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Study of Inheritance Pattern and Selection Index in Chickpea (Cicer Arietinum L.)

Hasan, Md. Tarikul

University of Rajshahi

Ph.D. Thesis

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A Thesis

Submitted to the University of Rajshahi in fulfillment of the requirements for the degree of DOCTOR OF PHILOSOPHY

by

MD. TARIKUL HASAN

December 2014

DECEMBER, 2014
UNIVERSITY OF RAJSHAHI

BIOMETRICAL GENETICS LABORATORY
DEPARTMENT OF GENETIC ENGINEERING AND BIOTECHNOLOGY
UNIVERSITY OF RAJSHAHI
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MD. TARIKUL HASAN
Roll No. 09820
Registration No. 3454
Session: 2009-2010

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Dedicated to My

Parents

Without whose loving care my existence on the earth would be impossible.

DECLARATION

I hereby declare that the whole of the work now submitted as a thesis towards the fulfillment for the degree of Doctor of Philosophy in Genetic Engineering and Biotechnology at the University of Rajshahi, Rajshahi-6205, Bangladesh is the results of my own investigation.

20.12.14
(Professor Dr. Anil Chandra Deb)
Supervisor

20.12.14
(Md. Tarikul Hasan)
Candidate

CERTIFICATION

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

20.12.14

(Professor Dr. Anil Chandra Deb)

Supervisor

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The Author

ABSTRACT

The whole work of the present investigation was carried out under three separate heads, such as part-I consist study of variability, heritability, genetic advance, correlation coefficient, path coefficient and selection index; part-II consist genotype × environment interaction and part-III consist genetic study. Again, part-III i.e. genetic study had been done following three biometrical model viz., genetic study-1 deals with generation mean analysis, genetic study-2 deals with biparental progeny (BIPs) analysis and genetic study-3 deals with triple test cross (TTC) analysis. The thirteen yield and yield contributing characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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 eight chickpea genotypes were taken for the analysis. The experiment was set up during the four consecutive robi seasons of 2009-2010, 2010-2011, 2011-2012 and 2012-2013 at the Botanical Research Field, University of Rajshahi, Rajshahi-6205, Bangladesh.

In part-I, the analysis of variance showed significant differences among the genotypes for all the thirteen studied characters. The phenotypic variation (σ^2_p) was greater than those of other components of variation for all the characters. The highest phenotypic variation was observed for NPd/P followed by NS/P and PWH. It is also noticed that phenotypic coefficient of variability (PCV) in general, was higher than the estimates of genotypic coefficient of variability (GCV) for all the characters. The highest GCV with high PCV were found for NS/P and NPd/P.

The heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GA %) were found to be low for most of the characters.

Regarding correlation coefficient, the most important trait SW/P that is yield per plant exhibited positive association with NPBFF, NPBMF, NPd/P, PdW/P and NS/P both at genotypic and phenotypic levels. The path coefficient analysis had been done based on SW/P as a dependent variable revealed that NS/P had the highest positive direct effect on seed weight, both at genotypic and phenotypic levels. On the other hand, the highest negative direct effect on SW/P was recorded for NPd/P both at genotypic and phenotypic levels but highest positive indirect effect of NS/P nullified its negative effect and finally it turn into positive. In the analysis of descriminant function, it showed that the combination of two attributes viz., NPBFF and NPBMF gave the highest expected genetic gain. Since these two traits exhibited highest genetic gain in the combination of selection index and showed positive correlation with SW/P both at genotypic and phenotypic levels hence considered as primary yield component. However during selection study emphasis may be given on PdW/P and NS/P as they showed high correlation and positive direct effect on seed yield. Considering heritability, genetic advance and positive association with SW/P, trait NPd/P should also be given importance during selection of chickpea trait.

In part-II, genotype × environment (G×E) interaction was carried out according to Freeman and Perkins (1971) model. The results of joint regression analysis exhibited that the mean square due to genotypes were significant for all the traits. All the studied traits except DMF exhibited significant variation due to environmental changes. Combined regression displayed significant values for PHFF, NPBFF, NSBFF, DMF, NPBMF, NPd/P, PdW/P and NS/P in comparison to residual-1. Resedual-1 item in comparison to error was significant for the traits DFF, NSBFF, PHMF and SW/P.

According to Freeman and Perkins (1971) model a desired genotype should be with high mean performance, a nearly unit regression coefficient (b_i=1.0) and non-significant deviation from regression ($\overline{S}^2_{di}$) irrespective of sign. On the basis of the above mentioned criteria the genotype-1 for DFF, NPBFF and DMF; genotype-2 for NSBFF and NPBMF; genotype-3 for NSBFF; genotype-4 for NSBMF; genotype-5 for NPBFF and NPBMF; genotype-6 for NSBMF and SW/P and genotype-7 for NPBFF and NPBMF were considered as stable genotypes. On the other hand, genotype-1 for PHFF and PHMF; genotype-2 for PHMF, NSBMF and SW/P; genotype-3 for DFF, NPBFF, DMF and PHMF; genotype-5 for NSBFF; genotype-6 for DMF, NPBMF and PdW/P and genotype-7 for DMF, NSBMF and SW/P were considered as suitable genotypes for favorable environments.

For the genetic study of chickpea, five different crosses were considered in part-III. Obtained results of genetic study-1 in part-III that is generation mean analysis is performed by Mather's (1949a) scaling test. In this case, scales (C and D) showed significant for most of the characters and crosses. C and D were found to be non-significant for PWH in cross-2; for NSBFF, PHMF and NSBMF in cross-3 and for NPBMF in cross-4 indicated additive-dominance model was adequate for these traits. On the other hand, Cavalli's (1952) joint scaling test showed significant χ^2 values in maximum cases. Non-significant χ^2 values observed for PWH, NPd/P and NS/P in cross-2; for NSBFF and NSBMF in cross-3 and for NPBMF in cross-4. In the present investigation, dominance effect [h] plays a greater role in the inheritance of most of the traits due to their higher magnitude than additive effect [d]. The negative sign of [h] indicated dominance towards decreasing parent. In the present study, most of the characters exhibited duplicate type epistasis. The character PWH in cross-5 exhibited complimentary type of epistasis. Complementary gene action could be successfully exploited in the selection programme. The values of degree of dominance ($\sqrt{H/D}$) for most of the characters in studied crosses showed over

dominance. The number of effective factor i.e. K_1 was found less than one for all the characters and crosses.

Heritability estimates both in broad (h^2_b) and narrow (h^2_n) senses were found to be high in majority cases. Both the high values of broad and narrow sense genetic advance (GA) as well as genetic advance as percentage of mean (GA%) indicated that improvement of these characters is possible through selection. The values of mid-parents (MP) heterosis were non-significant for most of the characters in studied crosses.

Results obtained from the genetic study-2 that is biparental progeny (BIPs) analysis, showed significant difference among the families (crosses) for all the characters except DMF in cross-1; NSBFF and NPd/P in cross-4 and DMF, NPBMF, NPd/P, PdW/P and SW/P in cross-5 which suggests considerable variation among the BIPs families.

In the present investigation, magnitude of additive (D_R) component was higher than that of dominance (H_R) component for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. This result indicated the relative important of additive gene action in the inheritance of these characters. Therefore, selection for these traits which exhibited additive gene action will be very effective. Over dominance for most of the characters and crosses were noted in the present study. The significant regression item in some cases revealed good relationship between biparental progenies and their parents.

Both broad and narrow sense heritability and genetic advance (GA) were low for most of the traits in each cross. In case of NPBFF, DMF, PWH, NS/P and SW/P in cross-1; PHFF, PWH, NPd/P, NS/P and SW/P in cross-2; PHFF, NSBFF and PWH in cross-3; NSBFF, NSBMF, NPd/P and PdW/P in cross-4 and DFF,

NSBFF, NPBMF, NSBMF and NPd/P in cross-5, both heritability and genetic advance in narrow sense were higher than broad sense heritability and genetic advance. This indicated that additive gene action was important in the expression of these traits. Thus additive gene action is a measure of breeding value of a genotype. Hence, for these traits which showed preponderance of additive gene action, reliance should be placed on pure line selection, mass selection and or progeny selection. By comparing total variances of F_2 BIPs, F_2 and $F_2 \times F_1$ generations, it found that the linkage was present in repulsion phage for most of the characters.

Again, in the genetic study-3 that is triple test cross (TTC) analysis; total epistatic effects were found to be non-significant for all the studied traits. But partitioning of total epistasis indicated the involvement of 'i' type (additive × additive) epistasis for DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; NPBFF and NSBFF in cross-3 and for PHFF, DMF, PHMF and NSBMF in cross-5 and involvement of 'j+l' type epistasis for DFF in cross-2; for PHMF, NSBMF and NS/P in cross-3 and for PHFF and NSBFF in cross-4. The magnitude of additive component was higher than that of dominance component for most of the traits. Incomplete dominance was noted for most of the traits in each cross which indicated that the predominant nature of additive genetic component. Both broad sense and narrow sense heritability estimates were found to be moderately high or high for most of the characters. Positive and significant correlation between sums and differences found for NSBFF, PHMF, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF and NSBMF in cross-3 and for DFF and NPBMF in cross-5 indicated that direction of dominance towards decreasing parents while, negative and significant correlation between sums and differences observed for DMF in cross-1; for NPd/P, PdW/P, NS/P and SW/P in cross-2; for PHMF in cross-3 and for DFF in cross-4 indicated the direction of dominance towards increasing parents.

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GENERAL INTRODUCTION

Among the major food crops, legumes (pulses) occupy a unique position in the world agriculture by virtue of their high protein content (23-25%), starch content (60-67%) and capacity of fixing atmospheric nitrogen. Especially in the Asia-Pacific region, particularly South, East and Southeast Asia, pulses as nutritionally rich food, play an important role in improving the diet of the people of these area. To meet the dietary requirements particularly for the poorer section of the society, to whom animal protein is less accessible pulse, is ideal crop. So, pulses bring formidable solution to the alarming problem of protein scarcity of the world. In many of the developing countries, pulses are the major source of dietary protein. Their amino acids pattern is close to the ideal amino gram with rich in lysine content. In fact lysine is the most limiting essential amino acid in cereals, which is very well supplemented by the pulses. Plant proteins have an important advantage over animal proteins – as plants they do not contain cholesterol at all and when they do have fat, it is in the form of unsaturated oil which is better than animal fat.

Bangladesh is mainly the great combined delta of the Ganges, Brahmaputra, and Meghna rivers. It is also a humid, low-lying, alluvial region and one of the world's ten most populated countries and has a predominantly rural population, with over 60% of the workforce engaged in agriculture (van Nes *et al*., 2005). The land of this country is very fertile and produces a great variety of crop. But, in this country the major part of the population suffer from malnutrition, mainly due to deficiency of protein, owing to expensive price of animal protein like meat, fish etc. Among the major food crops in Bangladesh, pulses as nutritionally rich food, play an important role in improving the overall value of cereal-based diets for low and medium income group of the people. Pulses are vital components in diversification of Bangladesh’s largely rice-based cropping system. In accordance to the availability of statistics, the total areas under

different crops as well as different pulse crop cultivation in Bangladesh are presented in the following Figure 1 and Figure 2, respectively.

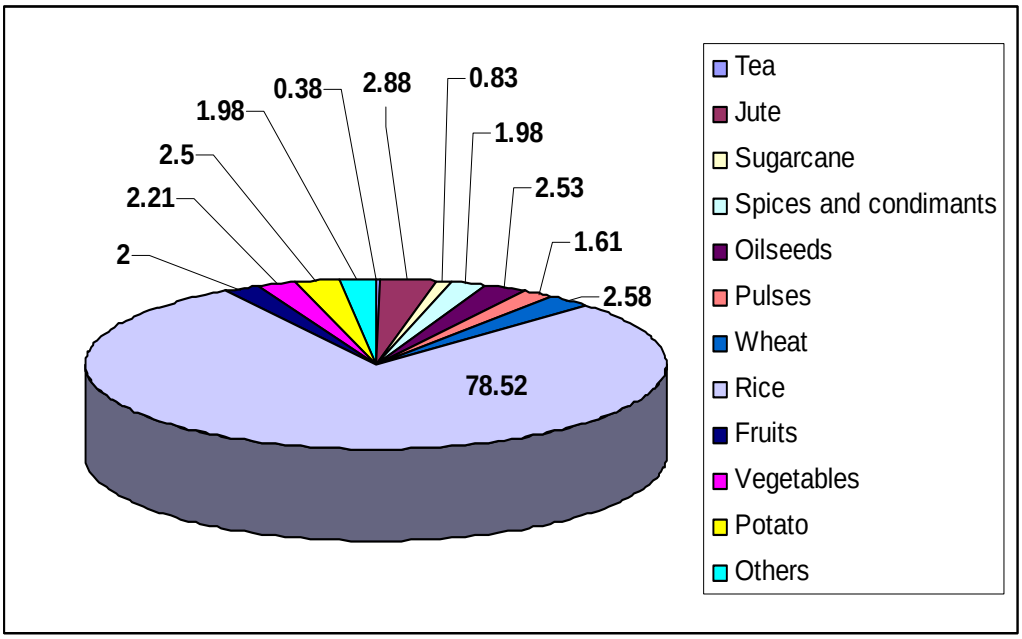


Figure 1. Area under different crop cultivation in Bangladesh, 2009-2010.

Source: Agriculture statistics wing BBS, 2010.

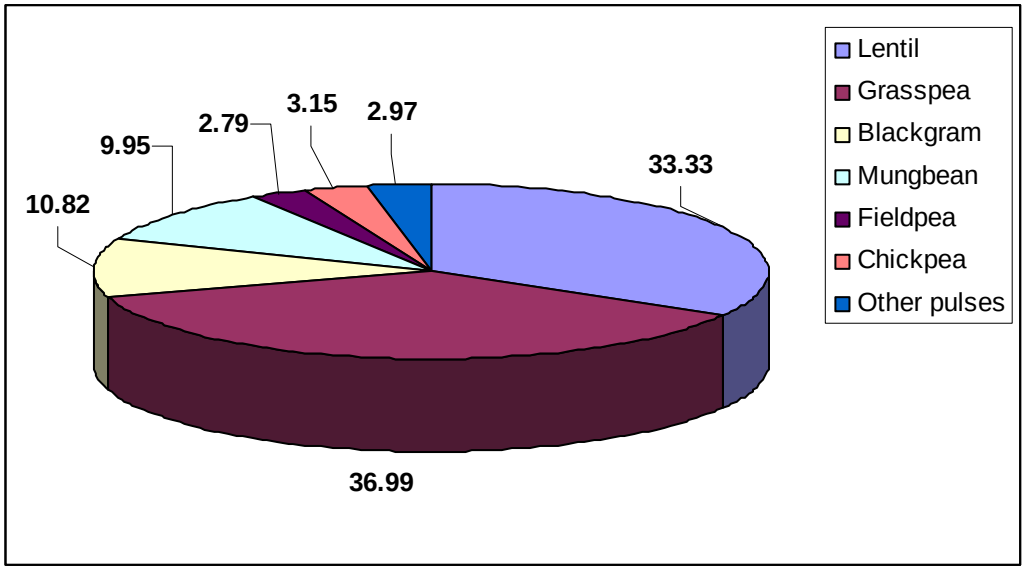


Figure 2. Area under different pulses in Bangladesh, 2009-2010.

Source: Agriculture statistics wing BBS, 2010.

In Bangladesh, a number of summer and winter pulses grow to meet the dietary requirements particularly for the poorer section of the society, to whom animal protein is less reachable. A large number of pulses are grown in Bangladesh. Presently about 1351000 acres are cultivated under pulses. This from is 3.52% of total cultivated land in Bangladesh (Agriculture statistics wing BBS, 2010). The major pulses are grasspea (*Lathyrus sativus* L.), lentil (*Lens culinaris* Medik.), mungbean (*Vinga radiate* L.Wilezek), blackgram (*Vinga mungo* L. Hepper), fieldpea (*Pisum sativum* L.), pigeonpea (*Cajanus cajan* L.) and chickpea (*Cicer arietinum* L.). Among the pulses grown in Bangladesh, chickpea contributes about 20% of the total pulses. Position of chickpea is present in Table 1.

Table 1. The position of chickpea.

Crop	Area (lac ha)	Production (lac ha)	Yield (t/ha)
Grasspea	2.41	2.36	0.98
Mungbean (summar)	1.63	1.50	0.90
Lentil	1.62	2.11	1.30
Blackgram (summar)	0.48	0.48	1.00
Chickpea	0.07	0.10	1.43

Source: Krishi Diary 2012.

Chickpea, an ancient crop of modern times, was first cultivated at least 9500 years ago in the Fertile Crescent, from Turkey to Iran, at the beginning of agriculture (Ladizinsky, 1975). Chickpea cultivation in the Indian subcontinent dates back at least 4000 years. Chickpea is cultivated in nearly 50 countries around the world. Due to its high nutritional value, it is an integral part of the daily dietary system for millions of people. Chickpea dominates international markets over other legume crops and it is traditionally a low-input crop and is grown extensively in the moisture stress environments. Thus, in the cropping intensity in Bangladesh on chickpea should be given more importance. The cropped area as well as production of chickpea has been decline over the past few years in our country mainly because of the increased emphasis on high yielding

variety (HYV) of rice, wheat and other cash crops. The area and yield of different pulses are shown in Figure 3 and Figure 4, respectively.

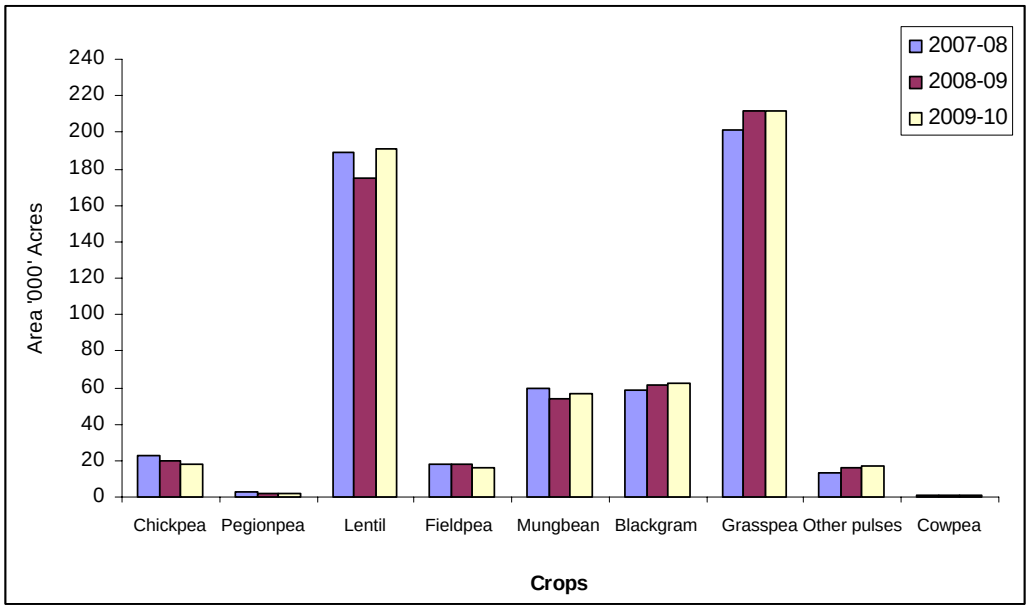


Figure 3. Areas of different pulse crop in Bangladesh.

Source: Agriculture statistics wing BBS, 2010.

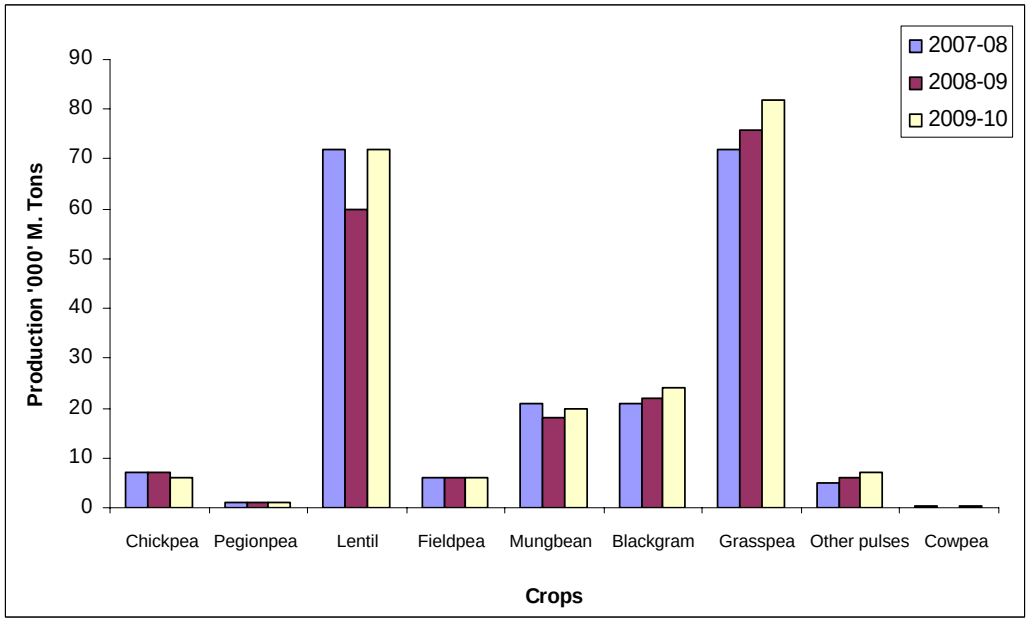


Figure 4. Yield of different pulse crop in Bangladesh.

Source: Agriculture statistics wing BBS, 2010.

Botany

Chickpea originated in southeastern Turkey (Ladizinsky, 1975). Duschak (1871) traced the origin of the word to the Hebrew *'kirkes'*, where *'kikar'* means round. The word *arietinum* is also Latin, translated from the Greek *'krios'*, another name for both ram and chickpea, an allusion to the shape of the seed which resembles the head of a ram (Aries) (van der Maesen, 1987). Chickpea is also called garbanzo (Spanish), hamaz (Arab world), shimbra (Ethiopia), nohud or lablabi (Turkey), chana (India), chola (Bangladesh), pois chiche (French), kichar or chicher (German), and gram or Bengal gram (English). In Turkey, Romania, Bulgaria, Afghanistan, and adjacent parts of Russia, chickpea is called 'nakhut' or 'nohut' (van der Maesen, 1987).

Chickpea (*Cicer arietinum* L.) belongs to genus *Cicer*, The genus *Cicer* L. (Leguminosae, *Cicereae*) comprises 9 annual and 35 perennial species that have a centre of diversity in south-western Asia, with remote, endemic species found in Morocco and the Canary Islands (van der Maesen, 1987). The genus is the member of the monogeneric tribe Cicereae Alef., subfamily Papilionoideae, family Fabaceae (Leguminosae). General information of chickpea as follows:

Table 2. General information of chickpea.

Features	Specification	References
Common name	Gram, Chola (in Bangla)	
Botanical genera	*Cicer*	
Cultivated species	*arietinum*	
Related wild species	*Cicer reticulatum*	
Ploidy level	*Diploid (2x)*	Millan *et al*.(2006)
Chrosome number	2n= 16	Millan *et al*.(2006)
Genome size	740 *Mbp*	Arumuganathan and Earle (1991)

Domestication

Chickpea was domesticated in association with other crops of wheat, barley, rye, peas, lentil, flax and vetch (Harlan, 1971; Abbo *et al*., 2003), and with sheep, goats, pigs and cattle (Diamond, 1997), as part of the evolution of agriculture in the Fertile Crescent 12,000–10,000 years ago (Zohary and Hopf, 1973; Bar-Yosef, 1998). The earliest records of chickpea used as food are: 8th millennium BC at Tell el-Kerkh (Tanno and Willcox, 2006) and Tell Abu Hureyra Syria (Hillman, 1975); 7500–6800 BC at Cayonu Turkey (van Zeist and Bottema, 1972); and 5450 BC at Hacilar Turkey (van der Maesen, 1984).

In the late Neolithic era chickpea spread westwards to modern Greece. By the Bronze Age chickpea had been disseminated widely to Crete in the west, upper Egypt in the south, eastwards through present-day Iraq to the Indian subcontinent, where remains have been found in Harrapan settlements in Pakistan (Vishnu-Mittre and Savithri, 1982) and a variety of sites in Uttar Pradesh and Maharashtra. By the Iron Age, chickpea consolidated its distribution in South and West Asia, and appeared in Ethiopia for the first time. Chickpea is used for both food and medicinal or herbal purposes by Homer in the *Iliad* (1000–800 BC), in Roman, Indian and medieval European literature (van der Maesen, 1972). The crop spread with the cluster of founder crops from the Fertile Crescent into Europe and west-central Asia from the c.5500 BC onwards (Harlan, 1992; Damania, 1998 and Harris, 1998). Chickpea was introduced to the New World by the Spanish and Portuguese in the 16th century AD, and kabuli types moved to India from the Mediterranean via the Silk Road in the 18th century (van der Maesen, 1972). Desi chickpea was probably imported to Kenya by Indian immigrants during the later 19th century (van der Maesen, 1972).

Phylogeny of the Genus *Cicer*

The genus *Cicer* has been traditionally classified into two sub genera (*Pseudononis* and *Viciastrum*) and four sections (*Cicer*, *Chamaecicer*,

Polycicer and *Acanthocicer*) based on morphological traits and geographical distribution (Popov, 1929; van der Maesen, 1972 and 1987). Morphological homoplasy (i.e. life cycle and flower size) and lack of diagnostic synapomorphies hinder sectional monophyly based on morphology in the infrageneric classification of van der Maesen (1972 and1987).

Plant Habit

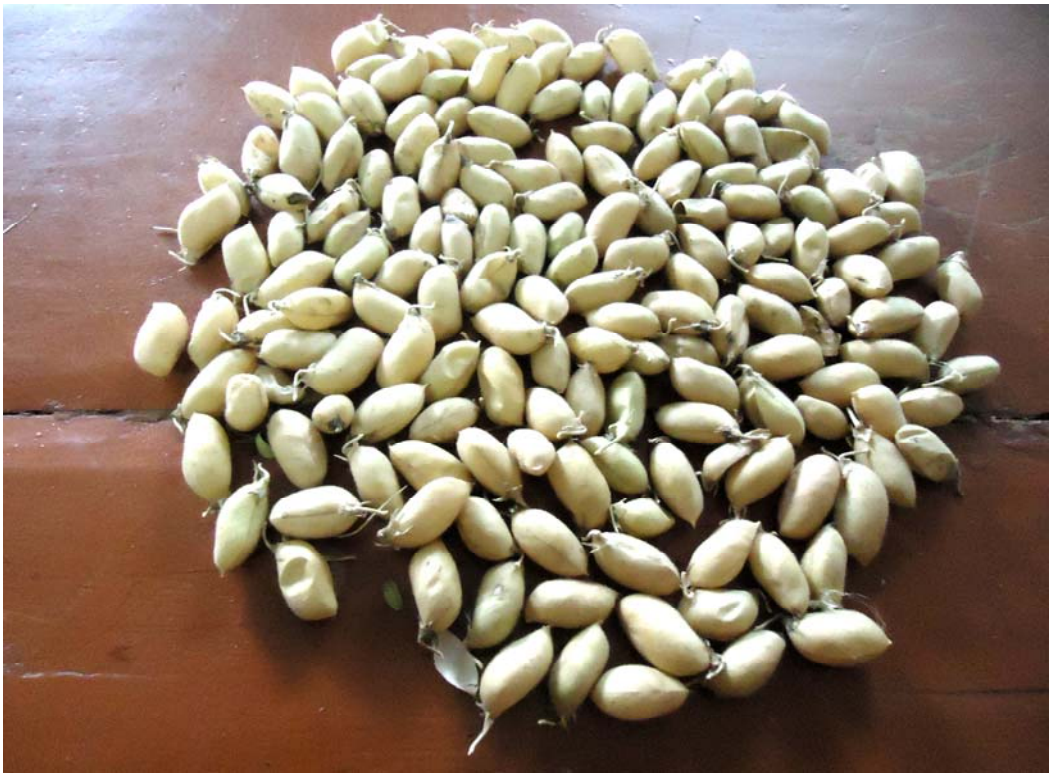
Chickpea is an herbaceous annual plant with plant height ranging 30-80 cm. which branches from the base. It is almost a small bush with diffused, spreading branches. The plant is mostly covered with glandular or non-glandular hairs but some genotypes do not possess hair and also the foliage is covered with glandular hairs which secrete highly acidic exudates and is considered important in conferring tolerance to insect pests, such as pod borer. Leaves are compound, arranged in an alternate phyllotaxy and generally imparipinnate with 11 to 13 leaflets. Flowers are axillary, solitary or in inflorescence of two or three. Flowers are white, pink and purplish in color. The plant has a deep root system and is consider a hardy crop. It produces nodules in common with other legumes and is efficient in fixing atmospheric nitrogen.

Based on seed size and color, cultivated chickpeas are of two types (Cubero, 1975). a). Macrosperma (kabuli type): the seeds of this type are large (100-seed mass >25 g), round or ram head, and cream-colored. The plant is medium to tall in height, with large leaflets and white flowers and contains no anthocyanin while, b). Microsperma (desi type): the seeds of this type are small and angular in shape. The seed color varies from cream, black, brown, yellow to green. There are 2-3 ovules per pod but on an average 1-2 seeds per pod are produced. The plants are short with small leaflets and purplish flowers and contain anthocyanin.

Photograph 1. Macrosperma (kabuli type - BARI Chola-8) type chickpea.

Photograph 2. Microsperma (desi type - BARI Chola-6) type chickpea.

Photograph 3. Mature chickpea plant.



Photograph 4. Harvested chickpea pod.

Chickpea Consumption in Bangladesh and Indian Subcontinent

Traditionally, chickpea is one of the most favoured of all pulses in Bangladeshi society. In Bangladesh and surrounding countries, chickpea serves as food in many ways. After harvesting and threshing, dried seeds of chickpea are used for the preparation of dhal, which has an attractive yellow colour, and is used in various preparations. The cooked dhal, called soopah (soup) in Sanskrit, constituted a common food item. We find it mentioned by Charaka (c. 700 BC), who states that chickpea soup has good food value and that it helps in the recovery from spleen and liver disorders (Vidyalankar, 1994). A common food since the time of the Rigveda (c. 8000 BC) was the 'instant' food sattoo, made by preparing flour from roasted chickpea and barley or wheat, and mixing it in milk or water with some cane jaggery. During the holy month of Ramadan, chickpea are used to make most favoured item *Ghugni* for iftary. During cropping season green leaves are used as a vegetable, fully developed green pods are used in vegetable dishes, rice and pulav and some are roasted with salt. Beside that, chickpea grain has been fed to horses since ancient times. Likewise, seed hulls were fed to cattle, a practice that continues to this day.

Nutritional Value of Chickpea

The World Health Organization (WHO) recognizes the importance of plant foods in the diet, recommending >400g/day consumption of fruits and vegetables, not including tubers (FAO/WHO, 2003). Chickpea and other pulse crops are staple foods in many countries and play an enhanced role in the diets of vegetarians around the world. Pulses are a primary source of nourishment and when combined with cereals, provide a nutritionally balanced amino acid composition with a ratio nearing the ideal for humans. Frequent consumption of pulses is now recommended by most health organizations (Leterme, 2002). Chickpea is a good source of energy, protein, minerals, vitamins, fibre, and also contains potentially health-beneficial phytochemicals. Nutritive value of different pulses with other pertinacious food is illustrated in Table 3.

Table 3. Nutritional value of different pulses with other pertinacious food.

Food staff	Energy (k. cal)	Protein (g)	Fat (g)	Carbohy (mg)	Calcium (mg)	Iron (mg)	Thiamin (mg)	Riboflavin (G)	B-Carotene
Lentil	347.00	24.50	1.40	59.60	154.00	9.10	0.42	0.37	38.00
Blackgram	343.00	25.10	0.60	59.00	69.00	4.80	0.45	0.49	270.00
Mungbean	348.00	24.50	1.20	59.90	75.00	8.50	0.72	0.15	49.00
Chickpea	**372.00**	**20.80**	**5.60**	**59.80**	**56.00**	**9.10**	**0.48**	**0.18**	**129.00**
Grasspea	345.00	28.20	0.60	56.60	90.00	6.30	0.39	0.41	120.00
Rice	356.00	6.40	0.40	79.00	9.00	4.00	0.21	0.09	-
Wheat flour	341.00	12.10	1.70	69.40	48.00	11.50	0.49	0.29	29.00
Wheat	348.00	11.00	0.90	73.90	23.00	2.50	0.12	0.70	25.00
Soybean	432.00	43.20	19.50	20.90	240.00	11.50	0.73	0.76	426.00
Groundnut	567.00	25.30	40.90	26.10	90.00	2.80	0.45	0.13	37.00
Goose egg	181.00	13.50	13.70	0.80	70.00	3.00	0.90	0.26	540.00
Cow milk	67.00	3.20	4.10	4.40	120.00	0.20	0.12	0.19	20.00
Ruhita fish	97.00	16.60	1.40	4.40	650.00	1.00	0.50	0.70	-
Chicken	109.00	25.90	0.60	-	25.00	-	-	0.14	145.00

Source**:** Afzal *et al*., 2003.

Cropping Systems

Chickpea cropping systems and production practices vary from region to region and also within a region. Chickpea is a temperate crop, which has become adapted to sub-tropical condition. This dry land pulse does not like at all excessive moisture in the soil, high humidity and cloudy weather; the crop is mostly grown on conserved moisture on well-drained soils. In Bangladesh, the crop is grown on sandy loam, alluvial to clay loam soils, which are normally well drained. The chickpea can be grown on soil with pH range of 6.0-9.0. However, it is sensitive to salinity and alkalinity. In the traditional chickpea growing areas about 60% to 65% of the crops grown under the aus (rain fed) rice / jute-fallow/chickpea cropping pattern. In this patterns, chickpea sown in early November (mid Kartic) and is harvested by early March (mid Falgune) in southern part of Bangladesh. In the northern districts it is sown in mid November (early Aghrayon) and harvest in last March or early April (mid Chaittra). The remaining 35%-40% is grown under the aman (rainy season) rice-chickpea-fallow cropping pattern under the late sowing condition. The mean yield of chickpea is 1.43 t/hac (Krishi Diary, 2012).

From the above discussion it is clear that chickpea is one of the most important pulses in Bangladesh but it’s per acre yield is low. It is very much neglected and very few works have been done for the improvement of this crop. On this ground chickpea cultivation should be taken with care in the country and high yielding heritable and stable line need to be developed and cultivated to meet up the nutritional needs of our people.

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. The main objective of chickpea research is to grow high yield and high quality crops. Improvement of yield is important in any breeding program. But, the success of breeding program depends on the knowledge of genetic variability of population about the nature and different gene actions governing the various quantitative characters. Although several information of the

genetical work on chickpea are available in the world but it is scanty in Bangladesh. Extensive research efforts are therefore, necessary for the improvement of chickpea crop in our country. So the present investigation has been done on different aspects as follows:

1. To study variability, heritability, genetic advance of the traits for understanding the performance of the traits and genotypes.
2. To study genotypic and phenotypic correlations along with path coefficient and to determined the discriminant function for the construction of a suitable selection index.
3. To study G×E interaction for recognizing better progeny lines.
4. To test the adequacy of additive-dominance model for identifying inheritance pattern.
5. To create heritable variation by means of forced recombination using biparental mating for breaking linkage.
6. To estimate the epistatic effect accurately.
7. To estimate and compare genetic parameters such as gene effects and heritability and also heterosis for some traits in chickpea.

Keeping this view in mind the eight chickpea genotypes were considered and the whole investigation was divided into three parts as follows:

Part I: Deals with variability, correlation, path coefficient and selection index.

Part II: Deals with genotype × environment interaction.

Part III: Deals with genetic study.

PART-I: STUDY OF VARIABILITY, CORRELATION, PATH COEFFICIENT AND SELECTION INDEX

INTRODUCTION

Food legumes are the important source of good quality protein in the diets of people and are valuable as animal feed. Legumes also increase and sustain the productivity of the soil by reducing chance of build-up of diseases, insect pests and obnoxious weeds in rotation with cereals (Zali *et al*., 2011). Pulse crops (food legumes) are the second most planted crops in Bangladesh after rice, reflecting the importance of pulses as a source of protein in Bangladeshi diets. Among the cultivated winter pulses in Bangladesh, chickpea with 17-24% protein, 41-50.8% carbohydrates and high percentage of other mineral nutrients and unsaturated linloeic and oliec acid is one of the most important crops for human consumption (Farshadfar and Farshadfar, 2008). Unfortunately despite its nutritional values, the average yield of chickpea is relatively low in Bangladesh. To improve the yield of this crop, plant breeders are continuously engaged to meet up the demands of an ever increasing population.

The information on nature and extent of variability is an important to make significant genetic improvement in chickpea. Therefore, the magnitude of genetic variability is a precondition for chickpea breeding program, which provides opportunity to a plant breeder or researcher for selecting high yielding genotypes. The estimates of genotypic and phenotypic variances as well as coefficient of variation provide information on the extent of variability. Several researchers such as Saleem *et al*. (2002), Arshad *et al*. (2003a), Pratap *et al*. (2004), Jeena *et al*. (2005), Saleem *et al*. (2005c), Khan *et al*. (2006), Atta *et al*. (2008), Ali *et al*. (2009), Tomar *et al*. (2009), Sharma and Saini (2010), Jivani *et al*. (2013), Sarker *et al*. (2013) and Zeeshan *et al*. (2013) have emphasized the utility of the estimates of genetic variability in chickpea. But genetic variability is uninformative for heritable portion of this variation. Knowledge on the heritability is important to a plant breeder since it indicates the possibility and extent to which improvement is possible through selection. Also

heritability is a parameter of tremendous significance to the breeder as its magnitude indicates the reliability with which genotypes can be recognized through its phenotypic expression. Johanson *et al*. (1955) and Arshad *et al*. (2004) suggested that heritability alone is not a very useful measure but this statistic together with genetic advance is more valuable. Several researchers such as Arshad *et al*. (2003a), Noor *et al*. (2003), Pratap *et al*. (2004), Jeena *et al*. (2005), Sharma *et al*. (2005), Yucel *et al*. (2006), Tomar *et al*. (2009), Sharma and Saini (2010), Srivastava *et al*. (2012) and Sarker *et al*. (2013) have emphasized the utility of the estimates of heritability and genetic advance in the prediction of response of quantitative characters to selection in chickpea.

Moreover, yield the ultimate goal of a breeding program, is very complex character, which is affected by many genetic as well as environmental factors. Hence the breeders need some index character in order to design the selection strategy for indirect selection towards higher yield. An improvement is one character is inheritable with positive or negative changes in another; association studies at genotypic as well as phenotypic level will help the breeder to select the genetic improvement of yield. It is also essential to establishing selection criteria. However, simple correlation coefficient between yield and yield components may not give satisfactory results. Because, the components do not only directly affect the yield, they also affect the yield indirectly by affecting other yield components in negative or positive manner. As a trait has helpful effect on a trait for yield, it can affect some other or all traits negatively (Walton, 1980). Under such situation, the path coefficient analysis helps to determine the direct contribution of these characters and their indirect contribution via other characters (Singh *et al*., 1990). For this reason, many of the studies on correlation and path analysis have been conducted in field crops. Correlation coefficient between yield and yield components and direct and indirect effect of various characters on yield and yield components have been reported by several researchers such as Bakhsh *et al*. (1999), Guler *et al*.

(2001), Narayana and Reddy (2002), Sial *et al*. (2003), Noor *at al*. (2003), Arshad *et al*. (2003a and 2004), Deb and Khaleque (2005), Jeena *et al*. (2005), Saleem *et al*. (2005c), Obaidullah *et al*. (2006), Yucel *et al*. (2006), Bakhsh *et al*. (2006), Khan *et al*. (2006), Renukadevi and Subbalakshmi (2006), Atta *et al*. (2008), Farshadfar and Farshadfar (2008), Ali *et al*. (2009), Tomar *et al*. (2009), Thakur and Sirohi (2009), Vaghela *et al*. (2009), Shahid *et al*. (2010), Sharma and Saini (2010), Yucel and Anlarsal (2010), Akhtar *et al*. (2011), Ali *et al*. (2011), Zali *et al*. (2011), Ali *et al*. (2012), Jivani *et al*. (2013), Mushtaq *et al*. (2013) and Zeeshan *et al*. (2013).

However, the information on the nature and extent of genetic variability present in a population for desirable character, their association and relative contribution to yield comprise the basic requirement of selection desirable genotypes but the discriminant function provides an efficient method for simultaneous selection (Smith, 1936). Thus construction of selection indices will be very helpful to differentiate desirable genotypes. This method have been successfully followed by various scientists in different crops such as Deb and Khaleque (2007) in chickpea, Sarker and Deb (2009) in blackgram, Ferdous *et al*. (2010) in spring wheat, Kumar *et al*. (2012) in rabi sorghum and Sarker *et al*. (2013) in chickpea.

The present investigation was therefore, undertaken to assess the magnitude of genetic variability, heritability and genetic advance to determine the nature and magnitude of correlations among different traits and their direct and indirect effect on seed yield and construction of selection indices in chickpea. Therefore, the available information will be helpful for an efficient selection criterion in selecting the most desirable and high yielding genotype of chickpea.

REVIEW OF LITERATURE

Grain yield in any crop is a complex character and is the final product of many contributory traits and their interaction. The knowledge of these factors and these relationships with each other and with yield provide the basic information on yield improvement. Therefore, for convenient of study and thorough understanding of variability, heritability, correlation coefficient, path coefficient and selection index, the available literature in chickpea has been reviewed as follows.

Saleem *et al*. (1999) worked with a set of twelve elite chickpea lines including one standard to evaluate for grain yield and other related character for path coefficient analysis. Seed yield was positively correlated with all attributes except days taken to flowering. Number of seeds per plant had maximum positive direct effect on yield. Number of pods per plant and plant weight had maximum negative direct effects on seed yield but contributed indirectly through other characters. The study related that selection may be done with optimistic compromise between number of seeds per pod, number of secondary branches per plant, number of seeds per plant, number of pods per plant and plant weight.

Jeena and Arora (2002) evaluated 40 genotypes of chickpea in a randomized experiment for yield and its components traits. Correlations among all the characters computed and subjected to path analysis. Biological yield exhibited highest positive correlations with seed yield coupled with highest positive direct effect on it. Biological yield, pods per plant, 100-seed weight and first pod forming node found to be the major yield contributing traits from selection point of view.

Saleem *et al*. (2002) worked with 20 elite chickpea genotypes. The genotypes showed highly significant difference for all the characters under studied. Seed yield per plant was positively and significantly correlated with days to flower,

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 plants had maximum positive direct effect on seed yield. The other traits in the study also exhibited considerable indirect effect on seed yield through number of pods per plant. It was concluded that number of pods per plants and 100-seed weight could be used as selection criteria to improve the yield.

Arshad *et al*. (2004) conducted the research work to determine variability, heritability, genetic advance, correlation and path coefficient for yield and its components in 24 advance lines of chickpea. High heritability with low genetic advance for days to flowering, days to maturity and 100-seed weight indicating the influence of dominant and epistatic genes for these traits. High heritability for secondary branches and biological yield coupled with high genetic advance reveled that additive gene effect is important in determining these characters. Grain yield had positive and significant correlations 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 emphasis while deciding about selection criteria of genotypes for rainfed conditions.

Ciftci *et al*. (2004) conducted an experiment 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. In this study, seed yield was positively and significantly related with plant height, number of branches, number of pods per plant, biological yield, harvest index and number of seeds per plant. Negative and non-significant relationship was determined between yield and 100-seed weight. According to

path coefficient analysis, they also observed that seed yield was highly influenced by biological yield, harvest index and number of seeds per plant.

Deb and Khaleque (2005) studied correlation, path coefficient in chickpea and found the significant correlation between pod weight per plant and seed weight per plant, number of seeds per plant and seed weight per plant. In path coefficient analysis, number of primary branches at first flower, number of secondary branches at first flower, plant weight at harvests, pod weight per plant and number of seeds per plant to be the most important yield component because these characters exhibited direct positive effect on seed weight per plant both at phenotypic and genotypic levels.

Khan *et al.* (2006) was carried out an investigation using thirteen chickpea cultivars for the magnitude of genetic variability, heritability and genetic advance. All the characters under studied showed significant genetic variability in the analysis of variance. The phenotypic coefficient of variation ranged from 2.23 for number of days to flowering to 15.47 for number of seeds per plant. The genotypic coefficient of variation was relatively low for days to flowering, days to maturity and plant height while it was high for seeds per plant. 100-seed weight and seed yield kg per hectare indicating low environmental impact for these characters. The magnitude of heritability was very high for days to flowering, days to maturity, pods per plant, 100-seed weight and seed yield kg per hectare and moderate for plant height. Genetic advance was high for seed yield kg per hectare followed by number of pods per plant indicating the greater effects of additive gene than the environment. Genotypic, phenotypic and environmental correlations revealed that days to flowering, days to maturity, pods per plant and 100-seed weight were positively correlated with seed yield both at phenotypic and genotypic levels while, plant height was found negatively correlated with seed yield.

Renukadevi and Subbalakshmi (2006) performed correlation and path coefficient for eleven characters including seed yield of fifty chickpea

genotypes during robi season in 2002. In this study, plant height, number of primary branches, number of pods per plant, 100-seed weight, biological yield per plant and harvest index had positive and significant correlation with seed yield. The positive direct effect on seed yield was reveled by plant height, number of primary branches per plant, number of pods per plant, biological yield per plant, harvest index, days to maturity and soluble protein content.

Yucel *et al*. (2006) studied variability, heritability and correlations between yields and its components and path coefficient in chickpea. Genotypic variance was the highest for 1000-seed weight followed by seed number per plant. They observed that the heritability for seed number, 1000-seed weight and number of full pods was greater than those for the other traits. Positive and significant relationship were determined between seed yield per plant with plant height, first pod height, secondary branches, total pods, number of full pods and seeds per plant. They also observed that the traits viz., number of seeds and number of full pods showed the highest direct effect on yield per plant.

Deb and Khaleque (2007) carried out an experiment in chickpea to construction an index for selection and found the maximum genetic gain of 98716.34% exhibited when number of primary branches at first flower, number of secondary branches at first flower, plant height at maximum flower, number of seeds per plant and seed weight per plant were included in the discriminant function. Among these four yield components such as number of seeds per plant and number of primary branches at first flower showed significant phenotypic and very high genotypic correlation with yield, respectively and plant height at maximum flower and number of secondary branches at first flower indicated high direct positive effect, hence these traits may be considered as primary yield components. The second highest genetic gain was noted as 89128.85% when all the characters under study were included in the discrinatnt function. This was followed by 85205.56% genetic gain when all

the characters except number of secondary branches at first flower were included in the discriminant function.

Singh (2007) analyzed correlation coefficient and path coefficient for getting appropriate information regarding interrelationship among different characters for effective selections program in forty five genotypes of chickpea. The genotypic correlation was higher than the corresponding phenotypic ones. Seed yield had highly significant positive correlation with biological yield per plant, pods per plant, harvest index and secondary branches per plant. Biological yield per plant and pods per plant had highly significant correlation with seed yield and its direct effects were very strong. Pods per plant, harvest index, 100-seed mass and secondary branches per plant were indirect contributory components, therefore, due emphasis may be given on these characters for selecting high yielding genotypes in 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 relationship between 100-seed weight and plant height, between number of secondary branches and plant height, between days to heading and days to maturity, between days to maturity and number of primary and secondary branches, between seed yield and number of pods per plant, between seed yield and biomass as harvest index and also found negative and significant relationships between number of pods per plant and 100-seed harvest, between seeds per plant and number of secondary branches. Harvest index had greatest direct effect on seed yield. Also, its indirect effect on seed yield more positive through plant height, number of pods per plant, number of seeds per plant 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.

Ali *et al*. (2008) studied twenty elite chickpea lines for variability and correlation for traits like number of days to flowering, number of days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height and seed yield per plant. Varietals differences among the genotypes were significant. Phenotypic and genotypic variances were higher for plant height and seed yield per plant. Broad sense heritability was the highest for plant height and seed yield per plant. Genetic advance was higher for seed yield per plant and plant height. High heritability for both the traits coupled with high genetic advance revealed that additive genetic effects were important for these characters. Positive genotypic correlation was detected between seed yield and number of primary branches per plant, while at phenotypic association was highly significant.

Farshadfar and Farshadfar (2008) made an experiment to determine the genetic variability among 360 chickpea land races and lines. Among the morphological characters, they observed that numbers of branches and pod numbers showed the higher variation while, leaflet had minimum variation. On the other hand, among the phonological traits the flowering period showed the highest and flowering time showed the least variability. In this study, the seed yield per plant exhibited the highest variation. The highest correlation coefficient observed between seed yield per plant and pod numbers. Path analysis revealed that the pods number, seeds number, 100-seed weight and single seed weight had highest direct effect on seed yield**.**

Ali *et al*. (2009) studied correlation and path analysis in chickpea. The results of correlation analysis reveled that the grain yield per plant had significant genotypic and phenotypic relationship with primary branches, pods per plant, seeds per plant, seeds per pod and total biological yield. The path coefficient analysis based on grain yield per plant, as a dependent variable, exposed that all of the traits, except days to flowering, days to maturity and secondary branches

exhibited positive direct effect. The path analysis confirmed that biological yield followed by number of seeds per plant and 100-grain weight had the maximum positive direct influence on grain yield per plant.

Malik *et al*. (2009) considered twenty chickpea genotypes for various yield parameters under field conditions to estimate correlation coefficient and linkage distance. Analysis of variance of yield and its components revealed significant differences between genotypes for six out of nine traits under studied. Maximum variation was recorded for pods per plant followed by secondary branches per plant, biological yield, grain yield and harvest index. Highly significant and positive correlation of grain yield was found with biological yield, secondary branches and number of pods per plant. Secondary branches were positively correlated with number of pods per plant and grain yield per plant, whereas it was negatively associated with 100-grain weight.

Thakur and Sirohi (2009) investigated correlations and path coefficient analysis in chickpea. Correlations studies indicated that seed yield per plant exhibited stable positive associations with biological yield per plant, pods per plant, primary branches per plant, plant height and harvest index both at genotypic and phenotypic levels in individually as well as combined over season. Path analysis revealed high positive and direct influence of biological yield per plant with seed yield per plant followed by harvest index and pods per plant in individuals as well as combined over the season. Pods per plant, primary branches per plant and plant height contributed to seed yield mainly through indirect effect via biological yield. Therefore, selection for high biological yield and harvest index would be lead to high seed yield and selection for pods per plant, primary branches per plant and plant height would facilitate for high biological yield.

Tomar *et al*. (2009) evaluated forty five genotypes of chickpea during 2004-2005 and 2005-2006 at two different locations under three planting dates. The genotypic and phenotypic coefficient of variation was found maximum for

number of seeds per plant. The high broad sense heritability was recorded for all the traits except days to maturity. The genetic advance as percentage of mean was high for seeds per plant. The genotypic correlation coefficient was observed to be higher than that of phenotypic correlation coefficient indicating the existence of strong inherent association for various traits and phenotypic selection may be rewarded. Grain yield per plant exhibited stable positive association with biological yield per plant, followed by seeds per plant, pods per plant and seeds per pod at genotypic and phenotypic levels.

Khan *et al*. (2010) was carried an investigation for the study of nature and magnitude of genetic variability using forty seven chickpea genotypes. The germplasm was grouped as deshi (pink flower, green with purplish tinge stem and colored seed coat) and kabuli (white flower, green stem and white seed coat) types. Highly significant differences were recorded among the genotypes for days to 50% flowering, days to maturity, leaf area, number of leaflets per leaf, plant height, 100-seed weight, biological yield per plant and grain yield per plant. Grain yield per plant had maximum phenotypic and genotypic coefficient of variation, followed by biological yield per plant. Heritability estimates of all the traits were high except leaf area which showed moderate heritability. Highest heritability was recorded for days to 50% flowering followed by biological yield per plant, plant height, 100 seed weight, grain yield per plant, leaflets per leaf and days to maturity.

Kobraee *et al*. (2010) worked on correlation analysis to detect the relationship between grain yield and other quantitative traits in chickpea. Early planting chickpea produce the highest plant height, distance of first pod from the earth surface, number of sub branch, number of pods per plant, number of seeds per plant, 100-seed weight, grain yield, biological yield and harvest index. Results showed that number of seeds per plant, number of pods per plant, plant height and biological yield had the highest positive

correlation with grain yield. The results of path coefficient analysis revealed that number of seed per plant had high and positive direct effect on seed yield, but number of pods per plant was an important constituent.

Sharma and Saini (2010) studied the genetic variability, heritability, genetic advance, correlation and path analysis in chickpea. Study of variability and heritability 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 development of high yielding genotypes of chickpea.

Yucel and Anlarsal (2010) carried out an experiment to determine selection criteria by using correlation and path coefficient analysis in chickpea. Among the studied characters, positive and significant relationships were found statistically between seed yield and harvest index and between seed yield and seeds number. The path coefficient analysis based on seed yield as a dependent variable revealed that harvest index had the highest direct effect on seed yield. Both correlation and path analysis indicated that harvest index was the major direct contributor to seed yield.

Akhtar *et al*. (2011) studied genetic variability, heritability and interrelationship for seed yield and its components in twenty advance genotypes of chickpea. Significant and positive correlations were found between yield and 100-seed weight and between number of pods per plant and plant height. Heritability for 100-seed weight and number of pods per plant was observed as higher than the other traits. Phenotypic coefficient of variability for days taken to flowering, days taken to maturity, plant height and seed yield was higher than genotypic coefficient of variation which means that the expression of these traits in more influenced by environmental effects. It is therefore, suggested that the grain yield could be improved by using the 100-seed weight and number of pods per plant as selection criterion in chickpea.

Ali *et al*. (2011) conducted an experiment to estimate the correlation for qualitative traits in chickpea. Correlation coefficient studies showed that bio-mass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per plant and 100-seed weight was positive and significant at genotypic level but positive and highly significant at phenotypic level with grain yield per plant. Number of days taken to flowering, number of days taken to maturity, primary branches per plant and secondary branches per plant were positively correlated with grain yield per plant at genotypic as well as phenotypic levels. Plant height was negative and non-significantly correlated with grain yield per pant both at genotypic and phenotypic levels.

Biabani *et al*. (2011) carried out an experiment in order to evaluate the relationship between grain yield and the other characteristics considering two cultivar of chickpea (Hashem and Arman) in determination (0 as control, 7 and 14 days). The experiment was a factorial completely randomized design with 2 factors. At harvest time, height of plant, filled and unfilled pods per plant, number of seeds per plant, plant dry weight and yield were measured. They observed that the yield was highly and positively correlated with filled pod per plant.

Zali *et al*. (2011) studied heritability, correlation and path coefficient in chickpea genotypes. Heritability values were greater for number of days to 50% maturity followed by number of days to 50% flowering, plant height, number of secondary branches, number of primary branches and number of seeds per plant indicating that these traits are controlled mainly by additive genes and that selection of such traits may be effective for improving seed yield. Number of seeds per plant and 100-seed weight had a positive direct effect on seed yield. Number of seed per plant, number of secondary branch, 100-seed weight, number of pods per plant, number of primary branch and plant height also had positive and highly significant phenotypic correlations with seed yield. They concluded that seed yield in chickpea can be improved by selecting an ideotype having greater number of

secondary and primary branches, as well as higher number of pods per plant, number of seeds per plant and 100-seed weight.

Kaloki and Kioko (2012) carried out an experiment at two different locations viz., Kabete (cool environment) and Kiboko (hot environment) to detect the genetic variability and heritability of 110 chickpea genotypes. Significant difference through the ANOVA indicated that there was genetic variability in most of the traits at both sites. Path coefficient analysis showed that number of pods per plant had the highest direct effect on grain yield in both locations. Heritability estimates were high for days to 50% flowering, days to 75% maturity and 100 seed mass hence, these characters can be effectively improved through selection.

Naveed *et al*. (2012) conducted an experiment in chickpea during the crop season of 2008-2009. The high heritability value was found for plant height while, genetic advance was noted for number of pods per plant. Correlation studies showed that the traits like as biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and 100-seed weight were positive and significant both at genotypic and phenotypic levels. Higher direct effect was found for number of days taken to flowering and maturity, biomass per plant and 100-seed weight on grain yield per plant. It was concluded that selection can be made on the basis of these traits.

Jivani *et al*. (2013) studied a set of 105 diverse genotypes of chickpea to estimate correlation and path coefficient analysis for seed yield per plant and its ten component characters. They reported that the seed yield per plant had significant and positive correlation with number of pods per plant, biological yield per plant and harvest index both at genotypic and phenotypic levels. Among the component traits, biological yield per plant had significant and positive association with plant height, number of pods per plant and 100-seed weight. Path coefficient analysis revealed that the maximum positive direct effect was observed for harvest index, followed by biological yield per plant, number of

pods per plant, and 100-seed weight towards seed yield and were considered to be the most promising traits for selection for higher seed yield in chickpea.

Mushtaq *et al*. (2013) carried out an investigation to estimate variability and path coefficient analysis in twenty elite chickpea genotypes including three standards. The material was also evaluated for means and components of variability and interrelationships (genotypic and phenotypic) for yield and yield components. High heritability values were noted for days taken to flowering, days taken to maturity, pods per plant, total weight of plant, secondary branches per plant, plant height, 100-grain weight and grain yield per plant while other characters exhibited moderate heritability. Seed yield was positively correlated with all attributes under study. Investigations regarding path coefficient showed that days taken to flowering had maximum direct influence on seed yield per plant followed by total weight of plant, 100-grain weight, primary branches and plant height.

Padmavathi *et al*. (2013) conducted an experiment with thirty genotypes of *kabuli* chickpea to study the extent of genetic variability, correlation and path analysis for yield and yield contributing characters. They found that wider genetic variability with high heritability and high genetic advance as percentage of mean was recorded for number of primary branches per plant, biological yield per plant and seed yield per plant. Correlation studies revealed that seed yield was significantly and positively correlated with plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, 100-seed weight, harvest index and biological yield per plant. Path coefficient analysis indicated that biological yield per plant, number of pods per plant and harvest index had high positive direct effect on seed yield signifying the importance of these traits in improvement of seed yield.

Sarker *et al*. (2013) studied variability, heritability, genetic advance, genetic advance as percentage of mean and selection index in chickpea applying four

irradiation treatments in two consecutive years. The lines were genetically well differentiated as indicated by the analysis of variance. The characters number of seeds per plant, number of pods per plant, plant weight after fully dried and 1000-seed weight showed the higher values for phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation which indicated a wide scope of improvement of these traits through selection. Estimates of broad sense heritability was found to be low. In the discriminant function analysis, single character indices like number of primary branches at maximum flower showed maximum genetic advance. Again, the highest expected genetic gain of 638.460 % was observed for characters combination viz., number of primary branches at maximum flower with number of secondary branches at maximum flower.

Zeeshan *et al*. (2013) conducted an experiment to estimate genotypic variability, heritability and correlation of 20 chickpea genotypes for yield and its related traits under rainfed conditions. There were significant genetic differences between genotypes for all the characters studied which suggested enormous scope of genotypes selection with desirable characters. High heritability for plant height and 100-seed weight coupled with high genetic advance revealed that additive gene effects were important in determining these traits. High heritability with low genetic advance for days to maturity indicated influence of dominant and epistatic genes. Estimation of correlation coefficient showed that pods per plant, plant biomass and 100-grain weight were positively correlated with grain yield. The traits, which revealed high amount of heritability and genetic advance, were controlled by additive genes, which advocated the chances of their improvement through selection.

MATERIALS AND METHODS

A. MATERIALS

The materials for the present study comprised eight genotypes of chickpea. The materials were collected from Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh.

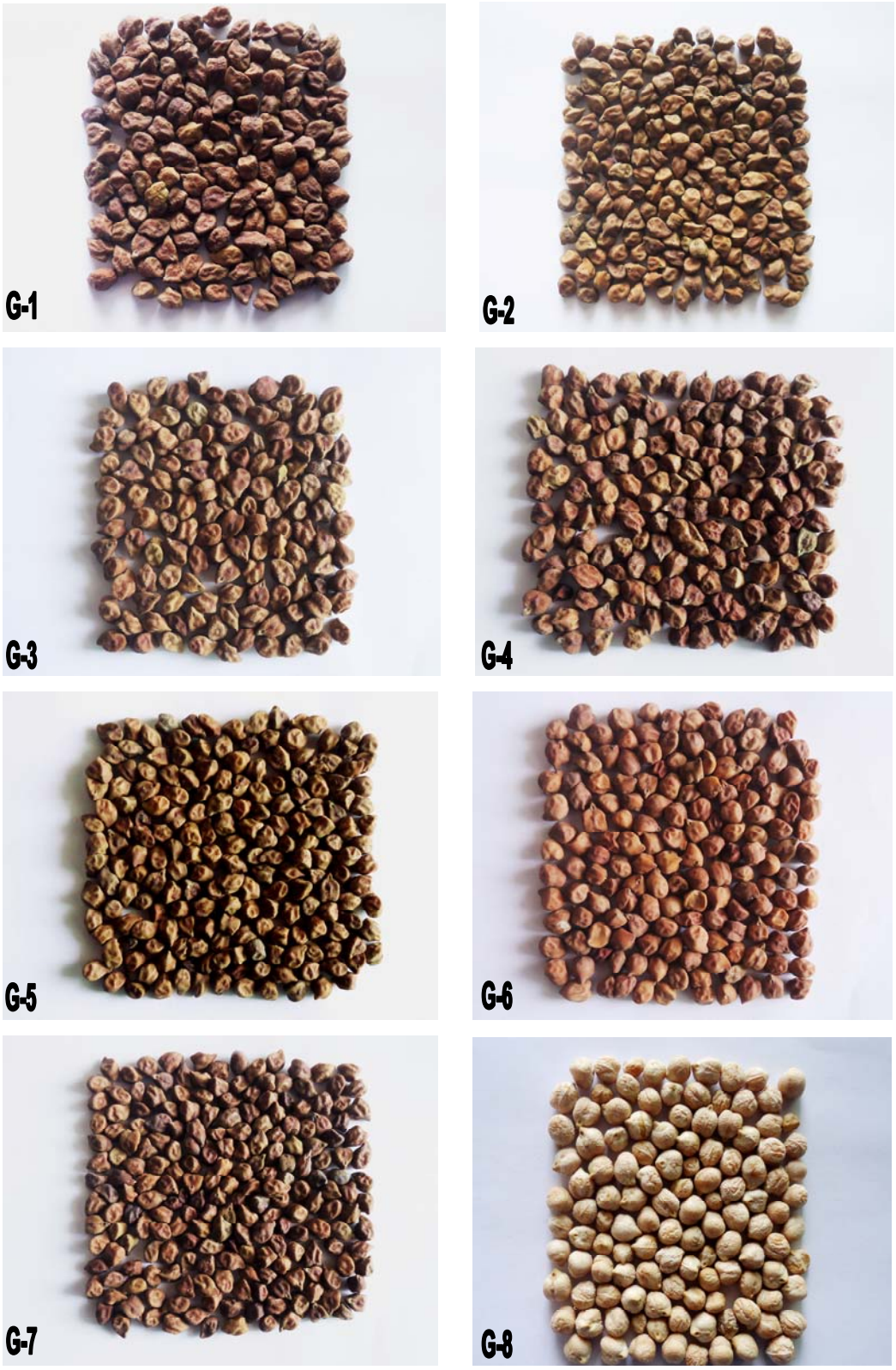
The eight chickpea genotypes are presented in Table 4.

Table 4. List of eight chickpea genotypes.

Sl. No.	Genotypes	Identifying Characteristics
1	BARI Chola-1 ICRISAT line	• Light green leaves with less waxy layer and spreading type canopy. • Absence of stem pigmentation, less nodulation capacity. • Each node contains only one flower and the flowers are light pink. • Seed color is light yellow.
2	BARI Chola-2 ICRISAT line, ICCL-83228	• Semi spreading type and tip of the branch is slender with long internodes. • Plant is green. • Seed size is 40-50% larger than the local variety. • Both sides of the seed are flattery and light brown in color.
3	BARI Chola-3 ICRISAT line, ICCL-83105	• Erect type and light green color. • Leaflets are large. • Seed size is 50-60% larger than the local variety and 40-50% from BARI chola-1. • This variety is specially suitable for the Barind region.
4	BARI Chola-4 ICRISAT line, ICCL-85222	• Two flower and pod in a same peduncle is the main identifying character of this variety. • Semi erect stature and light green color. • Grey color pigmentation presentation is stem. • Both sides of the seed is somewhat flattery, smooth and light brown in color.

Sl. No.	Genotypes	Identifying Characteristics
5	BARI Chola-5 Local Selection (local Cultivar of Pabna)	• Main identifying character of this variety is spread in stature and light green color. • No pigmentation observed at seedling stage but light grey pigmentation observed in the matured stage stem. • Seed size is small and seed coat is grey brown color. • Both sides of the seed are somewhat flattery, smooth.
6	BARI Chola-6 ICRISAT line, ICCL-83149	• Semi spreading type with medium and light green leaflets. • No pigmentation observed in stem at seedling stage but light grey pigmentation observed in the matured stage. • Small seed size, round shaped with deep brown color seed coat. • It is resistant to wilt.
7	BARI Chola-7 ICRISAT line, ICCL-3272	• Erect type stature with large and green leaflets. • Light brown color seed coat and larger than the local variety. • Resistant to wilt disease and tolerant to botrytis grey mold disease.
8	BARI Chola-8 ICRISAT line, ICCL-88003	• Erect type stature with large and green leaflets. • White color flower. • White color seed coat and larger than the desi variety. • Resistant to wilt.

Source: Pedigree of BARI Chola-1 to BARI Chola-8 Pulse Research Centre, BARI, Gazipur.



Photograph 5. Eight chickpea genotypes.

B. METHODS

The methods followed to conduct the experiment and analyses of the data are divided into the following sub-heads:

a. Preparation and Design of the Experimental Field,

b. Sowing of Seeds,

c. Maintenance of the Experimental Plants,

d. Collection of Data and

e. Techniques of Analysis of Data.

Descriptions of the sub-heads are as follows:

a. Preparation and Design of the Experimental Field

The experiment was set in the botanical research field behind the third science building, University of Rajshahi, during the consecutive four *rabi* crop seasons of 2009-2010, 2010-2011, 2011-2012 and 2012-2013. The experimental field was ploughed six times repeatedly. Weeds were removed completely before lay-out of the field and sowing of the seeds. The field was pulverized and leveled properly. Lay-out of the experimental field (Figure 5) considering randomized complete block design with three replications. Each replication having eight plots. Each plot contains five rows and per row having five hills. In each hill, single plant was maintained. Gap between replications, plots, rows and hills were 120 cm, 80 cm, 45cm and 45cm, respectively.

b. Sowing of Seeds

The seeds of eight genotypes were sown in the experimental field according to design on 11th November, 2009; 11th November, 2010; 11th November, 2011 and 11th November, 2012.

c. Maintenance of the Experimental Plants

When the seedlings were 15-16cm in heights, the excess seedlings were removed from the experimental field and regular weeding was done. As the soil

of the experimental field as moist sufficiently throughout the crop season, no irrigation was given.

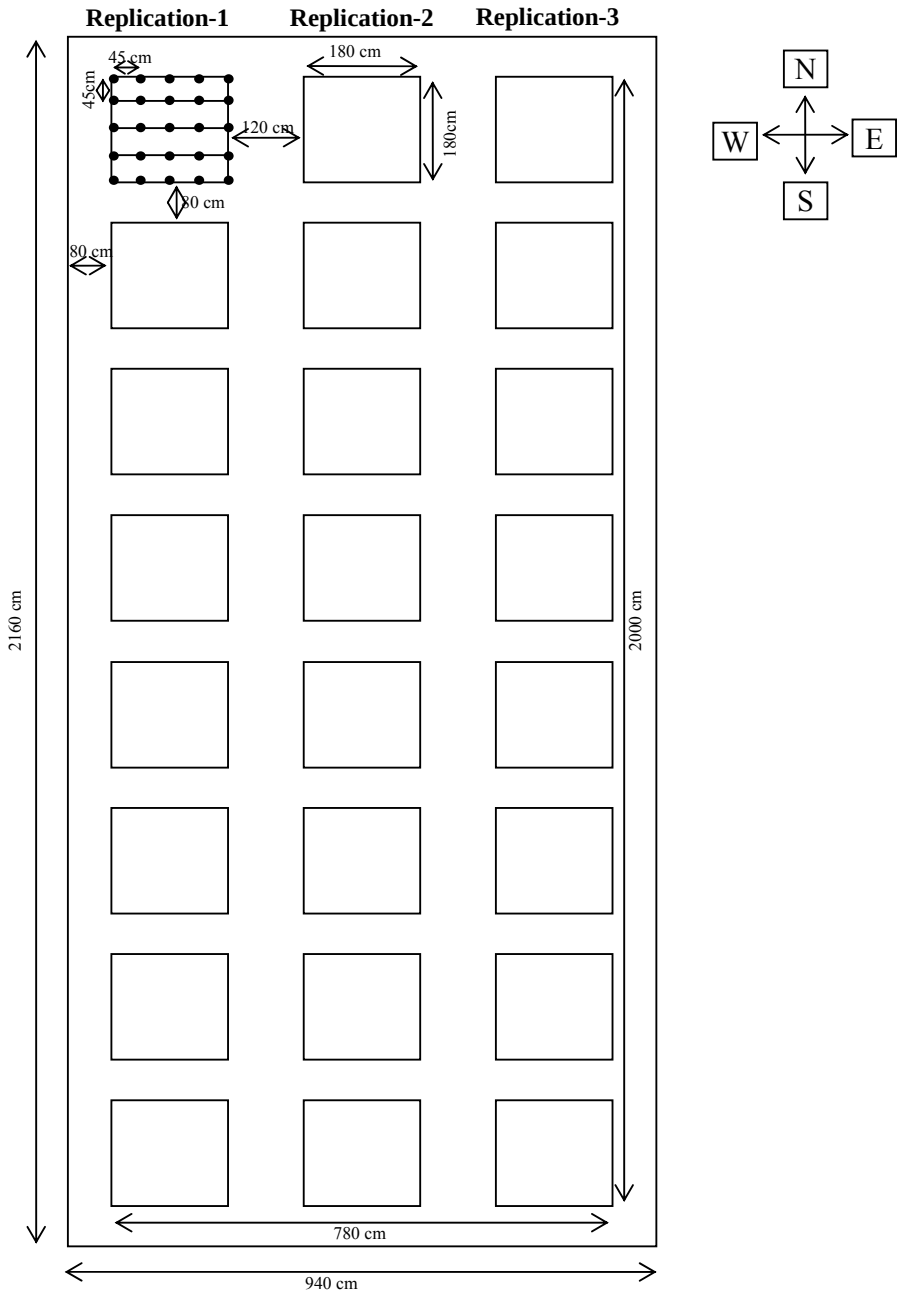


Figure 5. Design of lay-out of the experimental field.

Photograph 6. Experimental field of chickpea.

d. Collection of Data

Thirteen yield and yield contributing characters which are quantitative in nature were considered for the present investigation. Data were collected and recorded on individual plant basis of eight genotypes of chickpea. Following characters were measured and recorded.

i. Date of first flower (DFF): Date of first flower of the individual plant was recorded from the date of sowing.

ii. Plant height at first flower (PHFF): Height of the individual plant was recorded from the base of the stem to the top of the plant at the time of first flowering.

iii. Number of primary branches at first flower (NPBFF): The total number of primary branches from the main stem of the individual plant at the time of first flowering was counted and recorded.

iv. Number of secondary branches at first flower (NSBFF): The total number of secondary branches came out from the primary branches of the individual plant at the time of first flowering was counted and recorded.

v. Date of maximum flower (DMF): Date of maximum flower of the individual plant was recorded from the date of sowing.

vi. Plant height at maximum flower (PHMF): Height of the individual plant was recorded from the base of the stem to the top of the plant at the time of maximum flowering.

vii. Number of primary branches at maximum flower (NPBMF): The total number of primary branches from the main stem of the individual plant at the time of maximum flowering was counted and recorded.

viii. Number of secondary branches at maximum flower (NSBMF): The total number of secondary branches came out from the primary branches of the individual plant at the time of maximum flowering was counted and recorded.

ix. Plant weight at harvest (PWH): Weight of each plant was taken at the time of harvest of the plant and recorded.

x. Number of pods per plant (NPd/P): All the pods of the individual plant after harvesting were removed and counted.

xi. Pod weight per plant (PdW/P): All the pods of the individual plant were weighted and recorded.

xii. Number of seeds per plant (NS/P): All the pods of an individual plant were threshed and seeds were taken out from the pods and cleaned, then the total number of seeds was counted and recorded.

xiii. Seed weight per plant (SW/P): Total seeds of the individual plant were weighted and recorded.

e. Techniques of Analysis of Data

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

1. Mean

Data on individual plant was 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 from each plant.

n = number of observations.

i = 1, 2, 3…….n

∑= summation.

2. Standard deviation

Standard deviation is the root of the average of the deviation of the individual observations 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

3. Standard error of mean

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

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

Where,

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

S = standard deviation

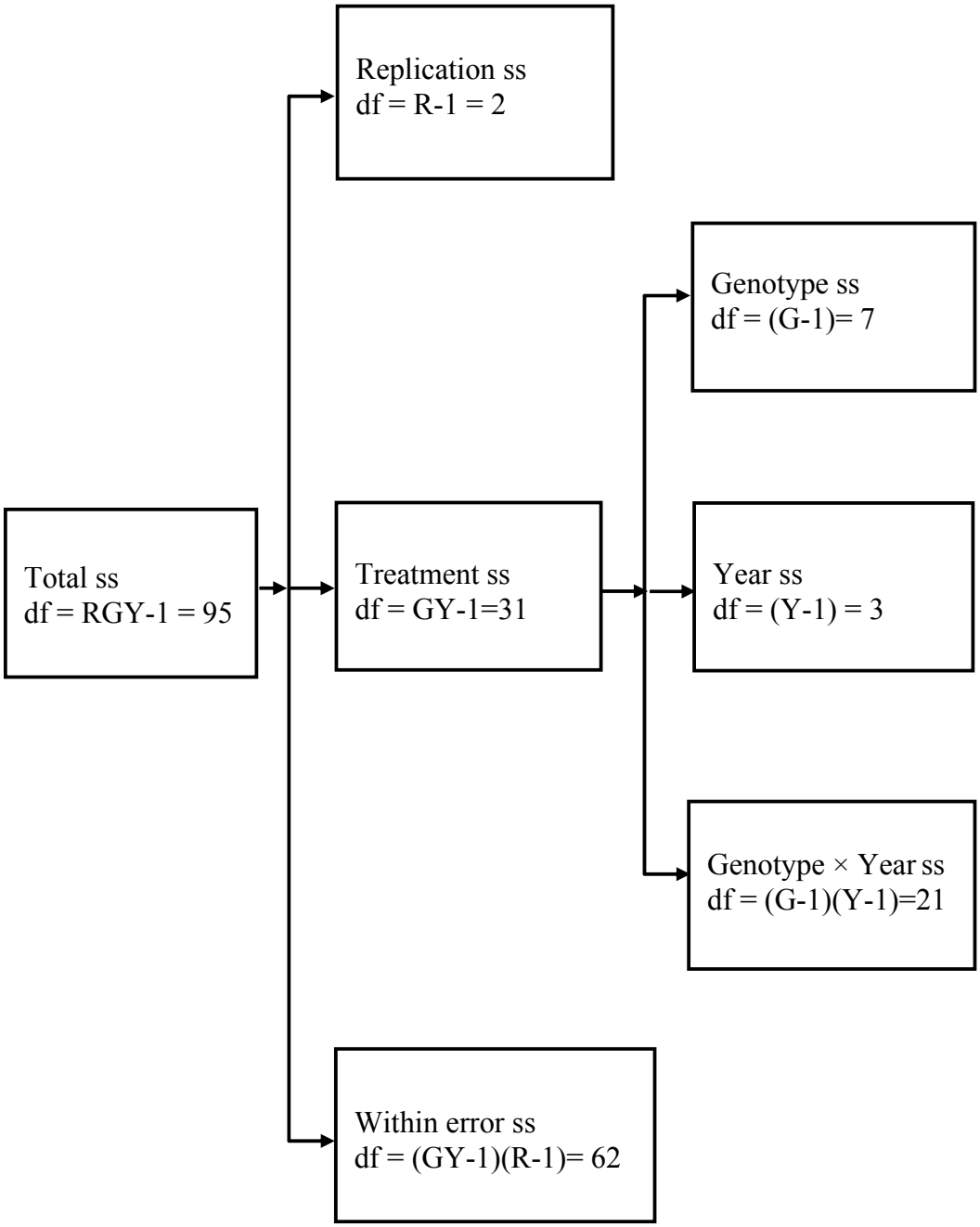
n = total number of individuals.

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

4. Analysis of variance

Variance is a measure of dispersion of a population. So, the analysis of variance is done for testing the significant differences among the genotypes. Variance analysis for each of the characters was carried out separately with raw data taken on individual plants.

The variances due to different sources such as replication (R), genotype (G), year (Y), genotype × year (G×Y) and within error of a population were calculated as per the following skeleton of analysis.



Where,

Genotype (G) = 8

Replication (R) = 3

Year (Y) = 4

The plant to plant variance of a population was calculated according to the following formula:

$$S^2 = \frac{\sum_{i=1}^{n} Xi^2 - \left(\sum_{i=1}^{n} Xi\right)^2 /n}{n-1}$$

Where,

S^2 = variance

X= the individual reading recorded on each plant

n = the total number of individuals.

∑= summation

i = 1, 2, 3…….n

n-1= degrees of freedom.

Furthermore where,

$$\text{Total}_{SS} = \sum (R_i G_j Y_k)^2 - CF$$

$$\text{Replication}_{SS} = \frac{\sum_{i} R_i^2}{G_j} - CF$$

$$\text{Treatment}_{SS} = \frac{\sum_{jk} (G_j Y_k)^2}{R_i} - CF$$

$$\text{Within Error}_{SS} = \text{Total}_{SS} - \text{Treatment}_{SS}$$

$$\text{Genotype}_{SS} = \frac{\sum_{j} G_j^2}{Y_k R_i} - CF$$

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

$$G \times Y_{SS} = \text{Treatment}_{SS} - \text{Genotype}_{SS} - \text{Year}_{SS}$$

Where,

R_i = the value of jth replication

G_i = the value of ith genotype

Y_k = the value of ith genotype

$G_j Y_k$= the value of jth genotype in kth Year

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

GT = grand total

N = total number of observations = (RGY)

The analysis of variance of a mixed model was used, where genotype (G) was fixed and Year (Y) effect was random. The expectation of mean square (EMS) was derived as follows.

Table 5. Analysis of variance.

Item	**df**	**MS**	**EMS**
Replication (R)	R-1	MS_1	$\sigma^2_E + GY\sigma^2_R$
Genotype (G)	G-1	MS_2	$\sigma^2_E + R\sigma^2_{GY} + RY\sigma^2_G$
Year (Y)	Y-1	MS_3	$\sigma^2_E + RG\sigma^2_Y$
Genotype × Year (G×Y)	(G-1)(Y-1)	MS_4	$\sigma^2_E + R\sigma^2_{GY}$
Within Error	(GY-1)(R-1)	MS_5	σ^2_E

Where,

G = genotype

R = replication

Y = year

MS_1= represents mean square of replication

MS_2= represents mean square of genotype

MS_3= represents mean square of year

MS_4= represents mean square of G×Y

MS_5= represents mean square of within error

$RY\sigma^2_G$ = variance due to genotype

$GY\sigma^2_R$ = variance due to replication

$R\sigma^2_{GY}$ = variance due to G×Y

σ^2_E = variance due to within error

5. Components of variation

It is a measure of variation among families/treatments or replications, etc. obtained by dividing the sum of squares by corresponding degrees of freedom to get mean sum of square, i.e. variances. Variance parameter is widely used in various statistical analyses. The phenotypic (σ^2_P), genotypic (σ^2_G), interaction ($\sigma^2_{GY,}$) and error (σ^2_E) variances were determined as follows:

Step-I:

$\sigma^2_G = (MS_2 - MS_4)/RY$

$\sigma^2_Y = (MS_3 - MS_5)/RG$

$\sigma^2_{GY} = (MS_4 - MS_5)/R$

$\sigma^2_E = MS_5$

Step-II:

Phenotypic variance (σ^2_P) = $\sigma^2_G + \sigma^2_{GY} + \sigma^2_E$

Genotypic variance (σ^2_G) = σ^2_G

Genotype × year variance = σ^2_{GY}

Error variance = σ^2_E

6. Coefficient of variability (CV)

When variation has to be compared for different characters, each represented by different units, variance, SD or SE are not adequate. However, by converting units of all characters on the same scale, the job can be done neatly. It is expressed as the percentage ratio of SD to corresponding mean, i.e.

$$CV = \frac{S^2}{\overline{X}} \times 100$$

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

i) Phenotypic coefficient of variability (PCV) $= \frac{\sigma_P^2}{\overline{X}} \times 100$

ii) Genotypic coefficient of variability (GCV) $= \frac{\sigma_G^2}{\overline{X}} \times 100$

iii) Error coefficient of variability (ECV) $= \frac{\sigma_E^{\ 2}}{\overline{X}} \times 100$

Where,

$\overline{X}$ = grand mean

σ^2_P = phenotypic variance

σ^2_G = genotypic variance

σ^2_E = error variance

7. Heritability (h^2_b)

Heritability (in broad sense) estimates was computed by dividing the genotypic variance with phenotypic variance and then multiplying by 100 as suggested by Warner (1952).

$$h^2_b = \frac{\sigma_G^{\ 2}}{\sigma^2_P} \times 100$$

Where,

h^2_b = heritability in broad sense

σ^2_P = phenotypic variance

σ^2_G = genotypic variance

8. Genetic Advance (GA)

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

$$GA = K \times \sigma_P \times h^2_b$$

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

h^2_b = broad sense heritability

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

It was calculated by the following formula:

$$\text{GA\% of Mean} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,

$\overline{\text{X}}$ = grand mean for a particular character.

10. Analysis of covariance

For the purpose of correlation coefficients and path coefficients, the analysis of both variance and covariance are required (Miller *et al.*, 1958). Nevertheless, covariances were calculated between all possible pairs of characters separately. For the analysis of covariance the raw data of individual plant were used according to the following formula.

$$\text{COV} = \frac{\sum_{i=1}^{n} \text{XiYi} - \left\{ \left(\sum_{i=1}^{n} \text{Xi} \right) \left(\sum_{i=1}^{n} \text{Yi} \right) \right\} / \text{n}}{\text{n} - 1}$$

Where,

COV = covariance

$\sum_{i=1}^{n} \text{XiYi}$ = sum of the X and Y

$\sum_{i=1}^{n} \text{Xi}$ = grand total of X

$\sum_{i=1}^{n} \text{Yi}$ = grand total of Y

n = number of observation

n-1= degrees of freedom

i = 1, 2, 3…….n

∑= summation

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

Table 6. Analysis of covariance.

Item	df	MS	MCP
Replication (R)	R-1	MCP_1	$\sigma^2_E + GY\sigma^2_R$
Genotype (G)	G-1	MCP_2	$\sigma^2_E + R\sigma^2_{GY} + RY\sigma^2_G$
Year (Y)	Y-1	MCP_3	$\sigma^2_E + RG\sigma^2_Y$
Genotype × Year (G×Y)	(G-1)(Y-1)	MCP_4	$\sigma^2_E + R\sigma^2_{GY}$
Within Error	(GY-1)(R-1)	MCP_5	σ^2_E

Where,

MCP_1= mean cross product of replication

MCP_2= mean cross product of genotype

MCP_3= mean cross product of year

MCP_4 = mean cross product of G×Y

MCP_5 = mean cross product of within error

$GY\sigma^2_R$ = covariance due to replication

$RY\sigma^2_G$ = covariance due to genotype

$GR\sigma^2_Y$ = covariance due to year

$R\sigma^2_{GY}$= covariance due to G×Y

σ^2_E = covariance due to within error

11. Components of covariation

The phenotypic (σ^2_P), genotypic (σ^2_G), interaction (σ^2_{GY}) and error (σ^2_E) components of covariance were measured as follows:

Step-I:

$\sigma^2_G = (MCP_2 - MCP_4)/RY$

$\sigma^2_Y = (MCP_3 - MCP_5)/RG$

$\sigma^2_{GY} = (MCP_4 - MCP_5)/R$

$\sigma^2_E = MCP_5$

Step-II:

Phenotypic variance (σ^2_P) = σ^2_G+ σ^2_{GY} + σ^2_E

Genotypic variance (σ^2_G) = σ^2_G

Genotype × year variance = σ^2_{GY}

Error variance = σ^2_E

12. Correlation coefficient

The correlation coefficient at phenotypic (r_P) and genotypic (r_g) levels were computed 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 $\sigma^2_{G12,}$ represent covariances at phenotypic and genotypic levels, respectively for characters 1 and 2.

σ^2_{P11} and σ^2_{G11} indicate variances at phenotypic and genotypic levels, respectively for character 1.

σ^2_{P22} and σ^2_{G22} represent variances at phenotypic and genotypic levels, respectively for character 2.

13. Path coefficient

The path coefficient analysis was done by using Wright's (1921 and 1923) formula as was extended by Dewey and Lu (1959). The path coefficient analysis was carried out both at phenotypic and genotypic levels were obtained by solving a set of simultaneous equations as follows.

$$r_{xy} = P_{xy} + r_{x2} P_{2y} + r_{x3} P_{3y} + r_{x4} P_{4y} + r_{x5} P_{5y} + r_{x6} P_{6y} + r_{x7} P_{7y} + r_{x8} P_{8y} + r_{x9} P_{9y} + r_{x10} P_{10y} + r_{x11} P_{11y} + r_{x12} P_{12y}$$

Where, the terms like

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

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

r_{x2}, $r_{x3,.....}r_{xn}$ = correlation between the same character and one of the remaining yield components in turn.

