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Study of Genetic Architecture on yield and Some of the Yield Components in Lentil (Lens Culinaris Medic.)

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STUDY OF GENETIC ARCHITECTURE ONYIELD AND SOME OF THE YIELD COMPONENTS IN LENTIL (*Lens culinaris* Medic.)

A Thesis

Submitted to the University of Rajshahi

in fulfillment of the requirements for the degree of

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in the
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and Biotechnology

BY

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DEPARTMENT OF GENETIC ENGINEERING
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UNIVERSITY OF RAJSHAHI
RAJSHAHI, BANGLADESH

Dedicated

To

My Beloved Parents

DECLARATION

I, hereby, declare that the research work as a thesis is the result of my own investigation, which is submitted for the fulfillment of the degree of Doctor of Philosophy in Genetic Engineering and Biotechnology, Faculty of Life and Earth Science of the University of Rajshahi, Bangladesh.

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Supervisor

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27.06.2013

(Anuradha Roy Chowdhury)
Candidate

CERTIFICATE

I, hereby, certify that the work embodied in this thesis has not been submitted in substance for any degree, and has not been concurrently submitted in candidature for any other degree.

Anuradha Roy Chowdhury
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ABSTRACT

Inheritance of the yield and yield contributing characters of six lines of lentil (*Lens culinaris* Medic.) was studied in 2005-2009 through diallel, combining ability, heterosis and model fitting in the first part (Part I) consisting of two experiments. Twelve yield contributing characters viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), number of secondary branches at maximum flower (NSBMF), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) were studied in a six parental half diallel analysis in experiment I. In experiment II, above characters were considered for study of heterosis and model fitting.

The combining ability analysis in lentil showed that the variation due to gca was found to be significant for the characters namedly DF, PHFF, CAMF and RW and variance due to sca was non significant for all of the characters. Component variance due to gca (σ^2g) was higher than that of due to sca (σ^2s) for DF, NPBFF, CAMF, PdWPP, SWPP and IPlW. Additive genetic component (σ^2A) was greater than dominance component (σ^2D) for DF, PHFF, NPBFF, CAMF, PdWPP, SWPP, IPlW and RW. From the comparison of gca effects of individual parents for twelve characters, positive significant gca effect was seen for DF by P_4, for PHFF by P_2 and P_3, for NSBFF by P_4, for CAMF by P_2 and P_3, for IPlW by P_2 and for RW by P_2 and P_4. The negative and significant gca effect was obtained for DF by P_3, for PHFF by P_1 and for NPBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW by P_6 in experiment I. P_4 for NSBFF, NPdPP, NSPP and RW, P_2 for PHFF, CAMF, PdWPP SWPP and IPlW, P_5 for NPBFF and NSBMF and P_3 for DF performed as better combiner. $P_1 \times P_2$ performed good specific combiner for NSBFF, PdWPP, SWPP and RW and $P_1 \times P_3$ for CAMF, NSBMF, NPdPP and IPlW. In the present study, the ratios of $[(H_1/D)]^{1/2}$ suggested over dominance for NSBFF, NSPP, SWPP, IPlW and RW, whereas partial dominance was recorded for the remaining characters except NPBFF, NPdPP and PdWPP in F_1 generation. In F_2 generation over dominance was found for DF, NPBFF, NSBFF, NSBMF, NPdPP, NSPP and SWPP, whereas partial dominance was shown by PHFF, CAMF, IPlW and RW. Only one group of genes controlled the characters namedly DF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW and two group of genes controlled PHFF in F_1 generation, whereas in F_2 generation one group of genes controlled the characters viz. DF, PHFF,

