revealed that there were statistically positive correlation between seed yield with the number of branch (r=0.219 **), with number of pods per plant (r=0.424 **), with the number of seeds per pod (r= 0.247 **), and with 1000-seed weight (r= 0.161*). Number of pods per plant, 1000-seed weight and number of seeds per pod have shown a considerable direct positive effect on seed yield. Positive direct effect of number of pods per plant, number of seeds per pod and number of branches per plant was associated with significant and positive correlation with seed yield. These yield components suggested good selection criteria to improve seed yield in rapeseed breeding.

Gul *et al.* (2008) conducted a study to determine correlation among different yield contributing traits of mungbean. Correlation was worked out among plant height, days to flowering, days to maturity, total dry weight plot^{-1}, yield plant^{-1}, 100-grain weight, harvest index and yield ha^{-1}. They found that significant differences were observed among different populations for all the parameters. Correlation analysis revealed that earliness had negative correlation with plant height and dry weight per plot, while 100-seed weight and harvest index were recorded to be positively correlated. Dry weight per plot was found to have positive correlation with days to maturity, seeds pod^{-1} and plant height, while negatively correlated with yield per hectare and harvest index. 100-grain weight showed positive correlation with pods plant^{-1} and harvest

index, while it had negative correlation with days to maturity, seeds pods^{-1} and plant height. Seed yield plot^{-1} was found to be non-significantly correlated with 100-grain weight. Harvest index had significant positive correlation with seed yield plant^{-1}, while it had significant negative correlation with days to maturity, seed pod-1, plant height and dry weight per plot. Similarly, seed yield per plant was positively correlated with pods plant^{-1}, yield ha^{-1} and harvest index. On the other hand, its correlation with plant height was significantly negative.

Rasheed *et al.* (2008) conducted a study at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad during the year 2006-2007. They evaluated fifteen lentil lines/varieties to exploit yield components to the maximum extent and to formulate selection criteria for the improvement of seed yield. Significant genetic variation was observed for all the traits. They found all the traits under study had high heritability values except number of primary branches. Higher values of heritability coupled with genetic advance were observed for seed yield (98.30%, 128.20%), harvest index (97.10%, 79.40%), biological yield (94.30%, 56.10%) and hundred seed weight (88.30%, 50.80%) which indicates the role of additive genes to control these traits. Hundred seed weight (0.67, 0.65), harvest index (0.94, 0.93) and biological yield (0.81, 0.80) had positive and highly significant correlation with seed yield at both genotypic and phenotypic levels. Number of primary branches, hundred seed weight, harvest index and biological yield showed positive direct effect along with positive genotypic correlation with seed yield. Finally, from this study they concluded that the traits like hundred seed weight, harvest index and biological yield can be exploited for the improvement of seed yield in lentil.

Togay *et al.* (2008) conducted an experiment to determine the relationship among yield and some of the yield components using correlation and path coefficient analysis. They used 12 pea genotypes in the experiment. The experiment was designed as randomized complete blocks with four replications. At the end of the study, positive and significant relationship were found among seed yield and pods per

plant and biological yield in both years. The strongest and direct positive effects were the biological yield (p = 0.6500), numbers of pods per plant (p = 0.3137) and the seed yield. These were followed by first pod height (p = 0.2398) and number of seeds per pod (p = 0.2227).

Younis *et al.* (2008) conducted a study to determine the genetic parameters and character association in elite lines of lentil (*Lens culinaris* Medik). Genetic parameters like genotypic and phenotypic variances, coefficients of variation, heritability, genetic advance, correlation coefficients and path coefficients were estimated. Significant variation was noted for all the traits. High heritability estimates were observed for all the traits except number of primary branches per plant. In general phenotypic coefficients of variability were greater than their corresponding genotypic coefficient of variability. Higher estimates of heritability and genetic advance were observed for seed yield (97.10%, 90.71%), harvest index (96.20%, 63.29%) and maturity days (95.90%, 63.39%) indicating that these characters are mainly controlled by additive genes and selection of such traits might be effective for the improvement of seed yield. Days to flower, plant height, number of primary branches, biological yield, harvest index and hundred seed weight had positive direct effect on seed yield. Biological yield, hundred seed weight and harvest index also had positive and highly significant genotypic and phenotypic correlation with seed yield. Hence these traits could be used for the improvement of seed yield resulting in the evaluation of high yielding varieties of lentil.

The evaluation of selection criteria using correlation coefficients and path analysis was carried out by Andrea *et al.* (2009) for a period of two years on forty pea genotypes. The correlation analysis revealed that grain yield had genotypic relationships with numbers of pods, seeds per plot, length of the internodes and plant height in 2007 and also with grain diameter, length and width of leaflets and number of nodes at the first pod in 2008. The highest positive direct effects in 2007 were length of the internodes (0.68), seeds per plot (0.38) and numbers of pods (0.26).

Length of leaflets exhibited a negative direct effect (-0.46). The highest positive indirect contribution of plant height mediated by length of the internodes was 0.50. The highest negative indirect contribution was pod length via length of the internodes (-0.35). In 2008, the highest positive direct effects were seeds per plot (0.67), width of leaflets (0.33) and numbers of pods (0.25). Length of leaflets presented the highest negative direct effect (-0.34). The indirect effects were observed via seeds per plot, length and width of leaflets; therefore number of pods and seeds per plot can be used for indirect selection. The parameter estimated showed that number of pods and seeds, and pod length determined the yield during 2007 and number of pods and seeds, and grain diameter during 2008. The R2 values for both models were 0.60 and 0.89, respectively. The number of pod and seeds per plot were the main components of seed yield, having the maximum direct effects on this trait. From this study they concluded that these results might be used as selection criteria in order to increase the selection efficiency in pea breeding programmes.

Khan (2009) studied correlation, path analysis and selection indices on twenty one yield and yield components of four high yielding varieties of potato (*Solanum tuberosum* L.). In most cases, the genotypic correlation was higher than that of corresponding phenotypic correlation suggesting that there was fairly a strong inherent relationship between the characters. Here X2 (NS/P) showed highly significant positive correlation both at phenotypic and genotypic levels with X7 (WT/P), X11 (NBST/P), X17 (WBST/P) and X18 (WNSST/P). The path coefficient analysis indicated that the characters X6 (NT/P), X9 (NSST/P) and X13 (NSEST/P) exhibited high direct positive effect on X21 (Y/P) both at phenotypic and genotypic levels. The discriminant function for selection was found to be superior over straight selection. The highest expected genetic gain of 529800.43% was observed with six characters combination followed by five and four characters combination.

Deb *et al.* (2009) made a study on correlation and path coefficient to determine the contribution of different traits to seed yield in lentil (*Lens culinaris* Medic). In

correlation analysis, they found that SWPP was positively correlated with all the characters but significantly correlated only with DFF, NPdPP, PdWPP and NSPP at genotypic levels. But at phenotypic level , SWPP significantly correlated only with NPdPP. Their path coefficient analysis revealed that NPdPP and NSPP had the highest direct effect on SWPP both at phenotypic and genotypic levels. The second highest direct effect on SWPP was noted for PdWPP at phenotypic level and NPdPP at genotypic level. From this study they concluded that NPdPP and NSPP were the most important yield components because they showed significant correlation with SWPP at genotypic level and highest direct positive effect on SWPP both at phenotypic and genotypic levels.

Ferdous *et al.* (2010) conducted a study with twenty bread wheat genotypes at the experimental field of Bangladesh Agricultural University (BAU), Mymensingh, during the period from November 2008 to March 2009 and assessed the relationship and selection index among yield and important yield attributing characters. Days to maturity, grains per spike, 100-grain weight and harvest index showed significant and positive correlation with grain yield per plant. Path coefficient analysis suggested that grains per spike followed by 100-grain weight and effective tillers per plant contributed maximum to grain yield positively and directly. Thus, selection based on these characters might be effective for improving grain yield. Selection indices were constructed through the discriminant functions using eight characters. From the results, the highest relative efficiency was observed with the selection index based on three characters viz, plant height and grains per spike and grain yield per plant. The present investigation indicates that the selection index based on these three characters might be more effective and efficient for selecting high yielding wheat genotypes.

Jonah *et al.* (2010) made a study on twelve cultivars of bambara groundnut those were sown for genetic correlation studies among agronomic characters and seed yield. The associations between seed yield and other quantitative characters showed positive correlation between seed yield per hectare, pod yield per plant and seed yield per

plant. There was a significant genotypic and phenotypic correlation coefficient in the association between pod length and pod width, seed length and seed width during the trial, which could be a good index for selecting high yielding cultivars, as plump pods appeared to compensate for an increase in the total yield through a relatively greater weight of seeds. The path coefficient analysis of characters showed that the seed yield per hectare indicated positive direct contribution with pod length, plant emergence at 2 WAS and stands count prior to harvest. Although these characters recorded a positive but a non-significant genotypic correlation coefficient of seed yield per hectare with other characters indicated the inefficiency of selection based on correlations alone.

Genetic variability and character association in 23 genotypes of mung bean for different quantitative characters were studied by Kumar *et al.* (2010) in ***kharif*** (summer or monsoon crop) 2007. In their study, analysis of variance revealed that there were highly significant differences among all the characters Genotypes under study indicating the presence of sufficient amount of variability among the varieties. Thus there was ample scope for selection of different quantitative characters for crop improvement. They also found that the highest GCV and PCV were observed for harvest index and pods per plant, respectively. High estimates of genetic advance as percent of mean were observed for 100-seed weight and harvest index. Highly significant correlation was recorded for pods per plant and harvest index at both genotypic and phenotypic levels with seed yield per plant and plant height, primary branch per plant, clusters per branch and days to maturity had direct positive effect on seed yield.

Ara (2010) carried out an experiment of F_1 materials of half diallel crosses, for nine quantitative characters viz., leaf length (LL), bulb diameter (BD), bulb length (BL), bulb weight (BW), neck diameter (ND), neck length (NL), plant height (PHt), number of leaves (NLS), and bulb yield/plot (BY) and studied correlation, path-coefficient and selection index. She found that phenotypic component of variation

(σ^2P) was higher than genotypic (σ^2G), interaction ((σ^2l) and within error (σ^2w) components of variation. The character, bulb weight showed the highest values for σ^2P, σ^2G, σ^2l and σ^2W components of variation. Regarding correlation studies, it was observed that genotypic correlations were higher than the respective phenotypic correlations. This situation was also marked in the path co-efficient analysis. All the characters have highly significant correlation co-efficient except neck length. Bulb yield/plot showed highly significant and positive correlation co-efficient at both phenotypic and genotypic levels. Among all the pairs of character associations, BW and BY showed the strongest correlation co-efficient at both levels. When all the nine characters were included in an index, it exhibited the highest genetic gain as percentage. The inclusion of BW (4), PHt (7), NLS (8) and BY (9) in an index together increases the value of expected gain greatly in the function. But the above mentioned characters in a combination of four had high correlation co-efficient as well as direct effect at both of phenotypic and genotypic levels may be considered as primary yield components. So, the four character combinations, such as LL (1), BW (4), PHt (7) and NLS (8) with the commendable expected gain of 330.729 may be considered as important selection index for this material.

Sharma and Saini (2010) conducted a study with the view to elucidate the genetic variability, heritability, genetic advance, correlation and path analysis in chickpea. They found that the study revealed the presence of sufficient variability with high heritability for most of the yield components. Correlation and path analysis indicated that number of pods per plant and branches per plant could be useful as selection indices for the development of high yielding genotypes of chickpea.

Tabasum *et al.* (2010) studied ten mungbean genotypes to assess variability and degree to which various plant traits associate with seed yield. Primary and secondary branches, pods per cluster and pod length showed lesser variability while clusters per plant, 100-seed weight and harvest index exhibited intermediate range of variability.

Sufficient genetic variability was observed for plant height, pods per plant, total plant weight and seed yield. Moderate to high heritability estimates were found for all traits. Primary and secondary branches per plant, pod length and 100-seed weight exhibited negative and non significant genotypic and phenotypic correlations with seed yield. Plant height showed positive non-significant and significant genotypic and phenotypic correlation. Pods per cluster correlated significantly negative with seed yield. Clusters per plant, pods per plant, total plant weight and harvest index showed positive significant genotypic and phenotypic correlations with seed yield. Positive direct effects were exerted through secondary branches, pods per plant, pod length, 100-seed weight, total plant weight and harvest index, while primary branches, plant height, clusters per plant and pods per cluster had negative direct effects. They concluded that the findings could be useful for establishing selection criteria for high seed yield in the mungbean breeding.

The genetic parameters, character association and path coefficient analysis between yield and yield contributing characters of 25 lentil genotypes were studied by Tyagi and Khan (2010) during 2007 – 2008. They found that the genotypes exhibited a wide range of variability for all the traits studied. High heritability accompanied by moderate to high GCV and genetic gain were observed for number of pods plant^{-1}, number of branches plant,$^{-1}$ 100-seed weight, seed yield plant^{-1} and harvest index. Correlation study indicated that number of pods plant^{-1}, biological yield and harvest index were positively and significantly correlated with seed yield at both phenotypic and genotypic levels. Path coefficient analysis showed that harvest index, biological yield and number of pods plant^{-1} showed maximum and positive direct effect on seed yield.

Yucel and Anlarsal (2010) carried out a research work to determine selection criteria by using correlation and path coefficient analysis in 22 genotypes of chickpea (*Cicer arietinum* L.) under Mediterranean conditions. They found positive and statistically significant relationships among seed yield and harvest index and seed

number. The path coefficients analysis based on seed yield, as a dependent variable, revealed that harvest index had the greatest direct effect on seed yield (0.4206) with the ratio of 56.04 %. Both correlation and path analyses indicated that harvest index was the major direct contributor to seed yield. Their study suggested that selection for high seed yield should be based on selecting plants having high harvest index in chickpea.

Biabani *et al.* (2011) carried out an experiment in order to evaluate the relationships between grain yield and the other characteristics with two cultivars of chickpea (Hashem and Arman) in deterioration (0 (control), 7 and 14 days). The experiment was a factorial completely randomized design with 2 factors. At harvest time, height of the plants, filled and unfilled pods per plant, number of seeds per plant, plant dry weight and yield were measured. Results showed the yield had highly positive correlation with filled pod per plant ($r = 0.96$)) ($p<0.01$). In Arman and Hashem cultivars, yield had high correlation with seed number per plant ($r = 0.95$) ($p<0.01$) Dependence of seed yield on height was great with deterioration of 14 days; and the correlation coefficient between filled pod number and height after 7 days deterioration was significantly ($P<0.01$) negative ($r = -0.95$) ($P<0.01$) but it was of greater in magnitude in 14 days deterioration ($r = 0.79$) ($P<0.01$).

Tadesse *et al.* (2011) needed to study the association among seed yield and related components due to lack of information on genetic diversity in Ethiopian faba bean (*Vicia faba* L.) germplasm. They grew fifteen genotypes at Sinana Agricultural Research Center and on two farmers' field at Sinja and Adaba, south Eastern Ethiopia in 2007-08 cropping season. At Sinana, they found that number of pods/plants, number of seeds/pod and plant height showed significant association with seed yield per plot. Whereas, At Adaba, thousand seed weight showed significant association with seed yield per plot. Path analysis for seed yield per plot at Sinana indicated number of pod/plants, seeds per pod, thousand seed weight, stand percent and plant height had high positive direct effect at genotypic level. At Sinja, days to flower, days

to maturity and number of pods/plant had positive direct effect on seed yield per plot whereas at Adaba stand percentage, days to flower, days to maturity, number of seeds/pod and thousand seed weight showed positive direct effect on seed yield per plot. Path analysis indicates that number of seeds/pod and thousand seed weight were the main determinants of yield per plot at Sinana and Adaba.

Tyagi and Khan (2011) carried out an experiment during winter (*rabi*) season of 2007 and 2008 to assess the correlation, path coefficient and genetic diversity in 30 morphological diverse accessions of lentil (*Lens culinaris* Medik) under rainfed conditions. Days to 50% flowering, biological yield/plant, seed yield/plant and 100-seed weight showed significant differences and wide variations during both years. Low differences between phenotypic coefficient of variability and genotypic coefficient of variability were observed for all the descriptors during both years. Pods/plant, days to 50% flowering, biological yield/plant, seed yield/plant and 100-seed weight in both the years showed high heritability coupled with high genetic advance (per cent of mean) signifying the influence of additive gene effects. The characters viz., biological yield/plant and number of primary branches/plant showed positive and significant correlations with seed yield/plant and exerted positive and high direct effects on seed yield/plant in both years.

MATERIALS AND MATHODS

This part of the present investigation described under the following heads:

A. MATERIALS

The materials used in this part were same as the materials of PART-II.

B. METHODS

The methods used in this study are described under following sub-heads:

1 Collection and Irradiation of the Experimental Seeds;
2 Preparation of the Experimental Field;
3 Design and Size of the Experimental Field;
4 Sowing of Seeds and Raising of Seedlings;
5 Maintenance of the Experimental Field;
6 Collection of Data and
7 Techniques of the Analyses of Data

The methods from 1 to 6 are the same as those described under the methods of PART-II. Layout of the experimental field and trial of the irradiated lines was conducted under randomized complete block design with 4 replications. Each replication having 4 blocks and each block having 8 plots. Each plot contains 3 rows and per row there are 5 hills. In each hill, one plant was maintained for data. Gap between block and that between plots were 50 cm. The same between rows and that between plants were 70 cm and 25 cm, respectively. Data of mutation generation 2 (M2) in year 2008-2009 and mutation generation 3 (M3) in year 2009-2010 were used for analysis in this part.

7. Techniques of the Analyses of Data

The collected data were analysed following the biometrical techniques of analysis as developed by Mather (1949) based on the mathematical model of Fisher *et al.* (1932). The techniques used are described under the following sub-heads:

a) Mean: Data on the individual plant basis were added together then divided by the total number of observations and the mean was obtained as follows:

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

Where,

X= The individual reading was recorded on each of the plants.

n= Number of observations

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

Σ= Summation.