The relationship used in this study for yield and yield components were as follows:

1. $r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + r_{14} P_{4y} + r_{15} P_{5y} + r_{16} P_{6y} + ...+ r_{112} P_{12y}$
2. $r_{2y} = P_{2y} + r_{21} P_{1y} + r_{23} P_{3y} + r_{24} P_{4y} + r_{25} P_{5y} + r_{26} P_{6y} + ...+ r_{212} P_{12y}$
3. $r_{3y} = P_{3y} + r_{31} P_{1y} + r_{32} P_{2y} + r_{34} P_{4y} + r_{35} P_{5y} + r_{36} P_{6y} + ...+ r_{312} P_{12y}$
4. $r_{4y} = P_{4y} + r_{41} P_{1y} + r_{42} P_{2y} + r_{43} P_{3y} + r_{45} P_{5y} + r_{46} P_{6y} + ...+ r_{412} P_{12y}$
5. $r_{5y} = P_{5y} + r_{51} P_{1y} + r_{52} P_{2y} + r_{53} P_{3y} + r_{54} P_{4y} + r_{56} P_{6y} + ...+ r_{512} P_{12y}$
6. $r_{6y} = P_{6y} + r_{61} P_{1y} + r_{62} P_{2y} + r_{63} P_{3y} + r_{64} P_{4y} + r_{65} P_{5y} + ...+ r_{612} P_{12y}$
7. $r_{7y} = P_{7y} + r_{71} P_{1y} + r_{72} P_{2y} + r_{73} P_{3y} + r_{74} P_{4y} + r_{75} P_{5y} + ...+ r_{712} P_{12y}$
8. $r_{8y} = P_{8y} + r_{81} P_{1y} + r_{82} P_{2y} + r_{83} P_{3y} + r_{84} P_{4y} + r_{85} P_{5y} + ...+ r_{812} P_{12y}$
9. $r_{9y} = P_{9y} + r_{91} P_{1y} + r_{92} P_{2y} + r_{93} P_{3y} + r_{94} P_{4y} + r_{95} P_{5y} + ...+ r_{912} P_{12y}$
10. $r_{10y} = P_{10y} + r_{101} P_{1y} + r_{102} P_{2y} + r_{103} P_{3y} + r_{104} P_{4y} + r_{105} P_{5y} +.....+ r_{1012} P_{12y}$
11. $r_{11y} = P_{11y} + r_{111} P_{1y} + r_{112} P_{2y} + r_{113} P_{3y} + r_{114} P_{4y} + r_{115} P_{5y} + ...+ r_{1112} P_{12y}$
12. $r_{12y} = P_{12y} + r_{121} P_{1y} + r_{122} P_{2y} + r_{123} P_{3y} + r_{124} P_{4y} + r_{125} P_{5y} +.....+ r_{1212} P_{12y}$

Where,

y, represent seed weight per plant (SW/P). The numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 and 12 represent date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at harvest (PWH), number of pods per plant (NPd/P), pod weight per plant (PdW/P) and number of seeds per plant (NS/P).

Residual effect (X) = 1- R^2

Where,

$R^2 = P_{1y} r_{1y} + P_{2y} r_{2y} + \ldots\ldots\ldots\ldots + P_{ny} r_{ny}$

14. 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 by solving the following equations of an index simultaneously. Similar equations were set up for each index and the values obtained for b_1, b_2, ……b_n were used in the discriminant function selection technique.

$b_1P_{11} + b_2P_{12} + \ldots\ldots\ldots\ldots + b_nP_{1n} = G_{1y}$

$b_1P_{12} + b_2P_{22} + \ldots\ldots\ldots\ldots + b_nP_{2n} = G_{2y}$

$b_1P_{1n} + b_2P_{2n} + \ldots\ldots\ldots\ldots + b_nP_{nn} = G_{ny}$

Where,

P_{11} = an estimate of the phenotypic variance of character 1

P_{12} = an estimate of phenotypic covariance of characters 1 and 2

$G_{1y}, G_{2y}, G_{3y}\ldots\ldots_{ny}$ = an estimate of genotypic covariance of character 1 and yield (seed weight per plant), etc.

The phenotypic and genotypic variances and covariances as obtained were used for constructing discriminant functions using different character combinations according to the method developed by Fisher (1936) and Smith (1936). Later on, Hazel (1943) developed a simultaneous selection model following path analysis approach. Since then, the theory of selection index has been extended and modified in various ways by various authors to suit the requirements of practical breeders (Robinson *et al*., 1951; Singh, 1972). The expected genetic advance from strait selection [GA (S)] and from the dicriminant function [GA (D)] was calculated as follows:

$$GA(S) = \frac{Z}{P}\left(\frac{g_{yy}}{\sqrt{t_{yy}}}\right) \quad \text{and}$$

$$GA(D) = \frac{Z}{P}\sqrt{\left(b_1 g_{1y} + b_2 g_{2y} + ... + b_n g_{ny}\right)}$$

Where,

$\frac{Z}{P}$ = 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} = genotypic and phenotypic variances of the character y

$b_1, b_2, \ldots\ldots\ldots b_n$ = relative weight for each character

$G_{1y}, G_{2y} \ldots G_{ny}$ = genetic covariances of independent characters with y.

The expected gain from the discriminant function over strait selection was calculated for all the functions and studied as follows:

Expected gain (%) = [{GA (D)/ GA(S)}-1] × 100

RESULTS

The present experiment was carried out to assess the nature and extent of genetic variability, heritability, genetic advance, correlation coefficient, path coefficient and construct the selection index in the material. The materials was comprised of eight genotypes of chickpea such as BARI chola-1, BARI chola-2, BARI chola-3, BARI chola-4, BARI chola-5, BARI chola-6, BARI chola-7 and BARI chola-8. Thirteen yield and yield components viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary brunches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) have been considered for this investigation. The obtained results are described as follows.

A. ANALYSIS OF VARIANCE

The results of the analysis of variance for all the quantitative characters were done separately and presented in Table 7A - 7M. For this investigation a mixed model was followed for testing the main items and their interaction. In the analysis of variance replication item was found to be non-significant for all the characters except DMF. Item genotype was highly significant for all the traits. Item year found to be highly significant for all the traits except DMF. Except NPBMF, the G×Y interaction item was significant for all the traits.

B. COMPONENTS OF VARIATION

Components of variation viz., phenotypic (σ^2_P), genotypic (σ^2_G), year (σ^2_Y), genotype × year interaction ($\sigma^2_{G\times Y}$) and error (σ^2_E) components of variation were estimates separately for all traits and presented in Table 8.

a. Phenotypic Variation (σ^2_P)

Phenotypic variation was greater than those of σ^2_G, $\sigma^2_{G\times Y}$ and σ^2_E components of variation for all the characters as expected. The highest phenotypic variation was found for NPd/P with a value of 1413.361 while the lowest recorded for NPBFF with a value of 0.290.

b. Genotypic Variation (σ^2_G)

The highest σ^2_G recorded for NS/P with a value of 499.591 while the lowest noted for NPBFF with a value of 0.047.

c. Year Variation (σ^2_Y)

The highest year variation noted for the character NPd/P with a value of 954.583 while the lowest recorded for DMF with a value of 0.009.

d. Genotypic × Year Interaction Variation ($\sigma^2_{G\times Y}$)

The highest and the lowest $\sigma^2_{G\times Y}$ were noted for NPd/P and NPBMF with the values of 362.413 and 0.024, respectively.

e. Error Variation (σ^2_E)

For this item, the highest variation was found for the trait NPd/P with a value of 588.795 while the lowest was found for the trait NPBFF with the value of 0.163.

C. COEFFICIENT OF VARIABILITY

Coefficient of variability viz., phenotypic (PCV), genotypic (GCV) and error (ECV) coefficient of variability were estimates separately for all traits and presented in Table 9.

a. Phenotypic Coefficient of Variability

Phenotypic coefficient of variability was found greater than genotypic and error coefficient of variability which was expected for all the traits. The height PCV was found for the trait NPd/P with a value of 1163.243 while the lowest was found for DMF with a value of 5.844.

b. Genotypic Coefficient of Variability

The values of 389.340 and 1.148 noted as the highest and the lowest genotypic coefficient of variability for NS/P and NSBMF, respectively.

c. Error Coefficient of Variability

Coefficient of variability due to error of 484.598 and 1.093 recorded as the highest and the lowest for NPd/P and DMF, respectively.

D. HERITABILITY (IN BROAD SENSE)

Heritability in broad sense (h^2_b) was calculated separately for all thirteen characters and presented in Table 9. Perusal the Table 9, the highest h^2_b was found for DMF with a value of 71.237 followed by PHFF (62.799) and DFF (60.685) while, the lowest was found for PdW/P (6.152).

E. GENETIC ADVANCE (GA)

Perusal the Table 9, genetic advance of the trait NS/P was found to be the highest with a value of 28.294 while the lowest was found for NSBMF with a value of 0.163.

F. GENETIC ADVANCE AS PARENTAGE OF MEAN (GA%)

Perusal the Table 9, the traits NS/P and NSBMF showed the highest and the lowest GA % of 22.050 and 2.190, respectively.

G. CORRELATION COEFFICIENT

The correlation coefficient between pairs of characters was computed both at phenotypic and genotypic levels to understand the relationship between the yield and other traits. The results are presented in Table 10A and 10B.

In the present investigation, correlation study showed that the most of character pairs both of genotypic and phenotypic associations were in same direction and genotypic correlation value was greater than respective phenotypic ones. NPBFF, NPBMF, NPd/P, PdW/P and NS/P were positively correlated with

SW/P both at genotypic and phenotypic levels. Seed yield was also positively correlated with NSBMF and PWH at phenotypic level whereas, rest of the traits were negatively correlated with seed yield at both levels.

Among the positive correlated traits, NPd/P, PdW/P and NS/P exhibited significant correlation with SW/P at both levels. Traits viz., NPBFF and NPBMF showed significant positive association with SW/P at genotypic level only. Again, the rest of the traits viz., DFF, PHFF, NSBFF, DMF, PHMF, NSBMF and PWH were negatively significant with SW/P at genotypic level.

Among the yield contributing traits, DFF showed positive correlation with PHFF, DMF, PHMF, PWH, NPd/P and NS/P both at genotypic and phenotypic levels and all were significant at genotypic level while, NPd/P and NS/P were non-significant at phenotypic level. On the other hand, DFF showed negative correlation with NPBFF, NSBFF, NPBMF, NSBMF and PdW/P both at genotypic and phenotypic levels. In that case, all traits exhibited significant value at genotypic level while, NSBFF and NSBMF showed significant value at phenotypic level.

Positive correlation of PHFF was observed with DFF, NPBFF, DMF, PHMF, PWH, NPd/P and NS/P at both levels and all were significant at genotypic level while, PWH, NPd/P and NS/P were non-significant at phenotypic level. On the other hand, it had negative association with NSBFF, NPBMF, NSBMF and PdW/P at both levels, where significant value showed only at genotypic level.

Character NPBFF showed positive and significant correlation with PHFF, DMF, PWH, NPd/P, PdW/P and NS/P while, negative and significant correlation with DFF and NSBMF at genotypic level. On the other hand at phenotypic level NPBFF showed positive and significant correlation with PHFF, NSBFF and DMF.

The trait NSBFF exhibited significant and positive correlation with NSBMF and NS/P at genotypic level while with NPBFF and NSBMF at phenotypic level. It also showed positive and non-significant correlation with DMF, PWH and NPd/P at genotypic level and with DMF, NPBMF, NPd/P and NS/P at phenotypic level. On the other hand, negative genotypic correlation with this trait was exhibited by DFF, PHFF, NPBFF, PHMF, NPBMF and PdW/P and among them correlation between NSBFF and NPBFF and NSBFF and PHMF were non-significant at genotypic level. Again, at phenotypic level, NSBFF exhibited negative correlation with DFF, PHFF, PHMF, PWH and PdW/P and among them correlation between NSBFF and PHFF, NSBFF and PHMF and NSBFF and PWH were non-significant.

DMF had positive and significant genotypic association with DFF, PHFF, NPBFF, PHMF, PWH, NPd/P and NS/P. Again, it had positive and significant phenotypic association with DFF, PHFF, NPBFF, PHMF and NS/P. It also showed positive but non-significant correlation with NSBFF at genotypic level while, NSBFF, PWH and NPd/P at phenotypic level. On the other hand, negative and significant genotypic correlation of DMF exhibited by NPBMF, NSBMF and PdW/P while, only PdW/P exhibited negative and significant correlation with this trait at phenotypic level. DMF also showed negative and non-significant phenotypic association with NPBMF and NSBMF.

The trait PHMF exhibited positive and significant correlation with DFF, PHFF, DMF and PWH at genotypic level while, with DFF, PHFF and DMF at phenotypic level. On the other hand, PHMF had negative and significant genotypic association with NPBMF, NSBMF and PdW/P while, it showed negative phenotypic association with NSBFF, NPBMF, NSBMF and PdW/P.

Character NPBMF had significant and positive genotypic correlation with NSBMF, NPd/P, PdW/P and NS/P while, it had positive but non-significant association with NPBFF at genotypic level. Whereas, this trait showed negative

and significant association with DFF, PHFF, NSBFF, DMF, PHMF and PWH at genotypic level. At phenotypic level, NPBMF had positive but non-significant relationship with NPBFF, NSBFF, NSBMF, PWH, NPd/P, PdW/P and NS/P while, DFF, PHFF, DMF and PHMF exhibited non-significant negative association with NPBMF.

NSBMF had positive and significant correlation with NSBFF and NPBMF at genotypic level while, with NSBFF at phenotypic level. The rest of the trait exhibited non-significant and positive correlation at the both levels. Whereas it had negative and significant genotypic association with DFF, PHFF, NPBFF, DMF, PHMF, PWH and PdW/P while, negative and significant phenotypic association only with DFF.

Positive and significant correlation showed by PWH with DFF, PHFF, NPBFF, DMF and PHMF at genotypic level while, with DFF at phenotypic level. PWH negatively associated with NPBMF, NSBMF, NPd/P, PdW/P and NS/P at genotypic level.

The trait NPd/P showed positive and significant association with DFF, PHFF, NPBFF, DMF, NPBMF and NS/P, but negative and significant association with PWH at genotypic level. Except PdW/P and NS/P, none of the traits significantly associated with NPd/P at phenotypic level. Simply all traits were positively correlated at phenotypic level. On the other hand, genotypic correlation of NPd/P with PWH and PdW/P was negative.

Positive and significant correlation was exhibited by PdW/P with NPBFF and NPBMF at genotypic level and with NPd/P and NS/P at phenotypic level. On the other hand, it had negative and significant correlation with DFF, PHFF, NSBFF, DMF, PHMF, NSBMF and PWH at genotypic level while, at phenotypic level PdW/P was negatively and significantly correlated with NSBFF and DMF.

NS/P had positive and significant association with DFF, PHFF, NPBFF, NSBFF, DMF, NPBMF and NPd/P at genotypic level while, with DMF, NPd/P and PdW/P at phenotypic level. The traits PHMF, PWH and PdW/P negatively correlated with NS/P at genotypic level while all the traits were positively correlated with NS/P at phenotypic level.

H. PATH COEFFICIENT

The path coefficients were estimated separately both at genotypic and phenotypic levels to understand the direct and indirect effect of yield components on seed yield. The obtained results are presented in Table 11A and 11B.

a. Path Coefficient Analysis at Genotypic Level

In the present experiment, characters DFF, NSBFF, PHMF, NSBMF, PdW/P and NS/P had positive direct effect on seed yield (SW/P) and among them NS/P had the highest positive direct effect with a value of 13.1562. While, negative direct effect showed by PHFF, NPBFF, DMF, NPBMF, PWH and NPd/P.

The indirect effects of DFF on seed yield via NPBFF, PHMF, NPBMF and NS/P were positive while, via PHFF, NSBFF, DMF, NSBMF, PWH, NPd/P and PdW/P were negative. Again, DFF had positive direct effect on seed yield (0.5425) which was nullified mainly due to DMF and NPd/P. As a result, the total effect was negative (-0.3065).

The indirect effects of PHFF were positive on seed yield via DFF, PHMF, NPBMF and NS/P while, negative via NPBFF, NSBFF, DMF, NSBMF, PWH, NPd/P and PdW/P. It had negative direct effect on seed yield as -0.3526 and the total effect was -0.6565.

The trait NPBFF had positive indirect effect on seed yield via PHMF, PdW/P and NS/P while, rest of the traits exhibited negative indirect effect on seed yield. The direct effect of NPBFF was -0.3699 which was compensated by high positive indirect effect via NS/P (11.8063) and the total effect was 0.5483.

NSBFF had second highest positive direct effect on seed yield (0.6365). The indirect effects of NSBFF on seed yield via DFF, DMF, PHMF, PWH, NPd/P and PdW/P were negative while, rest of the traits showed positive indirect effect on seed yield. The total effect of this trait was negative (-0.4632).

DMF had second highest negative direct effect on seed yield and it had negative indirect effect via PHFF, NPBFF, NSBMF, PWH, NPd/P and PdW/P while, rest of the traits exhibited positive indirect effect on seed yield in respect of this trait. The total effect of this trait on seed yield was -0.7263.

The trait PHMF had positive direct effect on seed yield (0.2840) which was turn into negative total effect via negative indirect effect of all the traits except DFF and NPBMF. The total effect of this trait was -1.0915.

NPBMF had negative direct effect which turns into positive via PHFF, DMF, NSBMF, PWH, PdW/P and NS/P and among them NS/P had a great role (10.6815) to reverse negative direct effect into positive total effect. Rest of the trait had negligible negative indirect effect on seed yield except NPd/P.

The trait NSBMF had positive but small direct effect on seed yield which turns into negative via DFF, PHMF, NPBMF, NPd/P and PdW/P. In this case, NPBMF (-0.9368) and NPd/P (-1.7156) had a great role to reverse its positive direct effect into negative total effect. Rest of the trait had small positive indirect effect on seed yield except NS/P.

The indirect effect of PWH were positive on seed yield via DFF, NSBFF, PHMF, NPBMF and NPd/P while, negative indirect effect via PHFF, NPBFF, DMF, NSBMF, PdW/P and NS/P. The direct effect of PWH was negative and very negligible (-0.0050). The total effect of PWH was -0.9923.

The trait NPd/P had the highest negative direct effect (-11.6785) on seed yield but this high value nullified by high indirect effect of NS/P (13.0785) and other

positive indirect effect via DFF, NSBFF, PHMF, NSBMF and PWH. Rest of the traits had negative and comparatively small indirect effect on seed yield in respect of this trait. The total effect of this trait was 0.2047.

PdW/P had positive and small direct effect of 0.3203 on seed yield. It exhibited positive indirect effect via PHFF, DMF, PWH and NPd/P while, it had negative indirect effect on seed yield via DFF, NPBFF, NSBFF, PHMF, NPBMF, NSBMF and NS/P which were comparatively low. The total effect was 0.9406.

The highest positive direct effect (13.1562) on seed yield was exhibited by NS/P. But this high value reduces by high negative indirect effect of NPd/P (-11.6096) and other small negative indirect effect via PHFF, NPBFF, DMF, PHMF, NPBMF and PdW/P. It had positive and comparatively low indirect effect on seed yield via DFF, NSBFF, NSBMF and PWH. The total effect of this trait was 0.3373.
The residual effect at genotypic level was -0.6876.

b. Path Coefficient Analysis at Phenotypic Level

At the phenotypic level of path analysis, the highest direct effect showed by NS/P (0.7995) followed by PdW/P (0.7615) while, the highest negative direct effect exhibited by NPd/P (-0.6776) followed by NPBMF (-0.0904).

The trait DFF had positive direct effect on seed yield with a value of 0.0402 however, it become negative due to negative indirect effect via PHFF, NPBFF, DMF, NSBMF, PWH, NPd/P and PdW/P. On the other hand, it had positive but low indirect effect on seed yield via NSBFF, PHMF and NPBMF. The total effect was -0.1572.

PHFF had positive indirect effect of on seed yield via DFF, NPBFF, NSBFF, PHMF, NPBMF and NS/P. On the other hand, it had negative indirect effect on seed yield through DMF, NSBMF, PWH, NPd/P and PdW/P. The direct effect of PHFF on seed yield and the total effect were negative.

The indirect effect on seed yield of NPBFF via DFF, PHFF, NSBFF, DMF, NPBMF, NSBMF and NPd/P was negative. Positive indirect effect via NS/P was comparatively high among the positive indirect effect showing traits. The direct and total effect for this trait was recorded as 0.1191 and 0.1145, respectively.

NSBFF had negative and negligible direct effect (-0.0031) on seed yield. This trait had negative indirect effect on seed yield via DFF, DMF, PHMF, NPBMF, NPd/P and PdW/P. Rest of the traits exhibited positive indirect effect on seed yield regarding NSBFF.

The direct effect of DMF on the seed yield was negative and small (-0.0664). It had negative indirect effect on seed yield via PHFF, NSBFF, NSBMF, PWH, NPd/P and PdW/P. The indirect effect on seed yield via DFF, NPBFF, PHMF, NPBMF and NS/P was positive. The total effect of DMF was negative (-0.1842).

The trait PHMF had positive but vary small direct effect (0.0005) on seed yield which turns into negative total effect via PHFF, DMF, NSBMF, PWH, NPd/P and PdW/P. Rest of the traits had small positive indirect effect on seed yield except NS/P in respect of NPBMF on seed yield.

NPBMF had negative direct effect (-0.0904) which was turn into positive total effect (0.0314) via positive indirect effect of PHFF, NPBFF, DMF, NSBMF, PdW/P and NS/P specially PdW/P and NS/P. It had negative indirect effect on yield via rest of the traits but they were lower than positive ones.

NSBMF had positive direct effect of 0.1029 on yield. It had positive indirect effect on seed yield via PHFF, DMF, PWH, PdW/P and NS/P while, negative indirect effect on seed yield via DFF, NPBFF, NSBFF, PHMF, NPBMF and NPd/P. The total effect was 0.1718.

The direct effect of PWH had negative and small (-0.0301) on yield. It had positive indirect effect on seed yield via DFF, NSBFF, PHMF, PdW/P and

NS/P while, negative indirect effect on seed yield via PHFF, NPBFF, DMF, NPBMF, NSBMF and NPd/P. The total effect was 0.1718.

The trait NPd/P had the highest negative direct effect (-0.6776) on seed yield but it become positive total effect due to the positive indirect effect via DFF, NPBFF, PHMF, NSBMF, specially PdW/P and NS/P which were higher than negative indirect effect via rest of the traits.

In the present experiment, the second highest positive direct effect of 0.7615 on seed yield was exhibited by PdW/P. PdW/P had positive indirect effect on seed yield via all the traits except DFF, NPBMF, PWH and NPd/P. The total effect was 0.9406.

The highest positive direct effect on seed yield (0.7995) exhibited by NS/P. It had also positive indirect effect via DFF, NPBFF, PHMF, NSBMF and PdW/P while, it had negative indirect effect which reduced its amount of total effect on seed yield via PHFF, NSBFF, DMF, NPBMF, PWH and NPd/P. The total effect was 0.4369. The residual effect at phenotypic level was 0.4608.

I. SELECTION INDEX

Selection index for yield were constructed for each set of data and different combinations were studied to identify the character which might be useful during selection program. For construct the selection indices, all the thirteen agronomical character viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P were considered. Here, SW/P was use as dependent character. The selection indices and the expected genetic gain in percentage over straight selection for yield and its components are presented in Table 12. In this study, 8750 different combinations were calculated and only high value showing combinations are presented in Table 12.

In the present investigation, the result showed that the character NPBMF had the highest (3286.72%) positive expected gain followed by NPBFF (2143.01%)

and NSBMF (942.67%) when individual traits were considered separately. In the discriminante function analysis, high value of expected gain exhibited by two characters in a combination with value of 1949.52% (NPBFF + NPBMF) followed by 1768.27% (NPBMF + NSBMF) and 1171.21% (NPBFF + NSBMF). Included three characters, the maximum genetic gain was recorded as 1350.99% for NPBFF + NPBMF + NSBMF followed by 382.68% for NPBFF + NPBMF + SW/P and 380.27% for NPBFF + NPBMF + PdW/P. When included four characters, the maximum genetic gain was recorded as 349.78% for NPBFF + NPBMF + NSBMF + SW/P followed by 340.70% for NPBFF + NPBMF + NSBMF + PdW/P and 227.54% for NPBFF + PHMF + NPBMF + NSBMF. The maximum genetic gain was recorded in a combination of five characters as 156% for NPBFF + NPBMF + NSBMF + PdW/P + SW/P followed by 139.69% for NPBFF + PHMF + NPBMF + NSBMF + SW/P and 124.6% for NPBFF + NSBFF + PHMF + NPBMF + NSBMF. Similarly, inoculation of six traits in a combination, the highest value was 78.39% noted for NPBFF + PHMF + NPBMF + NSBMF + PdW/P + SW/P followed by 75.75% for NPBFF + NSBFF + PHMF + NPBMF + NSBMF + SW/P and 52.41% for NPBFF + PHMF + NPBMF + NSBMF + PWH + SW/P, inclusion of seven traits the highest value was 24% recoded as for NPBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + SW/P followed by 20.45% for PHFF + NPBFF + PHMF + NPBMF + NSBMF + PdW/P + SW/P and 19.92% for NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + SW/P. On the other hand, when included eight and more traits in a combination the value of expected gain become negative such as, in case of eight combinations the value of -4.03% noted for PHFF + NPBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + SW/P followed by -7.82% for NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + SW/P and -7.85% for PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF+PWH +SW/P. In combination of nine traits, maximum gain of -25.26% recorded for PHFF + NPBFF + NSBFF + PHMF +

NPBMF + NSBMF + PWH + PdW/P + SW/P followed by -49.79% for DFF + PHFF + NPBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + SW/P and -54.48% for DFF + PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + SW/P. At ten traits combination, the highest value of -64.63% recoded for DFF + PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + SW/P followed by -71.79 % for PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + NS/P + SW/P and -74.82% for DFF + PHFF + NPBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + NS/P + SW/P. In the combination of eleven traits, the highest value was -79.12% noted for DFF + PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + PdW/P + NS/P + SW/P followed by -83.15% for PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + NPd/P + PdW/P + NS/P + SW/P and -83.99% for DFF + PHFF + NPBFF + PHMF + NPBMF + NSBMF + PWH + NPd/P + PdW/P + NS/P + SW/P. In the combination of twelve traits, the highest genetic gain was noted as -86.82% followed by -101.99% and -103.58% for DFF + PHFF + NPBFF + NSBFF + PHMF + NPBMF + NSBMF + PWH + NPd/P + PdW/P + NS/P + SW/P, DFF + PHFF + NPBFF + NSBFF + DMF + PHMF + NPBMF + PWH + NPd/P + NS/P + SW/P and DFF +PHFF + NPBFF + NSBFF + DMF + PHMF + NPBMF + PWH + NPd/P + PdW/P + NS/P + SW/P, respectively. While included all the traits under studied in a combination, the expected genetic gain was noted as -102.79%. In an overall basis the highest expected genetic gain was noted as 1949.5222 for the combination of NPBFF + NSBMF followed by 1768.277 for NSBMF + PWH and 1350.986 for NSBFF + NSBMF + PWH.

Table 7A-7M. Analysis of variances among genotypes and its interaction with year for thirteen characters in chickpea.

Table 7A. Date of first flower (DFF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	28.475	14.238	1.789^{NS}
Genotype (G)	7	1917.023	273.860	34.407**
Year (Y)	3	686.605	228.868	28.754**
G×Y	21	513.931	24.473	3.075**
Within Error	62	493.484	7.959	
Total	95	3639.519		

Table 7B. Plant height at first flower (PHFF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	25.000	12.500	2.182^{NS}
Genotype (G)	7	1368.412	195.487	34.117**
Year (Y)	3	118.561	39.520	6.897**
G×Y	21	319.936	15.235	2.659**
Within Error	62	355.258	5.730	
Total	95	2187.167		

Table 7C. Number of primary branches at first flower (NPBFF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	0.248	0.124	0.761^{NS}
Genotype (G)	7	6.729	0.961	5.889**
Year (Y)	3	102.825	34.275	209.975**
G×Y	21	8.462	0.403	2.469*
Within Error	62	10.121	0.163	
Total	95	128.385		

Table 7D. Number of secondary branches at first flower (NSBFF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	0.068	0.034	0.150^{NS}
Genotype (G)	7	10.816	1.545	6.816**
Year (Y)	3	69.080	23.027	101.576**
G×Y	21	12.756	0.607	2.679**
Within Error	62	14.055	0.227	
Total	95	106.774		

Table 7E. Date of maximum flower (DMF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	9.428	4.714	4.354*
Genotype (G)	7	366.141	52.306	48.315**
Year (Y)	3	3.888	1.296	1.197NS
G×Y	21	59.408	2.829	2.613**
Within Error	62	67.122	1.083	
Total	95	505.987		

Table 7F. Plant height at maximum flower (PHMF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	36.310	18.155	1.943NS
Genotype (G)	7	540.556	77.222	8.266**
Year (Y)	3	230.331	76.777	8.218**
G×Y	21	381.684	18.175	1.946*
Within Error	62	579.210	9.342	
Total	95	1768.091		

Table 7G. Number of primary branches at maximum flower (NPBMF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	0.260	0.130	0.449NS
Genotype (G)	7	7.142	1.020	3.530**
Year (Y)	3	100.029	33.343	115.362**
G×Y	21	7.605	0.362	1.253NS
Within Error	62	17.920	0.289	
Total	95	132.955		

Table 7H. Number secondary branches at maximum flower (NSBMF).

Source of variation	df	SS	MSS	F value
Replication (R)	2	3.811	1.906	2.783NS
Genotype (G)	7	20.279	2.897	4.231**
Year (Y)	3	42.690	14.230	20.781**
G×Y	21	39.272	1.870	2.731**
Within Error	62	42.455	0.685	
Total	95	148.508		

Table 7I. Plant weight at harvest (PWH).

Source of variation	df	SS	MSS	F value
Replication (R)	2	258.021	129.011	0.678NS
Genotype (G)	7	4645.178	663.597	3.487**
Year (Y)	3	4661.809	1553.936	8.166**
G×Y	21	7769.682	369.985	1.944*
Within Error	62	11797.802	190.287	
Total	95	29132.493		

Table 7J. Number of pods per plant (NPd/P).

Source of variation	df	SS	MSS	F value
Replication (R)	2	1542.492	771.246	1.310^{NS}
Genotype (G)	7	50553.113	7221.873	12.266**
Year (Y)	3	70496.386	23498.795	39.910**
G×Y	21	35196.702	1676.033	2.847**
Within Error	62	36505.303	588.795	
Total	95	194293.996		

Table 7K. Pod weight per plant (PdW/P).

Source of variation	df	SS	MSS	F value
Replication (R)	2	12.017	6.008	0.230^{NS}
Genotype (G)	7	690.067	98.581	3.778**
Year (Y)	3	2234.087	744.696	28.539**
G×Y	21	1412.494	67.262	2.578**
Within Error	62	1617.803	26.094	
Total	95	5966.468		

Table 7L. Number of seeds per plant (NS/P).

Source of variation	df	SS	MSS	F value
Replication (R)	2	1006.013	503.006	1.074^{NS}
Genotype (G)	7	52697.619	7528.231	16.067**
Year (Y)	3	51271.270	17090.423	36.476**
G×Y	21	32196.035	1533.145	3.272**
Within Error	62	29049.693	468.543	
Total	95	166220.630		

Table 7M. Seed weight per plant (SW/P).

Source of variation	df	SS	MSS	F value
Replication (R)	2	24.744	12.372	0.779^{NS}
Genotype (G)	7	577.359	82.480	5.196**
Year (Y)	3	1391.484	463.828	29.217**
G×Y	21	872.333	41.540	2.617**
Within Error	62	984.260	15.875	
Total	95	3850.180		

* = significant at 5% level
** = significant at 1% level
^{NS} = non-significant

Table 8. Phenotypic (σ^2_P), genotypic (σ^2_G), year (σ^2_Y), interaction ($\sigma^2_{G\times Y}$) and within error (σ^2_E) components of variation for thirteen characters in chickpea.

Character	σ^2_P	σ^2_G	σ^2_Y	$\sigma^2_{G\times Y}$	σ^2_E
DFF	34.246	20.782	9.205	5.504	7.959
PHFF	23.919	15.021	1.408	3.168	5.730
NPBFF	0.290	0.047	1.421	0.080	0.163
NSBFF	0.432	0.078	0.950	0.127	0.227
DMF	5.788	4.123	0.009	0.582	1.083
PHMF	17.207	4.921	2.810	2.944	9.342
NPBMF	0.368	0.055	1.377	0.024	0.289
NSBMF	1.165	0.086	0.564	0.395	0.685
PWH	274.654	24.468	56.819	59.899	190.287
NPd/P	1413.361	462.153	954.583	362.413	588.795
PdW/P	42.426	2.610	29.942	13.723	26.094
NS/P	1323.001	499.591	692.578	354.867	468.543
SW/P	27.842	3.412	18.665	8.555	15.875

Table 9. Phenotypic (PCV), genotypic (GCV) and error (ECV) coefficient of variability, heritability in broad sense (h^2_b), genetic advance (GA) and genetic advance as percent of mean (GA%) for thirteen characters in chickpea.

Character	PCV	GCV	ECV	h^2_b in %	GA	GA%
DFF	42.723	25.926	9.930	60.685	7.316	9.126
PHFF	66.871	41.994	16.019	62.799	6.327	17.688
NPBFF	9.903	1.591	5.581	16.062	0.178	6.088
NSBFF	14.980	2.711	7.865	18.099	0.245	8.500
DMF	5.844	4.163	1.093	71.237	3.530	3.565
PHMF	34.665	9.913	18.820	28.596	2.444	4.923
NPBMF	8.677	1.292	6.811	14.893	0.186	4.387
NSBMF	15.631	1.148	9.184	7.343	0.163	2.190
PWH	303.414	27.030	210.213	8.909	3.041	3.360
NPd/P	1163.243	380.368	484.598	32.699	25.324	20.842
PdW/P	131.690	8.101	80.994	6.152	0.825	2.562
NS/P	1031.038	389.340	365.144	37.762	28.294	22.050
SW/P	114.588	14.041	65.337	12.254	1.332	5.482

Table 10A. Genotypic (r_g) correlation coefficients between yield and yield contributing characters in chickpea.

Character	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
DFF	0.9111**	-0.3692**	-0.7813**	0.9074**	0.7414**	-0.3692**	-0.7813**	1.0193**	0.5371**	-0.2118*	0.5278**	-0.3065**
PHFF		0.2801**	-0.2150*	1.0041**	1.0104**	-0.4643**	-0.4883**	0.8286**	0.3374**	-0.7886**	0.3257**	-0.6565**
NPBFF			-0.0857NS	0.4015**	0.0840NS	0.1303NS	-0.7447**	1.3917**	0.8545**	0.7067**	0.8974**	0.5483**
NSBFF				0.0867NS	-0.1005NS	-0.4626**	0.6856**	0.1026 NS	0.4024 NS	-0.9067**	0.2864**	-0.4632**
DMF					0.9779**	-0.3947**	-0.3909**	0.9489**	0.4963**	-0.9980**	0.4590**	-0.7263**
PHMF						-0.5860**	-0.6910**	0.7430**	0.0042NS	-1.2284**	-0.0020NS	-1.0915**
NPBMF							1.0867**	-0.4930**	0.7977**	1.1047**	0.8119**	1.0673**
NSBMF								-0.3638**	0.1469 NS	-1.2831**	0.1281 NS	-0.3862**
PWH									-0.4089**	-1.3810**	-0.3438**	-0.9923**
NPd/P										-0.1796NS	0.9941**	0.2047*
PdW/P											-0.0302 NS	0.9406**
NS/P												0.3373**

* = Significant at 5% level
** = Significant at 1% level
NS = Non-significant.

Table 10B. Phenotypic (r_p) correlation coefficients between yield and yield contributing characters in chickpea.

Character	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
DFF	0.6143**	-0.0170NS	-0.2466*	0.5984**	0.3375**	-0.0170 NS	-0.2466*	0.2485*	0.1653NS	-0.1475NS	0.1871NS	-0.1572NS
PHFF		0.2488*	-0.0332NS	0.7396**	0.5252**	-0.0957NS	-0.1474NS	0.1320NS	0.1284NS	-0.1018NS	0.1594NS	-0.1239NS
NPBFF			0.3248**	0.2844**	0.1715NS	0.0482NS	-0.0089NS	-0.0036NS	0.1510NS	0.0060NS	0.1742NS	0.1145NS
NSBFF				0.0353NS	-0.1229NS	0.1552NS	0.2404*	-0.1921NS	0.0591NS	-0.2418*	0.0324NS	-0.1562NS
DMF					0.4774**	-0.1655NS	-0.0627NS	0.1265NS	0.1861NS	-0.2033*	0.2015*	-0.1842NS
PHMF						-0.1735NS	-0.1753NS	0.1339NS	0.0964NS	-0.0728NS	0.0523NS	-0.1252NS
NPBMF							0.1996NS	0.0046NS	0.0309NS	0.0435NS	0.0831NS	0.0314NS
NSBMF								-0.0508NS	0.1532NS	0.0828NS	0.1520NS	0.1718NS
PWH									0.0812NS	0.1374NS	0.0949NS	0.0806NS
NPd/P										0.3417**	0.9758**	0.3753**
PdW/P											0.3829**	0.8538**
NS/P												0.4369**

* = Significant at 5% level
** = Significant at 1% level
NS = Non-significant.

Table 11A. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at genotypic level.

Character	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P
DFF	**0.5425**	-0.3213	0.1366	-0.4973	-1.0997	0.2106	0.3183	-0.1987	-0.0051	-6.2725	-0.0678	6.9438
PHFF	0.4943	**-0.3526**	-0.1036	-0.1369	-1.2168	0.2870	0.4002	-0.1242	-0.0042	-3.9403	-0.2526	4.2850
NPBFF	-0.2003	-0.0988	**-0.3699**	-0.0546	-0.4866	0.0239	-0.1123	-0.1894	-0.0070	-9.9792	0.2264	11.8063
NSBFF	-0.4239	0.0758	0.0317	**0.6365**	-0.1051	-0.0285	0.3988	0.1743	-0.0005	-4.6994	-0.2905	3.7679
DMF	0.4923	-0.3541	-0.1485	0.0552	**-1.2119**	0.2778	0.3402	-0.0994	-0.0048	-5.7960	-0.3197	6.0387
PHMF	0.4022	-0.3563	-0.0311	-0.0640	-1.1851	**0.2840**	0.5051	-0.1757	-0.0037	-0.0490	-0.3935	-0.0263
NPBMF	-0.2003	0.1637	-0.0482	-0.2945	0.4783	-0.1664	**-0.8620**	0.2763	0.0025	-9.3159	0.3539	10.6815
NSBMF	-0.4239	0.1722	0.2754	0.4364	0.4737	-0.1963	-0.9368	**0.2543**	0.0018	-1.7156	-0.4110	1.6853
PWH	0.5530	-0.2922	-0.5147	0.0653	-1.1500	0.2110	0.4250	-0.0925	**-0.0050**	4.7753	-0.4424	-4.5231
NPd/P	0.2914	-0.1190	-0.3160	0.2561	-0.6015	0.0012	-0.6876	0.0374	0.0021	**-11.6785**	-0.0575	13.0785
PdW/P	-0.1149	0.2781	-0.2614	-0.5771	1.2095	-0.3489	-0.9523	-0.3263	0.0070	2.0975	**0.3203**	-0.3973
NS/P	0.2863	-0.1149	-0.3319	0.1823	-0.5563	-0.0006	-0.6999	0.0326	0.0017	-11.6096	-0.0097	**13.1562**

Residual effect = -0.6876

Table 11B. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at phenotype level.

Character	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P
DFF	**0.0402**	-0.0502	-0.0020	0.0008	-0.0397	0.0002	0.0015	-0.0254	-0.0075	-0.1120	-0.1123	0.1496
PHFF	0.0247	**-0.0818**	0.0296	0.0001	-0.0491	0.0002	0.0087	-0.0152	-0.0040	-0.0870	-0.0775	0.1274
NPBFF	-0.0007	-0.0203	**0.1191**	-0.0010	-0.0189	0.0001	-0.0044	-0.0009	0.0001	-0.1023	0.0046	0.1393
NSBFF	-0.0099	0.0027	0.0387	**-0.0031**	-0.0023	-0.0001	-0.0140	0.0247	0.0058	-0.0400	-0.1841	0.0259
DMF	0.0240	-0.0605	0.0339	-0.0001	**-0.0664**	0.0002	0.0150	-0.0065	-0.0038	-0.1261	-0.1548	0.1611
PHMF	0.0136	-0.0429	0.0204	0.0004	-0.0317	**0.0005**	0.0157	-0.0180	-0.0040	-0.0653	-0.0554	0.0418
NPBMF	-0.0007	0.0078	0.0057	-0.0005	0.0110	-0.0001	**-0.0904**	0.0205	-0.0001	-0.0209	0.0331	0.0664
NSBMF	-0.0099	0.0121	-0.0011	-0.0007	0.0042	-0.0001	-0.0181	**0.1029**	0.0015	-0.1038	0.0630	0.1215
PWH	0.0100	-0.0108	-0.0004	0.0006	-0.0084	0.0001	-0.0004	-0.0052	**-0.0301**	-0.0550	0.1046	0.0759
NPd/P	0.0066	-0.0105	0.0180	-0.0002	-0.0124	0.0001	-0.0028	0.0158	-0.0024	**-0.6776**	0.2602	0.7801
PdW/P	-0.0059	0.0083	0.0007	0.0007	0.0135	0.0001	-0.0039	0.0085	-0.0041	-0.2315	**0.7615**	0.3061
NS/P	0.0075	-0.0130	0.0207	-0.0001	-0.0134	0.0001	-0.0075	0.0156	-0.0029	-0.6612	0.2916	**0.7995**

Residual effect = 0.4608

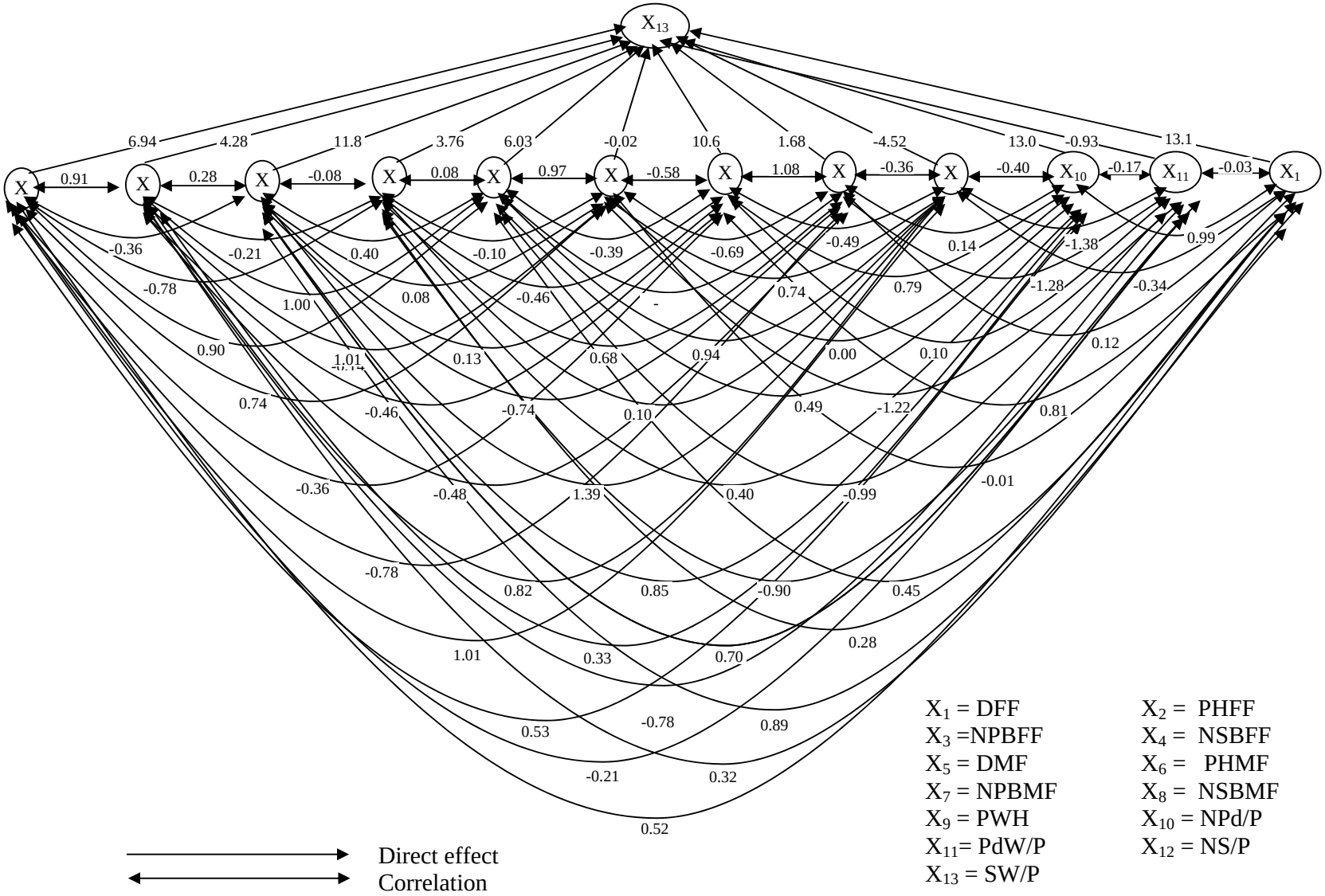


Figure 6. Path coefficient diagram of thirteen yield components at genotypic level.

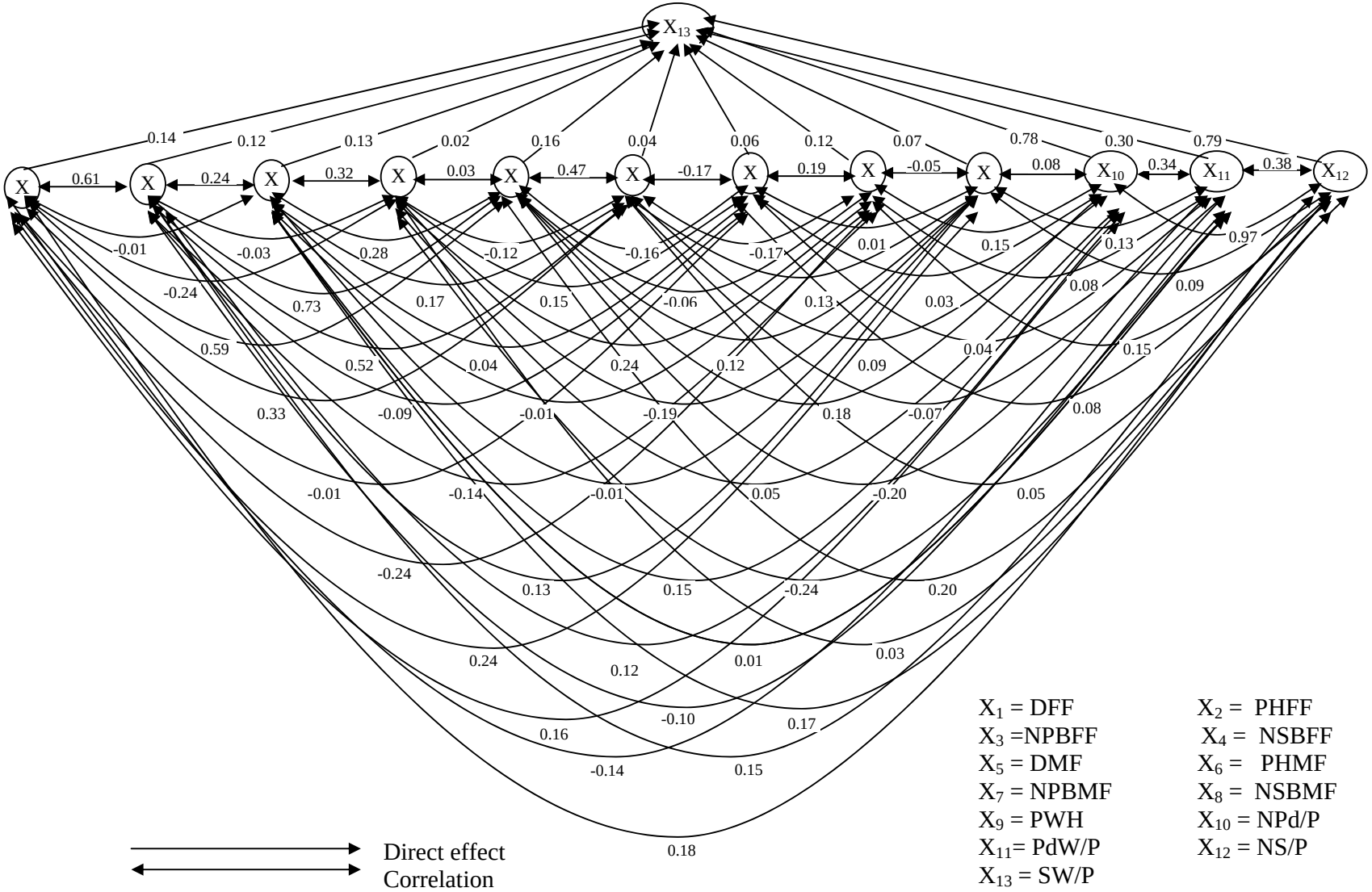


Figure 7. Path coefficient diagram of thirteen yield components at phenotypic level.

Table 12. Expected gain in percentage in seed weight per plant over straight selection from the use of various selection indices in chickpea genotypes (Index which, showed high value is presented only).

Combination	Gain %	Combination	Gain %
13	157.20	5+11	-349.489
1	-173.88	5+13	-288.191
2	19.16	6+7	231.3657
3	2143.01	6+8	140.6306
4	-2757.46	6+13	83.84756
5	-376.81	7+8	1768.277
6	147.08	7+9	136.794
7	3286.72	7+11	305.1981
8	942.67	7+13	371.1951
9	43.08	8+11	-549.435
10	-109.27	8+13	155.7536
11	-675.86	11+13	-252.77
12	-74.40	1+4+5	-216.576
1+4	-211.958	1+4+8	-207.374
1+5	-202.973	1+4+11	-215.777
2+3	67.1229	1+5+8	-200.273
2+4	-264.773	1+5+11	-204.003
2+5	-238.136	2+3+4	-206.185
2+7	124.7193	2+3+5	-220.937
3+4	-1322.4	2+3+7	142.924
3+5	-340.819	2+3+8	66.808
3+6	175.8112	2+4+5	-263.912
3+7	1949.522	2+4+8	-249.087
3+8	1171.211	2+4+11	-275.276
3+9	83.11538	2+4+13	-217.223
3+11	-360.659	2+5+8	-232.421
3+13	247.5535	2+5+11	-238.539
4+5	-411.069	2+5+13	-214.843
4+7	-503.165	2+6+7	66.404
4+8	-1642.03	2+7+8	119.709
4+9	-247.575	2+7+13	59.019
4+11	-853.026	3+4+5	-379.609
4+13	-451.063	3+4+6	-209.21
5+6	-228.671	3+4+7	-688.211
5+7	-301.551	3+4+8	-933.333
5+8	-360.598	3+4+11	-662.317
5+9	-233.186	3+4+13	-319.910

Combination	Gain %	Combination	Gain %
3+5+6	-206.971	5+9+11	-234.660
3+5+7	-263.075	5+9+13	-201.882
3+5+8	-326.491	5+11+13	-281.297
3+5+9	-215.552	6+7+8	217.912
3+5+11	-323.147	6+7+9	71.740
3+5+13	-263.572	6+7+11	111.208
3+6+7	241.223	6+7+13	136.292
3+6+8	166.744	6+8+13	81.440
3+6+11	57.87166	7+8+9	130.9166
3+6+13	102.343	7+8+11	277.7719
3+7+8	1350.986	7+8+13	337.385
3+7+9	153.0216	7+9+13	83.66271
3+7+11	380.2664	7+11+13	127.9177
3+7+13	382.6844	8+11+13	-221.817
3+8+9	81.38379	1+3+4+5	-209.189
3+8+11	-270.648	1+3+4+11	-203.451
3+8+13	229.732	1+4+5+7	-200.231
4+5+6	-262.015	1+4+5+8	-213.896
4+5+7	-350.589	1+4+5+11	-215.605
4+5+8	-395.088	1+4+5+13	-200.345
4+5+9	-260.059	1+4+8+11	-211.825
4+5+11	-375.369	1+5+8+11	-201.566
4+5+13	-319.906	2+3+4+5	-249.315
4+6+7	-301.194	2+3+4+7	-239.51
4+6+11	-252.242	2+3+4+11	-240.185
4+7+11	-502.972	2+3+5+8	-215.508
4+7+13	-267.635	2+3+5+11	-224.714
4+8+9	-231.72	2+3+6+7	75.09319
4+8+11	-739.085	2+3+7+8	136.6712
4+8+13	-402.945	2+3+7+11	59.87234
4+9+11	-265.201	2+3+7+13	88.97106
4+11+13	-403.733	2+4+5+6	-201.537
5+6+8	-222.168	2+4+5+7	-231.991
5+6+11	-232.935	2+4+5+8	-258.233
5+7+8	-288.075	2+4+5+9	-204.405
5+7+11	-295.342	2+4+5+11	-258.894
5+7+13	-231.899	2+4+5+13	-230.492
5+8+9	-227.501	2+4+8+11	-263.863
5+8+11	-337.557	2+4+11+13	-216.436
5+8+13	-278.941	2+5+7+11	-206.814

Combination	Gain %	Combination	Gain %
2+5+8+11	-233.686	3+7+8+13	349.7776
2+5+8+13	-202.049	3+7+9+11	69.71017
2+5+11+13	-210.627	3+7+9+13	95.69281
2+6+7+8	64.35695	3+7+11+13	164.0836
2+7+8+13	73.59978	3+8+11+13	-211.712
3+4+5+6	-244.76	4+5+6+7	-223.043
3+4+5+7	-319.805	4+5+6+8	-255.629
3+4+5+8	-365.37	4+5+6+11	-258.156
3+4+5+9	-245.29	4+5+6+13	-225.463
3+4+5+11	-351.788	4+5+7+8	-337.158
3+4+5+13	-298.797	4+5+7+9	-227.431
3+4+6+7	129.9546	4+5+7+11	-329.928
3+4+6+8	-217.555	4+5+7+13	-275.968
3+4+6+13	-210.558	4+5+8+9	-254.425
3+4+7+8	-613.585	4+5+8+11	-363.569
3+4+7+9	54.3383	4+5+8+13	-310.672
3+4+7+11	-318.91	4+5+9+11	-255.738
3+4+7+13	-355.221	4+5+9+13	-227.102
3+4+8+11	-582.713	4+5+11+13	-305.568
3+4+8+13	-280.758	4+6+7+8	98.44165
3+4+9+11	-228.449	4+6+7+13	-259.789
3+4+11+13	-337.327	4+6+8+11	-237.993
3+5+6+8	-200.689	4+7+8+11	-436.141
3+5+6+11	-216.37	4+7+8+13	-276.959
3+5+7+8	-250.838	4+7+11+13	-243.932
3+5+7+11	-268.102	4+8+9+11	-253.873
3+5+7+13	-202.258	4+8+11+13	-376.687
3+5+8+9	-210.128	4+9+11+13	-207.708
3+5+8+11	-312.364	5+6+8+11	-227.52
3+5+8+13	-255.065	5+6+11+13	-202.847
3+5+9+11	-220.593	5+7+8+11	-285.105
3+5+11+13	-262.253	5+7+8+13	-223.563
3+6+7+8	227.543	5+7+9+11	-201.984
3+6+7+9	79.87321	5+7+11+13	-239.301
3+6+7+11	128.7677	5+8+9+11	-229.835
3+6+7+13	145.7141	5+8+11+13	-273.855
3+6+8+11	57.91431	5+9+11+13	-207.133
3+6+8+13	98.66718	6+7+8+9	69.4649
3+7+8+9	146.1181	6+7+8+11	107.0889
3+7+8+11	340.6964	6+7+8+13	130.667

Combination	Gain %	Combination	Gain %
6+7+11+13	68.39016	3+4+5+7+13	-254.004
7+8+9+13	80.93732	3+4+5+8+9	-239.992
7+8+11+13	123.6122	3+4+5+8+11	-341.064
1+3+4+5+8	-206.606	3+4+5+8+13	-290.328
1+3+4+5+11	-209.07	3+4+5+9+11	-243.476
1+4+5+7+11	-201.324	3+4+5+9+13	-214.879
1+4+5+8+11	-213.179	3+4+5+11+13	-288.724
1+4+5+11+13	-200.706	3+4+6+7+8	124.6043
2+3+4+5+7	-216.227	3+4+6+7+11	-233.006
2+3+4+5+8	-243.98	3+4+6+7+13	78.12196
2+3+4+5+11	-246.744	3+4+6+8+13	-213.322
2+3+4+5+13	-218.464	3+4+7+8+9	54.31083
2+3+4+7+8	-240.779	3+4+7+8+11	-265.388
2+3+4+7+13	-223.195	3+4+7+8+13	-348.911
2+3+4+8+11	-229.57	3+4+8+9+11	-217.737
2+3+5+8+11	-220.105	3+4+8+11+13	-314.515
2+3+6+7+8	72.67581	3+5+6+8+11	-211.207
2+3+6+7+13	50.36936	3+5+7+8+11	-258.738
2+3+7+8+11	58.72243	3+5+7+11+13	-218.214
2+3+7+8+13	85.948	3+5+8+9+11	-216.002
2+4+5+6+11	-204.473	3+5+8+11+13	-255.345
2+4+5+7+8	-226.8	3+6+7+8+9	77.2654
2+4+5+7+11	-232.784	3+6+7+8+11	123.4761
2+4+5+7+13	-202.974	3+6+7+8+13	139.6862
2+4+5+8+9	-201.304	3+6+7+9+13	54.06544
2+4+5+8+11	-254.054	3+6+7+11+13	81.03654
2+4+5+8+13	-226.298	3+7+8+9+11	67.92662
2+4+5+9+11	-206.126	3+7+8+9+13	92.33651
2+4+5+11+13	-229.796	3+7+8+11+13	156.0004
2+4+7+8+13	-200.156	4+5+6+7+8	-217.179
2+4+8+11+13	-208.931	4+5+6+7+11	-227.303
2+5+7+8+11	-202.249	4+5+6+8+11	-252.782
2+5+8+11+13	-206.913	4+5+6+8+13	-220.831
3+4+5+6+7	-203.394	4+5+6+9+11	-201.708
3+4+5+6+8	-238.778	4+5+6+11+13	-226.546
3+4+5+6+11	-244.133	4+5+7+8+9	-222.264
3+4+5+6+13	-211.285	4+5+7+8+11	-319.712
3+4+5+7+8	-307.777	4+5+7+8+13	-267.864
3+4+5+7+9	-211.281	4+5+7+9+11	-229.171
3+4+5+7+11	-306.772	4+5+7+11+13	-270.913

Combination	Gain %
4+5+8+9+11	-250.933
4+5+8+9+13	-222.93
4+5+8+11+13	-298.137
4+5+9+11+13	-226.993
4+6+7+8+13	58.66331
4+7+8+11+13	-220.572
4+8+9+11+13	-200.108
5+7+8+11+13	-232.601
5+8+9+11+13	-203.427
6+7+8+11+13	66.4227
1+3+4+5+8+11	-206.728
2+3+4+5+7+8	-211.275
2+3+4+5+7+11	-219.982
2+3+4+5+8+11	-242.172
2+3+4+5+8+13	-214.461
2+3+4+5+11+13	-219.65
2+3+4+7+8+13	-223.774
2+4+5+6+8+11	-201.472
2+4+5+7+8+11	-228.334
2+4+5+7+11+13	-207.117
2+4+5+8+9+11	-203.356
2+4+5+8+11+13	-226.125
3+4+5+6+7+11	-212.083
3+4+5+6+8+11	-239.071
3+4+5+6+8+13	-206.849
3+4+5+6+11+13	-214.891
3+4+5+7+8+9	-206.331
3+4+5+7+8+11	-297.455
3+4+5+7+8+13	-246.492
3+4+5+7+9+11	-216.149
3+4+5+7+11+13	-253.653

Combination	Gain %
3+4+5+8+9+11	-238.935
3+4+5+8+9+13	-210.89
3+4+5+8+11+13	-281.83
3+4+5+9+11+13	-216.721
3+4+6+7+8+11	-234.382
3+4+6+7+8+13	75.75462
3+4+6+7+11+13	-218.854
3+5+7+8+11+13	-211.835
3+6+7+8+9+13	52.41296
3+6+7+8+11+13	78.38716
4+5+6+7+8+11	-222.367
4+5+6+8+11+13	-222.534
4+5+7+8+9+11	-224.746
4+5+7+8+11+13	-264.281
4+5+7+9+11+13	-203.841
4+5+8+9+11+13	-223.341
2+3+4+5+7+8+11	-215.742
2+3+4+5+8+11+13	-216.14
2+4+5+7+8+11+13	-203.662
3+4+5+6+7+8+11	-207.359
3+4+5+6+8+11+13	-211.054
3+4+5+7+8+9+11	-211.924
3+4+5+7+8+11+13	-247.461
3+4+5+8+9+11+13	-213.226
3+4+6+7+8+11+13	-219.503
4+5+7+8+9+11+13	-200.392

N.B. Numerical sign viz., 1, 2, 3 etc indicated different characters as follows:
1 = DFF, 2 = PHFF, 3 = NPBFF, 4 = NSBFF,
5 = DMF, 6 = PHMF, 7 = NPBMF, 8 = NSBMF,
9 = PWH, 10 = NPd/P, 11 = PdW/P, 12 = NS/P,
13 = SW/P,
Gain % = Expected Genetic gain.

DISCUSSION

The main objective of plant breeders have to improve yield in crop plants. The success of a breeder in the achievement of this objective largely depends upon his ability to identify the most appropriate breeding strategy, whereas the knowledge of a plant breeder about a population is an important requirement for the identification of this strategy (Bakhsh *et al*., 1999). In plant breeding research quantitative characters were no doubt important and most of quantitative characters are economically important. In the present investigation thirteen economically important quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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 eight chickpea genotypes were considered to estimate the variability, heritability, genetic advance, genetic advance as percentage of mean, correlation coefficient, path coefficient and construct the selection index in the material.

Analysis of variance revealed highly significant difference ($P<0.01$) among the chickpea genotypes for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among the experimental material and advocated that enough scope was present for the selection of good performing genotypes in relation to seed yield. Similar results were reported by Saleem *et al*. (2002), Khan *et al*. (2006), Atta *et al*. (2008), Ali *et al*. (2008 and 2009), Jivani *et al*. (2013), Sarker *et al*. (2013) and Zeeshan *et al*. (2013).

The year item was also highly significant (P<0.01) for all the characters except DMF, which indicated that year was also significantly different. This result was in agreement with the findings of Sarker *et al*. (2013). The interaction between year and genotypes was significant all the characters except NPBMF. Significant interaction item indicated that year interacted with genotypes significantly.

Variability is the prerequisite for the initiation of any breeding program for any crop (Ali and Khan, 2007). High magnitude of genetic variability gives free hand to plant breeder for selection and rejection of any character or genotypes have that specific character. The extent of variability with respect to thirteen quantitative characters in eight different genotypes of chickpea measured in terms of components of variation, coefficient of variability along with heritability, genetic advance and genetic advance as percentage of mean.

In the present study, different components of variation varied differently in different characters. Phenotypic component of variation (σ^2_P) was the higher than that of genotypic component of variation (σ^2_G), genotype × year interaction component of variation ($\sigma^2_{G\times Y}$) and within error component of variation (σ^2_E). In the present materials, high phenotypic value causes high genotypic value. The highest genotypic variation along with high phenotypic variation was recorded for NS/P flowed by NPd/P and PWH. Larger genotype value for any character is always helpful for effective selection. The highest value for $\sigma^2_{G\times Y}$ and σ^2_E component of variation also indicated better scope for the improvement of NPd/P, NS/P and PWH through selection, while rest of the traits exhibited low value for σ^2_P, $\sigma^2_{G,}$ $\sigma^2_{G\times Y}$ and σ^2_E which indicating difficulties regarding improvement of these traits through selection. Hasan (2001) and Sarker (2012) reported similar results in chickpea. The differences between phenotypic and genotypic component of variation were grater in magnitude was recorded for NPd/P, NS/P and PWH, which indicated that environment has considerable effect on these characters. This is accordance with Sarker *et al*. (2013).

In general, estimates of phenotypic coefficient of variability (PCV) for all the traits were compared with genotypic coefficient of variability (GCV). Wide difference between PCV and GCV indicated that susceptibility to environmental fluctuation and narrow different between phenotypic and genotypic coefficient of variation in traits implied relative resistance to environmental alteration (Singh *et al*., 2010). Relatively higher value of PCV and GCV are indicative of variability ensuring wide scope for improvement through selection and vice-versa (Gupta *et al*., 2009).

However, in the present investigation phenotypic coefficient of variability was higher than the GCV for all the traits indicating environmental factors influenced their expression. The results are in agreement with the findings of Arshad *et al*. (2003a), Tomar *et al*. (2009), Sharma and Saini (2010), Hasan and Deb (2013), Sarker *et al*. (2013) and Zeeshan *et al*. (2013). The highest GCV as well as high PCV was recorded for NS/P followed by NPd/P, PHFF, PWH and DFF. Thus, the major portion of variation for these traits was contributed by genotypic component, indicating the possibility of improving these traits by adopting proper selection method. This observation is conformity with the findings of earlier workers viz., Pratap *et al*. (2004), Jeena *et al*. (2005), Tomar *et al*. (2009), Hasan and Deb (2013) and Sarker *et al*. (2013). Remaining traits had low to moderate GCV as well as PCV. Sharma and Saini (2010) had also found high magnitude of GCV as well as PCV for number of pods per plant, plant height and days to flowering. Difference between PCV and GCV were greater in magnitude for PWH, NPd/P, PdW/P and NS/P which indicated that environment also had considerable effects on these characters. Similar findings have been reported by Hasan and Deb (2013) and Sarker *et al*. (2013).

The coefficient of variability indicates only the extent of variability present for different characters but do not indicates the heritable portion. The efficiency of selection not only depends on the magnitude of genetic variability but also the

heritability of that character. Heritability alone is not very useful but this statistic alone with genetic advance is valuable (Johanson *et al*., 1955)

In the present investigation, moderate to high heritability was recorded for DFF, PHFF, DMF, NPd/P and NS/P but rest of the trait had comparatively low heritability (<30%). Here, low values of heritability indicate that there is predominance of non-additive gene action and recombinant breeding may thus be useful (Arshad *et al*., 2003a). As per Johanson *et al*. (1955), the heritability value alone provides no indication in selecting the best individual and heritability should be considered along with genetic advance as percentage of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance. High genetic advance as percentage of mean (GA%>20%) with considerable amount of heritability (h^2_b) and high magnitude of GCV were observed for NS/P and NPd/P suggesting that these traits were genetically controlled by additive gene action and can be improved through mass selection, family selection or other modified selection. These results are very close to findings of Pratap *et al*. (2004), Jeena *et al*. (2005), Sharma *et al*. (2005) and Tomar *et al*. (2009). Date of first flower (DFF) and date of maximum flower (DMF) exhibited high heritability accompanied by low genetic advance as percentage of mean indicting the influence of dominant and epistatic genes for these traits and the high heritability may be due to the influence of environmental condition. Arshad *et al*. (2003a) observed similar results for days to flowering, days to maturity and 100-seed weight. Low heritability accompanied with low genetic advance as percentage of mean (GA%) observed for most of the traits which offers less scope for selection, as they were more influenced by the environment and accounted for non-additive gene effect (Srivastava *et al*., 2012). Low heritability and low genetic advance were also observed by Arshad *et al*. (2002), Noor *et al*. (2003), Yucel *et al*. (2006), Sharma and Saini (2010) and Sarker *et al*. (2013) in chickpea.

Grain yield is a complex character that is outcome of interaction between many plant traits, which are in turn influenced by their genetic make up and environment where plant is grown. Therefore the direct evaluation and improvement of grain yield itself may be misleading due to involvement of environmental components. Thus it is very important to analyses the data for relative contribution of various components to yield performance. The simple correlation analysis is an important tool for this purpose.

It was observed in correlation analysis that most of the character pairs both at genotypic and phenotypic levels were in same direction and genotypic estimates were higher than that of phenotypic ones indicating strong inherent association between the traits under studied and little role of environment in the expression of genetic relationship on the phenotypes (Singh *et al*., 2010). Similar results in chickpea were reported by Bakhsh *et al*. (1999), Thakur and Sirohi (2009), Tomar *et al*. (2009) and Sharma and Saini (2010).

However, seed weight per plant (SW/P) that is yield per plant which is the most important economic trait exhibited positive association with NPBFF, NPBMF, NPd/P, PdW/P and NS/P both at genotypic and phenotypic levels, in addition with NSBMF and PWH at phenotypic level. Among them NPd/P, PdW/P and NS/P exhibited significant positive association with SW/P both at genotypic and phenotypic levels while, NPBFF and NPBMF with SW/P only at genotypic level. Above information indicates that these characters are genetically related with SW/P more than those of the other yield related components (Deb and Khaleque, 2005) and suggested that any positive increase in such traits will improve the seed yield in chickpea. Thus it can be inferred that selection based on these traits in combination, will results in identifying high yielding genotypes. Similar findings for most of the traits have also been reported by Saleem *et al*. (2002), Jeena *et al*. (2005), Saleem *et al*. (2005c), Obaidullah *et al*. (2006), Yucel *et al*. (2006), Ali *et al*. (2009), Tomar *et al*. (2009), Thakur

and Sirohi (2009), Vaghela *et al*. (2009), Zali *et al*. (2011), Ali *et al*. (2012) and Jivani *et al*. (2013). Bakhsh *et al*. (2006) also reported primary branches and number of pods per plant in chickpea were positively correlated with grain yield. Significant and positive correlation of NS/P with seed yield has also reported by Yucel and Anlarsal (2010). Significant and positive correlation of NPd/P with seed yield were reported by Saleem *et al*. (2002), Narayana and Reddy (2002), Arshad *et al*. (2003a and 2004), Noor *et al*. (2003), Sial *et al*. (2003), Khan *et al*. (2006), Renukadevi and Subbalakshmi (2006), Atta *et al*. (2008), Thakur and Sirohi (2009), Sharma and Saini (2010), Shahid *et al*. (2010), Akhtar *et al*. (2011) and Zeeshan *et al*. (2013). The characters viz., DFF, PHFF, NSBFF, DMF and PHMF exhibited negative association with SW/P both at genotypic and phenotypic levels while, SW/P with NSBMF and PWH only at genotypic level. In this investigation, negatively correlated traits were all significant at genotypic level indicating a weak association. Khan *et al*. (2006) reported plant height was negatively correlated with seed yield, Sharma and Saini (2010) reported that 100-seed weight, days to maturity and plant height were negatively correlated with seed yield. Due to negative and significant genotypic association of DFF, PHFF, NSBFF, DMF, PHMF, NSBMF and PWH with seed weight per plant, it may suggested that decreasing of these characters seed weight per plant may be increased. In the other word, early flowering, short plant stature, less number of secondary branches both at first and maximum flowering stage and less vegetative growth of a chickpea plant gave more seed weight per plant.

Among the yield contributing traits, genotypic correlation of DFF was highly significant and positive with PHFF, DMF, PHMF, PWH, NPd/P and NS/P indicating that the increasing of DFF would increase plant height, date of maximum flower, plant weight at harvest, number of pods as well as number of seeds per plant. PHFF had positive and highly significant association with PWH, NPd/P and NS/P but negative and highly significant association with

PdW/P which indicated that taller plant at first flower gave more vegetative weight at harvest and more number of pods as well as seeds but pod or seed weight may be reduced while taller plant at maximum flower only gave more vegetative weight at harvest due to highly significant association with PWH. Almost similar result was reported by Zeeshan *et al*. (2013). Number of primary branches both at first flower and maximum flower had positive and highly significant association with NPd/P, PdW/P and NS/P reviled that more number of primary branches produce more large pods as well as seeds while, more number of secondary branches both at first flower and at maximum flower may be produce more pods as well as seeds but pod weight as well as seed weight may be reduced due to negative association with PdW/P. These findings are similar with Sharma and Saini (2010). PWH had significant and negative correlation with NPd/P, PdW/P and NS/P which indicated increase of PWH, yield may be significantly hampered.

Trait NPd/P showed non-significant and negative correlation with PdW/P while highly significant and positive correlation with NS/P at genotypic level which indicated that if the number of pods increased, the number of seeds will also increased significantly but weight of seed slightly reduced. Tomar *et al*. (2009) reported that seeds number per plant exhibited positive and significant association with number of pods per plant.

Correlation coefficient indicates only the general associations between any two traits without tracing any possible causes of such association. In such situations path coefficient analysis both at genotypic and phenotypic levels are worked out to partition the correlation coefficient into direct and indirect effects considering seed weight per plant as a dependent variable. A combination of direct and indirect selection will be effective to get a high selection response.

In the present study, highest positive direct effect of NS/P on seed yield coupled with a relatively high value of correlation both at genotypic and

phenotypic levels suggested that improvement of grain yield in chickpea in linked with this traits and selection of this character might have good impact on seed yield per plants. Saleem *et al*. (1999), Guler *et al*. (2001), Deb and Khaleque (2005), Yucel *et al*. (2006), Ali *et al*. (2009), Yucel and Anlarsal (2010) and Zali *et al*. (2011) reported the same result. On the other hand, the highest negative direct effect on seed yield per plant was recorded for NPd/P both at genotypic and phenotypic levels but highest positive indirect effect of NS/P nullified its negative effect and finally it turn into positive. It demands a good compromise between NPd/P and NS/P. This was an agreement with the findings of Saleem *et al*. (1999) and Deb and Khaleque (2005). Results of the path analysis revealed that most of the traits had great positive indirect effect on seed yield through NS/P. Thus improving of these traits may increase seed yield. It also indicated that NS/P exerted the greatest direct effect. This trait major contributes to seed yield could therefore be used to improve seed yield in chickpea breeding program. Similar reports have been noticed by Yucel *et al*. (2006), Ali *et al*. (2009) and Zali *et al*. (2011) however these finding are contrary with Renukadevi and Subbalakshmi (2006). They found NPd/P as positive and NS/P as negative direct effect on seed yield. Saleem *et al*. (2002), Noor *et al*. (2003), Atta *et al*. (2008), Farshadfar and Farshadfar (2008), Sharma and Saini (2010) and Ali *et al*. (2011) found NPd/P as the highest positive direct effect on yield. Ali *et al*. 2009 and Vaghela *et al*. (2009) found NPd/P and NS/P as positive direct effect on seed yield while, Mushtaq *et al*. (2013) found both NPd/P and NS/P as negative direct effect on seed yield.

Among the yield contributing traits at genotypic level, the trait DFF had positive direct effect on seed yield which was nullified mainly due to high negative indirect values of DMF and NPd/P, thus the total effect was negative but indirect effect of NS/P was high so, indirect selection for this trait to improve seed yield will be desirable. The direct effect of NPBFF and NPBMF had negative but total effect was positive mainly due to high positive indirect effect on seed yield via NS/P

indicating that indirect selection through this trait might be helpful in yield improvement but since the direct effect was negative, so direct selection for these traits to improve yield will not be desirable. This result is in line with the findings of Saleem *et al*. (1999). On the other hand, NSBFF, PHMF and NSBMF had positive direct effect on seed yield but low and the indirect effect of most of the traits also low and negative so, direct or indirect selection for these traits to improve yield will not be effective. At the phenotypic level, the results were almost same as genotypic level, though their direct and indirect values were very low. At the phenotypic level, the trait DFF and PHMF had positive direct effect on seed yield which was nullified mainly due to high negative indirect effect of NPd/P and PdW/P. The direct effect of PHFF, NSBFF and DMF on seed yield was negative and it remains unchanged due to high negative indirect effect of NPd/P and PdW/P. The positive direct effect of NPBFF, NSBMF, PdW/P and NS/P was unchanged due to comparatively high indirect effect of NS/P whereas the negative direct effect of NPBMF, PWH and NPd/P was changed into positive due to high positive indirect effect of PdWP and NS/P.

The residual effect permits precise explanation about the interaction of yield components. The results exhibited medium residual effect both at genotypic and phenotypic levels, which indicated that the variability in the seed yield was contributed by the character with environment included in the present study. Sharma and Saini (2010) also observed medium residual effect at genotypic level.

It is recognized that the yield is a complex character which depends upon the action and interaction of a number of factors and highly influenced by many genetic factors as well as environmental fluctuation. Therefore, it may be misleading to direct selections for yield. The methods of discriminant function are more helpful to estimates reliable effectiveness of the character and character combinations. This method has been successfully followed by various researchers in various crops such as Deb and Khaleque (2007) and Sarker *et al*.

(2013) in chickpea; Ferdous *et al*. (2010) in bread wheat; Kumar *et al*. (2012) in rabi sorghum and Sarker and Deb (2009) in blackgram. In the present study, characters such as PHFF, NPBFF, PHMF, NPBMF, NSBMF, PWH and SW/P exhibited positive expected genetic gain while rest of the characters show negative genetic gain alone. Deb and Khaleque (2007) in chickpea and Nahar (1997) in sugarcane also observed negative value of expected genetic gain. The highest positive genetic gain (3286.72%) was observed for the character NPBMF followed by NPBFF (2143.01%) and NSBMF (942.67%). The highest genetic gain over straight selection (1949.52%) was recorded when two character viz., NPBFF and NPBMF comprised the selection index and this was followed by 1768.28% when NPBMF and NSBMF included in a combinations. Further, the obtained results showed that with the inclusion of NPBFF and NPBMF in an index, the value of expected genetic gain was greatly increased, confirm, that these two traits are more important component for yield. Again, increases in the genetic gain with the addition of more traits were negligible. The results also revealed that, when the characters viz., NPBFF and NPBMF are common in different combination with SW/P gave the maximum expected gain. Therefore, these two yield components viz., NPBFF and NPBMF may be considered as the primary yield component and SW/P will increased by the improvement of the character NPBFF and NPBMF. It also revealed that the studied characters are quantitative in nature and are under polygenic control as they showed slightly under moderate heritability and genetic advance as percentage of mean. The genotypic correlation also indicates that NPBFF and NPBMF had highly significant and positive correlation with seed yield. Hence, those traits having significant correlation alone may be included to formulate selection indices for the improvement of seed yield. Inclusion of more traits may not be necessarily increasing the expected genetic gain and sometimes it may reduce the genetic gain. Moreover, selection of limited characters is more efficient and practical approach in breeding program than the inclusion of more character. Hence, in the

present study the selection index based on seed yield, NPBFF and NPBMF may be considered as appropriate selection index for seed yield improvement in chickpea genotypes. Character viz., NPBMF, NSBMF and RWFD considered as the primary yield components in chickpea by Sarker *et al*. (2013).

In the present study, moderate heritability and high genetic advance as percentage of mean were observed for NPd/P and NS/P which implies that these characters were under the control of additive type of gene action. Again, these two traits showed significant positive correlation with SW/P. Therefore, selection of these traits would better scope for improvement of seed yield in chickpea. Correlation and path analysis also indicated PdW/P as good yield component for chickpea improvement program due to its high positive correlation value and positive direct effect on seed yield.

SUMMARY

The present study was conducted considering thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) to assess variability, heritability, genetic advance, correlation coefficient, path analysis and selection index. The experiment was set in the botanical research field of the University of Rajshahi during the four consecutive robi seasons of 2009-2010, 2010-2011, 2011-2012 and 2012-2013 following randomized complete block design. Analysis of variance revealed that the genotypes were significantly different from each other, which indicating the presence of diversity in genotypes and hence justified their inclusion as materials in the study. The highest genotypic variation along with high phenotypic variation was recorded for the characters NS/P and NPd/P. The phenotypic coefficient of variability (PCV) was higher than that of the genotypic coefficient of variability (GCV) for all the traits which signifying environmental factor influenced their expression. The highest GCV with high PCV were found for the character NS/P followed by NPd/P and PHFF. Again, high genetic advance as percentage of mean with considerable amount of the heritability and high magnitude of GCV were observed for NS/P and NPd/P suggesting that these traits were genetically controlled by additive gene actions and this trait may be useful for further developing high yielding genotypes. Low heritability with low genetic advance as percentage of mean recorded for most of the traits which offer less scope of selection. In the correlation study,

the most of the character pairs exhibited same direction both at genotypic and phenotypic levels. In general, genotypic correlation coefficient observed to be higher than that of phenotypic correlation coefficient which indicated that the phenotypic selection may be rewarded. SW/P exhibited significant and positive association with NPd/P, PdW/P and NS/P at both levels indicating that these characters should given importance during selection to improve the yield potential of chickpea. The path coefficient analysis based on seed weight per plant as a dependent variable revealed that NS/P had the highest positive direct effect on seed weight both at genotypic and phenotypic levels. This observation suggested that improvement of seed yield in chickpea is linked with NS/P and this trait could be explored more confidently as selection criteria for yield improvement in chickpea. The descriminant function analysis showed that when a combination of two attributes viz., NPBFF and NPBMF in an index, gave the highest expected genetic gain. Since these two traits exhibited highest genetic gain in the combination of selection index and showed positive correlation with seed weight per plant both at genotypic and phenotypic levels hence considered as primary yield component. However during selection emphasis may also be given on PdW/P and NS/P as they showed high correlation and positive direct effect on seed yield. Besides this, NPd/P should given importance during selection considering its heritability, genetic advance and positive association with SW/P.

PART-II: STUDY OF GENOTYPE × ENVIRONMENT INTERACTION

INTRODUCTION

The climatic factors, such as rainfall and temperature change from year to year even in the same region. Therefore, a specific genotype does not always exhibit the same phenotypic performance under every year and different genotypes respond differently to a specific environment.

Environmental involvement in the expression of an individual phenotype was first recognized by Johannsen (1909) who worked with the dwarf bean (*Phaseolus vulgaries* L.). He observed heritable and non-heritable differences were jointly responsible for the variation in seed weight of bean and were of the same order of magnitude and effects. He showed that phenotype was the product of both heritable and non-heritable effects and phenotypic variation in any pure line was only due to environmental effects. All the different analyses of continuous variation undertaken over the years on many species of both plant and animal characters have revealed the combination of heritable and non-heritable agencies in the determination of continuous variation.

Latter on, Keeble and Pellow (1910) developed Johansen's findings and subsequently. Fisher (1918) for the first time provided statistical method for partitioning the variation of quantitative characters in segregating populations into genetic and environmental components. East (1915) studying the quantitative characters of *Nicotiana rustica* L., clearly showed that the quantitative characters were inherited with joint action of genetical and environmental variation and that they were inherited according to Mendel's law of inheritance. The influence of the test environments has been investigated by Horner and Frey (1957), Finlay and Wilkinson (1963), Abu El-Fittouh *et al*. (1969) and Shorter *et al*. (1977).

At present, it has become a challenge to breeders to understand fully the control of genetic variation due to the occurrence of genotype × environment (G×E) 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 breeders to face serious problem in the realization of breeding objective for any economic crop.

Some workers have tried to solve the problem created by G×E interaction. Comstock and Robinson (1952), Hanson *et al*. (1956) and Comstock and Moll (1963) mainly developed the analysis variance to estimate G×E interaction. It provides information on the existence and magnitude of G×E interaction only but they no measurement of response of individual genotype with the environment, as such stability measurement of individual genotype was not tested.

Considering regression, two main approaches have been used in the recent past for specifying, estimating and correcting the effects of G×E interaction. The first one is purely statistical analysis which was first proposed by Yates and Cochran (1938), but their ideas were not taken up until Finlay and Wilkinson (1963) rediscovered the same method. This method is based on regression analysis of stability parameters for cultivars by analyzing experiments conducted over years/locations. This model was later on modified by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). Finlay and Wilkinson (1963) reported that the regression coefficient (b_i) is a measure of stability. Eberhart and Russell (1966) proposed to consider two parameters to the first one is the regression coefficient (b_i) to compare relative responsiveness of a particular cultivar to the mean of all cultivars (environmental index) and the second one is the mean square deviation from the regression ($\overline{S}_{di}^2$) for measuring how well the predicted response compares with the observed response.

The second approach is based on fitting of models which specifying the contribution of genetic, environmental and G×E interaction to generation mean and variance due to the contribution of additive, dominance and epistatic gene effects to the genetic and interaction components. This approach has been used by Mather (1949b), Jinks (1954) and Jinks and Mather (1955) in *Nicotinia rustica* L. followed by Bucio Alanis (1966), Bucio Alanis and Hill (1966) and Perkins and Jinks (1968a).

Perkins and Jinks (1968a) formed a bridge over the gap between two alternative analyses. Later, 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 ($\overline{S}^2_{di}$) 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. Perkins and Jinks (1968a) used regression coefficient β_1, which is similar to Finlay and Wilkinson's (1963) regression coefficient (b_i) except the observed values which are adjusted for locations effects before the regression.

Among the models of first approach, models of Eberhart and Russell (1966) and Perkins and Jinks (1968b) are easier to use but these model has been criticized by Baker (1969), Freeman and Perkins (1971) and Easton and Clements (1973) because they are not estimate environmental index independently. In that connection, Freeman and Perkins (1971) proposed independent estimate of environmental index. They suggested that use of an independent measure like one replication to determine the environmental index and the remainder of replicates being used to determine genotype means. They also proposed two methods of stability analysis using regression coefficient (b_i)

and deviation from regression ($\overline{S}^2_{di}$) which is similar to proposed model of Eberhart and Russell (1966).

The joint regression analysis, a form of the analysis of variance, has been widely used in the study of G×E interaction. Its procedure and application were reviewed by Freeman (1973) and Hill (1975). The effectiveness of the analysis 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.

In Bangladesh, chickpea is an important pulse crop and grown as a winter crop. But the cropping pattern of chickpea does not permit sowing at the same time all over the country in each year. Chickpea shown in early November in the Southern part and mid November in the Northern part of our country following aus rice/jute - fallow/chickpea cropping pattern whereas some areas, chickpea grew up under the amon rice - chickpea - fallow cropping pattern which is the late sowing condition. Consequently the sowing time varies from early November to early December which may affect the yield potentials of chickpea, because, at the reproduction stage of chickpea, low temperature and excessive soil moisture or drought expressed various stress and limit its yield potentials. In this regards, it is essential to identify the suitable genotypes that could perform consistently well over a wide range of environments. Thus, understanding the nature of genotype × environment (G×E) interaction is very important. The adaptability of a genotype is usually tested by the degree of its interaction with different environments under which it is planted.