NSBFF; six groups of genes controlled the character NPBFF; four groups of genes controlled the characters viz., CAMF and NSBMF; three groups of genes controlled NPdPP; two groups of genes controlled PdWPP, NSPP and SWPP; ten groups of genes controlled IPlW and seven groups of genes controlled RW. From graphical analysis, it was evident that array 1 possessed dominant gene in excess for PHFF of replication 2, for CAMF of replication 2 and for IPlW of replication 2 in F_1 generation. Array 2 possessed dominant gene in excess for RW of replication 2, for DF and for NSPP of replication total in F_1 generation and this array possessed dominant gene in excess for NPBFF of replication 2, for NSBFF of replication 1, for PdWPP of replication 2, for NPBFF, NPdPP and PdWPP of replication total in F_2 generation. Array 3 possessed dominant gene in excess for NSBMF of replication 2 and for NPdPP of replication 2 in F_1 generation and for NPdPP of replication 1, for SWPP of replication 1 and for SWPP of replication 1 in F_2 generation. Array 4 possessed dominant gene in excess for NSPP of replication 1, for PHFF, NSBMF and NPdPP of replication total in F_1 generation and for NPBFF of replication 1, for CAMF of replication 2 and for IPlW in F_2 generation. Array 5 possessed dominant gene in excess for CAMF of replication 1, for NPdPP of replication 1, for IPlW of replication 1, for NPBFF, CAMF and IPlW of replication total in F_1 generation and for NSBMF of replication 2, for NSPP of replication 1, for SWPP of replication 2, for IPlW of replication 1, for RW of replication 1, for NSPP, SWPP and RW of replication total in F_2 generation. Array 6 possessed dominant gene in excess for PHFF of replication 1, for NPBFF of replication 1, for NSBMF replication 1, for NSPP of replication 2, for PdWPP and SWPP in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for CAMF of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 1 possessed recessive gene in excess for PHFF of replication 1, for CAMF of replication 1, for NSBMF of replication 1, for NPdPP of replication 1, for NPdPP of replication 2, for NSPP of replication 1, for IPlW of replication 1, for PHFF, CAMF, NSBMF, NPdPP, PdWPP, SWPP and IPlW of replication total in F_1 generation. Array 1 possessed recessive gene in excess for NPBFF of replication 1, for CAMF of replication 2, for PdWPP of replication 2, for NSPP of replication 1, for SWPP of replication 1, for SWPP of replication 2, for NPdPP, PdWPP, NSPP, SWPP and IPlW of replication total in F_2 generation. Array 2 possessed recessive gene in excess for NPBFF of replication 1 and for NSPP of replication 2 in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for IPlW of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 3 possessed recessive gene in excess for DF and NSPP of replication total in F_1 generation. This array possessed excess of recessive genes for NPBFF of replication 2, for CAMF of replication 1, for NSBMF of replication 2 and for NPBFF of replication total in F_2 generation. Array 4 possessed recessive gene in excess for PHFF of replication 2, for CAMF of replication 2, for IPlW of replication 2 and for RW of replication 2 in F_1 generation. This array possessed recessive in excess for NSBFF of replication 1, for RW of replication 1 and for RW of replication total in F_2 generation. Array 5 possessed recessive gene in excess for NSBMF of replication 2 in F_1 generation. Array 6 possessed recessive gene in excess for NPBFF in F_1 generation and for NPdPP of replication 1 in F_2 generation. Array 3 possessed more or less equal proportion of dominant and recessive genes for most of the characters in both generations. In heterosis study, $P_1 \times P_2$ showed the highest value of mid parent and better parent heterosis for NSBFF, PdWPP, SWPP and RW. From joint scaling test, it was revealed that non significant χ^2 value was obtained by all of the crosses for SWPP. From the inheritance study through diallel and heterosis, it was found that $P_1 \times P_2$ and $P_1 \times P_3$ was the promising crosses in respect of PdWPP, SWPP and RW. These crosses appeared important for heterosis study.