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

$$S = \sqrt{S^2}$$

Where,

S = Standard deviation

S^2 = Variance.

c) Standard error of mean: If instead of taking one sample, several samples are considered it will be found that the standard deviations of different samples also differ. This difference is measured by the standard error, which was calculated as follows:

$$S_{\bar{x}} = \frac{S}{\sqrt{n}}$$

Where,

$S_{\bar{x}}$ = Standard error of mean

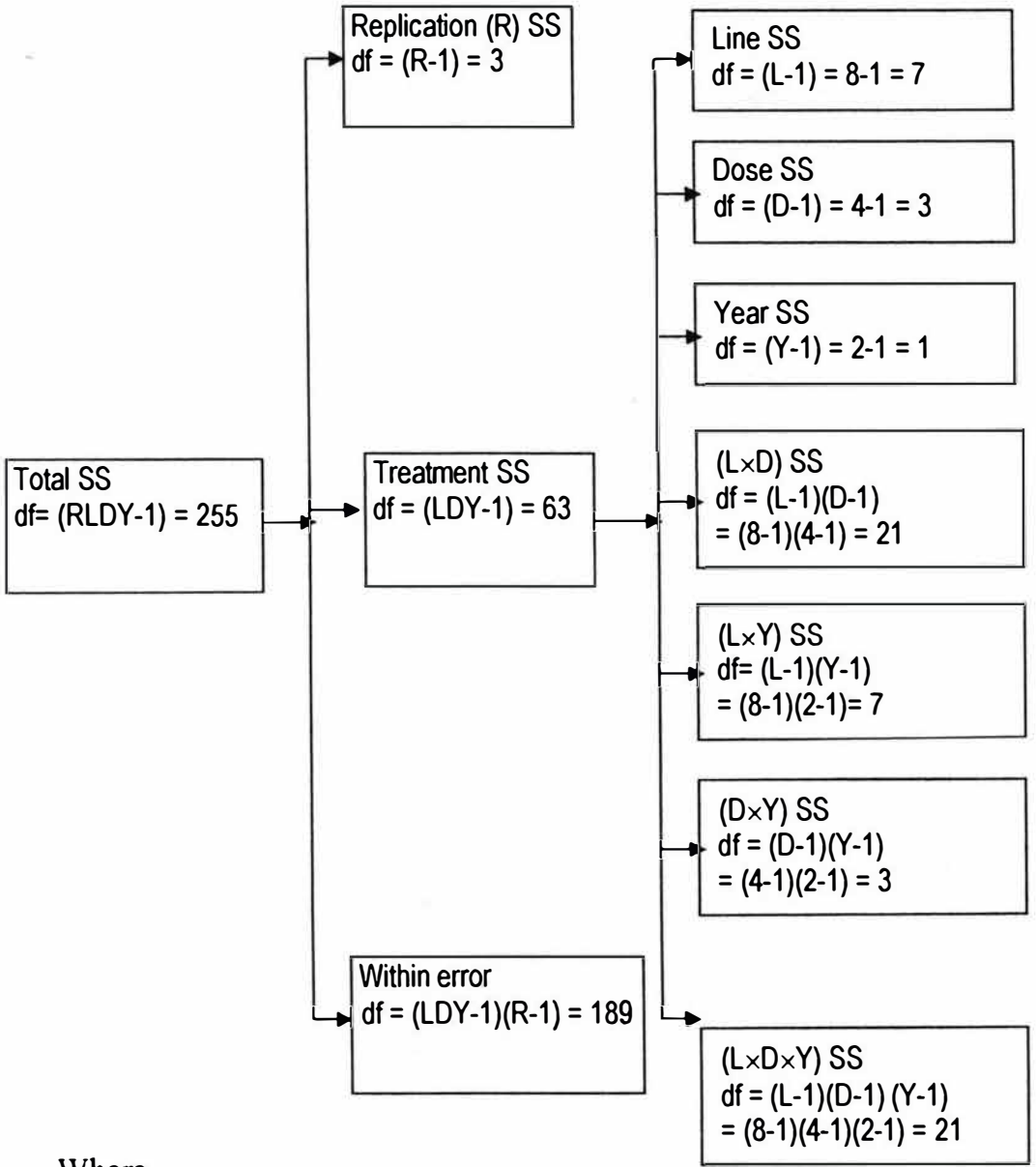
S= Standard deviation

n= Total number of individuals.

d) Analysis of variance: Variance analysis is a measure of dispersion of a population. So, for testing the significant differences among the population, the

analysis of variance is necessary. Variance analysis for each of the characters was carried out separately on mean value of 15 plants.

The variance due to different sources such as line (L), dose (D), year (Y), replication (R), their interactions L × D, L × Y, D × Y, L × D × Y and error of population were calculated as per the following skeleton of analysis:



Where,

$$\text{Total SS} = \sum(\text{RLDY})^2 - \text{CF}$$

$$\text{Replication SS} = \frac{\sum R^2_r}{r} - CF$$

$$\text{Treatment SS} = \frac{\sum_{ijk}(L_i D_j Y_k)^2}{R} - CF$$

Error SS = Total SS – Replication SS – Treatment SS

$$\text{Line SS} = \frac{\sum L_i^2}{RDY} - CF$$

$$\text{Dose SS} = \frac{\sum_{s} Dj^2}{RLY} - CF$$

$$\text{Year SS} = \frac{\sum_{k} Y_k^2}{RLD} - CF$$

$$(L \times D)\ SS = \frac{\sum_{ij}(LiDj)^2}{RY} - CF - L\,SS - D\,SS$$

$$(L \times Y)\ SS = \frac{\sum_{ik}(L_i Y_K)^2}{RD} - CF - L\,SS - Y\,SS$$

$$(D \times Y)\ SS = \frac{\sum_{jk}(D_j Y_K)^2}{RL} - CF - D\,SS - Y\,SS$$

$$(L \times D \times Y)\ SS = \frac{\sum_{ijk}(L_i D_j Y_K)^2}{R} - CF - LSS - DSS - YSS - (L \times D)SS - (L \times Y)SS - (D \times Y)SS$$

R_r= The value of the r^{th} replication

L_i = The value of i^{th} line

D_j = The total of j^{th} dose

Y_k= The value of k^{th} year

L_iD_j= The value of i^{th} line in j^{th} dose

L_iY_k= The value of i^{th} line in k^{th} year

D_jY_k= The value of j^{th} line in k^{th} year

$L_iD_jY_k$= The value of i^{th} line of j^{th} dose of k^{th} year

CF= Correction factor = $(GT)^2/N$

GT= Grand total

N= Total number of observation = (RLDY)

The analysis of variance of a mixed model was used, where line (L) and Dose (D) were fixed and year (Y) effect was random. The expectation of mean square (E. M. S) was derived as follows:

Analysis of variance (ANOVA):

Item	df	MS	EMS
Replication (R)	(R-1)=3	MS_1	$\sigma^2 + LDY\ \sigma^2_R$
Line (L)	(L-1)=7	MS_2	$\sigma^2+R\sigma^2_{LDY}+RD\sigma^2_{LY}+RDY\sigma^2_L$
Dose (D)	(D-1)=3	MS_3	$\sigma^2+R\sigma^2_{LDY}+RL\sigma^2_{DY}+RLY\sigma^2_D$
Year (Y)	(Y-I)=1	MS_4	$\sigma^2+RLD\sigma^2_Y$
L × D	(L-1) (D-I)=21	MS_5	$\sigma^2+R\sigma^2_{LDY}+RY\sigma^2_{LD}$
L × Y	(L-1) (Y-1)=7	MS_6	$\sigma^2+R\sigma^2_{LDY}+RD\ \sigma^2_{LY}$
D × Y	(D-1) (Y-I)=3	MS_7	$\sigma^2+R\sigma^2_{LDY}+RL\ \sigma^2_{DY}$
L × D × Y	(L-1)(D-1)(Y-1)=21	MS_8	$\sigma^2+R\sigma^2_{LDY}$
Error	(LDY-1) (R-1)=189	MS_9	σ^2

Where,

R, L, D and Y designate the number of replications, lines, doses and years, respectively.

MS_1 = Represents mean square of replication

MS_2 = Represents mean square of line

MS_3 = Represents mean square of dose

MS_4 = Represents mean square of year

MS_5 = Represents mean square of L × D

MS_6 = Represents mean square of L × Y

MS_7 = Represents mean square of D × Y

MS_8 = Represents mean square of L × D× Y

MS_9 = Represents mean square of error

and

LDY σ^2_R = Variance due to replication

RDY σ^2_L = Variance due to line

RLY σ^2_D = Variance due to dose

RLD σ^2_Y = Variance due to year

RY σ^2_{LD} = Variance due to L × D

RD σ^2_{LY} = Variance due to L × Y

RL σ^2_{DY} = Variance due to D × Y

R σ^2_{LDY} = Variance due to L × D × Y

e) Components of variation: The components of variation were phenotypic (σ^2_P), genotypic (σ^2_g), dose (σ^2_D), year (σ^2_Y), LD interaction (σ^2_{LD}), LY interaction (σ^2_{LY}), DY interaction (σ^2_{DY}) and error variance σ^2. These were measured as follows:

Step-I:

$\sigma^2_g = (MS_2 - MS_6)/_{RDY}$

$\sigma^2_D = (MS_3 - MS_7)/_{RLY}$

$\sigma^2_Y = (MS_4 - MS_9)/_{RLD}$

$\sigma^2_{LD} = (MS_5 - MS_8)/_{RY}$

$\sigma^2_{LY} = (MS_6 - MS_8)/_{RD}$

$\sigma^2_{DY} = (MS_7 - MS_8)/_{RL}$

$\sigma^2_{LDY} = (MS_8 - MS_9)/_{R}$

$\sigma^2 = MS_9$

Step – II:

a. Phenotypic variance (σ^2_P) = $\sigma^2_g + \sigma^2_{LY} + \sigma^2_{LDY} + \sigma^2$

b. Line variance = σ^2_g

c. Dose variance = σ^2_D

d. Year variance = σ^2_Y

e. Line × Dose variance = σ^2_{LD}

f. Line × Year variance = σ^2_{LY}

g. Dose × Year variance = σ^2_{DY}

h. Line × Dose × Year variance = σ^2_{LDY}

i. Error variance = σ^2

f) Coefficients of variability: Deviation is also expressed by the coefficient of variation. Coefficient of variability at different levels was calculated following Johnson *et al.* (1955).

a. Phenotypic coefficient of variability,

$$PCV = \frac{\sigma^2_p}{\bar{X}} \times 100$$

b. Genotypic coefficient of variability,

$$GCV = \frac{\sigma^2_g}{\bar{X}} \times 100$$

c. Dose coefficient of variability,

$$DCV = \frac{\sigma^2_D}{\bar{X}} \times 100$$

d. Year coefficient of variability,

$$YCV = \frac{\sigma^2_Y}{\bar{X}} \times 100$$

e. Genotype × dose coefficient of variability,

$$G\times DCV = \frac{\sigma^2_{GD}}{\bar{X}} \times 100$$

f. Genotype × year coefficient of variability,

$$G\times Y\ CV = \frac{\sigma^2_{GY}}{\bar{X}} \times 100$$

g. Dose × year coefficient of variability,

$$D\times YCV = \frac{\sigma^2_{DY}}{\bar{X}} \times 100$$

h. Genotype × dose × year coefficient of variability,

$$G\times D\times YCV = \frac{\sigma^2_{GDY}}{\bar{X}} \times 100$$

i. Error coefficient of variability,

$$ECV = \frac{\sigma^2}{\bar{X}} \times 100$$

g) Heritability (h^2_b): Heritability (in borad sense) estimates was computed by dividing the genotypic variance with phenotypic variance and then multiplying by 100 as suggested by Warner (1952).

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_P = Phenotypic variance

h) Genetic advance (GA): Genetic advance was calculated by the following formula as suggested by Lush (1949):

$$GA = K\sigma_p (\sigma^2_g/\sigma^2_p)$$

Where,

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

σ_P = Square root of the phenotypic variance

σ^2_P = Phenotypic variance

σ^2_g = Genotypic variance

i) Genetic advance as percentage of mean (GA%): It was calculated by the following formula:

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

Where,

$\bar{X}$ = Grand mean for a particular character.

j) Analysis of covariance: For the purpose of correlation coefficients and path-coefficient, the analysis of both variance and covariance are required (Miller *et al.* 1958). Therefore, covariances were calculated between all possible pairs of characters.

Mean value per replication per line (genotype) of five years were arranged in combined table and analysis of covariance were done as per following formula:

$$\text{Cov.} = \frac{\sum_{i=1}^{n} X_i Y_i - \left(\sum_{i=1}^{n} X_i\right)\left(\sum_{i=1}^{n} Y_i\right)/n}{n-1}$$

Where,

Cov. = Covariance

$\sum_{i=1}^{n} X_i Y_i$ = Sum of X and Y

$\sum_{i=1}^{n} X_i$ = Grand total of X

$\sum_{i=1}^{n} Y_i$ = Grand total Y

n = Number of observations

n-1 = Degrees of freedom

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

Σ = Summation

The expectation of mean cross product (MCP) was derived as follows:

Analysis of covariance

Item	df	MS	EMS
Replication (R)	3	MCP_1	$\sigma^2_{12}+LDY\sigma^2R_{12}$
Line (L)	7	MCP_2	$\sigma^2_{12} + R\sigma^2_{LDY12} + RD\sigma^2_{LY12} + RDY\sigma^2_{L12}$
Dose (D)	3	MCP_3	$\sigma^2_{12} + R\sigma^2_{LDY12} + RL\sigma^2_{DY12} + RLY\sigma^2_{D12}$
Year (Y)	1	MCP_4	$\sigma^2_{12} + RLD\sigma^2_{Y12}$
L × D	21	MCP_5	$\sigma^2_{12} + R\sigma^2_{LDY12} + RY\sigma^2_{LD12}$
L × Y	7	MCP_6	$\sigma^2_{12} + R\sigma^2_{LDY12} + RD\sigma^2_{LY12}$
D× Y	3	MCP_7	$\sigma^2_{12} + R\sigma^2_{LDY12} + RL\sigma^2_{DY12}$
L × D× Y	21	MCP_8	$\sigma^2_{12} + R\sigma^2_{LDY12}$
Error	189	MCP_9	σ^2_{12}

Where,

MCP_1 = Represent mean cross product of replication

MCP_2 = Represent mean cross product of line

MCP_3 = Represent mean cross product of dose

MCP_4 = Represent mean cross product of year

MCP_5 = Represent mean cross product of L × D

MCP_6 = Represent mean cross product of L × Y

MCP_7 = Represent mean cross product of D × Y

MCP_8 = Represent mean cross product of L × D × Y

MCP_9 = Represent mean cross product of error

and

LDY σ^2_{R12} = Covariance due to replication

RDY σ^2_{L12} = Covariance due to line

RLY σ^2_{D12} = Covariance due to dose

RLD σ^2_{Y12} = Covariance due to year

RYσ^2_{LD12} = Covariance due to L × D

RD σ^2_{LY12} = Covariance due to L × Y

RL σ^2_{DY12} = Covariance due to D × Y

R σ^2_{LDY12} = Covariance due to L × D × Y

σ^2_{12} = Covariance due to error

The phenotypic (σ^2_{P12}), genotypic (σ^2_{g12}), dose (σ^2_{D12}), Year (σ^2_{Y12}), interactions (σ^2_{LD12}, σ^2_{LY12}, σ^2_{DY12}, and σ^2_{LDY12}), and error covariances (σ^2_{12}) were determined as follows:

Step – I:

$\sigma^2_{g12} = (MCP_2 - MCP_6)/RDY$

$\sigma^2_{D12} = (MCP_3 - MCP_7)/RLY$

$\sigma^2_{Y12} = (MCP_4 - MCP_9)/RLD$

$\sigma^2_{LD12} = (MCP_5 - MCP_8)/RY$

$\sigma^2_{LY12} = (MCP_6 - MCP_8)/RD$

$\sigma^2_{DY12} = (MCP_7 - MCP_8)/RL$

$\sigma^2_{LDY12} = (MCP_8 - MCP_9)/R$

$\sigma^2_{12} = MS_9$

Step – II:

a. Phenotypic covariance (σ^2_{p12}) = $\sigma^2_{g12} + \sigma^2_{LY12} + \sigma^2_{LDY12} + \sigma^2_{12}$

b. Genotypic covariance = (σ^2_{g12})

c. Dose variance = σ^2_D

d. Year variance = σ^2_Y

e. Line × Dose variance = σ^2_{LD}

f. Line × Year variance = σ^2_{LY}

g. Dose × Year variance = σ^2_{DY}

h. Line × Dose × Year variance = σ^2_{LDY}

i. Error variance = σ^2

k) Correlation coefficient: The correlation coefficient at phenotypic (r_p) and genotypic (r_g) levels were calculated as follows:

$$r_p = (\sigma^2_{p12}) / (\sigma^2_{P11} \times \sigma^2_{P22})^{1/2}$$

$$r_g = (\sigma^2_{g12}) / (\sigma^2_{g11} \times \sigma^2_{g22})^{1/2}$$

Where,

σ^2_{P12} and σ^2_{g12} represent phenotypic and genotypic covariance of character 1 and 2.

σ^2_{P11} and σ^2_{g11} represent phenotypic and genotypic variance of character 1.

σ^2_{p22} and σ^2_{g22} indicate variance at phenotypic and genotypic levels of character 2.

l) Path-coefficient: The path-coefficient analysis was carried out using the formula of Wright (1921 and 1923) as illustrated by Dewey and Lu (1959). The path-coefficient analysis was done at both phenotypic and genotypic levels by solving the simultaneous equations using matrix method. The form of equation is as follows:

$$r_{xy} = p_{xy} + r_{x2} P_{2y} ++ r_{x3} p_{xy} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots r_{xn} P_{ny}$$

Where,

r_{xy} = correlation between one component character and yield.