Thus, the present investigation was therefore, deals with the study of stability parameters viz., regression coefficient (b_i), deviation mean square ($\overline{S}^2_{di}$) with standard error following the model of Freeman and Perkins (1971), on some of the quantitative traits such as date of first flower (DFF), plant height at first

flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) in eight genotypes of chickpea (*Cicer arietinum* L.). Chickpea as an important pulse crop in home and abroad are grown worldwide. So, the quality and stability of any quantitative character of chickpea over a range of environments undertaken in the present investigation is quite logical and extensive research effort would be needed on this aspect.

However, G×E interaction analysis are helpful to identify of adaptable genotypes over a wide range of environments, achieving stabilization in crop production over years and prediction of varietals response under changing environments. The genotype × environment interaction and stability parameter have been studied by different workers in chickpea as well as other pulses viz., in chickpea by Islam *et al*. (2000), Ashraf *et al*. (2001), Arshad *et al*. (2003b), Islam *et al*. (2003), Singh and Sandhu (2006), Durga (2008), Choudhary and Haque (2010), Tomar *et al*. (2010), Bakhsh *et al*. (2011) and Rao (2011); in mungbean by Swamy and Reddy (2004), Gomashe *et al*. (2008), Akhtar *et al*. (2010), Lal *et al*. (2013), Nath and Dasgupta (2013), Singh *et al*. (2013); in blackgram by Zubair *et al*. (2002), Pervin *et al*. (2007) and Vijaykumar *et al*. (2012); in grass pea by Tadesse (2003); in lentil by Islam *et al*. (2002); in navy bean by Gebeyehu and Assefa (2003); in french bean by Dethe and Dumbre (2005); in pigeon pea by Patel *et al*. (2009); in cluster bean by Jain and Patel (2012); in cowpea by Patel and Jain (2012) and in faba bean by Firas and AL-Aysh (2013) but still it is very important information that should be available for the forth-coming chickpea varieties.

REVIEW OF LITERATURE

In quantitative characters, the relative phenomenon of different genotypes often varies from one environment of another. This phenomenon is known as genotype × environment (G×E) interaction. There are three well known wide adapted regression based model viz., Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968a) have been used for measuring G×E interactions which have practical implications for stability of performance of many crop genotypes. Above three models are not estimate environmental index independently but Freeman and Perkins (1971) proposed independent estimate of environmental index. However, many papers have already been published in various crops and a few in chickpea concerning with the problem of genotype × environment interaction at different times and some of the papers regarding pulse crops are reviewed below to understand the phenomenon of genotype × environment interaction.

Islam *et al*. (2000) considered eighteen chickpea (*Cicer arietinum* L.) lines for genotype × environment interaction. 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 environment item also was highly significant. Moreover, significant G×E interaction indicated that different genotype responded differently in different environment.

Islam *et al*. (2002) carried out an investigation on genotype × environment interaction of yield and yield components viz., number of primary branches at first flower (NPBFF), number of secondary branches at maximum flower (NSBMF), dry weight per plant (DWPP), pod weight per plant (PdWPP),

number of pods per plant (NPdPP), number of seeds per plant (NSPP) and yield that is seed weight per plant (SWPP) of twelve genotypes of lentil in eight environments. They noticed that the item genotype was highly significant for all the characters, indicating the genotypes were genetically different. On the other hand, environment item was significant for all the characters except NSPP indicating that the genotypes interacted with the environments differently for all the characters under study except NSPP. In the joint regression analysis, the item heterogeneity of regression was non-significance for all the characters while remainder item was found to be highly significant for all the characters indicating that the major part of G×E interaction was not due to heterogeneity its due to non-linear components (reminder). 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 $\overline{S}_{di}^2$ values indicated the unstable performance for all the genotypes and characters under study.

Zubair *et al*. (2002) studied the genotype × environment interaction for grain yield in ten mash genotypes under six diverse environments. Significant differences among the genotypes and the environments indicated the presence of variability among the genotypes as well as the environments under study. 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. Genotype '9010' was the most adaptable showing highest grain yield, average response and non-significant deviation from regression.

Arshad *et al*. (2003b) evaluated twenty five genotypes of chickpea for stability of grain yield under 12 diverse environments. The interaction between the genotypes and environments 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 regression coefficient (b_i) was not significantly different from linearity, therefore, stable performance of the varieties could not be predicted on b_i alone. In this case, deviation from regression and the cultivars yield were used to judge the superior genotypes. The genotypes viz., '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.

Gebeyehu and Assefa (2003) studied genotype × environment interaction and stability for seed yield of navy bean (*Phaseolus vulgaris* L.) genotypes using linear regression. Sixteen genotypes were grown in a randomized complete block design with three replications at four locations. They found that there was considerable variation in seed yield within and across environments. They observed that the significance of the linear proportion demonstrated the adequacy of the regression model in describing the stability of the bean genotypes. Two genotypes viz., G-17450 and PAN-134 with respective regression coefficient (b_i) values of 1.04 and 1.09, smaller $\overline{S}_{di}^2$ values and relatively high mean value of seed yield could be considered the most widely adapted genotypes. The other test genotypes were sensitive to production-limiting factors, their wider adaptability, stability and general performance to the fluctuating growing conditions within and across sites being lowered.

Islam *et al*. (2003) carried out an experiment to study stability of six yield related characters viz., date of maximum flower (DMF), plant height at maximum flower (PHMF), plant weight (PW), number of pods per plant (NPd/P), pod weight per plant (PdW/P) and number of seeds per plant (NS/P)

using six lines of chickpea at four irrigation treatments viz., no irrigation, normal irrigation, below maximum irrigation and maximum irrigation during four consecutive rabi seasons. Genotype × environment interactions were observed for all the characters. Line ICCV-83105 for PHMF having above average mean performance, regression coefficient (b_i) close to 1 and non-significant mean square deviation from regression ($\overline{S}^2_{di}$) indicates this genotype showing stable performance over all the environments, while the lines ICCV- 11 for DMF, RBH-228 for PHMF, Nobin and CCL-85107 for PWH, ICCV-831 05 for NPd/P, ICCL-83149 and ICCL - 85107 both for PdW/P and NS/P were poorly adaptable to favorable environments with $P < \overline{X}$, $b > 1.0$ and minimum $\overline{S}^2_{di}$.

Tadesse (2003) conduct an experiment using ten grass pea varieties to identify the most stable varieties for oxalyl-diamino-propionic acid (ODAP) content and grain yield among the landraces and some Canadian varieties. According to the combined analysis genotypes and environments have significant effects on both ODAP content and grain yield, even though the relative importance of the environmental component of variance was larger than the genotype component for both grain yield and ODAP content. Acc. No. 201513 (a landrace) and LS 82 46 (a Canadian variety) had b values for ODAP content significantly different from unity indicating that these two genotypes are unstable over a wide range of environments. They suggest that environment, genotype and their interaction affect the ODAP content and grain yield performance of grass pea varieties. The ODAP content is significantly affected by both the genotype and environment thought the variation by the environmental component is high. A stable variety for grain yield may not be stable for ODAP content and vice versa.

Swamy and Reddy (2004) conducted an experiment with fifty mungbean genotypes in three different environments (different sowing dates) to study the environment and genotype × environment interaction components. Their study revealed significant differences for all the characters, indicating wide

differences between environments and differential behavior of genotypes in different environments. The linear and non-linear G×E components were significant for all the characters, indicating the importance of both predictable and unpredictable components in determining interaction of the genotypes with environments. The genotype LGG-460 was stable for seed yield per plant in average environmental conditions whereas genotypes Co-5, LGG-427 and LGG-470 considered being stable for poor environmental conditions. Hence these genotypes could be used in further breeding program.

Dethe and Dumbre (2005) carried out genotype × environment interaction on eighteen genotypes of french bean comprising the newly developed lines and certain existing variation under three district environments for nine quantitative traits including seed yield. The significant value of the G×E interaction revealed differential response of the genotypes viz., red clond, ACPR-94038, ACPR-90039, contender and HPR-35 possessed stability for seed yield. They found most of the high yielding genotypes were relatively stable in their study. Genotypes possessing stability indicated their suitability for general cultivations and also to use as donor parents in breeding program.

Singh and Sandhu (2006) had made a study with a set of 90 genotypes of chickpea for genotype × environment interaction for grain yield and its components over three environments created by different sowing dates. Genotypes and environments were found significantly diverse. The G×E interaction was highly significant for all the characters, except seeds per pod and harvest index.

Pervin *et al*. (2007) conducted an experiment to measure genetic variability and genotype × environment interaction using twenty four lines of balckgram for five yield and yield contributing characters, viz., plant height at first flower, number of branches at maximum flower, number of pods per plant, pod weight

per plant and seed weight per plant in four consecutive years. To calculate joint regression analysis they used Freeman and Perkins (1971) model and noticed that, genotype × environment interaction item was significant for plant height at first flower and pod weight per plant. In their study, line-5 for plant height at first flower, line-4 for number of brunches at maximum flower and line-8 for number of pods per plant and pod weight per plant considered as stable genotypes having unit regression coefficient and non-significant $\overline{S}_{di}^2$ values.

Durga (2008) evaluated fourteen genotypes of chickpea comprising desi and kabuli types during the 2000-2001, 2001-2002 and 2002-2003 rabi seasons. Data were recorded for days to 50% flowering, days to maturity, plant height, branches per plant, pods per plant, seed yield and seed weight. In their study a significant sum of squares due to variety × environment (linear) indicated significant differences among the regression coefficients for the 14 genotypes. Variation for pooled deviation, genotype × environment (linear) was be significant indicating some unpredictable causes of variation that are responsible for G×E interaction. High magnitude of environment effect (linear) over G×E (linear) interaction was recorded for days to maturity, branches per plant, pods per plant, plant height and seed yield indicating high adaptation for these traits. The values of environmental indices indicated that environment 1 (year 2000/01) was favorable for days to 50% flowering, days to maturity, plant height, pods per plant and test weight. Environment 1 followed by environment 2 (year 2001/02) was suitable for chickpea, while environment 3 (year 2002/03) was not ideal for growth and development of the crop.

Gomashe *et al*. (2008) done the experiment to evaluate stability parameters using twelve genotypes of mungbean [*Vigna radiata* (L.) Wilczek] for seven quantitative traits in three environments. In their study, genotype × environment interaction was found significant for all the traits. They noted that, the major portion of G×E interaction was due to the linear component. Hence, the prediction

of genotypic performance could be possible over environments. The genotypes TARM 18, PM 9377 and Vaibhav were found high yielding, responsive with non-significant deviation mean square for most of the yield traits.

Patel *et al*. (2009) studied eleven early maturing pigeon pea genotypes along with a check (ICPL-87) for their yield performance during four years (1997-1998, 1998-1999, 1999-2000 and 2000-2001). Highly significant genotype × environment interaction indicated differential response of the genotypes to the environmental changes. Stability analysis was carried out which showed significance of linear component of variation for important traits including grain yield. The genotype SKNP-9264 showed highest yield with high stability followed by SKNP-9256, SKNP-9203-1, SKNP-9217 and SKNP-9226. Genotypes SKNP-9264 and SKNP-9256 were also found stable for pods per plant, primary branches per plant, 100-seed weight, plant height and days to maturity. Similar trend for component traits was also observed for SKNP-9203-1, SKNP-9217 and SKNP-9226. SKNP-9260-2 was found unstable over environments for yield.

Akhtar *et al*. (2010) tested fifteen genotypes of mungbean at five locations in the Kharif season of 2006 to study their yield stability using pooled analysis of variance and stability analysis. They found the genotype × environment (G×E) interaction and both variances due to genotypes and environments were significant. The partitioning of G×E interaction into linear and non-linear components indicated that both predictable and unpredictable components shared the interaction. They computed three stability parameters viz., mean of grain yield over the five locations, regression coefficient (b_i) and deviation from regression ($\overline{S}_{di}^2$) to judge the stable and superior genotype. On the basis of these parameters, the top yielding genotype ‘2 (check) CGM-504’ exhibited the stable performance over all five locations. Results also showed that the

genotypes; BRM-288, NCM-257-2 and BRM-286 gave higher yield. But their performance was unstable due to high deviation from regression.

Choudhary and Haque (2010) cosidered forty two lines of chickpea including two checks for three years in twelve environments for stability parameters. Pooled analysis of variance revealed that the mean sum of square due to genotypes and environments for primary branches per plant, secondary branches per plant and grain yield per plant were highly significant for all the characters.

Tomar *et al*. (2010) conducted an experiment with a set of forty five genotypes of chickpea to measure stability parameters for grain yield and its components over 12 environments created by different sowing dates at two locations. The pooled analysis of variance revealed that mean square due to genotypes were highly significant for all the six characters viz., number of primary branches per plant, number of secondary branches per plant, days to maturity, 100-seed weight, biological yield per plant and grain yield per plant exhibiting enough genetic variability among the genotypes, the mean square due to environment were also highly significant for all the characters. The linear component due to environment was found to be significant for all the characters except secondary branches per plant. The significance of G×E interaction for various characters indicates that the performance of chickpea genotype is very much influenced by the environmental variations indicating scope for agronomical manipulations.

Bakhsh *et al*. (2011) conducted an experiment to quantify G×E interaction effect on grain yield in chickpea, sixteen chickpea genotypes were studied for grain yield at 6 different locations for two years using randomized complete block design. Combined analysis of variance showed significant effects of locations, genotypes, years and their interactions on grain yield. They noted none of the genotypes performed consistently across the environment. The parametric approach and stability parameters indicated that genotypes viz., G1 (BRC-l), G8 (BRC22O) and G9 (BRC-224) were relatively stable in different environments.

Rao (2011) studied twenty one advanced breeding chickpea lines and one local popular variety over three years to identify the high yielding stable genotypes. Genotype (G), environment (E) and G×E interaction variations were found to be significant. Genotypic variance over environments was significant for grain yield, pods per plant and 100-seed weight. Both linear and non-linear components were found to be important for the traits under studied. Significant non-linear component for grain yield indicated the predictability of the traits. Among all the genotypes, genotypes C-506 and C-527 were found to be stable.

Ceyhan *et al*. (2012) tested two cultivars and seven newly developed pea lines to determine stable ability of individual lines for seed yield and yield components. Genotypes were evaluated in three consecutive years viz., 2007, 2008 and 2009. Results from the combined analysis of variance indicated that there were significant differences between years and genotypes for the characters. The stability parameters were subjected to regression to determinate regression coefficient and deviations values. They found differences in the response of environment between genotypes for all traits. The genotypes PS57 and PS53-1 were well adapted for seed yield in good environments. The best-adapted genotypes for seed yield in various environments were PS29-1, PS49, PS100 and PS48 lines. The common parts of the examined genotypes were exhibited specific adaptation ability to different environment; therefore, they represented a target to developing individual plant material for the purpose of breeding programs.

Jain and Patel (2012) conducted an experiment for seed yield performances and stability indices using thirteen genotypes of cluster bean in two years (2008-2009 and 2009-2010) at two locations to identify phenotypically stable genotypes for seed yield and its component traits. Pooled analysis of variance for stability in the performance of different genotypes of guar were highly significant for all the characters viz., days to 50% flowering, days to 75% maturity, pods per plant, plant height and seed yield except pod length and seeds per pod. The G×E

interaction for all the characters was significant and the significant mean square due to environment (linear) indicated the existence of the real genotypic differences in the characters for regression over the environmental mean. The genotypes namely GAUG-0309, GAUG-0416, GAUG-0513 and GAUG-0522 were found stable for earliness and they can be directly used for breeding for earliness. For improvement of seed yield, the genotypes viz., GAUG-0309 and GAUG-0511 were the most stable under rainfed situation.

Patel and Jain (2012) carried out a study for stability analysis in eleven genotypes of cowpea over four different environments (two years and two locations) to identify stable genotypes for yield and their component traits. From the pooled analysis of variance for stability they found that the performance of different genotypes of cowpea were highly significant for all the characters viz., days to 50% flowering, days to maturity, pods per plant, plant height, seeds per pod and seed yield. The G×E interaction was significant for all the characters except days to 50% flowering and seeds per pod and the significant mean square due to the environment (linear) indicated the existence of the real genotypic differences in characters for regression over the environmental mean. The genotypes namely GC-0525 for earliness, GC-0521, GC-0510 and GC-0119 for plant height, GC-0203, GC-0119, and GC-5 for pods per plant and GC-04 for seeds per pod were found to stable and can be directly used for breeding program. For improvement of grain yield, the genotype GC-0121 was most stable and found 20 % superior over the popular check variety GC-5.

Revanappa *et al*. (2012) tested eleven genotypes of blackgram at three locations viz., Dharwad, Bidar and Gulbarga that represented different agro-climatic conditions of North-Karnataka during kharif season of 2009 to study their yield stability. Pooled analysis of variance and stability analysis were performed. The genotype × environment (G×E) interaction and both variance due to genotypes

and environments were significant. The partitioning of G×E interaction into linear and non-linear components indicated that both predictable and unpredictable components shared the interaction. On the basis of stability parameters, the top yielding genotypes viz., K-7-7 (1050 kg/ha) and DU-1 (1024 kg/ha) exhibited the stable performance over the locations. Results also revealed that the genotypes BDU-3-3, T-9 and DU-3 gave higher yield. But their performance was unpredictable due to high deviation from regression.

Firas and AL-Aysh (2013) carried out an experiment to study genotype × environment interaction and stability of performance over three environments (seasons) for seed yield and some of its components viz., number of podded branches per plant, number of seeds per pod, 10-green pod weight and seed yield per plant in 11 indigenous populations of faba bean. They were analyzed genotype × environment interaction using linear regression technique and investigated phenotypic stability using parameters of coefficient regression (b_i) and deviation from regression line ($\overline{S}_{di}^2$). They found the genotype × environment interaction was highly significant ($P \leq 0.01$) for all studied characters. The partitioning of genotype × environment interaction mean squares into linear and non-linear components showed that environments (linear) significantly differed and were quite diverse with regards to their effects on the performance of populations for seed yield and its components. Stable populations were identified for wide and specific environments along with desirable mean performance for all the investigated characteristics. The populations DAR 5, UD I, Q 2/1 and SU I were stable, having average responsiveness; hence, they are suited to all environments. Other populations like DAR 2 and DAR 4 were found suitable for favorable conditions, while populations such as UD II, Q 1/1 and SU II were adapted to low yielding environments for seed yield per plant.

Lal *et al*. (2013) performed an investigation to understand the role of genotype and environmental interactions in the expression of various characters and stability of mungbean genotypes in eight different environments. The significance of environmental component for all the characters except seed yield and protein content in pooled analysis indicated existence of substantial differences among the eight environments. Significant mean squares due to genotype × environment interaction for all the character except protein content suggested that the genotypes showed considerable differential interaction with different environments. The polled deviation was highly significant for all the characters except protein content and 100-seed weight indicating that the response of genotypes taken for this study was not predictable and non-linear component played an important role in the development of the characters. The overall results of the stability analysis indicated that the genotypes Ganga 1 and PS 16 exhibited stability across environment indicating their adoption to spring and kharif seasons, rain-fed as well as irrigated conditions. Thus, role of environment and G×E interactions must be taken into account while devising and implementing selection or breeding programmes in mungbean.

Nath and Dasgupta (2013) conducted an experiment to evaluate thirty mutant genotypes of mungbean at seven environments. They were computed stability parameters to know genotype × environment interaction and genotypic performance for yield per plant and its components viz., number of pods per plant, number of pods per cluster, pod length, number of seeds per pod, number of seeds per plant, 100-seeds weight and seed yield per plant. The analysis of variance indicated that highly significant differences were present among genotypes and environment for seven characters. The linear component of environments registered highly significant variation for the characters like number of pods per plant, pod length, number of seeds per pod, number of seeds per plant and seed yield per plant. In most of the cases, they found the stability for yield components was concomitant with stability for seed yield per plant. Four mutant genotypes

namely CUM1, CUM4, CUM10 and CUM13 registered average stability coupled with high mean performance for seed yield per plant and components consistently, based on regression parameters and sustainability index.

Singh *et al*. (2013) carried out an experiment with mungbean genotypes for their yield performance. In their study, pooled analysis of variance indicated highly significant differences for genotypes (G), environment (E) and G×E interaction. The partitioning of G×E interaction into linear and non-linear components indicated that both predictable and unpredictable components shared the interaction. They computed three stability parameters ($\overline{X}$, b_i and $\overline{S}^2_{di}$) to judge the suitable and superior genotype. The deviation from regression for majority of the genotypes was highly significant revealing the unpredictable response of these genotypes. On the basis of these parameters, three genotypes MH 565, SML 668 and ML 776 with higher performance for seed yield, protein, iron and zinc content and highly significant deviation from linearity may be recommended for better environment.

MATERIALS AND METHODS

A. MATERIALS

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

B. METHODS

The methods followed to conduct the experiment and analyses of the data are divided into the following sub-heads:

a. Preparation and Design of the Experimental Field,

b. Sowing of Seeds,

c. Maintenance of the Experimental Plants,

d. Collection of Data and

e. Techniques of Analysis of Data.

The methods from 'a' to'd' are the same as those described under the methods of PART-I. For this experiment, four consecutive year viz., 2009-2010, 2010-2011, 2011-2012 and 2012-2013 were considered as environments.

e. Techniques of Analysis of Data

1. Mean

Data on individual plant was 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 from each plant.

n = Number of observations.

i = 1, 2, 3…….n

∑= Summation.

2. Standard error of mean

Dispersion of family means around the experimental or estimated population mean is standard error of mean. The standard error of mean are determined 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.

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

3. Analysis of variance

Variance is a measure of dispersion of a population. So, the analysis of variance is done for testing the significant differences among the genotypes. Variance analysis for each of the characters was carried out separately following usual method of analysis of variance with raw data taken on individual plants. The variances due to different sources such as genotype, environment, replication in environments, genotype × environment (G×E) and error of a population were calculated as per the following table.

Table 13. The skeleton of analysis of variance of pooled data.

Source of variation	df	SS	MS	F value
Genotype (G)	G-1=7	SS_1	MS_1	MS_1/ MS_5
Environment (E)	E-1=3	SS_2	MS_2	MS_2/ MS_5
Replication in environment	E(R-1)=8	SS_3	MS_3	MS_3/ MS_5
Genotype × Environment	(G-1)(E-1)=21	SS_4	MS_4	MS_4/ MS_5
Error	E(G-1)(R-1)=56	SS_5	MS_5	
Total	GER-1=95	SS_6	MS_6	

4. Regression analysis

For describing performance in *k*th replication of *i*th genotype in the *j*th environment i.e.Y_{ijk}, Freeman and Perkins (1971) proposed the following model:

$$Y_{ijk} = m + d_i + e_j + g_{ij} + e_{ijk}.$$

Where,

m = general mean

d_i = additive genetic effect of *i*th genotype

e_j = additive environmental effect

g_{ij} = genotype × environment interaction effect and

e_{ijk} = the error associated with *k*th observation.

i = 1, 2, 3….. G (genotype)

j = 1, 2, 3……E (environment)

The collected data were analyzed following subheads:

i. Estimation of environment index

The values of replication 3 are used for measuring environmental index (Z_j) and the values of replication 1 and replication 2 are used for genotype mean and demonstrate the estimation of the stability parameters.

Here,

$$Z_j = Y_{.j} - \overline{Y}..$$

Where,

$Y_{.j}$ = the total over all the genotypes jth environment

$Y.. = \sum_i \sum_j Y_{ij}$ / total number of observations.

Z_j = environmental index,

Here,

$$\Sigma Z_j = 0$$

ii. Estimation of regression coefficient (b_i)

The regression coefficient (b_i) value was calculated as follows:

$$b_i = \sum_j \sum_k Y_{ij} / \sum_j \sum_k Z_j^2$$

But here K = 1

So,

$$b_i = \sum_j Y_{ij} Z_j / \sum_j \sum_k Z_j^2$$

Here,

$\sum_j Z_j^2$ = sum of square of various environmental index.

$\sum_j Y_{ij} Z_j$ = sum of products of environmental index (Z_j) with the corresponding mean of that variety at each location.

The values may be obtained in following manner:

$$\sum_j Y_{ij} Z_j = [Y][Z]=[S]$$

Here,

[Y] = Matrix of pooled data from replication 1 and 2.

[Z] = Vector for environmental index and

[S] = Vector for sum of products i.e. $\sum_j Y_{ij} Z_j$

Here, data was pooled from replication 1 and 2. So, the total values of different b_i are divided by two.

$$b_i = \frac{1}{2} \sum_j Y_{ij} / \sum_j Z_i^2 .$$

iii. Calculation of standard error of b_i

Standard error of b_i was calculated as follows:

$$\text{S.E. of } b_i = \frac{\sqrt{\text{MS due to pooled deviation of } i_{th} \text{ genotype}}}{\sum_j Z_j^2}$$

iv. Calculation of deviation mean square ($\bar{S}_{di}^2$)

- Calculate $\sigma^2 v_i$: which is ss due to i_{th} genotype,

$$\sigma^2_{V_i} = \sum_j Y_{ij}^2 - \left(1/E\right)\left(Y_{i.}^2\right)$$

- Calculate $\bar{S}^2_{d_i}$:

$$\bar{S}^2_{d_i} = \left[\sum \delta^2_{ij}/(E-2)\right] - \left(S^2_e/R\right)$$

Where, $\sum_j \delta^2_{ij} = \sigma^2_{vi} - b\sum_j Y_{ij}Z_j$

Here,

$\sum_j Y_{ij}Z_j$ values needed to be divided by number of replication i.e. R = 2

S^2_e = error mean square

R = replication = 2

v. Joint regression analysis

In the joint regression analysis, a standard two way analysis of variance was done separately for the main three components such as genotype, environment and genotype × environment (G×E) interaction. Again variance due to environment is divided into combined regression and environmental residual that is residual-1. Variance due to genotype × environment interaction is also divided into two parts (i) heterogeneity regression and (ii) interaction residual that is residual-2.

Various sums of squares (SS) are calculated as below:

- SS due to genotypes (G) = $\left(1/RE\right)\left(\sum_j Y_{i..}{}^2\right) - \left(1/GER\right)\left(Y_{...}^2\right)$
- SS due to environments (E) = $\left(1/GR\right)\left(\sum_j Y_{.j.}{}^2\right) - \left(1/GER\right)\left(Y_{...}^2\right)$
- SS due to G×E interaction

$$= \left(1/R\right)\left[\sum_i \sum_j Y^2_{ij.}\right] - \left(1/ER\right)\left[\sum_i Y^2_{i...}\right] - \left(1/GR\right)\left[\sum_j Y^2_{.j.}\right] + \left(1/GER\right)\left(Y_{...}^2\right)$$

- SS pooled error = $\sum_i \sum_j \sum_k Y^2_{ijk} - \left(1/R\right)\left[\sum_i \sum_j Y^2_{ij.}\right]$
- SS due to combined regression = $\left(\sum_j Y_{.j}Z_j\right)^2 / \left(GR\sum_j Z^2_j\right)$

- SS due to residual regression = SS due to environment – SS due to combined regression.
- SS due to heterogeneity of regression = SS due to regression – SS due to combined regression

$$= \left[\sum_j \left\{ \left(\sum_j Y_{ij.} Z_j \right)^2 / R \right\} - \left\{ \left(\sum_j Y_{.j.} Z_j \right)^2 / GR \right\} \right] / \sum_j Z_j^2$$

$$= \left[\left(\sum_j Y_{ij.} Z_j \right)^2 / R \sum_j Z_j^2 \right] - \left[\left(\sum_j Y_{.j.} Z_j \right)^2 / GR \sum_j Z_j^2 \right]$$

- SS residual = SS G×E – SS heterogeneity

Table 14. The skeleton of joint regression analysis according to Freeman and Perkins (1971) model.

Sources	df	SS	MS	F value
Genotype (G)	G-1=7	SS_1	MS_1	MS_1/MS_8
Environments (E)	E-1=3	SS_2	MS_2	MS_2/MS_8
Combined regression	1	SS_3	MS_3	MS_3/MS_4
Residual (1)	E-2=2	SS_4	MS_4	MS_4/MS_8
Interaction (G×E)	(E-1)(G-1)=21	SS_5	MS_5	MS_5/MS_8
Heterogeneity of regression	(G-1)=7	SS_6	MS_6	MS_6/MS_7
Residual (2)	(E-2)(G-1)=14	SS_7	MS_7	MS_7/MS_8
Error between replicates	GE(R-1)=32	SS_8	MS_8	

Where,

G = number of genotypes

E = number of environment

R = number of replication for this calculation

5. Graphical analysis

i. Curve

In the graphical analysis curve were drawn separately for all the thirteen yield and yield contributing traits of chickpea viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P. For

this purpose, environmental mean were plotted along the X-axis and the genotypic 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 environment values which are independent along horizontal axis. In the figure the straight line drawn in 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 estimated genotypic values given by an amount of X of the environment, 'a' is the intersect where regression line cut the Y-axis and it is equal to $\bar{Y}$ ($a = \bar{Y}$), $\bar{X}$ = environmental mean and b is the regression coefficient.

RESULTS

This part of investigation deals with the study of genotype × environment interaction and stability performance of eight genotypes of chickpea over four consecutive years viz., 2009-2010, 2010-2011, 2011-2012, 2012-2013 according to Freeman and Perkins (1971) model. Thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this study. The analyses were done separately and described in the below under different heads:

A. ENVIRONMENTAL AND GENOTYPIC MEAN

a. Environmental Mean (year mean)

The eight genotypes of chickpea were tested in four consecutive years viz., 2009-2010, 2010-2011, 2011-2012 and 2012-2013 on the basis of thirteen quantitative characters viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P. Mean performances of these characters of eight genotypes over four consecutive years (considered as environment) were computed and the results are presented in Table 15.

DFF: For this trait, the highest mean was recorded as 83.03±0.54 in 2010-2011, while the lowest mean was observed as 75.98±0.49 in 2009-2010.

PHFF: The highest environmental mean (37.17±0.42) for this character was noted in 2011-2012 and the lowest mean (34.61±0.34) was observed in 2012-2013.

NPBFF: The highest and the lowest mean were recorded as 4.61±0.09 and 1.53±0.34 in 2010-2011 and in 2012-2013, respectively.

NSBFF: For this character, the highest mean was exhibited by the year 2010-2011 while, the lowest mean was exhibited by the year 2009-2010.

DMF: Year 2011-2012 showed the highest mean and the year 2009-2010 showed the lowest mean for this trait.

PHMF: Regarding this trait, the values of 51.76±0.55 and 46.85±0.28 recorded as the highest and the lowest mean in 2012-2013 and in 2009-2010, respectively.

NPBMF: For this trait, the highest mean was exhibited by the year 2010-2011 with a value of 5.82±0.11 while, the lowest mean was recorded in the year 2012-2013 with a value of 3.26 ±0.10.

NSBMF: The highest mean performance (8.31±0.18) regarding this character was observed in 2011-2012 and the lowest mean performance (6.78±0.13) was recorded in 2012-2013.

PWH: For this character, the highest and the lowest mean were exhibited by the year 2011-2012 and 2012-2013, respectively.

NPd/P: Character number of pods per plant has the highest mean on 2011-2012 and the lowest mean on 2012-2013.

PdW/P: The values of 39.74±1.15 and 25.46±0.86 were noted as the highest and the lowest in 2011-2012 and in 2012-2013, respectively for this character.

NS/P: The highest mean regarding this character was recorded as 155.07±4.57 in 2011-2012 and the lowest mean was noted as 92.70±3.85 in 2012-2013.

SW/P: For this character, the highest and the lowest environmental means were recorded in 2011-2012 and in 2012-2013, respectively.

b. Genotypic Mean

Mean performances of thirteen characters of eight genotypes over four years (considered as environment) were computed according to Freeman and Perkins (1971) model and the results are presented in Table 17A-17M.

DFF: The highest mean (89.98±1.69) for this character was recorded in the genotype-3 and the lowest mean (73.31±1.19) was observed in the genotype-4.

PHFF: The values of 45.42±1.34 and 32.30±1.19 were noted as the highest and the lowest mean for this character in genotype-3 and in genotype-5, respectively.

NPBFF: For this trait, among the eight genotypes, genotype-7 showed the highest mean (3.22±0.48) and genotype-8 showed the lowest mean (2.63±0.39).

NSBFF: Regarding this trait, genotype-4 and genotype-6 showed the highest and lowest mean, respectively.

DMF: Genotype-3 and genotype-8 showed the highest (101.15±0.44) and the lowest (97.43±0.33) mean for this trait, respectively.

PHMF: Regarding this trait, the highest mean of 54.21±1.38 was recorded in genotype-3 and the lowest mean of 46.45±0.69 was noted in genotype-5.

NPBMF: The highest mean (4.95±0.44) was noted in genotype-2 and the lowest mean (3.81±0.42) was recorded in genotype-8 for this character.

NSBMF: Regarding this character, the highest (7.99±0.52) and the lowest (6.66±0.28) mean performance were exhibited by genotype-2 and genotype-8, respectively.

PWH: The value of 102.96±3.86 was recorded as the highest for genotype-7 and the value of 81.32±5.05 was noted as the lowest for genotype-1 for this trait.

NPd/P: For this character, genotype-5 and genotype-8 were exhibited the highest and the lowest mean performance, respectively.

PdW/P: The highest mean (36.10±3.69) was noted for genotype-1 and the lowest mean (27.85±2.51) was noted for genotype-3 regarding this trait.

NS/P: The highest (164.01±15.05) and the lowest (79.06±10.36) mean were recorded for genotype-5 and genotype-8, respectively for this character.

SW/P: For this character, genotype-7 and genotype-3 showed the highest (26.95±3.20) and lowest (19.46±1.66) mean performance, respectively.

B. ANALYSIS OF VARIANCE

The results of the analysis of variance for all the thirteen quantitative characters were done separately and presented in Table 16A-16M. In the analysis of variance, item replication in environment was non-significant for all the characters except NSBMF and PWH. Again, item genotype was highly significant for all the traits and environment item was also highly significant for all the characters except DMF. In this investigation, genotype × environment (G×E) interaction item was significant for all the traits except NPBMF.

C. REGRESSION ANALYSIS

According to Freeman and Perkins (1971) model, two stability parameters were calculated viz., a) the regression coefficient (b_i) which is the regression of the performance of each genotype under different environments on the environmental mean over all the genotypes and b) the mean square deviation from linear regression ($\overline{S}_{di}^2$). The results of these two parameters are shown in Table 17A-17M and are described separately in the below:

a. Regression Coefficient (b_i)

Regression coefficient is a measure of response of individual genotype in the different environments. Regression coefficient (b_i) in the present investigation

were b_i>1.0 and b_i<1.0 indicated an average and below average response, respectively. The b_i value which was near about 1.00 (0.90 to 1.10) indicated average responses. The responses of individual genotypes for each character to different environments are as follows:

DFF: Regarding this character, the regression coefficient was 1.0618±0.0897 for genotype-1 exhibited average response, genotype-3 (1.4725±0.1115), genotype-7 (1.300±0.1197) exhibit above average response while, rest of the genotypes performed below average response.

PHFF: Above average response exhibit by the genotype-1, genotype-2, genotype-3 and genotype-7 while, the rest of the genotypes exhibited bellow average response. Genotype-4 and genotype-8 showed negative value regarding this character.

NPBFF: Average response was exhibited by the genotype-1 (1.0314±0.1022), genotype-5 (0.9972±0.0465) genotype-6 (1.0496±0.0386) and genotype-7 (1.0311±0.2129). Genotype-3 exhibited slightly above average response and the value was 1.1526±0.1444 while, genotype-2, genotype-4 and genotype-8 showed bellow average response regarding this character.

NSBFF: Genotype-2, genotype-3 and genotype-6 showed average response with the values of 1.0509±0.2938, 0.9024±0.1053 and 1.0072±0.0785, respectively while, genotype-1, genotype-5 and genotype-7 showed above average response. Rest of the genotypes showed below average response regarding this trait.

DMF: Regarding this character, only genotype-1 showed average response while, genotype-2, genotype-5 and genotype-8 exhibit bellow average response. Rest of the genotypes viz., genotype-3 genotype-4 genotype-6 and genotype-7 showed above average response.

PHMF: Genotype-6 exhibited average response regarding this character while, above average response were exhibited by the genotype-1, genotype-2 genotype-3 and genotype-4 with the values of 2.2434±0.2263, 1.3021±0.3937, 1.5523±0.3990 and 1.2871±0.2581 respectively. Genotype-5 genotype-7 and genotype-8 were exhibited bellow average response. For this character, genotype-5 and genotype-8 exhibited negative value.

NPBMF: All the genotypes exhibited average response for this character except genotype-4 and genotype-6, where genotype-4 showed below average response (0.7962±0.0895) and genotype-6 exhibited above average response (1.3373±0.1942).

NSBMF: Regarding this character, the values of 1.0240±0.4289 and 0.9115±0.5885 noted for genotype-4 and genotype-6 which indicated average response. Genotype-2 and genotype-7 showed above average response and rest of the genotypes viz., genotype-1, genotype-3, genotype-5 and genotype-8 showed below average response.

PWH: Average response was exhibited by the genotype-2 (0.9558±0.0408). Genotype-1, genotype-3 and genotype-4 exhibit above average response while, genotype-5, genotype-6, genotype-7 and genotype-8 showed bellow average response. The negative b_i value exhibited by genotype-8.

NPd/P: Regarding this character, significant average response was exhibited by the genotype-4 (1.0445±0.0095). Genotype-1, genotype-2 and genotype-6 exhibited slightly above average response while, genotype-3, genotype-5 genotype-7 and genotype-8 exhibited below average response.

PdW/P: Genotype-4 (1.0519±0.0681) and genotype-6 (1.1037±0.0680) showed average response while, genotype-3 (0.7260±0.0754), genotype-5 (0.6046±0.1533) and genotype-8 (0.3937±0.0154) exhibited below average response and the rest of the genotypes showed above average response.

NS/P: For this character, genotypes-1, genotypes-2, genotypes-4 and genotypes-6 showed above average response. While, genotypes-3, genotypes-5, genotypes-7 and genotypes-8 showed below average response. None of the genotypes showed average response.

SW/P: Genotype-6 (1.0759±0.0716) showed average response while, genotypes-1, genotypes-2, genotypes-4 and genotypes-7 showed above average response. Rest of the genotypes viz., genotype-3 (0.8686±0.0636), genotype-5 (-0.3498±0.1572) and genotype-8 (0.2036±0.0548) were showed below average response regarding this character.

b. Deviation Mean Square ($\overline{S}_{di}^2$)

The deviation mean square measures the unpredictable irregularities in response to the environments. A genotype having non-significant deviation mean square ($\overline{S}_{di}^2$) is considered as stable one over a range of environments and its performance may be predictable. On the other hand, significant deviation mean square ($\overline{S}_{di}^2$) values indicate the unpredictable or unstable performance of a genotype. The value of $\overline{S}_{di}^2$ for all thirteen quantitative characters of eight genotypes of chickpea were calculated and presented in Table 17A-17M.

In the present study, deviation mean square ($\overline{S}_{di}^2$) values were found to be non-significant for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF and NSBMF regarding genotype-1; for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PdW/P and SW/P regarding genotype-2; for DFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PdW/P and SW/P regarding genotype-3; for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF and PdW/P regarding genotype-4; for PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF and NSBMF regarding genotype-5; for PHFF, NPBFF, NSBFF, DMF, NPBMF, NSBMF, PdW/P and SW/P regarding genotype-6; for DFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF and

SW/P regarding genotype-7 and for PHFF, NPBFF, NSBFF, DMF, NPBMF, NSBMF, NPd/P and SW/P regarding genotype-8.

D. JOINT REGRESSION ANALYSIS

The joint regression analysis of thirteen characters was done according to Freeman and Perkins (1971) model on eight chickpea genotypes over four consecutive years where, year considered as environment. In the present study, the degrees of freedom (df) for the main three items viz., genotype, environment and genotype × environment interaction were 7, 3 and 21, respectively. Environment item was again divided into combined regression (df=1) and residual-1 (df=2) and similarly, genotype × environment interaction item was divided into heterogeneity of regression (df=7) and residual-2 (df=14). In the joint regression analysis, a standard two way analysis of variance was done separately for the main three components such as genotype, environment and genotype × environment interaction. To tests the significance of these above three main items, error variance was included. According to Freeman and Perkins (1971) model following tests of significance are performed:

a) Genotype, environment and genotype × environment interaction are tested against error MS.
b) Residual for environment (residual-1) and residual for genotype × environment interaction (residual-2) are tested against error MS.
c) Combined regression is tested against residual-1 and
d) Heterogeneity of regression is tested against residual-2.

The degree of freedom, sum of squares and mean sum squares for thirteen quantitative characters are presented in Table 18A-18M and are described separately in the below:

DFF: Regarding this character, items genotype, environment and genotype × environment interaction were highly significant. Residual-1 and residual-2

were also highly significant, but combined regression and heterogeneity of regression were non-significant.

PHFF: Genotype, environment, genotype × environment interaction and combined regression were found to be significant while, residual-1, residual-2 and heterogeneity of regression items were non-significant for this trait.

NPBFF: Regarding this character, genotype, environment, genotype × environment interaction, combined regression and residual-2 were significant while, residual-1 and heterogeneity of regression items were non-significant.

NSBFF: All the items regarding this character were found as significant except residual-2.

DMF: Regarding this traits all the items were found as non-significant except genotype and combined regression.

PHMF: Genotype, environment and residual-1 were significant while, rest of the items were non-significant for PHMF.

NPBMF: Genotype, environment and combined regression were highly significant and rest of the items were non-significant regarding this character.

NSBMF: For NSBMF, genotype, environment, genotype × environment and residual-2 were significant but rest of the items were found as non-significant.

PWH: Regarding this character, genotype, environment, genotype × environment and residual-2 were significant and rest of the items were noted as non-significant.

NPd/P: The items genotype, environment, combined regression, genotype × environment and residual-2 were significant but residual-1 and heterogeneity of regression were recorded as non-significant regarding this trait.

PdW/P: The item genotype, environment, genotype × environment interaction, residual-2 and combined regression were significant. But residual-1 and heterogeneity of regression items were noted as non-significant regarding this character.

NS/P: Regarding this character, the main three items viz., genotype, environment and genotype × environment interaction with residual-2 and combined regression were significant. The items residual-1 and heterogeneity of regression were showed as non-significant values.

SW/P: Except combined regression and heterogeneity of regression all items viz., genotype, environment, genotype × environment interaction, residual-1 and residual-2 were found to be significant for this traits.

E. GRAPHICAL ANALYSIS

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

a. Curve

The performances of different genotypes in different environment regarding different characters are shown by the curves. For this purpose the mean performance of each of the individual genotypes against the mean performance of each of the environment are presented in Figure 8-20 for date of first flower, plant height at first flower, number of primary branches at first flower, number of secondary branches at first flower, date of maximum flower, plant height at maximum flower, number of primary branches at maximum flower, number of secondary branches at maximum flower, plant weight at harvest, number of pods per plant, pod weight per plant, number of seeds per plant and seed weight per plant, respectively. In each figure genotype-1, genotype-2, genotype-3, genotype-4, genotype-5, genotype-6, genotype-7 and genotype-8 were plotted.

DFF: The genotypic mean performance for this trait was represented by curves in Figure 8. It was observed from the figure that genotype-1, genotype-4, genotype-6 and genotype-7 in environment-4; genotype-2 and genotype-8 in environment-3; genotype-3 and genotype-5 in environment-2 exhibited the highest performance. On an overall basis, genotype-3 showed the highest performance in environment-2 and genotype-4 showed the lowest performance in environment-3. The figure also showed that individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction for this character.

PHFF: Regarding this character, the performance of eight genotypes was presented in Figure 9. This figure showed that in environment-2, genotypes viz., genotype-3, genotype-5 and genotype-7; in environment-3, genotype-1, genotype-2, genotype-6 and genotype-8 and in environment-4, only genotype-4 showed the highest performance. In all the four environments genotype-3 and genotype-5 showed the highest and the lowest performance in environment-3, respectively. The individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction.

NPBFF: Genotypic performance for this trait was shown in Figure 10. The figure exhibited that all the genotypes except genotype-2 and genotype-7 showed the highest performance in environment-2 where, these two genotypes showed highest performance in environment-3. The highest and the lowest performance showed by genotype-3 and genotype-8 in environment-2 and in environment-4, respectively. The figure also showed that individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction.

NSBFF: The genotypic mean performance for this trait was represented by curves in Figure 11. In this figure, genotype-2 and genotype-4 in environment-3 and rest of the genotypes in environment-2 exhibited the highest performance.

On an overall basis genotype-5 and genotype-7 showed the highest and the lowest performance in environment-2 and environment-1, respectively. At some points of the figure of individual curves are intersected among themselves which indicated that genotype × environment interaction be present for this character.

DMF: Eight genotypic performances for DMF were presented in Figure 12. For this trait, genotype-1 and genotype-5 in environment-2; genotype-2 and genotype-6 in environment-4; genotype-3, genotype-4, genotype-7 and genotype-8 in environment-3 displayed the highest performance. Genotype-3 showed the highest performance in environment-3 and genotype-8 showed the lowest performance in environment-2 on an overall basis of environment. Individual curves are intersected at some points among themselves in the figure indicating the existence of genotype × environment interaction for this character.

PHMF: The genotypic mean performance for this character was denoting in Figure 13. It was observed that genotype-1, genotype-2, genotype-3, genotype-4, genotype-6 and genotype-8 in environment-4 while, genotype-5 in environment-3 and genotype-7 in environment-2 exhibited the highest performance. On an overall basis genotype-3 showed the highest performance in environment-4 and genotype-5 showed the lowest performance in environment-4. The individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction.

NPBMF: The genotypic mean performance for NPBMF was illustrated in Figure 14. The figure showed that all genotypes were exhibited the highest performance in environment-2. On an overall basis, genotype-6 showed the highest performance in environment-2 and genotype-8 showed the lowest performance in environment-4. The existence of genotype × environment

interaction for this character is indicating by intersected at some points of individual curves among themselves.

NSBMF: Genotypic mean performance for this trait was shown in Figure 15. It was observed that all genotypes except genotype-3 showed the highest performance in the envronment-3. Again, genotype-2 showed the highest performance in environment-3 and genotype-1 showed the lowest performance in environment-4 on an overall basis. The existence of genotype × environment interaction was indicated by intersected individual curves at some points among themselves.

PWH: The genotypic mean performance of different genotypes for this trait shown in Figure 16. Perusal the figure it was observed that in environment-1, genotype-5 and genotype-7; in environment-2, genotype-8 and in environment-3, genotype-1, genotype-2, genotype-3, genotype-4 and genotype-6, exhibited the highest performance. Considering four environments genotype-3 and genotype-1 showed the highest and the lowest performance in environment-3 and environment-2, respectively. Individual curves are intersected at some points among themselves in the figure which indicated the existence of genotype × environment interaction.

NPd/P: The mean performance of different genotypes for this trait was represented in Figure 17. Perusal the figure it was observed that the genotypes viz., genotype-1, genotype-2, genotype-3, genotype-4 and genotype-6 in environment-3; genotype-5 and genotype-1 in environment-1 and genotype-7 only in environment-2 were showed the highest performance. Whereas, on the overall basis of the four environments genotype-5 showed the highest performance in environment-1 and genotype-8 showed the lowest performance in environment-4. The figure also showed that individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction for this character.

PdW/P: Regarding this character eight genotypic performance was illustrated in Figure 18. The figure showed that the five genotypes such as genotype-1, genotype-2, genotype-6, genotype-7 and genotype-8 exhibited the highest mean performance in environment-3 where, genotype-3 and genotype-5 in environment-1 and genotype-4 in environment-2 showed the highest mean performance. Whereas, genotype-1 and genotype-3 showed the highest and the lowest performance in environment-3 and environment-4, respectively among the four environments. The individual curves are intersected at some points among themselves indicating the existence of genotype × environment interaction.

NS/P: The performance of eight genotypes regarding this trait shown in Figure 19. The figure showed that only two genotypes showed the highest performance in environmnt-1 and these were genotype-5 and genotype-8 while, in environment-3 rest of the genotypes viz., genotype-1, genotype-2, genotype-3, genotype-4, genotype-6 and genotype-7 showed the highest mean performance. On the overall basis of the four environments genotype-5 showed the highest performance in environment-1 and genotype-8 showed the lowest performance in environment-4. Existence of genotype × environment was indicating by intersecting at some points of individual curves.

SW/P: Regarding this character, the performance of genotypes shown in Figure 20. From the figure it was observed that the genotypes such as, genotype-1, genotype-2, genotype-3, genotype-6 and genotype-7 in environment-3; genotype-5 and genotype-8 in the environment-1 and genotype-4 in environment-2 exhibited the highest performance. Whereas, in an overall basis of the four environments genotype-7 showed the highest performance in environment-3 and genotype-3 showed the lowest performance in environment-4. Individual curves are intersected at some points among themselves in the figure indicating the existence of genotype × environment interaction.

b. Regression Graph

The regression linens for each genotype against the corresponding environmental mean are shown in Figure 21-33, respectively for date of first flower, plant height at first flower, number of primary branches at first flower, number of secondary branches at first flower, date of maximum flower, plant height at maximum flower, number of primary branches at maximum flower, number of secondary branches at maximum flower, plant weight at harvest, number of pods per plant, pod weight per plant, number of seeds per plant and seed weight per plant. Plotting environmental means on X-axis and genotypic performance on Y-axis, the regression lines were drawn. Here, to avoid confusion individual points were not plotted in these figures. Intercrossing of the lines was prominent in all the characters, which indicated the presence of interaction between genotypes and environments.

Table 15. Mean performance of thirteen characters overall four consecutive years.

Character		2009-10	2010-11	2011-12	2012-13
DFF	Mean ± SE	75.98 ± 0.49	83.03 ± 0.54	82.00 ± 0.61	81.18 ± 0.51
PHFF	Mean ± SE	35.72 ± 0.41	36.92 ± 0.62	37.17 ± 0.42	34.61 ± 0.34
NPBFF	Mean ± SE	2.48 ± 0.05	4.61 ± 0.09	3.40 ± 0.07	1.53 ± 0.05
NSBFF	Mean ± SE	1.86 ± 0.08	4.01 ± 0.12	3.36 ± 0.09	2.25 ± 0.07
DMF	Mean ± SE	98.48 ± 0.23	99.16 ± 0.30	99.32 ± 0.23	99.18 ± 0.19
PHMF	Mean ± SE	46.85 ± 0.28	49.95 ± 0.53	48.72 ± 0.30	51.76 ± 0.55
NPBMF	Mean ± SE	3.34 ± 0.05	5.82 ± 0.11	4.74 ± 0.08	3.26 ± 0.10
NSBMF	Mean ± SE	6.89 ± 0.11	7.28 ± 0.10	8.31 ± 0.18	6.78 ± 0.13
PWH	Mean ± SE	89.59 ± 2.58	88.45 ± 2.13	100.19 ± 3.08	88.44 ± 2.29
NPd/P	Mean ± SE	120.21 ± 5.15	133.53 ± 4.07	150.40 ± 4.67	80.43 ± 3.83
PdW/P	Mean ± SE	29.82 ± 1.07	32.41 ± 1.05	39.74 ± 1.15	25.46 ± 0.86
NS/P	Mean ± SE	122.77 ± 5.09	135.87 ± 4.06	155.07 ± 4.57	92.70 ± 3.85
SW/P	Mean ± SE	21.60 ± 0.83	25.58 ± 0.90	30.42 ± 0.89	19.18 ± 0.61

Table 16A-16M. Analysis of variance of pooled data for genotype and environment (G×E) interaction of thirteen characters in chickpea.

Table 16A. Date of first flower (DFF).

Source of variation	df	SS	MS	F value
Genotype	7	1917.0233	273.8605	34.3878**
Environment	3	686.6047	228.8682	28.7383**
Replication in environments	8	75.9817	9.4977	1.1926NS
Genotype × Environment	21	513.9312	24.4729	3.0730**
Error	56	445.9776	7.9639	
Total	95	3639.5185	38.3107	

Table 16B. Plant height at first flower (PHFF).

Source of variation	df	SS	MS	F value
Genotype	7	1368.4123	195.4875	35.2068**
Environment	3	118.5610	39.5203	7.1175**
Replication in environments	8	69.3154	8.6644	1.5604NS
Genotype × Environment	21	319.9356	15.2350	2.7438**
Error	56	310.9424	5.5525	
Total	95	2187.1667	23.0228	

Table 16C. Number of primary branches at first flower (NPBFF).

Source of variation	df	SS	MS	F value
Genotype	7	6.7288	0.9613	5.5141**
Environment	3	102.8251	34.2750	196.6142**
Replication in environments	8	0.6067	0.0758	0.4350NS
Genotype × Environment	21	8.4621	0.4030	2.3115**
Error	56	9.7623	0.1743	
Total	95	128.3850	1.3514	

Table 16D. Number of secondary branches at first flower (NSBFF).

Source of variation	df	SS	MS	F value
Genotype	7	10.8155	1.5451	7.2574**
Environment	3	69.0803	23.0268	108.1599**
Replication in environments	8	2.2008	0.2751	1.2922NS
Genotype × Environment	21	12.7557	0.6074	2.8531**
Error	56	11.9222	0.2129	
Total	95	106.7744	1.1239	

Table 16E. Date of maximum flower (DMF).

Source of variation	df	SS	MS	F value
Genotype	7	366.1407	52.3058	45.3746**
Environment	3	3.8883	1.2961	1.1243NS
Replication in environments	8	11.9955	1.4994	1.3007NS
Genotype × Environment	21	59.4078	2.8289	2.4541**
Error	56	64.5543	1.1528	
Total	95	505.9867	5.3262	

Table 16F. Plant height at maximum flower (PHMF).

Source of variation	df	SS	MS	F value
Genotype	7	540.5557	77.2222	9.9443**
Environment	3	230.3315	76.7772	9.8870**
Replication in environments	8	180.6530	22.5816	2.9080NS
Genotype × Environment	21	381.6842	18.1754	2.3405**
Error	56	434.8668	7.7655	
Total	95	1768.0912	18.6115	

Table 16G. Number of primary branches at maximum flower (NPBMF).

Source of variation	df	SS	MS	F value
Genotype	7	7.1415	1.0202	3.5381**
Environment	3	100.0294	33.3431	115.6323**
Replication in environments	8	2.0317	0.2540	0.8807NS
Genotype × Environment	21	7.6046	0.3621	1.2558NS
Error	56	16.1479	0.2884	
Total	95	132.9551	1.3995	

Table 16H. Number secondary branches at maximum flower (NSBMF).

Source of variation	df	SS	MS	F value
Genotype	7	20.2794	2.8971	4.6695**
Environment	3	42.6905	14.2302	22.9360**
Replication in environments	8	11.5220	1.4403	2.3214*
Genotype × Environment	21	39.2715	1.8701	3.0142**
Error	56	34.7440	0.6204	
Total	95	148.5075	1.5632	

Table 16I. Plant weight at harvest (PWH).

Source of variation	df	SS	MS	F value
Genotype	7	4645.1784	663.5969	4.3615**
Environment	3	4661.8095	1553.9365	10.2134**
Replication in environments	8	3535.5853	441.9482	2.9047**
Genotype × Environment	21	7769.6824	369.9849	2.4318**
Error	56	8520.2379	152.1471	
Total	95	29132.4935	306.6578	

Table 16J. Number of pods per plant (NPd/P).

Source of variation	df	SS	MS	F value
Genotype	7	50553.113	7221.873	13.1291**
Environment	3	70496.386	23498.795	42.7199**
Replication in environments	8	7244.063	905.508	1.6462NS
Genotype × Environment	21	35196.702	1676.033	3.0470**
Error	56	30803.732	550.067	
Total	95	194293.996	2045.200	

Table 16K. Pod weight per plant (PdW/P).

Source of variation	df	SS	MS	F value
Genotype	7	690.0665	98.5809	3.5929**
Environment	3	2234.0871	744.6957	27.1413**
Replication in environments	8	93.3050	11.6631	0.4251NS
Genotype × Environment	21	1412.4945	67.2616	2.4514**
Error	56	1536.5150	27.4378	
Total	95	5966.4681	62.8049	

Table 16L. Number of seeds per plant (NS/P).

Source of variation	df	SS	MS	F value
Genotype	7	52697.6190	7528.2313	15.9013**
Environment	3	51271.2697	17090.4232	36.0987**
Replication in environments	8	3543.2870	442.9109	0.9355NS
Genotype × Environment	21	32196.0354	1533.1445	3.2383**
Error	56	26512.4187	473.4360	
Total	95	166220.6298	1749.6908	

Table 16M. Seed weight per plant (SW/P).

Source of variation	df	SS	MS	F value
Genotype	7	577.3592	82.4799	5.2994**
Environment	3	1391.4837	463.8279	29.8014**
Replication in environments	8	137.4233	17.1779	1.1037NS
Genotype × Environment	21	872.3326	41.5396	2.6690**
Error	56	871.5811	15.5639	
Total	95	3850.1799	40.5282	

* = significant at 5% level, ** = significant at 1% level, NS = non-significant.

Table 17A-17M. Stability test of thirteen characters of eight genotypes of chickpea according to Freeman and Perkins (1971) model.

Table 17A. Date of first flower (DFF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	80.12	1.54	1.0618	0.0897	-4.3677	-1.5557
2	79.62	1.17	0.4962	0.0881	-4.4941	-1.6007
3	89.98	1.69	1.4725	0.1115	-2.4514	-0.8732
4	73.31	1.19	0.6631	0.1554	2.6603	0.9475
5	82.92	1.82	0.8025	0.2191	13.0879	4.6617
6	79.87	0.89	0.5263	0.0170	-7.7554	-2.7624
7	80.03	1.59	1.3000	0.1197	-1.6267	-0.5794
8	78.50	2.32	0.7234	0.3621	49.3720	17.5856

Table 17B. Plant height at first flower (PHFF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	36.41	0.87	1.4261	0.3796	-4.7148	-1.9293
2	34.78	1.45	2.0685	1.0479	3.6079	1.4764
3	45.42	1.34	2.1964	1.2220	7.0550	2.8869
4	33.94	0.63	-0.3618	0.7106	-1.5663	-0.6409
5	32.30	1.19	0.0149	0.8485	0.3092	0.1265
6	37.24	1.06	0.6813	0.4379	-4.2990	-1.7592
7	35.63	0.76	1.4120	0.3345	-4.9958	-2.0443
8	33.12	0.82	-0.2030	0.7505	-1.0581	-0.4330

Table 17C. Number of primary branches at first flower (NPBFF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	2.92	0.44	1.0314	0.1022	-0.0584	-0.1532
2	2.77	0.29	0.5904	0.1969	0.1780	0.4667
3	3.12	0.49	1.1526	0.1444	0.0284	0.0744
4	2.67	0.31	0.7263	0.0015	-0.1455	-0.3815
5	3.21	0.43	0.9972	0.0465	-0.1275	-0.3342
6	2.76	0.43	1.0496	0.0386	-0.1331	-0.3490
7	3.22	0.48	1.0311	0.2129	0.2327	0.6100
8	2.63	0.39	0.8644	0.0980	-0.0655	-0.1716

Table 17D. Number of secondary branches at first flower (NSBFF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	2.72	0.51	1.4243	0.3584	0.3363	0.7050
2	2.86	0.40	1.0509	0.2938	0.1513	0.3171
3	2.92	0.30	0.9024	0.1053	-0.1789	-0.3750
4	3.39	0.20	0.2731	0.2255	-0.0044	-0.0092
5	3.04	0.45	1.3819	0.1074	-0.1769	-0.3708
6	2.52	0.36	1.0072	0.0785	-0.2005	-0.4203
7	2.57	0.40	1.1605	0.1326	-0.1504	-0.3153
8	2.93	0.30	0.6840	0.2486	0.0437	0.0917

Table 17E. Date of maximum flower (DMF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	98.24	0.33	0.9861	1.4661	-0.9516	-0.8553
2	98.18	0.29	0.1124	1.6164	-0.8899	-0.7999
3	101.15	0.44	1.4218	3.0071	-0.0341	-0.0306
4	98.25	0.31	1.6089	0.7663	-1.1596	-1.0423
5	98.29	0.39	0.6419	1.9692	-0.7216	-0.6486
6	98.44	0.50	1.4741	1.8440	-0.7851	-0.7057
7	98.31	0.35	2.5967	0.2845	-1.2269	-1.1028
8	97.43	0.33	0.4899	1.1021	-1.0760	-0.9672

Table 17F. Plant height at maximum flower (PHMF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	51.05	2.11	2.2434	0.2263	-3.5358	-1.2706
2	49.67	1.27	1.3021	0.3937	4.9873	1.7921
3	54.21	1.38	1.5523	0.3990	5.3374	1.9179
4	47.16	1.35	1.2871	0.2581	-2.2736	-0.8170
5	46.45	0.69	-0.5026	0.2043	-4.3138	-1.5501
6	48.90	0.98	0.9231	0.1023	-6.8842	-2.4738
7	48.52	0.79	0.4140	0.2809	-1.2609	-0.4531
8	48.63	0.36	-0.1085	0.0684	-7.3605	-2.6449

Table 17G. Number of primary branches at maximum flower (NPBMF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	4.01	0.47	1.0873	0.0499	-0.2582	-0.4875
2	4.95	0.44	1.0354	0.1663	-0.0333	-0.0629
3	4.02	0.36	0.9197	0.0311	-0.2717	-0.5132
4	4.15	0.33	0.7962	0.0895	-0.2087	-0.3942
5	4.43	0.41	0.9824	0.1406	-0.1037	-0.1958
6	4.39	0.54	1.3373	0.1942	0.0568	0.1072
7	4.30	0.43	0.9716	0.1472	-0.0866	-0.1636
8	3.81	0.42	0.9856	0.1927	0.0515	0.0973

Table 17H. Number secondary branches at maximum flower (NSBMF).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	6.68	0.36	0.7830	0.5900	0.1055	0.1486
2	7.99	0.52	1.4680	0.2471	-0.3974	-0.5595
3	6.95	0.30	-0.1960	0.8385	0.7272	1.0239
4	7.70	0.40	1.0240	0.4289	-0.1820	-0.2563
5	6.86	0.33	0.8192	0.4277	-0.1838	-0.2589
6	7.52	0.37	0.9115	0.5885	0.1023	0.1440
7	7.44	0.54	1.1883	0.9189	0.9749	1.3728
8	6.66	0.28	0.4625	0.1694	-0.4541	-0.6394

Table 17I. Plant weight at harvest (PWH).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	81.32	5.05	2.8150	0.0977	-73.0584	-6.7060
2	93.83	4.62	0.9558	0.0408	-110.7417	-10.1650
3	96.87	4.58	1.2079	0.2125	97.1690	8.9192
4	83.74	5.42	1.6743	0.0700	-95.2494	-8.7430
5	87.81	4.59	0.2308	0.2380	151.9872	13.9509
6	91.98	5.52	0.6929	0.2572	197.3794	18.1175
7	102.96	3.86	0.5359	0.0245	-115.8225	-10.6314
8	94.81	3.82	-0.2695	0.1845	43.9839	4.0373

Table 17J. Number of pods per plant (NPd/P).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	132.58	16.16	1.3931	0.0053	-476.3516	-19.8248
2	133.00	16.95	1.3848	0.0093	-270.2301	-11.2464
3	138.27	9.31	0.2660	0.0054	-473.1407	-19.6912
4	119.12	14.23	1.0445	0.0095	-256.8172	-10.6882
5	158.37	16.89	0.8073	0.0273	2073.982	86.3151
6	109.42	16.20	1.2143	0.0138	97.7154	4.0667
7	101.00	10.06	0.5205	0.0073	-388.4633	-16.1671
8	77.34	10.69	0.3780	0.0132	41.9761	1.7470

Table 17K. Pod weight per plant (PdW/P).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	36.10	3.69	2.0774	0.0306	-18.5244	-3.7826
2	31.36	3.29	1.6772	0.0660	1.5183	0.3100
3	27.85	2.51	0.7260	0.0754	9.2751	1.8939
4	29.51	2.22	1.0519	0.0681	3.1058	0.6342
5	32.69	3.32	0.6046	0.1533	113.4108	23.1580
6	34.96	2.80	1.1037	0.0680	3.0424	0.6213
7	34.44	3.69	2.2372	0.0406	-14.3491	-2.9300
8	29.35	1.55	0.3937	0.0154	-22.5977	-4.6144

Table 17L. Number of seeds per plant (NS/P).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	136.36	15.85	1.5295	0.0137	-78.427	-3.5905
2	137.98	15.30	1.3461	0.0168	118.962	5.4463
3	140.56	9.76	0.3910	0.0053	-417.242	-19.1021
4	122.14	13.83	1.2699	0.0072	-366.627	-16.7848
5	164.01	15.05	0.4751	0.0358	2245.421	102.7994
6	118.07	13.73	1.2342	0.0167	115.212	5.2746
7	114.54	6.85	0.5708	0.0033	-453.981	-20.7841
8	79.06	10.36	0.2652	0.0182	222.338	10.1790

Table 17M. Seed weight per plant (SW/P).

Variety	Mean	SE	b_i	Sb_i	$\overline{S}^2_{di}$	C test value
1	26.49	2.67	1.3767	0.1248	29.5975	7.9035
2	24.10	3.05	1.9570	0.0728	0.8152	0.2177
3	19.46	1.66	0.8686	0.0636	-2.7015	-0.7214
4	23.29	2.08	1.5252	0.0090	-13.7962	-3.6840
5	25.55	2.36	-0.3498	0.1572	55.2064	14.7419
6	25.23	1.97	1.0759	0.0716	0.3227	0.0862
7	26.95	3.20	2.3381	0.0728	0.8211	0.2193
8	21.66	1.50	0.2036	0.0548	-5.6190	-1.5005

Table 18A-18M. Analysis of variance for joint regression for thirteen characters of eight genotypes of chickpea according to Freeman and Perkins (1971) model.

Table 18A. Date of first flower (DFF).

Source of variation	df	SS	MS	F value
Genotype	7	1223.70	174.81	22.18**
Environment	3	472.84	157.61	20.00**
Combined Regression	1	382.15	382.15	8.43NS
Residual-1	2	90.69	45.34	5.75**
Genotype × Environment	21	395.31	18.82	2.39*
Heterogeneity of Regression	7	56.07	8.01	0.33NS
Residual-2	14	339.24	24.23	3.07**
Error between replicates	32	252.23	7.88	

Table 18B. Plant height at first flower (PHFF).

Source of variation	df	SS	MS	F value
Genotype	7	945.73	135.10	22.62**
Environment	3	66.83	22.28	3.73*
Combined Regression	1	64.84	64.84	65.12*
Residual-1	2	1.99	1.00	0.17NS
Genotype × Environment	21	238.08	11.34	1.90*
Heterogeneity of Regression	7	71.61	10.23	0.86 NS
Residual-2	14	166.47	11.89	1.99 NS
Error between replicates	32	191.10	5.97	

Table 18C. Number of primary branches at first flower (NPBFF).

Source of variation	df	SS	MS	F value
Genotype	7	3.31	0.47	3.25**
Environment	3	65.36	21.79	149.69**
Combined Regression	1	65.17	65.17	689.46 **
Residual-1	2	0.19	0.09	0.65 NS
Genotype × Environment	21	6.46	0.31	2.11*
Heterogeneity of Regression	7	2.35	0.34	1.15 NS
Residual-2	14	4.10	0.29	2.01*
Error between replicates	32	4.66	0.15	

Table 18D. Number of secondary branches at first flower (NSBFF).

Source of variation	df	SS	MS	F value
Genotype	7	4.33	0.62	2.72*
Environment	3	47.41	15.80	69.45**
Combined Regression	1	44.19	44.19	27.50*
Residual-1	2	3.21	1.61	7.06**
Genotype × Environment	21	8.98	0.43	1.88*
Heterogeneity of Regression	7	5.63	0.80	3.36*
Residual-2	14	3.35	0.24	1.05 NS
Error between replicates	32	7.28	0.23	

Table 18E. Date of maximum flower (DMF).

Source of variation	df	SS	MS	F value
Genotype	7	67.91	9.70	7.84**
Environment	3	8.26	2.75	2.22 NS
Combined Regression	1	7.53	7.53	20.82*
Residual-1	2	0.72	0.36	0.29 NS
Genotype × Environment	21	14.46	0.69	0.56 NS
Heterogeneity of Regression	7	2.96	0.42	0.51 NS
Residual-2	14	11.50	0.82	0.66 NS
Error between replicates	32	39.61	1.24	

Table 18F. Plant height at maximum flower (PHMF).

Source of variation	df	SS	MS	F value
Genotype	7	329.69	47.10	6.08**
Environment	3	205.10	68.37	8.83**
Combined Regression	1	123.64	123.64	3.04 NS
Residual-1	2	81.46	40.73	5.26*
Genotype × Environment	21	217.85	10.37	1.34 NS
Heterogeneity of Regression	7	112.71	16.10	2.14 NS
Residual-2	14	105.15	7.51	0.97 NS
Error between replicates	32	247.82	7.74	

Table 18G. Number of primary branches at maximum flower (NPBMF).

Source of variation	df	SS	MS	F value
Genotype	7	6.89	0.98	3.51**
Environment	3	67.66	22.55	80.43**
Combined Regression	1	67.05	67.05	221.71**
Residual-1	2	0.60	0.30	1.08 NS
Genotype × Environment	21	6.34	0.30	1.08 NS
Heterogeneity of Regression	7	1.39	0.20	0.56 NS
Residual-2	14	4.95	0.35	1.26 NS
Error between replicates	32	8.97	0.28	

Table 18H. Number secondary branches at maximum flower (NSBMF).

Source of variation	df	SS	MS	F value
Genotype	7	14.16	2.02	4.01**
Environment	3	29.95	9.98	19.79**
Combined Regression	1	26.88	26.88	17.52 NS
Residual-1	2	3.07	1.53	3.04 NS
Genotype × Environment	21	24.94	1.19	2.35*
Heterogeneity of Regression	7	9.10	1.30	1.15 NS
Residual-2	14	15.84	1.13	2.24*
Error between replicates	32	16.14	0.50	

Table 18I. Plant weight at harvest (PWH).

Source of variation	df	SS	MS	F value
Genotype	7	2832.10	404.59	3.41**
Environment	3	1564.29	521.43	4.39**
Combined Regression	1	1102.70	1102.70	4.78 NS
Residual-1	2	461.59	230.79	1.94 NS
Genotype × Environment	21	4623.07	220.15	1.85*
Heterogeneity of Regression	7	904.04	129.15	0.49 NS
Residual-2	14	3719.03	265.65	2.24 *
Error between replicates	32	3798.03	118.69	

Table 18J. Number of pods per plant (NPd/P).

Source of variation	df	SS	MS	F value
Genotype	7	35329.57	5047.08	8.74**
Environment	3	42683.15	14227.72	24.64**
Combined Regression	1	41651.87	41651.87	80.78*
Residual-1	2	1031.29	515.64	0.89 NS
Genotype × Environment	21	28474.36	1355.92	2.35*
Heterogeneity of Regression	7	9635.88	1376.55	1.02 NS
Residual-2	14	18838.48	1345.61	2.33*
Error between replicates	32	18475.09	577.35	

Table 18K. Pod weight per plant (PdW/P).

Source of variation	df	SS	MS	F value
Genotype	7	502.63	71.80	2.99**
Environment	3	1730.38	576.79	24.05**
Combined Regression	1	1663.02	1663.02	49.38*
Residual-1	2	67.35	33.68	1.40 NS
Genotype × Environment	21	1453.53	69.22	2.89**
Heterogeneity of Regression	7	453.90	64.84	0.91 NS
Residual-2	14	999.63	71.40	2.98**
Error between replicates	32	767.46	23.98	

Table 18L. Number of seeds per plant (NS/P).

Source of variation	df	SS	MS	F value
Genotype	7	34537.89	4933.98	10.34**
Environment	3	32954.57	10984.86	23.02**
Combined Regression	1	30339.37	30339.37	23.20*
Residual-1	2	2615.20	1307.60	2.74 NS
Genotype × Environment	21	26872.33	1279.63	2.68**
Heterogeneity of Regression	7	8677.54	1239.65	0.95 NS
Residual-2	14	18194.78	1299.63	2.72**
Error between replicates	32	15267.36	477.11	

Table 18M. Seed weight per plant (SW/P).

Source of variation	df	SS	MS	F value
Genotype	7	362.58	51.80	3.69**
Environment	3	1197.77	399.26	28.47**
Combined Regression	1	897.96	897.96	5.99 NS
Residual-1	2	299.82	149.91	10.69**
Genotype × Environment	21	894.03	42.57	3.04**
Heterogeneity of Regression	7	486.49	69.50	2.39 NS
Residual-2	14	407.54	29.11	2.08*
Error between replicates	32	448.77	14.02	

* = significant at 5% level, ** = significant at 1% level, NS = non-significant.

Figure 8-20. Performance graph for thirteen characters of eight genotypes of chickpea according to Freeman and Perkins (1971) model.

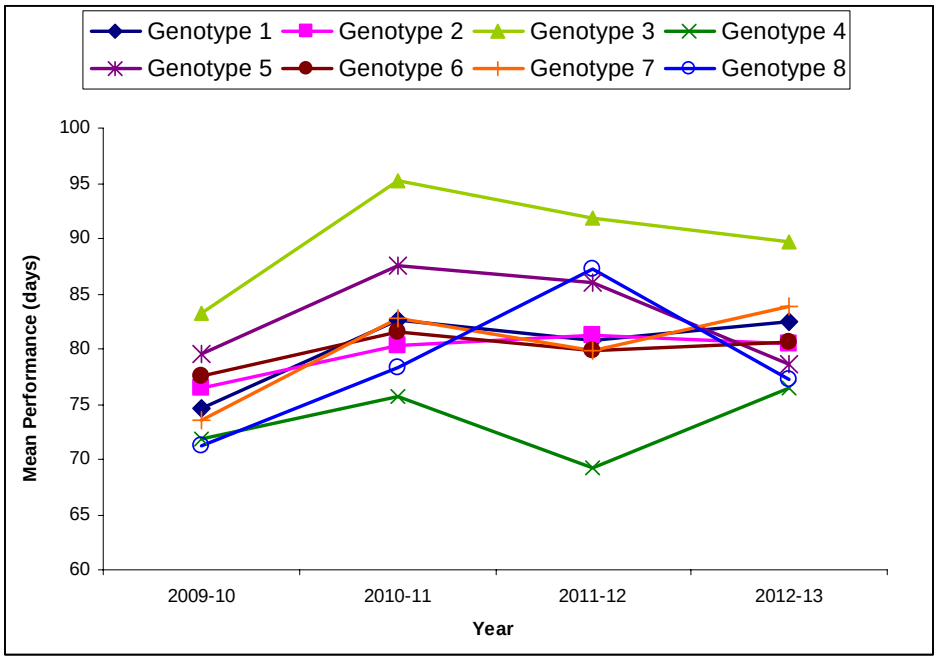


Figure 8. Curves of individual genotype mean on environmental mean of eight genotypes for DFF.

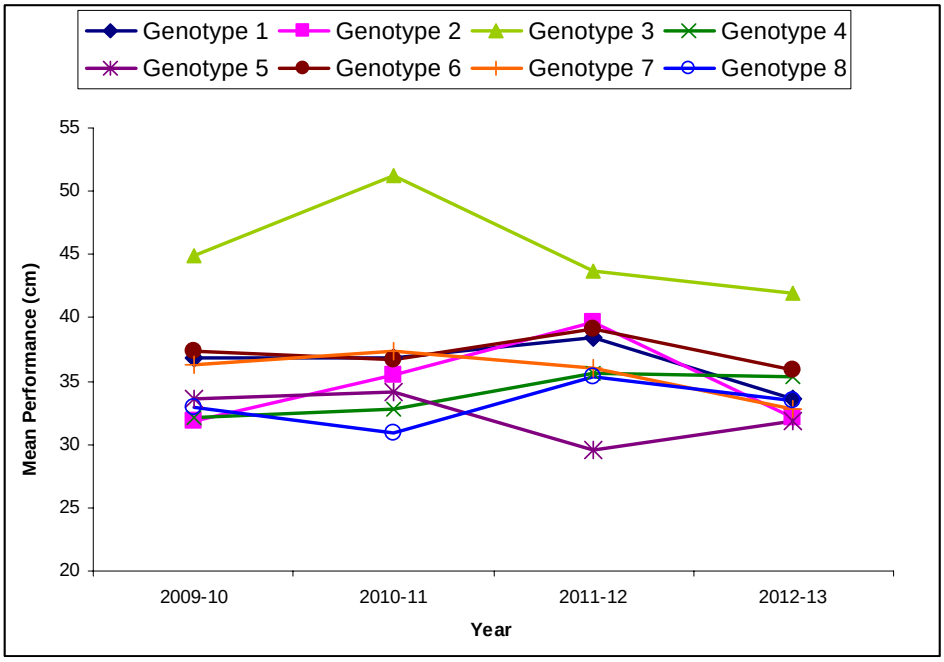


Figure 9. Curves of individual genotype mean on environmental mean of eight genotypes for PHFF.

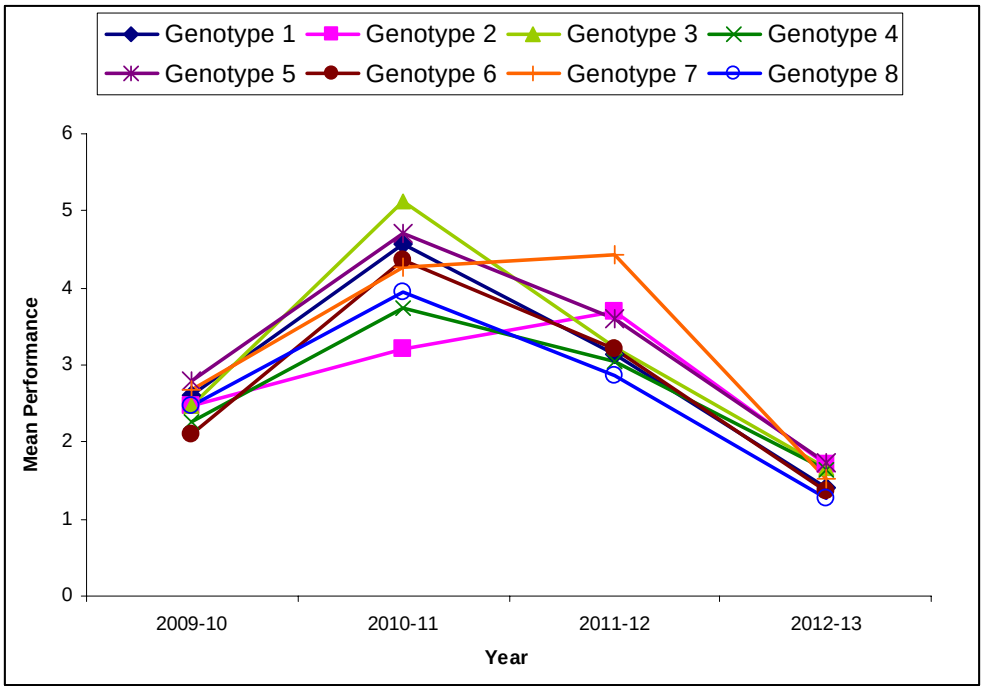


Figure 10. Curves of individual genotype mean on environmental mean of eight genotypes for NPBFF.

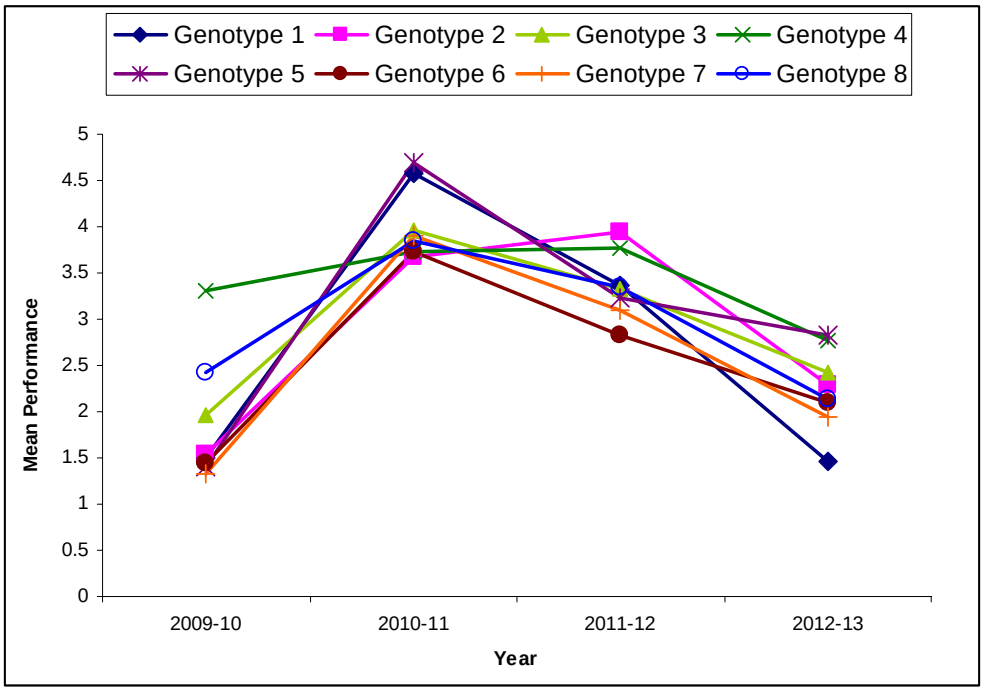


Figure 11. Curves of individual genotype mean on environmental mean of eight genotypes for NSBFF.

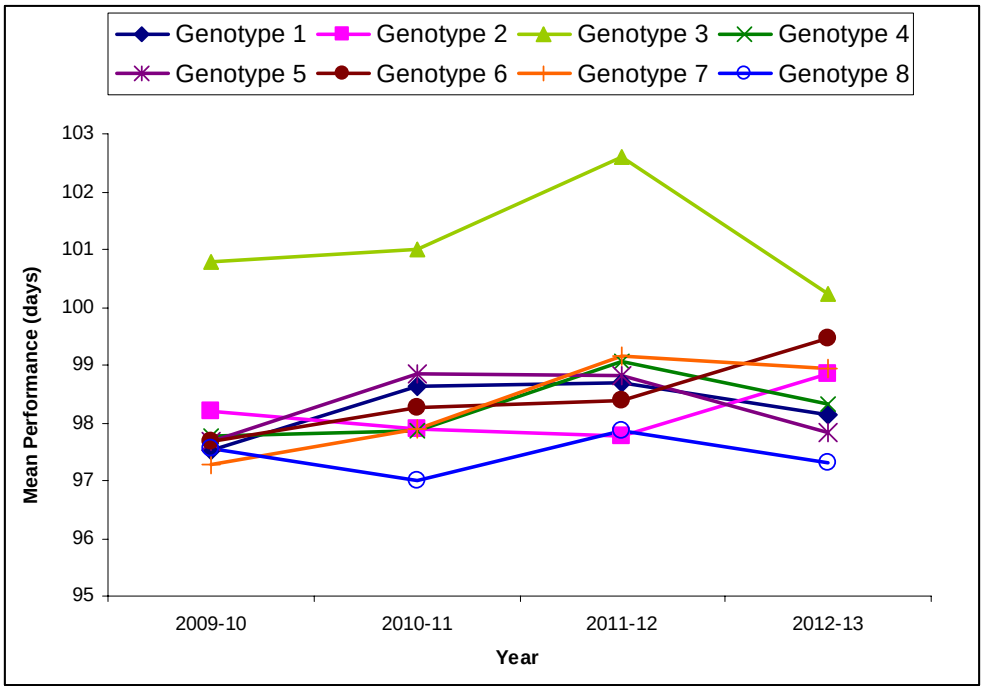


Figure 12. Curves of individual genotype mean on environmental mean of eight genotypes for DMF.

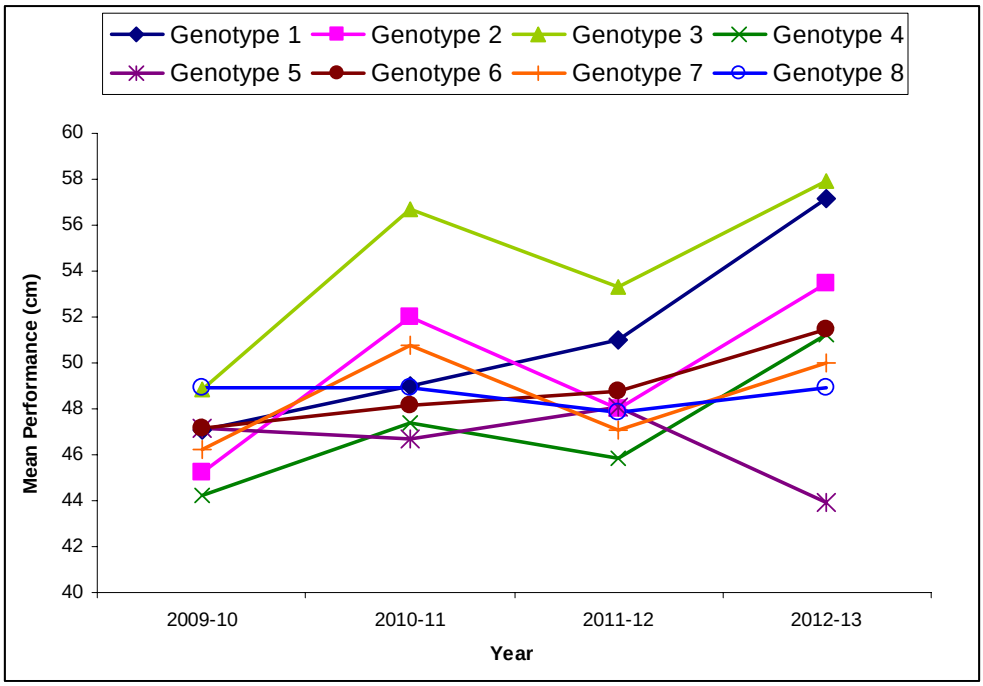


Figure 13. Curves of individual genotype mean on environmental mean of eight genotypes for PHMF.