In second part (Part-II) of the present investigation, F_1 materials of half diallel crosses for nine characters viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), pod weight per plant (PdWPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) were studied for correlation, path-coefficient and selection index. Phenotypic component of variation (σ^2p) was higher than genotypic (σ^2g) component of variation. The highest genotypic and phenotypic components of variations were obtained for CAMF. In the present materials, high genotypic values caused high phenotypic values. In this investigation, genotypic correlations were higher than the respective phenotypic correlations for most of the characters. SWPP showed highly significant and positive correlation co efficient with other characters except NPBFF at genotypic level and except NPBFF and DF at phenotypic level. The highest significant and positive genotypic correlation coefficient was recorded for NSBFF with PdWPP at genotypic level and PdWPP with SWPP at phenotypic level. PdWPP had the highest positive direct effect on SWPP at both genotypic and phenotypic level. The maximum expected genetic gain of 4603.196% was found when NPBFF and RW were included in the discriminant function. These two characters had high correlation coefficient with most of the characters studied as well as direct effect at genotypic level may be considered as primary yield components.

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GENERAL INTRODUCTION

GENERAL INTRODUCTION

Lentils, botanically known as *Lens culinaris* Medic. have been a source of sustenance for our ancestors since prehistoric times. The word lentil comes from the Latin lens, and indeed, this bean cousin is shaped like the double convex optic lens which took its name from the lentil. Lentil is a pulse (grain legume) crop. It is the most likely the oldest cultivated legume and is believed to be native to southwestern Asia, perhaps northern Syria. Evidences present that the spread of lentil eastward into the Indo-Gangetic Plain dates to around 2000 B.C., but previous contacts between Mohenjo-Daro and the Sumerians and Akkadians of Mesopotamia are well documented. Lentil might have been introduced into the Indus valley earlier (Cubero, 1981). It was written by De Candolle (1882) that on linguistic evidence 'it may be supposed that the lentil was unknown in this country (India) before the invasion of the Sanskrit-speaking race.'

The botanical features of *Lens culinaris* (cultivated lentil) can be described as annual bushy herb, slender almost erect or sub erect, much branched, stems slender, angular, 15-75 cm height. The leaves are alternate, compound, and pinnate and leaflets are 4-7 pairs, alternate or opposite and oval. Pods are oblong, flattened or compressed and smooth. Seed is biconvex, rounded and small. Flowers are small, pale blue, purple, and white or pink. In axillary, 1-4 flowered racemes are situated. 1-4 flowers are borne on a single peduncle in lentil. The flowers are hermaphrodite (have both male and female organs) and are pollinated by cheistogomy (self-pollinating without flowers ever opening).

Classification:
- Kingdom: Plantae
  - Division: Magnoliophyta
    - Class: Magnoliopsida
      - Order: Fabales
        - Family: Fabaceae
          - Subfamily: Faboideae
            - Tribe: Vicieae
              - Genus: *Lens*
                - Species: *L. culinaris*
                  - Binomial name
                  - *Lens culinaris* Medic.

The chromosome number of lentil is 2n=14.

There are many varieties of lentil grown and eaten throughout the world, but the three most common types used in cooking are brown, red and green.

Brown lentils: They also known as continental or Egyptian lentils, are generally the least expensive and more easily obtained. They are mild in flavour and hold their shape well after cooking, although they easily turn mushy if overcooked. They can be cooked in about 35 minutes although if anyone wants to ensure they remain firm, then add oil to the cooking water and cook them for a shorter period, about 20 minutes.

Red lentils: They are less common than brown lentils and have a slightly sweeter taste than the brown. They take a little less time to cook although they tend to become somewhat mushy and are therefore more suitable to soups and stews.

Green lentils: They, also known as Puy or French lentils, are the finest but most expensive lentils. They are the meatiest, richest tasting and remain quite firm after cooking making them an excellent choice for salads. Originally grown in the volcanic soils of Puy in France, these are now also grown in North America and Italy.

Two less common but interesting lentils are Beluga Lentils which, as the name implies, are black and once cooked they glisten which makes them look like beluga caviar and White Lentils (skinned and split Black Lentils) which having very smooth texture are suitable for chilled vegetable salads and stuffing mixes.