P_{xy} = Path-coefficient between the same character and yield.

r_{x2}, r_{x3},.... r_{xn} = Represent correlation coefficient between that character and each of the other yield components in turn.

The above equation was written in a matrix form as:

$$\underset{A}{\begin{bmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ r_{iy} \end{bmatrix}} = \underset{B}{\begin{bmatrix} r_{11} & r_{12} & r_{13} & r_{1J} \\ r_{21} & r_{22} & r_{23} & r_{2J} \\ r_{31} & r_{32} & r_{33} & r_{3J} \\ r_{i1} & ri_2 & ri_3 & r_{iJ} \end{bmatrix}} \times \underset{C}{\begin{bmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \\ Pi_y \end{bmatrix}}$$

$$A = B \times C; \text{ Then } C = B^{-1} A$$

Where,

P_{iy} = direct effect of the character i on the dependent trait y (yield).

The indirect effect of a particular character through other characters was obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

Indirect effect = $r_{ij} \times P_{iy}$

Where,

i = 1, ...n,

j = 1, ...n,

$P_{iy} = P_{1y}$ .....P_{ny}

Where,

r_{ij} = correlation coefficient between two independent characters.

m) Selection index: The coefficients, b_1, b_2 .....b_n used in the discriminant function technique were obtained from the genotypic and phenotypic variances and covariances arranged in the matrix form as follows:

$$\underset{X}{\begin{bmatrix} X_{11} & X_{12} & X_{13} & X_{1J} \\ X_{21} & X_{22} & X_{23} & X_{2J} \\ X_{31} & X_{32} & X_{33} & X_{3J} \\ X_{i1} & X_{i2} & X_{i3} & X_{iJ} \end{bmatrix}} \underset{b}{\begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_n \end{bmatrix}} = \underset{G}{\begin{bmatrix} G_{11} & G_{12} & G_{13} & G_{1J} \\ G_{21} & G_{22} & G_{23} & G_{2J} \\ G_{31} & G_{32} & G_{33} & G_{3J} \\ G_{i1} & G_{i2} & G_{i3} & G_{iJ} \end{bmatrix}} \underset{a}{\begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_n \end{bmatrix}}$$

The solution of this matrix gave the estimates of 'b' values in the following manner (Singh and Chaudhary, 1999).

$$b = X^{-1} Ga$$

Where,

'b' is the column vector, 'X^{-1}, is the inverse of phenotypic variance and covariance matrix, 'G' is the genotypic variance and covariance matrix and 'a' is the column vector for economic weights. Assuming that all the characters are of economically equal importance, i.e., $a_1 = a_2 = a_3 = 1$. The values obtained for b_1, b_2.....b_n were used in discriminant function selection technique. The phenotypic and genotypic variances and covariances as obtained were used for constructing the discriminant function using different character combinations according to the method as developed by Fisher (1936) and Smith (1936). Yield/plant was also included as one of the independent characters as suggested by Robinson *et al.* (1951). The expected genetic advance from straight selection {GA(S)} and from discriminant function {GA(D)} was calculated as follows:

$$GA\ (S) = (Z/P) \times (g_{yy})/(t_{yy})^{1/2} \text{ and}$$

$$GA\ (D) = (Z/P) \times (b_{1g1y} + b_{2g2y})^{1/2}$$

Where,

Z/P = the selection differential in standard units, for the present study it was 2.06 at 5% level of selection (Lush, 1949).

g_{yy} and t_{yy} = the genotyic and phenotypic variances of character.

$b_1, b_2, \ldots . b_n$ = the relative weights for character

$g_{1y}, g_{2y} \ldots .$ = the genotypic covariances of independent character with y.

The expected gain from the discriminant function over straight selection was calculated for all the functions as shown below:

$$\text{Expected gain (\%)} = [\{GA\ (D)/GA(S)\}-1] \times 100.$$

RESULTS

Results obtained for the eleven agronomical characters are quantitative in nature, which are days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD), number of pods per plant (NPPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and seed weight per plant (SWPP). The estimate of variance, component of variation, coefficient of variability, heritability, genetic advance, genetic advance expressed as percentage of mean, characters association, path coefficient and selection index are described separately.

A. ANALYSIS OF VARIANCE

The results of analysis of variance for all the eleven quantitative characters were done separately and are shown in table (19A-19K). For significant test the main item and their interaction effects, a mixed model was followed.

In the analysis, the replication item (R) was highly significant for NPBMF, NSBMF, PHMF, PWFD, NPPP, PdWPP, NSPP and SWPP, while for 1000-SW, it was significant at 5% level only and for DMF and RWFD it was non-significant.

The line item (L) was significant for all the characters when tested against the within error. This item was also significant (at 5% and 1% level) when it was tested against pooled error, except DMF which showed non-significant value.

The dose item (D) was highly significant for PdWPP, NSPP and SWPP and just significant (at 5% level) for 1000-SW, and non-significant only for DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD and NPPP when tested against within error and pooled error. Highly significant influence of year (Y) item was also observed for all the characters except 1000-SW where it was non-significant.

The L × D interaction was highly significant for PHMF and 1000-SW, where it was significant for DMF and RWFD when tested against both within error and pooled error. The interaction item was non-significant for NPBMF, NSBMF, PWPP, NPPP, PdWPP, NSPP and SWPP. The interaction L × Y was non-significant for all the characters except RWFD where it was significant at 5% level and 1000-SW where it was significant both at 5% and 1% level when tested against within error and pooled error.

Another interaction item D × Y was non-significant for all the characters except RWFD where it was significant at 5% level when tested both against within error and pooled error. The second order interaction L × D ×Y was non-significant for all the characters except DMF where it was highly significant when tested both against within and pooled error.

B. COMPONENTS OF VARIATION

The estimates of phenotypic (σ^2_p), genotypic (σ^2_g), dose (σ^2_D), year (σ^2_Y), interactions (σ^2_{LD}, σ^2_{LY}, σ^2_{DY}, and σ^2_{LDY}) and error (σ^2_w) components of variation were calculated separately for all the eleven quantitative characters. The results were presented in the table 20.

Phenotypic variation (σ^2_p): For all the characters, phenotypic variation (σ^2_p) was greater than those of σ^2_g, σ^2_D, σ^2_Y, σ^2_{LY}, σ^2_{LD}, σ^2_{DY}, σ^2_{LDY} and σ^2_w components of variation as expected, except σ^2_w for PWFD. The phenotype is the joint product of σ^2_g, σ^2_{LY}, σ^2_{LDY} and σ^2_w. Table 20 showed that the greater portion of the total phenotypic variation was appeared mostly due to error variation for all the characters. The maximum phenotypic variation was observed for NSPP with a value of 778.6894 and the lowest phenotypic variation was 0.2855 shown by NPBMF.

Genotypic variation (σ^2_g): The highest genotypic variation (σ^2_g) was found for 1000-SW with a value of 288.6634, while the lowest genotypic variation was recorded for NPBMF with a value of 0.0868.

Dose variation (σ^2_D): The variation due to dose (σ^2_D) was high with a value of 45.8948 for NSPP, while the lowest value was exhibited by PWFD with a value of -7.4114.

Year variation (σ^2_Y): The year component of variation (σ^2_Y) was high (194.6458) for PWFD. On the other hand, the lowest value of σ^2_Y was recorded as 0.0137 for NPBMF.

Line × year interaction variation (σ^2_{LY}): Regarding variation of the interaction between line and year, the highest value was found for 1000-SW with a value of 36.6838, while the lowest values was observed for NSPP with a value of -7.7862.

Line × dose interaction variation (σ^2_{LD}): The highest and the lowest values of this interaction variation were noted for 1000-SW and NPBMF with the values of 68.2366 and 0.0162, respectively.

Dose × year interaction variation (σ^2_{DY}): The highest value of dose and year interaction (σ^2_{DY}) variation was found for PWFD with a value of 13.6409 and the lowest value was recorded for NSPP with a value of -14.5011.

Line × dose × year interaction variation (σ^2_{LDY}): The second order interaction component of variation (σ^2_{LDY}) showed the maximum value of 18.9401 for DMF and the lowest was noted for PWFD with a value of -113.0526.

Error variation (σ^2_w): The highest error variation (σ^2_w) was recorded for PWFD with a value of 778.2597 and the lowest was noted for NPBMF with a value of 0.2235.

C. COEFFICIENT OF VARIABILITY

The estimates of phenotypic (PCV), genotypic (GCV), dose (DCV), year (YCV), interaction (L × DCV, L × YCV, D ×YCV and L ×D ×YCV) and within error coefficient of variability (ECV) for eleven quantitative characters of chickpea were computed. The results are presented in table 21.

Phenotypic coefficient of variability (PCV): In general, the phenotypic coefficient of variability (PCV), was greater than those of genotypic, dose, year, interactions and error coefficient of variability for all the characters except ECV for PWFD. PCV is the joint product of GCV, L ×YCV, L × DCV, D × YCV, L × D × YCV and ECV. Estimate of the phenotypic coefficient of variability was the highest for NSPP with a value of 1156.7980 and the lowest phenotypic coefficient of variability was estimated for NPBMF with a value of 9.5115.

Genotypic coefficient of variability (GCV): In GCV, NSPP showed the highest value (264.0330), while the lowest value was found for DMF with the value of 1.9649.

Dose coefficient of variability (DCV): The highest dose coefficient of variability (DCV) was exhibited by NSPP with a value of 68.1799 and the lowest was indicated by PWFD with a value of -9.7375.

Year coefficient of variability (YCV): This coefficient of variability was high for PWFD with a value of 255.7373, while the lowest was recorded for 1000-SW with a value of 0.3595.

L × Y interaction coefficient of variability (L × YCV): The maximum L × Y CV was exhibited by 1000-SW with a value of 23.6576 and the character, NSPP showed the lowest value of -11.5669.

L × D interaction coefficient of variability (L × DCV): The highest and the lowest values of this interaction coefficient of variability were noted for PWFD and DMF with the values of 69.2054 and -2.2648, respectively.

D × Y interaction coefficient of variability (D × YCV): The highest and the lowest values for this coefficient of variability were recorded as 17.9222 and -21.5424 for the characters PWFD and NSPP, respectively.

L × D × Y interaction coefficient of variability (L × D × YCV): The second order interaction coefficient of variability showed the highest value of 19.3658 for DMF and the character PWFD exhibited the lowest value of -148.5352.

Error coefficient of variability (ECV): The character, PWFD showed the highest value of 1022.5241 in case of error coefficient of variability followed by NSPP (934.8856) and NPPP (867.7029). The lowest value of 7.4439 was observed for NPBMF.

D. HERITABILITY (h^2_b)

Broad sense heritability (h^2_b) for eleven quantitative characters of chickpea was estimated and the results are shown in table 22. In the present investigation the highest heritability was estimated for 1000-SW with a value of 52.4637 followed by 30.3915 and 27.0965 for NPBMF and RWFD. The lowest h^2_b was recorded for DMF with a value of 2.2545.

E. GENETIC ADVANCE (GA)

Genetic advance for all the eleven characters are shown in table 22. The character, 1000-SW showed maximum genetic advance with a value of 25.3508. Next to this character, GA value of 13.1205 and 11.9868 were shown by NSPP and NPPP, respectively. The lowest GA was 0.3228 observed for NSBMF.

F. GENETIC ADVANCE AS PERCENTAGE OF MEAN (GA%)

The genetic advance as percentage of mean was shown in table 22.The highest value of genetic advance as percentage of mean was 19.4914 for NSPP followed by 19.4639 and 16.5458 for NPPP and RWFD, respectively. The lowest value was 0.4384 exhibited by DMF.

G. CORRELATION CO-EFFICIENT

The estimation of correlation co-efficient between pairs of characters were analyzed both at phenotypic and genotypic levels. In the present experiment, there

were eleven quantitative characters, so altogether 55 pairs of combination and hence 55 were obtained in each case of phenotypic and genotypic levels. The results are presented in table 23A-23B at phenotypic and genotypic levels.

Correlation Co-efficient at Phenotypic Levels

At phenotypic level the result (table 23A) indicated that SWPP showed positive highly significant correlation with NPPP, PdWPP and NSPP while it showed positive correlation with NPBMF and 1000-SW. Where as negative significant correlation was observed for PWFD. DMF, NSBMF, PHMF and RWFD showed negatively non-significant correlation with yield.

In case of yield associated characters like DMF showed positive and non-significant correlation with NSBMF, PHMF, PWFD, RWFD and NSPP, while it showed negative and non-significant correlation with NPBMF, NPPP, PdWPP and 1000-SW.

The characters NPBMF showed positive and non-significant correlation with the characters NSBMF, PHMF, PWFD, NPPP, PdWPP and NSPP. It showed negative and non-significant correlation with RWFD and 1000-SW. In case of NSBMF it showed positive and non-significant correlation with PHMF, PWFD and NPPP and negative and non-significant correlation with RWFD, PdWPP, NSPP and 1000-SW.

The character PHMF showed positive and non-significant correlation with PWFD, while it exhibited negative and non-significant correlation with RWFD, NPPP, PdWPP, NSPP and 1000-SW. It was observed from the result in table 23A that PWFD showed positive and non-significant correlation with RWFD and rest of the characters showed negative correlation.

RWFD showed positive and non-significant correlation with the characters 1000-SW and negative and non-significant correlation with NPPP, PdWPP and NSPP. The characters NPPP showed positive highly significant correlation with PdWPP and NSPP and this character showed negative and non-significant correlation with 1000-

SW. In case of PdWPP which showed positive highly significant correlation with NSPP, while 1000-SW showed positive correlation with PdWPP. The character NSPP showed negative non-significant correlation with the character 1000-SW.

Correlation Co-efficient at Genotypic Levels

It was observed from the table 23B that in most of the cases the genotypic correlation coefficients were higher than the phenotypic correlation coefficients. From the result it was observed that seed weight per plant (SWPP) showed positive significant correlation with NSBMF and positive highly significant correlation with NPBMF, NPPP, PdWPP and NSPP. On the other hand SWPP showed negative and significant correlation with PHMF. The characters DMF, PWFD, RWFD, and 1000-SW showed negative correlation.

The yield contributing character like DMF showed positive highly significant correlation with PWFD. The characters NPBMF, NSBMF, PHMF, NPPP and NSPP showed positive correlation with DMF. While DMF showed negatively significant correlation with RWFD and PdWPP and 1000-SW showed negative correlation.

In case of NPBMF it showed positive highly significant correlation with NSBMF, NPPP, PdWPP and NSPP, while it showed positive correlation with PHMF and RWFD. It showed negative and significant correlation with 1000-SW and negative correlation was observed for RWFD.

NSBMF showed positive significant correlation with NPPP and PdWPP and positive highly significant correlation with NSPP. While it showed positive non-significant correlation with PHMF and PWFD. Again NSBMF showed negative significant correlation with RWFD and 1000-SW.

PHMF exhibited positive correlation with PWFD, NPPP, PdWPP and NSPP while it showed negative correlation with RWFD and 1000-SW. The characters PWFD showed positive correlation with NPPP, PdWPP and NSPP and it showed negative correlation with RWFD and 1000-SW.

From the table 23B it was observed that RWFD showed positive highly significant correlation with 1000-SW. It showed negative significant correlation with NPPP and NSPP. While it showed negative correlation with PdWPP.

The character NPPP showed positive highly significant correlation with PdWPP and NSPP while it showed negative highly significant correlation with 1000-SW. PdWPP showed positive highly significant correlation with NSPP. The character PdWPP showed negative correlation with 1000-SW. NSPP showed negative highly significant correlation with 1000-SW.

H. PATH-COEFFICIENTS

The path-coefficient, measuring the direct as well as indirect (via other variables) effects of one variable on the end product (yield), was worked out for eleven quantitative characters of chickpea. Direct and indirect effects of component characters of seed weight per plant (SWPP) were estimated separately for each character both at phenotypic and genotypic levels. The results of the analyses are presented in table 24A and table 24B.

Path-coefficient at Phenotypic Levels

The result of path coefficient analysis at phenotypic level was presented in table 24A. This table exhibited that the highest positive direct effect (0.8483) was expressed by NSPP on SWPP and it was followed by 1000-SW, NSBMF, DMF, RWFD, PHMF, PdWPP, NPBMF and NPPP. PWFD showed negative direct effect.

The third highest direct effect of DMF on SWPP was 0.1573. DMF had low positive indirect effects on SWPP through NSBMF, PHMF, RWFD and NSPP. The indirect effects through NPBMF, PWFD, NPPP, PdWPP and 1000-SW were negative and negligible. The total effect was 0.2240.

NPBMF had low positive direct effect (0.0872) on SWPP. It had low positive indirect effects on SWPP through NSBMF, PHMF, NPPP, PdWPP and NSPP. DMF,

PWFD, RWFD and 1000-SW showed negligible negative indirect effects on SWPP. The total effect was 0.1426.

NSBMF had the second highest positive direct contributor (0.2864) to SWPP. NSBMF had positive and low indirect effects on SWPP via DMF, NPBMF, PHMF and NPPP. It also showed low negative indirect effects through PWFD, RWFD, PdWPP, NSPP and 1000-SW. Its total effect was 0.4608.

PFMF showed positive direct effect (0.1109) on seed weight per plant (SWPP). This character showed negligible positive indirect effects on SWPP for DMF, NPBMF and NSBMF. It also showed negative indirect effect on SWPP for PWFD, RWFD, NPPP, PdWPP, NSPP and 1000-SW. The total effect was 0.1112.

PWFD showed negative direct effect (-0.8886) on SWPP. It had positive indirect effects via DMF, NPBMF, NSBMF, PHMF and RWFD. The indirect effects through NPPP, PdWPP, NSPP and 1000-SW were negative on SWPP. The total effect was -1.7054

RWFD had low positive direct effect (0.1506) on seed weight per plant (SWPP). It had low positive indirect effects on SWPP via DMF and 1000-SW. It also showed negligible negative effects for rest of the characters. The total effect was 0.1267.