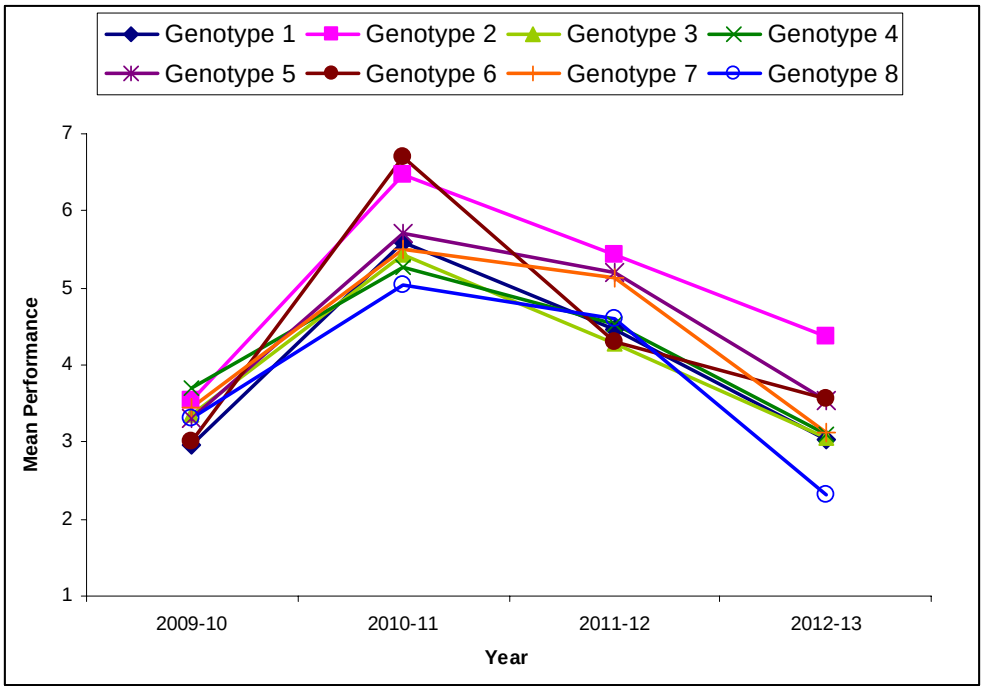


Figure 14. Curves of individual genotype mean on environmental mean of eight genotypes for NPBMF.

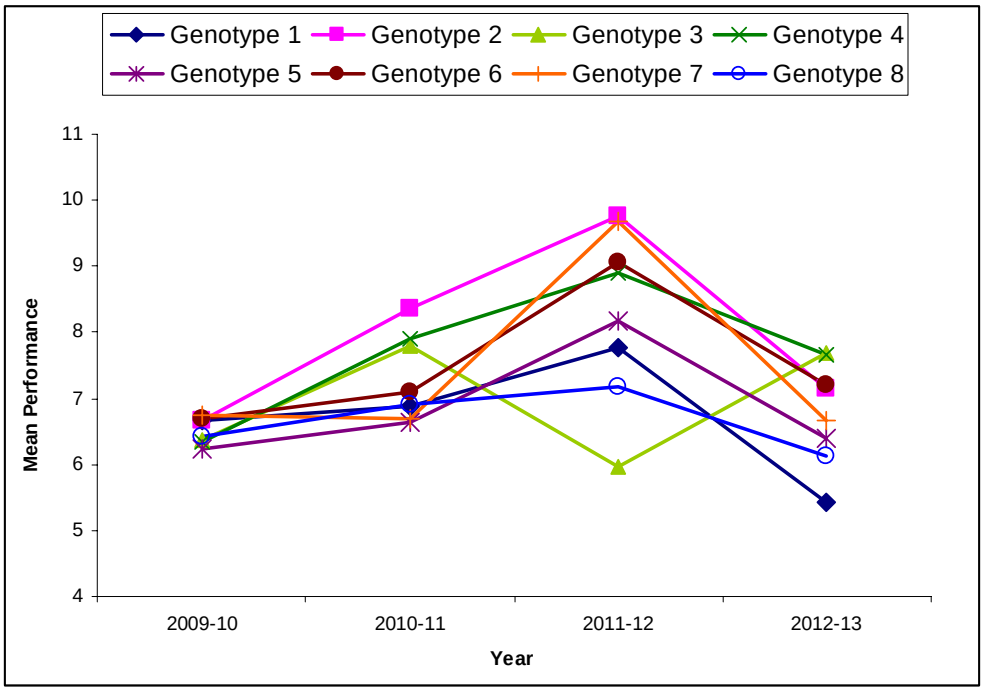


Figure 15. Curves of individual genotype mean on environmental mean of eight genotypes for NSBMF.

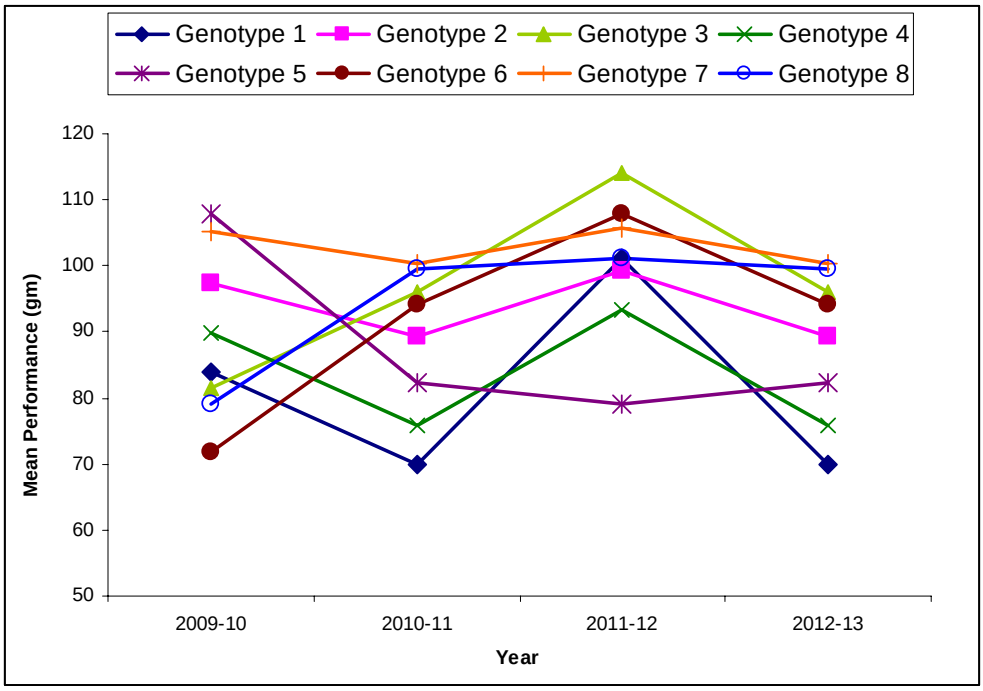


Figure 16. Curves of individual genotype mean on environmental mean of eight genotypes for PWH.

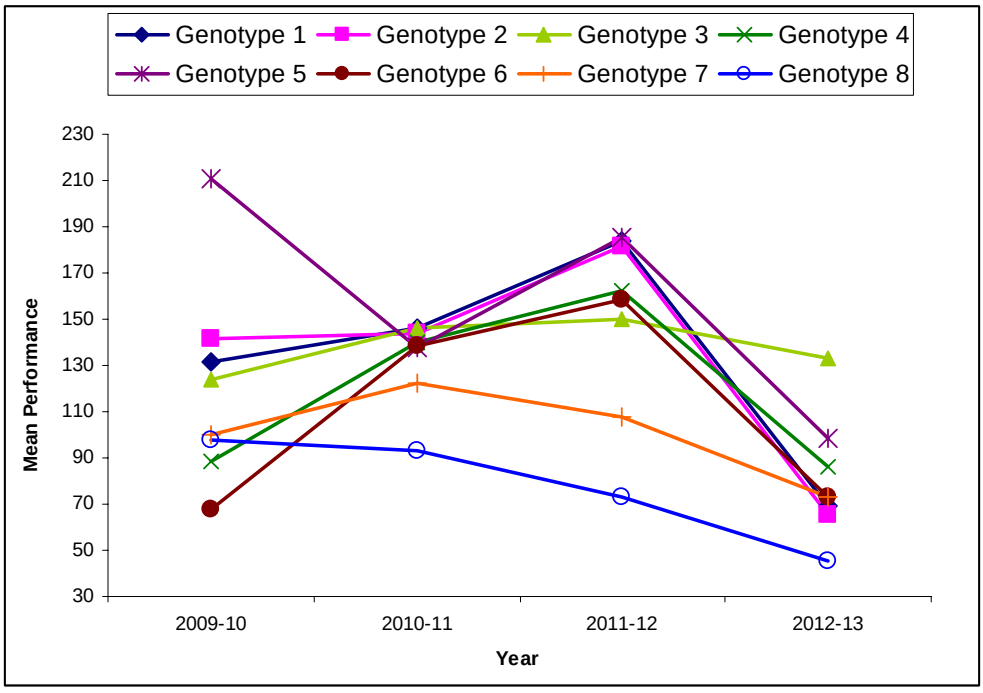


Figure 17. Curves of individual genotype mean on environmental mean of eight genotypes for NPd/P.

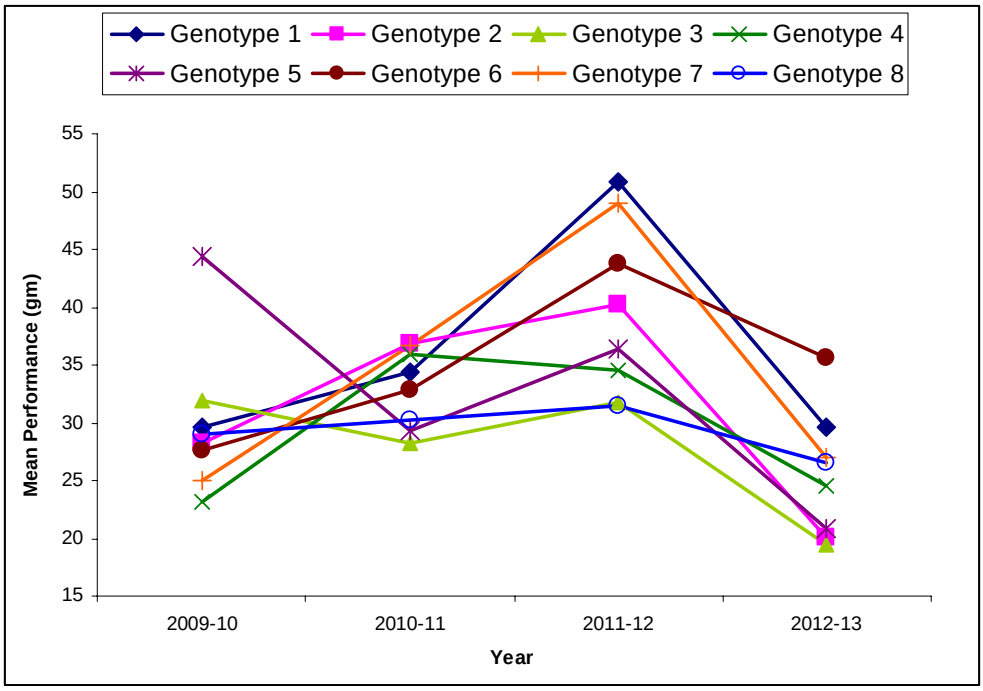


Figure 18. Curves of individual genotype mean on environmental mean of eight genotypes for PdW/P.

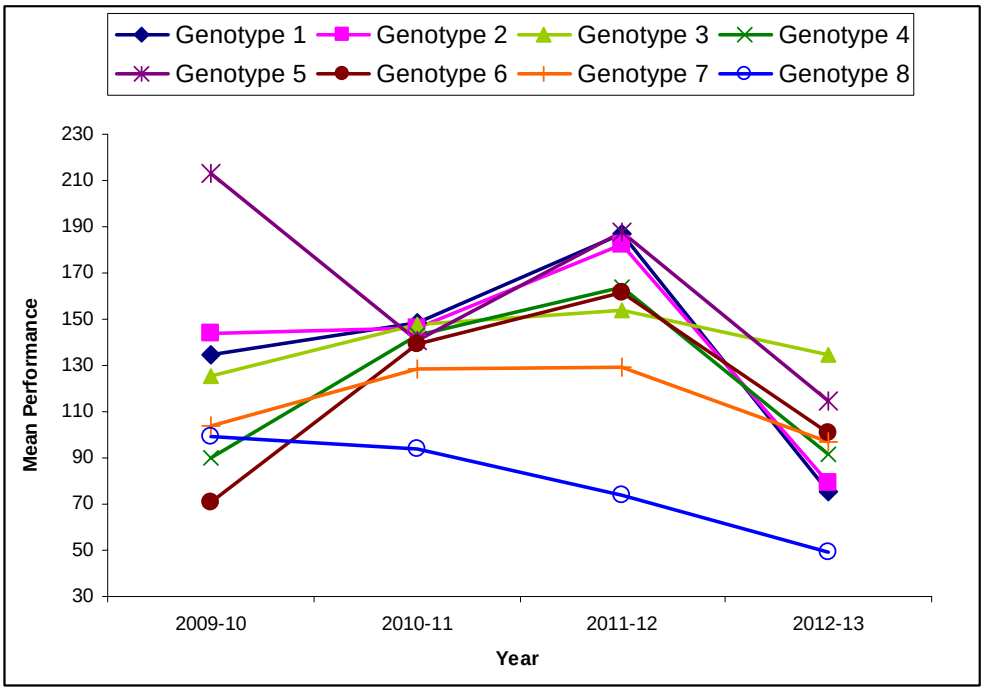


Figure 19. Curves of individual genotype mean on environmental mean of eight genotypes for NS/P.

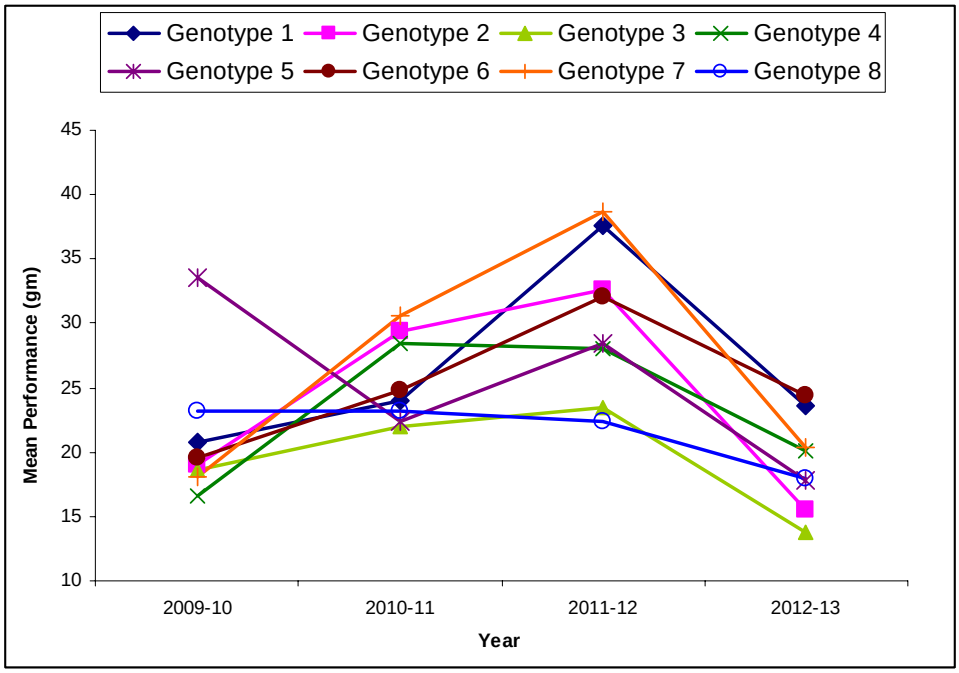


Figure 20. Curves of individual genotype mean on environmental mean of eight genotypes for SW/P.

Figure 21-33. Regression graph for thirteen characters of eight genotypes of chickpea according to Freeman and Perkins (1971) model.

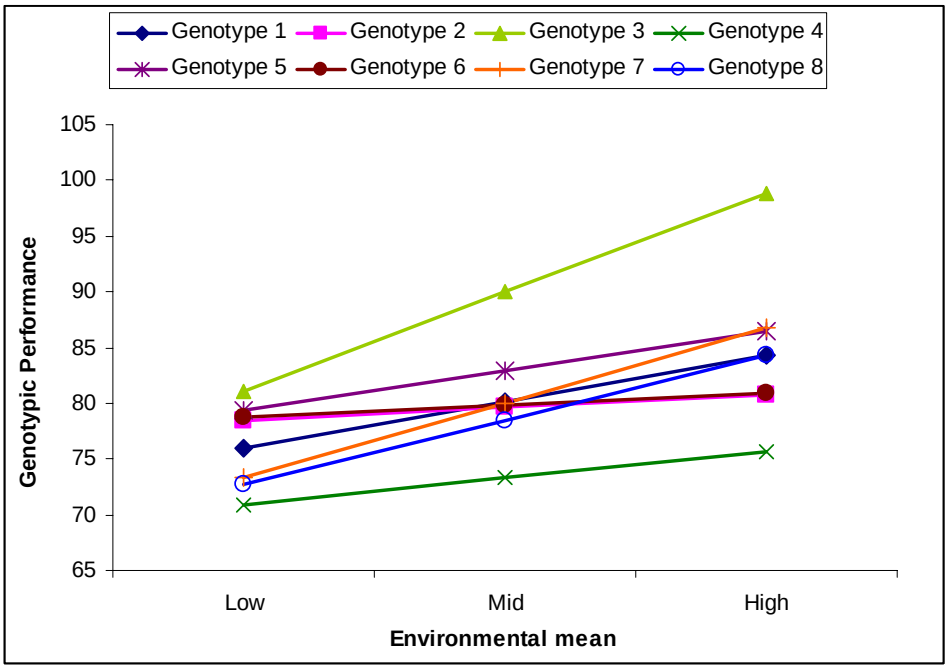


Figure 21. Regression of individual genotypic mean on environmental mean of eight genotypes for DFF.

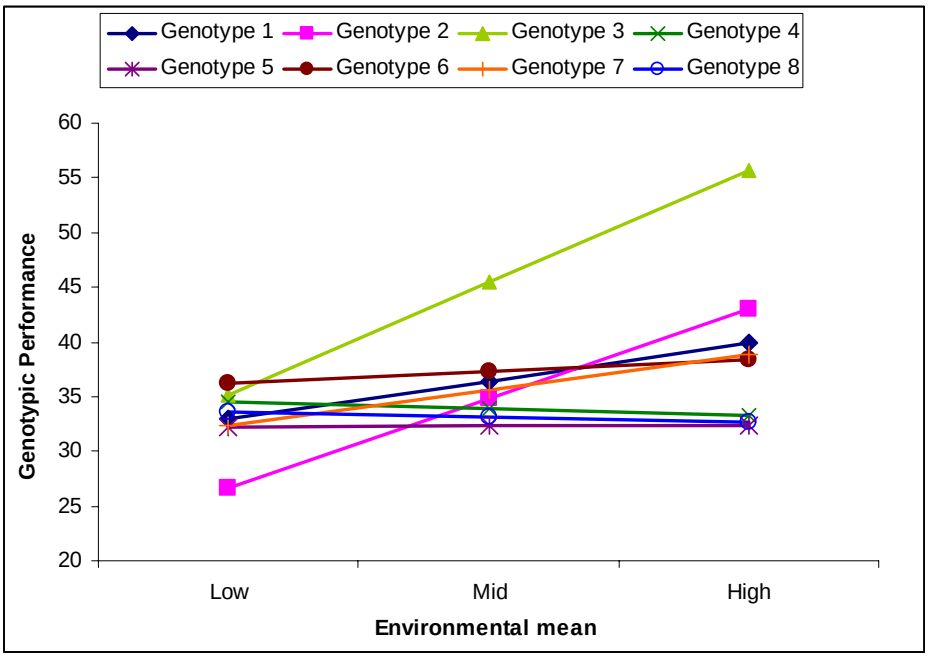


Figure 22. Regression of individual genotypic mean on environmental mean. of eight genotypes for PHFF.

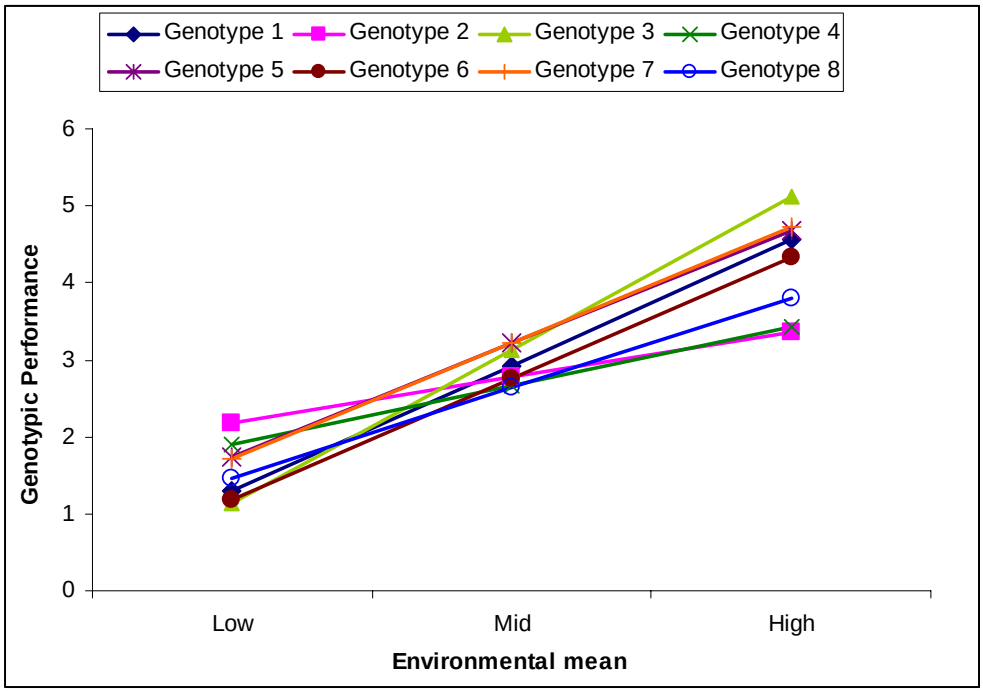


Figure 23. Regression of individual genotypic mean on environmental mean of eight genotypes for NPBFF.

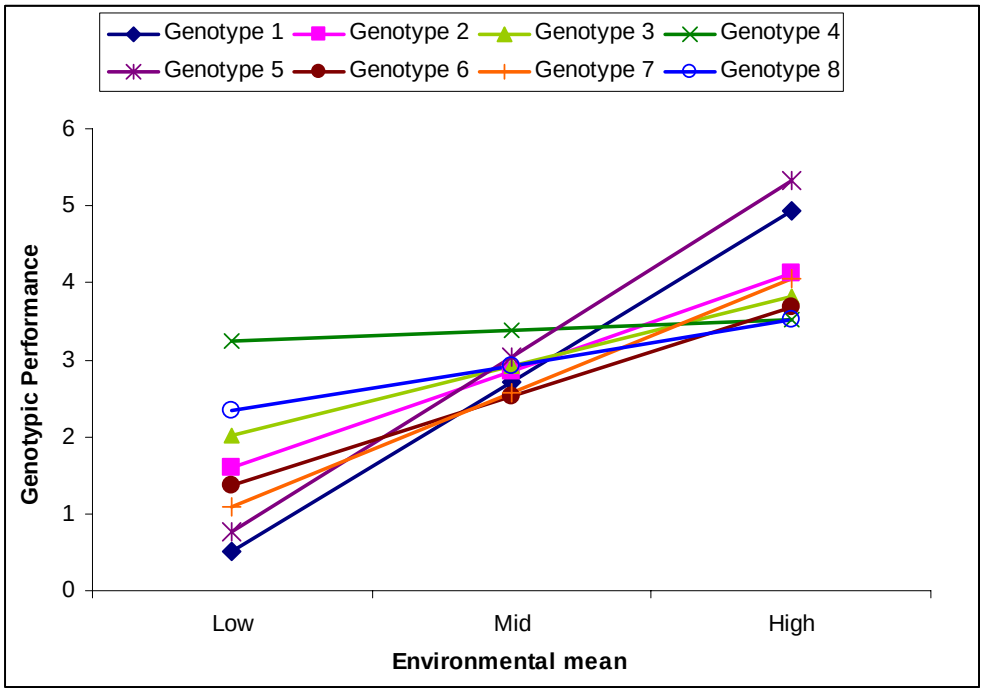


Figure 24. Regression of individual genotypic mean on environmental mean of eight genotypes for NSBFF.

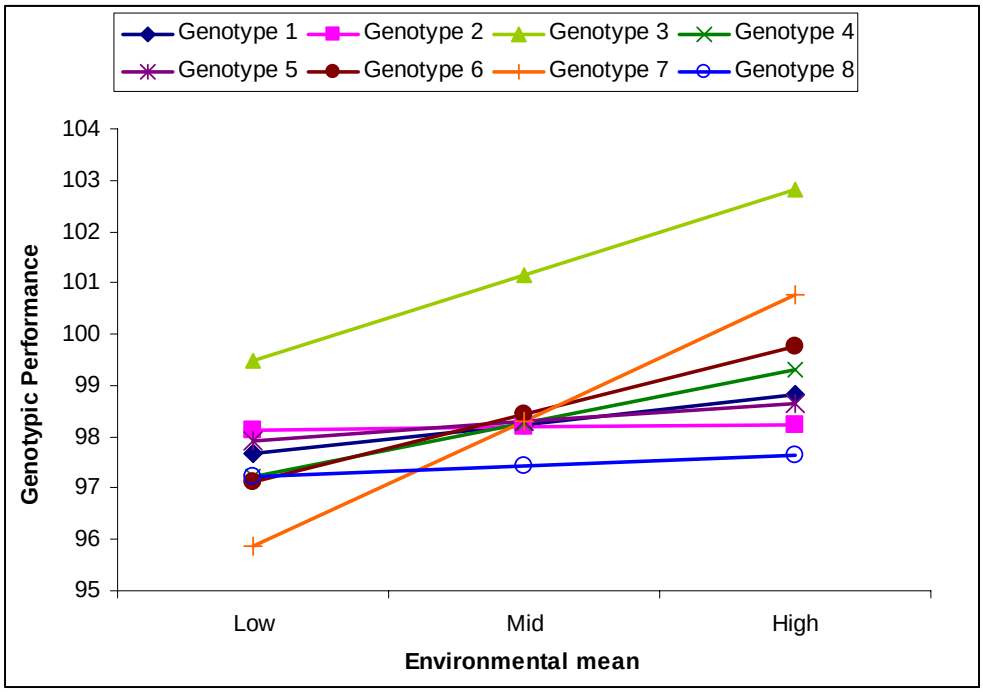


Figure 25. Regression of individual genotypic mean on environmental mean of eight genotypes for DMF.

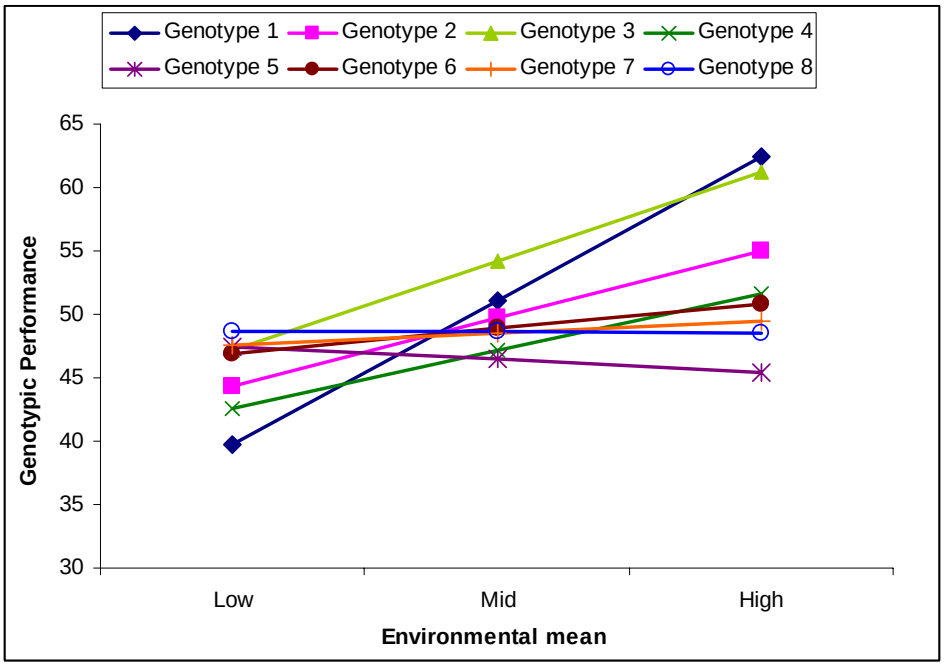


Figure 26. Regression of individual genotypic mean on environmental mean of eight genotypes for PHMF.

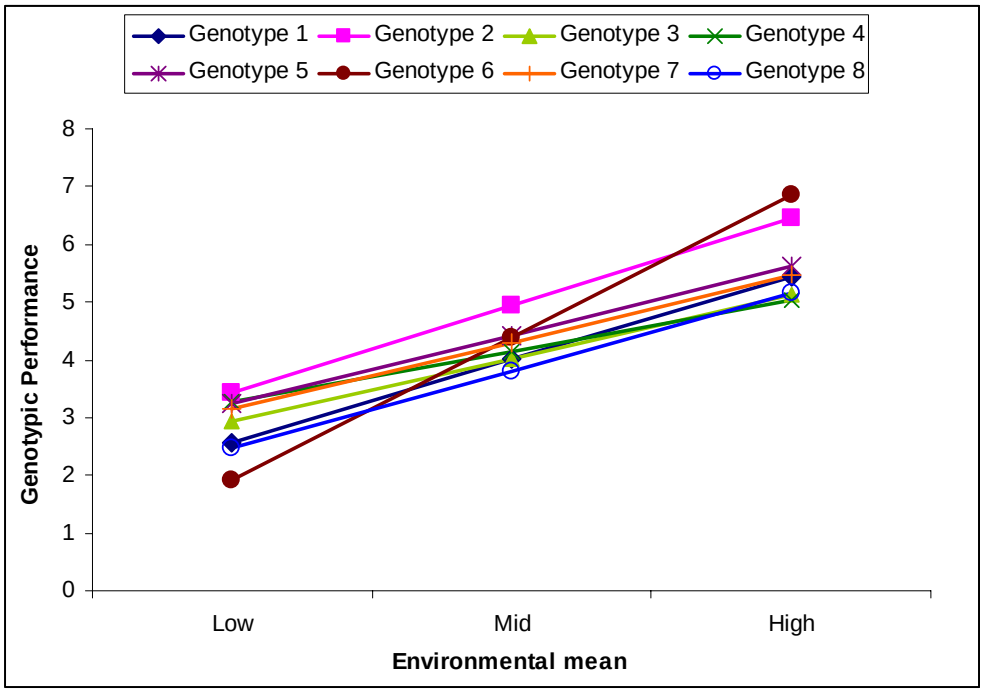


Figure 27. Regression of individual genotypic mean on environmental mean of eight genotypes for NPBMF.

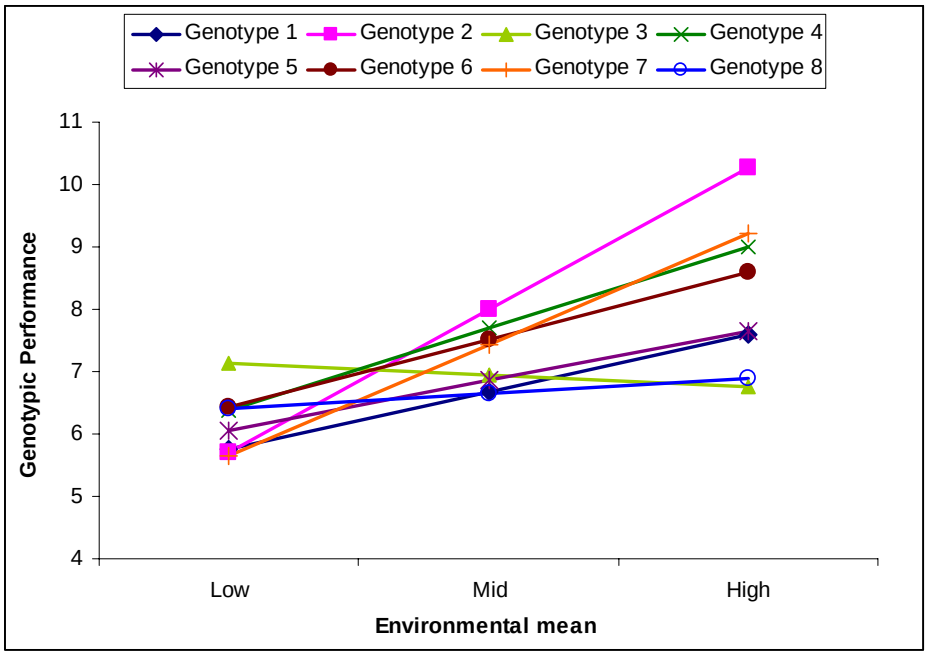


Figure 28. Regression of individual genotypic mean on environmental mean of eight genotypes for NSBMF.

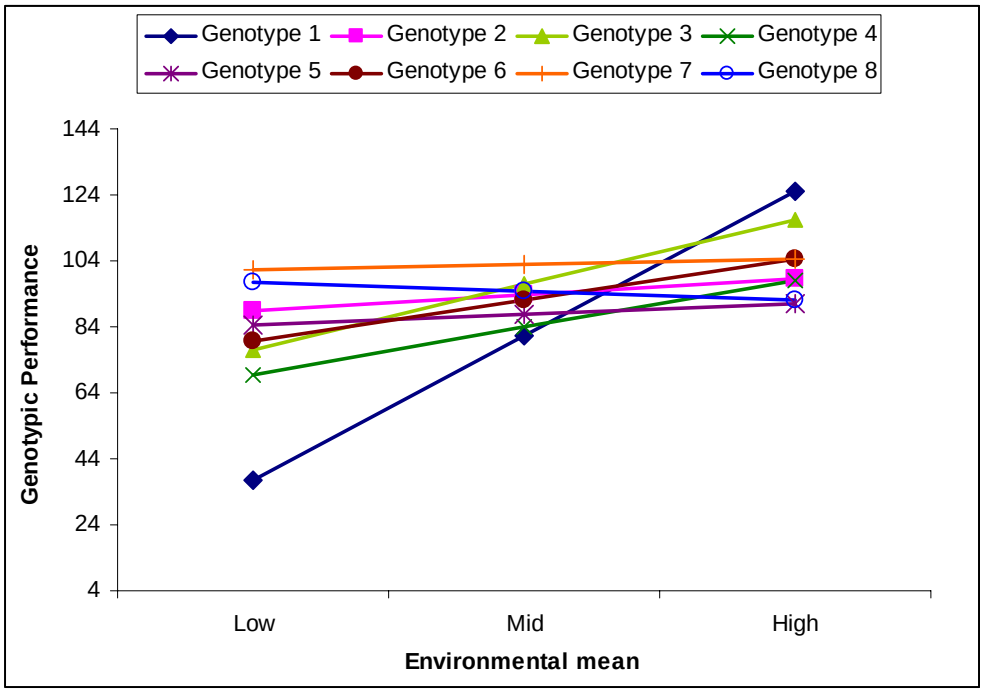


Figure 29. Regression of individual genotypic mean on environmental mean of eight genotypes for PWH.

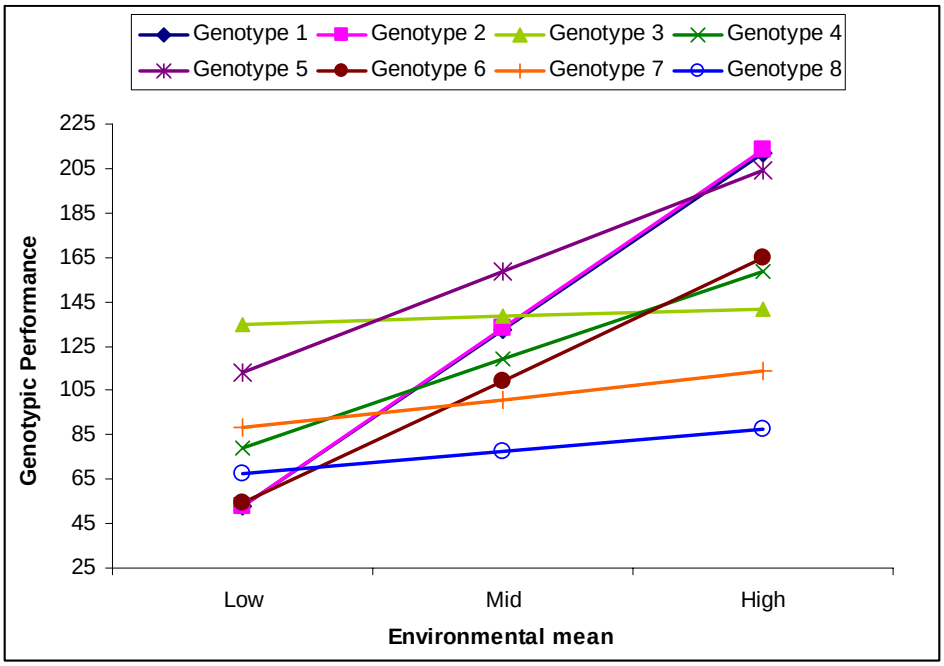


Figure 30. Regression of individual genotypic mean on environmental mean of eight genotypes for NPd/P.

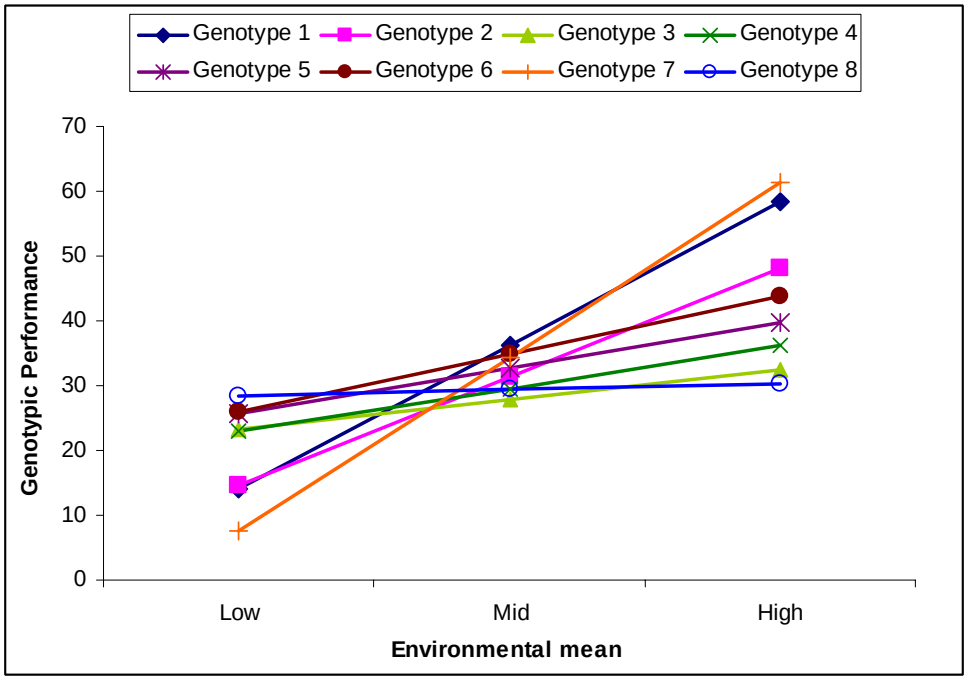


Figure 31. Regression of individual genotypic mean on environmental mean of eight genotypes for PdW/P.

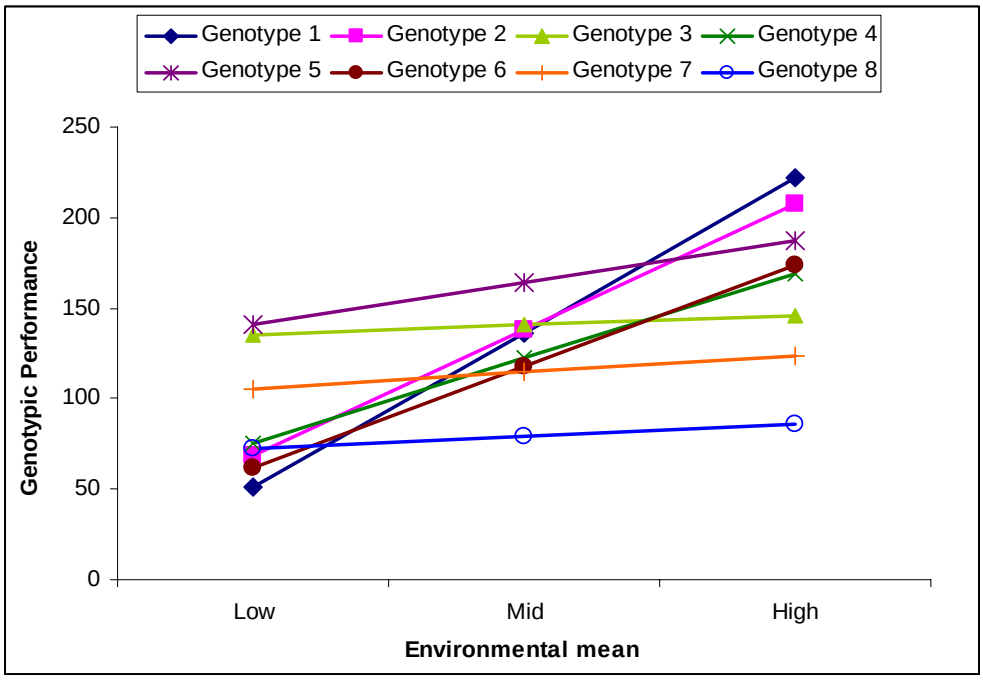


Figure 32. Regression of individual genotypic mean on environmental mean of eight genotypes for NS/P.

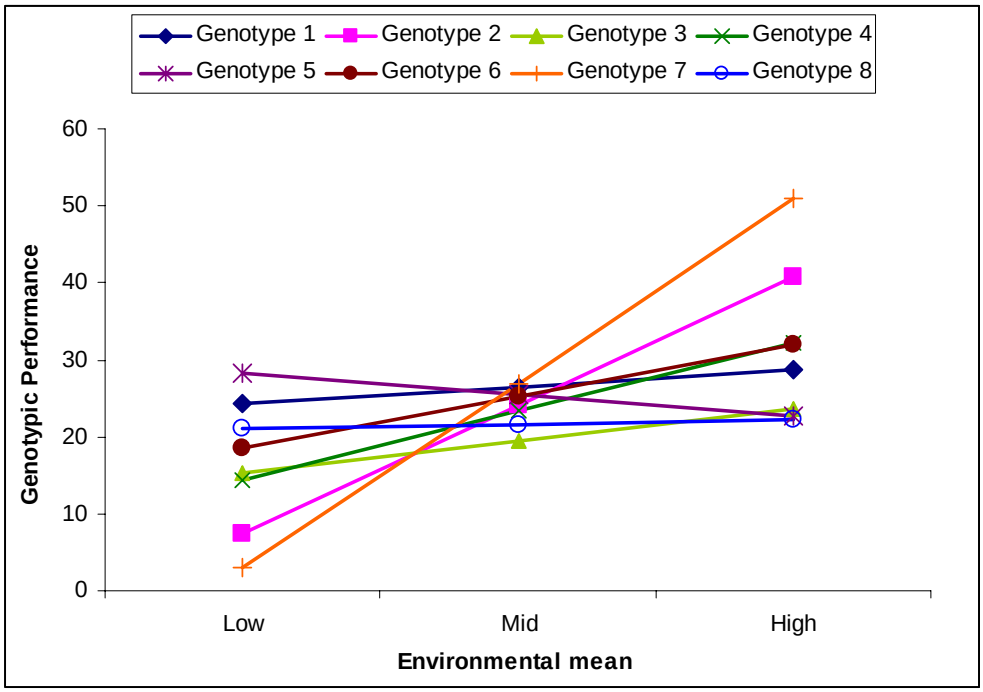


Figure 33. Regression of individual genotypic mean on environmental mean of eight genotypes for SW/P.

DISCUSSION

In plant breeding programs it is important to understanding the nature of genotype × environment interaction because a significant genotype × environment interaction can seriously impair efforts in selecting superior genotypes relation to new crop introductions and cultivar development programs (Danyali *et al*., 2012). Thus, major goal of plant breeding programs is to increase stability and stabilize crop yield across environments. In that context, in this investigation thirteen economically important characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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 eight chickpea genotypes over four consecutive years were considered for study the genotype × environment (G×E) interaction following Freeman and Perkins (1971) model which may assist understanding of nature of genotype × environment interaction as well as their stability.

In the present study, analysis of variance revealed highly significant difference ($P<0.01$) among the genotypes for all the characters under studied indicated genotypes were different form each other. The environment item was also highly significant ($P<0.01$) for all the characters except DMF, which indicated that year (environment) was also different. The interaction between genotypes and year that is environment was significant all the characters except NPBMF. Significant genotype × environment (G×E) interaction item indicated that year interacted with the genotypes significantly. This result reflects that the chickpea genotypes respond differently to the different environmental condition like year. This

finding suggested the importance of assessment of genotypes under different environments to identify the best genotypes of a crop.

However, analysis of variance is uninformative in the explanation of G×E interaction. It seems that the other statistical methods such as regression procedure are more useful for understanding and describing G×E interactions.

The joint regression analysis that is partitioning analysis of variance showed that the mean square due to genotypes exhibited significance for all studied characters. Moreover significant variations were noted for all studied characters except DMF due to environmental change. Combined regression displayed significant values for PHFF, NPBFF, NSBFF, DMF, NPBMF, NPd/P, PdW/P and NS/P in comparison to residual-1. Significant combined regression indicated that environments were well measured for these traits, that is, a large part of the observed differences between varieties was accounted for by a linear effect of the environments. Resedual-1 item in comparison to error is significant for the characters DFF, NSBFF, PHMF and SW/P suggesting that environmental index adequately is the index of additive environmental effect. Similar results were reported by Pervin *et al*. (2007) in blackgram. Significant residual-1 for different characters was also noted by Islam (2002) in blackgram. Significant G×E interaction for all the characters except DMF, PHMF and NPBMF were recorded which indicated that except these characters genotypes were interacted with environment differently. Pervin *et al*. (2007) reported that PHFF and PdW/P showed significant value of interaction between genotype and environment. There are several reports of G×E interactions in different crops by several researchers viz., Khan *et al*. (2002) and Islam *et al*. (2002 and 2004). The significant interaction of genotypes with environments warrants further computations of stability parameters.

Heterogeneity of regression item was found to be non-significant for all the characters except NSBFF. Significant value of this item against residual-2

mean square indicates a large portion of G×E interaction was predictable (Singh and Pawar, 2005), that is, there was a linear relationship between G×E interaction and the environmental values. On the other hand, residual-2 item was significant for all the characters except PHFF, NSBFF, DMF, PHMF and NPBMF indicating that these characters showed linear performance to the environments in which they are grown.

To estimate the response and to find out stability of a trait, Freeman and Perkins (1971) considered high mean overall the environments, less standard error with unite regression coefficient (b_i = 1.0) and mean square deviation from regression need to be zero or nearly zero ($\overline{S}_{di}^2 = 0$). This concept merits practical consideration. Further, Breese (1969), Parado *et al*. (1973) and Langer *et al*. (1979) stated that regression coefficient is a measure of response to varying environments and the mean square deviations from linear regression is a true measure of stability and the genotype with the lowest deviation being the most stable and vice versa. But, Banis and Gupta (1972) stated that the potentiality of a genotype to express greater mean over environments should be the most important criterion, since other two parameters may not have any particular utility if the genotype is potentiality weak. From the above discussion it may be stated that,

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

(2) Genotypes with above average mean performances and high regression coefficient with non-significant $\overline{S}_{di}^2$ are sensitive to environmental changes may be recommended for favorable environments.

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

(4) Genotypes having less mean performance, regression coefficients close to 1.00 and non-significant $\overline{S}^2_{di}$ indicating poor adaptability to all environments.

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

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

In addition to this, standard error of b_i (Sb_i) is also used to compare significance of b_i values and a genotypes having negative b_i values, it would be suggested to grow only in poor environment (Singh and Chaudhary, 1979). On the other hand, any type of b_i values (positive or negative) with significant $\overline{S}^2_{di}$ are unstable (Umadevi *et al*., 2009).

On the basis of above mentioned criterion, the experimental results concerning genotypic stability of various genotypes across the different conditions are discussed as follows:

In respect of the trait DFF, genotype-1 was found as a stable genotype to all environments with regression coefficient close to unity (b_i = 1.0) and non-significant deviation from regression but the mean performance was just under average indicating that moderate early flowering genotype was less sensitive to environmental change. Genotype-2 and genotype-4 were found to be poor adaptability to unfavorable environments with below average regression coefficient (b_i<1.0) and non-significant deviation from regression ($\overline{S}^2_{di}$) with below average mean performance indicating early genotype was

sensitive to the changing environment. Genotype-3 showed the high mean performance with high b_i values along with non-significant $\overline{S}^2_{di}$ indicating this genotype was sensitive to environmental change and recommended for favorable environment only. This result indicated that the late flowering genotypes are more sensitive to environment. On the other hand, genotype-7 having above average b_i value with non-significant $\overline{S}^2_{di}$ and below mean performance indicating this genotype was poorly adaptable in favorable environment while, rest of the genotype were not stable due to significant $\overline{S}^2_{di}$ value.

In respect of the trait PHFF, genotype-1 exhibited high mean performance with above average b_i value and had non-significant $\overline{S}^2_{di}$ which indicated that this genotype was sensitive to environmental changes and may be recommended for favorable environment. Genotype-6 showed the high mean performance with below average b_i value and had non-significant $\overline{S}^2_{di}$ indicated that this genotype may be adapted to poor environments. Genotype-2 exhibited below mean performance with high b_i value and had non-significant $\overline{S}^2_{di}$ indicated that this genotype was poorly adaptable to favorable environment. On the other hand, genotype-8 and genotype-4 may be suggested to grow in poor field management due to negative b_i value (Singh and Chaudhary, 1979). Genotype-3 and genotype-7 were unstable due to significant $\overline{S}^2_{di}$ values and genotype-5 was poorly adaptable in unfavorable environment having below average mean with below average regression coefficient value and non-significant $\overline{S}^2_{di}$. Shafi *et al*. (2012) and Malik *et al*. (1988) found that plant height is sensitive to environmental fluctuations and indicating that relative performance of genotypes was markedly inconsistent over the environment.

For the trait NPBFF, genotype-1, genotype-5 and genotype-7 showed the highest mean value, regression coefficient close to unity (bi = 1.00) and had non-significant $\overline{S}^2_{di}$ indicating stable all over the environments. Genotype-3 was found

to be sensitive to environmental condition which may be recommended for suitable environment only while, genotype-6 showed less men performance and average b_i value with non-significant $\overline{S}^2_{di}$ indicated that this genotype may be poorly adapted in all environment. Whereas, genotype-2, genotype-4 and genotype-8 showed poor adaptation to unfavorable environment.

Regarding NSBFF, genotype-4 and genotype-8 exhibited the high mean performances but b_i values were below average and non-significant $\overline{S}^2_{di}$ indicating these genotypes were adaptable in poor environment. The second highest mean performance showed by genotype-5. This genotype has above average b_i and non-significant $\overline{S}^2_{di}$ values indicated that this genotype was sensitive to environmental changes. Genotype-2 and genotype-3 showed stable performance with regression coefficient close to unity (b_i = 1.0) and had non-significant deviation from regression but the mean performance were average. Genotype-6 was poorly adapted to all environments due to their below average mean performance, b_i value was to unity and non-significant $\overline{S}^2_{di}$. Genotype-1 and genotype-7 also exhibited below average mean performance but b_i value was above average and had non-significant $\overline{S}^2_{di}$ value indicating poorly adaptable to favorable environment.

The character DMF showed non-significant $\overline{S}^2_{di}$ value for all the genotypes. The high mean performance was found in genotype-3, genotype-6 and genotype-7 but its b_i value was above average and this genotype may be recommended for favorable environment. Genotype-1 with regression coefficient close to unity (b_i = 1.0) and non-significant deviation from regression but the average mean performance indicating this genotype may be stable. Genotyp-2, genotype-5 and genotype-8 exhibited below average mean performances with below average b_i values indicated that these genotypes for this trait were poorly adaptable in unfavorable environments. While,

genotype-4 having below average mean performances with high b_i values indicating poor adaptable in favorable environments.

In respect of PHMF, genotype-1, genotype-2 and genotype-3 exhibited above average to high mean performance but these genotypes may be recommended for favorable environment due to their above average b_i with non-significant $\overline{S}_{di}^2$ values. Genotype-4 is poorly adaptable to favorable environment due to below average mean and above average b_i values. While, genotype-7 may be adapted in poor environments but genotype-6 and genotype-8 were completely unstable due to their significant $\overline{S}_{di}^2$ values. On the other hand, genotype-5 may be suggested to grow in poor field management (Singh and Chaudhary, 1979).

The trait NPBMF, genotype-2, genotype-5 and genotype-7 exhibited average mean performance and their b_i values also close to unity therefore, these genotypes for this character may be suitable for all environments. Genotype-1, genotype-3 and genotype-8 exhibited below average performance and their b_i values close to unity therefore these genotypes may suggested for poor adaptability for all environments. Genotype-4 showed below average mean with below b_i values indicating adaptability of this genotype was is unfavorable environment while, genotype-6 was sensitive to environmental change due to above average b_i value with non-significant $\overline{S}_{di}^2$.

Among all the genotypes, genotype-4 and genotype-6 showed high mean performance, average b_i value with non-significant $\overline{S}_{di}^2$ for NSBMF indicating stable performance over all the environments. Genotype-2 and genotype-7 may be considered as sensitive genotype to the environmental changes due to above average mean performance with above average b_i and having non-significant $\overline{S}_{di}^2$ values. Genotype-1, genotype-5 and genotype-8 may be considered as poor adaptable genotype in unfavorable environments due their below average mean

with less than one b_i value and non-significant $\overline{S}^2_{di}$. While, genotype-3 would be suggested to grow in poor field management due to negative b_i value.

In case of PWH and NS/P, all the genotypes were unstable due to their significant values of mean square deviation from regression ($\overline{S}^2_{di}$).

NPd/P is an important selection criterion for the development of high yielding genotypes and is strongly influenced by environment in chickpea (Malik *et al*., 1988). In the present investigation, all the genotypes except genotype-8 were unstable due to significant $\overline{S}^2_{di}$ value. Genotype-8 having less mean performance and less b_i value indicating poor adaptability to in unfavorable environments.

For the trait PdW/P, genotype-6 having average mean performance, high b_i value and non-significant $\overline{S}^2_{di}$ indicating that this genotype may be suitable for favorable environments. Genotype-4 having below average mean performance and regression coefficient closed to unity (b_i=1.0) and also had non-significant $\overline{S}^2_{di}$ value thus possessing poorly adaptable in the all environments. Genotype-2 having regression coefficient above 1.0 and below mean performance indicated that this genotypes may be poor adaptability in favorable environments, while genotype-3 having less mean performance and less b_i value indicated that this genotype have poor adaptability in unfavorable environments. Rest of the genotypes were unstable due to their significant $\overline{S}^2_{di}$ values.

In case of SW/P, genotype-6 having high mean performance and average regression value with non-significant mean square deviation indicated that this genotype was stable across the diverse environments. Genotype-2 and genotype-7 having average mean performance with high b_i and non-significant $\overline{S}^2_{di}$ values indicated that these two genotypes were sensitive to environmental changes and may be recommended for favorable environments. Whereas, genotype-3 and genotype-8 having less mean performance with bellow average

b_i and non-significant $\overline{S}^2_{di}$ values indicating that these two genotypes were poor adaptable to the unfavorable environments. Rest of the genotypes viz., genotype-1, genotype-4 and genotype-5 for this character were unstable due to their significant $\overline{S}^2_{di}$ values.

It is therefore, suggested that breeders are likely to select suitable genotypes (having high mean, unit regression and non-significant $\overline{S}^2_{di}$ values) by growing them under varied environmental conditions, which might lead, be able to increase the yield potential by increasing the performance of yield components in the suitable environments.

On the basis of the above discussion, genotype-1 for DFF, NPBFF and DMF; genotype-2 for NSBFF and NPBMF; genotype-3 for NSBFF; genotype-4 for NSBMF; genotype-5 for NPBFF and NPBMF; genotype-6 for NSBMF and SW/P and genotype-7 for NPBFF and NPBMF were considered as stable genotypes having unit regression coefficient (b_i), non-significant deviation from regression ($\overline{S}^2_{di}$) with high mean. Therefore these genotypes may be selected as stable genotypes for respective characters for further breeding research. The present findings are in agreement with the findings of Islam *et al*. (2002), Sharma *et al*. (2007), Kanouni *et al*. (2007), Atta *et al*. (2009), Akhter *et al*. (2010), Dehghani *et al*. (2010) and Sarker (2012).

Beside these, it was noted that the genotype-1 for PHFF and PHMF; genotype-2 for PHMF, NSBMF and SW/P; genotype-3 for DFF, NPBFF, DMF and PHMF; genotype-5 for NSBFF; genotype-6 for DMF, NPBMF and PdW/P, genotype-7 for DMF, NSBMF and SW/P were responsive to diverse environment, having high b_i values with non-significant $\overline{S}^2_{di}$ values. Thus the genotypes might be recommended only for favorable environments. Similar results are reported by Khan *et al*. (2001) in wheat, Akhtar *et al*. (2010) in

mungbean, Karadavut *et al*. (2010) in faba bean, Choudhary and Haque (2010) and Sarker (2012) in chickpea.

Again, genotype-1 for NPBMF; genotype-3 for NPBMF; genotype-4 for PdW/P; genotype-6 for NPBFF and NSBFF and genotype-8 for NPBMF exhibited poor adaptability to all environments due to below mean performance with average b_i values and non-significant $\overline{S}_{di}^2$ values. Researchers such as Sharma *et al*. (2007), Choudhary and Haque (2010) and Sarker (2012) obtained similar results in chickpea.

Genotype × environment (G×E) interaction has been an important and challenging issue for plant breeders, geneticists and agronomists who engaged in the performance testing. The genotype × environment interaction reduces association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters sensitive to environmental fluctuations. Such traits are less amenable to selection. Both yield and stability of performance should be considered simultaneously to reduce the effect of G×E interaction and to make selection of genotypes more precise and refined.

SUMMARY

To estimate genotype × environment (G×E) interaction and the stability parameters following Freeman and Perkins (1971) model using eight chickpea genotypes for thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) in four consecutive years viz., 2009-2010, 2010-2011, 2011-2012 and 2012-2013 were investigated.

In the present study, analysis of variance showed that the genotypes were significantly different for all the character and years were significantly different for all of the character except DMF. Again, significant genotype × environment (G×E) interaction item exhibited that the item year interacted with genotypes significantly which pointed out that the chickpea genotypes respond differently to the different environmental conditions like year.

The results of joint regression analysis exhibited that the mean square due to genotypes were significant for all the traits. Except DMF, all the studied traits exhibited significant variation due to environmental changes. Combined regression displayed significant values for PHFF, NPBFF, NSBFF, DMF, NPBMF, NPd/P, PdW/P and NS/P in comparison to residual-1 which, indicated that environments were well measured. Resedual-1 item in comparison to error was significant for the traits DFF, NSBFF, PHMF and SW/P suggesting that environmental index adequately is the index of additive environmental effect.

Heterogeneity of regression item was found to be non-significant for all the traits except NSBFF in comparison to residual-2 indicates a large portion of G×E interaction was predictable. On the other hand, residual-2 item was significant for all the characters except PHFF, NSBFF, DMF, PHMF and NPBMF indicating that these traits showed linear performance to the environments in which they are grown.

To estimate the response and find out stability of a trait, Freeman and Perkins (1971) considered high mean overall the environments, less standard error with unite regression coefficient ($b_i = 1.0$) and deviation from regression need to be zero or nearly zero ($\overline{S}_{di}^2 = 0$).

On the basis of the above mentioned criteria the genotype-1 for DFF, NPBFF and DMF; genotype-2 for NSBFF and NPBMF; genotype-3 for NSBFF; genotype-4 for NSBMF; genotype-5 for NPBFF and NPBMF, genotype-6 for NSBMF and SW/P and genotype-7 for NPBFF and NPBMF were considered as stable genotypes having unit regression coefficient (b_i), non-significant deviation from regression ($\overline{S}_{di}^2$) with average to high mean. Hence, above mentioned genotypes exhibited significant linear responses to the changing environments for respective traits. Therefore, these genotypes may be selected as stable genotypes for respective traits for further breeding research.

On the other hand, genotype-1 for PHFF and PHMF; genotype-2 for PHMF, NSBMF and SW/P; genotype-3 for DFF, NPBFF, DMF and PHMF; genotype-5 for NSBFF; genotype-6 for DMF, NPBMF and PdW/P and genotype-7 for DMF, NSBMF and SW/P were considered as suitable genotypes for favorable environments due to their above average b_i value, above average mean performance and non-significant ($\overline{S}_{di}^2$).

Beside these, genotype-1 for NPBMF; genotype-3 for NPBMF; genotype-4 for PdW/P; genotype-6 for NPBFF and NSBFF; genotype-8 for NPBMF were considered as poor adaptable genotype for all the environments.

PART-III: GENETIC STUDY

INTRODUCTION

To formulate an efficient breeding program for developing high yielding varieties, it is essential to understand the mode of inheritance, the magnitude of gene effects and their mode of action (Farshadfar *et al*., 2001 and 2008; Iqbal *et al*., 2007). Most agronomic and economic characters are quantitative in nature and show continuous variation, which might be produced by multitude of individual genes, each with a small effect on the measured character (Yule, 1906). Knowledge of genetic information on the inheritance of quantitative characters controlled by polygenic system having both additive and non-additive gene effects is essential. Such knowledge leads the plant breeder to develop commercial varieties. Gardner (1963) stated that information on variation attributable to genetic differences and also on the relationship among various quantitative traits is fundamentally significant in a crop improvement program.

Breeding methods are dictated by the gene action, interaction and linkage relationship of genes conditioning continuous phenotypic variation of various metric traits. Thus both additive and non-additive components of genetic variance, along with their allied parameters are of immense use for plant breeders under different situations. An estimate of additive and non-additive genetic variance provides a measure of how surely particular traits could be selected for or against a hybrid vigor or a population improvement program.

Thus, it is important to identify and estimate non-allelic interactions i.e. epistasis which could otherwise inflate the measures of additive and dominance components. To study the nature of gene action governing quantitative traits, various mating designs have been developed. The most frequent used designs namely, diallel and line × tester analysis do not provide the estimates of epistasis. The mating designs such as generation mean analysis, triple test cross and biparental cross provides information about all the three components of

variance viz., additive, dominance and epistatic. The generation mean analysis is based on first order statistics, whereas triple test cross and biparental cross are based on second degree statistics. Estimates based on first order statistics are statistically more robust and reliable than those based on second degree statistics (Singh and Narayanan, 1993). The analysis of generation mean provides the opportunity first to detect presence or absence of epistasis (by scaling test) and when present, it measures them appropriately. It also determines the components of heterosis in terms of gene effects and some other statistics. Such as potence ratio, levels of dominance, etc (Singh and Narayanan, 1993; Kearsey and Pooni, 1996 and Farshadfar, 1998). The present study has been undertaken to estimate the gene effects controlling yield and yield components using five generations viz., P_1, P_2, F_1, F_2 and F_3. Generation mean analysis considering this five generations provides information about the parameters of mean effects, additive, dominance, additive × additive gene interaction and dominance × dominance gene interaction and thereby helps in formulating the guidelines for handling the segregating material in the subsequent generations by the exploitation of fixable component. Further, Toledo *et al*. (1991) suggested that the five parameter model was good as the back cross studies for estimation of gene effects and gives satisfactory results.

Generation mean analysis was successfully used to estimate of main gene effects which help in understanding the nature of gene effects involved in different traits in chickpea genotypes by various researchers viz., Kidambi *et al*. (1988), Kumar and Singh (1995) and Deb and Khaleque (2009). Generation mean analysis also performed by Merrit (1988), Shekhawat *et al*. (2000), Rahman and Saad (2000), Hasib *et al*. (2002), Zewdie and Bosland (2003), Khattak *et al*. (2004), Novoselovic *et al*. (2004), Akhtar and Chowdhry (2006), Azizi *et al*.(2006), Marinković *et al*. (2006), Tabatabaei *et al*. (2007), Taiwo (2007), Sharmila *et al*. (2007), Singh *et al*. (2007), Farshadfar *et al*. (2008a), Ray and Islam (2008), Samad *et al*. (2009), Eshghi and Akhundova (2010), Kumar and Patra (2010),

Nahar *et al*. (2010), Payasi *et al*. (2010), Shoba *et al*.(2010), Ajay *et al*. (2011), Kumar *et al*. (2011b), Lyimo *et al*. (2011), Thangavel and Thirugnanakumar (2011) and Thangavel *et al*. (2011) in various crops.

Another mating design named biparental mating is one of the simplest random mating design available to effect forced recombination and breaking down undesirable linkages as pointed out by Comstock and Robinson (1952). However, the genetics of yield is extremely complex and hence one can face difficulties in genetical analysis. This complexity can be judged from the vide array of the type of gene action. Biparental intermating approach has been favoured to elevate the population mean and genetic variability in self pollinated crops like oat, barley and wheat (Srivastava *et al*., 1989). To develop high yielding genotypes coupled with good yield quality a population with high variability serves always as prime source for effective selection, particularly the role by F_2 segregants in throwing much variability is highly recognized. The intercrossing or intermating in the F_2 segregants provides chances of finding superior recombinants in F_3 or later generations and a greater amount of concealed genetic variations particularly of the additive type would be released there by improving response to selection (Moll and Robinson, 1967). Fredrickson and Kronsrad (1985) stressed that in autogamous crops, intermating among early segregants could open vistas to new levels of genetic variability by breaking up of the genetic recombination within the linkage group. Hence, the present investigation was aimed to find out the type of gene action for yield and its components through a biparental cross in chickpea. Thus, the present study was undertaken to know the genetics of yield and yield contributed traits in chickpea by following biparental mating. Biparental progeny analysis was successfully used in chickpea and other genotypes by other workers such as Kearsey (1965) in *Papaver dubium*, Husain (1997) in chilli, Nahar (1997) in sugarcane, Ojha and Roy (2001) in sunflower, Kampli *et al*. (2002) in chickpea, Kanwar and Karla (2004) in cauliflower, Jayaprada (2005) in mungbean,

Srividhya *et al*. (2005) in blackgram, Manickavelue *et al*. (2006) in rice, Alam *et al*. (2009) in sugarcane, Dhameliya and Dobariya (2009) in brinjal, Mahalingam *et al*. (2011) in rice and Alam (2012) in sugarcane.

On the other hand, most of genetic designs estimating second degree statistics (variance and covariance) depend on the assumption of no epistasis. However, there is no valid biological reason to exclude the possibility of epistasis acting on quantitative characters. It is recognized that, the estimation of additive and non-additive components gets significantly biased in presence of epistasis, which leads to erroneous estimation of genetic parameters and expected genetic grain under selection. Among the various mating designs estimating second degree statistics available to study the genetic variability, the triple test cross design developed by Kearsey and Jinks (1968) is an extension of North Carolina Design III of Comstock and Robinson (1952) is the most important. It provides precise estimates of various genetic parameters together with the availability of a test for epistasis which is not envisaged in other multiple mating designs. Triple test cross (TTC) that is applicable to any population irrespective of its mating system and its gene and genotype frequencies (Kearsey and Jinks, 1968). In the absence of epistasis TTC also provides unbiased estimates of additive (D) and dominance (H) components of genetic variation, degree of dominance $[(H/D)^{1/2}]$ as well as the direction of dominance (r_{sd}) with high degree of precision (Kearsey and Jinks, 1968). Therefore, an attempt was made to examine the role of various components of genetic variance in the inheritance of yield and its component traits using triple test cross analysis.

Triple test cross analysis was successfully used to estimate epistasis precisely and unbiased estimates of additive (D) and dominance (H) components of genetic variation in absence of epistasis which help in understanding the nature of gene effects involved in different traits in chickpea genotypes by Malhotra and Singh (1989). TTC also studied by different researchers in various crops such as

Verhalen *et al*. (1971) in cotton, Singh and Singh (1976) in wheat, Verma and Yunus (1986) in bread wheat, Garg *et al*.(1987) in upland cotton, Samad (1991) in rapeseed, Bhajan *et al*. (1994) in Indian mustered, Rathore *et al*. (1995) in peas, Husain (1997) in chilli, Khattak *et al*. (2002) in mungbean under spring/summer, Nagaraj *et al*. (2002) in cowpea, Subhan *et al*. (2002) in cotton, De-Lin and Yan (2004) in rice, Noori and Sokhansanj (2004) in spring wheat, Saravanan *et al*. (2005) in bhendi, Sofi *et al*. (2006) in maize, Ram *et al*. (2007) in rice, Zafar *et al*. (2008) in wheat, Kumar *et al*. (2011a) and Azad (2012) in lentil.

Thus, in this section genetic study have been done under three heads as follows:

Genetic study-1: Generation mean analysis

Genetic study-2: Biparental progeny (BIPs) analysis

Genetic study-3: Triple test cross (TTC) analysis.

REVIEW OF LITERATURE

Literatures in respect of genetic study of pulses 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 study" of different quantitative characters on various leguminous crop plants. A brief review of literatures on the leguminous crops, especially chickpea and other than leguminous crops regarding this study is narrated below.

Kearsey and Jinks (1968) improved a method of detecting additive, dominance and epistatic variation in a population derived by crossing F_2 males to their two inbred parents ($L_1 + L_2$) and their F_1s (L_3). They proposed that irrespective of the genetic constitution of this population (i.e., gene frequencies, linkage equilibrium etc.), the method will detect dominance and epistasis for those loci for which L_1 and L_2 differ. They advocated that, the method also allows one to estimate additive and dominance components with equal precision if no epistatis is detected and L_1 and L_2 are high and low selection lines for the trait investigated.

Verma and Yunus (1986) reported from their experiment in a modified triple test cross of bread wheat, that epistasis was important for most of the characters viz. tillers per plant, grains per ear and weight per ear. Both additive and dominance components were significant for all the characters except for 100-grain weight. Selection in later generation of these characters would be more effective as was suggested.

Garg *et al*. (1987) made a triple test cross analysis using 45 families of upland cotton and noted epistasis to be important for all the characters except seed-cotton yield, boll number and lint index. Additive component of variation was significant for all the characters. Dominance component of variation was significant for seed-cotton yield, boll number, boll size and lint index.

Kidambi *et al*. (1988) studied the inheritance of several developmental traits in three crosses of chickpea, viz., WFWG III'×'T20', 'T88'×'Bold Seeded', and 'NP34'×'P1528-1-1', each having seven generations. The seven generations were P_1, P_2, F_1, B_1, B_2, F_2, and F_3. The experimental lay-out was randomized complete block design with three replications. Data were collected on days to flowering (DF), days to maturity (DM), plant height in cm (PH), number of primary branches (PB), and number of secondary branches (SB). Generation mean analysis was used to estimate the genetic components, narrow sense heritability was estimated using variance components and correlation analysis to estimate correlation coefficients among different traits. Genetic differences were found in all the three crosses for all the traits under studied. Additive, dominance and epistatic effects were found for many traits. Duplicate epistasis was observed for all the traits except number of PB. Higher order interactions and/or linkage were detected for DM and SB. For many traits the relative magnitudes of the genetic effects differed among crosses, thus the extrapolation to other crosses may be difficult. The inheritance becomes more complex as the fate of the character is decided at a later stage in the life cycle. Positive heterosis was observed for some traits, but the exploitation of this component may not feasible since stable male sterile lines are not available. Early maturity and high yield may be selected independently because of the absence of any significant correlation between these two traits.

Malhotra and Singh (1989) carried out triple test cross analysis to detect epistasis in chickpea. None of the characters exhibited epistasis. In the absence of epistasis, additive and dominance effects were estimated. The results indicated the importance of additive genetic variance for seed yield, biological yield, number of primary branches, number of secondary branches, 100-seed weight, days to flower and number of seeds per pod, dominance genetic variance for days to maturity and both additive and dominance genetic variances for plant height.

Singh and Nanda (1989) estimated gene action through triple test cross in bread wheat. They detected epistasis by two independent comparisons ($2B_{1i}$-F_{1i}-P_i and $2BC_i$-F_{1i}) for grains per spike and yield per plant in both the years and for tillers per plant in 1981-82. Additive gene action was significant for all the traits in both the years, whereas dominance gene action was present for number of tillers/plant, harvest index and grain yield in both years. The degree of dominance varied from 0.41-0.62 in first year and that varied from 0.33-0.55 in the second year for the various traits.

Cheema *et al*. (1990) studied heterosis and inbreeding depression for yield components in six hybrids of four parents of basmati rice. Significant heterosis and inbreeding depression were estimated for traits studied. The maximum heterosis of 111.6% were observed for yield in hybrid D"A116-5-1 × Kashmir Basmati. Cross combinations of Basmati 370 × DM16-5-1 and DM16-5-1 × DM107-4 showed highly significant heterosis with a non-significant inbreeding depression.

Samad (1991) studied BIPs and triple test cross (TTC) in rape seed. Through triple test cross analysis, 'i' type epistasis was noted in cross-2 for plant height and seed yield per plant in cross-3 for number of seed per plant, while 'j+l' type epistasis was recorded in cross-3 for plant height, number of seed per plant and seed yield per plant in cross-l for number of seed per plant. Thus he found that linkage and epistasis played an important role in governing most of the characters in these materials. He also found that the relationship between BIPs progenies and their parents were mostly due to non-linear components. The contribution of H_R was greater than D_R, have over dominance resulted for most of the crosses and for a few partial dominance was observed. Both narrow and brood sense heritability were found to be low for biparental progenies.

Pooni *et al*. (1994) investigated both theoretically and experimentally the applicability of the triple test cross design to the genetic analysis of metrical traits. Theory has shown that the standard sets of triple test cross families

(L_1, L_2 and L_3) do not provide unambiguous tests of the additive, dominance and epistatic effects when reciprocal crosses were analysed separately. Analysis of the backcross families also suffers from similar problems but only in respect of the additive component and the tests of dominance and epistasis were not biased by the parentage of the families. Selfs of the standard families, on the other hand, did not display reciprocal differences (of heritable kind) and therefore, provides unambiguous tests of the additive, dominance and epistatic effects, but the dominance component was detected with reduced reliability as the level of heterozygosity was halved due to selfing. Theory further showed that biases of the various tests were eliminated rather easily by including the reciprocal families in the analysis. This was confirmed to a large extent by the analysis of amylose content in rice which also reveals that it was controlled by genes that display both interallelic and non-allelic interactions. Furthermore, dominance was showed to be partial but the dominance ratio seems to be high for both the $h_{a1}$and h_{a2} types of non-additive effects.

Kumar and Singh (1995) studied the inheritance of seed size in chickpea in two desi × desi crosses viz., ICCV 10 × ICCV 4958 and ICCV 10 × 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 come from additive gene effects, indicating that selection for seed size in early generations 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.

Chawla *et al*. (1999) carried out a triple test cross and developed sixty progeny families of two sets by crossing of 10 desi cotton varieties with male testers (G-1,

Lohit and their F_1 of G-1 × Lohit and K-359, RG-8 and their F_1 of K-359 × RG- 8) in a triple test cross fashion to detect epistasis and adequacy test and estimate additive and dominance components of genetic variation for all the traits studied. Both additive and non-additive genetic variance were important for most of the traits. Partial degree of dominance was detected for all the characters except seed index in cross G-1 × Lohit and for seed cotton yield, boll number per plant, boll weight, and lint yield and plant height in cross RG-8 × 359 indicated the preponderance of additive genetic variance for these characters. The remaining characters, seed index in G-1 × Lohit and ginning percentage, 2.5 per cent span length, seed index and lint index in cross RG-8 × K-359 indicated the preponderance of dominance genetic variance. The directional element of dominance 'F' was negative and significant for all the characters under study except ginning percentage and 2.5 per cent span length for which ambidirectional dominance was observed.

Bakheit *et al*. (2000) carried out an experiment during the three successive growing seasons of 1996, 1997 and 1998 to estimate the additive, dominance and epistatic components of genetic variation for the yield, yield components and wilt infection by using ninety triple test cross families and their parents, F_1 and F_2 in four sesame crosses. The results indicated that mean squares of the genetic analysis of variance and the overall epistatic gene effects for the crosses showed highly significant differences for all studied characters. The [i] type gene action (additive × additive) was considered as a major component of the overall epistatic effects for 1000-seed weight in cross-3, wilt infection percentage in cross-3 and cross-4, number of capsules per plant in cross-1, cross-2 and cross-4 and seed yield per plant in all crosses. The ratio of $(H/D)^{1/2}$ for all the crosses confirms the presence of partial dominance for all studied traits. The direction of dominance was positive and significant for wilt infection in cross-4, oil percentage in cross-1 and cross-4, number of capsules per plant and 1000-seed weight in cross-2 and seed yield per plant in all four

crosses. The results also revealed that the highest proportion of recombinant lines was obtained for number of capsules per plant, 1000-seed weight and oil percentage in the cross-2 cross and for seed yield per plant in cross-3.

Rahman and Saad (2000) investigated inheritance of yield and yield contributing characters using generation mean analysis, utilizing the means of six basic generations viz., P_1, P_2, F_1, F_2, B_1 and B_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 KU 7 × KU 8. Among the digenic epistatic interactions, both additive × additive [i] and dominance × dominance [l] contributed more for pod yield per plant and pods per plant.

Shekhawat *et al*. (2000) elucidate the inheritance of tillers per plant, grains per spike, 1000-grain weight and grain yield per plant by generation means analysis involving twelve generations in two crosses of wheat *(Triticum aestivum* L.). The grain yield per plant and tillers per plant were mostly governed by the dominance, dominance × dominance and dominance × dominance × dominance type of gene effects with larger magnitude but were unexploitable due to duplicate type of gene action. 1000-grain weight was found to be under control of both additive and non-additive gene effects with inadequate trigenic epistasis. Simultaneous utilization of both additve and non-additive genetic effects can be achieved by inter-mating of segregants in early segregating generation.

Khattak *et al*. (2001) studied the genetics of days to first flowering, first pod maturity, 90% pod maturity and duration of the period from first flower to 90% pod maturity(DDd_1) and from first pod maturity to 90% pod maturity (DDd_2) [degree of non-synchrony of pod maturity] in mungbean using the triple test

cross (TTC) technique. Ten diverse genotypes were crossed with two true breeding testers (L_1 and L_2) and the F_1 hybrid of the tester lines (L_3). The resultant single and three-way crosses were evaluated in two seasons (kharif and spring/summer). Epistatic variation was found to be an integral part of inheritance of days to first flower in both seasons and days to first pod maturity only in kharif season. Further, partitioning of total epistasis revealed that additive × additive (i type) interactions had a major role in the inheritance of these traits. In the absence of epistasis both additive and dominance genetic components were significant for days to 90% pod maturity, DDd_1 and DDd_2 in both seasons and for days to first flower in spring/summer season. The additive genetic component was predominant for days to 90% pod maturity and DDd_2 in both seasons and for DDd_1 in spring/summer season, whereas the dominance component was important for days to first flower and DDd_1 in the spring/summer season. The direction of dominance was towards early maturity of 90% pods and late maturity of the first pod. The significant additive genetic component in DDd_1 and DDd_2 could be exploited in later generations for developing mungbean genotypes with improved synchrony in pod maturity.

Chand and Raghunadha (2002) conducted an experiment during rabi seasons of 1993-1995 to find out the type of gene action for yield and its components through a biparental cross in blackgram [*Vigna mungo* (L.) Hepper]. They found additive genetic variance was higher in magnitude than the dominance genetic variances for all the traits except days to flowering, maturity and plant height which showed preponderance of additive genetic variance. They noted both additive and dominance genetic variances were significant for six characters viz., days to flowering, maturity, plant height, clusters per plant, pods per plant and grain yield per plant. The dominance ratio is more than one for all the characters except days to flowering suggesting the presence of intrallelic and interallelic interactions governing the expression of these characters and there are possibilities of getting transgressive segregants.

Hasib *et al*. (2002) set up an experiment to study 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 mutants and 'basmoti' varieties. Epistasis was noticed in the majority of characters of all crosses. Additive and dominance effects had major role in most of the crosses for the expression of plant height, days to flowering, panicle number per plant, panicle length, spikelet fertility percent, 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, 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 action were important for the expression of almost all characters studied.

Khattak *et al*. (2002) carried out the triple test cross analysis and thirty progenies of mungbean were produced by crossing 10 true-breeding genotypes with three testers (NM 92, 6601, and their F_1) in a Triple Test cross (TTC) fashion and evaluated with parents in the kharif (July-October) and spring/summer (March-June) seasons. The data on parents and F_1s were analysed for pod clusters on main stem, pod clusters on branches, node of the first peduncle, nodes on main stem and average internodes length to detect epistasis and estimate additive and dominance components of genetic variation. Epistasis was observed for node of the first peduncle and nodes on main stem in the kharif season. Partitioning of total epistasis revealed that both additive × additive (i type) and additive × dominance, and dominance × dominance (j and l types) interactions were significant with prevalent influence of i type interactions on these traits. Both additive and dominance components of genetic variation were significant for all those traits not significantly influenced by epistasis in either or both seasons. The additive component was predominant for pod clusters on main stem, pod clusters on branches and average internodes length in the kharif season, and for the node

of the first peduncle and nodes on main stem in spring/summer season whereas, dominance component was important for pod clusters on main stem, pod clusters on branches and average internodes length in the spring/summer season. These results suggested that particular generation of segregating population and specific breeding method for selection might be adopted in each season for the improvement of these traits in mungbean.

Pandey and Singh (2003) estimated the genetic components of variance following TTC mating design involving 10 diverse genotypes of wheat. Five traits viz., grain yield, biological yield, spikelets per panicle, spikes per plant, and spike length showed epistasis except 100-grain weight. Epistasis of 'i' and 'j+l' types were important in the genetic control of grain yield, biological yield, spikelets per plant and spike per plant whereas, only 'i' type interaction influence spike length expression. Both additive and dominance type of gene action were present for grain yield, biological yield, spikes per plant, grains per spike and spikelets per spike. Additive genetic variance was present only for spike length and 100-grain weight. The ambi-directional dominance was working for grain yield, biological yield and grains per spike, while dominance was absent for spike length and grain weight.

Zewdie and Bosland (2003) studied the mode of seed colour inheritance in capsicum via an inter-specific hybridization between *C. pubescens* Ruizand Pav. (black seed colour) and *C. eximium* Hunz. (yellow seed colour). Black seed colour was dominant over yellow seed colour. The F_2 segregation pattern showed continuous variation. The generation mean analysis indicated the presence of a significant effect of additive [d], dominance [h], and additive × additive [i] interaction for seed colour inheritance. The estimate for a minimum number of effective factors (genes) involved in seed colour inheritance was approximately 3.

De-Lin and Yan (2004) studied genetic analysis of heterosis for number of spikelets per panicle and panicle length of F_1 hybrid by using japonica rice

varieties, Bing 8979, C Bao, their F_1, F_2 and triple test cross (TTC) progenies. The two traits, panicle length and number of spikelets per panicle were controlled by polygenes, which were dispersed in the two parents. The dispersion of these polygenes was the genetic basis for the heterosis. Genetic variation in panicle length was mainly due to additive and dominant effects, and the dominant component played a determinative role. For number of spikelets per panicle, the effect of non-allelic genes was highly significant (1% probability level) and there existed epistasis including effects of additive × additive, additive × dominance and dominance × dominance.

Khattak *et al*. (2004) studied the genetic variation for yield and some important yield components in two sets of crosses involving four parents through generation mean analysis. The mean data of six populations (both parents, F_1, BC_1, BC_2 and F_2) were subjected to joint scaling test. In the presence of epistasis, six-parameter model was used to detect all types of gene actions. Both the crosses shown complex genetic behavior for all the traits examined, except branches per plant in cross 6601 × NM 92 and pod cluster per plant in cross ML-5 × NM 54. The additive (D) and dominant (H) components of genetic variation were significant for all the traits in both the crosses, but dominant (H) component was non-significant for branches per plant and 1000-seed weight in cross ML-5 × NM 54, and for pod bearing nodes on main stem in cross 6601 × NM 92. The duplicate type of non-allelic interactions were found for pod cluster per plant and 1000-seed weight in cross 6601 × NM92, and for 1000-seed weight in cross ML-5 × NM 54. The complementary type of non-allelic interaction for seed yield per plant was found in both crosses. The intercrossing of F_2 plants are recommended to produce best recombinants for the traits having complex genetic behavior and selection in the latter generations of segregating populations for developing high yielding mungbean genotypes.

Noori and Sokhansanj (2004) obtained the data from 75 families produced by crossing 25 F_2 plants derived from a cross between two spring hexaploid wheats, namely Siete Cerros (salt tolerant) and Axona (salt sensitive), to their parents and their F_1 progenies, was subjected to triple test cross analysis. The genetic components (epistasis, additive and dominance) and their interactions with the environment (control - salinity) were detected for heading date, days to maturity, final plant height, spike length, ear weight, straw weight, number of grains per ear, grain yield per plant, 1000-grain weight, whole plant weight and harvest index. Epistasis was presented only for days to maturity ('j' and 'l' types) and plant height ('i' type) at control and spike length ('j' and 'l' types) at salinity condition. Additive component of variation (D) was more important than dominance (H) especially in salinity condition. Dominance ratio, $(H/D)^{1/2}$, was less than unity in both environments and heritability (both broad and narrow sense) decreased for all traits at salinity condition.

Novoselovic *et al*. (2004) set up an experiment to estimate gene effects and genetic variability for some quantitative traits of two winter wheat crosses (Soissons × Zitarka and Soissons × Sana) following generation mean analysis. In the most cases, a digenic 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 culm. In two cases (grain yield per plant and single grain weight) these models failed to explain variation in generation means, implying the presence of higher order interactions or interactions between linked loci. Dominance effects and additive × additive epistasis were more important than additive effects and other epistatic components. Only complementary type epistasis was observed. The estimated values 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 (11-99.8%), grain weight per spike (23-73%), grain yield per plant (21-78%) and single grain weight (49.7-72%).