Lentil is an important crop in Bangladesh. It is the second most important pulse crop in terms of both area and production and rates the highest consumer preference in Bangladesh. It is generally grown in the traditional aus (rainfed) rice/jute/fallow-lentil cropping pattern. This is an annual semi erect temperate plant grows well in winter season. It provides a good yield on light, fertile and a well-drained soil. The black and alluvial type of soil has all these suitability factors. In case of excessive rainfall or humidity, these may affect the plantation of this crop negatively. This may reduce the yield of this crop. It takes of around 85 days to reach its maturity. The lower pods turn brown to yellowish brown in color at maturity. It is a winter season crop and most is planted after rice on a roughly prepared seed bed with one or two ploughing and then the seed is broadcast followed by one more ploughing. This crop matures in a shorter growing period than chickpea. This crop is cultivated as a sole or mixed crop with mustard (*Brassica campestris* L.) and to a very small extent as a relay crop with rainy season rice.

It is lens shaped edible seed, which is one of the most ancient cultivated food that has a great importance as in the case of the other dry seeds for the low water content and impervious seed coats which enhance this value for storage purposes and increase their longevity.

Masur crop is extremely good in nitrogen fixation from atmosphere. It forms nitrogen nodules in the soil and these rejuvenate the nutrients and keep the soil productive for a long time.

More than 80% people of Bangladesh are suffering from malnutrition. Lentil is a good source of protein and some other nutrients. So, by adding lentil to their daily diets, suffering people from malnutrition can be relieved to some extent. However, besides a high level of proteins, lentils also contain a rich supply of copper and selenium, and are a good source of iron, vitamin B_6, folate, and zinc (Bender and Bender, 2005). Iron is particularly important for adolescents, and menstruating or pregnant women. In general, lentils are a good source of dietary fiber, but red (or pink) lentils contain a lower concentration of fiber than green lentils (11 percent rather than 31 percent, ARS 2008). Pulses are the cheapest source of proteins and essential amino acid 'lysine', the deficiency of which in the dietary is likely to lead to mental and physical dwarfism.

Lentil is the oldest food legume which has been known to the mankind. The seeds of lentil are rich in carbohydrates also. For this above reasons, this plant is so popular in the vegetarian population of the world.

Health magazine has selected lentils as one of the five healthiest foods (Raymond, 2006). Lentils are often mixed with grains, such as rice, which results in a complete protein dish. The nutritional value of lentil is low because it is deficient in the amino acids methionine and cystine. It is used in soups, stews, casseroles and salad dishes.

Contribution of lentils to heart health lies not just in their fiber, but in the significant amounts of folate and magnesium they supply. Folate helps lower levels of homocysteine, an amino acid that is an intermediate product in an important metabolic process called the methylation cycle and when folate and vitamin B_6 are present, homocysteine is converted into cysteine or methionine and when these B vitamins are not available, levels of homocysteine increase in the bloodstream with potential for the homocysteine to damage artery walls and serve as a risk factor for heart disease.

Lentils' magnesium is a calcium channel blocker. Sufficient magnesium aid veins and arteries to relax, which lessens resistance and improves the flow of blood, oxygen, and nutrients throughout the body. Studies show that a deficiency of magnesium is not only associated with heart attack but that immediately following a heart attack, lack of sufficient magnesium promotes free radical injury to the heart.

In addition to its beneficial effects on the digestive system and the heart, soluble fiber helps stabilize blood sugar levels and legumes such as lentils can help balance blood sugar levels, while providing steady slow-burning energy.

Beside this, grain legumes provide rich fodder to the milch and draft animals.

Table 1. Nutrients of lentils.