NPPP had low positive direct effects (0.0691) on SWPP. NPPP showed high positive indirect effects on SWPP through NSPP, while it showed very low positive and negative indirect effects on SWPP for other examined characters. Its total effect was 0.1880.

PdWPP had positive direct effect (0.1020) on seed weight per plant. PdWPP had high positive indirect effects on SWPP via NSPP. It showed low positive indirect effects for NPBMF, PWFD, NPPP, NSPP and 1000-SW.. The indirect effects through DMF, NSBMF, PHMF and RWFD were negative and negligible. The total effect was 0.2929.

NSPP showed the greatest direct effect on SWPP which was 0.8483. Also it showed positive indirect effects on SWPP via DMF, NPBMF, PWFD, NPPP and PdWPP. It showed negative indirect effects on SWPP via NSBMF, PHMF, RWFD and 1000-SW. The total effect was 2.2024.

1000-SW had the second highest positive direct contribution (0.2857) with SWPP. In this case, PWFD, RWFD and PdWPP showed negligible positive indirect effects and the characters DMF, NPBMF, NSBMF, PHMF, NPPP and NSPP showed very low negative indirect effects on SWPP. The total effect was 0.0651.

The residual effect was 0.7793.

Path-coefficient at Genotypic Level

The result of path coefficient analysis at genotypic level was presented in table 24B. It was observed from the table that NSPP had the highest positive direct effect (1.0166) on SWPP followed by PdWPP, 1000-SW, RWFD, NSBMF, NPBMF and DMF. The characters PWFD, PHMF and NPPP showed negative direct effect on SWPP.

DMF had a negligible positive direct effect (0.000405) on SWPP. Here its indirect effects on SWPP were positive through NPBMF, NSBMF and NSPP. It showed negative indirect effects on SWPP through PHMF, PWFD, RWFD, NPPP, PdWPP and 1000-SW. The total effect was 0.00065.

The character NPBMF showed negligible positive direct effect (0.0042) on yield. The indirect effects on SWPP were positive through DMF, NSBMF, PdWPP and NSPP, while in case of PHMF, PWFD, RWFD, NPPP and 1000-SW it showed negative indirect effects. The total effect was 0.0165

NSBMF showed low positive direct effect (0.0454) on SWPP. DMF, NPBMF, PdWPP and NSPP had positive indirect effect on SWPP, while PHMF, PWFD,

RWFD, NPPP and 1000-SW had negative indirect effect on SWPP. Its total effect was 0.1887

PHMF also had negative direct effects (-0.1352) on SWPP. It showed positive indirect effects on SWPP with DMF, NPBMF, NSBMF, PdWPP and NSPP. It had negative indirect effects through PWFD, RWFD, NPPP and 1000-SW. The total effect was -0.2130

The characters PWFD had negative indirect effects of -0.0487 on SWPP. The indirect influence through PHMF, RWFD, NPPP and 1000-SW were also negative. It had positive indirect effects through DMF, NPBMF, NSBMF, PdWPP and NSPP. The total effect was -0.1227

Next RWFD showed positive direct effect (0.0511) on SWPP. It had positive indirect effect on SWPP via PHMF, PWFD, NPPP and 1000-SW but low and negative indirect effect via DMF, NPBMF, NSBMF, PdWPP and NSPP. The total effect was -0.1548

NPPP had negative direct effects (-0.1625) on SWPP. It had positive and high indirect effects (0.9971) on SWPP via NSPP, while positive negligible indirect effects via DMF, NPBMF, NSBMF and PdWPP. PHMF, PWFD, RWFD and 1000-SW had negative indirect effects on SWPP. Its total effect was -0.5490

The second highest direct effect of PdWPP on SWPP was 0.4007. PdWPP had high positive indirect effect on NSPP, while it showed negligible positive indirect effect on NPBMF and NSBMF. The indirect effects through DMF, PHMF, PWFD, RWFD, NPPP and 1000-SW were negative and negligible. The total effect was 1.4099

NSPP had the greatest direct effect on seed yield which was 1.0166. Also its indirect effects on SWPP were positive through DMF, NPBMF, NSBMF and PdWPP

but negative and low through PHMF, PWFD, RWFD, NPPP and 1000-SW. Its total effect was 3.5340

1000-SW had the third highest positive direct contribution to SWPP. It showed positive indirect effect through PHMF, PWFD, RWFD, NPPP and negative indirect effect via DMF, NPBMF, NSBMF, PdWPP and NSPP. The total effect was -1.0524.

The residual effect at genotypic level was 0.06388

I. SELECTION INDEX

Selection indices for yield were constructed for each set of data and different combinations were studied to identify the characters which might be useful during selection breeding. In constructing the selection indices, all the eleven agronomical characters viz, days to maximum flower (DMF); number of primary branches at maximum flower (NPBMF); number of secondary branches at maximum flower (NSBMF); plant height at maximum flower (PHMF); plant weight after fully dry (PWFD); root weight after fully dry (RWFD); number of pods per plant (NPPP); pod weight per plant (PdWPP); number of seeds per plant (NSPP); 1000-seed weight (1000-SW); and seed weight per plant (SWPP) were included of which SWPP was dependant character. The selection indices and the expected genetic gain in percentage over straight selection for yield and its component in each case are presented in table 25.

In the present investigation, the result revealed that when individual characters were judged separately the character number of primary branches at maximum flower showed highest (1329.525%) positive expected genetic gain followed by seed weight per plant (659.582%) and root weight after fully dry (379.339%). The high expected gains were more frequent through the different sets of data, when more character combinations were studied in the functions. In discriminant function analysis high values for expected gains were obtained when only two characters were included in a

combinations with value of 638.460 % (NPBMF + RWFD) followed by NPBMF + NSBMF (636.932 %) and NPBMF + SWPP (571.392 %).

In the discriminant function analysis when selection index included three characters, the maximum genetic gain was recorded as 463.078 % for NPBMF + NSBMF + SWPP followed by 459.846 % for NPBMF + RWFD + SWPP and 410.979 % for NSBMF + RWFD + SWPP.

In the same way when four characters were included in the discriminant function the highest genetic gain was 383.369 % for NPBMF + NSBMF + RWFD + SWPP next was 362.614 % for DMF + NPBMF + NSBMF + SWPP and 361.166 % for DMF + NPBMF + RWFD + SWPP. Similarly when five characters were included in the discriminant function, SWPP in combination with DMF, NPBMF, NSBMF and RWFD exhibited the highest genetic gain of 308.136 % followed by 241.602 % (NPBMF + NSBMF + PHMF + RWFD + SWPP) and 230.152 % (DMF + NPBMF + NSBMF + PHMF + SWPP).

In case of discriminant functions when six characters were included, SWPP combination with DMF, NPBMF, NSBMF, PHMF and RWFD showed the highest expected genetic gain of 202.295 % followed by 147.036 % (DMF + NPBMF + NSBMF + RWFD + PdWPP + SWPP) and 121.559 % (NPBMF + NSBMF + PHMF + RWFD + PdWPP + SWPP). In case of seven characters combination the characters DMF, NPBMF, NSBMF, PHMF, RWFD, PdWPP and SWPP showed the highest positive expected genetic gain with value of 104.590 %.

Table 19A: Analysis of variance for the character days to maximum flower.

Item	df	SS	MS	VR1	VR2
R	3	273.2641	91.088	1.344^{NS}	1.209^{NS}
L	7	1054.068	150.581	2.222*	1.998^{NS}
D	3	428.5172	142.839	2.107^{NS}	1.896^{NS}
Y	1	592.3474	592.347	8.739**	7.861**
L×D	21	2642.208	125.819	1.856*	1.670*
L×Y	7	623.6041	89.0863	1.314^{NS}	1.182^{NS}
D×Y	3	459.5754	153.192	2.26^{NS}	2.033^{NS}
L×D×Y	21	3014.331	143.54	2.118**	1.905**
ERROR	189	12810.238	67.779		
Pooled error	210	15824.569	75.3551		
Total	255	21898.153			

Table 19B: Analysis of variance for the character number of primary branches at maximum flower.

Item	df	SS	MS	VR1	VR2
R	3	5.323	1.774	7.941**	8.479**
L	7	21.225	3.032	13.57**	14.492**
D	3	0.66	0.22	0.984^{NS}	1.052^{NS}
Y	1	1.978	1.978	8.85**	9.454**
L×D	21	4.425	0.211	0.943^{NS}	1.009^{NS}
L×Y	7	1.788	0.255	1.143^{NS}	1.219^{NS}
D×Y	3	0.232	0.077	0.346^{NS}	0.368^{NS}
L×D×Y	21	1.702	0.081	0.363^{NS}	0.387^{NS}
ERROR	189	42.233	0.223		
Pooled error	210	43.935	0.20921		
Total	255	21898.153			

Table 19C: Analysis of variance for the character number of secondary branches at maximum flower.

Item	df	SS	MS	VR1	VR2
R	3	124.203	41.401	5.488**	5.433**
L	7	113.807	16.258	2.155*	2.133*
D	3	33.17	11.057	1.466^{NS}	1.451^{NS}
Y	1	59.549	59.549	7.894**	7.814**
L×D	21	134.363	6.398	0.848^{NS}	0.840^{NS}
L×Y	7	15.797	2.257	0.299^{NS}	0.296^{NS}
D×Y	3	11.087	3.696	0.49^{NS}	0.485^{NS}
L×D×Y	21	174.655	8.317	1.103^{NS}	1.091^{NS}
ERROR	189	1425.685	7.543		
Pooled error	210	1600.34	7.62067		
Total	255	21898.153			

Table 19D: Analysis of variance for the character plant height at maximum flower.

Item	df	SS	MS	VR1	VR2
R	3	376.317	125.439	8.503**	8.718**
L	7	507.852	72.55	4.918**	5.042**
D	3	16.731	5.577	0.378 NS	0.388 NS
Y	1	112.067	112.066	7.597**	7.789**
L×D	21	795.952	37.903	2.569**	2.634**
L×Y	7	86.988	12.427	0.842 NS	0.864 NS
D×Y	3	6.394	2.131	0.144 NS	0.148 NS
L×D×Y	21	233.43	11.116	0.754 NS	0.773 NS
ERROR	189	2788.142	14.752		
Pooled error	210	3021.572	14.3884		
Total	255	21898.153			

Table 19E: Analysis of variance for the character plant weight after fully dry.

Item	df	SS	MS	VR1	VR2
R	3	25415.811	8471.94	10.886**	11.557**
L	7	12502.108	1786.02	2.295*	2.436*
D	3	864.685	288.228	0.37 NS	0.393 NS
Y	1	25692.92	25692.9	33.013**	35.050**
L×D	21	15696.161	747.436	0.96 NS	1.020 NS
L×Y	7	3225.423	460.775	0.592 NS	0.629 NS
D×Y	3	2287.67	762.557	0.98 NS	1.040 NS
L×D×Y	21	6847.038	326.049	0.419 NS	0.445 NS
ERROR	189	147091.083	778.26		
Pooled error	210	153938.121	733.039		
Total	255	21898.153			

Table 19F: Analysis of variance for the character root weight after fully dry.

Item	df	SS	MS	VR1	VR2
R	3	0.094	0.031	0.118 NS	0.116 NS
L	7	28.53	4.076	15.3**	15.251**
D	3	1.491	0.497	1.865 NS	1.860 NS
Y	1	3.124	3.124	11.729**	11.689**
L×D	21	8.752	0.417	1.564*	1.560*
L×Y	7	4.36	0.623	2.338*	2.331*
D×Y	3	2.327	0.776	2.912*	2.903*
L×D×Y	21	5.777	0.275	1.033 NS	1.029 NS
ERROR	189	50.349	0.266		
Pooled error	210	56.126	0.26727		
Total	255	21898.153			

Table 19G: Analysis of variance for the character number of pods per plant.

Item	df	SS	MS	VR1	VR2
R	3	26717.118	8905.71	16.666**	17.198**
L	7	35128.207	5018.32	9.391**	9.691**
D	3	3860.477	1286.83	2.408^{NS}	2.485^{NS}
Y	1	6494.793	6494.79	12.154**	12.542**
L×D	21	12596.33	599.825	1.123^{NS}	1.158^{NS}
L×Y	7	2237.655	319.665	0.598^{NS}	0.617^{NS}
D×Y	3	1299.173	433.058	0.81^{NS}	0.836^{NS}
L×D×Y	21	7746.683	368.89	0.69^{NS}	0.712^{NS}
ERROR	189	100996.249	534.372		
Pooled error	210	108742.932	517.823		
Total	255	21898.153			

Table 19H: Analysis of variance for the character pod weight per plant.

Item	df	SS	MS	VR1	VR2
R	3	1270.915	423.638	13.983**	14.298**
L	7	1277.463	182.495	6.024**	6.159**
D	3	438.028	146.009	4.819**	4.928**
Y	1	438.845	438.845	14.485**	14.812**
L×D	21	816.873	38.899	1.284^{NS}	1.313^{NS}
L×Y	7	99.154	14.165	0.468^{NS}	0.478^{NS}
D×Y	3	31.856	10.619	0.351^{NS}	0.358^{NS}
L×D×Y	21	495.909	23.615	0.779^{NS}	0.797^{NS}
ERROR	189	5726.078	30.297		
Pooled error	210	6221.987	29.6285		
Total	255	21898.153			

Table 19I: Analysis of variance for the character number of seeds per plant.

Item	df	SS	MS	VR1	VR2
R	3	30772.777	10257.6	16.3**	16.516**
L	7	42769.15	6109.88	9.709**	9.837**
D	3	9060.824	3020.28	4.799**	4.863**
Y	1	8205.26	8205.26	13.038**	13.211**
L×D	21	18691.754	890.084	1.414^{NS}	1.433^{NS}
L×Y	7	2957.25	422.464	0.671^{NS}	0.680^{NS}
D×Y	3	249.026	83.0086	0.132^{NS}	0.134^{NS}
L×D×Y	21	11487.898	547.043	0.869^{NS}	0.881^{NS}
ERROR	189	118939.756	629.311		
Pooled error	210	130427.654	621.084		
Total	255	21898.153			

Table 19J: Analysis of variance for the character 1000-seed weight.

Item	df	SS	MS	VR1	VR2
R	3	2243.919	747.973	2.826*	3.007*
L	7	69506.871	9929.55	37.513**	39.915**
D	3	2699.428	899.809	3.399*	3.617*
Y	1	336.0487	336.049	1.27 NS	1.351 NS
L×D	21	13676.793	651.276	2.461**	2.618**
L×Y	7	4846.269	692.324	2.616**	2.783**
D×Y	3	539.208	179.736	0.679 NS	0.723 NS
L×D×Y	21	2213.053	105.384	0.398 NS	0.424 NS
ERROR	189	50027.767	264.697		
Pooled error	210	52240.82	248.766		
Total	255	21898.153			

Table 19K: Analysis of variance for the character seed weight per plant.

Item	df	SS	MS	VR1	VR2
R	3	824.626	274.875	17.533**	17.811**
L	7	679.14	97.02	6.188**	6.286**
D	3	182.394	60.798	3.878**	3.939**
Y	1	147.342	147.342	9.398**	9.547**
L×D	21	423.273	20.156	1.286 NS	1.306 NS
L×Y	7	77.221	11.032	0.704 NS	0.715 NS
D×Y	3	6.959	2.32	0.148 NS	0.150 NS
L×D×Y	21	277.846	13.231	0.844 NS	0.857 NS
ERROR	189	2963.11	15.678		
Pooled error	210	3240.956	15.433		
Total	255	21898.153			

*, ** indicated significant at 5% and 1% levels respectively.
NS indicated non-significant
VR1 denominator is within error and
VR2 denominator is pooled error

Table 20: Phenotypic (σ^2_p), Genotypic (σ^2_g), Dose (σ^2_D), Year (σ^2_Y), Interactions (σ^2_{LY}, σ^2_{LD}, σ^2_{DY} and σ^2_{LDY}) Error (σ^2_e) components of variation of eleven characters in chickpea.

Characters	σ^2_p	σ^2_g	σ^2_D	σ^2_Y	σ^2_{LY}	σ^2_{LD}	σ^2_{DY}	σ^2_{LDY}	σ^2_e
DMF	85.2376	1.9217	-0.1618	4.0982	-3.4033	-2.2150	0.3016	18.9401	67.7790
NPBMF	0.2855	0.0868	0.0022	0.0137	0.0109	0.0162	-0.0001	-0.0356	0.2235
NSBMF	7.7955	0.4375	0.1150	0.4063	-0.3788	-0.2398	-0.1444	0.1934	7.5433
PHMF	15.8038	1.8789	0.0538	0.7603	0.0819	3.3483	-0.2808	-0.9091	14.7521
PWFD	715.0412	41.4138	-7.4114	194.6458	8.4203	52.6734	13.6409	-113.0526	778.2597
RWFD	0.3982	0.1079	-0.0044	0.0223	0.0217	0.0177	0.0156	0.0022	0.2664
NPPP	636.7575	146.8328	13.3401	46.5658	-3.0765	28.8669	2.0052	-41.3705	534.3717
PdWPP	33.2959	5.2603	2.1155	3.1918	-0.5906	1.9105	-0.4061	-1.6705	30.2967
NSPP	778.6894	177.7317	45.8948	59.1871	-7.7862	42.8801	-14.5011	-20.5670	629.3109
1000-SW	550.2159	288.6634	11.2511	0.5574	36.6838	68.2366	2.3235	-39.8284	264.6972
SWPP	17.6158	2.6871	0.9137	1.0286	-0.1374	0.8656	-0.3410	-0.6118	15.6778

Table 21: Phenotypic (PCV), Genotypic (GCV), Dose (DCV), Year (YCV), Interactions (L × Y CV, L × D CV, D × Y CV and L × D × Y CV) Error (ECV) components of variation of eleven characters in chickpea.