Paramjit and Chahal (2004) developed two sets of generations of single tester analysis during the rainy seasons of 1999 and 2000 from crosses of 17 genetically diverse upland cotton (*Gossypium hirsutum* L.) genotypes, viz., 'LH 900' in Set I and 'LH 1832' in Set II, were grown in the rainy season of 2001 and evaluated for characters related to yield, fibre quality, earliness and plant type. The differences in the magnitude of additive and dominance components as estimated by single tester analysis in Set I and Set II and in means of different generations in both the sets indicated an improvement of seed-cotton yield (51.00 g from 35.89 g) and fibre quality characters in 'LH 1832' compared to 'LH 900'.While fibre length increased (29.13 mm from 25.30 mm) in the strain 'LH 1832' but there was decrease in ginning outturn (30.33% from 35.06%) compared to 'LH 900', which was the major constraint in the improvement of' LH 900'. The simplified triple test cross analysis indicated that a part of additive genetic variation was utilized for most of the characters as additive genetic component estimated from this analysis was lower than that of Set I and Set II as estimated by single tester analysis. On the basis of estimates of gene effects from analysis of generation means and high F_1 performance coupled with low inbreeding depression, 3 crosses, i. e., 'LH 1832' × 'RS 2013', 'LH 1832' × 'CIM 435' and 'LH 1832' × 'LH 1980', were selected for further improvement having good potential to further improvement of yield and fibre quality but no single cross was ideal to combine these characters with short height, early maturity and higher ginning outturn.

Jayaprada *et al*. (2005) conducted an experiment of biparental crosses derived from two F_2 populations (STV 2667 × MGG 330 and RMG 406 × LGG 407) of mungbean revealed that, variance due to females was higher than variance due to males for days to 50 per cent flowering, days to maturity and plant height. Variance due to males was higher for pods per plant, pods per cluster, seeds per pod, 100-seed weight and grain yield. Both additive and dominance genetic variance were significant for all the characters but the predominance of additive

variance was observed. The degree of dominance revealed partial dominance for all the characters except for days to 50 per cent flowering and days to maturity in BIP-I (STV 2667 x MGG 330) where as, over dominance was recorded for the later two characters. They suggested that the biparental mating or diallel selective mating system could be the best breeding method for improvement of the crop.

Khan and McNeilly (2005) used triple test cross analysis to examine the genetic base of salinity tolerance of maize. The triple test cross progenies were evaluated for seedling root growth in saline solutions with NaCl concentrations of 0 (control) and 80 mili mol (mM). Analysis of root length data of the progenies suggested that epistatic effects were important for salinity tolerance at the seedling stage. Additive × additive effects were more important for both absolute and relative root length under NaCl stress. Additive × treatment interaction was not significant, whereas epistasis × treatment interactions were significant. Non-additive effects predominantly controlled tolerance at the seedling stage and the dominance appeared to be ambi-directional for salinity tolerance.

Saleem *et al*. (2005b) studied genetic analysis to uncover the supremacy of additive, dominance and epistatic genetic variances following triple test cross analysis involving three testers (P_1, P_2 and F_1) and four lines of rice. Epistasis was found to be an integral part of genetic variation for days to flowering, plant height, number of tillers per plant and yield per plant. The partitioning of total epistasis revealed that 'i' type (additive × additive) were highly significant for days to flowering whilst 'j+l' type (additive × dominance and dominance × dominance) were important for plant height with predominant effect of 'i' type interaction. 'j+l' type epistasis also played significant role in the inheritance of number of tillers per plant and yield per plant, respectively. The additive and dominance effects were highly significant for number of grains per panicle and grain weight per panicle with the exception of 1000-grain weight where dominance effects were non-significant coupled with highly significant

additive effects. The degree of dominance was less than unity, indicating partial dominance for number of grains per panicle, grain weight per panicle and 1000-grain weight. The direction of dominance was observed towards less grain weight per panicle. Non-allelic interactions registered for days to flowering, plant height, number of tillers and yield per plant can be manipulated through recurrent selection technique for the improvement of these traits. The predominance of additive gene action for number of grains per panicle, grain weight per panicle and 1000-grain weight suggest that the selection may be delayed to later segregating populations for the improvements of yield through yield components in rice. The result shows that epistasis was found to be an integral part of genetic variation for most of the traits.

Saravanan *et al*. (2005) carried out triple test cross analysis in bhendi and brought· out that significant epistasis was present for most of the characters in the three crosses except for days to first flower in two crosses (Arka Anamika × Parbhani Kranti) and (Parbhani Kranti × MDU 1). Significant 'i' type epistasis (homozygote × homozygote) was recorded for fruit yield per plant in all the three crosses. While fruit yield per plant showed significant 'j+l' (homozygote × heterozygote and heterozygote × heterozygote) type epistasis in the cross Arka Anamika × Parbhani Kranti. The D and H component were significant for all the traits in the cross Arka Anamika × MDU 1. The estimated ratio of $(H/D)^{1/2}$ was less than unity for most of the characters.

Azizi *et al*. (2006) worked on corn inbreed lines to determine genetic parameters for yield and other traits including some of the yield components under three planting densities, using generation means analysis (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from crosses of B73 with Mo17 and K74/1. Analysis of variance reinforced the hypothesis that interaction of plant density on generation means depends on evaluating genotypes and the kind of trait. Generation mean analysis suggested that both additive and dominance effects

were important for most of the traits evaluated in this study, but dominance had a more pronounced effect. Epistasis affected the expression of nine traits in both crosses at three planting densities. Expression of epistasis and genetic parameters differed in the two crosses and were influenced by plant density. Plant densities interacted more strongly with epistasis gene action than with additive or dominance gene action in both crosses.

Bhatti *et al*. (2006) assessed the role of additive, dominance and epistatic components of genetic variance in the inheritance of staple length, fibre strength and fibre fineness in (*Gossypium hirsutum* L.) grown in 10 and 20 dSm-1 NaCl salinities by using triple test cross analysis. Results of the genetic analysis revealed that although both additive and non-additive genes affected the characters, genes acting cumulatively were predominant. It was further revealed that additive × dominance and dominance × dominance epistatic component was important in the inheritance of the characters under studies. Since there was strong evidence of the presence of significant epistasis in the inheritance of the characters, therefore no precise conclusion could be drawn about the relative importance of the three components of genetic variation. However, for the improvement of these fibre traits showing predominantly additive gene effects, early generation selection may be effective. The results of the genetic analysis revealed that the epistatic component was an important element for all the characters expression.

Dhillon and Singh (2006) carried out a triple test cross and (45 progenies) developed from J34 × SS67 *(Gossypium hirsutum)* studied at two sites. Additive × additive ('i') epistasis was significant for ginning outturn, lint index and halo length at Ludhiana and for ginning outturn, seed index and halo length at Faridkot, while its interaction with environment was significant for seed index only. Epistasis 'j+l' types was significant for all the characters except for bolls per plant at Ludhiana and ginning outturn, seed index, lint index and halo length

at Faridkot. Except for halo length, the cross showed significant interaction of epistasis 'j+l' with environment for all the characters. Both additive and dominance components of variation showed significant interaction with environment.

Marinković *et al*. (2006) analyzed the effects of additive and dominant genes and their interactions on the inheritance of hectoliter weight in 10 sunflower hybrids developed by crossing five inbred lines derived from the synthetic NS-S-1. The linkage among the expected progeny means was tested using the scaling tests method (Mather, 1949c), while the estimates of gene effects and mode of inheritance were made by generation mean analysis (Mather and Jinks, 1982). The additive-dominance model was not adequate for all crosses from the two years. In the hybrids for which the model was not adequate, epistatic gene effects were important in the inheritance of the studied characters. In the first year of study, duplicate epistasis between dominance increasers was expressed in crosses C2 and C9, while duplicate epistasis between dominance decreasers occurred in crosses C5 and C6. In the second year of study duplicate epistasis between dominance increasers was expressed only in the cross C5, while duplicate epistasis between dominance decreasers occurred in crosses C1, C4, C6, C7 and C10. In the crosses C1, C3, C4, C7, C8 and C10 in the first year and in the crosses C2, C3, C8 and C9 in the second year of investigation the type of epistasis could not be determined, because the values of the non-fixable components (dominance and dominance×dominance interaction) were insignificant.

Sofi *et al*. (2006) carried out triple test cross analysis by crossing fifteen diverse white maize inbred lines to three testers viz., W3, W5 and their F_1 of W3 × W5. The parents (lines and testers) and crosses were evaluated in randomized block design. Data were recorded on six quantitative traits governing yield, viz., grain yield, 100-seed weight, ear length, ear diameter, number of rows per ear and harvest index. Analysis of variance revealed significant differences among progenies. The epistasis was detected for all the traits except 100-seed weight.

Epistasis 'i' type was found only in case of ear diameter while as 'j+l' type epistasis was found in all the traits except 100-seed weight. Additive and dominance components of variances were significant for all the traits with preponderance of additive component. Degree of dominance was in the range of partial dominance. Correlation coefficient was non-significant for all the traits. Heritability (narrow sense) estimates were low to medium. So, result indicated that the success of plant breeding operations relies heavily on the nature and extent of genetic components of variation. Thus it is imperative to have reliable estimates of such components in order to formulate an efficient breeding strategy.

Esmail (2007) conducted an experiment to detect epistasis and to estimate genetic components for five quantitative traits viz., days to heading, plant height (cm), number of spikes per plant, 100-grain weight (g) and grain yield per plant (g) using triple test cross analysis and to determine the superior parents and hybrid combinations in respect to grain yield and its components through line × tester analysis. Ten bread wheat varieties were crossed with three testers. Result revealed the significant epistasis for number of spike per plant, 100-grain weight, plant height and days to heading. Additive × additive epistatic type of gene action was found to be much larger in magnitude than additive × dominance and dominance × dominance ('j+l') epistatic types for grain yield per plant, number of spikes per plant and 100-grain weight. Both additive (D) and dominance (H) genetic components play an important role in the inheritance of number of spikes per plant, plant height and days to heading. The average degree of dominance $(H/D)^{1/2}$ was in the range of partial dominance for all the traits studied.

Sharmila *et al*. (2007) carried out generation mean analysis considering four crosses of different sesame cultivars viz., VS 9510 × Co1; NIC 7907 × TMV 3; Cianno 13/10 × VRI 1; and Si 1115/1 × TMV 3. The P_1, P_2, F_1, F_2, BC_1 and BC_2 generations were studied for seven quantitative traits. The analysis showed the

presence of additive, dominance and epistatic gene interactions. The additive-dominance model was adequate for plant height in the NIC 7907 × TMV3 and Si 1115/1 × TMV 3 crosses and for capsule length in the VS 9510 × Co1, NIC 7907 × TMV 3 and Si 1115/1 × TMV 3 crosses. An epistatic digenic model was assumed for the remaining cross. Duplicate type epistasis played a greater role than complementary epistasis. The study revealed the importance of both additive and non-additive types of gene action for all the traits studied.

Singh *et al*. (2007) analyzed the nature of gene effects for yield and its components in four crosses involving seven diverse genotypes of mungbean through generation mean analysis. Presence of additive, dominance and epistatic gene effects were observed in almost all the crosses, indicating importance of both additive and non-additive gene actions for the expression of the characters namely, days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, number of pod per plant, pod length, seeds per pod, 100-seed weight and yield per plant. Duplicate type of epistasis was prevalent in most of the crosses. However, in certain crosses, *e.g.* BDYRI × HUM 1 for plant height and 100-seed weight and in PDM 84-139 × Pusa Bold 1 for pods per plant, additive and non-additive gene actions were important for the expression of the traits.

Taiwo (2007) used P_1, P_2, F_1, F_2, BC_1 and BC_2 generations derived from crosses between early and late maturing accessions of West African Okra to evaluate inheritance pattern of earliness. In the generation mean analysis, the additive gene effect was important in the inheritance of earliness as compared with other gene effects. A high additive gene accounts for high heritability estimates recorded for earliness. As found in the study, the relative proportion of additive gene effect was important for high estimates of heritability recorded.

Toklu and Yagbasanlar (2007) estimated genetic parameters, heterosis and heritability for the kernel size and kernel weight in three bread wheat genotypes

such as, 84 CZT 04 (large-kernelled), panda (medium-kernelled) and Bow S/ Crow S (small-kernelled) with reciprocal crossed in six combinations. Means of 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 15.42% for large kernel ratio and kernel weight, respectively. Higher heterosis was detected in the crosses where large-kernelled parent used as female. Narrow-sense heritability estimates ranged from 60 to 90% for large kernel ratio and 23 to 1005 for kernel ratio. Additive [d] and dominance [h] effects were more consistent and important in determining large kernel ratio and also epistatic gene action was effective for kernel weight.

Farshadfar *et al*. (2008a) estimated additive and dominant components of genetic variance and detection of non-allelic interaction for the salt tolerance criteria in barley with seven generations (P_1, P_2, F_1, F_2, F_3, BC_1 and BC_2) derived from the cross Wiesel burger/Abor × Lokus/Bda. Mean generation analysis indicated that the involvement of additive, dominance and epistatic type of gene action in the inheritance of leaf weight (additive, dominance and epistatic), biomass (additive and epistatic), K^+, Na^+ and K^+/Na^+ (dominance and epistatic). Heritability estimate was low for K^+ and Na^+, moderate for shoot length, leaf weight, biomass and K^+/Na^+ and high for root length. Over dominance type of gene action was found for shoot length, biomass, K^+, Na^+ and K^+/Na^+, while partial dominance for root length and leaf weight.

Zafar *et al*. (2008) carried out triple test cross analysis applied to study additive, dominance and epistatic components of genetic variation for five seedling traits namely shoot length, fresh shoot weight, root length, fresh root weight and root/shoot ratio at two salinity levels, 0 (control) and 10 dSm-1 in wheat. The results revealed that the epistatic component is an important

element for salinity tolerance at seedling stage in wheat. Both additive and dominance gene effects were involved in the inheritance of shoot length, fresh shoot weight, root length, fresh root weight and root/shoot ratio. Complete dominance was noted for shoot length, fresh root weight and root/shoot ratio and partial dominance was observed for other traits at control. On the other hand, over dominance was observed for shoot length, fresh shoot weight and root/shoot ratio, complete dominance noted for fresh root weight and partial dominance for root length at 10 dSm-1 salinity level. Significant epitasis was observed for all the traits except shoot length at both the salinity treatments.

Deb and Khaleque (2009) studied the nature of gene action of some quantitative traits in chickpea. In the analysis of scaling test, in cross-1 for number of primary branches at first flower, plant height at maximum flower, plant weight at harvest, pod weight per plant and number of seeds per plant; in cross-2 for number of primary branches at first flower, plant weight at harvest and pod weight per plant and in cross-3 for plant height at maximum flower, plant weight at harvest, number of pods per plant, pod weight per plant, number of seeds per plant and seed weight per plant additive-dominance model was found to be adequate. Dominance component of variation (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. GA and GA% were low in majority of the characters and crosses. The values of h^2_b and h^2_n were found to be low in majority cases. But in some cases theses values were high.

Husain *et al*. (2009) studied inheritance of six agronomical characters in chilli through biparantal progenies (BIPs) model. They found significant variance between family items, which indicated the presence of genetic variability in their materials. Significant regression item found in many cases which indicated that the biparental progenies were related to their parents and significant remainder item made the relationship complicated in this situation.

In most of the cases, additive components of variation (D_R) was greater than dominance components of variation (H_R) and few cases H_R was larger than D_R. As a result partial dominance was prevalent in their study. Both broad sense (h^2_b) and narrow sense (h^2_n) heritabilities were found to be low in most of the crosses. The characters such as plant height at maximum flower, number of fruits and date of early ripen having considerable amount of h^2_n may be the best improved by biparental matings in an advance generations. Significant greater variance of between families than within families in all the crosses and characters indicated the presence of significant genetic variability in different families of BIPs.

Saleem *et al*. (2009) investigated the genetic basis of flag leaf area, days to flowering, seed weight per panicle, biological yield per plant, harvest index and yield per plant by using triple test cross analysis in Basmati rice. Epistasis was detected for all the traits except biological yield per plant. Partition of epistasis into 'i' (additive × additive) and 'j+l' (additive × dominance and dominance × dominance) types showed that epistasis of i and j + l types were involved in the expression of those traits. Expression of epistasis was dependent on particular cultivars. Various lines contributed significant and positive epistatic deviations to the total epistasis. Additive (D) and dominance (H) genetic components controlled the manifestation of biological yield per plant. However, partial dominance was revealed by degree of dominance $(H/D)^{1/2}$ for this trait. Direction of dominance ($r_{s.d}$) was non-significant for biological yield per plant. The result shows that due to influence of epistatic effects for majority of the traits, recurrent selection may be recommended to develop high yielding Basmati rice varieties.

Samad *et al*. (2009) set up an experiment to study 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 and cross-II: 17 × 20). 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 in 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.

Abdelmageed (2010) investigated the inheritance of number of pods per plant, number of days to flowering and plant height in two okra cultivars, namely 'Kosti' and the Indian cultivar 'Pusa Sawani'. The experiment was carried out at Shambat, Sudan in a randomized complete block design with three replications. Gene effects, heritability in broad and narrow senses, number of effective factors and genetic advance were determined. No reciprocal differences were found between F_1 and F_2 generations for all the characters under studied. Three parameter additive-dominance model utilizing generation means was used to estimate gene effects. The results indicated that most of the genetic variance was accounted for by additive and dominance gene effects, with evidence of epistasis. High genetic variability, high heritability values and genetic gains support the above conclusions regarding the inheritance of these characters.

Bnejdi and Gazzah (2010) estimated epistasis and genotype × environment interaction of grain protein content in durum wheat considering parents, F_1, F_2, BC_1 and BC_2 generations of four crosses involving four cultivars were evaluated at two sites in Tunisia. A three-parameter model was found inadequate for all cases except crosses Chili × Cocorit 71 at site Sidi Thabet and Inrat 69 × Karim at both sites (Mograne and Sidi Thabet). 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 by environment interaction, the non-interactive model (m, d, h and e) was found to be adequate. Additive variance was higher than environmental variance in three crosses at both sites. The estimated values of narrow-sense heritability were dependent upon the cross and the sites and were 0%-85%. The results indicate that appropriate choice of environment and selection in later generations would increase grain protein content in durum wheat.

Eshghi and Akhundova (2010) estimated gene effects for some 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 and 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 and 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 [m, d, h, i and l] was adequate for number of grains per spike in cross ICNBF93-369 × ICNBF-582. Genetic variance 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.

Kumar and Patra (2010) were done four single crosses (VG20 × SGE48, SGE48 × SG35II, VG26 × SG35II, and SG35II × VG20) in opium poppy (*Papaver somniferum* L.) to study the gene actions involved in the inheritance of quantitative traits, namely plant height, branches per plant, capsules per plant, peduncle length, capsule index, stigmatic rays, straw yield per plant and morphine content. Simple additive, dominance and epistatic genetic components were found to be significant for inheritance pattern. Dominance gene effect [h]was higher than additive effect [d]. Digenic interaction indicated the prevalence of dominance × dominance [l] followed by additive × dominance [j] type epistasis. The significance of dominance [h] and dominance × dominance [l] interaction indicated duplicate epistasis for all the traits and crosses except SG35II × VG20 for stigmatic rays. Biparental mating followed by recurrent selection involving desired recombinants may be utilized to improve the component traits.

Nahar *et al*. (2010) studied on three lines of blackgram to get information about 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). 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. In RW non-significant χ^2 was found in both of the crosses. Non-significant χ^2 values indicated that only additive and dominant gene control these characters. Components of variation viz., D and H for all the characters in both of the crosses expressed negative values, except for NPdPP and NSPP where D was

positive. In almost all the cases over dominance was found in negative direction which indicates dominance towards decreasing parents. 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% were noted for NPdPP and NSPP, respectively in cross II. Selection practices may be fruitful with these characters and crosses as they showed positive and moderate genetic advance.

Payasi *et al*. (2010) estimated of various gene effects by generation mean analysis of P_1, P_2, F_1, F_2 and F_3 generations for twelve characters in mungbean. Additive-dominance model failed in all the cases, hence five parameter model were applied which gave the information about digenic interactions between genes at different loci.

Shoba *et al*. (2010) studied four groundnut genotypes of which three are late leaf spot (LLS) and rust resistant genotypes viz., COG 0437, COG 0438 and ICGV 97150 and one susceptible genotype TMV 2. Generation raising from the cross TMV 2 × ICGV 97150 showed additive gene action for most of the traits viz., plant height, number of pods per plant, pod yield per plant, kernel yield per plant, hundred kernel weight and shelling percentage and hence, early generation selection could be practiced in TMV 2 × ICGV 97150. However due to the presence of epistasis, especially for rust and LLS incidence in other two crosses viz., TMV 2 × COG 0437 and TMV 2 × COG 0438, selection should be postponed to later generations.

Sohu *et al*. (2010) carried out the triple test cross analysis and the analysis of variance for epistasis in cotton revealed the presence of epistasis for most of the characters studied. The analysis of variance for sums (D) indicated the presence of additive genetic component in the inheritance of most of the characters except for number of monopods and sympods per plant, plant height, bolls at first sympod, bolls at sympod at 50 per cent plant height, boll weight,

fibre strength and fibre quality index. Whereas, the analysis of variance for differences (H) indicated the involvement of dominance component in the inheritance of length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn, 2.5% span length, fibre fineness and fibre maturity. Both additive and dominance components of genetic variations were observed to be involved in the inheritance of length of first sympod, days to maturity, seed cotton yield, number of bolls per plant, lint yield, ginning outturn and 2.5% span length. Out of these, length of first sympod, days to maturity, number of bolls per plant, ginning outturn and 2.5% span length showed higher magnitude of dominance genetic component indicating degree of dominance to be in the range of over dominance. So, the simplified triple test cross analysis provides a precise test for epistasis along with unambiguous estimates of additive and dominance genetic variance.

Ajay *et al*. (2011) conducted an experiment of four pigeonpea crosses considering five generation to know the significance of additive-dominance model, gene action of quantitative characters, heritability and genetic advance. 'Scaling' and 'joint scaling test' was significant for most characters indicating that additive-dominance model alone is not enough to explain the inheritance pattern of the character. Though additive variance was more, dominance variance also played important role for most of the traits. Positive and negative alleles were found to be distributed between parents. Additive gene effect [d] was significant for pods per plant and seeds per pod whereas dominance gene effect [h] was more predominant among pod yield and seed yield. Dominance × dominance inter-allelic interaction [l] was more important than Additive × additive type [i] for most of the traits under studied which could be exploited by selecting individuals based on their performance in recurrent selection. Complementary gene action was observed among many traits with few exhibiting duplicate gene action. Heritability and genetic advance were high indicating the effectiveness of selection. Since dominance effects are also

present along with additive effects so selection could be practiced in later generations to identify high yielding genotypes.

Ezhilarasi and Thangavel (2011) studied the nature and magnitude of gene action with five families viz., P_1, P_2, F_1, F_2 and F_3 for fruit yield and its component characters in bhendi. It was found that the additive, dominance, additive × additive and dominance × dominance interaction with duplicate dominant type of epitasis was more important for the characters like plant height, number of fruits per plant, fruit weight and fruit yield per plant. The characters like number of nodes per plant and number of fruits per plant in all the crosses and fruit weight in TCR 852 × Mohanur local and TCR 2056 × Parbhani Kranti which were controlled by additive genetic variation could be improved by resorting to simple selection in early segregating generation.

Ghaderi *et al*. (2011) studied the genetics of resistance to damping off caused by *Pythium ultimum* was investigated in two different crosses of safflower, using generation means analysis (GMA). Generations P_1, P_2, F_1, F_2, F_3, BC_1 and BC_2 were developed to measure the percentage of un-emerged seeds (PUS), rate of seedling off (RSO), ratio of seedling off to total emerged seedlings (ROE), and disease susceptibility index (DSI). The ANOVA showed that seed emergence was faster in soil infected with the pathogen than in sterilized soil. GMA indicated that resistance was under genetic control with both simple and digenic interaction effects. The relative importance of additive and dominance genetic effects in controlling the resistance to the pathogen varied in two evaluated crosses.

Mahalingam *et al*. (2011) conducted an experiment to develop and evaluate the biparental progenies (BIPs) for important yield component traits in three rice cross combinations, namely, JGL 384 × Rasi (cross I), KJTCMS 5B × IR 64 (cross II) and WGL 14 × Rasi (cross III). They observed the traits namely, days to 50% flowering, plant height and number of productive tillers per plant in

cross I and number of productive tillers per plant in cross II were governed by additive gene action and for the improvement of these traits pure line selection, mass selection and or progeny selection and pedigree breeding method may be followed. Preponderance of non-additive type of gene action was observed for all the studied traits in cross III and remaining traits in cross I and cross II. Hence, improvement of these characters could possible through heterosis breeding or single plant selection at later generation after hybridization or two or more cycles of intermating among the selected segregants and to exploit the hidden genetic variability in heterozygous condition.

Namayandeh *et al*. (2011) have been done triple test cross analysis to assess gene action controlling resistance to common smut in maize. Epistasis was observed for resistance to maize common smut. Partitioning of the total epistasis which revealed both 'i' type and 'j+l' type were highly significant. Additive ($\overline{L}_{1i} + \overline{L}_{2i}$) and dominance ($\overline{L}_{1i} - \overline{L}_{2i}$) effects for resistance to maize common smut were also significant over two growing seasons. Dominance ratio $(H/D)^{1/2}$ indicated over dominance resistance to maize common smut. However, the direction of dominance ($r_{s,d}$) for this character in two growing seasons was non-significant which implies that dominant alleles were distributed in the parents, therefore they did not express any directional dominance for this attribute.

Kumar and Patra (2012) conduct an experiment of the families of two crosses (VG26 × VG20 and SG35II × VE01) of opium poppy to study the gene action involved in the inheritance of yield and component traits viz., plant height, leaves per plant, capsules per plant, peduncle length, capsule index, seed and straw yield per plant and morphine content. They found significant additive, dominance and epistatic genetic components. Dominance effect [h] was higher than additive effect [d] for capsule index and morphine content. In their study, digenic interaction indicated the prevalence of dominance × dominance [l] followed by additive × dominance [j] type epistasis. The opposite sign of [h]

and [l] indicated duplicate epistasis for all the traits. They concluded that biparental mating followed by recurrent selection involving desired recombinants may be utilized to improve the component traits.

Moreto *et al*. (2012) conducted an experiment to detect epistasis in Andean × Mesoamerican beans crosses using triple test cross (TTC) method. The parents of the segregating population were Carioca–MG (Mesoamerican) and BRS Radiante (Andean). They evaluate TTC families at two different locations for three characters viz., number of pods per plant, number of grains per plant and grain weight per plant. The presence of epistasis was detected for all yield components in their experiment. In the partitioning of epistasis in 'i' (additive × additive) and 'j+l' (additive × dominance and dominance × dominance) components and only 'j+l' type of epistasis was found to be significant for number of pods per plant and number of grains per plant. On the other hand, both types of epistasis were found to be significant for grain weight per plant.

Singh *et al*. (2012) done the triple test cross analysis to estimate additive, dominance and epistatic components of genetic variation for eleven quantitative characters in pea considering three testers such as, LFP 326, HUDP 15 and their hybrid. They noted total epistasis and its 'j+l' type component were highly significant for all the traits. The 'i' type epistasis was evident only for pods per plant and seed yield per plant. Additive (D) and dominance (H) components of genetic variation were highly significant for all the eleven traits. All traits showed partial dominance except for pods per plant and days to maturity. The non-significant directional element (F) for all traits indicated ambi-directional nature of dominance.

GENETIC STUDY-1: GENERATION MEAN ANALYSIS

MATERIALS AND METHODS

A. MATERIALS

The materials for the present study were collected from Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh. Five chickpea genotypes viz., BARI chola-1, BARI chola-3, BARI chola-4, BARI chola-7 and BARI chola-8 were taken as materials for this experiment. Five different crosses were made between the genotypes and raised the generations in the following manner as given in Table 19.

Table 19. Five single crosses of chickpea, their F_1, F_2 and F_3 generations.

Cross	P_1 ♀	P_2 ♂	F_1s	Selfing	F_2s	Selfing	F_3s
1.	G-8	G-3	8 × 3	→	8 × 3	→	8 × 3
2.	G-8	G-1	8 × 1	→	8 × 1	→	8 × 1
3.	G-8	G-4	8 × 4	→	8 × 4	→	8 × 4
4.	G-4	G-8	4 × 8	→	4 × 8	→	4 × 8
5.	G-8	G-7	8 × 7	→	8 × 7	→	8 × 7

B. METHODS

The methods followed to conduct the experiment and analyses of the data are divided into the following sub-heads:

a. Preparation of the Experimental Seeds,

b. Preparation of the Experimental Field,

c. Design of the Experimental Field,

d. Sowing of Seeds and Raising of the Seedlings,

e. Maintenance of the Experimental Field,

f. Collection of Data and

g. Techniques of Analysis of Data.

Descriptions of the sub-heads are as follows:

a. Preparation of the Experimental Seeds

Seeds were sown in the experimental 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 varieties/lines or genetically divergent individuals from the same varieties/lines. 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 stoppered 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 sniped off and the keel petal was pushed downwards by slitting it with a fine-pointed forceps to expose the anthers. The anthers were removed carefully and then were counted them and 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 colored cotton thread was tied loosely around the pedicel of the emasculated flower for identification.

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 between 8.30 to 10.30 (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.

b. Preparation of the Experimental Field

The experimental field was on the North-Western side of the third science building of the University of Rajshahi, Bangladesh. The experiments were conducted during the Rabi crop season of 2009-2010, 2010-2011, 2011-2012 and 2012-2013. 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.

c. Design of the Experimental Field

Lay-out of the experimental field and trial of the parents and other generations have been done under randomized complete block design.

d. Sowing of Seeds and Raising of the Seedlings

The seeds of different generations such as F_1, F_2 and F_3 along with their parents (P_1 and P_2) were sown on the 11th November, 2012. 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 plots. The gap between replications, plots, rows and hills were 120cm, 80cm, 45cm and 45cm, respectively. 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.

e. Maintenance of the Experimental Field

At the seedling stages, 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 15-16cm in height.

f. Collection of Data

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

i. Date of first flower (DFF),
ii. Plant height at first flower (PHFF),
iii. Number of primary branches at first flower (NPBMFF),
iv. Number of secondary branches at first flower (NSBFF),
v. Date of maximum flower (DMF),
vi. Plant height at maximum flower (PHMF),
vii. Number of primary branches at maximum flower (NPBMF),
viii. Number of secondary branches at maximum flower (NSBMF),
ix. Plant weight at harvest (PWH),
x. Number of pods per plant (NPd/P),
xi. Pod weight per plant (PdW/P),
xii. Number of seeds per plant (NS/P) and
xiii. Seed weight per plant (SW/P).

The thirteen recorded characters were described in Part-I.

g. Techniques of Analysis of Data

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

1. 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

2. 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

3. 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 means of the population. The standard error of mean could be determined as follows:

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

II. $S_{\bar{x}} = \sqrt{s^2 / n}$

Where,

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

S = standard deviation

n = total number of individuals.

S^2 = variance

4. Variance

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 and F_3 generations.

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

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

5. Analysis of components of mean

i. Mather's scaling test

Adequacy of scale must satisfy two conditions namely, additivity 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 are made assuming the absence of gene interaction. Mather (1949b) and Hayman and Mather (1955) gave following four tests for scale effects:

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

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

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

$D = 4\overline{F}_3 - 2\overline{F}_2 - \overline{P}_1 - \overline{P}_2$

In the present investigation, only two scales, C and D were used. With the F_3 population in absence of backcrosses, D scaling test is applied. Significance of any of these scales indicated the presence of epistasis/non-allelic interaction. It

is to be noted that, scale D provides a test largely of 'i' type (additive × additive) interaction and scale C indicates 'l' type (dominance × dominance) of gene interaction. When the scale is adequate, the values of C and D 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:

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

$$V_D = 16\ V(\bar{F}_3) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$$

Where,

VP_1, VP_2, VF_1, VF_2, and VF_3 are the variances of $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$ and $\bar{F}_3$ populations, respectively.

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

$$S.E.(_D) = (V_D)^{1/2}$$

't' values are calculated as follows:

$$t(_C) = C/\ S.E.(_C)$$

$$t(_D) = D/\ S.E.(_D)$$

ii. Test of potence

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

$$\begin{array}{r} \bar{F}_1 = m + [h] \\ -\bar{F}_2 = -m + -\tfrac{1}{2}[h] \\ \hline \bar{F}_1 - \bar{F}_2 = \tfrac{1}{2}[h] \end{array}$$

Test of significance by "t" test as $t = \dfrac{\text{Estimated value of } \bar{F}_1 - \bar{F}_2}{\text{Standard error of mean}}$

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:

- It can combine any combination of families at the same time
- It also estimates the parameters of the model viz., m, [d] and [h].
- 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 2-parameter (h-parameter excluded when potence found to be non-significant) and 3-parameter model for five generations. For testing the adequacy of additive-dominance model following weighted least square technique was done as proposed by Cavalli (1952) as follows.

Table 20. Generations, mean, weight and coefficients of 3-parameter model.

Generation	Mean	Weight	Coefficients of parameters		
			m	[d]	[h]
P_1			1	1	0
P_2			1	-1	0
F_1			1	0	1
F_2			1	0	½
F_3			1	0	¼

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 = estimated value 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 five generations following two steps are involved:

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

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

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

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

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

$\overline{F}_3 = m + \frac{1}{4}[h]$

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

- Calculation of the squared deviation of the observed mean from the expected mean for each family and calculation of the χ^2 values as follows:

Generation	**Observed (O)**	**Expected (E)**	**(O-E)**	**$(O-E)^2$**	**$\chi^2 = (O-E)^2 \times$ Weight**
P_1					
P_2					
F_1					
F_2					
F_3					
					$\sum\chi^2 =$

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

iv. Study of gene action

In the present experiment, instead of backcrosses F_3 generation is included and Hayman (1958) five parameters model is used to estimation of various genetic components to know the gene action as follows:

$$m = \overline{F}_2$$
$$d = 1/2\overline{P}_1 - 1/2\overline{P}_2$$
$$h = 1/6\left(4\overline{F}_1 + 12\overline{F}_2 - 16\overline{F}_3\right)$$
$$i = \overline{P}_1 - \overline{P}_2 + (1/2)(\overline{P}_1 - \overline{P}_2 + h) - 1/4l$$
$$l = 1/3\left(16\overline{F}_3 - 24\overline{F}_2 + 8\overline{F}_1\right)$$

Variances of this model are,

$$V(m) = V\overline{F}_2$$
$$V(d) = 1/4(V\overline{P}_1 + V\overline{P}_2)$$
$$V(h) = 1/36\left(16V\overline{F}_1 + 144V\overline{F}_2 + 256V\overline{F}_3\right)$$
$$V(i) = V\overline{P}_1 - V\overline{P}_2 + (1/4)(V\overline{P}_1 - V\overline{P}_2 + Vh) - 1/16\,Vl$$
$$V(l) = 1/9\left(256V\overline{F}_3 + 576V\overline{F}_2 + 64V\overline{F}_1\right)$$

Now, 't' values are obtained as follows:

$S.E.m = V(m)^{1/2}$	$t_m = m/S.E.m$
$S.E.d = V(d)^{1/2}$	$t_d = d/S.E.d$
$S.E.h = V(h)^{1/2}$	$t_h = h/S.E.h$
$S.E.i = V(i)^{1/2}$	$t_i = i/S.E.i$
$S.E.l = V(l)^{1/2}$	$t_l = l/S.E.l$

6. Analysis of components of variation

The variance of segregating generations viz., F_2 and F_3 consisted of both heritable and non-heritable components. The heritable components consist of fixable heritable (D) and non-fixable heritable (H) types of variation. Variation in the non-segregating generation viz., P_1, P_2 and F_1 are non-heritable (E) in nature. Based on the additive (D) - dominance (H) model variances of different generations under study can be written following Mather and Jinks (1977).

$$V_{F2} = \frac{1}{2}D + \frac{1}{4}H + E$$

$$\overline{V}_{F3} = \frac{1}{4}D + \frac{1}{8}H + E$$

$$V_{\bar{F}3} = \frac{1}{2} D + \frac{1}{16} H + E_2$$

Where,

V_{F2} = variance of F_2 family

$\overline{V}_{F3}$ = mean variance of F_3 families and

$V_{\bar{F}3}$ = variance of F_3 family means.

The non-heritable components of variation (E) in a generation were found out from the variance of non-segregating generations as follows:

$$E = {}^1/_3\, VP_1 + {}^1/_3\, VP_2 + {}^1/_3\, VF_1$$

E measure the non-heritable variance of individuals whereas, E_2 measure the non- heritable variances of F_3 family means. In general E_2 is lesser than E because each family means is based on 'm' number of individuals and it will be $({}^1/_m)$ E. Whereas, the differences in environment between individuals in different families were not high than those to which members of the same family were subjected. Therefore E_2 was measured as follows:

E_2 = E/(harmonic mean number per F_3 families).

The composition of each of the variances of segregating generations was determined in terms of single gene differences. For F_2 the composition of V_{F2} shown above was determined as follows:

Genotype	Frequency (f)	Effect (e)	f × e	f × $(e)^2$
AA	¼	+ d	¼ × d	¼ × d^2
Aa	½	h	½ × h	½ × h^2
aa	¼	- d	¼ × -d	¼ × d^2
Totals		h	½ h	½ d^2 + ½h^2

Variances of $F_2 = V_{F2} = \frac{1}{2} d^2 + \frac{1}{2} h^2 - (-\frac{1}{2} h)^2$

$$= \frac{1}{2} d^2 + \frac{1}{4} h^2$$

Where,

There are ‘k’ gene differences between two parents,

$$V_{F2} = \frac{1}{2}\, kd^2 + \frac{1}{4} kh^2$$

Substituting D for kd^2 and H for kh^2

$$V_{F2} = \frac{1}{2} D + \frac{1}{4}\, H$$

Since, VF_2 includes non-heritable variance (E) also

$$V_{F2} = \frac{1}{2} D + \frac{1}{4} H + E$$

In terms of‘d’ and ‘h’ the variance of F_3 family as follows:

F_2:	AA	Aa	aa	Mean
Frequency	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{1}{4}$	
Effect:	d	h	-d	$\frac{1}{2}$ h
F_3:	All AA	$\frac{1}{4}$ AA $\frac{1}{2}$ Aa $\frac{1}{4}$ aa	All aa	
Effect:	d	d h -d → $\frac{1}{2}$ h	-d	$\frac{1}{4}$ h
σ^2_{F3}:	0	$(\frac{1}{2} d^2 + \frac{1}{4} h^2)$	0	

Therefore, mean variance of F_3 families.

$$\overline{V}_{F3} = \frac{1}{4} \times (0) + \frac{1}{2}(\frac{1}{2} d^2 + \frac{1}{4} h^2) + \frac{1}{4} \times (0)$$

$$= \frac{1}{4} d^2 + \frac{1}{8} h^2$$

Considering other gene (k), total mean variance of F_3 families is

$$\overline{V}_{F3} = \underbrace{\frac{1}{4}D + \frac{1}{8}H}_{\text{Heritable effect}} + \underbrace{E_1}_{\text{Non-heritable effect}}$$

and variance of F_3 family means is

$$V_{\bar{F}3} = \frac{1}{4}d^2 + \frac{1}{2}\left(\frac{1}{2}h\right)^2 + \frac{1}{4}(-d)^2 - \left(\frac{1}{4}h\right)^2$$

$$= \frac{1}{4}d^2 + \frac{1}{8}h^2 + \frac{1}{4}d^2 - \frac{1}{16}h^2$$

$$= \frac{1}{2}d^2 + \frac{1}{16}h^2$$

Where, considering 'k' genes, the total heritable variances of F_3 family means is

$$V_{\bar{F}3} = \underbrace{\frac{1}{2}D + \frac{1}{16}H}_{\text{Heritable effect}} + \underbrace{E_2}_{\text{Non-heritable effect}}$$

7. 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, 1949b).

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

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

8. Number of effective factors

The number of effective factors was estimated using the formula of Mather (1949a) as follows:

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

Where,

D = least square estimate of component of genetic variation.

9. Heritability

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

i. Broad sense heritability (h^2_b)

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

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

ii. Narrow sense heritability (h^2_n)

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

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

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

10. Genetic advance (GA)

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

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

It was measured by the following formula:

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

Where,

$\overline{X}$ = grand mean for a respective character

12. Heterosis

Heterosis was expressed as increase of F_1 hybrid over the average of the parent (mid-parent or over better-parent). It was calculated as follows:

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

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

t = estimated value of the parameter / standard error of the parameter

13. Inbreeding depression

Inbreeding depression was the reduction of F_2 below the F_1 performance. It was estimated as follows.

$$\text{Inbreeding depression} = \frac{\overline{F}_1 - \overline{F}_2}{\overline{F}_1}$$

t = estimated value of the parameter / standard error of the parameter

In order to test each of the values (heterosis and inbreeding depression) 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

Generation mean analysis i.e. first order statistics based biometrical techniques was applied to determine the nature and magnitude of gene action in the expression of characters in chickpea. Thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

We know that phenotypic mean is consummated by additive, dominance and interaction effects of gene in point. The interaction effect is again of two kinds: (i) complimentary and (ii) duplicate at digenetic level. The analysis of generation mean provides measurement of these effects very efficiently, it provides the opportunity first to detect the presence or absence of epistasis (by scaling tests) and when present, it measures them appropriately. It also determines the component of heterosis in term of gene effects. Besides, based on generation mean data, some other statistic, like potence ratio, levels of dominance, number of effective factors can be developed. The results obtained through generation mean analysis are described under the different sub-heads as follows:

A. ANALYSIS OF COMPONENTS OF MEAN

a. Mather's Scaling Test

In the analysis of the components of means viz., m, [d] and [h], first Mather's scaling test was done to see whether additive-dominance model was adequate or not. It is noticed that the additive-dominance model was considered

inadequate when any one of the two scales was found to deviate significantly from zero. Mather's scaling test for C and D scales are done for all the characters in all the five different crosses separately and are presented in Table 21A-21E. Table showed that in cross-1 (8×3), all studied traits were significant for at least one of the scale tests. Regarding cross-2 (8×1), all the studied traits except PWH were significant for at least one of the scale tests. In respect of cross-3 (8×4), at least one of the scales either C or D was found to be significant for all the characters except NSBFF, PHMF and NSBMF which showed non-significant for both the scales. In the cross-4 (4×8), at least one of the scale was significant for all the traits except NPBMF. In this cross, in maximum cases scale C was found to be non-significant whereas, scale D was found to be significant. Regarding cross-5 (8×7), scale C was noted as significant for DFF, PHFF, NSBFF, NSBMF, PWH, NS/P and SW/P and scale D was significant for all traits except DFF and PWH. But both scales are significant for PHFF, NSBFF, NSBMF, NS/P and SW/P.

b. Test of Potence

The test of potence was done in five different crosses for all the characters and the results are given in Table 21A-21E. Table showed that in cross-1 (8×3), potence was significant for all the characters except DFF, NPd/P and NS/P. In cross-2 (8×1), all the characters showed significant potence except PHFF and NPBFF. Regarding cross-3 (8×4), except NPBFF, DMF and PHMF, all traits were significant for potence. In cross-4 (4×8), potence was significant for all the traits except DFF and PdW/P. All the characters except PHFF showed significant potence in cross-5 (8×7).

c. Joint Scaling Test

The significance of any one of the scale reveals the presence of non-allelic interaction. Depending on potence, in this investigation 2-parameter ($\hat{m}$ and $\hat{d}$)

and 3-paramenter ($\hat{m}$, $\hat{d}$ and $\hat{h}$) models were used in which 'm' measures a constant value (base population mean) and $\hat{d}$ and $\hat{h}$ estimate the algebraic sum of the additive and dominance effects, respectively. Thus the values of m, $\hat{d}$ and $\hat{h}$ were calculated in terms of 2 and 3-parameter 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 2 and 3-parameter model. χ^2 values obtained for each of the characters are shown in Table 21A-21E.

In this study, most of the studied traits of five different crosses exhibited significant χ^2 values. The characters showing non-significant χ^2 values indicated an adequacy of the additive-dominance model while, characters showing significant χ^2 values exhibited inadequacy of the additive-dominance model. Table 21A-21E showed that in cross-1, all the traits showed significant χ^2 values. Regarding cross-2, except PWH, NPd/P and NS/P all the traits showed significant χ^2 values. All the characters showed significant χ^2 values except NSBFF and NSBMF in cross-3. Regarding cross-4, all traits exhibited significant χ^2 values except NPBMF and regarding cross-5 none of the traits showed non-significant χ^2 values. In the present experiment, in most of the cases, the significant χ^2 values indicated that the additive-dominance model is inadequate to explain the relationship among the generation.

d. Study of Gene Action

For gene action, values of five parameters viz., m, [d], [h], [i] and [l] are estimated for thirteen characters in five crosses according to Hayman (1958) and presented in Table 22A-22E.

The mean effect 'm' was significant and positive for all the crosses and characters. In cross-1, traits viz., DFF, PHFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P and NS/P were found to be significant in respect of additive effect [d] on the other hand, traits viz., DFF, PHFF, NPBFF, DMF, NPBMF,

NSBMF, NPd/P, PdW/P, NS/P and SW/P were found to be significant in case of dominance effect [h]. The additive × additive interaction [i] exhibited significant value for DFF, DMF, PHMF, NPBMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P while, dominance × dominance gene interaction [l] showed significant value for DFF, DMF, PHMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P. Regarding cross-2, parameter [d] found to be significant for NSBFF, PHMF, NSBMF, NPd/P and NS/P and dominance [h] for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF and NPd/P. Additive × additive [i] gene action had significant effect on NPBFF, NSBFF, DMF and NS/P whereas, dominance × dominance [l] gene effect played significant role on DFF, PHFF, NPBFF, NSBFF, DMF and PdW/P. In cross-3, [d] had significant effect on NPBMF, NSBMF, NPd/P and NS/P while dominance [h] had significant effect on PHFF, NPBFF, NSBFF, DMF, PWH and PdW/P. The non-allelic parameter [i] was significant for PHFF, DMF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P while, [l] was significant for DFF, PHFF, DMF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P. In cross-4, the fixable heritable effect i.e. [d] was significant for NPBMF, NSBMF, NPd/P and NS/P while, un-fixable heritable effect i.e. [h] was significant for most of the characters except DFF, NSBFF and NSBMF. The estimated [i] for most of the traits found to be significant on the other hand, estimated [l] expressed significant values only for PHFF, NSBFF, DMF, PHMF and NSBMF. In cross-5, estimated [d] noted as significant for NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P whereas, estimated [h] exhibited significant values for most of the traits except DFF, PHMF and NSBMF. Additive × additive gene effect i.e. fixable gene interaction had significant effect for most of the traits except DFF, NSBFF and PHMF, while, dominance × dominance gene effect i.e. un-fixable gene interaction had significant effect for most of the traits except NPBFF, NSBFF, PHMF and NPBMF. In this study, the gene effects viz., additive [d], dominance [h], additive× additive [i] and dominance × dominance [l] were

significant for different crosses and characters indicating involvement of additive, dominance, additive × additive and dominance × dominance gene interactions in the control of these traits.

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 22A-22E complementary type of epistasis was observed for NPBFF, NSBFF and PHMF in cross-1; for PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; for NPBMF, NSBMF and NPd/P in cross-3; for NSBFF in cross-4 and for NSBFF, PHMF, NPBMF and PWH in cross-5. Among these traits, only PWH in cross-5 showed significant value of [h] and [l]. On the other hand, duplicate type of epistasis was noted for DFF, PHFF, DMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF, PHFF, NPBFF, NSBFF and DMF in cross-2; for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, PWH, PdW/P, NS/P and SW/P in cross-3; for DFF, PHFF, NPBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHFF, NPBFF, DMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P in cross-5. Among these, traits viz., DFF, DMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P in cross-1; DFF, PHFF, NPBFF, NSBFF and DMF in cross-2; PHFF, DMF, PWH and PdW/P in cross-3; PHFF, DMF and PHMF in cross-4 and PHFF, DMF, NPd/P, PdW/P, NS/P and SW/P in cross-5 shown significant value of [h] and [l]. It was noted from this work that when none of [i] and [l] interactions were significant and also [h] is non-significant revealed the absence of non-allelic gene interaction. So it was a perfect fit to the model ‘m’ and [d].

B. ANALYSIS OF COMPONENTS OF VARIATION (D, H and E)

Information of the genetic components of variation assist the breeder in the selection of desirable parents for crossing programs and also in deciding a

suitable breeding procedure for the genetic improvement of various quantitative traits (Singh and Narayanan, 1993). The estimates of variance components viz. D, H and E are presented in Table 23A-23E. During the estimation of components of variation, both additive genetic variation (D) and dominance genetic variation (H) were estimated from the variances of F_2 and F_3 generations while, environmental variation (E) was found out as the mean of P_1, P_2 and F_1 variances. Having only three parameters (D, H and E) a perfect fit solution was possible and for the test of the goodness of fit, the estimate of the standard deviation was done. Perusal the Table 23A-23E, it was noted that additive component (D) exhibited positive value in 61 cases and negative in 4 cases. On the other hand, dominance component H expressed positive value in 8 cases and negative in 57 cases. Both components, that is, D and H exhibited positive values in 5 cases in all the crosses. A universal characteristic of D, H, and E is that, being a component of variances, they cannot be negative. Sometimes the estimates of D, H, and E may be negative due to sampling error (Mather, 1949b) and genotype × environment interaction (Hill, 1966).

C. DEGREE OF DOMINANCE

The degrees of dominance as measured from the estimate of components of variation are shown in Table 23A-23E. The values for degree of dominance for most of the characters in studied five crosses showed over dominance. Partial degree of dominance was exhibited for PWH in cross-1 and NSBMF, NPd/P, NS/P and SW/P in cross-4. The highest dominance ratio of -3.8181 found for PWH in cross-5 but with negative sign. The negative sign indicated that the dominance towards decreasing parent.

D. NUMBER OF EFFECTIVE FACTORS (K_1)

Effective factors was estimated following Mather (1949a) and presented in Table 23A-23E. It was noted from this table that the value of K_1 was less than one for all the characters and crosses. Among the characters and crosses of this

work, the highest value of K_1 was recorded as 0.8334 for NPd/P in cross-1 and the lowest value of K_1 was noted as -0.4131 for NS/P in cross-4.

E. HERITABILITY

Heritability estimates, both in broad sense (h^2_b) and narrow sense (h^2_n) based on the components of variation and the result shown in Table 24A-24E. The major part of the total phenotypic variation of yield and yield contributing characters were of heritable in nature, as the estimates in broad sense heritability were found to be high in all the crosses for most of the characters. The highest broad sense heritability (-7.8841) was found for PdW/P in cross-2 but with negative sign which is due to the negative value of dominance component (H). However, in some cases values of h^2_b were low. Again, the estimates of narrow sense heritability was also found to be high for most the characters in different crosses. Regarding narrow sense heritability the traits viz., NPd/P and PdW/P in cross-1; NSBMF in cross-3; PWH, NPd/P, PdW/P and NS/P in cross-4 and DFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-5 found to be low. Narrow sense heritability found to be higher than broad sense heritability for most of the cases. Again, in some cases viz., PWH in cross-1; NPd/P and NS/P in cross-4 and DFF, NPd/P, PdW/P, NS/P and SW/P in cross-5 the values of broad sense heritability was higher than narrow sense heritability.

F. GENETIC ADVANCE (GA)

Both broad sense genetic advance (GA_b) and narrow sense genetic advance (GA_n) were calculated for thirteen characters in studied crosses and are presented in Table 24A-24E.

The highest value of genetic advance in broad sense was noted as 99.9467 for PWH in cross-1, as -345.0171 for NPd/P in cross-2, as -128.4259 for NS/P in cross-3, as -34.886 for NS/P in cross-4 and as -172.6964 for PWH in cross-5. On the other hand, the highest value for genetic advance in narrow sense was recorded as 195.3934 for NS/P in cross-1, as 513.9944 for PdW/P in cross-2, as 287.3275

for NS/P in cross-3, as 115.8458 for PHFF in cross-4 and as 95.0475 for NS/P in cross-5. Both the high values of broad and narrow sense genetic advance indicated that improvement of these characters was possible through selection.

G. GENETIC ADVANCE AS PERCENTAGE OF MEAN (GA%)

Both broad sense and narrow sense genetic advance as percentage of mean in different crosses for all the characters were estimated and are presented in Table 24A-24E. In the present study, most of the characters in the crosses GA% in broad and narrow senses were found to be high. The highest GA% in broad sense was noted as -142.7485 for SW/P in cross-1, as -485.9800 for PdW/P in cross-2, as -175.0036 for NPd/P in cross-3, as -117.2160 for SW/P in cross-4 and as 178.9026 for SW/P in cross-5. While, GA% in narrow sense, the highest value was noted as 358.3123 for NPBFF in cross-1, as 2497.7760 for PdW/P in cross-2, as 633.6172 for NSBFF in cross-3, as 462.2061 for NSBFF in cross-4 and as 381.9026 for NPBMF in cross-5.

H. HETEROSIS

Both mid-parent (MP) and better-parent (BP) heterosis were estimated for all the characters in studied crosses and are presented in Table 25. The mid-parent heterosis was found to be significant for NPBFF and NPBMF in cross-1; NPBFF, NSBFF and NPBMF in cross-2; NPBMF and NS/P in cross-3; NPBFF, NSBFF and NPBMF in cross-4 and NPBFF, NSBFF and NPBMF in cross-5. On the other hand, the better-parent heterosis was found to be significant for NPBFF and NPBMF in cross-2; NPBFF, NSBFF and NPBMF in cross-4 and NPBFF and NPBMF in cross-5.

I. INBREEDING DEPRESSION (ID)

Inbreeding depression (ID) was calculated and is presented in Table 26. Non-significant inbreeding depression was observed for all characters and crosses. Among the characters and crosses, negative inbreeding depression recorded in 14 cases and positive inbreeding depression noted in 51 cases.

Table 21A-21E. Mather's scaling test (C and D), test of potence and joint scaling test for thirteen characters of five crosses in chickpea.

Table 21A. Cross-1

Character	C	D	Potence	$\hat{m}$	$\hat{d}$	$\hat{h}$	χ^2
DFF	6.25*±2.39	-3.37±2.00	-1.12±0.68	80.97±0.23	-3.15±0.29	-	22.82**
PHFF	-9.96*±3.14	-12.35*±2.62	13.90*±0.75	32.49±0.43	-8.07±0.59	13.90±0.75	30.07**
NPBFF	-1.55*±0.76	-0.90*±0.43	1.85*±0.29	1.61±0.07	-0.06±0.09	1.85±0.29	12.99**
NSBFF	-3.55*±1.09	-1.51*±0.65	2.09*±0.34	1.77±0.11	0.40±0.17	0.50±0.30	24.70**
DMF	-5.09*±1.84	25.56*±2.05	5.45*±0.63	99.58±0.19	-0.40±0.19	2.63±0.49	156.74**
PHMF	-22.61*±2.59	2.12±2.49	19.25*±0.71	50.63±0.40	-2.59±0.51	8.69±0.66	77.18**
NPBMF	1.89*±0.91	1.39*±0.47	1.15*±0.35	2.53±0.07	-0.60±0.08	2.73±0.25	24.04**
NSBMF	-4.35*±1.85	4.27*±0.95	3.91*±0.72	6.62±0.14	-1.03±0.15	1.25±0.49	20.66**
PWH	83.87*±41.37	-7.90±26.30	-43.22*±10.80	101.68±2.61	-7.44±2.89	-1.56±4.94	6.69*
NPd/P	93.22*±45.41	-138.1±724.02	1.63±16.71	81.14±2.58	-24.39±6.26	-	57.85**
PdW/P	-7.37±10.10	-43.57*±6.31	7.75*±3.70	19.61±1.20	1.36±1.62	6.98±3.26	52.50**
NS/P	108.45*±44.13	-146.37*±26.09	-16.06±16.11	95.23±3.06	-30.15±6.29	-	54.91**
SW/P	-3.48±8.39	-29.69*±4.81	7.36*±3.39	15.47±0.91	2.70±1.11	5.75±2.64	40.62**

Table 21B. Cross-2

Character	C	D	Potence	$\hat{m}$	$\hat{d}$	$\hat{h}$	χ^2
DFF	15.39*±2.59	1.81±2.36	-4.60*±0.94	77.94±0.47	-1.21±0.64	4.67±1.00	35.32**
PHFF	7.74*±3.77	-4.03±3.55	1.54±1.04	36.20±0.37	1.43±0.84	-	31.05**
NPBFF	2.35*±0.69	-3.47*±0.42	0.13±0.24	1.79±0.05	-0.02±0.09	-	137.95**
NSBFF	1.10±0.97	-2.35*±0.69	0.59*±0.29	2.09±0.10	0.30±0.14	1.32±0.23	11.92**
DMF	-8.10*±1.70	25.42*±1.65	7.08*±0.68	99.99±0.25	-0.67±0.28	-0.12±0.58	253.38**
PHMF	-11.87*±3.93	-6.55±3.94	10.21*±1.38	51.28±0.59	-1.30±0.70	3.25±1.29	13.33**
NPBMF	0.84±0.95	1.27*±0.43	3.06*±0.37	2.14±0.06	-0.01±0.08	4.05±0.24	18.05**
NSBMF	0.50±1.73	1.86*±0.88	1.99*±0.54	5.51±0.11	0.25±0.14	2.62±0.37	11.55**
PWH	-34.58±39.61	-3.00±19.45	49.06*±13.61	82.39±2.94	4.84±3.98	25.78±10.31	1.41NS
NPd/P	-109.13*±53.01	-8.51±20.57	113.78*±23.66	66.09±4.61	-12.67±6.27	23.38±15.05	4.63NS
PdW/P	-46.37*±11.72	-13.42±7.03	26.36*±5.27	31.68±1.54	-1.68±1.65	-20.98±3.56	83.70**
NS/P	-106.93*±53.39	6.42±21.78	110.42*±23.70	79.59±4.73	-16.66±6.03	19.93±15.18	4.01NS
SW/P	-38.11*±9.93	-19.39*±4.91	19.66*±4.47	18.54±1.04	0.13±1.23	-10.47±2.84	31.22**

Table 21C. Cross-3

Character	C	D	Potence	$\hat{m}$	$\hat{d}$	$\hat{h}$	χ^2
DFF	12.75*±2.00	3.40±2.31	-4.07*±0.52	76.93±0.35	0.99±0.46	1.22±0.50	46.35**
PHFF	27.34*±4.55	-13.50*±3.27	-9.49*±1.34	32.98±0.57	0.52±0.83	6.09±1.26	45.80**
NPBFF	0.45±0.70	-1.04*±0.44	0.51±0.28	1.93±0.05	-0.16±0.09	-	21.37**
NSBFF	-0.82±0.97	-1.21±0.64	1.12*±0.37	2.56±0.11	-0.17±0.13	0.58±0.30	5.49NS
DMF	3.10*±1.71	22.22*±1.91	0.19±0.59	100.52±0.17	-0.17±0.26	-	161.43**
PHMF	6.66±4.16	1.12±3.38	0.56±1.24	52.07±0.36	1.18±0.60	-	19.17**
NPBMF	-0.24±0.74	2.49*±0.46	2.24*±0.29	2.81±0.09	-0.73±0.10	1.97±0.24	30.39**
NSBMF	-1.78±1.15	-0.53±0.84	1.96*±0.39	5.72±0.16	-0.28±0.21	1.05±0.37	3.19NS
PWH	-129.00*±35.03	96.99*±19.88	80.70*±13.39	95.80±3.50	-2.41±4.28	-8.84±10.58	29.06**
NPd/P	-244.28*±34.19	-29.88±22.35	164.40*±12.31	56.58±4.48	-14.38±7.05	21.32±11.83	52.34**
PdW/P	-69.89*±8.31	-1.79±5.74	36.47*±3.07	19.90±1.17	2.29±1.69	-7.62±2.92	70.87**
NS/P	-262.68*±38.50	6.65±22.42	175.50*±14.67	75.97±4.59	-20.80±6.65	-0.02±13.12	46.58**
SW/P	-54.13*±7.05	2.38±4.03	31.36*±2.86	16.64±0.80	2.03±1.02	-8.81±2.27	59.30**

Table 21D. Cross-4

Character	C	D	Potence	$\hat{m}$	$\hat{d}$	$\hat{h}$	χ^2
DFF	8.07*±2.48	9.17*±1.83	0.09±0.94	77.89±0.25	-1.12±0.46	-	56.90**
PHFF	16.98*±3.27	-3.75±2.96	-4.72*±0.98	34.36±0.56	-1.42±0.83	4.46±1.12	32.51**
NPBFF	-0.85±0.69	-1.08*±0.45	1.54*±0.22	1.54±0.07	0.03±0.10	1.15±0.19	11.40**
NSBFF	-9.98*±0.94	1.04±0.62	7.42*±0.28	2.03±0.10	0.14±0.13	2.05±0.23	124.53**
DMF	-10.60*±2.19	31.80*±1.98	11.42*±0.87	99.69±0.24	0.15±0.26	11.42±0.87	263.29**
PHMF	-4.21±2.63	35.07*±2.45	5.24*±0.79	54.27±0.43	-1.48±0.60	5.24±0.79	205.05**
NPBMF	1.13±0.78	-0.62±0.53	1.93*±0.23	2.51±0.08	0.54±0.10	2.63±0.18	3.23NS
NSBMF	-4.33*±1.84	4.11*±1.10	4.71*±0.50	6.36±0.15	0.75±0.20	2.13±0.34	13.95**
PWH	-31.86±35.19	-37.37*±17.66	33.35*±12.46	81.06±2.99	-1.88±4.25	11.92±10.12	8.95*
NPd/P	-44.10±50.06	-143.30*±25.37	43.03*±17.06	45.53±4.06	8.92±6.99	33.65±14.85	43.22**
PdW/P	-12.35±13.19	-44.99*±6.43	2.19±4.71	14.42±0.50	-4.54±1.64	-	68.47**
NS/P	-31.76±61.24	-122.10*±28.46	45.52*±22.25	68.28±4.84	16.73±6.70	17.80±17.74	26.82**
SW/P	-14.54±11.19	-25.37*±5.40	9.33*±4.45	16.14±0.88	-2.15±1.03	-5.55±3.07	33.62**

Table 21E. Cross-5

Character	C	D	Potence	$\hat{m}$	$\hat{d}$	$\hat{h}$	χ^2
DFF	27.48*±4.30	1.91±2.67	-12.81*±1.23	77.95±0.39	-0.05±0.55	0.66±0.91	65.69**
PHFF	13.84*±3.40	-7.42*±2.53	-0.40±0.97	35.70±0.25	2.15±0.59	-	94.20**
NPBFF	-0.29±0.61	-1.42*±0.39	1.71*±0.20	1.44±0.06	0.08±0.08	1.71±0.20	17.58**
NSBFF	-2.91*±0.83	-1.44*±0.56	3.08*±0.29	2.18±0.10	-0.03±0.13	1.36±0.26	25.21**
DMF	4.67±2.85	40.12*±2.26	-2.24*±0.82	100.86±0.22	-0.23±0.24	0.49±0.53	467.02**
PHMF	2.18±2.95	5.68*±2.56	4.61*±0.86	51.53±0.44	0.68±0.63	4.97±0.83	6.17*
NPBMF	1.16±0.75	1.84*±0.53	2.28*±0.25	2.61±0.08	-0.56±0.09	2.98±0.20	22.25**
NSBMF	-5.32*±1.53	3.31*±0.95	5.30*±0.50	6.03±0.15	-0.57±0.18	2.09±0.40	16.64**
PWH	-192.98*±54.40	25.33±21.08	178.84*±23.31	98.24±3.40	-10.69±3.86	20.75±13.16	12.60**
NPd/P	83.99±44.81	-144.22*±23.87	-32.26*±12.62	50.05±2.77	-22.58±4.74	22.31±8.52	47.99**
PdW/P	8.03±11.07	-33.76*±6.91	-8.01*±2.98	18.06±0.88	2.66±1.12	-1.66±1.81	33.72**
NS/P	204.62*±68.62	-179.22*±36.23	-79.62*±18.91	71.28±3.29	-20.49±4.00	22.64±10.01	28.69**
SW/P	26.72*±11.27	-41.29*±6.11	-16.63*±2.96	14.92±0.55	-0.10±0.69	-1.89±1.33	82.06**

* = Significant at 5% level, ** = Significant at 1% level, NS = non-significant.

Table 22A-22E. Estimates of gene effects using 5-parameter model of parents, F_1, F_2 and F_3 for thirteen characters of five crosses in chickpea.

Table 22A. Cross-1

Character	m	[d]	[h]	[i]	[l]
DFF	82.47*±0.52	-4.19*±0.37	5.28*±1.49	-5.10*±1.71	-12.82*±4.81
PHFF	38.93*±0.59	-4.18*±0.93	15.49*±1.55	-1.78±2.59	-3.19±5.24
NPBFF	1.93*±0.14	-0.12±0.09	1.42*±0.37	0.11±0.43	0.86±1.33
NSBFF	1.77*±0.22	0.07±0.19	0.72±0.52	0.56±0.65	2.72±1.95
DMF	99.47*±0.37	-0.71*±0.20	-14.98*±1.49	-19.32*±1.38	40.86*±4.10
PHMF	51.07*±0.54	-1.65*±0.53	2.76±1.73	-8.49*±1.96	32.98*±5.21
NPBMF	3.90*±0.16	-0.48*±0.09	1.48*±0.43	-1.57*±0.49	-0.66±1.58
NSBMF	6.23*±0.32	-0.98*±0.16	-1.84*±0.88	-5.53*±1.00	11.50*±3.22
PWH	118.89*±10.04	-9.01*±2.98	17.96±22.86	1.23±26.56	-122.36±83.73
NPd/P	129.90*±8.04	-24.81*±6.49	155.89*±20.52	58.03*±25.36	-308.52*±77.04
PdW/P	27.46*±1.74	-1.12±1.66	31.88*±4.93	25.58*±5.86	-48.26*±17.30
NS/P	140.60*±7.71	-29.79*±7.00	153.82*±20.89	56.08*±24.94	-339.75*±75.27
SW/P	21.40*±1.27	1.20±1.14	24.83*±3.99	21.62*±4.54	-34.95*±13.91

Table 22B. Cross-2

Character	m	[d]	[h]	[i]	[l]
DFF	81.30*±0.33	-0.19±0.69	4.45*±1.49	0.98±1.66	-18.10*±4.27
PHFF	37.80*±0.70	-0.36±1.00	9.39*±2.27	3.25±2.99	-15.70*±6.88
NPBFF	2.93*±0.14	-0.02±0.09	4.01*±0.35	2.66*±0.41	-7.76*±1.25
NSBFF	3.13*±0.21	0.29*±0.14	2.89*±0.54	2.32*±0.63	-4.61*±1.88
DMF	98.37*±0.24	-0.31±0.29	-15.27*±1.17	-18.91*±1.12	44.69*±3.24
PHMF	51.80*±0.70	-1.54*±0.70	6.66*±2.78	-0.69±2.76	7.11±7.87
NPBMF	3.90*±0.17	-0.05±0.08	2.77*±0.43	-0.80±0.50	0.58±1.63
NSBMF	6.43*±0.38	0.29*±0.14	1.08±0.83	-0.59±1.02	1.82±3.25
PWH	92.45*±7.98	4.35±4.01	28.01±18.30	4.94±22.48	42.11±71.02
NPd/P	74.30*±5.84	-14.31*±6.38	46.70*±20.61	-41.14±24.99	134.17±78.34
PdW/P	15.96*±1.12	0.19±1.66	4.39±5.62	1.60±6.02	43.93*±18.13
NS/P	83.93*±6.13	-17.57*±6.18	34.85±21.43	-57.24*±25.35	151.14±80.22
SW/P	13.37*±1.00	-1.93±1.29	7.18±4.29	2.71±4.77	24.96±14.92

Table 22C. Cross-3

Character	m	[d]	[h]	[i]	[l]
DFF	79.37*±0.42	0.69±0.46	2.17±1.56	1.24±1.63	-12.47*±4.30
PHFF	41.48*±0.90	0.24±0.98	17.74*±2.30	14.04*±3.22	-54.46*±8.07
NPBFF	2.27*±0.11	-0.12±0.10	1.50*±0.35	0.53±0.39	-1.98±1.17
NSBFF	2.87*±0.16	-0.14±0.13	1.38*±0.51	0.38±0.57	-0.52±1.70
DMF	100.33*±0.33	-0.12±0.26	-12.56*±1.36	-14.53*±1.27	25.50*±3.71
PHMF	53.78*±0.90	0.93±0.60	4.26±2.56	2.22±2.82	-7.39±8.30
NPBMF	3.50*±0.11	-0.60*±0.11	0.42±0.37	-2.89*±0.41	3.64*±1.25
NSBMF	6.07*±0.20	-0.50*±0.24	1.13±0.59	-0.94±0.69	1.67±1.99
PWH	66.34*±6.02	-0.93±4.35	-69.96*±16.91	-88.01*±19.53	301.32*±60.38
NPd/P	47.47*±5.20	-29.74*±7.71	21.47±15.22	-80.27*±19.62	285.87*±53.74
PdW/P	9.92*±1.25	-0.48±1.78	-8.93*±3.99	-11.41*±4.87	90.80*±13.44
NS/P	52.20*±5.84	-31.17*±7.28	-4.05±16.89	-110.55*±21.04	359.10*±61.19
SW/P	7.89*±1.02	1.39±1.04	-6.31±3.29	-7.84*±3.83	75.35*±11.48

Table 22D. Cross-4

Character	m	[d]	[h]	[i]	[l]
DFF	79.10*±0.38	-0.69±0.46	-0.65±1.33	-6.15*±1.51	1.48±4.26
PHFF	38.68*±0.50	-0.24±0.98	9.10*±1.74	4.85*±2.09	-27.64*±5.27
NPBFF	2.13*±0.14	0.12±0.10	1.70*±0.35	0.82±0.44	-0.31±1.27
NSBFF	1.43*±0.20	0.14±0.13	0.07±0.50	-2.07*±0.59	14.69*±1.77
DMF	99.10*±0.35	0.12±0.26	-16.85*±1.48	-22.73*±1.42	56.53*±4.25
PHMF	50.68*±0.50	-0.93±0.60	-20.95*±1.66	-25.94*±1.86	52.39*±4.98
NPBMF	4.03*±0.17	0.60*±0.11	3.10*±0.42	1.79*±0.51	-2.34±1.49
NSBMF	6.17*±0.42	0.50*±0.24	-0.92±0.93	-2.47*±1.20	11.26*±3.54
PWH	91.23*±6.72	0.93±4.35	37.02*±15.94	21.45±20.30	-7.34±61.41
NPd/P	86.87*±9.59	29.74*±7.71	109.16*±21.75	147.66*±30.14	-132.26±85.85
PdW/P	21.55*±2.46	0.48±1.78	23.95*±5.78	28.90*±7.64	-43.52±22.58
NS/P	102.67*±11.39	31.17*±7.28	105.75*±26.77	138.44*±34.85	-120.46±105.10
SW/P	16.68*±1.87	-1.39±1.04	16.56*±5.10	11.72±6.01	-14.44±18.92

Table 22E. Cross-5

Character	m	[d]	[h]	[i]	[l]
DFF	82.50*±0.97	0.55±0.56	4.23±2.22	4.40±2.68	-34.09*±8.23
PHFF	39.64*±0.59	-0.13±0.94	13.77*±1.52	6.99*±2.62	-28.34*±5.41
NPBFF	2.33*±0.12	0.05±0.08	2.47*±0.32	0.99*±0.37	-1.51±1.11
NSBFF	2.70*±0.15	-0.05±0.13	2.09*±0.43	0.38±0.51	1.97±1.48
DMF	100.17*±0.66	-0.38±0.24	-25.87*±1.80	-26.73*±1.90	47.27*±5.92
PHMF	53.84*±0.59	0.65±0.63	2.27±1.78	-2.13±2.08	4.67±5.62
NPBMF	4.10*±0.15	-0.48*±0.09	1.83*±0.42	-1.98*±0.46	0.90±1.43
NSBMF	5.97*±0.32	-0.50*±0.18	-0.45±0.80	-4.10*±0.92	11.52*±2.86
PWH	93.35*±7.78	-10.86*±3.86	33.29*±2.81	-70.78*±26.55	291.09*±86.95
NPd/P	99.70*±10.31	-16.17*±4.86	119.88*±21.71	77.81*±27.61	-304.28*±85.28
PdW/P	21.96*±2.61	4.21*±1.16	19.86*±5.91	32.27*±7.10	-55.73*±21.84
NS/P	143.33*±16.35	-16.21*±4.16	176.28*±34.45	121.16*±41.96	-511.79*±134.40
SW/P	23.81*±2.74	1.90*±0.73	28.71*±5.73	35.78*±7.00	-90.68*±22.30

* = Significant

Table 23A-23E. Estimates of components of variation (D, H and E), degree of dominance (√H/D) and effective factor (K_1) for thirteen characters of five crosses in chickpea.

Table 23A. Cross-1

Character	Additive (D)	Dominance (H)	Environment (E)	√H/D	K_1
DFF	66.6335±8.1629	-119.6229±10.9372	4.8464±2.2015	-1.3398	0.2635
PHFF	70.4541±8.3937	-180.4860±-13.4345	20.3035±4.5059	-1.6005	0.2474
NPBFF	4.7808±2.1865	-10.7540±-3.2793	0.8452±0.9194	-1.4998	0.0030
NSBFF	4.0237±2.0059	-7.6944±-2.7739	1.4071±1.1862	-1.3828	0.0013
DMF	130.2452±11.4125	-258.6690±-16.0832	3.5952±1.8961	-1.4092	0.0039
PHMF	103.1897±10.1582	-203.8370±-14.2772	8.1875±2.8614	-1.4054	0.0265
NPBMF	0.9878±0.9939	-3.3875±-1.8405	1.1357±1.0657	-1.8517	0.2295
NSBMF	22.6485±4.7590	-52.0377±-7.2137	4.8357±2.1990	-1.5157	0.0001
PWH	4367.8770±66.0899	1932.8230±43.9639	354.8270±18.8369	0.6652	0.0186
NPd/P	738.5295±27.1759	-6261.9460±-79.1325	3137.6940±56.0151	-2.9118	0.8334
PdW/P	67.8171±8.2351	-450.1792±-21.2174	169.5262±13.0202	-2.5764	0.0184
NS/P	8010.9257±89.5038	-21411.5400±-146.3268	3130.7060±55.9527	-1.6348	0.1107
SW/P	174.5375±13.2113	-680.6707±-26.0897	130.9890±11.4450	-1.9748	0.0083

Table 23B. Cross-2

Character	Additive (D)	Dominance (H)	Environment (E)	√H/D	K_1
DFF	138.6066±11.7731	-336.9870±-18.3572	18.1262±4.2575	-1.5592	0.0003
PHFF	531.6352±23.0572	-1114.3896±33.3825	27.4280±5.2372	-1.4478	0.0003
NPBFF	4.8437±2.2008	-9.7465±-3.1219	0.5619±0.7496	-1.4185	0.0001
NSBFF	19.1014±4.3705	-35.8306±-5.9859	0.7679±0.8763	-1.3696	0.0043
DMF	101.9809±10.0986	-220.8320±-14.8604	5.9750±2.4444	-1.4715	0.0009
PHMF	757.0895±27.5153	-1556.6023±-39.4538	25.2541±5.0253	-1.4338	0.0031
NPBMF	4.4874±2.1184	-10.5728±-3.2516	1.2512±1.1186	-1.5349	0.0005
NSBMF	9.7753±3.1266	-9.7495±-3.1224	1.9417±1.3934	-0.9986	0.0001
PWH	2933.2141±54.1592	-4685.5382±-68.4510	1614.4387±40.1801	-1.2638	0.0065
NPd/P	9724.5584±98.6132	-40861.1780±-202.1415	6374.5429±79.8407	-2.0498	0.0211
PdW/P	3072.7131±55.4321	-7341.1127±-85.6803	336.8358±18.3531	-1.5456	0.0001
NS/P	11859.3318±108.9006	-44447.3320±-210.8254	6307.7488±79.4213	-1.9359	0.0260
SW/P	1185.2548±34.4275	-3188.8824±56.4702	234.3630±15.3089	-1.6402	0.0032

Table 23C. Cross-3

Character	Additive (D)	Dominance (H)	Environment (E)	√H/D	K_1
DFF	115.6477±10.7540	-232.1868±-15.2377	5.4286±2.3299	-1.4169	0.0041
PHFF	194.7758±13.9562	-415.0620±-20.3731	30.6408±5.5354	-1.4597	0.0003
NPBFF	4.9038±2.2145	-12.0944±-3.4777	0.9119±0.9549	-1.5704	0.0029
NSBFF	14.9985±3.8728	-32.7602±-5.7236	1.5000±1.2247	-1.4779	0.0014
DMF	182.3754±13.5046	-367.6027±-19.1730	3.9083±1.9770	-1.4197	0.0001
PHMF	222.2622±14.9085	-408.2403±-20.2050	15.1922±3.8977	-1.3552	0.0039
NPBMF	11.5092±3.3925	-25.5085±-5.0506	1.0190±1.0095	-1.4887	0.0308
NSBMF	1.2618±1.1233	-6.8956±-2.6260	2.3298±1.5264	-2.3376	0.0001
PWH	8085.0711±89.9170	-19412.1300±-139.3274	1897.4666±43.5599	-1.5495	0.0001
NPd/P	4599.3712±67.8187	-16186.1300±-127.2247	2557.6571±50.5733	-1.8759	0.1923
PdW/P	142.71906±11.9465	-693.2105±-26.3289	148.8036±12.1985	-2.2038	0.0016
NS/P	8920.7882±94.4499	-25816.1700±-160.6741	3016.2976±54.9208	-1.7011	0.1089
SW/P	75.8874±8.7113	-416.3368±-20.4043	97.5612±9.8773	-2.3422	0.0253

Table 23D. Cross-4

Character	Additive (D)	Dominance (H)	Environment (E)	√H/D	K_1
DFF	155.6716±12.4768	-342.4963±-18.5067	12.2262±3.4966	-1.4832	0.0031
PHFF	305.0763±17.4664	-692.0464±-26.3068	27.8309±5.2755	-1.5061	0.0002
NPBFF	4.8148±2.1943	-9.3253±-3.0537	0.5262±0.7254	-1.3916	0.0029
NSBFF	12.8629±3.5865	-23.9905±-4.8980	0.7857±0.8864	-1.3656	0.0016
DMF	126.4505±11.2450	-270.3509±-16.4424	8.1107±2.8479	-1.4621	0.0001
PHMF	169.6064±13.0233	-356.1026±-18.8707	11.5799±3.4029	-1.4489	0.0051
NPBMF	11.3817±3.3737	-21.3007±-4. 6153	0.4952±0.7037	-1.3680	0.0311
NSBMF	10.4139±3.2271	-7.2352±-2.6898	1.9869±1.4096	-0.8335	0.0001
PWH	64.3113±8.0194	-920.6537±-30.3423	1552.6514±39.4037	-3.7835	0.0133
NPd/P	-1745.0446±-41.7737	1180.0411±34.3517	3338.1143±57.7764	-0.8223	-0.2068
PdW/P	52.9240±7.2749	-322.3040±-17.9528	235.6147±15.3497	-2.4677	0.0044
NS/P	-2351.1427±-48.4886	479.5953±21.8997	4949.9024±70.3555	-0.4516	-0.4131
SW/P	-157.4579±-12.5482	-41.6661±6.4549	193.5843±13.9135	0.5144	-0.0122

Table 23E. Cross-5

Character	Additive (D)	Dominance (H)	Environment (E)	√H/D	K_1
DFF	20.3313±4.5090	21.5014±4.6370	12.5107±3.5370	1.0283	0.0147
PHFF	34.8476±5.9032	-127.2928±-11.2824	24.9033±4.9903	-1.9112	0.0005
NPBFF	0.7564±0.8697	-1.4800±-1.2166	0.4286±0.6547	-1.3987	0.0030
NSBFF	2.0756±1.4407	-5.4227±-2.3287	1.0179±1.0089	-1.6163	0.0011
DMF	104.1448±10.2051	-171.1145±-13.0811	3.7464±1.9356	-1.2818	0.0014
PHMF	105.6952±10.2808	-218.7471±-14.7901	12.3430±3.5133	-1.4386	0.0039
NPBMF	11.4005±3.3765	-22.2458±-4.7166	0.5750±0.7583	-1.3968	0.0199
NSBMF	21.5338±4.6405	-40.3912±-6.3554	2.3298±1.5264	-1.3695	0.0001
PWH	1135.5616±33.6981	-16554.3900±-128.6639	5385.0929±73.3832	-3.8181	0.1039
NPd/P	-834.0530±-28.8800	10229.3200±28.8800	1051.3619±32.4247	-3.5020	-0.3134
PdW/P	94.0971±9.7004	426.9712±20.6633	50.1499±7.0817	2.1301	0.1884
NS/P	8264.6257±90.9100	10309.1110±101.5338	1311.6048±36.2161	1.1168	0.0318
SW/P	71.9016±8.4795	656.9019±25.6301	24.4129±4.9409	3.0226	0.0503

Table 24A-24E. Estimates of heritability (h^2_b, h^2_n), genetic advanced (GA_b, GA_n) and genetic advanced as percentage of mean ($GA\%_b$, $GA\%_n$) for thirteen characters of five crosses in chickpea.

Table 24A. Cross-1

Character	h^2_b	h^2_n	GA_b	GA_n	$GA\%_b$	$GA\%_n$
DFF	0.413086	4.034741	2.445293	23.883961	3.027458	29.570161
PHFF	-0.950537	3.384227	-6.317492	22.492382	-16.947261	60.337881
NPBFF	-0.544868	4.368964	-0.830237	6.657169	-44.686312	358.312300
NSBFF	0.059021	1.345357	0.148679	3.389095	7.413691	168.993012
DMF	0.112413	16.07737	0.466060	66.656212	0.453206	64.817932
PHMF	0.072025	5.847772	0.440716	35.782080	0.827926	67.219982
NPBMF	-0.450913	0.631023	-0.821814	1.150076	-24.062711	33.674232
NSBMF	-0.534867	3.594352	-1.955727	13.142640	-27.594311	185.435921
PWH	0.882584	0.722686	99.946720	81.839402	94.485611	77.367682
NPd/P	-0.616141	0.190198	-55.925940	17.263920	-61.824611	19.084812
PdW/P	-0.865180	0.373072	-16.991500	7.326878	-75.648961	32.620472
NS/P	-0.755586	2.246117	-65.729620	195.393401	-65.913312	195.939411
SW/P	-1.723825	1.814692	-24.625680	25.923770	-142.748512	150.273222

Table 24B. Cross-2

Character	h^2_b	h^2_n	GA_b	GA_n	$GA\%_b$	$GA\%_n$
DFF	-4.695121	21.774611	-17.255031	80.023851	-21.926721	101.689922
PHFF	-0.872442	18.146685	-6.878546	143.073142	-19.549223	406.620321
NPBFF	-0.027011	4.426503	-0.041157	6.744844	-2.139724	350.655321
NSBFF	0.435781	7.017842	1.047252	16.865032	42.306222	681.302423
DMF	-2.399771	29.013546	-6.553618	79.234121	-6.416182	77.572442
PHMF	-0.724032	25.842275	-5.708445	203.747213	-10.982721	391.995423
NPBMF	-0.469012	2.634347	-0.891657	5.008294	-26.970812	151.490521
NSBMF	0.557904	1.112871	2.408548	4.804423	38.936781	77.668682
PWH	0.154594	0.767993	13.916774	69.135782	15.216722	75.593662
NPd/P	-5.240212	4.759812	-345.017113	313.387821	-438.522514	398.319124
PdW/P	-7.884160	40.521954	-100.005464	513.994412	-485.982151	2497.776145
NS/P	-4.603991	5.268090	-318.192654	364.090214	-352.648142	403.515614
SW/P	-6.872511	19.907005	-77.245016	223.749214	-468.091121	1355.879145

Table 24C. Cross-3

Character	h^2_b	h^2_n	GA_b	GA_n	$GA\%_b$	$GA\%_n$
DFF	-0.042803	11.107712	-0.201181	52.207497	-0.259635	67.376391
PHFF	-0.262849	4.013806	-2.667155	40.728459	-7.614214	116.271921
NPBFF	-1.680260	7.206697	-2.018971	8.659439	-104.076512	446.388212
NSBFF	-0.853693	9.267522	-1.581960	17.173450	-58.366721	633.617221
DMF	-0.223111	28.537169	-0.821584	105.085038	-0.803151	102.727412
PHMF	0.373859	4.580227	3.793583	46.475984	7.263204	88.983031
NPBMF	-1.569772	14.511676	-2.036356	18.824988	-58.870972	544.229542
NSBMF	-0.883729	0.510145	-2.024571	1.168711	-33.348021	19.250641
PWH	-0.745646	3.719084	-50.641796	252.587666	-53.659643	267.639842
NPd/P	-2.154450	2.836284	-126.375531	166.370513	-175.003624	230.388221
PdW/P	-2.175459	1.522808	-30.677616	21.474142	-155.408841	108.785212
NS/P	-1.949496	4.361611	-128.425972	287.327577	-153.231721	342.837212
SW/P	-2.104991	1.207621	-24.306703	13.944366	-157.850341	90.556191

Table 24D. Cross-4

Character	h^2_b	h^2_n	GA_b	GA_n	$GA\%_b$	$GA\%_n$
DFF	-1.754931	17.538764	-7.615831	76.112590	-9.727092	97.212473
PHFF	-2.782651	20.732291	-15.548632	115.845801	-44.381432	330.665832
NPBFF	0.126363	3.997076	0.202022	6.390219	10.502732	332.218863
NSBFF	0.355729	5.273671	0.809254	11.997152	31.177566	462.206153
DMF	-1.163851	16.867833	-4.641742	67.273233	-4.486084	65.017173
PHMF	-0.573891	11.526068	-3.206713	64.404182	-5.825173	116.99376
NPBMF	0.424757	6.610226	0.811874	12.634712	24.316372	378.42069
NSBMF	0.631034	0.966928	3.016581	4.622283	44.021876	67.454372
PWH	-0.146171	0.023737	-11.082532	1.799751	-12.565632	2.040605
NPd/P	-0.209211	-0.316062	-22.642621	-34.209112	-31.462568	-47.530736
PdW/P	-0.298151	0.145794	-8.274453	4.046198	-44.571423	21.795372
NS/P	-0.271091	-0.301875	-34.848625	-38.806623	-40.058412	-44.608163
SW/P	-0.853572	-0.753829	-17.969552	-15.869821	-117.216325	-103.526983

Table 24E. Cross-5

Character	h^2_b	h^2_n	GA_b	GA_n	$GA\%_b$	$GA\%_n$
DFF	0.554013	0.362389	6.044588	3.953871	7.698772	5.035903
PHFF	-1.370858	1.658792	-9.152408	11.074771	-25.771271	31.184251
NPBFF	0.018797	0.865915	0.025591	1.178893	1.334233	61.463671
NSBFF	-0.454082	1.482595	-0.782619	2.555282	-29.408462	96.019841
DMF	0.712702	3.993214	5.301735	29.705231	5.078609	28.455041
PHMF	-0.175109	5.031231	-1.168971	33.590552	-2.197606	63.148571
NPBMF	0.194444	7.985873	0.338414	13.898753	9.298776	381.902611
NSBMF	0.223115	3.590345	0.795927	12.807992	11.909632	191.648512
PWH	-1.968178	0.312952	-172.696431	27.459731	-156.865701	24.942563
NPd/P	0.670591	-0.130661	78.042991	-15.206251	115.074302	-22.421635
PdW/P	0.754096	0.230697	22.184352	6.786741	127.925720	39.135646
NS/P	0.836483	0.515174	154.327601	95.047541	177.354710	109.229591
SW/P	0.891302	0.160074	27.516010	4.941759	178.902630	32.130166

h^2_b = Heritability at broad sense, h^2_n = Heritability at narrow sense, GA_b = Genetic advance at broad sense, GA_n = Genetic advance at narrow sense, $GA\%_b$ = Genetic advance as percentage of mean at broad sense, $GA\%_n$ = Genetic advance as percentage of mean at narrow sense.