Nutrient	Amount per 100 grams
Carbohydrates	57.09 g
Fat (Lipids)	0.96 g
Fiber, total dietary	30.5 g
Protein	28.06 g
Water	11.19 g
Calcium, Ca	51 mg
Copper, Cu	0.852 mg
Iron, Fe	9.02 mg
Magnesium, Mg	107 mg
Manganese, Mn	1.429 mg
Phosphorus, P	454 mg
Potassium, K	905 mg
Sodium, Na	10 mg
Zinc, Zn	3.61 mg
Niacin	2.621 mg
Riboflavin	0.245 mg
Thiamin	0.475 mg
Vitamin A, IU	39 IU
Vitamin B-6	0.535 mg
Vitamin C, total ascorbic acid	6.2 mg

Lentil is a self-pollinated species and very little cross pollination has been observed in this plant. The breeding methods common for self-pollinated crops, viz. pure-line selection, pedigree method, bulk method and back cross method are all followed by lentil breeders and sometimes some modifications are done with these. Mutagenesis has also been used to improve existing cultivars for specific traits.

This crop faced tough competition in the recent past from cereals, particularly wheat and boro (winter) rice, due to the expansion of irrigation facilities and the availability of high-yielding varieties. A tremendous diversion of land from winter pulses to these cereals is seen. Therefore, there is a need to increase the productivity of lentil.

Looking to the importance and production of this crop, greater attention is needed for its improvement. In this regard, efforts should be made to develop high yielding varieties through breeding research. The aim of any breeding programme is to develop commercial varieties having high production potential and this potentiality of materials may be due to inherent genetic superiority of yield or quality and resistance to pests and diseases. But the success of breeding programme depends on the knowledge about the nature of different gene actions governing the various quantitative characters. Breeders should be able to determine and predict the magnitudes.

The present investigation was conducted to study the gene action, characters association and selection index. For the ease of study the whole work has been divided into two parts and is described under the following heads.

Part I: Deals with the study of inheritance (Diallel, Combining ability, Heterosis analysis and Model fitting).

Part II: Deals with character association and selection index.

PART I

INHERITANCE STUDY THROUGH DIALLEL, COMBINING ABILITY, HETEROSIS AND MODEL FITTING

INTRODUCTION

Lentil is very important crop in our country and it is poor man's meat also. For developing high yielding varieties of this crop, the information of the genetic nature of the yield and yield contributing characters is necessary. Most of the agronomic and economic characters are quantitative in nature and controlled by polygenes.

In the study of these characters, the analyses are done by following biometrical techniques based on mathematical methods of Fisher *et al.* (1932) and Mather and Jinks (1971).

The genetic variance in relation to environmental effects was studied by Fisher (1918) and he was the first to provide statistical methods of partitioning the total variation into genetic and environmental components.

In case of the development of first (mean) and second (variance and co-variance) degree statistics, two distinct lines were developed for the measurement of gene action and interaction which were involved in the phenomenon of continuous variation in later. According to the first degree statistics, Mather (1949) developed biometrical techniques based on mathematical models of Fisher *et al.* (1932).

Another line of study was developed where second degree statistics (variance and covariance) are used for the analysis of continuous variation present in random mating groups and the diallel cross technique as a mean of early generation evaluation came into existence. It provides the estimation of genetic parameters regarding combining ability as well as a rapid overall picture of the dominance relationship of the parents studied using the first filial generations (F_1) with or without reciprocals. The combining ability study is more reliable as it provides useful information for selection of parents in terms of performance of F_1 and elucidates the nature and magnitude of various types of gene action involved in the expression of quantitative characters.

The exploitation of heterosis in the breeding method and development of crop hybrids have made an enormous contribution to the 20th century agriculture, although the genetic basis of the phenomenon remains unclear (Mc Daniel, 1986 and Sinha and Khanna, 1975). Geneticist and plant breeders describe heterosis as the manifestation of greater vigour, growth and yield in a hybrid in comparison with parents (Allard, 1960).