Characters	PCV	GCV	DCV	YCV	L × Y CV	L × D CV	D × Y CV	L × D × Y CV	ECV
DMF	87.1534	1.9649	-0.1654	4.1903	-3.4798	-2.2648	0.3084	19.3658	69.3025
NPBMF	9.5115	2.8907	0.0743	0.4565	0.3631	0.5400	-0.0040	-1.1862	7.4439
NSBMF	48.0760	2.6984	0.7093	2.5057	-2.3359	-1.4791	-0.8906	1.1927	46.5207
PHMF	28.6248	3.4031	0.0975	1.3770	0.1484	6.0647	-0.5085	-1.6466	26.7199
PWFD	939.4639	54.4119	-9.7375	255.7373	11.0631	69.2054	17.9222	-148.5352	1022.5241
RWFD	18.7052	5.0685	-0.2046	1.0488	1.0212	0.8317	0.7348	0.1021	12.5135
NPPP	1033.9551	238.4244	21.6615	75.6127	-4.9956	46.8736	3.2561	-67.1767	867.7029
PdWPP	245.3096	38.7556	15.5859	23.5157	-4.3514	14.0757	-2.9921	-12.3075	223.2128
NSPP	1156.7980	264.0330	68.1799	87.9266	-11.5669	63.7014	-21.5424	-30.5538	934.8856
1000-SW	354.8374	186.1607	7.2559	0.3595	23.6576	44.0061	1.4984	-25.6856	170.7047
SWPP	172.9297	26.3790	8.9698	10.0978	-1.3493	8.4978	-3.3472	-6.0056	153.9056

Table 22: Heritability (h^2_b), Genetic advance (GA) and Genetic advance as percentage of mean (GA%) of different characters in chickpea.

Characters	h^2_b	GA	GA%
DMF	2.2545	0.4288	0.4384
NPBMF	30.3915	0.3345	11.1442
NSBMF	5.6128	0.3228	1.9909
PHMF	11.8887	0.9736	1.7634
PWFD	5.7918	3.1904	4.1918
RWFD	27.0965	0.3522	16.5458
NPPP	23.0595	11.9868	19.4639
PdWPP	15.7987	1.8779	13.8359
NSPP	22.8245	13.1205	19.4914
1000-SW	52.4637	25.3508	16.3489
SWPP	15.2542	1.3189	12.9472

Table 23A: Phenotypic correlation coefficient between yield and yield contributing characters in chickpea.

Characters	Characters									
	NPBMF	**NSBMF**	**PHMF**	**PWFD**	**RWFD**	**NPPP**	**PdWPP**	**NSPP**	**1000-SW**	**SWPP**
DMF	-0.0582	0.2193	0.0370	0.2486	0.0232	-0.0024	-0:0013	0.0149	-0.0572	-0.0022
NPBMF		0.1586	0.1613	0.0711	-0.1652	0.2893	0.2436	0.2611	-0.3252	0.2267
NSBMF			0.2335	0.3446	-0.1371	0.0041	-0.0086	-0.0169	-0.1885	-0.0351
PHMF				0.1857	-0.0400	-0.1395	-0.1199	-0.1033	-0.2125	-0.1436
PWFD					0.1477	-0.0216	-0.0228	-0.0256	-0.0084	-0.7297*
RWFD						-0.1404	-0.0417	-0.1777	0.3731	-0.0932
NPPP							0.9119**	0.9558**	-0.1381	0.9422**
PdWPP								0.9059**	0.0028	0.9537**
NSPP									-0.2179	0.9495**
1000-SW										0.0403

Table 23B: Genotypic correlation coefficient between yield and yield contributing characters in chickpea.

Characters	Characters									
	NPBMF	**NSBMF**	**PHMF**	**PWFD**	**RWFD**	**NPPP**	**PdWPP**	**NSPP**	**1000-SW**	**SWPP**
DMF	0.0682	0.6475	0.1541	0.9545**	-0.9089**	0.1008	-0.0037	0.1782	-0.5827	-0.0734
NPBMF		0.9003**	0.0385	0.3164	-0.6759	1.0045**	1.0297**	0.9806**	-0.7303*	1.0445**
NSBMF			0.3441	0.5189	-0.7294*	0.7866*	0.7387*	0.8463**	-0.8939**	0.7342*
PHMF				0.4148	-0.1819	0.1700	0.0541	0.2566	-0.6743	-0.0710
PWFD					-0.3094	0.0256	0.0294	0.1194	-0.5478	-0.1102
RWFD						-0.7855*	-0.4716	-0.8268*	0.8637**	-0.6207
NPPP							0.9416**	0.9808**	-0.8459**	0.9654**
PdWPP								0.8692**	-0.6687	0.9608**
NSPP									-0.9281**	0.9217**
1000-SW										-0.6934

Table 24A: Path-coefficient analysis showing direct and indirect effects of yield and yield components of chickpea at phenotypic level.

Characters	Characters									
	DMF	**NPBMF**	**NSBMF**	**PHMF**	**PWFD**	**RWFD**	**NPPP**	**PdWPP**	**NSPP**	**1000-SW**
DMF	**0.1573**	-0.0051	0.0628	0.0041	-0.2209	0.0035	-0.0002	-0.0001	0.0127	-0.0163
NPBMF	-0.0091	**0.0872**	0.0454	0.0179	-0.0632	-0.0249	0.0200	0.0249	0.2215	-0.0929
NSBMF	0.0345	0.0138	**0.2864**	0.0259	-0.3062	-0.0207	0.0003	-0.0009	-0.0143	-0.0539
PHMF	0.0058	0.0141	0.0669	**0.1109**	-0.1650	-0.0060	-0.0096	-0.0122	-0.0876	-0.0607
PWFD	0.0391	0.0062	0.0987	0.0206	**-0.8886**	0.0222	-0.0015	-0.0023	-0.0218	-0.0024
RWFD	0.0037	-0.0144	-0.0393	-0.0044	-0.1312	**0.1506**	-0.0097	-0.0043	-0.1508	0.1066
NPPP	-0.0004	0.0252	0.0012	-0.0155	0.0192	-0.0211	**0.0691**	0.0931	0.8108	-0.0395
PdWPP	-0.0002	0.0212	-0.0025	-0.0133	0.0202	-0.0063	0.0630	**0.1020**	0.7685	0.0008
NSPP	0.0023	0.0228	-0.0048	-0.0114	0.0228	-0.0268	0.0661	0.0924	**0.8483**	-0.0623
1000-SW	-0.0090	-0.0284	-0.0540	-0.0236	0.0075	0.0562	-0.0095	0.0003	-0.1849	**0.2857**
Total	0.2240	0.1426	0.4608	0.1112	-1.7054	0.1267	0.1880	0.2929	2.2024	0.0651

The residual effect = 0.7793

Under line value denote the direct effect

Table 24B: Path-coefficient analysis showing direct and indirect effects of yield and yield components of chickpea at genotypic level.

Characters	Characters									
	DMF	**NPBMF**	**NSBMF**	**PHMF**	**PWFD**	**RWFD**	**NPPP**	**PdWPP**	**NSPP**	**1000-SW**
DMF	**0.000405**	0.0003	0.0294	-0.0208	-0.0465	-0.0465	-0.0164	-0.0015	0.1812	-0.1530
NPBMF	0.000028	**0.0042**	0.0409	-0.0052	-0.0154	-0.0346	-0.1632	0.4126	0.9969	-0.1917
NSBMF	0.000262	0.0038	**0.0454**	-0.0465	-0.0253	-0.0373	-0.1278	0.2960	0.8604	-0.2347
PHMF	0.000062	0.0002	0.0156	**-0.1352**	-0.0202	-0.0093	-0.0276	0.0217	0.2608	-0.1770
PWFD	0.000386	0.0013	0.0235	-0.0561	**-0.0487**	-0.0158	-0.0042	0.0118	0.1213	-0.1438
RWFD	-0.000368	-0.0028	-0.0331	0.0246	0.0151	**0.0511**	0.1276	-0.1890	-0.8405	0.2267
NPPP	0.000041	0.0042	0.0357	-0.0230	-0.0012	-0.0402	**-0.1625**	0.3773	0.9971	-0.2221
PdWPP	-0.000001	0.0043	0.0335	-0.0073	-0.0014	-0.0241	-0.1530	**0.4007**	0.8837	-0.1756
NSPP	0.000072	0.0041	0.0384	-0.0347	-0.0058	-0.0423	-0.1593	0.3483	**1.0166**	-0.2437
1000-SW	-0.000236	-0.0031	-0.0406	0.0912	0.0267	0.0442	0.1374	-0.2680	-0.9435	**0.2625**
Total	0.00065	0.0165	0.1887	-0.2130	-0.1227	-0.1548	-0.5490	1.4099	3.534	-1.0524

The residual effect = 0.06388. Under line value denote the direct effect

Table 25: Expected genetic gain in % for yield over straight selection from the use of various selection indices. Indices showing values over 100 are shown only.

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
SWPP(x_{11})	659.582	x_5+x_7	-122.270	$x_2+x_3+x_4$	200.541	$x_4+x_5+x_7$	-121.434
DMF(x_1)	-146.364	x_5+x_9	-166.921	$x_2+x_3+x_6$	408.132	$x_4+x_5+x_9$	-163.003
NPBMF(x_2)	1329.525	x_5+x_{11}	122.167	$x_2+x_3+x_7$	-146.714	$x_4+x_6+x_9$	-174.470
NSBMF(x_3)	139.412	x_6+x_9	-180.044	$x_2+x_3+x_8$	108.512	$x_4+x_6+x_{11}$	285.174
PHMF(x_4)	-23.168	x_6+x_{11}	507.932	$x_2+x_3+x_9$	-170.995	$x_4+x_7+x_9$	-139.692
PWFD(x_5)	-98.336	x_7+x_9	-141.339	$x_2+x_3+x_{11}$	463.078	$x_4+x_8+x_9$	-166.881
RWFD(x_6)	379.339	x_8+x_9	-171.396	$x_2+x_4+x_6$	208.750	$x_4+x_8+x_{11}$	146.171
NPPP(x_7)	-128.194	x_8+x_{11}	220.290	$x_2+x_4+x_9$	-167.807	$x_4+x_9+x_{11}$	-127.700
PdWPP(x_8)	12.695	x_9+x_{11}	-130.018	$x_2+x_4+x_{11}$	323.525	$x_5+x_6+x_9$	-164.718
NSPP(x_9)	-183.194	$x_1+x_2+x_3$	345.632	$x_2+x_5+x_9$	-158.947	$x_5+x_6+x_{11}$	108.976
1000-SW(x_{10})	-5.274	$x_1+x_2+x_4$	178.441	$x_2+x_5+x_{11}$	129.179	$x_5+x_7+x_9$	-136.678
x_1+x_2	525.964	$x_1+x_2+x_6$	354.269	$x_2+x_6+x_8$	392.331	$x_5+x_8+x_9$	-158.872
x_1+x_5	-105.294	$x_1+x_2+x_9$	-170.688	$x_2+x_6+x_9$	-170.005	$x_5+x_9+x_{11}$	-124.584
x_1+x_6	114.676	$x_1+x_2+x_{11}$	433.048	$x_2+x_6+x_{11}$	459.846	$x_6+x_7+x_9$	-140.224
x_1+x_7	-127.173	$x_1+x_3+x_7$	-127.170	$x_2+x_7+x_9$	-136.207	$x_6+x_8+x_9$	-168.886
x_1+x_9	-180.575	$x_1+x_3+x_9$	-178.502	$x_2+x_8+x_9$	-162.487	$x_6+x_8+x_{11}$	192.397
x_1+x_{11}	473.108	$x_1+x_3+x_{11}$	385.189	$x_2+x_8+x_{11}$	220.014	$x_6+x_9+x_{11}$	-126.989
x_2+x_3	636.932	$x_1+x_4+x_7$	-125.809	$x_2+x_9+x_{11}$	-113.676	$x_7+x_8+x_9$	-137.654
x_2+x_4	270.022	$x_1+x_4+x_9$	-174.996	$x_3+x_4+x_7$	-126.699	$x_7+x_9+x_{11}$	-110.270
x_2+x_6	638.460	$x_1+x_4+x_{11}$	269.090	$x_3+x_4+x_9$	-175.345	$x_8+x_9+x_{11}$	-123.182
x_2+x_8	136.368	$x_1+x_5+x_7$	-121.620	$x_3+x_4+x_{11}$	285.254	$x_1+x_2+x_3+x_4$	137.780
x_2+x_9	-172.925	$x_1+x_5+x_9$	-165.217	$x_3+x_5+x_7$	-122.369	$x_1+x_2+x_3+x_6$	256.389
x_2+x_{11}	571.392	$x_1+x_5+x_{11}$	102.835	$x_3+x_5+x_9$	-165.457	$x_1+x_2+x_3+x_9$	-168.867
x_3+x_6	175.071	$x_1+x_6+x_9$	-122.846	$x_3+x_5+x_{11}$	107.940	$x_1+x_2+x_3+x_{11}$	362.614
x_3+x_7	-128.163	$x_1+x_6+x_{11}$	383.704	$x_3+x_6+x_9$	-177.970	$x_1+x_2+x_4+x_6$	145.197
x_3+x_9	-180.993	$x_1+x_7+x_9$	-140.652	$x_3+x_6+x_{11}$	410.979	$x_1+x_2+x_4+x_9$	-165.863
x_3+x_{11}	512.031	$x_1+x_8+x_9$	-169.424	$x_3+x_7+x_9$	-140.701	$x_1+x_2+x_4+x_{11}$	264.039
x_4+x_7	-126.707	$x_1+x_8+x_{11}$	182.357	$x_3+x_8+x_9$	-169.710	$x_1+x_2+x_5+x_9$	-157.479
x_4+x_9	-177.265	$x_1+x_9+x_{11}$	-129.183	$x_3+x_8+x_{11}$	191.740	$x_1+x_2+x_5+x_{11}$	110.508
x_4+x_{11}	338.210	$x_1+x_{10}+x_{11}$	-196.016	$x_3+x_9+x_{11}$	-128.891	$x_1+x_2+x_6+x_9$	-167.911

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
$x_1+x_2+x_6+x_{11}$	361.166	$x_1+x_6+x_8+x_{11}$	160.831	$x_2+x_6+x_8+x_9$	-160.128	$x_4+x_6+x_8+x_9$	-164.615
$x_1+x_2+x_7+x_9$	-135.615	$x_1+x_6+x_9+x_{11}$	-126.261	$x_2+x_6+x_8+x_{11}$	194.219	$x_4+x_6+x_8+x_{11}$	130.048
$x_1+x_2+x_8+x_9$	-160.801	$x_1+x_7+x_8+x_9$	-137.072	$x_2+x_6+x_9+x_{11}$	-117.408	$x_4+x_6+x_9+x_{11}$	-124.873
$x_1+x_2+x_8+x_{11}$	185.320	$x_1+x_7+x_9+x_{11}$	-110.133	$x_2+x_7+x_8+x_9$	-132.816	$x_4+x_7+x_8+x_9$	-136.244
$x_1+x_2+x_9+x_{11}$	-113.226	$x_1+x_8+x_9+x_{11}$	-122.619	$x_2+x_7+x_9+x_{11}$	-114.714	$x_4+x_7+x_9+x_{11}$	-109.522
$x_1+x_3+x_4+x_7$	-125.824	$x_2+x_3+x_4+x_6$	161.413	$x_2+x_8+x_9+x_{11}$	-117.572	$x_4+x_8+x_9+x_{11}$	-121.444
$x_1+x_3+x_4+x_9$	-173.181	$x_2+x_3+x_4+x_9$	-166.116	$x_3+x_4+x_5+x_7$	-121.531	$x_5+x_6+x_7+x_9$	-135.744
$x_1+x_3+x_4+x_{11}$	230.923	$x_2+x_3+x_4+x_{11}$	278.084	$x_3+x_4+x_5+x_9$	-161.692	$x_5+x_6+x_8+x_9$	-157.032
$x_1+x_3+x_5+x_7$	-121.731	$x_2+x_3+x_5+x_9$	-157.646	$x_3+x_4+x_6+x_9$	-172.654	$x_5+x_6+x_9+x_{11}$	-122.198
$x_1+x_3+x_5+x_9$	-163.823	$x_2+x_3+x_5+x_{11}$	115.379	$x_3+x_4+x_6+x_{11}$	244.259	$x_5+x_7+x_8+x_9$	-133.673
$x_1+x_3+x_6+x_9$	-175.632	$x_2+x_3+x_6+x_9$	-168.187	$x_3+x_4+x_7+x_9$	-139.098	$x_5+x_7+x_9+x_{11}$	-109.162
$x_1+x_3+x_6+x_{11}$	320.463	$x_2+x_3+x_6+x_{11}$	383.369	$x_3+x_4+x_8+x_9$	-165.384	$x_5+x_8+x_9+x_{11}$	-119.389
$x_1+x_3+x_7+x_9$	-140.034	$x_2+x_3+x_7+x_9$	-135.627	$x_3+x_4+x_8+x_{11}$	129.131	$x_6+x_7+x_8+x_9$	-136.652
$x_1+x_3+x_8+x_9$	-167.824	$x_2+x_3+x_8+x_9$	-161.000	$x_3+x_4+x_9+x_{11}$	-126.683	$x_6+x_7+x_9+x_{11}$	-107.935
$x_1+x_3+x_8+x_{11}$	160.009	$x_2+x_3+x_8+x_{11}$	193.894	$x_3+x_5+x_6+x_9$	-163.324	$x_6+x_8+x_9+x_{11}$	-120.306
$x_1+x_3+x_9+x_{11}$	-128.106	$x_2+x_3+x_9+x_{11}$	-114.329	$x_3+x_5+x_7+x_9$	-136.164	$x_7+x_8+x_9+x_{11}$	-106.003
$x_1+x_4+x_5+x_7$	-120.845	$x_2+x_4+x_5+x_9$	-155.528	$x_3+x_5+x_8+x_9$	-157.695	$x_1+x_2+x_3+x_4+x_6$	114.783
$x_1+x_4+x_5+x_9$	-161.488	$x_2+x_4+x_6+x_9$	-165.198	$x_3+x_5+x_9+x_{11}$	-123.755	$x_1+x_2+x_3+x_4+x_9$	-164.261
$x_1+x_4+x_6+x_9$	-172.335	$x_2+x_4+x_6+x_{10}$	-190.906	$x_3+x_6+x_7+x_9$	-139.607	$x_1+x_2+x_3+x_4+x_{11}$	230.049
$x_1+x_4+x_6+x_{11}$	231.375	$x_2+x_4+x_6+x_{11}$	277.727	$x_3+x_6+x_8+x_9$	-167.286	$x_1+x_2+x_3+x_5+x_9$	-156.237
$x_1+x_4+x_7+x_9$	-139.058	$x_2+x_4+x_7+x_9$	-134.758	$x_3+x_6+x_8+x_{11}$	168.761	$x_1+x_2+x_3+x_6+x_9$	-166.192
$x_1+x_4+x_8+x_9$	-165.143	$x_2+x_4+x_8+x_9$	-158.577	$x_3+x_6+x_9+x_{11}$	-125.912	$x_1+x_2+x_3+x_6+x_{11}$	308.136
$x_1+x_4+x_8+x_{11}$	123.179	$x_2+x_4+x_8+x_{11}$	151.402	$x_3+x_7+x_8+x_9$	-137.101	$x_1+x_2+x_3+x_7+x_9$	-135.052
$x_1+x_4+x_9+x_{11}$	-126.979	$x_2+x_4+x_9+x_{11}$	-113.682	$x_3+x_7+x_9+x_{11}$	-109.726	$x_1+x_2+x_3+x_8+x_9$	-159.386
$x_1+x_5+x_6+x_9$	-163.105	$x_2+x_5+x_6+x_9$	-156.864	$x_3+x_8+x_9+x_{11}$	-115.635	$x_1+x_2+x_3+x_8+x_{11}$	164.431
$x_1+x_5+x_7+x_9$	-136.137	$x_2+x_5+x_6+x_{11}$	116.100	$x_4+x_5+x_6+x_9$	-160.998	$x_1+x_2+x_3+x_9+x_{11}$	-113.875
$x_1+x_5+x_8+x_9$	-157.526	$x_2+x_5+x_7+x_9$	-132.172	$x_4+x_5+x_7+x_9$	-135.366	$x_1+x_2+x_4+x_5+x_9$	-154.220
$x_1+x_5+x_9+x_{11}$	-124.025	$x_2+x_5+x_8+x_9$	-151.724	$x_4+x_5+x_8+x_9$	-155.745	$x_1+x_2+x_4+x_6+x_9$	-163.373
$x_1+x_6+x_7+x_9$	-139.565	$x_2+x_5+x_9+x_{11}$	-111.251	$x_4+x_5+x_9+x_{11}$	-122.948	$x_1+x_2+x_4+x_6+x_{11}$	230.152
$x_1+x_6+x_8+x_9$	-167.026	$x_2+x_6+x_7+x_9$	-135.108	$x_4+x_6+x_7+x_9$	-138.639	$x_1+x_2+x_4+x_7+x_9$	-134.210