Table 25. Estimates of heterosis (mid-parent and better-parent) for thirteen characters of five crosses in chickpea.

Character	Mid-parent heterosis					Better-parent heterosis				
	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5
DFF	0.0250	0.0408	0.0308	0.0549	0.0124	-0.0260	0.0382	0.0214	0.0453	0.0050
PHFF	0.2411	0.1633	0.1285	0.1158	0.1980	0.1151	0.1506	0.1202	0.1075	0.1932
NPBFF	0.6000*	0.7746*	0.4133	0.6267*	0.9706*	0.5000	0.7500*	0.3250	0.5250*	0.9143*
NSBFF	0.1238	0.5000*	0.2632	0.8947*	0.6182*	0.0926	0.3333	0.2000	0.8000*	0.5893
DMF	0.0293	0.0306	0.0176	0.0620	0.0010	0.0219	0.0274	0.0164	0.0607	-0.0029
PHMF	0.1506	0.0812	0.0775	0.0624	0.1129	0.1156	0.0505	0.0580	0.0432	0.0989
NPBMF	0.8800*	1.7805*	0.8476*	1.0000*	1.2000*	0.5667	1.7143*	0.4923	0.6154*	0.8333*
NSBMF	0.2694	0.4312	0.1793	0.4263	0.4422	0.1026	0.5146	0.0882	0.3162	0.3309
PWH	-0.0131	0.3729	0.1791	0.1925	0.8200	-0.0957	0.3062	0.1671	0.1804	0.6423
NPd/P	0.5849	0.8227	0.4835	0.2400	0.1319	0.2184	0.5204	0.1069	-0.0748	-0.0714
PdW/P	0.1491	0.1221	0.0571	-0.1496	-0.1819	0.1038	0.1140	0.0384	-0.1647	0.0124
NS/P	0.4043	0.6929	0.4611*	0.3095	0.2807	0.0675	0.3947	0.1024	-0.0120	0.0667
SW/P	0.2887	0.0266	0.2229	0.1072	-0.1742	0.2137	-0.0543	0.1408	0.0329	-0.2502

* = Significant

Table 26. Estimates of inbreeding depression for thirteen characters of five crosses in chickpea.

Character	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5
DFF	-0.0068±0.6821	-0.0283±0.9444	-0.0256±0.5154	0.0005±0.9420	-0.0776±1.2253
PHFF	0.1784±0.7515	0.0204±1.0422	-0.1144±1.3395	-0.0610±0.9813	-0.0051±0.9732
NPBFF	0.4778±0.2855	0.0227±0.2373	0.1134±0.2760	0.3616±0.2195	0.3673±0.2033
NSBFF	0.5903±0.3387	0.0942±0.2853	0.1960±0.3667	2.5880±1.2930	0.5697±0.2912
DMF	0.0274±0.6324	0.0360±0.6804	0.0009±0.5853	0.0576±0.8725	-0.0112±0.8216
PHMF	0.1885±0.7102	0.0985±1.3792	0.0052±1.2395	0.0517±0.7929	0.0428±0.8581
NPBMF	0.1477±0.3457	0.3919±0.3686	0.3197±0.2948	0.2397±0.2291	0.2776±0.2479
NSBMF	0.3140±0.7194	0.1547±0.5403	0.1617±0.3850	0.3822±0.5039	0.4445±0.5046
PWH	-0.1818±10.8035	0.2653±13.6103	0.6082±13.3851	0.1828±12.4597	0.9578±23.3139
NPd/P	0.0063±16.7149	0.7657±23.6569	1.7317±12.3114	0.2477±17.0556	-0.1618±12.6190
PdW/P	0.1411±3.6968	0.8257±5.2725	1.8377±3.0657	0.0508±4.7068	-0.1823±2.9843
NS/P	-0.0571±16.1081	0.6578±23.7044	1.6811±14.6728	0.2217±22.2523	-0.2777±18.9132
SW/P	0.1719±3.3892	0.7350±4.4732	1.9864±2.8627	0.2798±4.4468	-0.3492±2.9571

DISCUSSION

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 character. This study was conducted to estimate the relative importance of additive, dominance and epistatic gene effects in the inheritance of thirteen yield and yield related characters in five chickpea crosses viz., cross-1(8×3), cross-2 (8×1), cross-3 (8×4), cross-4 (4×8) and cross-5 (8×7). The characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

It is recognized that, generation mean analysis provide the estimates of main gene effects (additive and dominance) along with their digenic interactions (additive × additive and dominance × dominance) which help in understanding the nature of gene effects involved in different trait concern and accordingly the breeding procedure could be applied in developing superior expected lines. Thus, both additive and non-additive components of genetic variations along with their allied parameters are of immense use for plant breeders under different situations. For this purpose, generation mean analysis is used to studying the inheritance of thirteen quantitative traits of chickpea. In this

context, analyses have been done on the basis of parents and subsequent generations viz., P_1, P_2, F_1, F_2 and F_3 generations.

To find out presence or absence of non-allelic gene interaction in the expression of studied characters, Mather's (1949b) scaling test was done and hence C and D scales were used for this investigation. In the present study, at least one of the scale i.e., C or D noted significant for all the studied characters in all the crosses except PWH in cross-2; NSBFF, PHMF and NSBMF in cros-3 and NPBMF in cross-4. Significant of any one of the scale indicating that additive-dominance model is inadequate to explain the variation in the character and non-allelic interaction as well as other disturbing factors viz., genotype × environment (G×E) interaction or linkage may associate with these generations. Scale C and D found to be inadequate and also adequate for different characters and crosses were reported by several researchers in their materials such as, Rahman and Saad (2000) in *Vigna sesquipedalis*, Singh *et al*. (2007) in mungbean, Deb and Khaleque (2009) in chickpea and Shoba *et al*. (2010) in groundnut. Shahid (1996) also made a result from Mather's scaling test on wheat and observed that additive-dominance model was inadequate for most of the cases. The test of potence was noted as significant for all the characters except DFF, NPd/P and NS/P in cross-1; PHFF and NPBFF in cross-2; NPBFF, DMF and PHMF in cross-3; DFF and PdW/P in cross-4 and only PHFF in cross-5. Non-significance of this test indicating no difference between F_1 and F_2 and there will be no dominance and vise-versa.

Though the Mather's scaling test (C and D) can detect adequacy of additive-dominance model but not so effective, because in this test only a few combination of families is used one at a time. For example, scale 'C' involved with F_2, F_1, P_1 and P_2 families, but not other families at a time. An elaborated procedure which is an effective combination of a whole set of scaling tests into one was suggested by Cavalli (1952) named 'joint scaling test'. The method is thus more convenient,

more informative and more reliable. It is based on weighted least squares technique and is superior to other scaling test mainly in three ways:

i) In addition to the precise estimates of the three parameters viz., m, (d), (h) of the additive-dominance model, it provides the test of adequacy of the model, as χ^2, for g-p degrees of freedom if the number of generation (g) available is more than the number of parameters (p) to be estimated.

ii) With a minimum of three generations, the method can accommodate any number of generations contrary to other scaling tests where number of generation s is mostly fixed.

iii) Since the means of different generations are not generally known with a equal precision, appropriate weights are given to the generation means and their expectations.

Thus joint scaling test of Cavalli (1952) was calculated. In the present study, non-significant χ^2 values observed for PWH, NPd/P and NS/P in cross-2; NSBFF and NSBMF in cross-3 and NPBMF in cross-4 which, indicated that the additive-dominance model is adequate to explain the relationship among the generations and hence additive and dominant genes are responsible in the inheritance of these characters and crosses. As per Deb and Khaleque (2009) it also indicated that, only the additive-dominance relationship for those characters and crosses would likely be helpful in doing successful breeding plan easily for the development of potential lines in chickpea. Several worker such as Deb and Khaleque (2009) reported the adequacy of the additive-dominance model for NPBFF, PHMF, PWH, PdW/P and NS/P in cross-1; NPBFF, PWH and PdW/P in cross-2 and for PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3 in chickpea. Besides, Farshadfar *et al*. (2008a) in barley, Samad *et al*. (2009) in blackgram, Nahar *et al*. (2010) in blackgram and Eshghi *et al*. (2010) in barley also got the non-significant χ^2-values for different characters and crosses. On the other hand, most of the traits showed significant χ^2 values which indicated that the additive-dominance model was

inadequate to explain the relationship among the generations. Inadequacy of the model indicated that except the additive and dominance gene effects, non-allelic interaction and linkage may be a part to the inheritance of these characters. As the model is inadequate, further analysis is required in two lines

i) model must be extended to include those components such as non-allelic interactions, which were excluded from the simple model,

ii) on alternatively, a scale must be sought on when the simple model is adequate,

before design that is as general method of testing expected relationship between generation mean on the additive-dominance model. A procedure is known as the joint scaling test was proposed by Cavalli (1952). It contains of estimates the parameters viz., $\hat{m}$, $\hat{d}$ and $\hat{h}$ from the means of the available type of generations followed by a comparison of observed generation means with expected values derived from the estimates of the three parameter. Significant χ^2 values were reported by Ray and Islam (2008) in rice, Deb and Khaleque (2009) in chickpea, Nahar *et al*. (2010) in blackgram and Kumar *et al*. (2011b) in sweet sorghum for different characters and crosses.

The presence of non-allelic gene interactions was confirmed due to the inadequacy of additive-dominance model, then data were further analyzed employing five parameters viz., m, [d], [h], [i] and [l] model of generation mean analysis and this is happen due to the presence of F_3 generation instead of backcrosses. These genetic parameters provide information about the gene action involved for a particular trait under investigation. Estimates of genetic effects for the five parameters model indicated that mean effect 'm' of each cross was significant. Among the main effects, only additive effect [d] was noted as significant for PHMF and PWH in cross-1; for NSBMF and NS/P in cross-2; for NPBMF, NSBMF, NPd/P and NS/P in cross-3; for NSBMF in cross-4 and for NSBMF in cross-5 indicating importance of additive effect in the inheritance of these characters. On the other hand, only dominance [h]

effect was recorded as significant for NPBFF, PdW/P and SW/P in cross-1; for DFF, PHFF, NPBFF, DMF and NPBMF in cross-2; for PHFF, NPBFF, NSBFF, DMF, PWH and PdW/P in cross-3; for PHFF, NPBFF, DMF, PHMF, PWH, PdW/P and SW/P in cross-4 and for PHFF, NPBFF, NSBFF and DMF in cross-5. In this investigation, higher magnitude of dominance than additive in most of the cases indicated the greater role of dominance effect in the inheritance of these traits. Some of the characters exhibited both significant additive and dominance gene action in all the studied crosses. Among the interaction effects, additive × additive [i] and dominance × dominance [l] effects were also found to be significant for most of the characters except in few cases with a greater magnitude of dominance × dominance interaction which indicated the importance of dominance × dominance interaction in controlling the inheritance of these traits. However, the significant values of additive [d] and absence of digenic non-allelic interaction noted in cross-1 for PWH and in cross-2 and cross-3 for NSBMF revealed that selection for these traits would be useful to start from the early segregating generation. In the present study, all types of gene interactions viz., m, [d], [h], [i] and [l] were significant for DFF, DMF, NSBMF, NPd/P and NS/P in coss-1; for NSBFF in cross-2 and for PWH, NPd/P, PdW/P, NS/P and SW/P in cross-5. Many researchers such as, Sangha *et al*. (1990) in groundnut reported additive × additive gene action for plant height, Makne (1992) in groundnut observed the involvement of both additive and non-additive gene action for number of primary and secondary branches per plant, Venkateswarlu *et al*. (2007) in groundnut reported additive and non-additive gene action for kernel yield per plant and Jivani *et al*. (2009) reported additive and non-additive gene effects with preponderance of dominance for hundred kernel weight in groundnut. The significance of additive [d] and dominance [h] effects were reported for number of branches per plant by Manoharan and Thangavelu (2009) in groundnut, Jivani *et al*. (2009) noticed additive and non-additive effects with

preponderance of dominance effect for number of pods per plant in groundnut, Shoba *et al*. (2010) observed the significance of additive [d], dominance [h], additive × additive [i], dominance × dominance [l] and duplicate effect of different traits in different crosses in groundnut, Ezhilarasi and Thangavel (2011) reported the significance of [d], [h], [i], [l] and duplicate effect of plant height in different crosses in bhendi, Samad (2012) reported the significance of additive [d], dominance [h], additive × additive [i], dominance × dominance [l] and duplicate effect of different traits in six different crosses in chickpea and Sarker (2012) also observed significance of [d], [h], [i], [l] and duplicate effect of different traits and different crosses in chickpea.

The dominance [h] and dominance × dominance [l] gene effects were in the opposite direction, suggesting the duplicate type epistasis occurred in the present study. The characters viz., DFF, PHFF, DMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF, PHFF, NPBFF, NSBFF and DMF in cross-2; for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, PWH, PdW/P, NS/P and SW/P in cross-3; for DFF, PHFF, NPBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHFF, NPBFF, DMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P in cross-5 shown opposite direction of [h] and [l]. Among these traits, due to negative sign of [h] and positive sign of [l] the characters viz., DMF and NSBMF in cross-1; DMF in cross-2; DMF, PWH, PdW/P, NS/P and SW/P in cross-3; DFF, DMF, PHMF and NSBMF in cross-4 and DMF and NSBMF in cross-5 shown duplicate epistasis between dominant increaser while rest of the traits shown duplicate epistasis between dominant decreaser. Again the traits viz., DFF, DMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P in cross-1; DFF, PHFF, NPBFF, NSBFF and DMF in cross-2; PHFF, DMF, PWH and PdW/P in cross-3; PHFF, DMF and PHMF in cross-4 and PHFF, DMF, NPd/P, PdW/P, NS/P and SW/P in cross-5 shown significant value of [h] and [l], it will refer to as duplicate type of epistasis. Duplicate type of epistasis badly effects the crop

improvement and generally hinders the pace of progress in selection and hence, a higher magnitude of dominance and dominance × dominance type of interaction effects would not be expected. It also indicated that selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. Subsequent intermatings between promising lines may be important in accumulating favorable genes (Azizi *et al*., 2006). The duplicate type of epistasis further confirms the prevalence of dominance effects for these characters. Khattak *et al*. (2004) found duplicate type of non-allelic interactions for the number of clusters per plant when studied six basic generations from one cross in mungbean. Duplicate type of non-allelic interaction was also reported for plant height and number of tillers in wheat by Dashti *et al*. (2010) and in lentil by Khodambashi *et al*. (2012) for all the traits except pod length. On the other hand, unidirectional sign of [h] and [l] indicating the presence of complimentary type of gene interaction. The characters viz., NPBFF, NSBFF and PHMF in cross-1; PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; NPBMF, NSBMF and NPd/P in cross-3; NSBFF in cross-4 and NSBFF, PHMF, NPBMF and PWH in cross-5 showed complimentary type of epistasis but all are non-significant except PWH in cross-5. Due to positive sign of [h] and [l] all the above traits in the respective crosses showed complementary epistasis between dominant increaser. Kumar and Prakash (2010) found the complimentary type of gene interaction for seed protein content in all the studied crosses in mungbean. Kiani *et al*. (2013) noted complimentary type of epistasis for 1000-grain weight in cross Sang-e-Tarrom × Gerdeh and flag leaf length, panicle length and 1000-grain weight in cross IRRI2 × IR229 in rice. Between the two types of epistatic interactions, complementary gene action could be successfully exploited in the selection programme (Kumar *et al*., 2005).

Components of variation were computed on the basis of additive-dominance model. For three equations of three parameters viz., D, H and E, a perfect fit

solution was obtained. The estimates of additive component (D) expressed positive value in all the crosses for all the characters except NPd/P, NS/P and SW/P in cross-4 and NPd/P in cross-5 where it was negative. Considerable amount of additive component (D) indicated that additive component of variation was important in the present investigation. Similar results were reported by Adeniji *et al*.(2007) in West African okra, Farshadfar *et al*. (2008b) in chickpea Deb and Khaleque (2009) in chickpea, Samad *et al*. (2009) in blackgram, Nahar *et al*. (2010) in blackgram and Bnejdi and Gazzah (2010) in durum wheat reported positive value for all studied traits of his experiment.

On the other hand, dominance component (H) exhibited negative value in all the crosses for all the characters except PWH in cross-1; NPd/P and NS/P in cross-4 and DFF, NPd/P, PdW/P, NS/P and SW/P in cross-5. These results corroborate with the findings Adeniji *et al*. (2007) in West African okra, Deb and Khaleque (2009) in chickpea, Samad *et al*. (2009) in blackgram and Nahar *et al*. (2010) in blackgram. Negative estimation of component of variation, however might arise from genotype × environment interaction (Hill, 1966) and sampling errors (Mather, 1949b). These results confirmed by the work of Deb and Khaleque (2009), Samad (2012) and Sarker (2012) in chickpea; Samad *et al*. (2009) in blackgram and Nahar *et al*.(2010) in blackgram.

The values of degree of dominance (√H/D) for most of the characters in studied crosses showed over dominance. Nahar *et al*. (2010) in blackgram recorded over dominance for all the traits in their materials. Similar results were also obtained by Deb and Khaleque (2009) in chickpea and by Samad *et al*. (2009) in blackgram. Farshadfar *et al*. (2008b) in chickpea reported over dominance for number of pods per plant, earliness and proline content while grain yield, biological yield, harvest index, seed weight and number of seeds per plant showed average dominance. The negative sign of √H/D indicated dominance towards decreasing parents.

According to Mather (1949a), the effective factors (K_1) are 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 genes, 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 exist 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 were low for all the characters and crosses under study, which was due to the non-fulfillment of any one of the above assumptions. The present findings agree with the reports of different workers viz., Deb (2002), Samad (2012) and Sarker (2012) in chickpea.

Heritability estimates both in broad (h^2_b) and narrow (h^2_n) senses were found to be high in majority cases. However, in some cases these values were low. Adeniji *et al*. (2007) reported high broad sense heritability in their study and suggested that the earliness in West African okra was highly heritable. Farshadfar *et al*. (2008b) reported high broad sense heritability for all studied traits in chickpea. On the other hand, Novoselovic *et al*. (2004) reported high 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 in wheat. Aliyu (2006) observed high narrow sense heritability for pubescent density and pubescent length in cowpea. Toklu and Yagbasanlar (2007) reported higher narrow sense heritability for two crosses in bread wheat viz., Panda × 84CZT04 and Panda × Bow "S". Farshadfar *et al*. (2008b) reported high narrow sense heritability for grain yield, biological yield, seed weight, number of seeds per plant and earliness. Bnejdi and Gazzah (2010) reported moderate to high (48% - 85%) narrow sense heritability in durum

wheat. In the present study, broad sense heritability were low for DFF, NSBFF, DMF, PHMF and NPBMF in cross-1; NPBFF, NSBFF, NPBMF and PWH in cross-2; for DFF, PHFF, DMF and PHMF in cross-3; for NPBFF, NSBFF, NPBMF, PWH, NPd/P, PdW/P and NS/P in cross-4 and NPBFF, NSBFF, PHMF, NPBMF and NSBMF in cross-5. Again, in narrow sense, the heritability values were low for NPd/P and PdW/P in cross-1; PWH, NPd/P, PdW/P and NS/P in cross-4; DFF, PWH, NPd/P, PdW/P and SW/P in cross-5. Farshadfar *et al*. (2008b) reported low narrow sense heritability for number of pods per plant in chickpea and suggested that environmental effects constitute a major portion of the total phenotypic variation for this character.

Khodambashi *et al*.(2012) reported high value of narrow sense heritability for pods per plant, seeds per plant and seeds per pod suggesting that selection of these three yield components is likely be helpful to gain more yield. 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. Gangele and Rao (2005) in lentil, reported low heritability for pod length and seed yield per plant. Hinkossa *et al*. (2013) in common bean found both broad sense and narrow sense heritability as high for most of the morpho-physiological characters for both crosses and under the two growth conditions. Eshghi and Akundova (2010) estimated broad and narrow sense heritability for five characters in two crosses and found high as well as low heritability. Low broad sense and narrow sense heritability ware also observed by Alam *et al*. (2009) in sugarcane, Husain *et al*. (2009) in chilli, Deb and Khaleque (2009) in chickpea, Samad *et al*.(2009) and Nahar *et al*. (2010) in blackgram. In this investigation, the low and moderate values of heritability indicated that the non-additive and environmental effects were more prominent in the expression of traits and selection should be delayed for some generations, when the additive component of genetic variation get increased at the cost of non-additive components of genetic variations.

More or less, the values for genetic advance (GA) in broad and narrow senses were high in maximum cases. Both the high values of broad and narrow sense genetic advance indicated that improvement of these characters is possible through selection. Besides, in the present work, the genetic advance was lower in some of the cases. Farshadfar *et al*. (2008a) found that the genetic advance for grain yield and proline content was moderate (14%-40%) while, genetic advance for biological yield, harvest index, number of pods per plant, number of seeds per plant, seed weight and earliness was low (less than 14%) in chickpea. Deb and Khaleque (2009) in chickpea recorded low to high GA both in broad and narrow sense for different characters in studied crosses, whereas Samad *et al*. (2009) and Nahar *et al*. (2010) in blackgram reported low GA. Akhshi *et al*. (2014) reported that the genetic advance (GA) was low for node number of main stem, node number of lateral branches, internode length and internode diameter in both crosses, and also for plant height in DER.×A.1007 cross, whereas it was moderate for plant height in GOLI×D81 cross in common bean.

In the present study, most of the characters in all studied crosses genetic advance as percentage of mean (GA %) in broad and narrow senses were high. Sarker (2012) studied chickpea and recorded broad sense GA% as well as narrow sense GA% as moderate to high. However, heritability estimates along with the genetic gain is usually more useful than heritability values alone in predicting the resultant effect from selecting the best individuals as was indicated by Johanson *et al*. (1955) in soybean and Swarup and Chaugale (1962) in sorghum. The high heritability and high genetic gain are the indication of additive gene effects (Panse, 1957). Deb and Khaleque (2009) in chickpea reported high GA% for different characters in studied crosses.

Heterosis as a measure of the superior performance of hybrid relative to the average of parents is a means of identifying superior genotypes. In the present investigation, the values of mid-parents (MP) heterosis was found to be significant

for NPBFF and NPBMF in cross-1; NPBFF, NSBFF and NPBMF in cross-2; NPBMF and NS/P in cross-3; NPBFF, NSBFF and NPBMF in cross-4 and NPBFF, NSBFF and NPBMF in cross-5. On the other hand, better-parent heterosis (BP) was found to be significant for NPBFF and NPBMF in cross-2; for NPBFF, NSBFF and NPBMF in cross-4 and for NPBFF and NPBMF for cross-5. Abdullah *et al*. (2002) observed significant heterosis over mid-parent and better-parent for various characters in wheat. Iqbal and Nadeem (2003) observed that mid parent heterosis were significant for all the crosses except Albacala (69) × S-12 in seed cotton. Alam *et al*. (2004) in rice reported non-significant MP values in 8 crosses out of 10 only for 1000-SW. Reddy (2004) also reported significant MP values in most of the characters and crosses in rice.

Non-significant inbreeding depression (ID) values were observed for all the characters and crosses indicating absent inbreeding depression in this materials. In all the crosses, negative ID values showed in 14 cases, whereas, positive ID values exhibited in 51 cases. Gutierrez and Singh (1985) in bush bean recorded non-significant ID values for most of the characters and crosses. Cheema *et al*. (1990) in rice found non-significant ID values in cross Basmati-370/DM107-4, DM16-5-1/ DM107-4 and Basmati-370/DM16-5-1 for number of tillers per plant, number of primary branches per panicles, number of total spikelets per panicle and panicle weight. Alam *et al*. (2004) in rice also found non-significant ID values in most of the crosses for the studied characters. Reddy (2004) in rice observed non-significant ID values in 9 crosses under late planting for 100-grain weight and panicle length. Farshadfar *et al*. (2008b) reported positive ID for grain yield, biological yield, number of pods per plant and number of seeds per plant whereas, negative ID for harvest index, seed weight earliness and proline content. Positive ID revealed that the value of progenies in the F_2 generation in comparison with F_1 reduced, while negative ID indicated the increase of F_2 in relation to F_1 progenies.

From the above discussion, it may be summarized that scaling test of Mather (1949b) and Cavalli's (1952) joint scaling tests indicated the presence of epistastic

gene interaction in maximum cases. Five parameters model of generation mean analysis revealed the importance of additive [d], dominance [h] and epistastic gene interactions viz., additive × additive [i] and dominance × dominance [l] for studied characters with predominance of non-additive gene action for majority of the traits. The role of duplicate epistasis was found to important in majority of the traits under studied. On the other hand, character PWH in cross-5 exhibited complimentary type of epistasis which could be effectively exploited in the selection program. The dominance and epistastic components of variation could be exploited for the development of hybrids while the biparental hybridization between recombinants in early segregating generation (F_2) would produce better genetic combinations through which the accumulations of desirable genes could be achieved for high yield potential in an individual line.

The present investigation indicated that further breeding experiment could be done considering two lines of research 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., PWH, NPd/P and NS/P in cross-2 showed non-significant χ^2 values which, implied that the additive-dominance model found to be adequate. We know that the selection efficiency is related to the magnitude of heritability and genetic advance (Johanson *et al*., 1955). These three characters also exhibit high narrow sense heritability and genetic advance. Therefore, these characters would likely be good genetic materials for the development of prospective pure lines for further breeding works.

In second line of fruitful research would likely be with the crosses for the character NS/P in cross-3 showing the high heterosis for mid-parent and also showing over whelming dominance and duplicate type of epistasis suggesting that this trait for this cross be utilized for commercial exploitation of hybrid vigour.

SUMMARY

Inheritance pattern of yield and yield contributing characters of five crosses in chickpea were studied through generation mean analysis. Thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

Results obtained from the genetic study-1 that is generation mean analysis which is performed by Mather's (1949b) scaling test and found significant C and D scales in maximum cases which indicated that the additive-dominance model was inadequate. This result was supported by the Cavalli's (1952) joint scaling test. Inadequacy of the model indicated except additive and dominance gene effects, non-allelic interaction and linkage may be a part of the inheritance of most of the characters under studied. On the other hand, non-significant χ^2 values observed for PWH, NPd/P and NS/P in cross-2; for NSBFF and NSBMF in cross-3 and for NPBMF in cross-4. Among these characters and crosses, PWH in cross-2; NSBFF and NSBMF in cross-3 and NPBMF in cross-4 were also non-significant regarding C and D scales indicated that only the additive-dominance relationship for those characters and crosses would likely be helpful in doing successful breeding plan easily for the development of potential lines in chickpea. In the present investigation, dominance effect [h] plays a greater role in the inheritance of most of the traits due to their higher magnitude than additive effect [d]. The negative sign of [h] indicated

dominance towards decreasing parent. Among the interaction effects, dominance × dominance interaction [l] was found an important in controlling the inheritance for most of the characters due to their significant value. In the present study, most of the characters exhibited duplicate type epistasis having the opposite direction of dominance [h] and dominance × dominance [l] gene effects while, PWH in cross-5 exhibited complimentary type epistasis having unidirectional sign for [h] and [l]. Between these two types of epistatic interactions, complementary gene action could be successfully exploited in the selection breeding programme whereas duplicate type of epistasis will decrease the variation in F_2 and subsequent generations, and will also hinder the pace of progress through selection. The values of degree of dominance for most of the characters in studied crosses showed over dominance. The number of effective factor i.e. K_1 was found less than one for all the characters and crosses. It indicated that minimum one group of gene controlled the characters.

Heritability estimates both in broad (h^2_b) and narrow (h^2_n) senses were found to be high in majority cases which indicate that selection for high heritability showing traits is likely to be successful. However, in some cases these values were low, it is apparent that selection for low heritability showing traits will be difficult and high environmental influence will be a problem. Both the high values of broad and narrow sense genetic advance as well as genetic advance as percentage of mean indicated that improvement of these characters are possible through selection. In the present investigation, the values of mid-parents (MP) and better-parent heterosis were non-significant for most of the characters in studied crosses. Again, non-significant inbreeding depression was observed in all the characters and crosses.

GENETIC STUDY-2: BIPARENTAL PROGENY (BIPs) ANALYSIS

MATERIALS AND METHODS

A. MATERIALS

In this experiment five chickpea genotypes viz., BARI chola-1, BARI chola-3, BARI chola-4, BARI chola-7 and BARI chola-8 were taken as material. Five different crosses were made between the genotypes to raised F_1, F_2 and BIPs family in the following manner as given in Table 27.

Table 27. Five single crosses of chickpea, their selfing, F_2 and BIPs family.

Cross	P_1 ♀	P_2 ♂	F_1s	Selfing	F_2s	F_2s × F_2s	BIPs family
1.	G-8	G-3	8 × 3	→	8 × 3	8 × 3	8 × 3
2.	G-8	G-1	8 × 1	→	8 × 1	8 × 1	8 × 1
3.	G-8	G-4	8 × 4	→	8 × 4	8 × 4	8 × 4
4.	G-4	G-8	4 × 8	→	4 × 8	4 × 8	4 × 8
5.	G-8	G-7	8 × 7	→	8 × 7	8 × 7	8 × 7

The materials of the present investigation were the $10F_1$ families obtained from the cross between 10 pairs of plants which were randomly selected from the F_2 population. The plants of the F_2 population were considered as parental families and the crosses between these selected parental families acted as F_1 families. In a crossing program, 20 plants of the F_2 population were randomly selected and among the 20 plants, 10 plants were marked as male (♂) and the rest 10 plants were marked as female (♀). Crossings were done in a single cross fashion and $10F_1$ families were raised. The crossing patterns for cross-1 shown as follows:

Cross-1:

P_1 (F_2) × P_2 (F_2)

↓

F_1

(selling)

↓

F_2

(20 F_2 plants were randomly selected in pairs)

No. of families	Generations	(F_{1i})	Number of sibs
1	$F_{2i} \times F_{2i}$	F_{1_1}	1, 2, 3……5
2	$F_{2ii} \times F_{2ii}$	F_{1_2}	1, 2, 3……5
⋮			
10	$F_{2x} \times F_{2x}$	$F_{1_{10}}$	1, 2, 3……5

The same procedure was followed for cross-2, cross-3, cross-4 and cross-5

B. METHODS

The methods followed to conduct the experiment and analyses of the data are divided into the following sub-heads:

a. Techniques of Cross Pollination and Production of the Experimental Seeds,
b. Preparation and Design of the Experimental Field,
c. Sowing of Seeds,
d. Maintenance of the Experimental Plants,
e. Collection of Data and
f. Techniques of Analysis of Data.

Descriptions of the sub-heads are as follows:

a. Techniques of Cross Pollination and Production of the Experimental Seeds

Techniques of cross pollination were same as described in genetic study-1. In the first year, F_1 seeds were collected, in the second year F_1 plants were raised and in that year selfing were allowed to get F_2 seeds. In the third year, from each F_2 population 20 plants were selected randomly in pairs and marked as male and female parents and crosses were made between the mates of a pair. Thus, seeds of 10 F_1 families were obtained for each cross. Seeds from each mate of a pair (10 pairs) treated as P_1 and P_2 of the F_2 population were also collected and were marked as 10 P_1 and P_2 families.

In this way, seeds of 10 F_1, 10 P_1, and 10 P_2 families were produced which constituted the materials of the present investigation.

b. Preparation and Design of the Experimental Field

The experimental research field was conducted at the North-Western side of the third science building, University of Rajshahi, Bangladesh. Lay-out of the experimental field was conducted under randomized complete block design with three replications. Each replication having fifty plots. Each plot contains three rows and different rows with five hills were considered for F_1, P_1 and P_2 families. In each hill, single plant was maintained. Gap between replications, plots, rows and hills were 120 cm, 80 cm, 45cm and 45cm, respectively.

c. Sowing of Seeds

The seeds of 10 F_1, 10 P_1 and 10 P_2 families for each cross were sown in the experimental field according to design on the 11th November, 2012.

d. Maintenance of the Experimental Plants

Weeding and hoeing was done whenever necessary. Insecticide and fungicide were sprayed regularly to keep plants free from insect and fungal attack.

e. Collection of Data

Data on thirteen quantitative characters (same as genetic study-1) were collected and recorded on individual plant basis. All the plants were labeled properly before harvesting. Total number of plants from which data were taken from each cross of each family per generation and per replication is as follows:

Families	Number of families	Number of plants (sibs) per family	Total number of plants per families per replication per cross
F_1 families	10	5	10×5=50
P_1families	10	5	10×5=50
P_2 families	10	5	10×5=50

The thirteen recorded characters were described in Part-I.

f. Techniques of Analysis of Data

Techniques of Analysis of data are described under the following sub-heads:

1. Analysis of means and variance

Mean of five sibs per family per replication was taken. The analysis of variance of biparental progenies (BIPs) was computed following Kearsey (1965). The expected mean squares (EMS) were expressed as follows:

Table 28. EMS of biparental progeny analysis.

Item	df	MS	Expected MS
Replication (R)	R- 1 = 2	MS_1	$\sigma^2_W + SF\sigma^2_R$
Between families (F)	F- 1 = 9	MS_2	$\sigma^2_W + S\sigma^2_{FR} + SR\sigma^2_F$
F×R	(R-1)(F-1)= 18	MS_3	$\sigma^2_W + S\sigma^2_{FR}$
Within families	FR (S-1)=120	MS_4	σ^2_W

Where,

R = designated for number of replications

F = designated for number of family

F × R = designated for interaction of F × R

S = designated for number of sibs

σ^2_F = variance due to families

σ^2_R = variance due to replications

σ^2_{FR} = variance due to interaction of F × R

σ^2_W = variance due to within families.

2. Regression analysis

Considering the values of biparental progeny family means as dependent variable and parental family means as independent variable, regression analysis as well as regression graph was done following standard procedure. The skeleton of regression analysis as follows:

Table 29. The skeleton of regression analysis.

Source of variation	df	SS	MS	VR
Between families (F)	F-1= 9	SS_1	MS_1	MS_1/MS_4
Regression	1	SS_2	MS_2	MS_2/MS_4
Remainder	F-2 = 8	SS_3	MS_3	MS_3/MS_4
Within families	FR(S-1)=120	SS_4	MS_4	

Where,

R = designated for number of replications

F = designated for number of family

S = designated for number of sibs

3. Components of variation

Components of variation i. e. additive (D_R), dominance (H_R) and environmental (E_w) components of variation were calculated from the variance of between (σ^2_b) and within (σ^2_w) families and covariance between parent and offspring's ($Cov._{po}$). Hence,

Between family variance (σ^2_b) = 1/4 D_R + 1/16 H_R

Within family variance (σ^2_w) = 1/4 D_R + 3/16 H_R + E_w and

W_{por} = 1/4 D_R

From the above,

$D_R = W_{por} \times 4$

$H_R = 16 (\sigma^2_b - W_{por})$

$E_w = \sigma^2_w - 1/4\ D_R - 3/16\ H_R$

4. Degree of dominance

The degree of dominance was calculated as follows:

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

5. Heritability

Narrow sense (h^2_n) and broad sense (h^2_b) heritability were calculated as follows:

$$h^2_n = \frac{\frac{1}{2}D_R}{\frac{1}{2}D_R + \frac{1}{4}H_R + E_w}$$

$$h^2_b = \frac{\frac{1}{2}D_R + \frac{1}{4}H_R}{\frac{1}{2}D_R + \frac{1}{4}H_R + E_w}$$

Where,

$$E_W = \sigma^2_W - (\frac{1}{4}D + \frac{3}{16}H)$$

6. Genetic advance (GA)

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 = square root of $1/2D_R + 1/4H_R + E_W$

h^2_b = heritability in broad sense

h^2_n = heritability in narrow sense

RESULTS

Biparental mating (BIPs) is one of the simplest random mating design available to effect forced recombination and braking down undesirable linkage as pointed out by Comstock and Robinson (1952). The biparental mating design was suggested by Mather (1949a) to partition the total phenotypic variance of random mating population into between crosses and within crosses components. The great utility of BIPs is in estimating additive (D_R), dominance (H_R) and environmental (E_W) component of variation from the total variation. To secure these estimates viz., D_R, H_R and E_W, BIPs are developed following different designs of mating. In the present study, among the BIPs designs, Kearsey's (1965) paired mating design was followed. Same thirteen characters like genetic study-1 were considered for BIPs study and the obtained results are described as follows.

A. ANALYSIS OF VARIANCE

Analysis of variance was done with the biparental progenies among 10 families in five different cross following paired mating design. Thirteen quantitative characters such as DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, PdW/P, NS/P and SW/P are included in this analysis. The results of BIPs are presented in Table 30A-30M. All the items of the ANOVA of BIPs were tested by within family error.

It is noted from the Table 30A-30M that item replication showed non-significant values for all characters and crosses except NPd/P, PdW/P and NS/P in cross-2. Between family item was significant for all the characters and crosses except DMF in cross-1; NSBFF and NPd/P in cross-4 and DMF, NPBMF, NPd/P, PdW/P and SW/P in cross-5. The significant between family item indicated that there were real differences among the families. In this investigation, interaction item (F×R) was found to be non-significant in maximum cases. The characters viz., PHMF, PdW/P, NS/P and SW/P in cross-1; PHMF, NPd/P, PdW/P, NS/P and SW/P in cross-2 and DFF, PHFF, DMF, PHMF, PWH, NPd/P, PdW/P,

NS/P and SW/P in cross-3 were found to be significant regarding F×R interaction item. Non-significant interactions indicated that family and replication were not interacted each other significantly.

B. REGRESSION ANALYSIS

In the regression analysis, progeny means of biparental populations were regressed against the mid-parental values for all the thirteen traits in five single crosses. The results obtained each of the crosses and characters are shown in Table 31A-31M. Table 31A-31M showed that the regression item was found to be non-significant in most of the cases. Regression item was found to be significant only in two crosses viz., only NPBMF in cross-4 and PHFF, NPBMF and PdW/P in cross-5. For the remainder item, it was non-significant in majority cases except NPBFF in cross-2; NPBFF in cross-3; NPBFF, NPBMF and PWH in cross-4 and NPBFF and NPBMF in cross-5. Regression coefficients (b_i) when tested with their standard error, in most of the cases standard errors were greater than the regression coefficient.

C. GRAPHICAL ANALYSIS

Regression graphs were made by plotting biparental progeny means on y-axis against their respective mid-parents on x-axis for all the crosses and characters which are presented in Figures 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45 and 46. Each of the figure having five crosses and represents single character. It was observed from the graphs that the parent-offspring relationship was non-linear with below unity b value.

D. ADDITIVE COMPONENT, DOMINANCE COMPONENT AND DEGREE OF DOMINANCE

In the present study, additive (D_R) and dominance (H_R) components were estimated for all the studied characters and crosses and presented in Table 32A-32E.

Additive and Dominance Components: Table 32A-32E showed that the magnitude of additive component (D_R) was higher than that of the respective dominance component (H_R) for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. The rest of the characters and crosses showed lower D_R values than H_R. In this work, the dominance component was minus in sign in very few cases.

Degree of Dominance: In respect of degree of dominance ($\sqrt{H_R/D_R}$), complete dominance was noted for NSBFF, NSBMF and PdW/P, while NPBMF recorded as partial dominance and rest of the traits noted as over dominance in cross-1. The degree of dominance was recorded as partial for DFF, DMF, PHMF and NPBMF; as complete dominance for NSBFF and NSBMF and as over dominance for PHFF, NPBFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2. Characters viz., NPBMF, PdW/P and NS/P exhibited complete dominance; NPBFF and SW/P showed partial dominance and rest of the traits showed over dominance in cross-3. The characters viz., DMF, PHMF and SW/P showed complete dominance; NPBMF, NPd/P, PdW/P and NS/P showed partial dominance, while rest of the traits showed over dominance in cross-4. In cross-5, over dominate showed by PHFF, DMF and NPd/P; partial dominance by PdW/P, NS/P and SW/P and rest of the characters showed complete dominance.

E. HERETABILITY BOTH NARROW AND BROAD SENSES

In the present investigation, both narrow sense (h^2_n) and brood sense (h^2_b) heritability values were estimated for all the cases and are presented in Table 32A-32E. Both heritability values were found to be low and among them comparatively the high narrow sense heritability value was noted as 0.3261 for PWH in cross-1; as 0.3860 for PWH in cross-2; as 0.3340 for NSBFF in cross-3; as 0.1633 for NSBFF in cross-4 and as 0.1309 for NSBMF in cross-5. On the other hand, the high broad sense heritability value was noted as -0.2362 for PWH

in cross-1; as -0.1692 for PWH in cross-2; as 0.2079 for NPBFF in cross-3; as 0.1960 for PWH in cross-4 and as 0.1439 for PHFF in cross-5.

F. GENETIC ADVANCE (GA)

Both broad sense genetic advance (GA_b) and narrow sense genetic advance (GA_n) were calculated for thirteen characters in studied crosses and are presented in Table 32A-32E. The highest value of genetic advance in broad sense was noted as -21.2749 for PWH in cross-1, as -15.691 for PWH in cross-2, as -11.5253 for PWH in cross-3, as 22.3138 for PWH in cross-4 and as 12.7896 for PWH in cross-5. On the other hand, the highest value for genetic advance in narrow sense was recorded as 29.3791 for PWH in cross-1, as 35.7990 for PWH in cross-2, as 13.4223 for PWH in cross-3, as 4.6407 for PWH in cross-4 and as 8.4999 for PWH in cross-5. Both the high values of broad and narrow sense genetic advance indicated that improvement of these characters was possible through selection.

G. TEST OF LINKAGE

Comparison between total variance (σ^2) of different generations such as F_2, F_2 (BIPs) and $F_1 \times F_2$ (L_{3i}) was made for four different crosses viz., cross-2, cross-3, cross-4 and cross-5 for all the thirteen characters to observed the presence of linkage following Jinks and Perkins (1970) and the results are presented in Table 33A-33M. Linkage test was not done for cross-1 due to not available material of L_{3i} families. The test of linkage has been done by comparing variances of any pair of the total variances of these three generations. In calculating F value for significance test, the lower variance was considered as denominator. In the presence of linkage greater variance between the total variances as shown in F_2 (BIPs) and $F_1 \times F_2$ (L_{3i}) families in this investigation. Further in many cases F_2 and $F_1 \times F_2$ (L_{3i}) were intermediate. Hence in most of the comparison total variances (σ^2_s) of the F_2 (BIPs) and $F_1 \times F_2$ (L_{3i}) families provided a sensitive test of the presence of

linkage in this materials. Test of significance shows that linkage was present in most of the cases. Linkage in repulsion phage was noted for DFF, PHFF, DMF, PHMF, NPd/P, PdW/P, NS/P and SW/P in cross-2; for DFF, NPBFF, DMF, PHMF and NSBMF in cross-3; for DFF, PHFF, DMF, PHMF and PWH in cross-4 and for PHFF, NSBFF, DMF, PHMF and NSBMF in cross-5 due to smaller F_2 values. On the other hand, linkage in coupling phage was observed for NPBFF, NSBFF, NPBMF, NSBMF and PWH in cross-2; for PHFF, NSBFF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3; for NPBFF, NSBFF, NPBMF, NSBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, NPBFF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-5 due to larger F_2 values.

Table 30A-30M. Analysis of variance of biparental progeny (BIPs) for thirteen characters of five crosses in chickpea.

Table 30A. Date of first flower (DFF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	12.7760	6.3880	0.9109^{NS}
Between families (F)	9	127.4667	14.1630	2.0195^{*}
F × R	18	115.9973	6.4443	0.9189^{NS}
Within families	120	841.5520	7.0129	
Total	149	4464.0000		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	6.2160	3.1080	0.3927^{NS}
Between families (F)	9	249.0133	27.6681	3.4961^{**}
F × R	18	174.3707	9.6873	1.2241^{NS}
Within families	120	949.6800	7.9140	
Total	149	5178.0000		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	1.1760	0.5880	0.1488^{NS}
Between families (F)	9	94.3747	10.4861	2.6544^{**}
F × R	18	145.1173	8.0621	2.0408^{*}
Within families	120	474.0544	3.9505	
Total	149	2610.9400		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	3.8747	1.9373	0.2986^{NS}
Between families (F)	9	194.8013	21.6446	3.3360^{**}
F × R	18	156.2587	8.6810	1.3380^{NS}
Within families	120	778.5877	6.4882	
Total	149	4247.8733		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	6.1307	3.0653	0.5629^{NS}
Between families (F)	9	153.9680	17.1076	3.1416^{**}
F × R	18	77.0160	4.2787	0.7857^{NS}
Within families	120	653.4517	5.4454	
Total	149	3504.3733		

Table 30B. Plant height at first flower (PHFF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	24.9527	12.4763	2.8459^{NS}
Between families (F)	9	134.5770	14.9530	3.4108**
F × R	18	126.7871	7.0437	1.6067^{NS}
Within families	120	526.0838	4.3840	
Total	149	2916.7357		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	12.4148	6.2074	0.7994^{NS}
Between families (F)	9	227.3001	25.2556	3.2523**
F × R	18	217.1680	12.0649	1.5537^{NS}
Within families	120	931.8520	7.7654	
Total	149	5116.1426		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	2.3194	1.1597	0.2349^{NS}
Between families (F)	9	95.9683	10.6631	2.1601**
F × R	18	179.4016	9.9668	2.0190*
Within families	120	592.3651	4.9364	
Total	149	3239.5150		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	0.3912	0.1956	0.0240^{NS}
Between families (F)	9	492.6989	54.7443	6.7286**
F × R	18	119.5996	6.6444	0.8167^{NS}
Within families	120	976.3215	8.1360	
Total	149	5494.2971		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	11.7387	5.8693	1.2244^{NS}
Between families (F)	9	213.5298	23.7255	4.9494**
F × R	18	40.3770	2.2432	0.4680^{NS}
Within families	120	575.2309	4.7936	
Total	149	3141.7998		

Table 30C. Number of primary branches at first flower (NPBFF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	0.3227	0.1613	1.2318^{NS}
Between families (F)	9	4.1133	0.4570	3.4894^{**}
F × R	18	1.8107	0.1006	0.7680^{NS}
Within families	120	15.7173	0.1310	
Total	149	84.8333		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	0.2747	0.1373	1.2892^{NS}
Between families (F)	9	3.3453	0.3717	3.4894^{**}
F × R	18	1.4587	0.0810	0.7607^{NS}
Within families	120	12.7829	0.1065	
Total	149	68.9933		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0427	0.0213	0.1328^{NS}
Between families (F)	9	11.8520	1.3169	8.1969^{**}
F × R	18	1.1040	0.0613	0.3818^{NS}
Within families	120	19.2789	0.1607	
Total	149	109.3933		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0347	0.0173	0.2107^{NS}
Between families (F)	9	1.5253	0.1695	2.0604^{*}
F × R	18	0.5787	0.0321	0.3908^{NS}
Within families	120	9.8709	0.0823	
Total	149	51.4933		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	0.2427	0.1213	1.5275^{NS}
Between families (F)	9	2.9547	0.3283	4.1331^{**}
F × R	18	0.3173	0.0176	0.2219^{NS}
Within families	120	9.5317	0.0794	
Total	149	51.1733		

Table 30D. Number of secondary branches at first flower (NSBFF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0667	0.0333	0.1129^{NS}
Between families (F)	9	13.5200	1.5022	5.0881^{**}
F × R	18	2.6000	0.1444	0.4892^{NS}
Within families	120	35.4293	0.2952	
Total	149	193.3333		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	1.4907	0.7453	2.0429^{NS}
Between families (F)	9	7.2333	0.8037	2.2029^{*}
F × R	18	5.2027	0.2890	0.7922^{NS}
Within families	120	43.7813	0.3648	
Total	149	232.8333		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	1.2347	0.6173	2.9327^{NS}
Between families (F)	9	6.9347	0.7705	3.6605^{**}
F × R	18	3.4053	0.1892	0.8988^{NS}
Within families	120	25.2597	0.2105	
Total	149	137.8733		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	0.9627	0.4813	1.9979^{NS}
Between families (F)	9	2.5187	0.2799	1.1616^{NS}
F × R	18	3.3573	0.1865	0.7742^{NS}
Within families	120	28.9109	0.2409	
Total	149	151.3933		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	1.0347	0.5173	1.9888^{NS}
Between families (F)	9	5.7987	0.6443	2.4769^{*}
F × R	18	5.6853	0.3159	1.2142^{NS}
Within families	120	31.2149	0.2601	
Total	149	168.5933		

Table 30E. Date of maximum flower (DMF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	21.1760	10.5880	2.7264^{NS}
Between families (F)	9	64.7053	7.1895	1.8513^{NS}
F × R	18	112.0507	6.2250	1.6029^{NS}
Within families	120	466.0256	3.8835	
Total	149	2528.0600		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	25.8667	12.9333	2.5396^{NS}
Between families (F)	9	236.5600	26.2844	5.1612^{**}
F × R	18	81.2800	4.5156	0.8867^{NS}
Within families	120	611.1253	5.0927	
Total	149	3399.3333		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	5.6747	2.8373	0.5689^{NS}
Between families (F)	9	152.5813	16.9535	3.3992^{**}
F × R	18	156.7787	8.7099	1.7463^{*}
Within families	120	598.5077	4.9876	
Total	149	3307.5733		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	5.7707	2.8853	1.7267^{NS}
Between families (F)	9	43.1320	4.7924	2.8679^{**}
F × R	18	32.2560	1.7920	1.0724^{NS}
Within families	120	200.5269	1.6711	
Total	149	1083.7933		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	14.6907	7.3453	2.2457^{NS}
Between families (F)	9	24.2987	2.6999	0.8254^{NS}
F × R	18	66.4293	3.6905	1.1283^{NS}
Within families	120	392.4949	3.2708	
Total	149	2067.8933		

Table 30F. Plant height at maximum flower (PHMF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	31.5906	15.7953	1.7606^{NS}
Between families (F)	9	239.0547	26.5616	2.9607**
F × R	18	351.3257	19.5181	2.1756**
Within families	120	1076.5752	8.9715	
Total	149	6004.8469		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	51.3982	25.6991	1.7676^{NS}
Between families (F)	9	444.3031	49.3670	3.3955**
F × R	18	495.9413	27.5523	1.8951*
Within families	120	1744.6651	14.5389	
Total	149	9714.9680		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	4.6896	2.3448	0.6490^{NS}
Between families (F)	9	125.0528	13.8948	3.8458**
F × R	18	125.6722	6.9818	1.9324*
Within families	120	433.5597	3.6130	
Total	149	2423.2133		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	52.6352	26.3176	2.4317^{NS}
Between families (F)	9	456.1173	50.6797	4.6828**
F × R	18	129.4992	7.1944	0.6648^{NS}
Within families	120	1298.7150	10.8226	
Total	149	7131.8267		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0464	0.0232	0.0037^{NS}
Between families (F)	9	250.3999	27.8222	4.4214**
F × R	18	144.0454	8.0025	1.2717^{NS}
Within families	120	755.1191	6.2927	
Total	149	4170.0873		

Table 30G. Number of primary branches at maximum flower (NPBMF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	0.2747	0.1373	0.7368^{NS}
Between families (F)	9	8.7587	0.9732	5.2212^{**}
F × R	18	2.5253	0.1403	0.7527^{NS}
Within families	120	22.3669	0.1864	
Total	149	123.3933		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	0.5947	0.2973	2.3091^{NS}
Between families (F)	9	2.3213	0.2579	2.0031^{*}
F × R	18	2.4987	0.1388	1.0781^{NS}
Within families	120	15.4517	0.1288	
Total	149	82.6733		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	0.3547	0.1773	1.3309^{NS}
Between families (F)	9	3.6067	0.4007	3.0076^{**}
F × R	18	2.9253	0.1625	1.2197^{NS}
Within families	120	15.9893	0.1332	
Total	149	86.8333		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0240	0.0120	0.1140^{NS}
Between families (F)	9	2.5453	0.2828	2.6863^{**}
F × R	18	1.9227	0.1068	1.0146^{NS}
Within families	120	12.6336	0.1053	
Total	149	67.6600		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	0.0347	0.0173	0.1388^{NS}
Between families (F)	9	1.9467	0.2163	1.7325^{NS}
F × R	18	2.4453	0.1359	1.0882^{NS}
Within families	120	14.9813	0.1248	
Total	149	79.3333		

Table 30H. Number secondary branches at maximum flower (NSBMF).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	2.3547	1.1773	2.2730^{NS}
Between families (F)	9	21.3880	2.3764	4.5880^{**}
F × R	18	7.7520	0.4307	0.8315^{NS}
Within families	120	62.1557	0.5180	
Total	149	342.2733		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	2.6347	1.3173	1.3271^{NS}
Between families (F)	9	41.7920	4.6436	4.6779^{**}
F × R	18	17.4720	0.9707	0.9778^{NS}
Within families	120	119.1189	0.9927	
Total	149	657.4933		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	0.2480	0.1240	0.1651^{NS}
Between families (F)	9	23.5253	2.6139	3.4799^{**}
F × R	18	12.4987	0.6944	0.9244^{NS}
Within families	120	90.1376	0.7511	
Total	149	486.9600		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	5.2827	2.6413	2.2378^{NS}
Between families (F)	9	23.6867	2.6319	2.2298^{*}
F × R	18	29.6773	1.6487	1.3969^{NS}
Within families	120	141.6373	1.1803	
Total	149	766.8333		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	2.6480	1.3240	1.1620^{NS}
Between families (F)	9	47.7813	5.3090	4.6596^{**}
F × R	18	17.7787	0.9877	0.8669^{NS}
Within families	120	136.7264	1.1394	
Total	149	751.8400		

Table 30 I. Plant weight at harvest (PWH).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	64.4627	32.2314	0.0862^{NS}
Between families (F)	9	8760.4773	973.3864	2.6038^{**}
F × R	18	5908.9023	328.2723	0.8781^{NS}
Within families	120	44859.9871	373.8332	
Total	149	239033.7777		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	774.8086	387.4043	1.0105^{NS}
Between families (F)	9	19542.4341	2171.3816	5.6638^{**}
F × R	18	9422.8270	523.4904	1.3655^{NS}
Within families	120	46005.7712	383.3814	
Total	149	259768.9255		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	42.1322	21.0661	0.0965^{NS}
Between families (F)	9	5049.7947	561.0883	2.5707^{**}
F × R	18	8039.0057	446.6114	2.0462^{*}
Within families	120	26191.7972	218.2650	
Total	149	144089.9187		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	2466.4635	1233.2317	2.1458^{NS}
Between families (F)	9	28109.7995	3123.3111	5.4344^{**}
F × R	18	7406.8309	411.4906	0.7160^{NS}
Within families	120	68967.7105	574.7309	
Total	149	382821.6465		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	702.9074	351.4537	0.8180^{NS}
Between families (F)	9	18993.5263	2110.3918	4.9117^{**}
F × R	18	4739.9912	263.3328	0.6129^{NS}
Within families	120	51559.5180	429.6626	
Total	149	282234.0146		

Table 30J. Number of pods per plant (NPd/P).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	1435.4160	717.7080	2.0757^{NS}
Between families (F)	9	12690.3200	1410.0356	4.0780**
F × R	18	9580.4240	532.2458	1.5393^{NS}
Within families	120	41491.5680	345.7631	
Total	149	231164.0000		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	2963.3387	1481.6693	4.1819*
Between families (F)	9	9406.2347	1045.1372	2.9499**
F × R	18	13478.4213	748.8012	2.1135**
Within families	120	42516.1557	354.3013	
Total	149	238428.7733		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	7.0907	3.5453	0.0161^{NS}
Between families (F)	9	6359.9533	706.6615	3.2018**
F × R	18	7710.6427	428.3690	1.9409*
Within families	120	26484.6293	220.7052	
Total	149	146500.8333		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	781.0907	390.5453	1.6168^{NS}
Between families (F)	9	4171.7080	463.5231	1.9190^{NS}
F × R	18	3639.5760	202.1987	0.8371^{NS}
Within families	120	28985.8997	241.5492	
Total	149	153521.8733		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	39.3307	19.6653	0.0587^{NS}
Between families (F)	9	5870.3587	652.2621	1.9473^{NS}
F × R	18	7208.1893	400.4550	1.1956^{NS}
Within families	120	40193.9829	334.9499	
Total	149	214087.7933		

Table 30K. Pod weight per plant (PdW/P).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	181.8455	90.9228	2.4849^{NS}
Between families (F)	9	923.1577	102.5731	2.8033**
F × R	18	1278.1774	71.0099	1.9407*
Within families	120	4390.7934	36.5899	
Total	149	24337.1475		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	260.2612	130.1306	3.4296*
Between families (F)	9	1013.6758	112.6306	2.9684**
F × R	18	1557.4235	86.5235	2.2804**
Within families	120	4553.1605	37.9430	
Total	149	25597.1629		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	4.8354	2.4177	0.1039^{NS}
Between families (F)	9	481.5622	53.5069	2.2988*
F × R	18	924.9553	51.3864	2.2077**
Within families	120	2793.0751	23.2756	
Total	149	15376.7283		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	94.4159	47.2080	1.3108^{NS}
Between families (F)	9	815.2573	90.5841	2.5153*
F × R	18	500.6651	27.8147	0.7723^{NS}
Within families	120	4321.6652	36.0139	
Total	149	23018.6641		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	137.4432	68.7216	1.6304^{NS}
Between families (F)	9	672.0566	74.6730	1.7716^{NS}
F × R	18	968.9545	53.8308	1.2771^{NS}
Within families	120	5058.0379	42.1503	
Total	149	27068.6438		

Table 30L. Number of seeds per plant (NS/P).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	2516.5227	1258.2613	2.8383^{NS}
Between families (F)	9	15500.5720	1722.2858	3.8850**
F × R	18	13479.5840	748.8658	1.6892*
Within families	120	53198.0629	443.3172	
Total	149	297486.9933		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	3759.7787	1879.8893	4.0323*
Between families (F)	9	10727.6747	1191.9639	2.5567*
F × R	18	18153.8213	1008.5456	2.1633**
Within families	120	55945.1797	466.2098	
Total	149	312367.1733		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	2.6880	1.3440	0.0054^{NS}
Between families (F)	9	6683.8147	742.6461	3.0009**
F × R	18	8205.4453	455.8581	1.8420*
Within families	120	29697.0784	247.4757	
Total	149	163377.3400		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	1055.5280	527.7640	1.2734^{NS}
Between families (F)	9	10485.9480	1165.1053	2.8112**
F × R	18	8182.4720	454.5818	1.0968^{NS}
Within families	120	49734.7584	414.4563	
Total	149	268397.7400		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	23.8160	11.9080	0.0255^{NS}
Between families (F)	9	8755.3813	972.8201	2.0842*
F × R	18	10992.2107	610.6784	1.3084^{NS}
Within families	120	56010.2464	466.7521	
Total	149	299822.6400		

Table 30M. Seed weight per plant (SW/P).

Cross-1

Source of variation	df	SS	MS	F value
Replication (R)	2	133.9979	66.9989	2.8052^{NS}
Between families (F)	9	602.2039	66.9115	2.8015**
F × R	18	743.8644	41.3258	1.7303*
Within families	120	2866.1078	23.8842	
Total	149	15810.6052		

Cross-2

Source of variation	df	SS	MS	F value
Replication (R)	2	142.2607	71.1304	2.3844^{NS}
Between families (F)	9	671.3410	74.5934	2.5005*
F × R	18	1092.2440	60.6802	2.0341*
Within families	120	3579.8142	29.8318	
Total	149	19804.9167		

Cross-3

Source of variation	df	SS	MS	F value
Replication (R)	2	0.1828	0.0914	0.0064^{NS}
Between families (F)	9	321.9950	35.7772	2.4961*
F × R	18	580.9149	32.2731	2.2516**
Within families	120	1719.9981	14.3333	
Total	149	9503.0834		

Cross-4

Source of variation	df	SS	MS	F value
Replication (R)	2	61.9979	30.9990	1.4505^{NS}
Between families (F)	9	690.6081	76.7342	3.5906**
F × R	18	237.0172	13.1676	0.6162^{NS}
Within families	120	2564.4926	21.3708	
Total	149	13812.0861		

Cross-5

Source of variation	df	SS	MS	F value
Replication (R)	2	100.0411	50.0205	1.5286^{NS}
Between families (F)	9	488.6571	54.2952	1.6592^{NS}
F × R	18	717.3664	39.8537	1.2179^{NS}
Within families	120	3926.8909	32.7241	
Total	149	20940.5192		

* = Significant at 5% level, ** = Significant at 1% level and ^{NS} = non-significant.

Table 31A-31M. Regression analysis of ten families of biparental progeny (BIPs) against their mid-parent values for thirteen characters of five crosses in chickpea.

Table 31A. Date of first flower (DFF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	265.3533	29.4837	4.2042**
Regression	1	2.6377	2.6377	0.3761NS
Remainder	8	50.4329	6.3041	0.8989 NS
Within families	120	841.5520	7.0129	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	415.0222	46.1136	5.8268**
Regression	1	8.3066	8.3066	1.0496 NS
Remainder	8	74.6979	9.3372	1.1798 NS
Within families	120	949.6800	7.9140	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	169.9467	18.8830	4.7799**
Regression	1	9.3128	9.3128	2.3574NS
Remainder	8	24.6766	3.0846	0.7808 NS
Within families	120	474.0544	3.9505	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	324.6689	36.0743	5.5600**
Regression	1	1.0464	1.0464	0.1613 NS
Remainder	8	63.8874	7.9859	1.2308 NS
Within families	120	778.5877	6.4882	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	454.4800	50.4978	9.2734**
Regression	1	21.2170	21.2170	3.8963 NS
Remainder	8	69.6790	8.7099	1.5995 NS
Within families	120	653.4517	5.4454	

Table 31B. Plant height at first flower (PHFF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	155.2333	17.2481	3.9343**
Regression	1	2.1759	2.1759	0.4963 NS
Remainder	8	28.8708	3.6088	0.8232 NS
Within families	120	526.0838	4.3840	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	378.8335	42.0926	5.4205**
Regression	1	5.6283	5.6283	0.7248 NS
Remainder	8	70.1384	8.7673	1.1290 NS
Within families	120	931.8520	7.7654	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	235.8703	26.2078	5.3091**
Regression	1	5.0023	5.0023	1.0134 NS
Remainder	8	42.1718	5.2715	1.0679 NS
Within families	120	592.3651	4.9364	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	852.1898	94.6878	11.6381**
Regression	1	25.7573	25.7573	3.1658 NS
Remainder	8	144.6806	18.0851	2.2228 NS
Within families	120	976.3215	8.1360	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	314.1617	34.9069	7.2820**
Regression	1	36.2900	36.2900	7.5705**
Remainder	8	26.5424	3.3178	0.6921 NS
Within families	120	575.2309	4.7936	

Table 31C. Number of primary branches at first flower (NPBFF)**.**

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	6.8556	0.7617	5.8157**
Regression	1	0.0782	0.0782	0.5974 NS
Remainder	8	1.2929	0.1616	1.2339 NS
Within families	120	15.7173	0.1310	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	13.2200	1.4689	13.7892**
Regression	1	0.4153	0.4153	3.8991NS
Remainder	8	2.2287	0.2786	2.6152*
Within families	120	12.7829	0.1065	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	19.7533	2.1948	13.6614**
Regression	1	0.4467	0.4467	2.7805 NS
Remainder	8	3.5040	0.4380	2.7263**
Within families	120	19.2789	0.1607	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	8.0578	0.8953	10.8842**
Regression	1	0.2535	0.2535	3.0820 NS
Remainder	8	1.3580	0.1698	2.0637*
Within families	120	9.8709	0.0823	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	9.1383	1.0154	12.7830**
Regression	1	0.0928	0.0928	1.1688 NS
Remainder	8	1.7348	0.2169	2.7301**
Within families	120	9.5317	0.0794	

Table 31D. Number of secondary branches at first flower (NSBFF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	22.5333	2.5037	8.4801**
Regression	1	0.1085	0.1085	0.3677 NS
Remainder	8	4.3981	0.5498	1.8621 NS
Within families	120	35.4293	0.2952	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	12.5606	1.3956	3.8252**
Regression	1	0.0718	0.0718	0.1968 NS
Remainder	8	2.4403	0.3050	0.8361 NS
Within families	120	43.7813	0.3648	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	11.5578	1.2842	6.1008**
Regression	1	0.5847	0.5847	2.7777 NS
Remainder	8	1.7269	0.2159	1.0255 NS
Within families	120	25.2597	0.2105	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	4.1978	0.4664	1.9360NS
Regression	1	0.3912	0.3912	1.6236 NS
Remainder	8	0.4484	0.0560	0.2326 NS
Within families	120	28.9109	0.2409	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	9.6644	1.0738	4.1281**
Regression	1	0.0303	0.0303	0.1165 NS
Remainder	8	1.9026	0.2378	0.9143 NS
Within families	120	31.2149	0.2601	

Table 31E. Date of maximum flower (DMF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	107.8422	11.9825	3.0854**
Regression	1	0.4455	0.4455	0.1147 NS
Remainder	8	21.1230	2.6404	0.6799 NS
Within families	120	466.0256	3.8835	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	394.2667	43.8074	8.6020**
Regression	1	15.9217	15.9217	3.1264 NS
Remainder	8	62.9316	7.8665	1.5446 NS
Within families	120	611.1253	5.0927	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	254.3022	28.2558	5.6653**
Regression	1	1.4281	1.4281	0.2863 NS
Remainder	8	49.4324	6.1790	1.2389 NS
Within families	120	598.5077	4.9876	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	71.8867	7.9874	4.7799**
Regression	1	0.2820	0.2820	0.1687 NS
Remainder	8	14.0954	1.7619	1.0544 NS
Within families	120	200.5269	1.6711	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	40.4978	4.4998	1.3757NS
Regression	1	0.0232	0.0232	0.0071 NS
Remainder	8	8.0764	1.0095	0.3087 NS
Within families	120	392.4949	3.2708	

Table 31F. Plant height at maximum flower (PHMF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	331.8578	36.8731	4.1100**
Regression	1	2.9376	2.9376	0.3274 NS
Remainder	8	63.4340	7.9292	0.8838 NS
Within families	120	1076.5752	8.9715	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	731.8065	81.3118	5.5927**
Regression	1	1.8865	1.8865	0.1298 NS
Remainder	8	144.4748	18.0594	1.2421 NS
Within families	120	1744.6651	14.5389	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	167.1002	18.5667	5.1389**
Regression	1	9.2191	9.2191	2.5516 NS
Remainder	8	24.2009	3.0251	0.8373 NS
Within families	120	433.5597	3.6130	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	488.5414	54.2824	5.0156**
Regression	1	32.0194	32.0194	2.9586 NS
Remainder	8	65.6889	8.2111	0.7587 NS
Within families	120	1298.7150	10.8226	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	417.3331	46.3703	7.3690**
Regression	1	2.6659	2.6659	0.4237 NS
Remainder	8	80.8007	10.1001	1.6051 NS
Within families	120	755.1191	6.2927	

Table 31G. Number of primary branches at maximum flower (NPBMF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	14.5978	1.6220	8.7020**
Regression	1	0.0515	0.0515	0.2762 NS
Remainder	8	2.8681	0.3585	1.9234 NS
Within families	120	22.3669	0.1864	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	3.8689	0.4299	3.3385**
Regression	1	0.0229	0.0229	0.1781 NS
Remainder	8	0.7508	0.0939	0.7289 NS
Within families	120	15.4517	0.1288	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	9.2494	1.0277	7.7130**
Regression	1	0.1105	0.1105	0.8289 NS
Remainder	8	1.7394	0.2174	1.6318 NS
Within families	120	15.9893	0.1332	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	14.8561	1.6507	15.6789**
Regression	1	0.8112	0.8112	7.7051**
Remainder	8	2.1600	0.2700	2.5646*
Within families	120	12.6336	0.1053	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	16.1028	1.7892	14.3314**
Regression	1	0.7247	0.7247	5.8050*
Remainder	8	2.4958	0.3120	2.4989*
Within families	120	14.9813	0.1248	

Table 31H. Number secondary branches at maximum flower (NSBMF).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	35.6467	3.9607	7.6467**
Regression	1	0.0512	0.0512	0.0989 NS
Remainder	8	7.0781	0.8848	1.7082 NS
Within families	120	62.1557	0.5180	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	69.6533	7.7393	7.7965**
Regression	1	1.0827	1.0827	1.0907 NS
Remainder	8	12.8480	1.6060	1.6179 NS
Within families	120	119.1189	0.9927	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	29.8228	3.3136	4.4114**
Regression	1	1.8691	1.8691	2.4883 NS
Remainder	8	4.0955	0.5119	0.6815 NS
Within families	120	90.1376	0.7511	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	39.4778	4.3864	3.7163**
Regression	1	2.7380	2.7380	2.3197 NS
Remainder	8	5.1576	0.6447	0.5462 NS
Within families	120	141.6373	1.1803	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	79.6356	8.8484	7.7659**
Regression	1	1.2164	1.2164	1.0676 NS
Remainder	8	14.7107	1.8388	1.6139 NS
Within families	120	136.7264	1.1394	

Table 31I. Plant weight at harvest (PWH).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	14600.7956	1622.3106	4.3397**
Regression	1	820.5829	820.5829	2.1951 NS
Remainder	8	2099.5762	262.4470	0.7020 NS
Within families	120	44859.9871	373.8332	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	32570.7235	3618.9693	9.4396**
Regression	1	1105.9468	1105.9468	2.8847 NS
Remainder	8	5408.1979	676.0247	1.7633 NS
Within families	120	46005.7712	383.3814	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	8416.3245	935.1472	4.2845**
Regression	1	130.6375	130.6375	0.5985 NS
Remainder	8	1552.6273	194.0784	0.8892 NS
Within families	120	26191.7972	218.2650	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	46849.6659	5205.5184	9.0573**
Regression	1	68.7056	68.7056	0.1195 NS
Remainder	8	9301.2276	1162.6534	2.0230**
Within families	120	68967.7105	574.7309	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	31655.8772	3517.3197	8.1862**
Regression	1	108.2844	108.2844	0.2520 NS
Remainder	8	6222.8911	777.8614	1.8104 NS
Within families	120	51559.5180	429.6626	

Table 31J. Number of pods per plant (NPd/P).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	18164.2133	2018.2459	5.8371**
Regression	1	279.4496	279.4496	0.8082 NS
Remainder	8	3353.3931	419.1741	1.2123 NS
Within families	120	41491.5680	345.7631	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	15677.0578	1741.8953	4.9164**
Regression	1	66.4779	66.4779	0.1876 NS
Remainder	8	3068.9337	383.6167	1.0827 NS
Within families	120	42516.1557	354.3013	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	10599.9222	1177.7691	5.3364**
Regression	1	55.5744	55.5744	0.2518 NS
Remainder	8	2064.4100	258.0513	1.1692 NS
Within families	120	26484.6293	220.7052	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	7360.4800	817.8311	3.3858**
Regression	1	3.5822	3.5822	0.0148 NS
Remainder	8	1468.5138	183.5642	0.7599 NS
Within families	120	28985.8997	241.5492	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	9783.9311	1087.1035	3.2456**
Regression	1	12.5719	12.5719	0.0375 NS
Remainder	8	1944.2144	243.0268	0.7256 NS
Within families	120	40193.9829	334.9499	

Table 31K. Pod weight per plant (PdW/P).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	1290.8037	143.4226	3.9197**
Regression	1	2.5337	2.5337	0.0692 NS
Remainder	8	255.6270	31.9534	0.8733 NS
Within families	120	4390.7934	36.5899	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	1689.4597	187.7177	4.9474**
Regression	1	45.3762	45.3762	1.1959 NS
Remainder	8	292.5157	36.5645	0.9637 NS
Within families	120	4553.1605	37.9430	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	828.4879	92.0542	3.9550**
Regression	1	24.2872	24.2872	1.0435 NS
Remainder	8	141.4104	17.6763	0.7594 NS
Within families	120	2793.0751	23.2756	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	1358.7621	150.9736	4.1921**
Regression	1	7.1134	7.1134	0.1975 NS
Remainder	8	264.6390	33.0799	0.9185 NS
Within families	120	4321.6652	36.0139	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	3127.4295	347.4922	8.2441**
Regression	1	256.0582	256.0582	6.0749*
Remainder	8	369.4277	46.1785	1.0956 NS
Within families	120	5058.0379	42.1503	

Table 31L. Number of seeds per plant (NS/P).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	25834.2867	2870.4763	6.4750**
Regression	1	169.2921	169.2921	0.3819 NS
Remainder	8	4997.5652	624.6957	1.4091 NS
Within families	120	53198.0629	443.3172	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	17879.4578	1986.6064	4.2612**
Regression	1	283.0368	283.0368	0.6071 NS
Remainder	8	3292.8548	411.6068	0.8829 NS
Within families	120	55945.1797	466.2098	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	10503.2111	1167.0235	4.7157**
Regression	1	46.9920	46.9920	0.1899 NS
Remainder	8	2053.6502	256.7063	1.0373 NS
Within families	120	29697.0784	247.4757	

Cross-4

Source of variation	df	SS	MS	VR
Between families	9	17476.5800	1941.8422	4.6853**
Regression	1	27.8989	27.8989	0.0673 NS
Remainder	8	3467.4171	433.4271	1.0458 NS
Within families	120	49734.7584	414.4563	

Cross-5

Source of variation	df	SS	MS	VR
Between families	9	14592.3022	1621.3669	3.4737**
Regression	1	461.3387	461.3387	0.9884 NS
Remainder	8	2457.1218	307.1402	0.6580 NS
Within families	120	56010.2464	466.7521	

Table 31M. Seed weight per plant (SW/P).

Cross-1

Source of variation	df	SS	MS	VR
Between families	9	1003.6732	111.5192	4.6692**
Regression	1	16.6276	16.6276	0.6962 NS
Remainder	8	184.1071	23.0134	0.9635 NS
Within families	120	2866.1078	23.8842	

Cross-2

Source of variation	df	SS	MS	VR
Between families	9	1118.9017	124.3224	4.1674**
Regression	1	12.3326	12.3326	0.4134 NS
Remainder	8	211.4478	26.4310	0.8860 NS
Within families	120	3579.8142	29.8318	

Cross-3

Source of variation	df	SS	MS	VR
Between families	9	475.2641	52.8071	3.6842**
Regression	1	2.9456	2.9456	0.2055 NS
Remainder	8	92.1073	11.5134	0.8033 NS
Within families	120	1719.9981	14.3333	

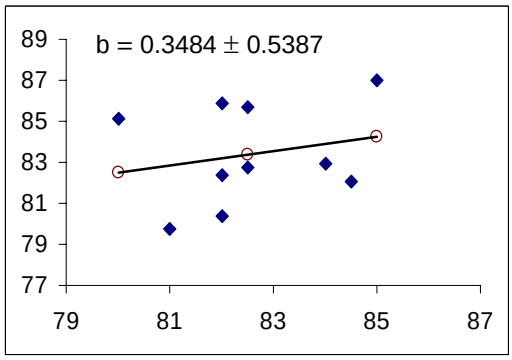
Cross-4

Source of variation	df	SS	MS	VR
Between families	9	1151.0135	127.8904	5.9844**
Regression	1	5.0284	5.0284	0.2353NS
Remainder	8	225.1743	28.1468	1.3171NS
Within families	120	2564.4926	21.3708	

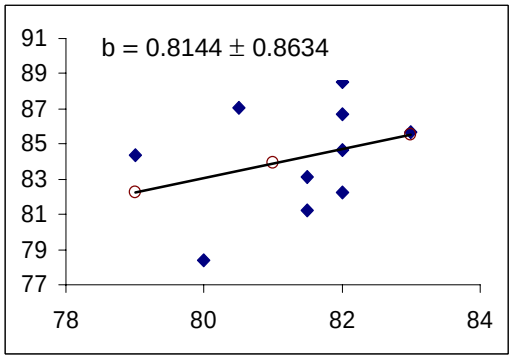
Cross-5

Source of variation	df	SS	MS	VR
Between families	9	814.4286	90.4921	2.7653**
Regression	1	10.8485	10.8485	0.3315 NS
Remainder	8	152.0372	19.0047	0.5808 NS
Within families	120	3926.8909	32.7241	

* = Significant at 5% level, ** = Significant at 1% level and NS = non-significant.



Cross-1



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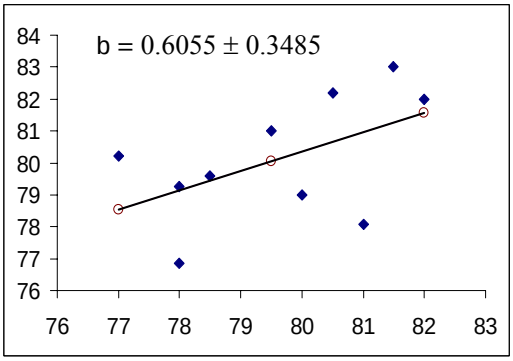

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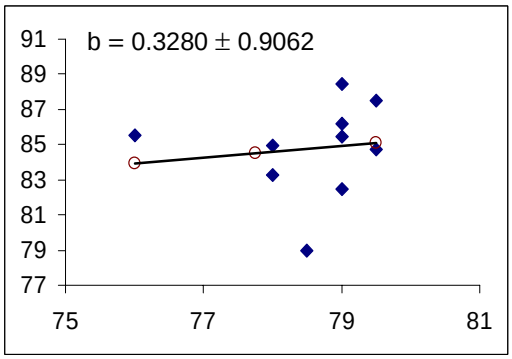

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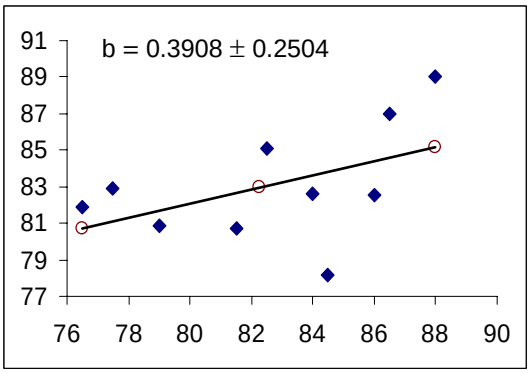
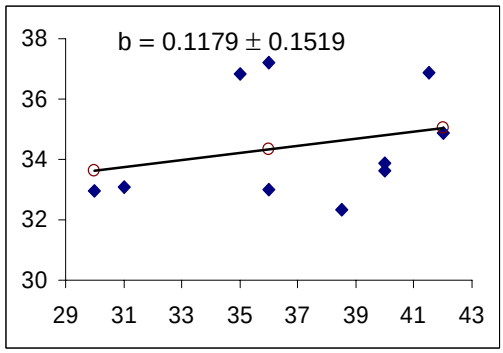
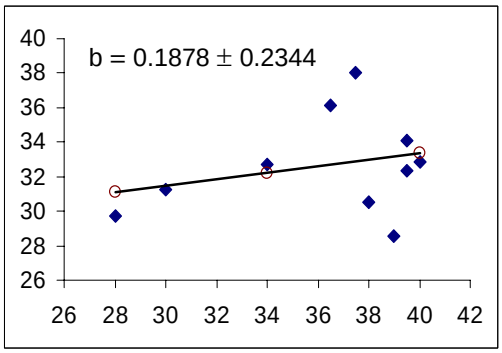


Cross-5

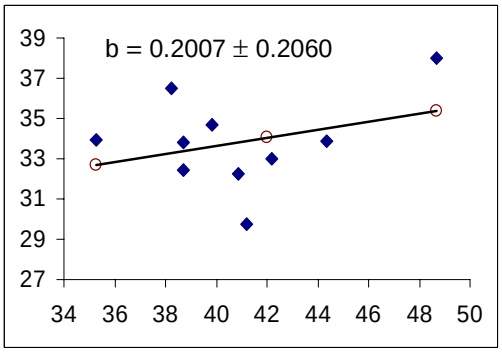
Figure 34. Regression of offspring means on mid-parental values of DFF.



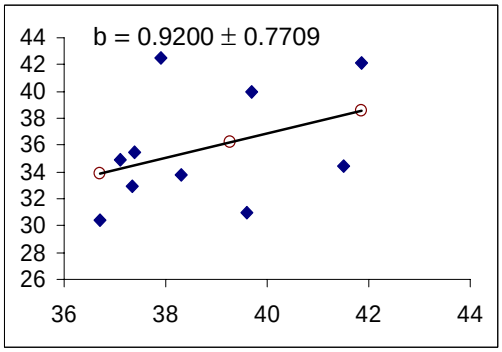
Cross-1



Cross-2



Cross-3



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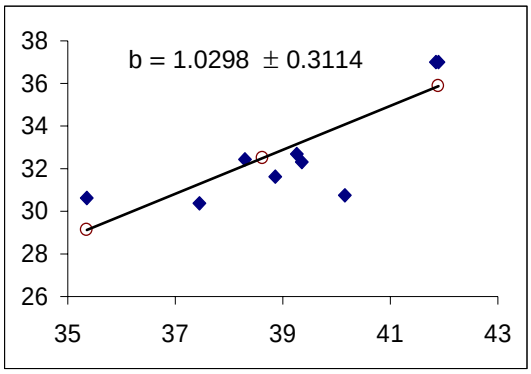
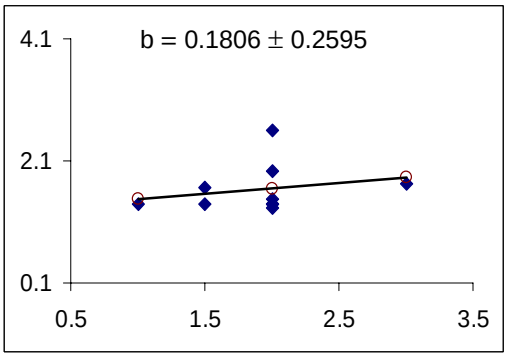
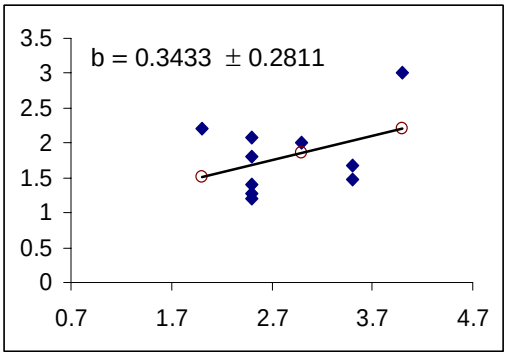


Cross-5

Figure 35. Regression of offspring means on mid-parental values of PHFF.



Cross-1



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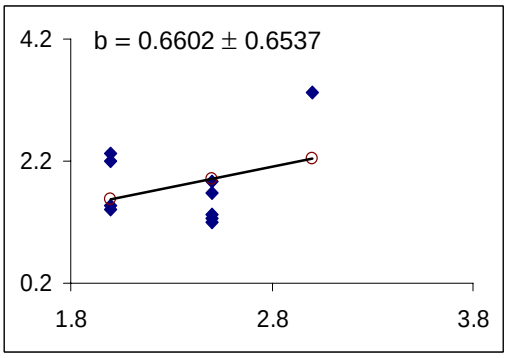
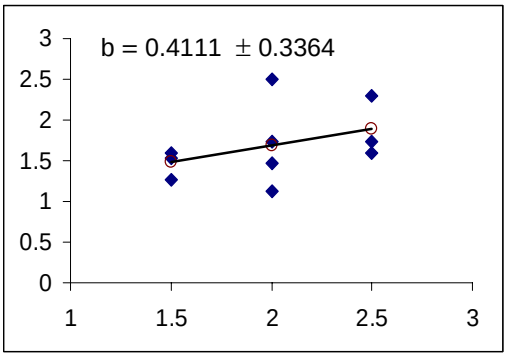
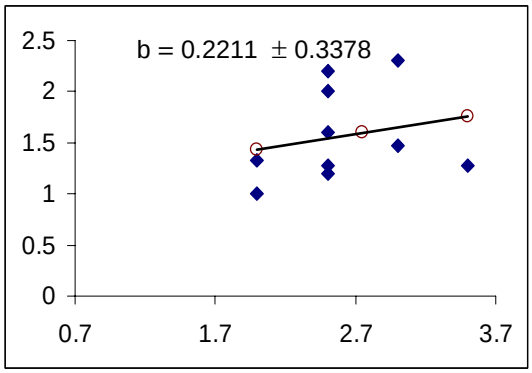


Cross-3



Cross-4



Cross-5

Figure 36. Regression of offspring means on mid-parental values of NPBFF.