The present study deals with the following aspects:

1. To determine the mode of gene action of yield and yield contributing characters in different generations.
2. To get information for identification of good general and specific combiners for the improvement of yield and its attributes.
3. To obtain the information on the magnitude of heterosis and direction of heterosis and
4. To obtain genetical information from joint scaling test.

REVIEW OF LITERATURE

Works on diallel analysis, combining ability, heterosis and generation mean analysis in lentil are scanty. Therefore, for convenience of study, review of literatures of diallel analysis, combining ability, heterosis and generation mean analysis are made not only on lentil but also on other crops.

The existence and magnitude of heterosis was affected by the day length studied by Sharma (1991) in lentil. Heterosis for seed yield and its components, such as, harvest index, pods per plant and pod clusters per plant, was more rewarding in cross-combinations involving Precoz as one of the parents studied by him. He found that the relationship between heterosis in F_1 and inbreeding depression in F_2 was variable for different crosses and characters. He suggested that L-9-12 × Precoz and L-830 × Precoz crosses should be exploited to produce biparental progenies to get superior segregants.

Tabassum and Saleem (1993) worked on the gene action. They conducted an experiment to do 6 × 6 diallel cross analysis in all the possible combinations of maize inbred lines. In their study, it was found that number of ears per plant was controlled by over-dominance type of gene action, while number of kernel rows per ear, 100-grain weight and grain yield per plant were controlled by additive type of gene action. Epistasis was observed for the characters, number of ears per plant and grain yield per plant.

Heterosis in relation to gca and sca was studied in a 14 × 14 diallel for fibre strength in tossa jute (*Corchorus olitorius* L.) by Chaudhury and Sasmal (1992). Manifestation of heterosis in general was very low, but a definite trend was observed in relation to genetic divergence of the parent revealed by their results. The importance of both additive and non-additive gene effects was evident in the inheritance of fibre strength. In their study, it was found that the per se performance of the parents was highly associated with their gca effects. Among the parents, Tanganika 1, IC 15901, JRO 632 and Bangkon were the best general combiners for fibre strength. In most of the crosses with significant sca effects involved one parent with high gca effect and the promising crosses were JRO 632 × JRO 620, Bangkok ×

Tanganika 1, Tanganika 1 × JRO 620, Bangkok × JRO 524 and Bangkok × JRO 620. As both additive and non-additive gene effects played role in the inheritance of fibre strength, their simultaneous exploitation through adoption of biparental approach in early generation mating were advocated by them.

Kumar *et al.* (1994) conducted an experiment to study heterosis over the better and standard parent for yield and its components in 30 hybrid lentils (*Lens culinaris* Medic.) derived by crossing three well-adapted varieties as testers and 10 eco-geographically diverse genotypes as lines. The range of heterosis over better parent (in percentage) varied from -10.1 to 49.9 for days to initial flowering, -16.6 to 33.7 for plant height, -17.1 to 21.0 for primary branches per plant, -16.7 to 42.7 for secondary branches per plant, 16.7 to 42.7 for secondary branches per plant, -24.7 to 81.7 for pods per plant, -11.1 to 15.8 for seeds per pod, -48.8 to 19.6 for 100-seed weight and -23.5 to 106.4 for yield per plant. In their study, the majority of crosses exhibited negative heterosis over better parent for 100-seed weight. The heterosis observed for yield was mainly attained through major yield components, pods per plant and secondary branches per plant. The hybrid Pusa 4 × Pant L-234 exhibited maximum better and standard parent heterosis for yield per plant. It also shown that the highest better parent heterosis for pods per plant along with high heterosis for seeds per pod and 100-seed weight was present.