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
$x_1+x_2+x_4+x_8+x_9$	-157.089	$x_1+x_3+x_7+x_8+x_9$	-136.535	$x_2+x_3+x_4+x_9+x_{11}$	-114.243
$x_1+x_2+x_4+x_8+x_{11}$	129.518	$x_1+x_3+x_7+x_9+x_{11}$	-109.601	$x_2+x_3+x_5+x_6+x_9$	-155.626
$x_1+x_2+x_4+x_9+x_{11}$	-113.262	$x_1+x_3+x_8+x_9+x_{11}$	-115.287	$x_2+x_3+x_5+x_6+x_{11}$	103.941
$x_1+x_2+x_5+x_6+x_9$	-155.477	$x_1+x_4+x_5+x_6+x_9$	-159.560	$x_2+x_3+x_5+x_7+x_9$	-131.701
$x_1+x_2+x_5+x_7+x_9$	-131.705	$x_1+x_4+x_5+x_7+x_9$	-134.862	$x_2+x_3+x_5+x_8+x_9$	-150.672
$x_1+x_2+x_5+x_8+x_9$	-150.565	$x_1+x_4+x_5+x_8+x_9$	-154.534	$x_2+x_3+x_5+x_9+x_{11}$	-111.833
$x_1+x_2+x_5+x_9+x_{11}$	-110.936	$x_1+x_4+x_5+x_9+x_{11}$	-122.455	$x_2+x_3+x_6+x_7+x_9$	-134.547
$x_1+x_2+x_6+x_7+x_9$	-134.542	$x_1+x_4+x_6+x_7+x_9$	-138.030	$x_2+x_3+x_6+x_8+x_9$	-158.717
$x_1+x_2+x_6+x_8+x_9$	-158.541	$x_1+x_4+x_6+x_8+x_9$	-162.972	$x_2+x_3+x_6+x_8+x_{11}$	172.259
$x_1+x_2+x_6+x_8+x_{11}$	164.924	$x_1+x_4+x_6+x_8+x_{11}$	110.088	$x_2+x_3+x_6+x_9+x_{11}$	-117.763
$x_1+x_2+x_6+x_9+x_{11}$	-116.879	$x_1+x_4+x_6+x_9+x_{11}$	-124.246	$x_2+x_3+x_7+x_8+x_9$	-132.312
$x_1+x_2+x_7+x_8+x_9$	-132.317	$x_1+x_4+x_7+x_8+x_9$	-135.704	$x_2+x_3+x_7+x_9+x_{11}$	-114.816
$x_1+x_2+x_7+x_9+x_{11}$	-114.463	$x_1+x_4+x_7+x_9+x_{11}$	-109.402	$x_2+x_3+x_8+x_9+x_{11}$	-117.829
$x_1+x_2+x_8+x_9+x_{11}$	-123.023	$x_1+x_4+x_8+x_9+x_{11}$	-120.955	$x_2+x_4+x_5+x_6+x_9$	-153.622
$x_1+x_3+x_4+x_5+x_7$	-120.952	$x_1+x_5+x_6+x_7+x_9$	-135.224	$x_2+x_4+x_5+x_7+x_9$	-131.011
$x_1+x_3+x_4+x_5+x_9$	-160.235	$x_1+x_5+x_6+x_8+x_9$	-155.752	$x_2+x_4+x_5+x_8+x_9$	-148.991
$x_1+x_3+x_4+x_6+x_9$	-170.616	$x_1+x_5+x_6+x_9+x_{11}$	-121.708	$x_2+x_4+x_5+x_9+x_{11}$	-111.380
$x_1+x_3+x_4+x_6+x_{11}$	200.740	$x_1+x_5+x_7+x_8+x_9$	-133.207	$x_2+x_4+x_6+x_7+x_9$	-133.715
$x_1+x_3+x_4+x_7+x_9$	-138.480	$x_1+x_5+x_7+x_9+x_{11}$	-109.056	$x_2+x_4+x_6+x_8+x_9$	-156.436
$x_1+x_3+x_4+x_8+x_9$	-163.718	$x_1+x_5+x_8+x_9+x_{11}$	-118.998	$x_2+x_4+x_6+x_8+x_{11}$	135.748
$x_1+x_3+x_4+x_8+x_{11}$	109.131	$x_1+x_6+x_7+x_8+x_9$	-136.093	$x_2+x_4+x_6+x_9+x_{11}$	-117.002
$x_1+x_3+x_4+x_9+x_{11}$	-126.005	$x_1+x_6+x_7+x_9+x_{11}$	-107.844	$x_2+x_4+x_7+x_8+x_9$	-131.577
$x_1+x_3+x_5+x_6+x_9$	-161.776	$x_1+x_6+x_8+x_9+x_{11}$	-119.831	$x_2+x_4+x_7+x_9+x_{11}$	-114.451
$x_1+x_3+x_5+x_7+x_9$	-135.636	$x_1+x_7+x_8+x_9+x_{11}$	-105.954	$x_2+x_4+x_8+x_9+x_{11}$	-117.135
$x_1+x_3+x_5+x_8+x_9$	-156.399	$x_2+x_3+x_4+x_5+x_9$	-154.358	$x_2+x_5+x_6+x_7+x_9$	-131.243
$x_1+x_3+x_5+x_9+x_{11}$	-123.226	$x_2+x_3+x_4+x_6+x_9$	-163.599	$x_2+x_5+x_6+x_8+x_9$	-149.964
$x_1+x_3+x_6+x_7+x_9$	-138.967	$x_2+x_3+x_4+x_6+x_{11}$	241.602	$x_2+x_5+x_6+x_9+x_{11}$	-114.378
$x_1+x_3+x_6+x_8+x_9$	-165.506	$x_2+x_3+x_4+x_7+x_9$	-134.216	$x_2+x_5+x_7+x_8+x_9$	-129.384
$x_1+x_3+x_6+x_8+x_{11}$	141.921	$x_2+x_3+x_4+x_8+x_9$	-157.252	$x_2+x_5+x_7+x_9+x_{11}$	-113.147
$x_1+x_3+x_6+x_9+x_{11}$	-125.230	$x_2+x_3+x_4+x_8+x_{11}$	135.137	$x_2+x_5+x_8+x_9+x_{11}$	-114.749

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
$x_2+x_6+x_7+x_8+x_9$	-131.819	$x_4+x_5+x_8+x_9+x_{11}$	-118.102	$x_1+x_2+x_4+x_5+x_9+x_{11}$	-111.081
$x_2+x_6+x_7+x_9+x_{11}$	-115.801	$x_4+x_6+x_7+x_8+x_9$	-135.293	$x_1+x_2+x_4+x_6+x_7+x_9$	-133.192
$x_2+x_6+x_8+x_9+x_{11}$	-119.867	$x_4+x_6+x_7+x_9+x_{11}$	-107.167	$x_1+x_2+x_4+x_6+x_8+x_9$	-155.032
$x_2+x_7+x_8+x_9+x_{11}$	-115.609	$x_4+x_6+x_8+x_9+x_{11}$	-118.711	$x_1+x_2+x_4+x_6+x_8+x_{11}$	116.592
$x_3+x_4+x_5+x_6+x_9$	-159.746	$x_4+x_7+x_8+x_9+x_{11}$	-105.211	$x_1+x_2+x_4+x_6+x_9+x_{11}$	-116.517
$x_3+x_4+x_5+x_7+x_9$	-134.882	$x_5+x_6+x_7+x_8+x_9$	-132.821	$x_1+x_2+x_4+x_7+x_8+x_9$	-131.113
$x_3+x_4+x_5+x_8+x_9$	-154.678	$x_5+x_6+x_7+x_9+x_{11}$	-107.088	$x_1+x_2+x_4+x_7+x_9+x_{11}$	-114.213
$x_3+x_4+x_5+x_9+x_{11}$	-122.184	$x_5+x_6+x_8+x_9+x_{11}$	-117.042	$x_1+x_2+x_4+x_8+x_9+x_{11}$	-116.692
$x_3+x_4+x_6+x_7+x_9$	-138.063	$x_5+x_7+x_8+x_9+x_{11}$	-105.393	$x_1+x_2+x_5+x_6+x_7+x_9$	-130.795
$x_3+x_4+x_6+x_8+x_9$	-163.192	$x_1+x_2+x_3+x_4+x_5+x_9$	-153.100	$x_1+x_2+x_5+x_6+x_8+x_9$	-148.865
$x_3+x_4+x_6+x_8+x_{11}$	115.313	$x_1+x_2+x_3+x_4+x_6+x_9$	-161.856	$x_1+x_2+x_5+x_6+x_9+x_{11}$	-114.009
$x_3+x_4+x_6+x_9+x_{11}$	-123.896	$x_1+x_2+x_3+x_4+x_6+x_{11}$	202.295	$x_1+x_2+x_5+x_7+x_8+x_9$	-128.984
$x_3+x_4+x_7+x_8+x_9$	-135.726	$x_1+x_2+x_3+x_4+x_7+x_9$	-133.684	$x_1+x_2+x_5+x_7+x_9+x_{11}$	-112.945
$x_3+x_4+x_7+x_9+x_{11}$	-108.988	$x_1+x_2+x_3+x_4+x_8+x_9$	-155.825	$x_1+x_2+x_5+x_8+x_9+x_{11}$	-114.403
$x_3+x_4+x_8+x_9+x_{11}$	-120.589	$x_1+x_2+x_3+x_4+x_8+x_{11}$	115.923	$x_1+x_2+x_6+x_7+x_8+x_9$	-131.341
$x_3+x_5+x_6+x_7+x_9$	-135.245	$x_1+x_2+x_3+x_4+x_9+x_{11}$	-113.821	$x_1+x_2+x_6+x_7+x_9+x_{11}$	-115.539
$x_3+x_5+x_6+x_8+x_9$	-155.906	$x_1+x_2+x_3+x_5+x_6+x_9$	-154.294	$x_1+x_2+x_6+x_8+x_9+x_{11}$	-119.345
$x_3+x_5+x_6+x_9+x_{11}$	-121.394	$x_1+x_2+x_3+x_5+x_7+x_9$	-131.246	$x_1+x_2+x_7+x_8+x_9+x_{11}$	-115.363
$x_3+x_5+x_7+x_8+x_9$	-133.220	$x_1+x_2+x_3+x_5+x_8+x_9$	-149.556	$x_1+x_3+x_4+x_5+x_6+x_9$	-158.363
$x_3+x_5+x_7+x_9+x_{11}$	-108.688	$x_1+x_2+x_3+x_5+x_9+x_{11}$	-111.513	$x_1+x_3+x_4+x_5+x_7+x_9$	-134.391
$x_3+x_5+x_8+x_9+x_{11}$	-118.670	$x_1+x_2+x_3+x_6+x_7+x_9$	-133.998	$x_1+x_3+x_4+x_5+x_8+x_9$	-153.510
$x_3+x_6+x_7+x_8+x_9$	-136.117	$x_1+x_2+x_3+x_6+x_8+x_9$	-157.199	$x_1+x_3+x_4+x_5+x_9+x_{11}$	-121.716
$x_3+x_6+x_7+x_9+x_{11}$	-107.304	$x_1+x_2+x_3+x_6+x_8+x_{11}$	147.036	$x_1+x_3+x_4+x_6+x_7+x_9$	-137.470
$x_3+x_6+x_8+x_9+x_{11}$	-119.394	$x_1+x_2+x_3+x_6+x_9+x_{11}$	-117.238	$x_1+x_3+x_4+x_6+x_8+x_9$	-161.616
$x_3+x_7+x_8+x_9+x_{11}$	-105.286	$x_1+x_2+x_3+x_7+x_8+x_9$	-131.827	$x_1+x_3+x_4+x_6+x_9+x_{11}$	-123.307
$x_4+x_5+x_6+x_7+x_9$	-134.477	$x_1+x_2+x_3+x_7+x_9+x_{11}$	-114.567	$x_1+x_3+x_4+x_7+x_8+x_9$	-135.200
$x_4+x_5+x_6+x_8+x_9$	-154.050	$x_1+x_2+x_3+x_8+x_9+x_{11}$	-117.352	$x_1+x_3+x_4+x_7+x_9+x_{11}$	-108.880
$x_4+x_5+x_6+x_9+x_{11}$	-120.685	$x_1+x_2+x_4+x_5+x_6+x_9$	-152.384	$x_1+x_3+x_4+x_8+x_9+x_{11}$	-120.130
$x_4+x_5+x_7+x_8+x_9$	-132.532	$x_1+x_2+x_4+x_5+x_7+x_9$	-130.576	$x_1+x_3+x_5+x_6+x_7+x_9$	-134.738
$x_4+x_5+x_7+x_9+x_{11}$	-108.527	$x_1+x_2+x_4+x_5+x_8+x_9$	-147.947	$x_1+x_3+x_5+x_6+x_8+x_9$	-154.673