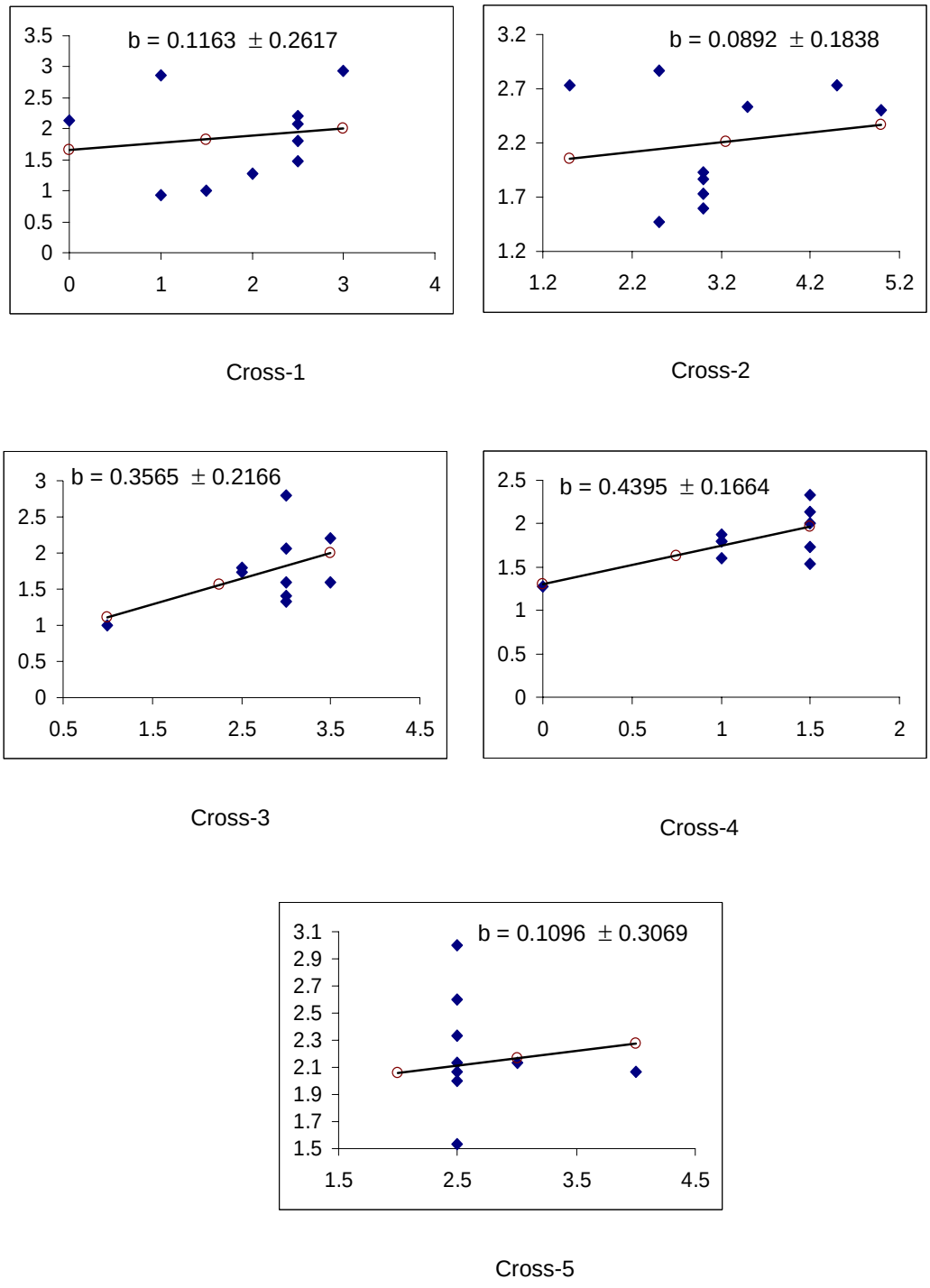


Figure 37. Regression of offspring means on mid-parental values of NSBFF.

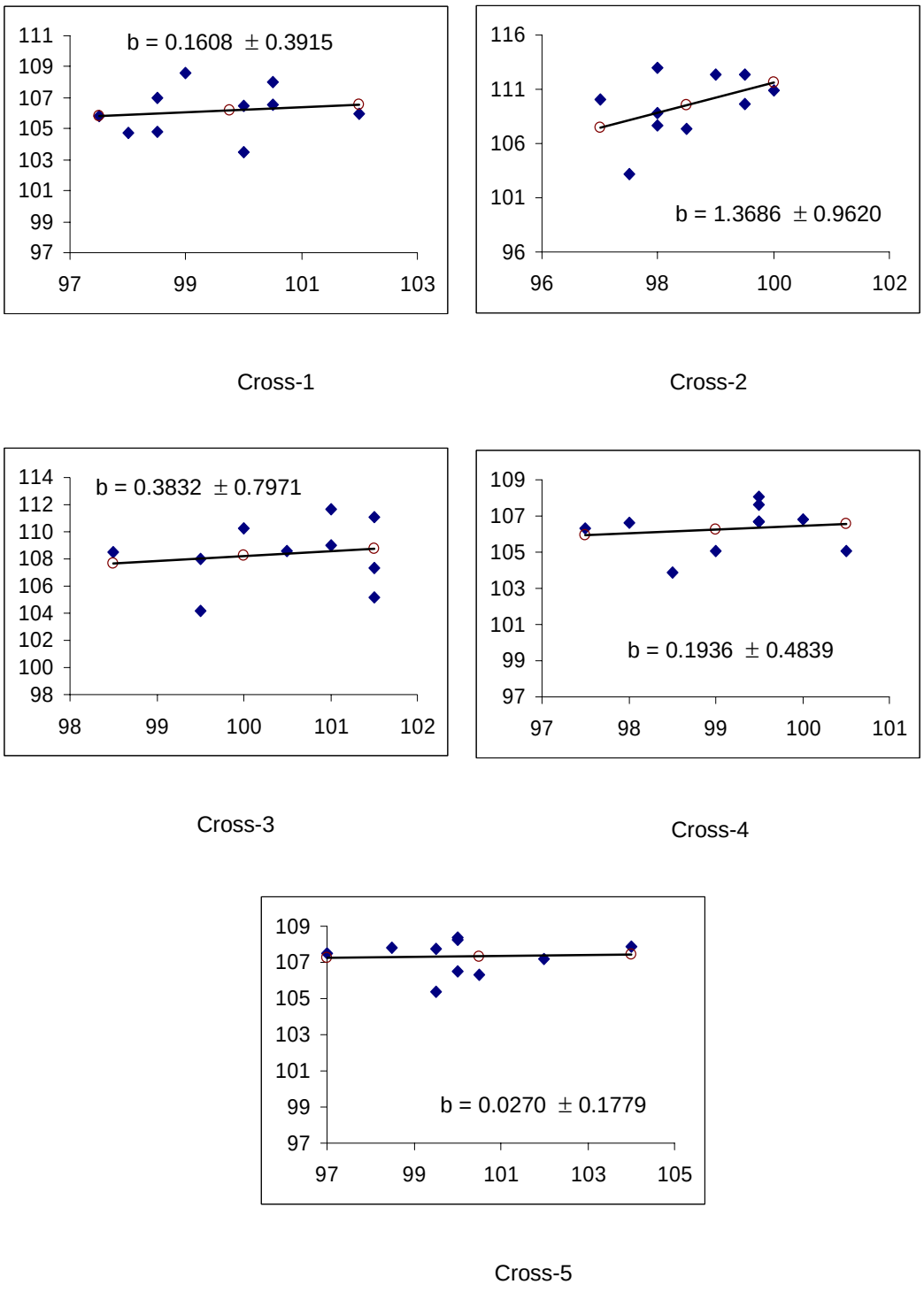


Figure 38. Regression of offspring means on mid-parental values of DMF.

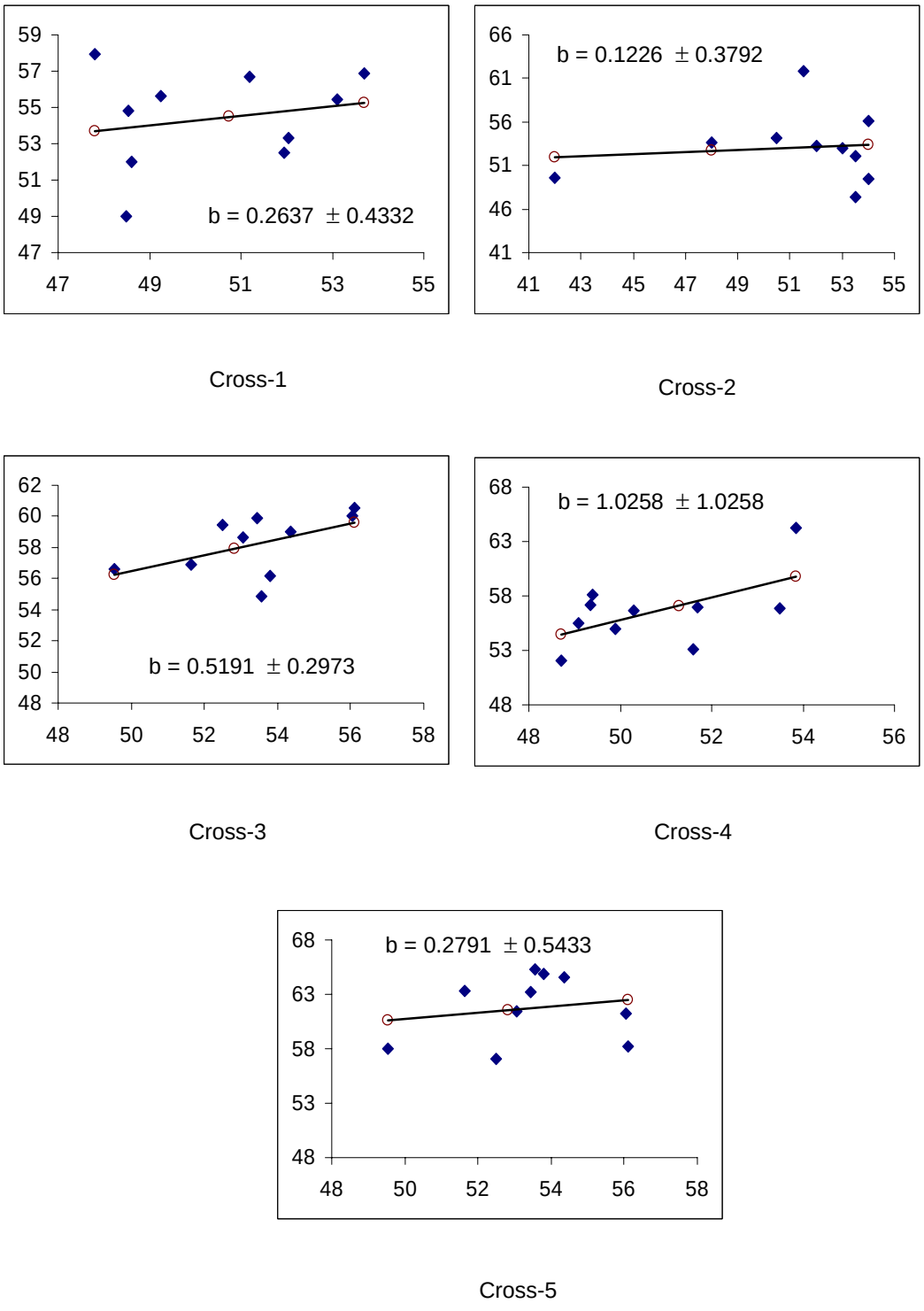


Figure 39. Regression of offspring means on mid-parental values of PHMF.

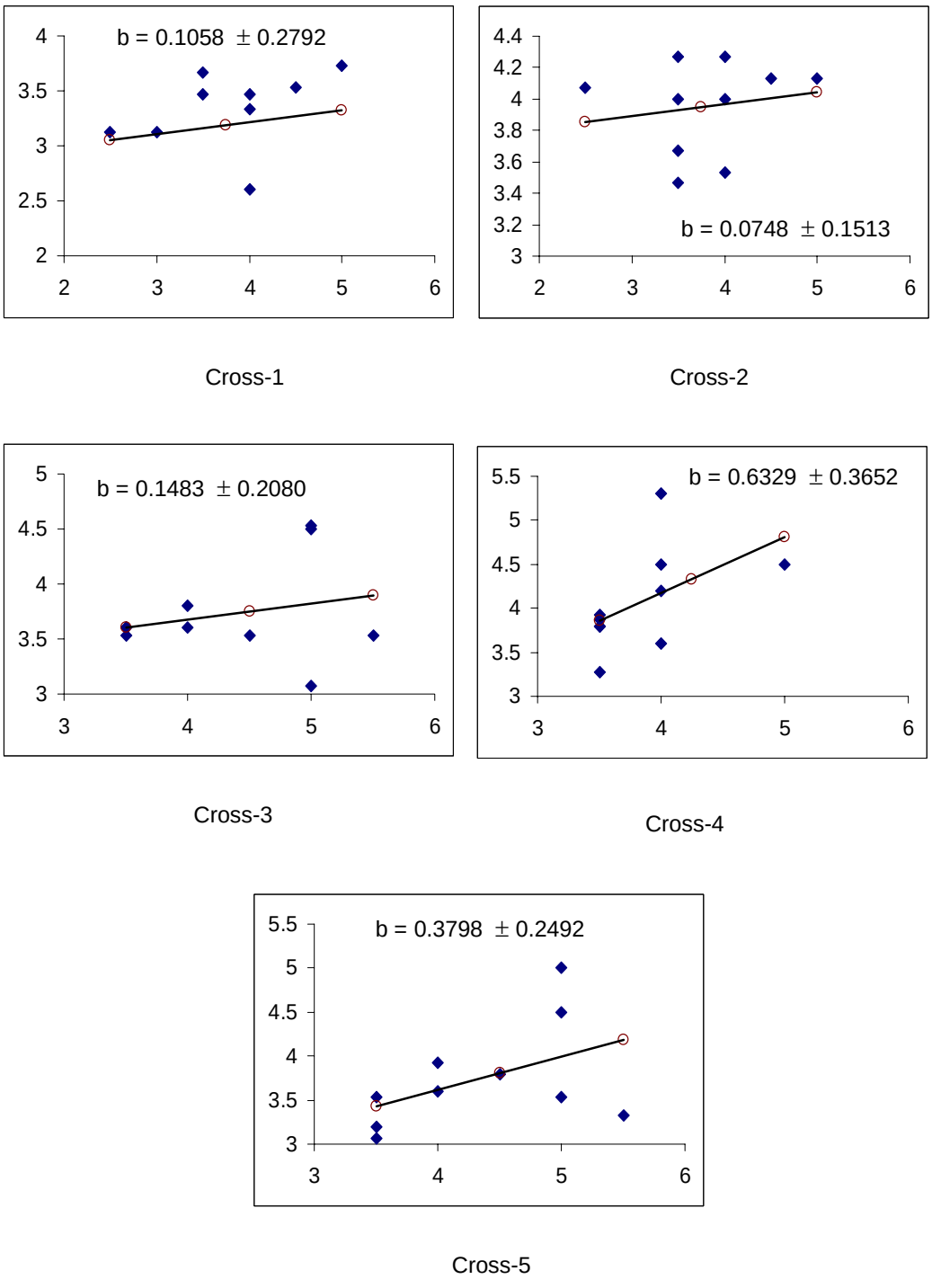


Figure 40. Regression of offspring means on mid-parental values of NPBMF.

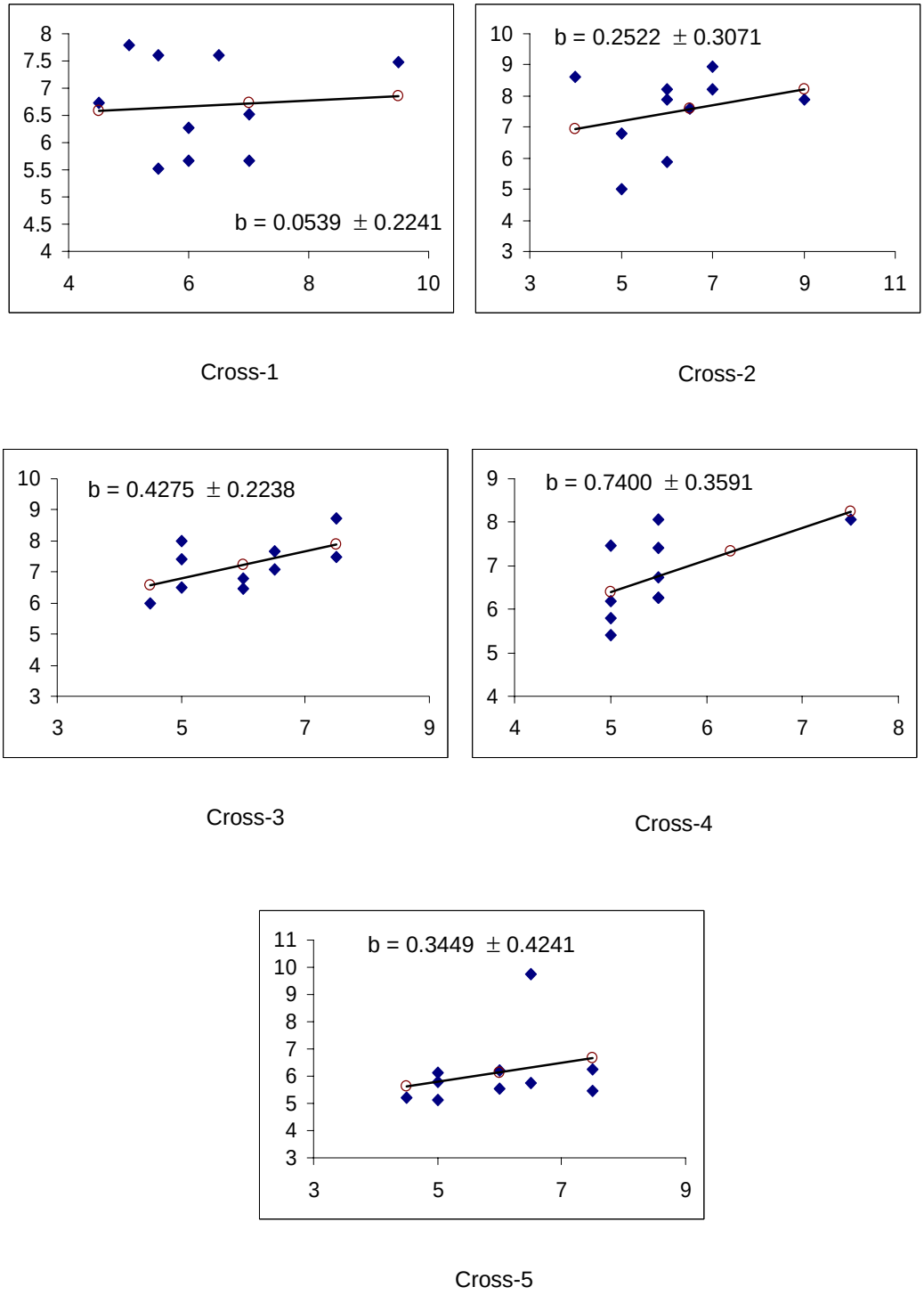


Figure 41. Regression of offspring means on mid-parental values of NSBMF.

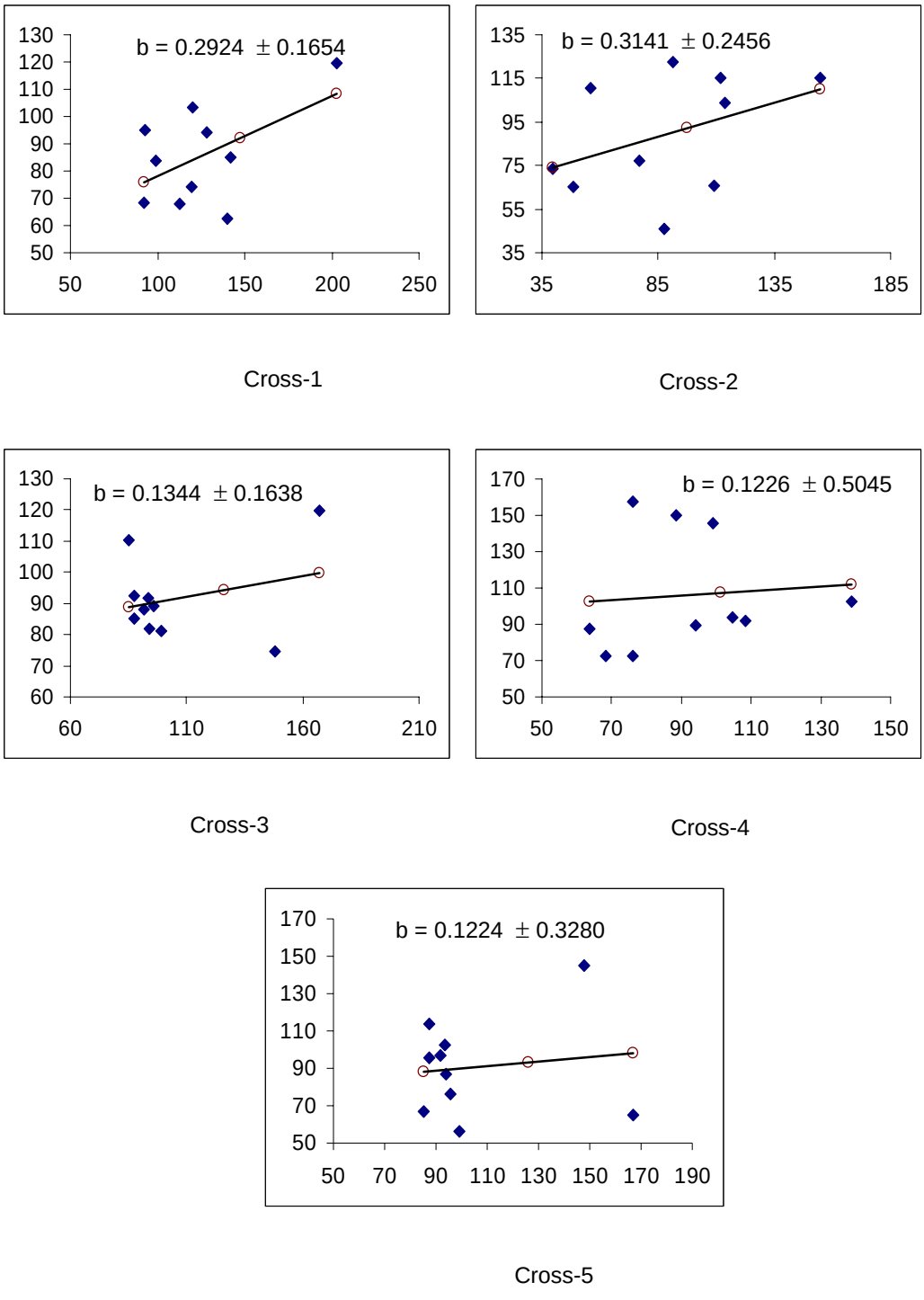


Figure 42. Regression of offspring means on mid-parental values of PWH.

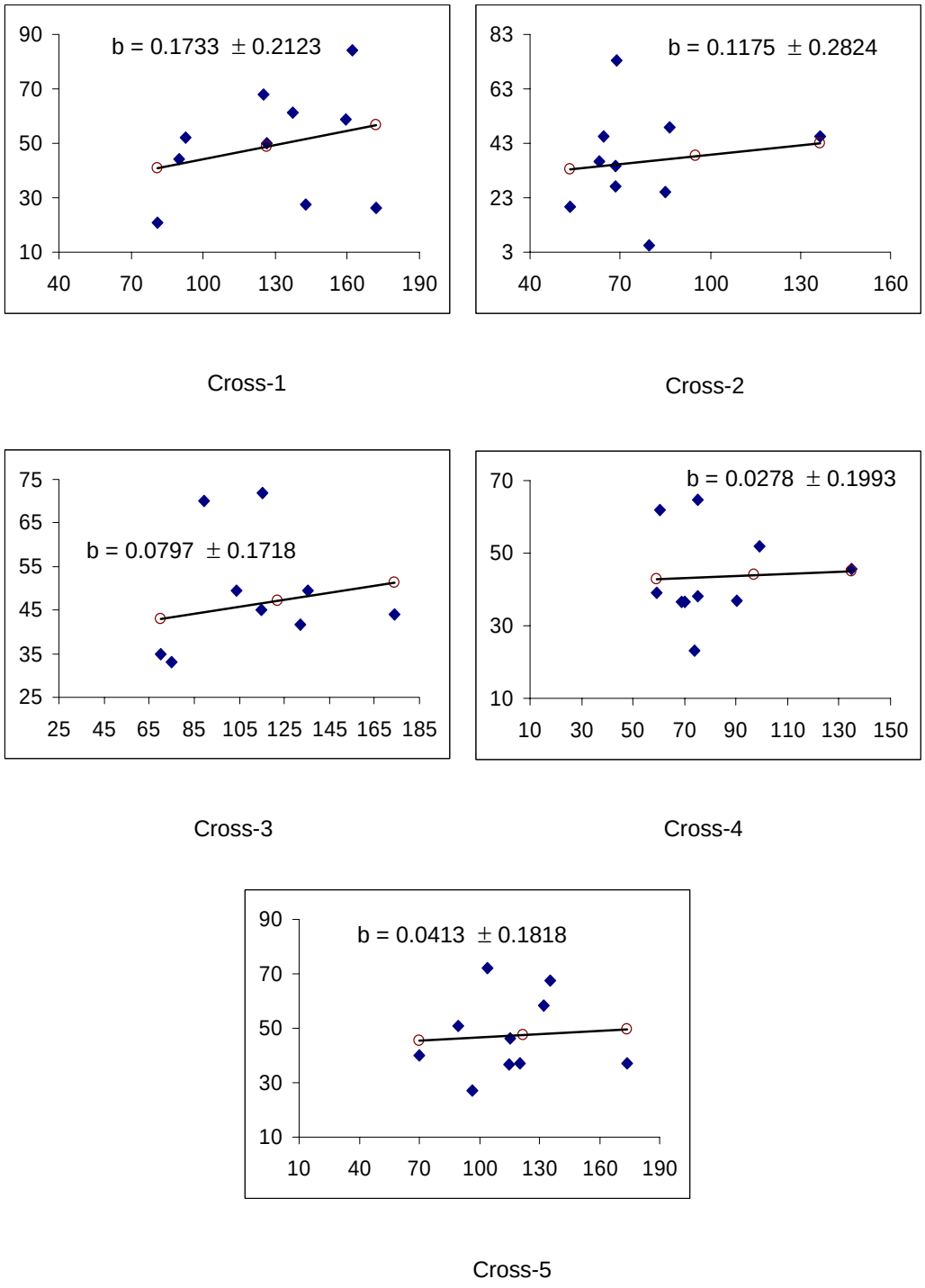


Figure 43. Regression of offspring means on mid-parental values of NPd/P.

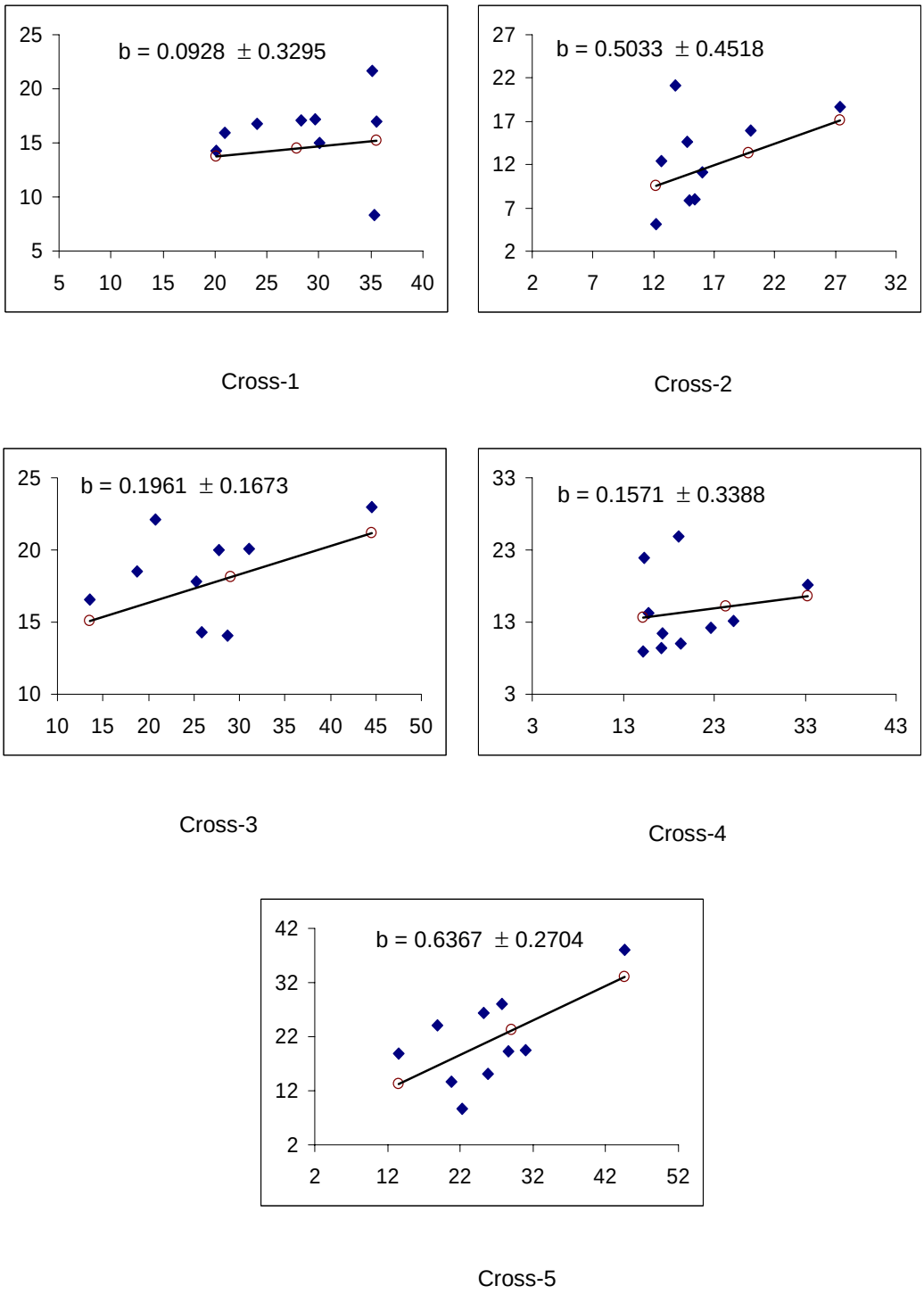


Figure 44. Regression of offspring means on mid-parental values of PdW/P.

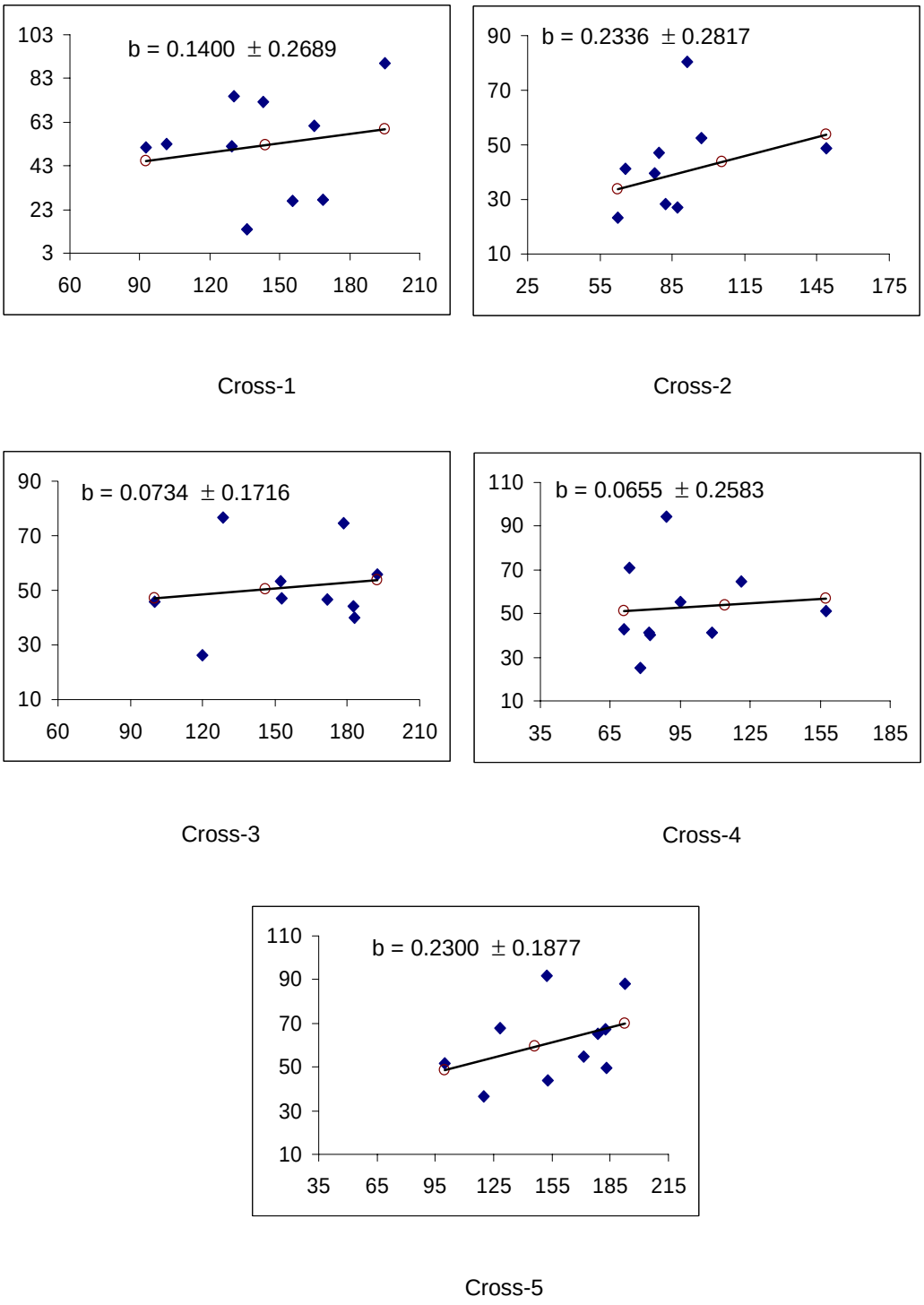


Figure 45. Regression of offspring means on mid-parental values of NS/P.

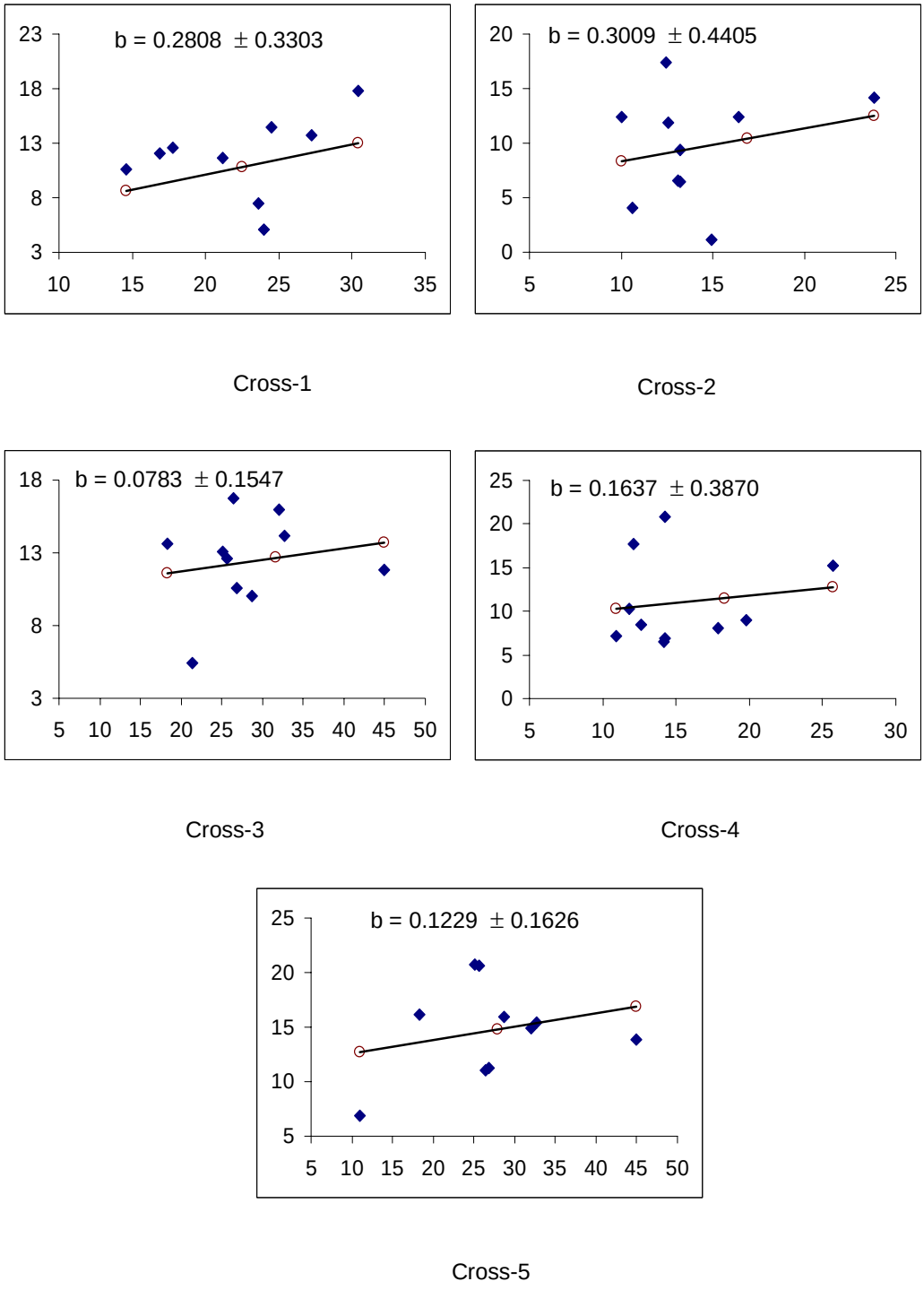


Figure 46. Regression of offspring means on mid-parental values of SW/P.

Table 32A-32E. Estimates of components of variation (D_R, H_R and E_W), degree of dominance ($\sqrt{H_R/D_R}$), heritability (h^2_b, h^2_n) and genetic advance (GA_b, GA_n) of biparental progeny for thirteen characters of five crosses in chickpea.

Table 32A. Cross-1

Character	D_R	H_R	E_W	$\sqrt{H_R/D_R}$	h^2_n	h^2_b	GA_n	GA_b
DFF	1.2593	3.1962	34.1506	1.5932	0.0177	0.0402	0.2174	0.4934
PHFF	1.2978	3.2454	20.9872	1.5814	0.0289	0.0651	0.2821	0.6349
NPBFF	0.1926	-0.3902	0.6799	-1.4233	0.1419	-0.0018	0.2408	-0.0031
NSBFF	0.2815	0.3224	1.3454	1.0702	0.0898	0.1413	0.2316	0.3643
DMF	1.2311	-3.8957	19.8404	1.7789	0.0316	-0.0184	0.2873	-0.1673
PHMF	1.2891	2.3566	44.0932	1.3521	0.0142	0.0272	0.1972	0.3775
NPBMF	0.2163	0.0232	0.8735	0.3277	0.1095	0.1154	0.2242	0.2362
NSBMF	0.4222	0.3866	2.4118	0.9569	0.0776	0.1132	0.2637	0.3844
PWH	1247.2814	-4301.0038	2363.7840	-1.8570	0.3261	-0.2362	29.3791	-21.2749
NPd/P	98.8889	540.7535	1602.7018	2.3384	0.0277	0.1033	2.4092	8.9965
PdW/P	6.8448	6.2883	180.0595	0.9585	0.0185	0.0270	0.5183	0.7563
NS/P	537.4430	-1111.4572	2290.6234	-1.4381	0.1178	-0.0040	11.5894	-0.3943
SW/P	26.3195	-77.9864	127.4637	-1.7214	0.1086	-0.0523	2.4632	-1.1861

Table 32B. Cross-2

Character	D_R	H_R	E_W	$\sqrt{H_R/D_R}$	h^2_n	h^2_b	GA_n	GA_b
DFF	4.5333	1.0463	38.2405	0.4804	0.0556	0.0620	0.7313	0.8157
PHFF	7.1250	-14.4301	39.7515	-1.4231	0.0897	-0.0011	1.1646	-0.0147
NPBFF	0.0341	0.1737	0.4915	2.2581	0.0309	0.1096	0.0472	0.1677
NSBFF	0.1111	0.1045	1.7768	0.9699	0.0299	0.0440	0.0839	0.1234
DMF	5.1704	2.5387	23.6950	0.7007	0.0961	0.1196	1.0265	1.2785
PHMF	5.7821	0.1406	71.2225	0.1559	0.0390	0.0395	0.6916	0.7000
NPBMF	0.0281	0.0145	0.6341	0.7167	0.0216	0.0271	0.0359	0.0451
NSBMF	0.8000	0.7177	4.6287	0.9472	0.0768	0.1113	0.3611	0.5230
PWH	1564.7142	-4501.1063	2369.6860	-1.6961	0.3860	-0.1692	35.7990	-15.6912
NPd/P	251.3659	-689.3720	1837.9223	-1.6561	0.0702	-0.0260	6.1174	-2.2711
PdW/P	40.0662	-132.4172	204.5267	-1.8180	0.1046	-0.0683	2.9825	-1.9460
NS/P	538.5452	-1958.5346	2563.6381	-1.9070	0.1149	-0.0940	11.4590	-9.3776
SW/P	18.2145	-58.0170	155.4835	-1.7847	0.0607	-0.0360	1.5314	-0.9075

Table 32C. Cross-3

Character	D_R	H_R	E_W	$\sqrt{H_R/D_R}$	h^2_n	h^2_b	GA_n	GA_b
DFF	0.4652	0.7249	19.5001	1.2483	0.0208	0.0117	0.1074	0.1910
PHFF	2.3977	-8.8480	25.7415	-1.9210	0.0485	-0.0410	0.4966	-0.4197
NPBFF	0.3007	0.1363	0.7025	0.6732	0.1695	0.2079	0.3289	0.4034
NSBFF	0.7289	-2.2955	1.3007	-1.7746	0.3340	-0.1919	0.7187	-0.4130
DMF	1.6563	2.1679	24.1173	1.1441	0.0325	0.0538	0.3379	0.5591
PHMF	1.3028	2.1626	17.3338	1.2884	0.0352	0.0643	0.3118	0.5705
NPBMF	0.0519	0.0467	0.6445	0.9490	0.0380	0.0551	0.0647	0.0938
NSBMF	0.3348	0.7083	3.5392	1.4544	0.0431	0.0887	0.1750	0.3601
PWH	431.9965	-1605.8773	1284.4278	-1.9280	0.1965	-0.1688	13.4223	-11.5253
NPd/P	45.1556	116.2231	1070.4455	1.6043	0.0201	0.0460	1.3885	3.1753
PdW/P	0.4567	0.4352	116.1824	0.9762	0.0020	0.0029	0.0436	0.0643
NS/P	62.6444	55.3294	1211.3429	0.9398	0.0249	0.0359	1.8203	2.6241
SW/P	0.8362	0.3931	71.3838	0.6856	0.0058	0.0072	0.1016	0.1254

Table 32D. Cross-4

Character	D_R	H_R	E_W	$\sqrt{H_R/D_R}$	h^2_n	h^2_b	GA_n	GA_b
DFF	1.4178	8.1567	30.5573	2.3986	0.0213	0.0825	0.2530	0.9809
PHFF	8.7471	16.3181	35.4336	1.3658	0.0997	0.1926	1.3600	2.6285
NPBFF	0.0148	0.0872	0.3912	2.4265	0.0176	0.0695	0.0235	0.0928
NSBFF	0.3956	-1.4827	1.3837	-1.9361	0.1633	-0.1428	0.3703	-0.3237
DMF	0.6474	0.6108	8.0789	0.9714	0.0378	0.0557	0.2280	0.3355
PHMF	8.9702	10.5037	49.9011	1.0821	0.0787	0.1247	1.2236	1.9401
NPBMF	0.0400	0.0277	0.5112	0.8327	0.0372	0.0500	0.0562	0.0756
NSBMF	1.6444	-5.5291	6.5272	-1.8337	0.1378	-0.0939	0.6934	-0.4723
PWH	249.0062	1896.5837	2455.7936	2.7598	0.0408	0.1960	4.6407	22.3138
NPd/P	78.1215	-33.7399	1194.5417	-0.6572	0.0319	0.0250	2.2988	1.8024
PdW/P	20.1232	-13.5389	177.5771	-0.8202	0.0546	0.0362	1.5270	1.0133
NS/P	189.2133	1.0385	2024.7836	0.0741	0.0446	0.0448	4.2331	4.2447
SW/P	13.6508	13.2012	100.9659	0.9834	0.0614	0.0911	1.3340	1.9790

Table 32E. Cross-5

Character	D_R	H_R	E_W	$\sqrt{H_R/D_R}$	h^2_n	h^2_b	GA_n	GA_b
DFF	4.4652	-4.1766	26.8940	-0.9671	0.0795	0.0423	0.8679	0.4620
PHFF	4.1453	6.3335	21.7441	1.2361	0.0816	0.1439	0.8472	1.4944
NPBFF	0.0652	0.0706	0.3676	1.0410	0.0780	0.1203	0.1039	0.1601
NSBFF	0.1230	-0.1415	1.2964	-1.0728	0.0465	0.0197	0.1101	0.0468
DMF	0.3822	-2.5856	16.7432	-2.6009	0.0117	-0.0280	0.0975	-0.2324
PHMF	4.2449	4.1616	29.6218	0.9901	0.0647	0.0965	0.7636	1.1379
NPBMF	0.0296	-0.0327	0.6229	-1.0507	0.0235	0.0105	0.0385	0.0172
NSBMF	1.5674	-1.6602	5.6164	-1.0292	0.1309	0.0616	0.6599	0.3104
PWH	393.3046	396.9777	1975.5538	1.0047	0.0866	0.1303	8.4999	12.7896
NPd/P	135.1348	-271.9450	1691.9553	1.4186	0.0399	-0.0002	3.3843	-0.0210
PdW/P	5.1192	1.7549	209.1427	0.5855	0.0121	0.0141	0.3620	0.4241
NS/P	92.7407	15.3216	2307.7023	0.4065	0.0197	0.0213	1.9672	2.1297
SW/P	3.3686	1.9301	162.4164	0.7569	0.0102	0.0132	0.2705	0.3479

Table 33A-33M. Specific test of linkage based on comparisons of the total variance between the generations for thirteen characters of four crosses in chickpea.

Table 33A. Date of first flower (DFF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	34.7517	10.9187 **
F_2	29	3.1828	
$F_1 \times F_2$	149	30.7606	9.6647 **

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	17.5231	3.3661 **
F_2	29	5.2057	
$F_1 \times F_2$	149	19.4284	3.7321 **

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	28.5092	6.4240 **
F_2	29	4.4379	
$F_1 \times F_2$	149	16.7315	3.7701 **

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	23.5193	1.0269 NS
F_2	29	28.0517	1.2248 NS
$F_1 \times F_2$	149	22.9024	

Table 33B. Plant height at first flower (PHFF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	34.3365	2.3110 **
F_2	29	14.6483	
$F_1 \times F_2$	149	21.4537	1.4645 NS

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	21.7417	1.7446 **
F_2	29	24.2632	1.9470 **
$F_1 \times F_2$	149	12.4617	

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	36.8745	5.0118 **
F_2	29	7.3575	
$F_1 \times F_2$	149	14.8233	2.0147 **

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	21.0859	2.0074 *
F_2	29	10.5039	
$F_1 \times F_2$	149	14.9990	1.4279 NS

Table 33C. Number of primary branches at first flower (NPBFF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.4630	1.2999 ^{NS}
F_2	29	0.5471	1.5360 ^{NS}
$F_1 \times F_2$	149	0.3562	

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.7342	2.1579 **
F_2	29	0.3402	
$F_1 \times F_2$	149	0.4922	1.4465 ^{NS}

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.3456	1.2022 ^{NS}
F_2	29	0.6023	2.0952 **
$F_1 \times F_2$	149	0.2875	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.3434	
F_2	29	0.4368	1.2718 ^{NS}
$F_1 \times F_2$	149	0.6361	1.8520 **

Table 33D. Number of secondary branches at first flower (NSBFF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	1.5626	1.6474 **
F_2	29	1.3609	1.4347 NS
$F_1 \times F_2$	149	0.9485	

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.9253	1.2310 NS
F_2	29	0.8092	1.0765 NS
$F_1 \times F_2$	149	0.7517	

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	1.0161	1.1914 NS
F_2	29	1.2195	1.4300 NS
$F_1 \times F_2$	149	0.8528	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	1.1315	1.6164 NS
F_2	29	0.7000	
$F_1 \times F_2$	149	1.5257	2.1796 **

Table 33E. Date of maximum flower (DMF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	22.8143	12.9813 **
F_2	29	1.7575	
$F_1 \times F_2$	149	31.2573	17.7853 **

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	22.1985	6.9470 **
F_2	29	3.1954	
$F_1 \times F_2$	149	17.9597	5.6205 **

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	7.2738	1.9406 *
F_2	29	3.7483	
$F_1 \times F_2$	149	17.2440	4.6005 **

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	13.8785	1.0643 NS
F_2	29	13.0402	
$F_1 \times F_2$	149	32.3132	2.4780 **

Table 33F. Plant height at maximum flower (PHMF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	65.2011	4.4511 **
F_2	29	14.6483	
$F_1 \times F_2$	149	45.7651	3.1242 **

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	16.2632	1.5483 NS
F_2	29	10.5039	
$F_1 \times F_2$	149	33.8901	3.2264 **

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	47.8646	6.5055 **
F_2	29	7.3575	
$F_1 \times F_2$	149	33.9210	4.6104 **

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	27.9872	2.6644 **
F_2	29	10.5039	
$F_1 \times F_2$	149	56.8368	5.4110 **

Table 33G. Number of primary branches at maximum flower (NPBMF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.5549	1.5350 **
F_2	29	0.8517	1.5721 *
$F_1 \times F_2$	149	0.8723	

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.5828	
F_2	29	0.7138	1.2248 NS
$F_1 \times F_2$	149	0.5865	1.0064 NS

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.4541	
F_2	29	0.8609	1.8959 **
$F_1 \times F_2$	149	0.5235	1.1528 NS

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	0.5324	
F_2	29	0.7138	1.3406 NS
$F_1 \times F_2$	149	0.7161	1.3449 *

Table 33H. Number secondary branches at maximum flower (NSBMF).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	4.4127	1.3132 *
F_2	29	4.4931	1.3371 NS
$F_1 \times F_2$	149	3.3604	

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	3.2682	1.0898 NS
F_2	29	2.9989	
$F_1 \times F_2$	149	4.4201	1.4739 NS

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	5.1465	1.2749 NS
F_2	29	5.3851	1.3340 NS
$F_1 \times F_2$	149	4.0367	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	5.0459	1.6826 **
F_2	29	2.9989	
$F_1 \times F_2$	149	3.9374	1.3130 NS

Table 33I. Plant weight at harvest (PWH).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	1743.4156	1.1415 ^{NS}
F_2	29	1909.6612	1.2503 ^{NS}
$F_1 \times F_2$	149	1527.3209	

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	967.0464	
F_2	29	1814.2755	1.8761 **
$F_1 \times F_2$	149	1409.2199	1.4572 *

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	2569.2728	1.8966 *
F_2	29	1354.6437	
$F_1 \times F_2$	149	1508.6107	1.1137 ^{NS}

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	1894.1880	1.4832 **
F_2	29	1814.2755	1.4206 ^{NS}
$F_1 \times F_2$	149	1277.1343	

Table 33J. Number of pods per plant (NPd/P).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	1600.1931	1.5665 ^{NS}
F_2	29	1021.5276	
$F_1 \times F_2$	149	1618.3291	1.5842 ^{NS}

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	983.2271	
F_2	29	3191.0486	3.2461 **
$F_1 \times F_2$	149	1315.0486	1.3375 *

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	1030.3481	1.3765 *
F_2	29	2760.6023	3.6880 **
$F_1 \times F_2$	149	748.5324	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	1436.8308	
F_2	29	3191.6655	2.2213 **
$F_1 \times F_2$	149	2018.6264	1.4049 *

Table 33K. Pod weight per plant (PdW/P).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	171.7930	4.5311 **
F_2	29	37.9142	
$F_1 \times F_2$	149	207.0988	5.4623 **

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	103.1995	
F_2	29	203.9413	1.9762 **
$F_1 \times F_2$	149	123.7511	1.1991 NS

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	154.4877	1.8180 **
F_2	29	181.5006	2.1359 **
$F_1 \times F_2$	149	84.9751	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	181.6688	1.5084 **
F_2	29	203.9413	1.6933 *
$F_1 \times F_2$	149	120.4420	

Table 33L. Number of seeds per plant (NS/P).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	2096.4240	1.8625 *
F_2	29	1125.5816	
$F_1 \times F_2$	149	2179.4016	1.9362 *

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	1096.4922	
F_2	29	8021.1954	7.3153 **
$F_1 \times F_2$	149	1577.3479	1.4385 *

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	1801.3271	1.5134 **
F_2	29	3894.2299	3.2717 **
$F_1 \times F_2$	149	1190.2640	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	2012.2325	
F_2	29	8021.1954	3.9862**
$F_1 \times F_2$	149	4748.1845	2.3597 **

Table 33M. Seed weight per plant (SW/P).

Cross-2

Source of variation	df	Total variance	F
F_2(BIPs)	149	132.9189	4.4649 **
F_2	29	29.7698	
$F_1 \times F_2$	149	126.2954	4.2424 **

Cross-3

Source of variation	df	Total variance	F
F_2(BIPs)	149	63.7794	1.0614 NS
F_2	29	224.5893	3.7374**
$F_1 \times F_2$	149	60.0923	

Cross-4

Source of variation	df	Total variance	F
F_2(BIPs)	149	92.6986	1.8091 **
F_2	29	104.4388	2.0383 **
$F_1 \times F_2$	149	51.2393	

Cross-5

Source of variation	df	Total variance	F
F_2(BIPs)	149	140.5404	1.8203 **
F_2	29	224.5893	2.9090 **
$F_1 \times F_2$	149	77.2059	

* = Significant at 5% level, ** = Significant at 1% level and NS = non-significant.

DISCUSSION

The genetics of yield is extremely complex and hence one can face difficulties in genetical analysis. This complexity can be judged from the vide array of the type of gene action. This study was aimed to find out the type of gene action through biparental progeny analysis for yield and yield related components of five crosses viz., cross-1(8×3), cross-2 (8×1), cross-3 (8×4), cross-4 (4×8) and cross-5 (8×7) in chickpea. The characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

Successful breeding program depends on the knowledge of genetic architecture and inheritance pattern of the quantitative traits of the crop. But the main weak point in breeding for high yield is that, quantitative character is very complex in nature. Biparental mating (BIPs) is one of the simplest random mating design available to effect forced recombination and breaking down undesirable linkage as pointed out by Comstock and Robinson (1952). The underlying concept of biparental mating is that rare recombinants which remain restricted due to linkage disequilibrium are promptly released by forced recombination and become available for selection in early segregating generations. The biparental mating design was suggested by Mather (1949a) to partition the total phenotypic variance of random mating population into between families (σ^2_b) and within families (σ^2_w) components. The analysis has two assumption viz., a) it assumes the absence of non-heritable variance of cross (family) means, i.e.

$E_2 = 0$ and b) the absence of dominance, i.e. $H_R = 0$. By ignoring these two parameters (E_2 and H_R), the values of D_R and E_1 are estimated. Still further, that the great utility of BIPs is in getting precise estimates of additive and dominance components of genetic variance and average level of dominance. To secure these estimates, BIPs have been developed following different designs of mating. Kearsey's (1965) paired mating is one such mating design.

Analysis of variance showed significant difference among the families (crosses) for all the characters in all the crosses except DMF in cross-1; NSBFF and NPd/P in cross-4 and DMF, NPBMF, NPd/P, PdW/P and SW/P in cross-5. Significance of family variance suggests considerable variation among BIPs families indicating thereby individuals involvement in paired mating contributed differentially to respective families. It also suggests the suitability of the present materials for further breeding research. Kearsey (1965) and Sharma *et al*. (1979) also obtained a greater extent of genetic variability in the population of BIPs in their materials. Similar results were reported by Ojha and Roy (2001) in sunflower and Husain *et al*. (2009) in chilli.

The replication item was non-significant for all the crosses and characters except NPd/P, PdW/P and NS/P in cross-2. Non-significant replication indicated that the research field was homogeneous. The non-significant replication item was reported by Kearsey (1965) in *Papaver dubium*, Husain (1997) in chilli, Nahar (1997) in sugarcane and Ojha and Roy (2001) in sunflower. The interaction (F×R) found non-significant in 47 cases while it was significant only in 18 cases viz., PHMF, PdW/P, NS/P and SW/P in cross-1; PHMF, NPd/P, PdW/P, NS/P and SW/P in coroos-2 and DFF, PHFF, DMF, PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3. Similar results were reported Husain *et al*. (2009) in chilli.

In the present study, the regression item was non-significant due to high standard error in maximum cases, which indicated complex situation present in

the parent-offspring relationship. It is therefore, suggested that biparental progenies and their mid-parents were related regarding the inheritance of these characters in the crosses. However, regression for NPBMF in cross-4 and for PHFF, NPBMF and PdW/P in cross-5 noted significant which indicated a good relationship between biparental progenies and their parents. Husain *et al*. (2009) reported non-significant regression item for most of the characters and crosses in chilli. In contrast, Nahar and Khaleque (2000) found significant regression for all the characters and population except population 2 and 3 for tiller per clump and leaf area in sugarcane. For the remainder item, it was non-significant in majority cases except for NPBFF in cross-2; for NPBFF in cross-3; for NPBFF, NPBMF and PWH in cross-4 and for NPBFF and NPBMF in cross-5, suggested that some non-linear components were involved in the inheritance of the biparental progenies. Nahar and Khaleque (2000) in sugarcane and Husain *et al*. (2009) in chilli reported that few traits were significant regarding remainder item. Regression coefficients (b_i) when tested with their standard error, in most of the cases standard errors were greater than the regression coefficient indicated that the parent-offspring relationship bear the complex situations and there were involved non-linear components. Similar findings were reported by Husain *et al*. (2009) in chilli.

As the plants were randomized individually in the present experiment, σ^2_b and σ^2_w were estimated for different characters. Thus there were two statistics for the estimation of three parameters, such as D_R, H_R and E_W. In this investigation, magnitude of additive (D_R) component was higher than that of the dominance (H_R) component for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF, NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. Higher magnitude of D_R indicated the relative important of additive gene action in the inheritance of these characters. Additive component of variation are associated

with homozygosity and also fixable in nature. Therefore, selection for these traits governed by additive component of variation will be very effective. Existence of additive component of variation is prerequisite for the improvement through selection because this is the only component of variation that responds to selection. Additive component of variation is a measure of additive gene action and this gene action is the chief cause of resemblance between relatives and progress by selection is directly proportional to the degree of resemblance between parents and progeny. Thus, additive gene action is a measure of breeding value of a genotype. Hence, for the traits which showed preponderance of additive gene action, reliance should be placed on pure line selection, mass selection and or progeny selection. This is in agreement with the findings of Shanthi *et al*. (2004), Manickavelue *et al*. (2006) and Thirugnana *et al*. (2007). Further this trait could be improved by pedigree breeding method while going for hybridization and selection. This finding corroborated with the findings of Husain *et al*. (2009) in chilli. The importance of additive gene action were reported by several workers in their materials following different methods of BIPs such as, Srividhya *et al*. (2005), Manickavelue *et al*. (2006), Dhameliya and Dobariya (2009) and Mahalingam *et al* (2011).

On the other hand, the magnitude of dominance (H_R) components were higher than that of additive (D_R) component for most of the characters in all crosses which indicated the relative importance of dominance type of gene actions in the inheritance of these traits. Kanwar and Karla (2004) obtained the same results in their material following NCD-1. The magnitude of H_R in some cases was negative. Science H_R is a variance components, it should not be negative. The probable cause of negative value of H_R may be first due to lack of random mating amounting to assertive mating, secondly due to sampling error (Mather,1949b) and lastly due to genotype × environment interaction (Hill, 1966). The negative dominance component was also reported by Moll *et al*. (1960), Husain *et al*. (2009) and Alam (2012). Normally dominance component of variation is

associated with heterozygosity and it is not fixable, therefore, selection for these traits is not effective. Dominance component of variation is the chief cause of heterosis or hybrid vigor. The preponderance of non–additive gene action for these traits under study indicated that improvement of these characters could be possible through heterosis breeding. But, chickpea being a self pollinated crop, heterosis breeding is not widely adopted, unlike recombination breeding. Therefore, to get better genotypes by the way of recombination breeding hybridization followed by selection at later generations is suggested for exploiting dominance gene action. Alternatively, two or more cycles of intermating among the selected segregants might not only break the undesirable linkages if any, but also allow accumulation of favorable alleles for the improvement of traits of interest. In the present study, the degree of dominance was measured separately for different characters and observed over dominance for most of the crosses and characters indicating the high influence of dominance components. The presence of over dominance was reported by Sharma *et al*. (1979), Nahar and Khaleque (2000), Kanwar and Karla (2004), Jayaprada (2005) and Husain *et al*. (2009).

Both broad sense and narrow sense heritability were estimated and in most of the cases these were low. In this study, E_w estimates were higher than that of D_R and H_R in most of the cases. It seems that high estimates of environmental variations and their prevalence of H_R components in this material deflated both narrow and broad sense heritability. Most of the traits showed higher heritability in broad sense than heritability in narrow sense except NPBFF, DMF, PWH, NS/P and SW/P in cross-1; PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; DFF, PHFF, NSBFF and PWH in cross-3; NSBFF, NSBMF, NPd/P and PdW/P in cross-4 and DFF, NSBFF, NPBMF, NSBMF and NPd/P in cross-5. Sharma *et al*. (1979), Alam *et al*. (2009), Husain *et al*. (2009) and Alam (2012) reported low narrow and broad sense heritability for most of the traits.

Genetic advance (GA) was estimated as low both in broad sense and narrow sense for most of the traits in each cross. GA in narrow sense was higher than that of broad sense for NPBFF, DMF, PWH, NS/P and SW/P in cross-1; PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; PHFF, NSBFF and PWH in cross-3; NSBFF, NSBMF, NPd/P and PdW/P in cross-4 and for DFF, NSBFF, NPBMF, NSBMF and NPd/P in cross-5. This indicated that additive gene action was important in the expression of these traits.

In the present materials, significant linkage in both coupling and repulsion phases were detected. According to Mather and Jinks (1982), linkage can affect the generation means in the presence of epistasis only, and it has no effect on the means of generations if epistasis is absent. If epistasis is present, its contribution to the mean of any segregating generation is determined by the degree of linkage. So, the presence of significant linkage is the indication of biased estimates of additive and dominance components of variation in the present materials. Significant linkage was reported by Joarder *et al*. (1977) in *Brassica campestries* L. and Husain (1997) in chilli.

To sum up the above discussion, magnitude of additive (D_R) component was higher than that of dominance (H_R) component for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. These results signify the relative important of additive gene action in the inheritance of these characters. Thus additive gene action is a measure of breeding value of a genotype. Hence, for the trait which showed preponderance of additive gene action, reliance should be placed on pure line selection, mass selection and or progeny selection. The significant regression item in some cases revealed good relationship between biparental progenies and their parents.

SUMMARY

To partition the total phenotypic variance into between crosses and within crosses components, the biparental progeny analysis of five crosses in chickpea was performed. Thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

Biparental progeny (BIPs) analysis is one of the simplest random mating design available to effect forced recombination and breaking down undesirable linkages. The great utility of BIPs is in estimating additive, dominance and environmental variation from total variation. To secure these estimates, BIPs are developed following different designs of mating. Kearsey's paired mating is one such mating design. Analysis of variance showed significant difference among the families (crosses) for all the characters except DMF in cross-1; NSBFF and NPd/P in cross-4 and DMF, NPBMF, NPd/P, PdW/P and SW/P in cross-5 suggested considerable variation among BIPs families indicating thereby individuals involvement in paired mating contributed differentially to respective families. The interaction between family × replication (F×R) item was non-significant for most of the characters and crosses indicated that family and replication (F×R) were not interacted with each other significantly. The characters viz., PHMF, PdW/P, NS/P and SW/P in cross 1; PHMF, NPd/P, PdW/P, NS/P and SW/P in coroos-2 and DFF, PHFF, DMF, PHMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3 found to be significant regarding F×R interaction.

In the present investigation, magnitude of additive (D) components was higher than that of dominance (H) components for NPBMF, NSBMF and PdW/P in cross-1; for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF in cross-2; for NPBFF, NPBMF, PdW/P, NS/P and SW/P in cross-3; for DMF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-4 and for DFF, PHMF, PdW/P, NS/P and SW/P in cross-5. This result indicated the relative important of additive gene action in the inheritance of these characters. On the other hand, the magnitude of dominance components was higher than that of additive component for rest of the characters and respective crosses indicated the relative importance of dominance type of gene actions on these traits. Regarding degree of dominance, over dominance for most of the characters and crosses were noted in the present study. The significant regression item in some cases revealed good relationship between biparental progenies and their parents, while significant remainder item made the relationship complicated in some cases.

Both broad sense and narrow sense heritability and genetic advance (GA) were low for most of the traits in each cross. In case of NPBFF, DMF, PWH, NS/P and SW/P in cross-1; PHFF. PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; PHFF, NSBFF and PWH in cross-3; NSBFF, NSBMF, NPd/P and PdW/P in cross-4 and DFF, NSBFF, NPBMF, NSBMF and NPd/P in cross-5, GA in narrow sense was higher than broad sense GA. This indicated that additive gene action was important in the expression of these traits. Therefore, selection for these traits which showed additive gene action will be very effective. By comparing total variances of F_2, F_2 BIPs and $F_2 \times F_1$, most of the characters showed linkage in repulsion phase.

GENETIC STUDY-3: TRIPLE TEST CROSS (TTC) ANALYSIS

MATERIALS AND METHODS

A. MATERIALS

In this experiment, five chickpea genotypes viz., BARI chola-1, BARI chola-4, BARI chola-6, BARI chola-7 and BARI chola-8 were taken as material. Five different crosses were made between the genotypes for raising triple test cross materials in the following manner as given in Table 34.

Table 34. Five single crosses of chickpea, their selfing, F_2 and TTC family.

Cross	P_1 ♀	P_2 ♂	F_1s	Selfing	F_2s	L_{1i}	L_{2i}	L_{3i}
1.	G-6	G-8	6 × 8	→	6 × 8	$P_1 \times F_2$s	$P_2 \times F_2$s	F_1s × F_2s
2.	G-8	G-1	8 × 1	→	8 × 1	$P_1 \times F_2$s	$P_2 \times F_2$s	F_1s × F_2s
3.	G-8	G-4	8 × 4	→	8 × 4	$P_1 \times F_2$s	$P_2 \times F_2$s	F_1s × F_2s
4.	G-4	G-8	4 × 8	→	4 × 8	$P_1 \times F_2$s	$P_2 \times F_2$s	F_1s × F_2s
5.	G-8	G-7	8 × 7	→	8 × 7	$P_1 \times F_2$s	$P_2 \times F_2$s	F_1s × F_2s

The materials for the present investigation comprised $10P_1$, $10P_2$ and $10F_1$ families leading to L_{1i}, L_{2i} and L_{3i} families, respectively. As a result, 30 families were obtained for each of the five separate crosses. The experimental families viz., L_{1i}, L_{2i} and L_{3i} were raised by crossing 10 male plants, randomly selected from the F_2 population, with P_1, P_2 and F_1 plants considered as female. The materials used in this experiment were raised in the following manner.

Cross-1:

$P_1 \times P_2$

↓

F_1

(selfing)

↓

F_2

(10 F_2 plants selected as male)

No. of families	L_{1i} ♀ × ♂	Number of sibs	L_{2i} ♀ × ♂	Number of sibs	L_{3i} ♀ × ♂	Number of sibs
1	$P_1 \times F_2$	1, 2.....5	$P_2 \times F_2$	1, 2.....5	$F_1 \times F_2$	1 ,2.....5
2	$P_1 \times F_2$	1, 2.....5	$P_2 \times F_2$.	1, 2.....5	$F_1 \times F_2$	1, 2.....5
.	.	.	.	.	.	.
.	.	.	.	.	.	.
10	$P_1 \times F_2$	1, 2.....5	$P_2 \times F_2$	1, 2.....5	$F_1 \times F_2$	1, 2.....5

The same procedure of crossing was followed in the other four crosses.

B. METHODS

The methods followed to conduct the experiment and analyses of the data are divided into the following sub-heads:

a. Techniques of the Cross Pollination and Production of the Experimental Seeds,

b. Preparation and Design of the Experimental Field,

c. Sowing of Seeds,

d. Maintenance of the Experimental Plants,

e. Collection of Data and

f. Techniques of Analysis of Data.

Descriptions of the sub-heads are as follows:

a. Techniques of the Cross Pollination and Production of the Experimental Seeds

The cross pollination techniques was same as which is mentioned earlier in genetic study-1 of generation mean analysis. The cross seeds were collected in packets separately for each F_1. In the second year, F_1s and parents were raised in the research field. F_1s were allowed for selfing to get F_2 seeds. At the same time fresh F_1s were also made. In the third year, parent 1 (P_1), parent 2 (P_2), F_1 and F_2 generations were grown in the field. From the F_2 generations, 10 plants were randomly selected and marked as males, and 10 plants from each of P_1, P_2 and F_1 populations were selected randomly as females. For getting TTC materials, crosses of selected F_2 males were made with the selected female plants of P_1, P_2 and F_1 populations. Thus seeds of 10 P_1 families as L_{1i}, $10P_2$ families as L_{2i} and 10 F_1 families as L_{3i} were produced and collected separately with proper labeling.

b. Preparation and Design of the Experimental Field

The experiment was conducted in the research field of the North-Western side of the third science building of University of Rajshahi, Bangladesh during the crop season of 2009-2010, 2010-2011, 2011-2012 and 2012-2013. 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.

Lay-out of the experimental field and trial of the L_{1i}, L_{2i} and L_{3i} families following randomized complete block design with three replications (blocks). The distance between replications was 120cm and that between rows was 45cm. The space between hills was 45cm. In each hill, one plant was maintained. The seeds of L_{1i}, L_{2i} and L_{3i} families were sown according to design.

c. Sowing of Seeds

The seeds of 30 families (L_{1i}, L_{2i} and L_{3i} families) were sown in the experimental field according to design on the 11th November, 2012.

d. Maintenance of the Experimental Plants

Weeding and hoeing was done whenever necessary. Insecticide and fungicide were sprayed regularly to keep plants free from insect and fungal attack.

e. Collection of Data

Under this model (TTC), data on thirteen quantitative characters like as genetic study-1 were collected and recorded on individual plant basis. All the plants were labeled properly before harvesting. Total number of plants from which data were taken from each family per replication is as follows:

Families	Number of families	Number of plants per family	Total number of plants per families per replication per cross
L_{1i} families	10	5	10×5=50
L_{2i} families	10	5	10×5=50
L_{3i} families	10	5	10×5=50

Recorded thirteen characters were described in Part-I.

f. Techniques of Analysis of Data

Biometrical technique of analysis which is devised by Kearsey and Jinks (1968) as an extension of the North Carolina Design III (NCD III) of Comstock and Robinson (1952) was followed. This design follows to produce the progeny families, such as L_{1i}, L_{2i} and L_{3i} by crossing each individual (i) in the population sample (F_2 population) is crossed to both of the parental lines i.e., (P_1 and P_2) and F_1. The progeny families were then raised in a replicated experiment. The contribution to the progeny family means due to single gene difference is shown in the following Table 35.

Table 35. Back crosses of F_2 population to contrasting inbred lines and their F_1s.

Frequency	$\mathbf{u_a^2}$	$\mathbf{2u_a v_a}$	$\mathbf{v^2_a}$	**Mean**
Genotype	**AA**	**Aa**	**aa**	
$\bar{L}_1$ AA	d_a	$\frac{1}{2}d_a + \frac{1}{2}h_a$	h_a	$u_a d_a + v_a h_a$
$\bar{L}_2$ aa	h_a	$-\frac{1}{2}d_a + \frac{1}{2}h_a$	$-d_a$	$-v_a d_a + u_a h_a$
$\bar{L}_3$ Aa	$\frac{1}{2}d_a + \frac{1}{2}h_a$	$\frac{1}{2}h_a$	$-\frac{1}{2}d_a + \frac{1}{2}h_a$	$\frac{1}{2}(u_a - v_a)d_a + \frac{1}{2}h_a$
$\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$	$\frac{3}{2}(d_a + h_a)$	$\frac{3}{2}h_a$	$\frac{3}{2}(-d_a + h_a)$	$\frac{3}{2}[(u_a - v_a)d_a + h_a]$
$\bar{L}_{1i} - \bar{L}_{2i}$	$d_a - h_a$	d_a	$d_a + h_a$	$d_a + (u_a - v_a)h_a$
$\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$	0	0	0	0

Jinks and Perkins (1970) suggested a modification in the analysis of Kearsey and Jinks (1968) estimates of additive and dominance component of variation as well as epistasis considering orthogonal comparison shown in Table 36.

Table 36. Orthogonal comparison between mean of different families.

Comparison	$\bar{L}_{1i}$	$\bar{L}_{2i}$	$\bar{L}_{3i}$
Additive	1	1	1
Dominance	1	-1	
Epistasis	1	1	-2

Thus, for each individual (i), orthogonal comparison between the family means are

for additivity = $\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$

for dominance = $\bar{L}_{1i} - \bar{L}_{2i}$ and

for epistasis = $\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$

1. Test of epistasis

The test of significance of the differences $\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$ provides information about presence or absence of epistasis. If epistasis does not exist in the material under investigation, the quantity of $\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$ should not be significantly different from zero. The presence of non-allelic interaction and its significance test was done through the analysis of variance. The test of significance of total epistasis, 'i' type epistasis and 'j+l' type epistasis are tested against their respective interaction with blocks. However, before testing individual epistasis effect, the homogeneity of the interaction was first tested. As there were only two variances (i type epistasis × blocks and j+l type epistasis × blocks) homogeneity was first tested as *F* test i.e. MS of 'i' type epistasis × blocks divided by 'j+l' type epistasis. If it non-significant suggesting homogeneity of interaction variances. It is therefore, recommended that 'i' type and 'j+l' type epistasis should also be tested against the pooled error, i.e., total epistasis × blocks interaction. The whole analysis is illustrated in Table 37.

Table 37. The skeleton of the analysis of variance for testing epistasis.

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	n	SS_1	MS_1		MS_1/ MS_4
i type epistasis	1	SS_2	MS_2		MS_2/ MS_4
j+l type epistasis	n-1	SS_3	MS_3		MS_3/ MS_4
Total epistasis × blocks	n(B-1)	SS_4	MS_4		
i type epistasis × blocks	1(B-1)	SS_5	MS_5	MS_5 /MS_6	MS_5/MS_4
j+l type epistasis × blocks	(n-1)(B-1)	SS_6	MS_6		MS_6/MS_4

Where,

n = number of families

B = number of blocks (replications)

2. Calculation of Additive ($\hat{D}$) and Dominance ($\hat{H}$) Component

For the estimation of sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) in the analysis of variance, the expectation mean squares (EMS) are shown in the following Table 38 and Table 39, respectively.

Table 38. ANOVA for sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$).

Item	df	MS	EMS
Sums	n-1 = 9	MS_1	$\sigma^2_{WS}+15(\sigma^2_{B\times F2}+5\sigma^2_P)+30\sigma^2_S$
Sums × blocks	(B-1)(n-1)=18	MS_2	$\sigma^2_{WS}+15(\sigma^2_{B\times F2}+5\sigma^2_P)$
Within families	nBT(P-1)=360	MS_3	σ^2_{WS}

Table 39. ANOVA for differences ($\bar{L}_{1i} - \bar{L}_{2i}$).

Item	df	MS	EMS
Differences	n-1 = 9	MS_1	$\sigma^2_{WD}+10(\sigma^2_{B\times F2}+5\sigma^2_P)+20\sigma^2_D$
Differences × blocks	(B-1)(n-1)=18	MS_2	$\sigma^2_{WD}+10(\sigma^2_{B\times F2}+5\sigma^2_P)$
Within families	nBT(P-1)=240	MS_3	σ^2_{WD}

Where

n = number of families
B = number of blocks (replications)
T = number of testers
P = number of progenies (sibs)
σ^2_S = variance for sums
σ^2_D = variance for differences
σ^2_{WS} = within family variance for sums
σ^2_{WD} = within family variance for differences

From EMS of sums due to additive variance (σ^2_S) and EMS of differences due to dominance variance (σ^2_D), additive genetic component ($\hat{D}$) and dominance genetic component ($\hat{H}$) of variation were measured separately as follows:

i. Additive component ($\hat{D}$)

σ^2_S = [Sums - Sums × blocks]/30

σ^2_S = (MS_1- MS_2)/30

$\sigma^2_S = 1/8\,\hat{D}$

$\hat{D} = \sigma^2_S \times 8$

ii. Dominance component ($\hat{H}$)

σ^2_D = [Differences - Differences × blocks]/20

σ^2_D = (MS_1- MS_2)/20

$\sigma^2_D = 1/8\,\hat{H}$

$\hat{H} = \sigma^2_D \times 8$

In the absence of epistasis, σ^2_S is an estimate of 1/8 additive genetic variance ($\hat{D}$) and σ^2_D is an estimate of 1/8 dominance genetic variance ($\hat{H}$).

3. Degree of dominance

The degree of dominance was calculated as follows:

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

Where

H = dominance genetic component

D = additive genetic component

4. Heritability

Heritability in narrow sense (h^2_n) and broad sense (h^2_b) was computed as follows:

$$h^2_n = \frac{\frac{1}{2}D}{\frac{1}{2}D + \frac{1}{4}H + E_W + (E_P + G \times E)}$$

$$h^2_b = \frac{\frac{1}{2}D + \frac{1}{4}H}{\frac{1}{2}D + \frac{1}{4}H + E_W + (E_P + G \times E)}$$

Where,

$$E_W = \sigma^2_{WD} - (\frac{1}{8}D + \frac{1}{8}H)$$

$$E_P + G \times E = \frac{\text{Differences} \times \text{blocks} - \text{Within family variance for differences}}{10}$$

$$E_P + G \times E = \frac{MS_2 - MS_3}{10}$$

5. Direction of dominance ($r_{s,d}$)

Direction of dominance was determined by calculating the linear correlation coefficient ($r_{s,d}$) between the sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) and differences ($\overline{L}_{1i} - \overline{L}_{2i}$) for all the genotypes. Significant and positive correlation ($r_{s,d}$) would indicate a predominant direction towards decreasing alleles while, significant and negative correlation ($r_{s,d}$) indicated the direction of dominance towards increasing alleles of a trait (Jinks *et al.*, 1969).

RESULTS

In genetic study-3, i.e. triple test cross analysis was applied to detect the epistasis of thirteen agronomic characters of five different crosses in chickpea. The thirteen quantitative characters are date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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.

Since most of the economic traits in crop plants are governed by polygene, therefore it is hard to imagine a situation where epistasis can be thought of being absent. Triple test cross (TTC) analysis give exact information about epistasis. The information obtained through triple test cross would help in understanding the genetic basis and making breeding strategy for the development of high yielding cultivar or valuable germplasm in chickpea. TTC has wide applicability as it can be used to investigate both segregating and non-segregating populations arising from different generations such as F_2, backcross and homozygous lines. TTC analysis provides unambiguous test for the presence of epistasis regardless of gene frequencies, degree of inbreeding and linkage relationships. In the absence of epistasis TTC also provides unbiased estimates of additive ($\hat{D}$) and dominance ($\hat{H}$) components of genetic variation, degree of dominance [$(H/D)^{1/2}$] as well as the direction of dominance ($r_{s.d}$) with high degree of precision (Kearsey and Jinks, 1968). The results obtained in the experiment have been described under three sub-heads as follows:

A. ANALYSIS OF VARIANCE FOR EPISTASIS

To detect epistatic effect, analysis of variance was done according to Kearsey and Jinks (1968) for all the thirteen characters in all the five different crosses separately and are presented in Table 40A-40M. The method allows partitioning of the item total epistasis into fixable ('i' type i.e., additive × additive interaction) and unfixable epistasis ('j+l' type i.e., additive × dominance and dominance × dominance interaction) for 1 and 9 degrees of freedom, respectively. Similarly, total epiatsis × blocks was partitioned into 'i' type epistasis × blocks and 'j+l' type epistasis × blocks for 2 and 18 degrees of freedom. Before testing individual epistasis, the homogeneity of the interaction is first tested. So for homogeneity, at first 'i' type eplstasis × blocks was tested against 'j+l' type epistasis × blocks (VR_1). In this study, this test was found to be non-significant for all the characters and crosses, suggesting homogeneity of interaction variances. It is therefore, items viz., total epistasis, 'i' type epistasis, 'j+l' type epistasis, 'i' type epistasis × blocks and 'j+l' type epistasis × blocks in all cases were tested against total epistasis × blocks (VR_2).

Cross-1: Non-significant total epistasis was found for all traits regarding this cross. 'i' (additive × additive) type epistasis was found to be significant for the traits DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P. The item 'j+l' (additive × dominance and dominance × dominance) type epistasis was non-significant for all traits. Most of the traits showed high magnitude of 'i' type epistasis than 'j+l' type epistasis. Other items viz., 'i' type epistasis × blocks and 'j+l' type epistasis × blocks were found to be non-significant for all the traits.

Cross-2: Non-significant total epistasis was found for all the studied traits regarding this cross. All the characters showed non-significant 'i' type epistasis but 'j+l' type epistasis was found to be significant only for DFF. The magnitude of additive type of epistasis was found higher than additive and

dominance i.e., ‘j+l’ type epistasis for most of the traits. Other items were found to be non-significant for all the traits.

Cross-3: Effect of total epistasis was non-significant for all the traits regarding this cross. Partitioning the total epistasis into ‘i’ type epistasis and ‘j+l’ type epistasis and it was found that the ‘i’ type epistasis for NPBFF and NSBFF was significant while, ‘j+l’ type epistasis was significant for PHMF, NSBMF and NS/P. The item ‘i’ type epistasis × blocks and ‘j+l’ type epistasis × blocks were non-significant for all traits. High magnitude of ‘i’ type epistasis than ‘j+l’ type epistasis was found for most of the trait regarding this cross.

Cross-4: Similarly to other crosses, the total epistasis was found non-significant for all the traits regarding this cross. ‘i’ type epistasis was found to be non-significant for all the studied traits and ‘j+l’ type epistasis was found to be significant for PHFF and NSBFF. Rest of the traits found to be non-significant for both ‘i’ type and ‘j+l’ type epistasis. ‘i’ type epistasis found higher magnitude than ‘j+l’ type epistasis. Other items were found to be non-significant for all the trait in this cross.

Cross-5: The item total epistasis was non-significant for all the traits in this cross. Significant ‘i’ type epistasis was noted for PHFF, DMF, PHMF and NSBMF. The item ‘j+l’ type epistasis was non-significant for all the traits regarding this cross. Again, ‘i’ type epistasis × blocks was found to be non-significant for all the traits. High magnitude of ‘i’ type epistasis was found than ‘j+l’ type epistasis for most of the traits.

B. ANALYSIS OF VARIANCE FOR SUMS (σ^2_S) AND DIFFERENCES (σ^2_D)

Analysis of variance for sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) provides direct tests of the significance of additive and dominance components. The ten (10) sums of means of the families provided a variance of sums with 9 degrees of freedom. Similarly, the variance of differences was also obtained with 9 degrees of

freedom. Variances of sums × blocks and differences × blocks were computed each for 18 degrees of freedom. At first, the items viz., sums, differences, sums × blocks and differences × blocks were tested against their respective within family error (VR_1). Later on sums and differences were also tested against sums × blocks and differences × blocks, respectively (VR_2). In this way, test of significance of variance for sums and differences were done separately for all the characters and the results obtained are presented in Table 41A-41M.

Cross-1: Regarding this cross, sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) item was found to be significant for all characters when tested against within families while, it is found to be significant for PHFF, DMF, PHMF, NSBMF, PWH, NPd/P, PdW/P and NS/P when tested against sums × blocks interaction. Except PHFF and PWH, all characters found to be significant regarding sums × blocks item when tested against within families. On the other hand, item differences noted significant for DFF, PHFF, DMF, PWH, NPd/P, PdW/P, NS/P and SW/P when tested against within families whereas this item was found to be significant for DFF, PHFF, DMF, PWH, NPd/P, PdW/P, NS/P and SW/P when tested against differences × blocks. NS/P is the only trait which noted significant regarding differences × blocks item.

Cross-2: In this cross, when tested against respective within families, item sums was found to be significant for all the characters except NSBFF but noted significant only for three characters viz., PWH, NS/P and SW/P when tested against sums × blocks interaction. All characters also found to be significant regarding sums × blocks item when tested against within families except NPBFF. Item differences showed significant values for NPBFF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P when tested against respective within families whereas this item showed significant values for NSBMF and PWH when tested against differences × blocks. Differences × blocks item when tested against respective within families recorded significant for NPBFF, DMF, NPd/P and PdW/P.

Cross-3: Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) item was found to be significant for all characters when tested against within families while, it found to be significant only for DFF, PHFF, NSBMF and PWH when tested against sums × blocks interaction. Item sums × blocks found to be significant for all characters except DFF and PHFF when tested against within families. On the other hand, item differences ($\overline{L}_{1i} - \overline{L}_{2i}$) noted significant for DFF, NSBFF, DMF, PHMF, NPBMF and NSBMF when tested against within families whereas, this item was found to be significant for DFF, PHFF, PHMF and NPBMF when tested against interaction viz., differences × blocks. Differences × blocks item noted significant only for NPBFF and DMF.

Cross-4: Regarding this cross, sums was found to be significant for all the characters and sums × blocks item noted significant for all the characters except NSBMF when tested against respective within families. Whereas, sums item was noted significant only for PHFF when it was tested against sums × blocks item. Again, item differences showed significant value for DFF, PHFF, NPBFF, PHMF, NSBMF and PWH when tested against respective within families, whereas this item showed significant value only for NSBMF when tested against differences × blocks. Differences × blocks item showed significant values for PHFF, NPBFF, PHMF and NPBMF when tested against respective within families.

Cross-5: Significant sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) item was noted for all the characters when tested against within families and at the same time as it was noted significant for DFF, NPBMF, NPd/P, PdW/P, NS/P and SW/P when tested against sums × blocks interaction. All characters also found to be significant regarding sums × blocks item when tested against within families except NSBFF and NSBMF. On the other hand, item differences showed significant value for DFF, NSBFF, DMF, PHMF and NPBMF when tested against respective within families whereas this item showed significant value for DFF, NSBFF, DMF, PHMF and NPBMF when tested against differences × blocks.

Only NSBMF and PWH showed significant value regarding differences × blocks item when tested against respective within families.