Six lentil genotypes (microsperma types, KL 86-2, L 4136, PL 406, PL 639 and HUL 12; and macrosperma type Precoz Sel.) and their 15 F_1s, including reciprocals, were grown during the winter season of 1992-93 and 1993-94 at Pantnagar, Uttar Pradesh, India by Chauhan and Singh (2000). Relative heterosis and heterobeltiosis for 9 quantitative characters were estimated by them. The heterotic response for various characters was influenced by the environment observed by them. They found that the highest heterotic effect was observed for the number of fruiting nodes per plant (81-82%), followed by seed yield per plant (47.52%) in F_1 of Precoz Sel. × KL 86-2 and this cross was the best heterotic combination for plant spread, seeds per pod and harvest index. The F_1s of Precoz Sel. × L 4136 showed high heterobeltiosis for germination percentage, nodes up to first flower and plant height. In their study, F_1 plants exhibiting heterosis for seed yield also exhibited high heterotic response for major yield attributes.

Five best yielding hybrids among 90 F_1 of lentil were evaluated by Rathi *et al.* (2001) for their 9 component characters to understand the basis of heterosis for yield. Hybrid showing negative heterosis for either test weight or pods per cluster showed that it declined 21.24% heterosis in yield, and if heterosis is negative for both the characters, 35% decline occured in yield. It was asserted that heterosis for yield has positive association with vigours of its component characters like test weight and pods per clusters.

Solanki and Sharma (2002) studied dry, healthy and uniform seeds of a *macrosperma* lentil (*Lens culinaris* Medic.) cv., 'Precoz Selection' which were treated with three doses (0.005, 0.01 and 0.02%) each of ethylene imine (EI) and N-nitroso-N-ethyl urea (NEU) and gamma rays (5, 10 and 20 kR). In M_1 generation, different groups of mutagenic damage were identified in each treatment *viz.*, low seedling damage and low sterility (LL), high seedling damage and low sterility (HL), low seedling damage and high sterility (LH), and high seedling damage and high sterility (HH). Effective selection was attempted in M_2 based on desired shift in character mean and higher CV than the highest observed in the control, followed by identification of M_3 families with higher mean than the highest in the control. Among the mutagens tested, NEU induced the highest frequencies of mutated and promising progenies with multiple characters in both the M_2 and M_3, followed by EI and gamma rays, and different groups of mutagenic damage were observed to follow the pattern: HH>HL>LH >LL in the M_2 and HH >LL in the M_3 families.

Vanaja *et al.* (2003) worked on rice varieties of diverse origin. Twenty-eight hybrids were produced from diallel crossing excluding reciprocals among eight parents. These hybrids were studied along with the parents for combining ability for yield and 17 yield components. The study revealed the importance of both additive and non-additive gene effects in governing yield and most of the yield components. Additive gene action was found important for 1000-grain weight, second uppermost internodal length and height of plant at harvest. The parent Vyttila 3 was found to be a good general combiner and the hybrids PK3355-5-1-4 × Hraswa, Vyttila 3 × IR60133-184-3-2-2, Vyttila 3 × IR36, Vyttila 3 × Mattatriveni and IR36 × Mattatriveni showed significant favourable *sca* effect for yield and different yield components in their study.

The genetic basis of heterosis was studied by Alam *et al.* (2004). They studied heterosis through mid-parent, standard variety and better parent for 11 quantitative characters in 17 parental lines and their 10 selected hybrids in rice (*Oryza sativa* L.). The studied characters were plant height, days to flag leaf initiation, days to first panicle initiation, days to 100% flowering, panicle length, flag leaf length, days to maturity, number of fertile spikelet per panicle, number of effective tillers per hill, grain yield per 10-hill and 1000-grain weight. In general the hybrids performed significantly better than the respective parents. Significant heterosis was observed for most of the characters. It was found that among the 10 hybrids, four hybrids viz., 17A × 45R, 25A × 37R, 27A × 39R, 31A × 47R and 35A × 47R showed the highest heterosis in 10-hill grain yield per 10-hill. Inbreeding depression of F_2 progenies was also studied for 11 characters of 10 hybrids by them. Both positive and negative inbreeding depressions were found in many crosses for the studied characters, but any character was not significant.