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
$x_1+x_3+x_5+x_6+x_9+x_{11}$	-120.931	$x_2+x_3+x_4+x_7+x_8+x_9$	-131.103	$x_3+x_4+x_5+x_6+x_9+x_{11}$	-119.940
$x_1+x_3+x_5+x_7+x_8+x_9$	-132.765	$x_2+x_3+x_4+x_7+x_9+x_{11}$	-114.548	$x_3+x_4+x_5+x_7+x_8+x_9$	-132.104
$x_1+x_3+x_5+x_7+x_9+x_{11}$	-108.590	$x_2+x_3+x_4+x_8+x_9+x_{11}$	-117.369	$x_3+x_4+x_5+x_7+x_9+x_{11}$	-108.059
$x_1+x_3+x_5+x_8+x_9+x_{11}$	-118.302	$x_2+x_3+x_5+x_6+x_7+x_9$	-130.786	$x_3+x_4+x_5+x_8+x_9+x_{11}$	-117.430
$x_1+x_3+x_6+x_7+x_8+x_9$	-135.572	$x_2+x_3+x_5+x_6+x_8+x_9$	-148.959	$x_3+x_4+x_6+x_7+x_8+x_9$	-134.791
$x_1+x_3+x_6+x_7+x_9+x_{11}$	-107.226	$x_2+x_3+x_5+x_6+x_9+x_{11}$	-114.725	$x_3+x_4+x_6+x_7+x_9+x_{11}$	-106.528
$x_1+x_3+x_6+x_8+x_9+x_{11}$	-118.951	$x_2+x_3+x_5+x_7+x_8+x_9$	-128.968	$x_3+x_4+x_6+x_8+x_9+x_{11}$	-117.864
$x_1+x_3+x_7+x_8+x_9+x_{11}$	-105.253	$x_2+x_3+x_5+x_7+x_9+x_{11}$	-113.255	$x_3+x_4+x_7+x_8+x_9+x_{11}$	-104.444
$x_1+x_4+x_5+x_6+x_7+x_9$	-133.992	$x_2+x_3+x_5+x_8+x_9+x_{11}$	-115.010	$x_3+x_5+x_6+x_7+x_8+x_9$	-132.381
$x_1+x_4+x_5+x_6+x_8+x_9$	-152.898	$x_2+x_3+x_6+x_7+x_8+x_9$	-131.331	$x_3+x_5+x_6+x_7+x_9+x_{11}$	-106.532
$x_1+x_4+x_5+x_6+x_9+x_{11}$	-120.253	$x_2+x_3+x_6+x_7+x_9+x_{11}$	-115.867	$x_3+x_5+x_6+x_8+x_9+x_{11}$	-116.326
$x_1+x_4+x_5+x_7+x_8+x_9$	-132.096	$x_2+x_3+x_6+x_8+x_9+x_{11}$	-120.001	$x_3+x_5+x_7+x_8+x_9+x_{11}$	-104.753
$x_1+x_4+x_5+x_7+x_9+x_{11}$	-108.433	$x_2+x_3+x_7+x_8+x_9+x_{11}$	-115.664	$x_3+x_6+x_7+x_8+x_9+x_{11}$	-102.584
$x_1+x_4+x_5+x_8+x_9+x_{11}$	-117.756	$x_2+x_4+x_5+x_6+x_7+x_9$	-130.124	$x_4+x_5+x_6+x_7+x_8+x_9$	-131.718
$x_1+x_4+x_6+x_7+x_8+x_9$	-134.773	$x_2+x_4+x_5+x_6+x_8+x_9$	-147.364	$x_4+x_5+x_6+x_7+x_9+x_{11}$	-106.426
$x_1+x_4+x_6+x_7+x_9+x_{11}$	-107.093	$x_2+x_4+x_5+x_6+x_9+x_{11}$	-114.193	$x_4+x_5+x_6+x_8+x_9+x_{11}$	-115.844
$x_1+x_4+x_6+x_8+x_9+x_{11}$	-118.300	$x_2+x_4+x_5+x_7+x_8+x_9$	-128.376	$x_4+x_5+x_7+x_8+x_9+x_{11}$	-104.696
$x_1+x_4+x_7+x_8+x_9+x_{11}$	-105.179	$x_2+x_4+x_5+x_7+x_9+x_{11}$	-112.961	$x_4+x_6+x_7+x_8+x_9+x_{11}$	-102.441
$x_1+x_5+x_6+x_7+x_8+x_9$	-132.373	$x_2+x_4+x_5+x_8+x_9+x_{11}$	-114.511	$x_1+x_2+x_3+x_4+x_5+x_6+x_9$	-151.315
$x_1+x_5+x_6+x_7+x_9+x_{11}$	-107.019	$x_2+x_4+x_6+x_7+x_8+x_9$	-130.626	$x_1+x_2+x_3+x_4+x_5+x_7+x_9$	-130.143
$x_1+x_5+x_6+x_8+x_9+x_{11}$	-116.710	$x_2+x_4+x_6+x_7+x_9+x_{11}$	-115.484	$x_1+x_2+x_3+x_4+x_5+x_8+x_9$	-147.028
$x_1+x_5+x_7+x_8+x_9+x_{11}$	-105.356	$x_2+x_4+x_6+x_8+x_9+x_{11}$	-119.246	$x_1+x_2+x_3+x_4+x_5+x_9+x_{11}$	-111.584
$x_2+x_3+x_4+x_5+x_6+x_9$	-152.507	$x_2+x_4+x_7+x_8+x_9+x_{11}$	-115.306	$x_1+x_2+x_3+x_4+x_6+x_7+x_9$	-132.682
$x_2+x_3+x_4+x_5+x_7+x_9$	-130.568	$x_2+x_5+x_6+x_7+x_8+x_9$	-128.529	$x_1+x_2+x_3+x_4+x_6+x_8+x_9$	-153.829
$x_2+x_3+x_4+x_5+x_8+x_9$	-148.035	$x_2+x_5+x_6+x_7+x_9+x_{11}$	-114.139	$x_1+x_2+x_3+x_4+x_6+x_8+x_{11}$	104.590
$x_2+x_3+x_4+x_5+x_9+x_{11}$	-111.887	$x_2+x_5+x_6+x_8+x_9+x_{11}$	-116.730	$x_1+x_2+x_3+x_4+x_6+x_9+x_{11}$	-116.838
$x_2+x_3+x_4+x_6+x_7+x_9$	-133.191	$x_2+x_5+x_7+x_8+x_9+x_{11}$	-114.045	$x_1+x_2+x_3+x_4+x_7+x_8+x_9$	-130.652
$x_2+x_3+x_4+x_6+x_8+x_9$	-155.176	$x_2+x_6+x_7+x_8+x_9+x_{11}$	-116.482	$x_1+x_2+x_3+x_4+x_7+x_9+x_{11}$	-114.312
$x_2+x_3+x_4+x_6+x_8+x_{11}$	121.559	$x_3+x_4+x_5+x_6+x_7+x_9$	-134.008	$x_1+x_2+x_3+x_4+x_8+x_9+x_{11}$	-116.929
$x_2+x_3+x_4+x_6+x_9+x_{11}$	-117.320	$x_3+x_4+x_5+x_6+x_8+x_9$	-153.028	$x_1+x_2+x_3+x_5+x_6+x_7+x_9$	-130.349

Selection index	Genetic gain	Selection index	Genetic gain	Selection index	Genetic gain
$x_1+x_2+x_3+x_5+x_6+x_8+x_9$	-147.900	$x_1+x_3+x_4+x_6+x_7+x_8+x_9$	-134.284	$x_2+x_4+x_5+x_6+x_7+x_9+x_{11}$	-113.906
$x_1+x_2+x_3+x_5+x_6+x_9+x_{11}$	-114.356	$x_1+x_3+x_4+x_6+x_7+x_9+x_{11}$	-106.467	$x_2+x_4+x_5+x_6+x_8+x_9+x_{11}$	-116.347
$x_1+x_2+x_3+x_5+x_7+x_8+x_9$	-128.578	$x_1+x_3+x_4+x_6+x_8+x_9+x_{11}$	-117.481	$x_2+x_4+x_5+x_7+x_8+x_9+x_{11}$	-113.818
$x_1+x_2+x_3+x_5+x_7+x_9+x_{11}$	-113.054	$x_1+x_3+x_4+x_7+x_8+x_9+x_{11}$	-104.430	$x_2+x_4+x_6+x_7+x_8+x_9+x_{11}$	-116.141
$x_1+x_2+x_3+x_5+x_8+x_9+x_{11}$	-114.666	$x_1+x_3+x_5+x_6+x_7+x_8+x_9$	-131.944	$x_3+x_4+x_5+x_6+x_7+x_8+x_9$	-131.302
$x_1+x_2+x_3+x_6+x_7+x_8+x_9$	-130.866	$x_1+x_3+x_5+x_6+x_7+x_9+x_{11}$	-106.473	$x_3+x_4+x_5+x_6+x_7+x_9+x_{11}$	-105.859
$x_1+x_2+x_3+x_6+x_7+x_9+x_{11}$	-115.607	$x_1+x_3+x_5+x_6+x_8+x_9+x_{11}$	-116.015	$x_3+x_4+x_5+x_6+x_8+x_9+x_{11}$	-115.168
$x_1+x_2+x_3+x_6+x_8+x_9+x_{11}$	-119.485	$x_1+x_3+x_5+x_7+x_8+x_9+x_{11}$	-104.730	$x_3+x_4+x_5+x_7+x_8+x_9+x_{11}$	-104.008
$x_1+x_2+x_3+x_7+x_8+x_9+x_{11}$	-115.421	$x_1+x_3+x_6+x_7+x_8+x_9+x_{11}$	-102.455	$x_3+x_4+x_6+x_7+x_8+x_9+x_{11}$	-103.534
$x_1+x_2+x_4+x_5+x_6+x_7+x_9$	-129.706	$x_1+x_4+x_5+x_6+x_7+x_8+x_9$	-131.299	$x_3+x_5+x_6+x_7+x_8+x_9+x_{11}$	-102.334
$x_1+x_2+x_4+x_5+x_6+x_8+x_9$	-146.373	$x_1+x_4+x_5+x_6+x_7+x_9+x_{11}$	-106.369	$x_1+x_2+x_3+x_4+x_5+x_6+x_7+x_9$	-129.286
$x_1+x_2+x_4+x_5+x_6+x_9+x_{11}$	-113.847	$x_1+x_4+x_5+x_6+x_8+x_9+x_{11}$	-115.552	$x_1+x_2+x_3+x_4+x_5+x_6+x_8+x_9$	-145.492
$x_1+x_2+x_4+x_5+x_7+x_8+x_9$	-128.002	$x_1+x_4+x_5+x_7+x_8+x_9+x_{11}$	-104.674	$x_1+x_2+x_3+x_4+x_5+x_6+x_9+x_{11}$	-114.160
$x_1+x_2+x_4+x_5+x_7+x_9+x_{11}$	-112.768	$x_1+x_4+x_6+x_7+x_8+x_9+x_{11}$	-102.314	$x_1+x_2+x_3+x_4+x_5+x_7+x_8+x_9$	-127.618
$x_1+x_2+x_4+x_5+x_8+x_9+x_{11}$	-114.187	$x_2+x_3+x_4+x_5+x_6+x_7+x_9$	-129.694	$x_1+x_2+x_3+x_4+x_5+x_7+x_9+x_{11}$	-112.872
$x_1+x_2+x_4+x_6+x_7+x_8+x_9$	-130.182	$x_2+x_3+x_4+x_5+x_6+x_8+x_9$	-146.448	$x_1+x_2+x_3+x_4+x_5+x_8+x_9+x_{11}$	-114.427
$x_1+x_2+x_4+x_6+x_7+x_9+x_{11}$	-115.236	$x_2+x_3+x_4+x_5+x_6+x_9+x_{11}$	-114.505	$x_1+x_2+x_3+x_4+x_6+x_7+x_8+x_9$	-129.735
$x_1+x_2+x_4+x_6+x_8+x_9+x_{11}$	-118.767	$x_2+x_3+x_4+x_5+x_7+x_8+x_9$	-127.983	$x_1+x_2+x_3+x_4+x_6+x_7+x_9+x_{11}$	-115.302
$x_1+x_2+x_4+x_7+x_8+x_9+x_{11}$	-115.073	$x_2+x_3+x_4+x_5+x_7+x_9+x_{11}$	-113.064	$x_1+x_2+x_3+x_4+x_6+x_8+x_9+x_{11}$	-118.899
$x_1+x_2+x_5+x_6+x_7+x_8+x_9$	-128.145	$x_2+x_3+x_4+x_5+x_8+x_9+x_{11}$	-114.750	$x_1+x_2+x_3+x_4+x_7+x_8+x_9+x_{11}$	-115.128
$x_1+x_2+x_5+x_6+x_7+x_9+x_{11}$	-113.926	$x_2+x_3+x_4+x_6+x_7+x_8+x_9$	-130.167	$x_1+x_2+x_3+x_5+x_6+x_7+x_8+x_9$	-127.751
$x_1+x_2+x_5+x_6+x_8+x_9+x_{11}$	-116.354	$x_2+x_3+x_4+x_6+x_7+x_9+x_{11}$	-115.548	$x_1+x_2+x_3+x_5+x_6+x_7+x_9+x_{11}$	-114.005
$x_1+x_2+x_5+x_7+x_8+x_9+x_{11}$	-113.845	$x_2+x_3+x_4+x_6+x_8+x_9+x_{11}$	-119.373	$x_1+x_2+x_3+x_5+x_6+x_8+x_9+x_{11}$	-116.519
$x_1+x_2+x_6+x_7+x_8+x_9+x_{11}$	-116.228	$x_2+x_3+x_4+x_7+x_8+x_9+x_{11}$	-115.359	$x_1+x_2+x_3+x_5+x_7+x_8+x_9+x_{11}$	-113.911
$x_1+x_3+x_4+x_5+x_6+x_7+x_9$	-133.534	$x_2+x_3+x_5+x_6+x_7+x_8+x_9$	-128.125	$x_1+x_2+x_3+x_6+x_7+x_8+x_9+x_{11}$	-116.261
$x_1+x_3+x_4+x_5+x_6+x_8+x_9$	-151.915	$x_2+x_3+x_5+x_6+x_7+x_9+x_{11}$	-114.216	$x_1+x_2+x_4+x_5+x_6+x_7+x_8+x_9$	-127.197
$x_1+x_3+x_4+x_5+x_6+x_9+x_{11}$	-119.532	$x_2+x_3+x_5+x_6+x_8+x_9+x_{11}$	-116.892	$x_1+x_2+x_4+x_5+x_6+x_7+x_9+x_{11}$	-113.703
$x_1+x_3+x_4+x_5+x_7+x_8+x_9$	-131.679	$x_2+x_3+x_5+x_7+x_8+x_9+x_{11}$	-114.111	$x_1+x_2+x_4+x_5+x_6+x_8+x_9+x_{11}$	-115.996
$x_1+x_3+x_4+x_5+x_7+x_9+x_{11}$	-107.974	$x_2+x_3+x_6+x_7+x_8+x_9+x_{11}$	-116.513	$x_2+x_3+x_4+x_5+x_6+x_7+x_8+x_9$	-127.174
$x_1+x_3+x_4+x_5+x_8+x_9+x_{11}$	-117.103	$x_2+x_4+x_5+x_6+x_7+x_8+x_9$	-127.557	$x_1+x_2+x_3+x_4+x_5+x_6+x_7+x_8+x_9$	-126.823

DISCUSSION

The present investigation was carried out with the eleven quantitative characters viz, days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD), number of pods per plant (NPPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and seed weight per plant (SWPP) in two consecutive years in four irradiation doses. Analyses were done for variability, heritability, genetic advance, genetic advance as percentage of mean, correlation, path-coefficient and selection index.

In the analysis, the replication item (R) was highly significant for NPBMF, NSBMF, PHMF, PWFD, NPPP, PdWPP, NSPP and SWPP, while for 1000-SW it was significant at 5% level only and for DMF and RWFD it was non-significant.

In the analysis of variance the line (L) item was significant for all the characters when tested against within error. Again it was significant (at 5% and 1% level) for all the characters except DMF which showed non-significant value when tested against pooled error. These results indicated that genotypes were significantly and genetically different from each other and it justifies their inclusion in the present investigation as materials. Similar result was obtained by Mahmood-ul-Hasan *et al.* (2003) and Pervin *et al.* (2007) in blackgram; Deb and Khaleque (2009) and Ali *et al.* (2009) in chickpea; Azad (2008), Younis *et al.* (2008), Azizi *et al.* (2010); Salehi *et al.* (2007) and Abdipur *et al.* (2011) in lentil and Samad (1991) in rapeseed and Nahar (1997) in sugarcane. The dose item (D) was highly significant for PdWPP, NSPP and SWPP and just significant (at 5% level) for 1000-SW, and non-significant for DMF, NPBMF, NSBMF, PHMF, PWFD, RWFD and NPPP when tested against within error and pooled error. Significant differences among the doses for most of the characters indicated that the four doses included in the analysis were different from each other.

Similar results were obtained by Azad (2008) in lentil; Nahar (1997) in sugarcane and Deb (2002) in chickpea.

The L×D interaction was highly significant for PHMF and 1000-SW, where it was significant for DMF and RWFD when tested against both within error and pooled error. The interaction item was non-significant for NPBMF, NSBMF, PWPP, NPPP, PdWPP, NSPP and SWPP. The significance of this item indicated that there was evidence of L×D interaction in the present investigation. These results also indicated that the lines significantly interacted with the doses. Similar results were obtained by Bicer and Sarker (2004) and Azad (2008) in lentil and Nahar (1997) in sugarcane. The non-significant L × D indicated that genotypes (lines) and doses did not interacted significantly. Hasan (2001) in chickpea obtained similar results.

The year (Y) item was highly significant for all the characters except 1000-SW, where it was non-significant. The interaction L × Y was non-significant for all the characters except RWFD where it was significant at 5% level and also in case of 1000-SW it was significant both at 5% and 1% level when tested against within error and pooled error. Significant L × Y indicated that the genotype (L) interacted with the year. Nahar (1997) obtained similar result in sugarcane; Deb (2002) in chickpea and Azad (2008) in lentil. On the other hand, the interaction item D × Y was non-significant for all the characters except RWFD when tested against both within error and pooled error. Non-significant D × Y item indicated that year did not interacted with doses. Similar result was obtained by Deb (2002) in chickpea and Azad (2008) in lentil. The second order interaction, L × D × Y was non-significant for all the characters except DMF where it was highly significant when tested against both within error and pooled error. Non-significant values of this interaction indicated that genotypes (L), Dose (D) and Year (Y) did not interact among themselves. This result was in agreement with the findings of Hasan (2001); Tomar *et al.* (1982); Arshad *et al.* (2002); Bakhsh *et al.* (2006); Deb (2002) in chickpea.

The different components of variation varied differently in different characters. Phenotypic component of variation (σ^2_p) was higher than that of genotypic (σ^2_g) and interactions (σ^2_{LD}, σ^2_{DY}, σ^2_{LY}, σ^2_{LDY}) components of variations. These results are in conformity with the findings of Samad (1991) in rapeseed; Nahar (1997) in sugarcane; Deb (2002) in chickpea; Azad (2008) and Abdipur *et al.* (2011) in lentil; Majid *et al.* (1982) in blackgram and Ara (2010) in onion..

The difference between phenotypic and genotypic variation were greater in magnitude for DMF, PWFD, NPPP, PdWPP and NSPP which indicated that the environment had considerable effects on these characters. These results are in agreement with the findings of Mohamed *et al.* (1991), Nahar and Khaleque (1996) and Nahar (1997) in sugarcane; Deb (2002) in chickpea and Azad (2008) in lentil. In the present materials, high genotypic value causes high phenotypic value. Larger genotypic value for any character is always helpful for effective selection. These results are in agreements with the findings of Mian and Awal (1979) in sugarcane; Deb (2002) in chickpea and Azad (2008) in lentil.