C. ADDITIVE ($\hat{D}$) AND DOMINANCE ($\hat{H}$) COMPONENTS, DEGREE OF DOMINANCE ($\sqrt{H/D}$), HERITABILITY (h^2_n & h^2_b) AND DIRECTION OF DOMINANCE

In the absence of epistasis an additive-dominance model would be adequate to explain the genetic variation. The results of additive and dominance components, degree of dominance, heritability in narrow sense and broad sense with direction of dominance for all crosses and characters are presented in Table 42A-42E and cross-wise description as are follows:

Cross-1: Both additive ($\hat{D}$) and dominance ($\hat{H}$) components of variationwere highly significant for most of the traits. Additive component was higher than that of dominance component for DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH and PdW/P. In respect of degree of dominance ($\sqrt{H/D}$), over dominance was noted for NPd/P and SW/P and complete dominance was noted for PWH, PdW/P and NS/P while rest of traits exhibited partial dominance. Both narrow sense (h^2_n) and broad sense (h^2_b) heritability for most of the traits regarding this cross showed moderately high to high value. Broad sense heritability was found to be higher than that of narrow sense heritability for most of the characters. Correlation between sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) and differences ($\overline{L}_{1i} - \overline{L}_{2i}$) were positive and significant for NSBFF, PHMF, NPd/P, PdW/P, NS/P and SW/P indicated direction of dominance towards decreasing parents while, negative and significant for DMF indicates direction of dominance towards increasing parents. Rest of traits showed non-significant correlation indicates no effect of direction of dominance.

Cross-2: Most of the traits were highly significant in respect of both additive ($\hat{D}$) and dominance ($\hat{H}$) components and additive component was higher than

dominance components for all the traits regarding this cross. The degree of dominance was partial for all the traits and no over dominance or complete dominance was noted for this cross. The characters viz., DFF, NSBFF, DMF and PWH exhibited high narrow sense heritability whereas, DFF, NSBFF, NSBMF and PWH showed high broad sense heritability. The broad sense heritability was found higher than that of narrow sense heritability for most of the characters. Negative and significant correlation between sums and difference were observed for NPd/P, PdW/P, NS/P and SW/P.

Cross-3: In this cross, both additive and dominance component were highly significant for most of the studied traits. Component $\hat{D}$ was higher than that of component $\hat{H}$ for DFF, PHFF, NPBFF, DMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P. In respect of degree of dominance ($\sqrt{H/D}$), partial dominance was found for most of the traits while complete dominance was noted for DFF and over dominance was recorded for NSBFF, PHMF and NPBMF. Regarding this cross, both broad sense and narrow sense heritability were found to be low and broad sense heritability (h^2_b) was higher than narrow sense heritability (h^2_n) for most of the traits. Comparatively high narrow sense and broad sense heritability were noted for DFF, PHFF and NSBMF. The positive and significant correlation between sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) and differences ($\overline{L}_{1i} - \overline{L}_{2i}$) noted for DFF and NSBMF while, negative and significant correlation recorded for PHMF. Rest of the trait showed non-significant correlation between sum and differences.

Cross-4: In this cross, both additive ($\hat{D}$) and dominance ($\hat{H}$) components were highly significant for most of the traits. Higher additive component than dominance component was found for PHFF, NSBFF, DMF, PHMF, NPBMF, NS/P and SW/P. Over dominance was noted for DFF, NSBMF, PWH, NPd/P and PdW/P whereas character NPBFF, PHMF and NPBMF exhibited complete dominance and character PHFF, NSBFF, DMF, NS/P and SW/P exhibited partial dominance. Regarding this cross, both broad and narrow sense heritability

were found to be low but the value of broad sense heritability was higher than narrow sense heritability for most of the traits. Negative and significant correlation between sums and difference was noted only for DFF.

Cross-5: In cross-5, most of the traits were highly significant for both additive ($\hat{D}$) and dominance ($\hat{H}$) components. Characters viz., DFF, PHFF, PHMF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P showed higher $\hat{D}$ value than respective $\hat{H}$. Regarding degree of dominance, over dominance was observed for NPBFF, NSBFF, DMF and NSBMF and complete dominance was observed for PHMF while rest of the traits exhibited partial dominance. For this cross, the high narrow sense and broad sense heritability was noted for DFF, PHMF and NPBMF. Positive and significant correlation between sums and differences showed by DFF and NPBMF. Rest of the traits showed non-significant correlation between sums and differences.

Table 40A-40M. Analysis of variance for epistasis ($\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$) for thirteen characters of five crosses in chickpea.

Table 40A. Date of first flower (DFF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	777.1867	77.7187		2.10 ^{NS}
i type epistasis	1	404.8013	404.8013		10.94**
j+l type epistasis	9	372.3853	41.3761		1.12^{NS}
Total epistasis × blocks	20	739.9187	36.9959		
i type epistasis × blocks	2	157.5480	78.7740	2.43 ^{NS}	2.12 ^{NS}
j+l type epistasis × blocks	18	582.3707	32.3539		0.87 ^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	450.9867	45.0987		2.26 ^{NS}
i type epistasis	1	6.5333	6.5333		0.33 ^{NS}
j+l type epistasis	9	444.4533	49.3837		2.47 *
Total epistasis × blocks	20	399.2480	19.9624		
i type epistasis × blocks	2	2.9493	1.4747	0.07^{NS}	0.07 ^{NS}
j+l type epistasis × blocks	18	396.2987	22.0166		1.10 ^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	305.9467	30.5947		1.69^{NS}
i type epistasis	1	1.7280	1.7280		0.10^{NS}
j+l type epistasis	9	304.2187	33.8021		1.86^{NS}
Total epistasis × blocks	20	362.6720	18.1336		
i type epistasis × blocks	2	6.1947	3.0973	0.16^{NS}	0.17 ^{NS}
j+l type epistasis × blocks	18	356.4773	19.8043		1.09 ^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	547.7867	54.7787		2.25 ^{NS}
i type epistasis	1	84.6720	84.6720		3.48 ^{NS}
j+l type epistasis	9	463.1147	51.4572		2.12 ^{NS}
Total epistasis × blocks	20	486.1120	24.3056		
i type epistasis × blocks	2	43.0267	21.5133	0.87 ^{NS}	0.88 ^{NS}
j+l type epistasis × blocks	18	443.0853	24.6159		1.01 ^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	327.9600	32.7960		1.35^{NS}
i type epistasis	1	12.0333	12.0333		0.50^{NS}
j+l type epistasis	9	315.9267	35.1030		1.44^{NS}
Total epistasis × blocks	20	485.9827	24.2991		
i type epistasis × blocks	2	85.9853	42.9927	1.93^{NS}	1.76 ^{NS}
j+l type epistasis × blocks	18	399.9973	22.2221		0.91 ^{NS}

Table 40B. Plant height at first flower (PHFF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	421.7065	42.1707		2.25^{NS}
i type epistasis	1	114.0750	114.0750		6.09^{*}
j+l type epistasis	9	307.6315	34.1813		1.83^{NS}
Total epistasis × blocks	20	374.4137	18.7207		
i type epistasis × blocks	2	50.2852	25.1426	1.40^{NS}	1.34^{NS}
j+l type epistasis × blocks	18	324.1285	18.0071		0.96^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	699.6167	69.9617		2.00^{NS}
i type epistasis	1	139.8816	139.8816		4.00^{NS}
j+l type epistasis	9	559.7351	62.1928		1.78^{NS}
Total epistasis × blocks	20	698.8696	34.9435		
i type epistasis × blocks	2	50.7631	25.3815	0.70^{NS}	0.73^{NS}
j+l type epistasis × blocks	18	648.1066	36.0059		1.03^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	296.5539	29.6554		2.24^{NS}
i type epistasis	1	52.9075	52.9075		3.99^{NS}
j+l type epistasis	9	243.6463	27.0718		2.04^{NS}
Total epistasis × blocks	20	265.3569	13.2678		
i type epistasis × blocks	2	28.8564	14.4282	0.10^{NS}	1.08^{NS}
j+l type epistasis × blocks	18	236.5005	13.1389		0.99^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	241.4703	24.1470		2.24^{NS}
i type epistasis	1	0.3808	0.3808		0.04^{NS}
j+l type epistasis	9	241.0895	26.7877		2.48^{*}
Total epistasis × blocks	20	215.9226	10.7961		
i type epistasis × blocks	2	23.7942	11.8971	1.11^{NS}	1.10^{NS}
j+l type epistasis × blocks	18	192.1284	10.6738		0.98^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	506.8567	50.6857		1.70^{NS}
i type epistasis	1	158.9761	158.9761		5.33^{*}
j+l type epistasis	9	347.8805	38.6534		1.30^{NS}
Total epistasis × blocks	20	596.7251	29.8363		
i type epistasis × blocks	2	83.1918	41.5959	1.46^{NS}	1.39^{NS}
j+l type epistasis × blocks	18	513.5333	28.5296		0.95^{NS}

Table 40C. Number of primary branches at first flower (NPBFF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	2.5600	0.2560		0.54^{NS}
i type epistasis	1	0.0053	0.0053		0.01^{NS}
j+l type epistasis	9	2.5547	0.2839		0.60^{NS}
Total epistasis × blocks	20	9.5147	0.4757		
i type epistasis × blocks	2	0.6053	0.3027	0.61^{NS}	0.64^{NS}
j+l type epistasis × blocks	18	8.9093	0.4950		1.04^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	3.3467	0.3347		0.61^{NS}
i type epistasis	1	2.0280	2.0280		3.71^{NS}
j+l type epistasis	9	1.3187	0.1465		0.27^{NS}
Total epistasis × blocks	20	10.9213	0.5461		
i type epistasis × blocks	2	1.8600	0.9300	1.85^{NS}	1.70^{NS}
j+l type epistasis × blocks	18	9.0613	0.5034		0.92^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	7.1067	0.7107		2.30^{NS}
i type epistasis	1	1.6333	1.6333		5.28^{*}
j+l type epistasis	9	5.4733	0.6081		1.96^{NS}
Total epistasis × blocks	20	6.1907	0.3095		
i type epistasis × blocks	2	0.5880	0.2940	0.94^{NS}	0.95^{NS}
j+l type epistasis × blocks	18	5.6027	0.3113		1.01^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	4.6133	0.4613		1.38^{NS}
i type epistasis	1	0.1920	0.1920		0.57^{NS}
j+l type epistasis	9	4.4213	0.4913		1.46^{NS}
Total epistasis × blocks	20	6.7093	0.3355		
i type epistasis × blocks	2	1.4747	0.7373	2.54^{NS}	2.20^{NS}
j+l type epistasis × blocks	18	5.2347	0.2908		0.87^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	6.4800	0.6480		1.76^{NS}
i type epistasis	1	1.0453	1.0453		2.84^{NS}
j+l type epistasis	9	5.4347	0.6039		1.64^{NS}
Total epistasis × blocks	20	7.3600	0.3680		
i type epistasis × blocks	2	1.3627	0.6813	2.04^{NS}	1.85^{NS}
j+l type epistasis × blocks	18	5.9973	0.3332		0.91^{NS}

Table 40D. Number of secondary branches at first flower (NSBFF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	7.4267	0.7427		0.78^{NS}
i type epistasis	1	1.1213	1.1213		1.18^{NS}
j+l type epistasis	9	6.3053	0.7006		0.74^{NS}
Total epistasis × blocks	20	18.9320	0.9466		
i type epistasis × blocks	2	1.0813	0.5407	0.55^{NS}	0.57^{NS}
j+l type epistasis × blocks	18	17.8507	0.9917		1.05^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	9.2533	0.9253		1.24^{NS}
i type epistasis	1	0.0213	0.0213		0.03^{NS}
j+l type epistasis	9	9.2320	1.0258		1.37^{NS}
Total epistasis × blocks	20	14.9813	0.7491		
i type epistasis × blocks	2	1.2933	0.6467	0.85^{NS}	0.86^{NS}
j+l type epistasis × blocks	18	13.6880	0.7604		1.02^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	9.0400	0.9040		1.71^{NS}
i type epistasis	1	2.3520	2.3520		4.44^{*}
j+l type epistasis	9	6.6880	0.7431		1.40^{NS}
Total epistasis × blocks	20	10.6027	0.5301		
i type epistasis × blocks	2	1.5547	0.7773	1.55^{NS}	1.47^{NS}
j+l type epistasis × blocks	18	9.0480	0.5027		0.95^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	19.4667	1.9467		2.25^{NS}
i type epistasis	1	0.6453	0.6453		0.75^{NS}
j+l type epistasis	9	18.8213	2.0913		2.42^{*}
Total epistasis × blocks	20	17.2853	0.8643		
i type epistasis × blocks	2	1.2667	0.6333	0.71^{NS}	0.73^{NS}
j+l type epistasis × blocks	18	16.0187	0.8899		1.03^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	15.2400	1.5240		2.25^{NS}
i type epistasis	1	1.6333	1.6333		2.41^{NS}
j+l type epistasis	9	13.6067	1.5119		2.23^{NS}
Total epistasis × blocks	20	13.5347	0.6767		
i type epistasis × blocks	2	2.2893	1.1447	1.83^{NS}	1.69^{NS}
j+l type epistasis × blocks	18	11.2453	0.6247		0.92^{NS}

Table 40E. Date of maximum flower (DMF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	261.4533	26.1453		1.36^{NS}
i type epistasis	1	38.0813	38.0813		1.98^{NS}
j+l type epistasis	9	223.3720	24.8191		1.29^{NS}
Total epistasis × blocks	20	384.5267	19.2263		
i type epistasis × blocks	2	17.7507	8.8753	0.44^{NS}	0.46^{NS}
j+l type epistasis × blocks	18	366.7760	20.3764		1.06^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	242.3733	24.2373		0.64^{NS}
i type epistasis	1	33.2853	33.2853		0.88^{NS}
j+l type epistasis	9	209.0880	23.2320		0.61^{NS}
Total epistasis × blocks	20	758.2987	37.9149		
i type epistasis × blocks	2	12.2267	6.1133	0.15^{NS}	0.16^{NS}
j+l type epistasis × blocks	18	746.0720	41.4484		1.09^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	117.5333	11.7533		0.81^{NS}
i type epistasis	1	7.1053	7.1053		0.49^{NS}
j+l type epistasis	9	110.4280	12.2698		0.84^{NS}
Total epistasis × blocks	20	291.8493	14.5925		
i type epistasis × blocks	2	37.7213	18.8607	1.34^{NS}	1.29^{NS}
j+l type epistasis × blocks	18	254.1280	14.1182		0.97^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	138.3333	13.8333		1.12^{NS}
i type epistasis	1	11.0413	11.0413		0.90^{NS}
j+l type epistasis	9	127.2920	14.1436		1.15^{NS}
Total epistasis × blocks	20	246.2120	12.3106		
i type epistasis × blocks	2	4.1880	2.0940	0.16^{NS}	0.17^{NS}
j+l type epistasis × blocks	18	242.0240	13.4458		1.09^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	631.1867	63.1187		0.94^{NS}
i type epistasis	1	404.8013	404.8013		6.03^{*}
j+l type epistasis	9	226.3853	25.1539		0.37^{NS}
Total epistasis × blocks	20	1341.8333	67.0917		
i type epistasis × blocks	2	242.0707	121.0353	1.98^{NS}	1.80^{NS}
j+l type epistasis × blocks	18	1099.7627	61.0979		0.91^{NS}

Table 40F. Plant height at maximum flower (PHMF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	434.5112	43.4511		0.74^{NS}
i type epistasis	1	51.5354	51.5354		0.87^{NS}
j+l type epistasis	9	382.9758	42.5529		0.72^{NS}
Total epistasis × blocks	20	1181.2972	59.0649		
i type epistasis × blocks	2	80.8159	40.4080	0.66^{NS}	0.68^{NS}
j+l type epistasis × blocks	18	1100.4813	61.1378		1.04^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	477.6472	47.7647		0.99^{NS}
i type epistasis	1	25.7613	25.7613		0.54^{NS}
j+l type epistasis	9	451.8859	50.2095		1.05^{NS}
Total epistasis × blocks	20	960.5105	48.0255		
i type epistasis × blocks	2	46.2622	23.1311	0.46^{NS}	0.48^{NS}
j+l type epistasis × blocks	18	914.2482	50.7916		1.06^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	488.1796	48.8180		2.31^{NS}
i type epistasis	1	5.5815	5.5815		0.26^{NS}
j+l type epistasis	9	482.5981	53.6220		2.53^{*}
Total epistasis × blocks	20	423.3777	21.1689		
i type epistasis × blocks	2	48.1847	24.0923	1.16^{NS}	1.14^{NS}
j+l type epistasis × blocks	18	375.1930	20.8441		0.98^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1392.9019	139.2902		2.14^{NS}
i type epistasis	1	83.8675	83.8675		1.29^{NS}
j+l type epistasis	9	1309.0343	145.4483		2.24^{NS}
Total epistasis × blocks	20	1301.3730	65.0687		
i type epistasis × blocks	2	84.7439	42.3720	0.63^{NS}	0.65^{NS}
j+l type epistasis × blocks	18	1216.6291	67.5905		1.04^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1100.6164	110.0616		2.32^{NS}
i type epistasis	1	248.0263	248.0263		5.23^{*}
j+l type epistasis	9	852.5901	94.7322		2.00^{NS}
Total epistasis × blocks	20	947.6248	47.3812		
i type epistasis × blocks	2	113.6883	56.8442	1.2^{NS}	1.20^{NS}
j+l type epistasis × blocks	18	833.9365	46.3298		0.98^{NS}

Table 40G. Number of primary branches at maximum flower (NPBMF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	9.0533	0.9053		1.00^{NS}
i type epistasis	1	1.1213	1.1213		1.23^{NS}
j+l type epistasis	9	7.9320	0.8813		0.97^{NS}
Total epistasis × blocks	20	18.1853	0.9093		
i type epistasis × blocks	2	1.7613	0.8807	0.97^{NS}	0.97^{NS}
j+l type epistasis × blocks	18	16.4240	0.9124		1.00^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	19.4167	1.9417		1.26^{NS}
i type epistasis	1	0.8003	0.8003		0.52^{NS}
j+l type epistasis	9	18.6163	2.0685		1.34^{NS}
Total epistasis × blocks	20	30.9317	1.5466		
i type epistasis × blocks	2	2.6910	1.3455	0.86^{NS}	0.87^{NS}
j+l type epistasis × blocks	18	28.2407	1.5689		1.01^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	9.4800	0.9480		1.85^{NS}
i type epistasis	1	1.2813	1.2813		2.50^{NS}
j+l type epistasis	9	8.1987	0.9110		1.78^{NS}
Total epistasis × blocks	20	10.2333	0.5117		
i type epistasis × blocks	2	0.4440	0.2220	0.41^{NS}	0.43^{NS}
j+l type epistasis × blocks	18	9.7893	0.5439		1.06^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	6.4667	0.6467		1.17^{NS}
i type epistasis	1	0.0120	0.0120		0.02^{NS}
j+l type epistasis	9	6.4547	0.7172		1.30^{NS}
Total epistasis × blocks	20	11.0600	0.5530		
i type epistasis × blocks	2	2.8227	1.4113	3.08^{NS}	2.55^{NS}
j+l type epistasis × blocks	18	8.2373	0.4576		0.83^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	12.7100	1.2710		2.12^{NS}
i type epistasis	1	0.1470	0.1470		0.24^{NS}
j+l type epistasis	9	12.5630	1.3959		2.32^{NS}
Total epistasis × blocks	20	12.0117	0.6006		
i type epistasis × blocks	2	0.1977	0.0988	0.15^{NS}	0.16^{NS}
j+l type epistasis × blocks	18	11.8140	0.6563		1.09^{NS}

Table 40H. Number secondary branches at maximum flower (NSBMF).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	63.4133	6.3413		1.76^{NS}
i type epistasis	1	6.1653	6.1653		1.71^{NS}
j+l type epistasis	9	57.2480	6.3609		1.77^{NS}
Total epistasis × blocks	20	71.9200	3.5960		
i type epistasis × blocks	2	8.6960	4.3480	1.24^{NS}	1.21^{NS}
j+l type epistasis × blocks	18	63.2240	3.5124		0.98^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	50.9867	5.0987		1.89^{NS}
i type epistasis	1	0.6453	0.6453		0.24^{NS}
j+l type epistasis	9	50.3413	5.5935		2.07^{NS}
Total epistasis × blocks	20	53.9680	2.6984		
i type epistasis × blocks	2	0.6053	0.3027	0.10^{NS}	0.11^{NS}
j+l type epistasis × blocks	18	53.3627	2.9646		1.10^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	43.1600	4.3160		2.33^{NS}
i type epistasis	1	0.3853	0.3853		0.21^{NS}
j+l type epistasis	9	42.7747	4.7527		2.57^{*}
Total epistasis × blocks	20	37.0227	1.8511		
i type epistasis × blocks	2	1.0413	0.5207	0.26^{NS}	0.28^{NS}
j+l type epistasis × blocks	18	35.9813	1.9990		1.08^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	73.6267	7.3627		2.05^{NS}
i type epistasis	1	14.4213	14.4213		4.01^{NS}
j+l type epistasis	9	59.2053	6.5784		1.83^{NS}
Total epistasis × blocks	20	71.9840	3.5992		
i type epistasis × blocks	2	7.6053	3.8027	1.06^{NS}	1.06^{NS}
j+l type epistasis × blocks	18	64.3787	3.5766		0.99^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	41.3467	4.1347		1.50^{NS}
i type epistasis	1	14.7000	14.7000		5.34^{*}
j+l type epistasis	9	26.6467	2.9607		1.08^{NS}
Total epistasis × blocks	20	55.0440	2.7522		
i type epistasis × blocks	2	6.5747	3.2873	1.22^{NS}	1.19^{NS}
j+l type epistasis × blocks	18	48.4693	2.6927		0.98^{NS}

Table 40I. Plant weight at harvest (PWH).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	22330.8863	2233.0886		2.12^{NS}
i type epistasis	1	5288.0963	5288.0963		5.02^{*}
j+l type epistasis	9	17042.7899	1893.6433		1.80^{NS}
Total epistasis × blocks	20	21048.0983	1052.4049		
i type epistasis × blocks	2	3564.6973	1782.3486	1.84^{NS}	1.69^{NS}
j+l type epistasis × blocks	18	17483.4010	971.3001		0.92^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	9128.2052	912.8205		0.83^{NS}
i type epistasis	1	388.3681	388.3681		0.35^{NS}
j+l type epistasis	9	8739.8371	971.0930		0.89^{NS}
Total epistasis × blocks	20	21897.7304	1094.8865		
i type epistasis × blocks	2	2289.8180	1144.9090	1.05^{NS}	1.05^{NS}
j+l type epistasis × blocks	18	19607.9124	1089.3285		0.99^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	21756.8871	2175.6887		2.01^{NS}
i type epistasis	1	2493.4083	2493.4083		2.30^{NS}
j+l type epistasis	9	19263.4787	2140.3865		1.98^{NS}
Total epistasis × blocks	20	21671.7823	1083.5891		
i type epistasis × blocks	2	1808.7297	904.3648	0.82^{NS}	0.83^{NS}
j+l type epistasis × blocks	18	19863.0527	1103.5029		1.02^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	40977.4875	4097.7487		1.51^{NS}
i type epistasis	1	6290.1120	6290.1120		2.32^{NS}
j+l type epistasis	9	34687.3755	3854.1528		1.42^{NS}
Total epistasis × blocks	20	54214.8042	2710.7402		
i type epistasis × blocks	2	3796.0394	1898.0197	0.68^{NS}	0.70^{NS}
j+l type epistasis × blocks	18	50418.7648	2801.0425		1.03^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	11071.3979	1107.1398		0.54^{NS}
i type epistasis	1	1349.3813	1349.3813		0.65^{NS}
j+l type epistasis	9	9722.0165	1080.2241		0.52^{NS}
Total epistasis × blocks	20	41322.1758	2066.1088		
i type epistasis × blocks	2	11051.5634	5525.7817	3.29^{NS}	2.67^{NS}
j+l type epistasis × blocks	18	30270.6124	1681.7007		0.81^{NS}

Table 40J. Number of pods per plant (NPd/P).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	12181.1600	1218.1160		1.90^{NS}
i type epistasis	1	5264.2253	5264.2253		8.21^{**}
j+l type epistasis	9	6916.9347	768.5483		1.20^{NS}
Total epistasis × blocks	20	12821.0280	641.0514		
i type epistasis × blocks	2	1811.7187	905.8593	1.48^{NS}	1.41^{NS}
j+l type epistasis × blocks	18	11009.3093	611.6283		0.95^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	13651.3600	1365.1360		1.53^{NS}
i type epistasis	1	3456.1333	3456.1333		3.86^{NS}
j+l type epistasis	9	10195.2267	1132.8030		1.27^{NS}
Total epistasis × blocks	20	17896.2347	894.8117		
i type epistasis × blocks	2	1747.7893	873.8947	0.97^{NS}	0.98^{NS}
j+l type epistasis × blocks	18	16148.4453	897.1359		1.00^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	27968.7867	2796.8787		1.40^{NS}
i type epistasis	1	1657.6333	1657.6333		0.83^{NS}
j+l type epistasis	9	26311.1533	2923.4615		1.47^{NS}
Total epistasis × blocks	20	39862.3347	1993.1167		
i type epistasis × blocks	2	3200.9960	1600.4980	0.79^{NS}	0.80^{NS}
j+l type epistasis × blocks	18	36661.3387	2036.7410		1.02^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	34379.5067	3437.9507		2.27^{NS}
i type epistasis	1	5707.6813	5707.6813		3.77^{NS}
j+l type epistasis	9	28671.8253	3185.7584		2.10^{NS}
Total epistasis × blocks	20	30293.9400	1514.6970		
i type epistasis × blocks	2	5160.9773	2580.4887	1.85^{NS}	1.70^{NS}
j+l type epistasis × blocks	18	25132.9627	1396.2757		0.92^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	46045.0000	4604.5000		1.69^{NS}
i type epistasis	1	11579.7453	11579.7453		4.26^{NS}
j+l type epistasis	9	34465.2547	3829.4727		1.41^{NS}
Total epistasis × blocks	20	54400.9267	2720.0463		
i type epistasis × blocks	2	8558.8493	4279.4247	1.68^{NS}	1.57^{NS}
j+l type epistasis × blocks	18	45842.0773	2546.7821		0.94^{NS}

Table 40K. Pod weight per plant (PdW/P).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1019.5848	101.9585		1.03^{NS}
i type epistasis	1	448.2241	448.2241		4.55^{*}
j+l type epistasis	9	571.3607	63.4845		0.64^{NS}
Total epistasis × blocks	20	1970.8127	98.5406		
i type epistasis × blocks	2	200.2937	100.1468	1.02^{NS}	1.02^{NS}
j+l type epistasis × blocks	18	1770.5190	98.3622		1.00^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1266.4695	126.6469		0.86^{NS}
i type epistasis	1	616.3520	616.3520		4.20^{NS}
j+l type epistasis	9	650.1175	72.2353		0.49^{NS}
Total epistasis × blocks	20	2935.2783	146.7639		
i type epistasis × blocks	2	313.0683	156.5342	1.07^{NS}	1.07^{NS}
j+l type epistasis × blocks	18	2622.2099	145.6783		0.99^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	2339.7051	233.9705		1.94^{NS}
i type epistasis	1	58.2413	58.2413		0.48^{NS}
j+l type epistasis	9	2281.4637	253.4960		2.11^{NS}
Total epistasis × blocks	20	2407.4599	120.3730		
i type epistasis × blocks	2	271.2106	135.6053	1.14^{NS}	1.13^{NS}
j+l type epistasis × blocks	18	2136.2493	118.6805		0.99^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1796.7044	179.6704		1.41^{NS}
i type epistasis	1	495.6455	495.6455		3.90^{NS}
j+l type epistasis	9	1301.0589	144.5621		1.14^{NS}
Total epistasis × blocks	20	2542.4516	127.1226		
i type epistasis × blocks	2	402.1221	201.0611	1.69^{NS}	1.58^{NS}
j+l type epistasis × blocks	18	2140.3294	118.9072		0.94^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	3219.8068	321.9807		1.41^{NS}
i type epistasis	1	930.4351	930.4351		4.07^{NS}
j+l type epistasis	9	2289.3716	254.3746		1.11^{NS}
Total epistasis × blocks	20	4569.3900	228.4695		
i type epistasis × blocks	2	1259.8731	629.9365	3.43^{NS}	2.76^{NS}
j+l type epistasis × blocks	18	3309.5169	183.8620		0.80^{NS}

Table 40L. Number of seeds per plant (NS/P).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	20765.5467	2076.5547		1.78^{NS}
i type epistasis	1	10319.3653	10319.3653		8.84^{**}
j+l type epistasis	9	10446.1813	1160.6868		0.99^{NS}
Total epistasis × blocks	20	23355.6960	1167.7848		
i type epistasis × blocks	2	3469.1813	1734.5907	1.57^{NS}	1.49^{NS}
j+l type epistasis × blocks	18	19886.5147	1104.8064		0.95^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	13946.4533	1394.6453		0.64^{NS}
i type epistasis	1	6026.5013	6026.5013		2.79^{NS}
j+l type epistasis	9	7919.9520	879.9947		0.41^{NS}
Total epistasis × blocks	20	43255.0080	2162.7504		
i type epistasis × blocks	2	3834.0000	1917.0000	0.88^{NS}	0.89^{NS}
j+l type epistasis × blocks	18	39421.0080	2190.0560		1.01^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	52078.5067	5207.8507		2.25^{NS}
i type epistasis	1	1218.5813	1218.5813		0.53^{NS}
j+l type epistasis	9	50859.9253	5651.1028		2.44^{*}
Total epistasis × blocks	20	46303.4720	2315.1736		
i type epistasis × blocks	2	5635.9813	2817.9907	1.25^{NS}	1.22^{NS}
j+l type epistasis × blocks	18	40667.4907	2259.3050		0.98^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	21660.1867	2166.0187		1.61^{NS}
i type epistasis	1	5647.1520	5647.1520		4.20^{NS}
j+l type epistasis	9	16013.0347	1779.2261		1.32^{NS}
Total epistasis × blocks	20	26922.0000	1346.1000		
i type epistasis × blocks	2	5708.3227	2854.1613	2.42^{NS}	2.12^{NS}
j+l type epistasis × blocks	18	21213.6773	1178.5376		0.88^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	79085.8533	7908.5853		1.39^{NS}
i type epistasis	1	8676.8013	8676.8013		1.53^{NS}
j+l type epistasis	9	70409.0520	7823.2280		1.38^{NS}
Total epistasis × blocks	20	113546.8840	5677.3442		
i type epistasis × blocks	2	17876.6520	8938.3260	1.68^{NS}	1.57^{NS}
j+l type epistasis × blocks	18	95670.2320	5315.0129		0.94^{NS}

Table 40M. Seed weight per plant (SW/P).

Cross-1

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	705.3592	70.5359		1.45^{NS}
i type epistasis	1	341.3813	341.3813		7.03^{*}
j+l type epistasis	9	363.9779	40.4420		0.83^{NS}
Total epistasis × blocks	20	970.6324	48.5316		
i type epistasis × blocks	2	127.4277	63.7138	1.36^{NS}	1.31^{NS}
j+l type epistasis × blocks	18	843.2048	46.8447		0.97^{NS}

Cross-2

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	681.4235	68.1423		0.97^{NS}
i type epistasis	1	293.2813	293.2813		4.16^{NS}
j+l type epistasis	9	388.1421	43.1269		0.61^{NS}
Total epistasis × blocks	20	1408.9290	70.4465		
i type epistasis × blocks	2	108.7344	54.3672	0.75^{NS}	0.77^{NS}
j+l type epistasis × blocks	18	1300.1946	72.2330		1.03^{NS}

Cross-3

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1170.7764	117.0776		1.78^{NS}
i type epistasis	1	27.4563	27.4563		0.42^{NS}
j+l type epistasis	9	1143.3201	127.0356		1.93^{NS}
Total epistasis × blocks	20	1315.1976	65.7599		
i type epistasis × blocks	2	233.0182	116.5091	1.94^{NS}	1.77^{NS}
j+l type epistasis × blocks	18	1082.1794	60.1211		0.91^{NS}

Cross-4

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	1451.3616	145.1362		2.32^{NS}
i type epistasis	1	181.7449	181.7449		2.91^{NS}
j+l type epistasis	9	1269.6167	141.0685		2.26^{NS}
Total epistasis × blocks	20	1250.2944	62.5147		
i type epistasis × blocks	2	305.9352	152.9676	2.92^{NS}	2.45^{NS}
j+l type epistasis × blocks	18	944.3592	52.4644		0.84^{NS}

Cross-5

Source of variation	df	SS	MS	VR_1	VR_2
Total epistasis	10	2024.0199	202.4020		1.02^{NS}
i type epistasis	1	841.2167	841.2167		4.23^{NS}
j+l type epistasis	9	1182.8032	131.4226		0.66^{NS}
Total epistasis × blocks	20	3973.0193	198.6510		
i type epistasis × blocks	2	1090.3321	545.1661	3.40^{NS}	2.74^{NS}
j+l type epistasis × blocks	18	2882.6872	160.1493		0.81^{NS}

* = Significant at 5% level, ** = Significant at 1% level and ^{NS} = non-significant.

Table 41A-41M. Analysis of variance for sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$) and differences ($\bar{L}_{1i} - \bar{L}_{2i}$) for thirteen characters of five crosses in chickpea.

Table 41A. Date of first flower (DFF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	874.6613	97.1846	12.3362 **	2.2563 NS
Sums × blocks	18	775.3147	43.0730	5.4675 **	
Within families	360	2836.0846	7.8780		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	311.3080	34.5898	3.8732 **	2.8089 *
Differences × blocks	18	221.6560	12.3142	1.3789 NS	
Within families	240	2143.3191	8.9305		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	963.9733	107.1081	14.8124 **	2.2768 NS
Sums × blocks	18	846.7627	47.0424	6.5057 **	
Within families	360	2603.1502	7.2310		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	141.1147	15.6794	1.8082 NS	2.3839 NS
Differences × blocks	18	118.3893	6.5772	0.7585 NS	
Within families	240	2081.1451	8.6714		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	1101.4787	122.3865	17.0612 **	9.3821 **
Sums × blocks	18	234.8053	13.0447	1.8185 NS	
Within families	360	2582.4176	7.1734		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	687.6587	76.4065	8.7395 **	7.1998 **
Differences × blocks	18	191.0213	10.6123	1.2138 NS	
Within families	240	2098.2469	8.7427		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	125.9587	13.9954	3.5517**	1.8062 NS
Sums × blocks	18	139.4773	7.7487	1.9665*	
Within families	360	1418.5616	3.9404		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	121.1947	13.4661	3.4723**	2.4478 NS
Differences × blocks	18	99.0213	5.5012	1.4185 NS	
Within families	240	930.7557	3.8781		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	878.0747	97.5639	13.5792 **	3.3551 *
Sums × blocks	18	523.4213	29.0790	4.0473 **	
Within families	360	2586.5220	7.1848		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	411.5213	45.7246	5.2670 **	3.8758 **
Differences × blocks	18	212.3547	11.7975	1.3589 NS	
Within families	240	2083.5324	8.6814		

Table 41B. Plant height at first flower (PHFF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	413.5336	45.9482	7.8398 **	4.2340 **
Sums × blocks	18	195.3410	10.8523	1.8516 NS	
Within families	360	2109.9158	5.8609		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	195.4941	21.7216	3.6198 **	3.4623 *
Differences × blocks	18	112.9288	6.2738	1.0455 NS	
Within families	240	1440.1984	6.0008		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	451.3040	50.1449	6.0520 **	2.0260 NS
Sums × blocks	18	445.5199	24.7511	2.9872 **	
Within families	360	2982.8270	8.2856		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	129.0203	14.3356	1.4005 NS	1.2401 NS
Differences × blocks	18	208.0772	11.5598	1.1293 NS	
Within families	240	2456.6448	10.2360		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	303.3550	33.7061	10.7445 **	5.7167 **
Sums × blocks	18	106.1291	5.8961	1.8795 NS	
Within families	360	1129.3388	3.1371		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	36.3891	4.0432	1.1843 NS	2.5013 *
Differences × blocks	18	29.0958	1.6164	0.4735 NS	
Within families	240	819.3337	3.4139		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	174.1231	19.3470	6.0555**	2.4872*
Sums × blocks	18	140.0152	7.7786	2.4347**	
Within families	360	1150.1767	3.1949		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	86.2265	9.5807	3.0738**	1.3603NS
Differences × blocks	18	126.7763	7.0431	2.2597**	
Within families	240	748.0551	3.1169		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	217.3708	24.1523	5.8131 **	1.6072 NS
Sums × blocks	18	270.4965	15.0276	3.6169 **	
Within families	360	1495.7179	4.1548		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	64.1692	7.1299	1.5770 NS	1.9928 NS
Differences × blocks	18	64.4000	3.5778	0.7913 NS	
Within families	240	1085.0965	4.5212		

Table 41C. Number of primary branches at first flower (NPBFF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	4.2187	0.4687	4.9380 **	2.0452 NS
Sums × blocks	18	4.1253	0.2292	2.4144 *	
Within families	360	34.1732	0.0949		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	1.2480	0.1387	1.4099 NS	1.0722 NS
Differences × blocks	18	2.3280	0.1293	1.3150 NS	
Within families	240	23.6037	0.0983		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	2.8267	0.3141	3.4983 **	2.1766 NS
Sums × blocks	18	2.5973	0.1443	1.6073 NS	
Within families	360	32.3200	0.0898		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	2.2147	0.2461	2.7306 **	1.0165 NS
Differences × blocks	18	4.3573	0.2421	2.6862 **	
Within families	240	21.6284	0.0901		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	2.9933	0.3326	3.2287 **	1.4111 NS
Sums × blocks	18	4.2427	0.2357	2.2882 *	
Within families	360	37.0836	0.1030		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	1.3667	0.1519	1.6131 NS	0.8065 NS
Differences × blocks	18	3.3893	0.1883	2.0003 *	
Within families	240	22.5927	0.0941		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	3.0413	0.3379	4.4781**	2.1641NS
Sums × blocks	18	2.8107	0.1561	2.0692**	
Within families	360	27.1664	0.0755		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	2.4533	0.2726	3.4346**	1.8236NS
Differences × blocks	18	2.6907	0.1495	1.8834*	
Within families	240	19.0480	0.0794		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	3.5147	0.3905	2.9302 **	1.0209 NS
Sums × blocks	18	6.8853	0.3825	2.8702 **	
Within families	360	47.9780	0.1333		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	0.3413	0.0379	0.2995 NS	0.2368 NS
Differences × blocks	18	2.8827	0.1601	1.2647 NS	
Within families	240	30.3904	0.1266		

Table 41D. Number of secondary branches at first flower (NSBFF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	6.2253	0.6917	2.3077 *	1.1681 NS
Sums × blocks	18	10.6587	0.5921	1.9756 *	
Within families	360	107.9038	0.2997		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	2.8280	0.3142	0.9996 NS	0.9847 NS
Differences × blocks	18	5.7440	0.3191	1.0151 NS	
Within families	240	75.4471	0.3144		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	3.1520	0.3502	1.4826 NS	0.1896 NS
Sums × blocks	18	33.2560	1.8476	7.8210 **	
Within families	360	85.0425	0.2362		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	2.5653	0.2850	1.0971 NS	0.7542 NS
Differences × blocks	18	6.8027	0.3779	1.4546 NS	
Within families	240	62.3563	0.2598		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	9.4880	1.0542	4.9279 **	1.3719 NS
Sums × blocks	18	13.8320	0.7684	3.5921 **	
Within families	360	77.0144	0.2139		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	5.3813	0.5979	2.5539 **	1.6281 NS
Differences × blocks	18	6.6107	0.3673	1.5686 NS	
Within families	240	56.1904	0.2341		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	6.5453	0.7273	3.8022**	1.5975NS
Sums × blocks	18	8.1947	0.4553	2.3801**	
Within families	360	68.8585	0.1913		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	2.5813	0.2868	1.4936NS	1.4267NS
Differences × blocks	18	3.6187	0.2010	1.0469NS	
Within families	240	46.0864	0.1920		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\bar{L}_{1i} + \bar{L}_{2i} + \bar{L}_{3i}$)	9	9.3897	1.0433	2.9990 **	1.5932 NS
Sums × blocks	18	11.7873	0.6549	1.8824 NS	
Within families	360	125.2381	0.3479		
Differences ($\bar{L}_{1i} - \bar{L}_{2i}$)	9	11.2213	1.2468	3.6584 **	3.2085 *
Differences × blocks	18	6.9947	0.3886	1.1402 NS	
Within families	240	81.7931	0.3408		

Table 41E. Date of maximum flower (DMF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	606.1720	67.3524	9.9730 **	3.2264 *
Sums × blocks	18	375.7520	20.8751	3.0910 **	
Within families	360	2431.2425	6.7535		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	158.4547	17.6061	2.2239 *	3.3167 *
Differences × blocks	18	95.5493	5.3083	0.6705 NS	
Within families	240	1900.0337	7.9168		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1250.6080	138.9564	19.0559 **	2.2401 NS
Sums × blocks	18	1116.5680	62.0316	8.5067 **	
Within families	360	2625.1353	7.2920		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	55.8400	6.2044	0.6745 NS	0.2527 NS
Differences × blocks	18	441.9920	24.5551	2.6694 **	
Within families	240	2207.6987	9.1987		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	467.0680	51.8964	12.2011 **	2.0461 NS
Sums × blocks	18	456.5440	25.3636	5.9631 **	
Within families	360	1531.2286	4.2534		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	100.7853	11.1984	2.1955 *	1.1969 NS
Differences × blocks	18	168.4107	9.3561	1.8343 *	
Within families	240	1224.1596	5.1007		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	283.8680	31.5409	7.9677**	1.7572NS
Sums × blocks	18	323.0960	17.9498	4.5344**	
Within families	360	1425.1006	3.9586		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	55.9320	6.2147	1.4776NS	1.0607NS
Differences × blocks	18	105.4640	5.8591	1.3931NS	
Within families	240	1009.4236	4.2059		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	219.7013	24.4113	2.6150 **	1.6129 NS
Sums × blocks	18	272.4347	15.1353	1.6214 *	
Within families	360	3360.5860	9.3350		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	270.4387	30.0487	3.0321 **	3.6531 **
Differences × blocks	18	148.0613	8.2256	0.8300 NS	
Within families	240	2378.4636	9.9103		

Table 41F. Plant height at maximum flower (PHMF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	2194.5723	243.8414	17.4633 **	4.0097 **
Sums × blocks	18	1094.6333	60.8130	4.3553 **	
Within families	360	5026.6972	13.9630		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	198.8041	22.0893	1.2335 NS	1.2097 NS
Differences × blocks	18	328.6783	18.2599	1.0196 NS	
Within families	240	4297.9762	17.9082		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	525.1301	58.3478	5.8476 **	1.1952 NS
Sums × blocks	18	878.7309	48.8184	4.8925 **	
Within families	360	3592.1196	9.9781		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	138.2238	15.3582	1.4161 NS	1.0762 NS
Differences × blocks	18	256.8716	14.2706	1.3159 NS	
Within families	240	2602.8221	10.8451		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	645.4113	71.7124	7.0120 **	0.9416 NS
Sums × blocks	18	1370.9403	76.1633	7.4472 **	
Within families	360	3681.7394	10.2271		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	391.6580	43.5176	3.3900 **	2.8922 *
Differences × blocks	18	270.8330	15.0463	1.1721 NS	
Within families	240	3080.9237	12.8372		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	226.4940	25.1660	3.2767**	0.4242NS
Sums × blocks	18	1067.8760	59.3264	7.7246**	
Within families	360	2764.8739	7.6802		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	329.8817	36.6535	4.5506**	2.0259NS
Differences × blocks	18	325.6592	18.0922	2.2462**	
Within families	240	1933.1109	8.0546		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	288.7860	32.0873	3.6126 **	0.4604 NS
Sums × blocks	18	1254.4969	69.6943	7.8467 **	
Within families	360	3197.5231	8.8820		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	267.9913	29.7768	3.8783 **	3.2977 *
Differences × blocks	18	162.5338	9.0297	1.1761 NS	
Within families	240	1842.6757	7.6778		

Table 41G. Number of primary branches at maximum flower (NPBMF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	6.4920	0.7213	4.4942 **	1.9298 NS
Sums × blocks	18	6.7280	0.3738	2.3288 **	
Within families	360	57.7812	0.1605		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	0.8920	0.0991	0.6251 NS	0.6904 NS
Differences × blocks	18	2.5840	0.1436	0.9054 NS	
Within families	240	38.0529	0.1586		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	16.4403	1.8267	10.2394 **	1.5422 NS
Sums × blocks	18	21.3207	1.1845	6.6395 **	
Within families	360	64.2240	0.1784		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	2.7283	0.3031	1.5122 NS	1.8531 NS
Differences × blocks	18	2.9447	0.1636	0.8161 NS	
Within families	240	48.1117	0.2005		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	5.6747	0.6305	4.1936 **	1.2558 NS
Sums × blocks	18	9.0373	0.5021	3.3393 **	
Within families	360	54.1273	0.1504		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	3.8787	0.4310	2.6894 **	2.4507 *
Differences × blocks	18	3.1653	0.1759	1.0974 NS	
Within families	240	38.4583	0.1602		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	3.4147	0.3794	3.8283**	0.8678NS
Sums × blocks	18	7.8693	0.4372	4.4113**	
Within families	360	35.6784	0.0991		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	1.3667	0.1519	1.6196NS	0.8259NS
Differences × blocks	18	3.3093	0.1839	1.9609*	
Within families	240	22.5020	0.0938		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	25.2808	2.8090	15.0879 **	6.3587 **
Sums × blocks	18	7.9515	0.4418	2.3728 **	
Within families	360	67.0227	0.1862		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	4.5387	0.5043	2.2291 *	4.2872 **
Differences × blocks	18	2.1173	0.1176	0.5200 NS	
Within families	240	54.2949	0.2262		

Table 41H. Number of secondary branches at maximum flower (NSBMF).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	70.7520	7.8613	13.3836 **	6.1889 **
Sums × blocks	18	22.8640	1.2702	2.1625 **	
Within families	360	211.4585	0.5874		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	5.7600	0.6400	1.1157 NS	0.6860 NS
Differences × blocks	18	16.7920	0.9329	1.6262 NS	
Within families	240	137.6747	0.5736		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	78.0053	8.6673	10.8428 **	2.3998 NS
Sums × blocks	18	65.0107	3.6117	4.5183 **	
Within families	360	287.7678	0.7994		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	23.1787	2.5754	2.9743 **	2.5132 *
Differences × blocks	18	18.4453	1.0247	1.1835 NS	
Within families	240	207.8096	0.8659		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	76.2987	8.4776	10.8968 **	4.6687 **
Sums × blocks	18	32.6853	1.8159	2.3340 *	
Within families	360	280.0772	0.7780		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	12.0013	1.3335	1.9175 *	2.0602 NS
Differences × blocks	18	11.6507	0.6473	0.9307 NS	
Within families	240	166.9031	0.6954		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	32.3533	3.5948	3.6573**	2.4207 NS
Sums × blocks	18	26.7307	1.4850	1.5109 NS	
Within families	360	353.8462	0.9829		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	32.3467	3.5941	3.4535**	22.1755**
Differences × blocks	18	2.9173	0.1621	0.1557 NS	
Within families	240	249.7680	1.0407		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	22.8587	2.5399	2.3819 *	1.7623 NS
Sums × blocks	18	25.9413	1.4412	1.3516 NS	
Within families	360	383.8656	1.0663		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	10.6147	1.1794	1.0776 NS	0.4116 NS
Differences × blocks	18	51.5733	2.8652	2.6179 **	
Within families	240	262.6684	1.0945		

Table 41I. Plant weight at harvest (PWH).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	23091.9130	2565.7681	9.0213 **	5.8109 **
Sums × blocks	18	7947.8352	441.5464	1.5525 NS	
Within families	360	102387.8846	284.4108		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	14473.3059	1608.1451	5.5684 **	3.4855 *
Differences × blocks	18	8304.8633	461.3813	1.5976 NS	
Within families	240	69312.1505	288.8006		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	45382.1566	5042.4618	12.6472 **	3.6884 **
Sums × blocks	18	24608.0534	1367.1141	3.4289 **	
Within families	360	143532.8159	398.7023		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	12005.4179	1333.9353	2.9532 **	3.2559 *
Differences × blocks	18	7374.4969	409.6943	0.9070 NS	
Within families	240	108406.7025	451.6946		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	11635.4608	1292.8290	4.3980 **	2.1270 *
Sums × blocks	18	10940.5093	607.8061	2.0676 *	
Within families	360	105826.0166	293.9612		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	3957.6801	439.7422	1.5670 NS	1.5450 NS
Differences × blocks	18	5123.3207	284.6289	1.0143 NS	
Within families	240	67350.6589	280.6277		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	26107.9166	2900.8796	4.3584 **	1.1762 NS
Sums × blocks	18	44391.8729	2466.2152	3.7053 **	
Within families	360	239609.8764	665.5830		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	16533.1445	1837.0161	2.1334 *	1.5756 NS
Differences × blocks	18	20985.8655	1165.8814	1.3540 NS	
Within families	240	206657.4371	861.0727		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	18139.8739	2015.5415	4.2141 **	0.8708 NS
Sums × blocks	18	41661.2869	2314.5159	4.8392 **	
Within families	360	172180.8112	478.2800		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	9727.2550	1080.8061	1.8238 NS	0.8972 NS
Differences × blocks	18	21684.0298	1204.6683	2.0328 **	
Within families	240	142229.5314	592.6230		

Table 41J. Number of pods per plant (NPd/P).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	10825.4947	1202.8327	7.7302 **	2.6730 *
Sums × blocks	18	8099.9653	449.9981	2.8920 **	
Within families	360	56016.6206	155.6017		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	8015.3880	890.5987	5.3279 **	6.1415 **
Differences × blocks	18	2610.2320	145.0129	0.8675 NS	
Within families	240	40117.5591	167.1565		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	22894.4587	2543.8287	6.0276 **	1.7353 NS
Sums × blocks	18	26386.3013	1465.9056	3.4735 **	
Within families	360	151930.8238	422.0301		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	8528.5067	947.6119	1.9659 *	1.0931 NS
Differences × blocks	18	15604.1253	866.8959	1.7985 *	
Within families	240	115685.2613	482.0219		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	21088.4653	2343.1628	7.2176 **	1.2272 NS
Sums × blocks	18	34368.3547	1909.3530	5.8814 **	
Within families	360	116871.6798	324.6436		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	2926.7480	325.1942	0.9021 NS	0.8314 NS
Differences × blocks	18	7040.1760	391.1209	1.0849 NS	
Within families	240	86519.3084	360.4971		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	12910.6253	1434.5139	4.2017**	1.0784NS
Sums × blocks	18	23944.1627	1330.2313	3.8963**	
Within families	360	122908.2665	341.4119		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	6176.9347	686.3261	1.5568NS	1.5328NS
Differences × blocks	18	8059.4853	447.7492	1.0156NS	
Within families	240	105807.0844	440.8629		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	65798.3747	7310.9305	7.6968 **	2.5322 *
Sums × blocks	18	51968.3253	2887.1292	3.0395 **	
Within families	360	341950.8286	949.8634		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	11551.1320	1283.4591	0.9425 NS	0.8153 NS
Differences × blocks	18	28336.2480	1574.2360	1.1561 NS	
Within families	240	326806.5756	1361.6941		

Table 41K. Pod weight per plant (PdW/P).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1572.8511	174.7612	9.0863 **	2.6902 *
Sums × blocks	18	1169.3251	64.9625	3.3776 **	
Within families	360	6924.0723	19.2335		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	792.9995	88.1111	4.3752 **	4.4602 **
Differences × blocks	18	355.5865	19.7548	0.9809 NS	
Within families	240	4833.3399	20.1389		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	3253.2791	361.4755	8.0742 **	2.4103 NS
Sums × blocks	18	2699.4293	149.9683	3.3498 **	
Within families	360	16116.9387	44.7693		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	1074.0721	119.3413	2.5061 **	1.5296 NS
Differences × blocks	18	1404.3662	78.0203	1.6384 *	
Within families	240	11428.9770	47.6207		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	2442.7309	271.4145	9.5607 **	1.3115 NS
Sums × blocks	18	3725.1749	206.9542	7.2900 **	
Within families	360	10219.8976	28.3886		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	439.4262	48.8251	1.5631 NS	1.1916 NS
Differences × blocks	18	737.5144	40.9730	1.3117 NS	
Within families	240	7496.8340	31.2368		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1610.7613	178.9735	4.7586**	1.0438NS
Sums × blocks	18	3086.3128	171.4618	4.5589**	
Within families	360	13539.8678	37.6107		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	467.9460	51.9940	1.0442NS	1.1666NS
Differences × blocks	18	802.2390	44.5688	0.8951NS	
Within families	240	11950.6251	49.7943		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	6165.5942	685.0660	9.7549 **	2.5295 *
Sums × blocks	18	4874.9256	270.8292	3.8565 **	
Within families	360	25281.9217	70.2276		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	812.7999	90.3111	0.8498 NS	0.5747 NS
Differences × blocks	18	2828.8366	157.1576	1.4788 NS	
Within families	240	25505.2869	106.2720		

Table 41L. Number of seeds per plant (NS/P).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	28077.7013	3119.7446	10.5001 **	2.9612 *
Sums × blocks	18	18963.8427	1053.5468	3.5459 **	
Within families	360	106961.3753	297.1149		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	17062.2987	1895.8110	5.5825 **	6.0097**
Differences × blocks	18	5678.2693	315.4594	0.9289 *	
Within families	240	81503.1056	339.5963		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	44619.4520	4957.7169	8.6937 **	3.0625*
Sums × blocks	18	29139.0160	1618.8342	2.8387**	
Within families	360	205296.5438	570.2682		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	15754.3787	1750.4865	2.7056**	1.7197NS
Differences × blocks	18	18322.3413	1017.9079	1.5733NS	
Within families	240	155278.9803	646.9958		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	34104.4653	3789.3850	8.6961 **	1.5631NS
Sums × blocks	18	43635.8987	2424.2166	5.5632 **	
Within families	360	156873.3492	435.7593		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	6984.4267	776.0474	1.5471 NS	1.0212NS
Differences × blocks	18	13679.1013	759.9501	1.5150 NS	
Within families	240	120389.5120	501.6230		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	16713.5147	1857.0572	4.6094**	1.8216NS
Sums × blocks	18	18350.4853	1019.4714	2.5305**	
Within families	360	145037.0984	402.8808		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	4407.0880	489.6764	1.0388NS	1.1994NS
Differences × blocks	18	7348.6160	408.2564	0.8660NS	
Within families	240	113137.5444	471.4064		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	184065.9320	20451.7702	9.1197 **	2.6649 *
Sums × blocks	18	138138.5360	7674.3631	3.4221 **	
Within families	360	807330.9918	2242.5861		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	24188.1453	2687.5717	0.8274 NS	0.6349NS
Differences × blocks	18	76190.0987	4232.7833	1.3031 NS	
Within families	240	779583.0929	3248.2629		

Table 41M. Seed weight per plant (SW/P).

Cross-1

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	836.2068	92.9119	7.9273 **	2.0520 NS
Sums × blocks	18	815.0019	45.2779	3.8631 **	
Within families	360	4219.3651	11.7205		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	680.2173	75.5797	6.0286 **	5.6267 **
Differences × blocks	18	241.7807	13.4323	1.0714 NS	
Within families	240	3008.8688	12.5370		

Cross-2

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1947.3032	216.3670	7.7856**	2.5217*
Sums × blocks	18	1544.4570	85.8032	3.0875**	
Within families	360	10004.6883	27.7908		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	609.9198	67.7689	2.2559*	1.6055NS
Differences × blocks	18	759.7774	42.2099	1.4051NS	
Within families	240	7209.6937	30.0404		

Cross-3

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1762.5033	195.8337	12.0929 **	1.9204 NS
Sums × blocks	18	1835.5545	101.9753	6.2971 **	
Within families	360	5829.8739	16.1941		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	323.9624	35.9958	1.8812 NS	1.3176 NS
Differences × blocks	18	491.7447	27.3192	1.4278 NS	
Within families	240	4592.1634	19.1340		

Cross-4

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	1281.8396	142.4266	7.3683**	1.5161 NS
Sums × blocks	18	1690.9385	93.9410	4.8599**	
Within families	360	6958.6673	19.3296		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	213.3299	23.7033	0.9543NS	1.0699 NS
Differences × blocks	18	398.7969	22.1554	0.8920 NS	
Within families	240	5961.2543	24.8386		

Cross-5

Item	df	SS	MS	VR_1	VR_2
Sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$)	9	4543.3311	504.8146	11.8936 **	3.2533 *
Sums × blocks	18	2793.0560	155.1698	3.6559 **	
Within families	360	15279.8747	42.4441		
Differences ($\overline{L}_{1i} - \overline{L}_{2i}$)	9	362.8940	40.3216	0.6280 NS	0.4522 NS
Differences × blocks	18	1604.8734	89.1596	1.3887 NS	
Within families	240	15409.3929	64.2058		

* = Significant at 5% level, ** = Significant at 1% level and NS = non-significant.

Table 42A-42E. Estimates of additive ($\hat{D}$) and dominance ($\hat{H}$) components of variation, degree of dominance ($\sqrt{H/D}$), heritability and direction of dominance ($r_{s,d}$) for thirteen characters of five crosses in chickpea.

Table 42A. Cross-1

Character	$\hat{D}$	$\hat{H}$	$\sqrt{H/D}$	h^2_n	h^2_b	r_{sd}
DFF	14.4297±1.4150	8.9102±0.7926	0.7891	0.4568	0.5979	-0.1395
PHFF	9.3589±1.1316	6.1791±0.6848	0.8110	0.4539	0.6037	0.1478
NPBFF	0.0639±0.1246	0.0037±0.0648	0.2402	0.2538	0.2612	0.1573
NSBFF	0.0265±0.2326	-0.0020±0.1293	-0.2714	0.0409	0.0394	0.5865**
DMF	12.3940±1.3648	4.9191±0.5808	0.6269	0.4797	0.5749	-0.4059*
PHMF	48.8076±2.8758	1.5318±1.0596	0.1811	0.6697	0.6802	0.4334*
NPBMF	0.0927±0.2089	-0.0178±0.0786	-0.4380	0.2444	0.2210	-0.2305
NSBMF	1.7576±0.3289	-0.1172±0.1631	-0.2582	0.7008	0.6774	0.0331
PWH	566.4591±7.3297	458.7055±5.4201	0.9010	0.4919	0.6910	-0.1136
NPd/P	200.7559±5.8852	298.2343±3.6373	1.2212	0.3617	0.6304	0.5600**
PdW/P	29.2797±2.1432	27.3425±1.2042	0.9701	0.4244	0.6225	0.6523**
NS/P	550.9861±8.7280	632.1406±5.4222	1.0702	0.4423	0.6961	0.6991**
SW/P	12.7024±1.6179	24.8590±1.0728	1.4010	0.3099	0.6131	0.6900**

Table 42B. Cross-2

Character	$\hat{D}$	$\hat{H}$	$\sqrt{H/D}$	h^2_n	h^2_b	r_{sd}
DFF	16.0175±1.6302	3.6409±0.6189	0.4812	0.5366	0.5976	0.2286
PHFF	6.7717±1.0858	1.1103±0.6283	0.4014	0.2595	0.2808	-0.1152
NPBFF	0.0453±0.0983	0.0016±0.0903	0.1952	0.1848	0.1881	-0.2280
NSBFF	-0.3993±0.2096	-0.0372±0.1088	0.3121	-1.7027	-1.7819	0.0999
DMF	20.5133±1.8933	-7.3403±0.7737	-0.5982	0.5858	0.4810	0.0263
PHMF	2.5412±1.6502	0.4350±0.7390	0.4014	0.1042	0.1131	-0.2193
NPBMF	0.1713±0.2199	0.0558±0.0825	0.5714	0.3195	0.3716	0.2776
NSBMF	1.3481±0.4125	0.6203±0.2315	0.6874	0.4602	0.5660	0.0614
PWH	980.0927±9.0809	369.6964±4.7318	0.6112	0.5690	0.6763	-0.0073
NPd/P	287.4462±10.7791	32.2864±6.6351	0.3414	0.2273	0.2401	-0.8861**
PdW/P	56.4019±3.6922	16.5284±2.1249	0.5410	0.3817	0.4377	-0.8693**
NS/P	890.3687±12.3035	293.0315±7.7335	0.5701	0.4221	0.4916	-0.8083**
SW/P	34.8170±2.9220	10.2236±1.6402	0.5401	0.3818	0.4379	-0.8898**

Table 42C. Cross-3

Character	$\hat{D}$	$\hat{H}$	$\sqrt{H/D}$	h^2_n	h^2_b	r_{sd}
DFF	29.1578±1.2480	26.3177±1.0056	0.9431	0.6297	0.9138	0.5963**
PHFF	7.4160±0.6943	0.9707±0.2806	0.3612	0.6043	0.6438	-0.1051
NPBFF	0.0258±0.0930	-0.0146±0.0780	-0.7511	0.1159	0.0832	-0.1723
NSBFF	0.0762±0.1654	0.0923±0.1267	1.1012	0.1325	0.2127	-0.0202
DMF	7.0754±1.2839	0.7369±0.5750	0.3210	0.4277	0.4500	-0.0805
PHMF	-1.1869±1.8651	11.3885±1.0593	-3.0976	-0.0423	0.1606	-0.5338**
NPBMF	0.0343±0.1429	0.1020±0.0937	1.7323	0.0914	0.2275	-0.0765
NSBMF	1.7765± 0.3664	0.2745± 0.1652	0.3912	0.6385	0.6878	0.4346*
PWH	182.6728± 5.7912	62.0453± 3.3049	0.5753	0.2991	0.3660	0.2556
NPd/P	115.6826± 8.0391	-26.3707± 3.5009	-0.4682	0.1433	0.1270	0.0400
PdW/P	17.1894± 2.6710	3.1408± 1.2386	0.4310	0.2201	0.2402	0.2062
NS/P	364.0449± 9.4552	6.4389± 5.2695	0.1312	0.2738	0.2762	-0.0867
SW/P	25.0289± 2.0556	3.4707± 1.0104	0.3711	0.4203	0.4495	0.0495

Table 42D. Cross-4

Character	$\hat{D}$	$\hat{H}$	$\sqrt{H/D}$	h^2_n	h^2_b	r_{sd}
DFF	1.6658±0.6543	3.1860±0.5338	1.3812	0.1645	0.3218	-0.3837*
PHFF	3.0849±0.6877	1.0150±0.4949	0.5710	0.3218	0.3747	-0.1687
NPBFF	0.0485±0.1025	0.0492±0.0881	1.0101	0.2189	0.3301	0.1935
NSBFF	0.0725±0.1548	0.0343±0.0903	0.6945	0.1616	0.1998	-0.0908
DMF	3.6243±0.8755	0.4377±0.1422	0.2012	0.3153	0.3214	-0.1463
PHMF	-9.1095±1.3697	7.4245±0.8755	-0.9028	-0.6932	-0.4107	-0.2931
NPBMF	-0.0154±0.1414	-0.0128±0.0778	0.9112	-0.0808	-0.1143	-0.2238
NSBMF	0.5626±0.3851	1.3728±0.2033	1.5614	0.2106	0.4676	-0.1807
PWH	115.9105±11.1067	268.4539±6.9530	1.5212	0.0598	0.1291	-0.0968
NPd/P	27.8087±7.4714	95.4308±4.5211	1.8512	0.0300	0.0814	0.0752
PdW/P	2.0031±2.7479	2.9701±1.2871	1.2211	0.0199	0.0346	-0.2071
NS/P	223.3562±6.7897	32.5680±4.1958	0.3810	0.2020	0.2167	0.1443
SW/P	12.9295±2.0448	0.6192±0.9817	0.2210	0.2192	0.2244	-0.2517

Table 42E. Cross-5

Character	$\hat{D}$	$\hat{H}$	$\sqrt{H/D}$	h^2_n	h^2_b	r_{sd}
DFF	18.2626±1.3472	13.5708±0.8786	0.8621	0.5207	0.7141	0.4011*
PHFF	2.4333±0.7623	1.4209±0.4690	0.7612	0.2205	0.2849	-0.1300
NPBFF	0.0021±0.1186	-0.0489±0.0721	-4.7871	0.0086	-0.0895	0.0871
NSBFF	0.1036±0.1722	0.3433±0.1460	1.8210	0.1212	0.3220	0.0823
DMF	2.4736±0.9803	8.7292±0.8267	1.8812	0.1052	0.2907	-0.2285
PHMF	-10.0285±1.6822	8.2989±0.8028	-0.9097	-0.9852	-0.5776	-0.2733
NPBMF	0.6313±0.2034	0.1547±0.0970	0.4924	0.6695	0.7515	0.4617*
NSBMF	0.2930±0.2559	-0.6743±0.2713	-1.5171	0.1129	-0.0170	-0.0479
PWH	-79.7265±9.3318	-49.5449±6.2607	0.7914	-0.0645	-0.0846	0.2849
NPd/P	1179.6804±17.9259	-116.3108±7.1808	-0.3140	0.3257	0.3097	-0.3021
PdW/P	110.4632±5.2044	-26.7386±2.0697	-0.4920	0.3696	0.3249	0.1338
NS/P	3407.3086±27.9208	-618.0846±10.8414	-0.4259	0.3747	0.3407	0.0774
SW/P	93.2386±4.1328	-19.5352±1.5190	-0.4577	0.4698	0.4206	0.1851

* = Significant at 5% level and ** = Significant at 1% level.

DISCUSSION

Epistasis plays a major role in the inheritance of quantitative traits in several crops (Thimmappa, 1987; Mukher *et al*., 1988 and Ram, 1997). Consequently, the estimates of additive and dominance components of genetic variation are biased due to presence of epistasis. Kearsey and Jinks (1968) suggested an extension of the design III of Comstock and Robinson (1952) to detect epistasis and estimates of additive ($\hat{D}$) and dominance ($\hat{H}$) components of variation with a high degree of accuracy. This procedure fulfils most of the requirements of a good genetical model and is superior to other multiple mating designs in many ways (Singh and Pawar, 2005) as follows:

i) The method allows unambiguous detection and partitioning of epistasis and its interaction with environment,

ii) provides unbiased estimates of additive ($\hat{D}$) and dominance ($\hat{H}$) components of genetic variation and their interactions with environment if epistasis is absent,

iii) the $\hat{D}$ and $\hat{H}$ components are estimated with equal statistical precision as the sampling errors associated with these two components are similar,

iv) the method has least restrictions and widest applicability as it is independent of allelic frequency, gene correlation and mating system and thus can be used to investigate both the segregating and non-segregating plant populations arising from different generations (F_2, backcross and homozygous lines),

v) requires relatively less experimental efforts as the number of crosses in this design does not increase tremendously with an increase in the number of parents as it does in other mating designs (particularly diallel, triallel and quadriallel),

vi) allows test of adequacy of the testers used to produce the experimental material and provides unbiased estimates of $\hat{D}$ and $\hat{H}$ components if inadequacy of testers is solely responsible for the failure of the additive-dominance model and

vii) if epistasis is present in the material investigated, the method provides relatively better estimates of $\hat{D}$ and $\hat{H}$ components than other multiple mating designs (Chahal and Singh, 1974; Pooni *et al*., 1978).

Furthermore, this approach is independent of both the gene frequencies and the mating system of the population to be investigated. Singh and Pawar (1998) advocated the use of TTC method in plant breeding for obtaining scientifically relevant results. In the present investigation, the inheritance of thirteen yield and yield related traits viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P has been studied to detect epistasis as well as estimates of additive and dominance component of variation in an unbiased way in five chickpea crosses viz., cross-1(6×8), cross-2 (8×1), cross-3 (8×4), cross-4 (4×8) and cross-5 (8×7).

Presence of epistasis was evidenced by the significance of variance of $\bar{L}_{1i} + \bar{L}_{2i} - 2\bar{L}_{3i}$. In the present study, total epistatic effect was non-significant for all the traits. This is in conformity with the study of Ram *et al*. (2007) in rice. Division of total epistasis into 'i' type (additive × additive) epistasis and 'j+l' type (additive × dominance and dominance × dominace) epistasis which indicated the involvement of 'i' type (additive × additive) epistasis for DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; NPBFF and NSBFF in cross-3 and PHFF, DMF, PHMF and NSBMF in cross-5 due to their significant values. The greater magnitude of 'i' type epistasis for these traits has significance in chickpea breeding where a linear directional and fixable component of genetic variation can be effectively exploited compared to non-directional and unfixable components (Ram *et al*., 2007). The influence of

additive × additive type of epistasis for plant height was also reported by Saleem *et al*. (2005b), Verma *et al.* (2006) and Ram *et al*. (2007) in rice. On the other hand, involvement of another epistatic component viz., additive × dominance and dominance × dominance i.e. 'j+l' type epistasis was found for DFF in cross-2; PHMF, NSBMF and NS/P in cross-3 and PHFF, NSBFF in cross-4. 'j+l' type epistasis noted for days to maturity in chickpea by Malhotra and Singh (1989), for pod length in peas by Rathore *et al*. (1995) and cowpea by Nagaraj *et al*. (2002). The result of the present study revealed that 'i' type epistasis was higher in magnitude than 'j+l' type epistasis for most of the studied character in all the crosses reflecting the importance of additive × additive non-allelic interaction in the genetic system controlling such characters. Similar results were reported by Allam (2003) and El-Mansy (2005). On the other hand, 'j+l' (unfixable) type epistasis was higher in magnitude than that of 'i' type epistasis for few of the traits in all the crosses. Ketata *et al*. (1976) proposed that standard hybridization and selection procedures could take benefit of epistasis if it is 'i' type epistasis (additive × additive) whereas, 'j+l' types of epistasis (additive × dominance + dominance × dominance) are not fixable by selection under self fertilization and therefore they would not be favourable for developing pure lines. Ketata *et al*. (1976) and Subbaraman and Rangaswamy (1989) reported that 'j+l' types of epistatic interactions could be useful in the development of hybrids. In the development of pure line cultivars, the masking effect of epistasis is of no importance if selection is postponed until virtually homozygosity is achieved because only additive type of epistasis is present in pure lines (Ketata *et al*., 1976). Because of additive and fixable nature of 'i' type epistasis, it has more importance for the development of pure line cultivars than 'j+l' types of epistasis in cereals (Subbaraman and Rangaswamy, 1989 and Dhiman *et al*., 1999). The interaction of total, 'i' type and 'j+l' types of epistasis with blocks were non-significant which indicated that these interactions were not sensitive to the

environments (blocks). These results were in line with those of many researchers viz., Kulshreshtha *et al*.(1993), Verma *et al*. (1994), Saleem *et al*. (2005a) and Saleem *et al*. (2005b) in rice and Prakash *et al*. (2004) in barley. However, most of the traits of the studied crosses showed non-significant epistatic effects indicating that there were no significant roles of epistasis in expression of these traits. Absence of epistasis was reported by several investigators for different traits in deferent crops. Khattak *et al*. (2002) reported no epistasis for pod clusters on main stem, pod clusters on branches, node of the first peduncle, node on main stem and average internodal length in mungbean under spring/summer. Verhalen *et al*. (1971) detected absence of epistasis for seed cotton yield, lint percentage and fiber properties of cotton. Subhan *et al*. (2002) observed non-significant epistasis for fiber length of cotton. De-Lin and Yan (2004) found no evidence of epistatic effect of panicle length and Saleem *et al*. (2005a) for number of grains per panicle, grain weight per panicle (g) and 1000 grain weight (g) in rice. Noori and Sokhansanj (2004) reported absence of epistasis for days to heading, spike weight, straw weight number of grains per spike, grain yield per plant, 1000 grain weight, whole plant weight and harvest index in spring wheat. Saravanan *et al* (2005) observed non-significant epistasis for days to first flower (cross-1 and 3) and fruit weight (cross-1) in bhendi. Husain (1997) reported absence of epistasis for plant height at maximum flower (cross 1, 2 and 3), number of fruits (cross-2 and 5), fruit weight at harvest (cross 4 and 5), number of secondary branch (cross 1, 3, 4 and 5) maximum flower (cross 1, 3, 4 and 5), number of leaf at maximum flower (cross 3, 4 and 5) and date of fruit ripening (cross 1, 2, 3 and 5) in chilli. Azad (2012) also reported absence of epistasis for plant height at first flower, number of primary branches at maximum flower, plant area per plant, pod weight per plant, number of pods per plant, number of seeds per plant and seed weight per plant in lentil. The non-significant estimates of epistasis may be due to involvement of common alleles or limited number of lines used (Wan

et al., 2005) or may be the environmental influences (Khattak *et al*., 2002). Therefore, more elaborate experiments are to be conducted to get a clear picture about the genetic systems controlling these characters and for in developing more efficient breeding procedure.

In the analysis of variance, sums ($\overline{L}_{1i} + \overline{L}_{2i} + \overline{L}_{3i}$) item was found to be significant for all the traits in all the crosses except NSBFF in cross-2 and differences ($\overline{L}_{1i} - \overline{L}_{2i}$) found to be significant for most of the traits when tested against their respective within families whereas, these two item when tested against their respective interaction (sums × blocks and differences × blocks), few traits were found to be significant. Sums was found to be significant for PHFF, DMF, PHMF, NSBMF, PWH, NPd/P, PdW/P and NS/P in cross-1; for PWH, NS/P and SW/P in cross-2; for DFF, PHFF, NSBMF and PWH in cross-3; for PHFF in cross-4 and for DFF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-5 when tested against sums × blocks interaction. These results revealed the present of additive genetic variance for these traits. Significant sums item for different characters in different crosses were reported by several workers such as, Singh and Singh (1976) in wheat, Randhawa *et al.* (1986) and Garg *et al*. (1987) in upland cotton, Verma and Yunus (1986) in bread wheat, Malhotra and Singh (1989) in chickpea and Azad (2012) in lentil. On the other hand, item differences was recorded as significant for DFF, PHFF, DMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for NSBMF and PWH in cross-2; for DFF, PHFF, PHMF and NPBMF in cross-3; only for NSBMF in cross-4 and for DFF, NSBFF, DMF, PHMF and NPBMF in cross-5 when tested against differences × blocks. These results indicated importance of dominance genetic variance for the inheritance of these traits. Significant differences for different characters in different crosses were obtained in chickpea by Malhotra and Singh (1989) and in bhendi by Saravanan *et al* (2005). The significant differences indicated that L_1 and L_2 testers were different from each others and

model provide precise test for epistasis and unbiased estimates of additive and dominance genetic components of variation if non-allelic interaction are absent as suggested by Kearsey and Jinks (1968) and Virk and Jinks (1977). The significant sums and differences observed in the present investigation indicated the importance of both additive and dominance variance in controlling the expression of these traits in chickpea.

Since most of the studied traits showed non-significant effect of epistasis, further analysis of additive and dominance genetic components were computed. In the absence of epistasis, unbiased estimation of additive and dominance components are possible (Jinks and Perkins, 1970). The results revealed that the magnitude of additive ($\hat{D}$) component was higher than that of dominance ($\hat{H}$) component for most of the traits viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH and PdW/P in cross-1; DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; DFF, PHFF, NPBFF, DMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3; PHFF, NSBFF, DMF, PHMF, NPBMF, NS/P and SW/P in cross-4 and DFF, PHFF, PHMF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-5 which indicated the presence of common alleles in testers increased the magnitude of additive components. The higher magnitude of additive components for most of the traits in each cross indicated the presence of common alleles in the testers and their cumulative effects in the expression of the traits which can be improved by pedigree method of selection. Again, high magnitude of additive variance in the above crosses for respective characters indicated the relative importance of fixable type of gene action in their inheritance. Usually the magnitude of additive component is higher than that of the dominance component for most of the quantitative traits (Singh *et al.*, 1997). On the other hand, the magnitude of dominance component ($\hat{H}$) was higher than that of the additive component for NPd/P, NS/P and SW/P in cross-1; for NSBFF, PHMF, NPBMF in cross-3; for DFF, NPBFF, NSBMF, PWH,

NPd/P and PdW/P in cross-4 and for NPBFF, NSBFF, DMF and NSBMF in cross-5 which indicated the presence of common alleles in testers increased the magnitude of the dominance components. The high magnitudes of dominance variance in the above crosses for the respective characters signify thereby the relative importance of non-fixable type of gene action. These results are in conformity with the findings of Khattak *et al.* (2002) in mungbean, Saravanan *et al*. (2005) in bhendi and Kumar *et al*. (2011a) in lentil. Both additive and dominance components were found to be significant in each cross for most of the characters which indicated the importance of both additive and dominance gene action. Similar results were obtained by Verma and Yunus (1986) in bread wheat, Khattak *et al*. (2002) in mungbean, Saleem *et al*. (2005b) in rice, Saravanan *et al.* (2005) in bhendi, Sofi *et al*. (2006) in maize and Kumar *et al*. (2011a) and Azad (2012) in lentil. The predominance of additive and non-additive gene action for yield and yield traits in rice have also been reported by Swain et *al.* (2003). Additive values are expected to be higher in self-pollinated crops like chickpea but the environment may influence the gene action. Jinks and Perkins (1970) observed that the components of variance changed to different degrees over environments if different kind of gene action were not equally sensitive to the environment.

Regarding degree of dominance, most of the traits in each cross showed incomplete dominance which indicated that the predominant nature of additive genetic component. Similar result were reported by Khattak *et al*. (2002) in mungbean, by Saravanan *et al*. (2005) in bhendi, by Zafar *et al*. (2008) in wheat and by Kumar *et al.* (2011a) in lentil. Over dominance gene effects were also noted in this materials for NPd/P and SW/P in cross-1; for NSBFF, PHMF and NPBMF in cross-3; for DFF, NSBMF, PWH, NPd/P and PdW/P in cross-4 and for NPBFF, NSBFF, DMF and NSBMF in cross-5 indicating the high influence of dominance component in the inheritance of these characters.

In the present investigation, both narrow sense and broad sense heritability were found as moderate to high for most of the characters and crosses. The high narrow sense heritability was noted for PHMF and NSBMF in cross-1; for DFF, NSBFF, DMF and PWH in cross-2; for DFF, PHFF and NSBMF in cross-3; only for PHMF in cross-4 and for DFF, PHMF and NPBMF in cross-5. On the other hand, high broad sense heritability was noted for DFF, PHFF, DMF, PHMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF, NSBFF, NSBMF and PWH in cross-2; for DFF, PHFF and NSBMF in cross-3 and for DFF, PHMF and NPBMF in cross-5. The high estimates of narrow sense heritability indicate the characters are largely governed by additive genes and simple selection for improvement of such characters would be rewarding. Noori and Sokhansanj (2004) found high narrow and high broad sense heritability in control but decreased in salinity condition. Sofi *et al.* (2006) and Azad (2012) found low to medium heritability in their study. Furthermore, the broad sense heritability was higher than narrow sense heritability in almost all the crosses for all the characters, as would be expected, because a greater portion of environmental and dominance components accounted for in the estimation of genotypic variance. Similar findings were reported by Khan and McNeilly (2005) in maize and Azad (2012) in lentil.

Positive and significant correlation between sums and differences was observed for NSBFF, PHMF, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF and NSBMF in cross-3 and for DFF and NPBMF in cross-5 indicated the direction of dominance towards decreasing parents whereas, negative and significant correlation between sums and differences was noted for DMF in cross-1; for NPd/P, PdW/P, NS/P and SW/P in cross-2; for PHMF in cross-3 and only for DFF in cross-4 indicated the direction of dominance towards increasing parents. The direction of dominance ($r_{s.d}$) of rest of the traits in different crosses was non-significant suggested dominant alleles

were dispersed between testers; therefore did not show any proof of directional dominance for these characters (Saleem *et al*., 2009).

Though, the estimation of total epistasis was non-significant for all the traits that indicated there was no significant roles of epistatic effect in expression of any traits in this study but after partitioning of epistasis, it was found the involvement of 'i' type (additive × additive) of epistasis for DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for NPBFF and NSBFF in cross-3 and for PHFF, DMF, PHMF and NSBMF in cross-5. It is recognized that the additive × additive ('i') type of epistasis can be fixed in early generation due to its linear directional nature. Therefore, pure lines can be developed through simple selection procedure of the above characters in the respective crosses. The predominance of additive and dominance type of gene action for yield and some of the important yield traits also observed in the present work, as both additive and dominance gene effects were significant for most of the characters, simple selection procedures in the immediate progenies will not help in achieving improvement in the characters. Thus, it can be exploited effectively following random intermating in segregating generations and selection in later generation.

Considering all the three genetic study viz., generation mean analysis, biparental progeny analysis (BIPs) and triple test cross analysis (TTC), the traits such as PWH, NPd/P and NS/P in cross-2; NSBFF and NSBMF in cross-3 and NPBMF in cross-4 showed non-significant χ^2-values regarding Cavalli's joint scaling test suggesting additive-dominance model was adequate for these characters in respective crosses. Among these traits, PWH and NPd/P in cross-2 showed no linkage and no epistasis regarding BIPs and TTC analysis which confirmed that only the additive-dominance model is really adequate to explain the relationship among the generations and hence only additive and dominant genes are responsible in the inheritance of these two characters which would likely be helpful in doing successful breeding plan easily for the development of potential

lines in chickpea. Rest of the characters viz., NSBFF and NSBMF in cross-3 showed no linkage but epistasis is present suggesting except additive and dominant gene, non-allelic interaction can play an important role in the inheritance of these characters. While, the character NS/P in cross-2 and NPBMF in cross-4 exhibited no epistasis but linkage is present suggesting linkage may be a part to the inheritance of these characters. Again, magnitude of additive genetic component of variation was higher than that of the dominance component for NSBMF in cross-2 and NS/P and SW/P in cross-4. Besides, the traits viz., DFF, NSBFF, DMF, PHMF and NPBMF in cross-2; NPBFF, PdW/P, NS/P and SW/P in cross-3; DMF and NPBMF in cross-4 and DFF, PHMF, PdW/P, NS/P and SW/P in cross-5 showed higher additive component than that of dominance component in both genetic study-2 and genetic study-3. Therefore, selection for these traits governed by additive component of variation will be very effective for further breeding work. Regarding heritability in narrow sense characters viz., DFF, NSBFF, DMF and PWH in cross-2; DFF, PHFF and NSBMF in cross-3; PHMF in cross-4 and PHMF and NPBMF in cross-5 were found to be high in both genetic study-1 and genetic study-3. High heritability indicates that the environment have least influenced to these characters and selection based on mean would be successful in improving these traits.

Again on the basis of TTC, the traits viz., DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; NPBFF and NSBFF in cross-3 and PHFF, DMF, PHMF and NSBMF in cross-5 exhibited ‘i’ type of epistasis suggesting pure lines can be developed for these traits through simple selection procedure.

SUMMARY

Epistatic genetic effects play an important role in determining genetic differences in several plant populations but all biometrical genetic procedures except triple test cross analysis have one of their important assumptions that there is absence of epistasis in populations. Thus, the triple test cross analysis of five crosses in chickpea was performed to detect epistasis precisely. Thirteen quantitative characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at 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) were considered for this work.

In the present study, total epistatic effect was found to be non-significant for all the traits under studied. But partitioning of total epistasis indicated the involvement of 'i' type (additive × additive) epistasis for DFF, PHFF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for NPBFF and NSBFF in cross-3 and for PHFF, DMF, PHMF and NSBMF in cross-5 and involvement of 'j+l' type epistasis for DFF in cross-2; for PHMF, NSBMF and NS/P in cross-3 and for PHFF, NSBFF in cross-4. In present study, 'i' type epistasis was higher in magnitude than 'j+l' type epistasis in maximum cases which reflecting the importance of additive × additive genetic interaction controlling such characters. Whereas, 'i' type, 'j+l' type or total epistasis was found to be non-significant for most of the traits indicating that there were no significant roles of epistasis in expression of these traits in this study. Item sums were significant for PHFF, DMF, PHMF, NSBMF, PWH, NPd/P, PdW/P and NS/P in cross-1; PWH, NS/P

and SW/P in cross-2; for DFF, PHFF, NSBMF and PWH in cross-3; for PHFF in cross-4 and for DFF, NPBMF, NPd/P, PdW/P, NS/P and SW/P in cross-5 revealed the importance of additive genetic variance for these traits. On the other hand, item differences was significant for DFF, PHFF, DMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-1; for NSBMF and PWH in cross-2; for DFF, PHFF, PHMF and NPBMF in cross-3; for NSBMF in cross-4 and for DFF, NSBFF, DMF, PHMF and NPBMF in cross-5 indicated importance of dominance genetic variance for the inheritance of these traits.

In the absence of epistasis, unbiased estimation of additive and dominance components were computed and noted that the magnitude of additive component was higher than that of dominance component for most of the traits viz., DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH and PdW/P in cross-1; DFF, PHFF, NPBFF, NSBFF, DMF, PHMF, NPBMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-2; DFF, PHFF, NPBFF, DMF, NSBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-3; PHFF, NSBFF, DMF, PHMF, NPBMF, NS/P and SW/P in cross-4 and DFF, PHFF, PHMF, NPBMF, PWH, NPd/P, PdW/P, NS/P and SW/P in cross-5 indicated the presence of common alleles in testers increased the magnitude of additive components. These traits can be improved by pedigree method of selection. On the other hand, the magnitude of dominance component was higher than that of the additive component for NPd/P, NS/P and SW/P in cross-1; for NSBFF, PHMF and NPBMF in cross-3; for DFF, NPBFF, NSBMF, PWH, NPd/P and PdW/P in cross-4 and for NPBFF, NSBFF, DMF and NSBMF in cross-5 indicated the presence of common alleles in testers increased the magnitude of the dominance components. The high magnitudes of dominance variance in above crosses for the respective characters signify thereby the relative importance of non-fixable type of gene actions.

Incomplete dominance was noted for most of the traits in each cross which indicated that the predominant nature of additive genetic component. In the present work, both broad sense and narrow sense heritability estimates were found to be moderate to high for most of the characters. The broad sense heritability was found higher than that of narrow sense heritability in all the crosses for most of the characters. Positive and significant correlation between sums and differences found for NSBFF, PHMF, NPd/P, PdW/P, NS/P and SW/P in cross-1; for DFF and NSBMF in cross-3 and for DFF and NPBMF in cross-5 indicated that the direction of dominance towards decreasing parents while, negative and significant correlation between sums and differences observed for DMF in cross-1; for NPd/P, PdW/P, NS/P and SW/P in cross-2; for PHMF in cross-3 and only for DFF in cross-4 indicated the direction of dominance towards increasing parents. The rest of the traits showed non-significant correlation indicating no evidence of directional dominance in these traits.

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