The pronounced environmental variation indicated that greater portion of the phenotypic variation was environmental in nature. Chandra (1968) reported in gram that variability was affected by environment. Similar results were also obtained in chickpea by Deb (2002) and Azad (2008) in lentil. The character NSPP also showed the highest values for σ^2_D, σ^2_Y and σ^2_L component of variation which indicated better scope for the development of these characters through selection. On the other hand, σ^2_{LY} and σ^2_{LD} showed the highest value for 1000-SW and σ^2_{DY} showed the highest value for PWFD and σ^2_{LDY} showed the highest value for DMF. Again σ^2_p, σ^2_g, σ^2_Y and σ^2_L for NPBMF; σ^2_D, and σ^2_{LDY} for PWFD; σ^2_{LY} and σ^2_{DY} for NSPP and σ^2_{LD} for DMF showed the lowest values in the present materials indicating difficulties in improvement of these traits through selection.

In the analysis, phenotypic coefficient of variability was greater than that of genotypic and all other coefficient of variabilities except ECV for PWFD. Similar

observation found by Samad (1991) in rapeseed; Nahar (1997) in sugarcane; Deb (2002) in chickpea; Azad (2008), Younis *et al.* (2008) and Abdipur *et al.* (2011) in lentil; Alam *et al.* (2004) in rice and Pervin *et al.* (2007) in blackgram. According to Shaha *et al.* (1981) with high value of genotypic and phenotypic coefficient of variabilities. These are the good scopes for the improvement of characters through selection. The difference between PCV and GCV were greater in magnitude for DMF, NSBMF, PWFD, NPPP, PdWPP and NSPP which indicated that environment had considerable effects on these characters. These results are in agreement with the findings of Singh and Sharma (1984); Podder (1993) and Deb (2002). The highest amount of PCV, GCV, and DCV were observed for NSPP; the highest value of YCV, L × DCV, D × YCV and ECV were recorded for PWFD; the highest value of L × YCV for 1000-SW and the highest value of L × D × YCV were observed for DMF, which indicated wide scope of selection for these traits.

Again, PCV and ECV the lowest values were shown by the components like NPBMF; GCV and L × DCV exhibited lowest value fro DMF; DCV and L × D × YCV for PWFD; L × YCV and D × YCV for NSPP and YCV for 1000-SW. These results are in conformity with the results of Singh *et al.* (1981) in mustard; Main and Awal (1979), Podder (1993) and Nahar (1997) in sugarcane; Deb (2002) in chickpea and Azad (2008) in lentil. Although GCV is an indicative of the presence of high degree of genetic variation, the amount of heritable portion of variation can be determined with the help of heritability estimates coupled with genetic advance (Punia *et al.*, 2011).

On an overall basis the heritability estimates in the present investigation was found to be low. Among these the high heritability was observed for 1000-SW. The lowest values of heritability indicated that there is preponderance of non additive gene action and recombinant breeding may thus be useful. Becer and Sarker (2004) found low heritability for biological yield per plant, seed yield per plant, number of pods per plant and number of seeds per plant in lentil. Podder (1993) observed low heritability for MCC and Nahar (1997) got low heritability for TC and MCC in sugarcane. Deb

(2002) also obtained low heritability for the nine yield and yield contributing characters (DFF, NPBFF, NSBFF, PWH, NPd/P, PdW/P, NS/P and SW/P) in chickpea. However, heritability alone does not provide indication of amount of genetic progress that would result from selecting the best individuals. Johnson *et al.* (1955), Ramanujam and Thirumalachar (1967) and Singh *et al.* (1981), Punia *et al.* (2011) suggested that heritability estimate with genetic gain are more useful for effective improvement than heritability alone in predicting the resultant effect for selecting the best genotype for a given trait. In the present materials, comparatively high value of heritability (h^2_b) with high genetic advance (GA) and genetic advance expressed as percentage of mean (GA%) were observed for NPPP and 1000-SW indicating that these traits were under the additive genetic control and simple selection for improvement of such characters would be rewarding. Different workers obtained high to moderate values for h^2_b, GA and GA% for different characters in different crops viz, Khatun (1997) for PHMF in lentil, Kabir (1997) for 100-SW in lentil and Deb (2002) for DFF and NS/P in chickpea; Younis *et al.* (2008) for grain yield, harvest index and days to maturity in lentil; Punia *et al.* (2011) for days to flowering and plant height in lentil; Rasheed *et al.* (2008) for harvest index, biological yield and 1000-seed weight in lentil.

Low heritability and low genetic advance were also observed by Longanathan *et al.* (2001) for days to flowering, plant height, number of branches per plant, pod length and 100-seed weight in green gram; by Noor *et al.* (2003) in chickpea; by Pervin *et al.* (2007) for most of the characters in blackgram.

The results of the present study revealed that the studied characters are quantitative in nature and are under polygenic control because they showed wide range of phenotypic and genotypic coefficient of variabilities. Therefore, the genetic progress may be achieved with the effective selection of these characters. The characters NSPP, NPPP, PWFD and 1000-SW showed the higher values for σ^2_p, σ^2_g, PCV and GCV, provided environmental factors are to be controlled as for as possible as low heritability was observed in these materials in maximum characters.

Correlation studies done in the present work showed that genotypic correlations were higher than the respective phenotypic correlation in most of the characters. This situation was also marked in the path–coefficient analysis. The high genotypic correlation, indicating the strong inherent association between pairs of characters dose not always reflects nature and magnitude of phenotypic variation indicating an apparent association due to genetic reason. Higher magnitude of genotypic correlations than phenotypic one were also found by several workers (Gupta, 1972 in Rye; Ramana Rao *et. al.*, 1974 in chilli; Khaleque, 1975 in rice; Kumar *et. al.* 1988 in mustard; Nahar 1997 in sugarcane and Husain *et. al.* 1997 in chilli; Sharma, 1999 in lentil; Younis *et al.*, 2008 in lentil; Sharma and Saini, 2010 and Ali *et al.*, 2009 in chickpea). The low phenotypic correlation due to modifying effect of environment on association of characters at genotypic level was reported by Salehuzzaman *el al.* (1979).

In the present investigation, SWPP showed positive significant correlation with NPBMF, NSBMF and highly positive significant correlation with NPPP, PdWPP and NSPP at genotypic level and in phenotypic level SWPP showed positive and highly significant correlation with NPPP, PdWPP and NSPP. Above information indicated that these characters are genetically related with SWPP more than those of the other yield components. The highly significant positive correlation of SWPP with NPPP, PdWPP and NSPP at both the genotypic and phenotypic levels indicated the effectiveness for directional selection for genetic improvement of chickpea yield and suggested that with the increase of NPPP, PdWPP and NSPP, SWPP will also be increased. Similar result obtained by several workers such as Erman *et al.* (1997); Guler *et al.* (2001); Ciftci *et al.* (2004) stated that positive and significant relationship were found between seed yield and number of pods plant^{-1} and harvest index. Talebi *et al.* (2007) observed high and positive relation between the number of pods plant-1 and seed yield (r = 0.5**) which was similar to the result of Gular *et al.* (2001) and Singh *et al.* (1990).

Ghafoor *et al.* (1990) also reported positive and highly significant correlation between number pods per plant and yield per plant. Biabani *et al.* (2011) observed that seed yield had a highly significant positive correlation with seed numbers and significant positive correlation with plant height and dry weight. Abdipur *et al.* (2011) found that seed yield was associated positively ($p>0.01$) with yield contributing characters like plant height, no. of branches per plant, no. pods per plant, no. seeds per plant and 1000-SW. Significant and positive relation between seed yield and seed number and harvest index was also obtained by Yucel *et al.* (2006) and Yucel and Anlarsal (2010). Similarly Singh and Singh (1989); Kumar and Arora (1991); Erman *et al.* (1997) showed positive significant relationship between seed yield and number pods per plant and also negative relationship between seed yield and 1000-seed weight. Ferdous *et al.* (2010) found that grain yield per plant was positively and significantly correlated with grains per spike, 100-grain weight and harvest index. Togay *et al.* (2008) also observed positive significant relationship between seed yield and number of branches, number of pods per plant, biological yield and 1000-SW. Ali *et al.* (2009) found that grain yield per plant had significant genotypic and highly significant phenotypic relationship with primary branches, pods plant^{-1}, seeds plant^{-1}, seeds pods^{-1} and total biological yield. Sharma and Saini (2010) revealed that yield per plant exhibited highest significant positive association with number of pods per plant. Younis *et al.* (2008) observed that biological yield, 100-SW and harvest index also had positive and highly significant genotypic and phenotypic correlation with seed yield. Roy *et al.* (2006) observed significant positive correlation of seed yield with pods per plant and seeds per pods.

To determine the linear relations among components affecting yield was insufficient to determine selection in chickpea breeding. Also, it was essential that the amount of direct and indirect effect of the causal components on the effect components were determined. A path-coefficient, measuring the direct as well as indirect effects of one variable through another on the end product, was worked out separately for each set of data at phenotypic and genotypic levels. At genotypic level the highest positive direct effect was observed for NSPP followed by PdWPP, 1000-

SW, RWFD, NSBMF and DMF and the rest of characters showed negative direct effect. In case of phenotypic level the highest positive direct effect was expressed by NSPP on SWPP and it was followed by 1000-SW, NSBMF, DMF, RWFD, PHMF, PdWPP, NPBMF, NPPP. Only PWFD showed negative direct effect. Similar results were obtained by several workers in different crops, like Khaleque *et al.* (1977) in rice, Togay *et al.* (2008) in pea; Deb (2002), Ali *et al.* (2009), Talebi *et al.* (2007), Sharma and Saini (2010), Yucel and Anlarsal (2010) and Ciftci *et al.* (2004) in chickpea; Younis *et al.* (2008) and Abdipur *et al.* (2011) in lentil; Ferdous *et al.* (2010) in wheat; Roy *et al.* (2006) in Bush bean; Khan (2009) in potato and Ara (2010) in onion.

From the result it revealed that the main reason for strong direct effect of number of seeds per plant was due to the strong positive correlation of this character with seed yield at both genotypic and phenotypic levels. The relationship between correlation and direct positive effect was at conformity with the findings of Talebi *et al.* (2007), Sharma and Saini (2010), Yucel and Anlarsal (2010) and Ciftci *et al.* (2004) in chickpea; Togay *et al.* (2008) in pea and Younis *et al.* (2008) in lentil.

It was observed that the highest indirect contributions were exhibited by DMF, NPBMF, NSBMF, PHMF, PWFD, NPPP and PdWPP on seed yield via NSPP at genotypic level and at phenotypic level NSBMF, NPPP and PdWPP showed highest indirect effect on seed yield via NSPP. Similar observations are made by Talebi *et al.* (2007), Erman *et al.* (1997), Singh *et al.* (1995), Yousefi *et al.* (1997), Noor *et al.* (2003) and Yucel *et al.* (2006) in chickpea.

Genetic improvement in chickpea is mainly focused on seed yield by breeders. Yield and yield components are strongly affected by biotic and abiotic factors. The residual effect at genotypic level was 0.0639 and phenotypic level was 0.7793. According to Yucel and Anlarsal (2010) 78.7% residual effect indicates that there were many other factors than these included in the present study affecting seed yield. In this manner, the path-coefficient was calculated by using seed yield as a dependant variable. While Roy *et al.* (2006) found that residual effect was low (0.251) which

indicated that about 75% of the variability in seed yield was contributed by the plant characters studied. This residual effect towards seed yield in the present study might be due to other factors of the environments.

Yield is a complex character which depends upon the action and interaction of yield contributing characters and is highly influenced by many genetic factors as well as environmental fluctuations (Choudhury and Joshi, 1996; Singh and Khan, 1998; Paul *et al.*, 1976; Nasker *et al.*, 1982; Uddin, 1983 and Uddin *et al.*, 1985; Simth, 1936). Thus direct selection for yield may be misleading. Nevertheless, to ensure the high yield, selection index is an effective approach in plant breeding programme. In this connection, the multiple selection criteria based on the selection index for most of the contributing characters to yield would be the most effective. Index selection is superior to improving yield alone.

In selection breeding experiments, a breeder generally comes across the problem of selecting a component character or characters which will give a high genetic gain through selection. For this purpose, considering the importance of selection index in improving economic characters, several workers worked on different crops and constructed selection model using discriminant function, (such as Balyan and Verma, 1985; Raut and Khorgade, 1989; Zhu *et al.*, 1991; Collaku, 1994; Agarwal *et al.*, 2001; Saifuzzaman, 2003; Parth *et al.*, 1988; Singh *et al.*, 1991; Singh and Singh, 1974; Khaleque, 1975; Joarder *et al.*, 1978; Samad, 1991; Nahar, 1997; Husain, 1997; Kumar *et al.*, 1988; Zuberi and Eunus, 1972; Salehuzzaman and Joarder, 1979; Deb, 2002; Khan, 2009 and Ara, 2010).

When individual characters were judged separately (table 25) the highest and positive expected genetic gain was observed for NPBMF followed by SWPP, RWFD, NSBMF and PdWPP. The highest genetic gain NPBMF (x_2) as shown individually might be due to the environmental influence on individual character is more than over multiple characters. The negative expected genetic gain reflects that it itself is not a complete characters for higher yield rather it depends on other components characters

for higher yield. Similar result was obtained by Khaleque (1975) in rice; Nahar (1997) in sugarcane and Deb (2002) in chickpea. From the table 25 it was observed that in the combination, which included SWPP gave maximum expected genetic gain. These results are in partial agreement with the findings of Punia *et al.* (1982) in sugarcane and Deb (2002) in chickpea.

It is always preferable to use a discriminant function containing a minimum number of characters which may lead to the maximum genetic advance. In the present study, among all the selection indices, the highest expected genetic gain were obtained when two characters were included in a combination viz, NPBMF + RWFD with a value of 638.460% followed by NPBMF + NSBMF (636.932%) and NPBMF + SWPP (571.392%).

In all the cases two, three, four, five, six and seven characters combinations, the characters like NPBMF, NSBMF and RWFD where common in combination with SWPP gave the maximum expected genetic gain. Therefore, these three yield components may be considered as the primary yield component. In addition, from selection point of view, SWPP will be increased by the improvement of the characters, like NPBMF, NSBMF and RWFD.

It would thus appear that among them NPBMF is the most important character for selection because with yield it gave the highest expected genetic gain and it also showed moderate heritability, significant positive correlation and positive direct effect with both at phenotypic genotypic levels. Nevertheless, to make the selection breeding programme effective with NPBMF emphasis should be given on other yield contributing characters, like PdWPP and NSPP as they showed highly significant positive correlation and high positive direct effect on yield.

SUMMARY

In the present investigation, components of variation, coefficient of variability, heritability, genetic advance, genetic advance as percentage of mean, correlation, path-coefficients and selection index were studied with eight chickpea (*Cicer arietinum* L.) lines in two consecutive years with four doses. In the analysis, eleven agronomical characters viz, days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD), number of pods per plant (NPPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), 1000-seed weight (1000-SW) and seed weight per plant (SWPP) were included.

In the analysis of variance, the significant line item indicated that the lines were genetically different from each other, which justifies the inclusion of them as breeding materials. Significant dose (D) item and its interaction with line (L × D) indicated dose to dose variation and interaction with lines differently. Significant year item and its interaction with line (L × Y) indicated the variation of environment in different years and its interaction with lines differently. The second order interaction L × D × Y was non-significant for all the characters except DMF which revealed that lines, years and doses did not interact among themselves.

Wide range of variation was shown by different component of variation and co-efficient of variability which indicated that the characters are quantitative in nature and are under polygenic control. Therefore, the genetic progress may be achieved with the effective selection of these characters. The characters NSPP, NPPP, PWFD and 1000-SW showed the higher value for σ^2_p, σ^2_g, PCV and GCV which indicated a wide scope of improvement of these traits through selection.

Broad sense heritability (h^2_b) estimates found to be low in maximum cases. The highest value of h^2_b was found for 1000-SW followed by NPBMF, RWFD and NSPP. Genetic advance (GA) and genetic advance as percentage of mean (GA%) were high

for 1000-SW and NSPP. The low heritability and low genetic advance showed that selection may be done with the controlled environment.

In most of the characters, the genotypic correlation was higher than the respective phenotypic correlation. In the present investigation the characters NPPP, PdWPP and NSPP showed positive and highly significant correlation with SWPP both at phenotypic and genotypic levels indicated the effectiveness for directional selection for genetic improvement of chickpea yield and suggested that with the increase of NPPP, PdWPP and NSPP, SWPP will also be increased.

Path coefficient analysis revealed that at phenotypic level the highest positive direct effect was found for NSPP followed by 1000-SW, NSBMF, DMF, RWFD, PHMF, PdWPP, NPBMF and NPPP on SWPP and at genotypic level the highest positive direct effect was observed for NSPP followed by PdWPP, 1000-SW, RWFD, NSBMF and DMF.

In the discriminant function analysis, when individual characters were judged, the character NPBMF showed highest expected genetic gain followed by SWPP and RWFD. The highest expected genetic gain of 638.460 % was observed with two characters combination viz, NPBMF + NSBMF followed by 636.932 % for NPBMF + RWFD and 571.392 % for NPBMF + SWPP. From the result it was observed that NPBMF, NSBMF and RWFD in combination with SWPP gave the maximum expected genetic gain. Therefore, these three yield components may be considered as the primary yield components and improvement of these characters, would likely increase seed yield.

From the result it was concluded that NPBMF is the most important character for selection because with yield it gave the highest expected genetic gain and it also showed moderate heritability, significant positive correlation and positive direct effect with SWPP both at phenotypic and genotypic levels. Nevertheless, to make the selection breeding programme effective with the character NPBMF, emphasis should also be given on other yield contributing characters, like PdWPP and NSPP as they showed highly significant positive correlation and high positive direct effect on yield.

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