Ahmad *et al.* (2005) conducted a 7×7 half diallel cross of sunflower at NWFP Agricultural University, Peshawar to study heterosis and inbreeding depression. The planted materials consisted of parental inbred lines, their F_1 hybrids and F_2 populations using randomized complete block design with three replications and data were recorded on yield and other important agronomic characters. Significant genetic differences were observed among the parents, their F_1 hybrids and F_2 populations for all the characters under study. They observed that yield and leaf area showed highly significant heterosis in F_1 hybrids ranging from 102 to 309% and 46.3 to 163.9%, respectively, while inbreeding depression in the F_2 populations ranged from 17-71% and -9.7-43% for these two characters, respectively. The character, leaves per plant showed low level of heterosis in F_1 hybrids (-0.9 to 39.7%), whereas the effect of inbreeding depression in F_2 populations was comparatively high (1.1 to 22.2%). The parent RHA-822 proved itself to be a good general combiner by making higher contribution towards heterosis both in F_1 hybrids and in F_2 populations studied by them.

Shanmuganathan *et al.* (2006) conducted a diallel set of 11 pearl millet genotypes to evaluate general combining ability (gca) effects of parents and specific combining ability (sca) effects of cross combinations. The analysis of variance of diallel progenies exhibited significant genotypic differences in their study. Different analyses, i.e., combining ability analysis and genetic component analysis revealed that both additive and non additive gene effect were significant. Four parents in their study had negative gca estimates.

Subramanian and Subbaraman (2006) conducted an experiment to study the genetics of yield and its components in diallel cross (excluding reciprocals) of maize involving 11 inbreds. All the 11 parents and 55 hybrids generated were raised in a randomised block design (RBD) with three replications in their experiment. Analysis of variance components revealed the importance of over dominance and epistasis in the inheritance of plant height, leaf length, number of kernels per row and seed yield per plant. It was found that dominance effect influenced the inheritance of ear length. Over dominance was preponderant in the expression of ear diameter. Correlation between parental order of dominance for each array and mean of common parents of the array was negative for plant height, leaf length, ear length, ear diameter, number of grains per row and seed yield per plant indicated that increasing genes contained in the parents were dominant. All the six characters recorded low heritability in their investigation. They suggested that heterosis breeding, population improvement through reciprocal recurrent selection, bi-parental mating and diallel selective mating could be employed for improvement of these characters.

Heterosis over better parent for seed yield and its component characters were studied in 28 crosses derived from a diallel mating involving 8 diverse parents of lentil by Singh and Singh (2006). They recorded that for seed yield heterosis ranged from -1.73 to 48.35 (%). It was observed that twenty two crosses had positive and significant heterosis for seed yield and out of them 9 crosses viz., DPL 62 × K 75, PL 4 × K 75, B 18 × Lens 830, PL 4 × B 18, B 18 × K 75, PL 4 × DPL 62, DPL 62 × L9-12, DPL 62 × B 18 and K 75 × Lens 830 were the best hybrids having high heterosis for seed yield per plant, plant height and pods per plant. It was revealed that high heterosis was attributed due to luxuriant plant growth coupled with high frequency of pods seed in their experiment. By considering heterosis, inbreeding depression, sca effect of crosses and gca effect of parents involved in crosses, grossly non additive gene action played major role for expression of high heterosis for seed yield.

A full diallel cross comprising seven inbred lines was studied by Uddin *et al.* (2006) for ten characters to determine the nature of gene action in parents and hybrid population in corn (*Zea mays* L.). From the analysis of variance, significant differences for general combining ability (gca) and specific combining ability (sca) indicated the presence of additive as well as non additive gene effects for controlling the characters. However, relative magnitude of these variances revealed that additive gene effects were more prominent for all the characters studied except grain yield per plant. Parent P_1 was the best general combiner for grain yield and P_7 for both earliness and dwarf plant type observed by them. It was found that the crosses showing significant sca effects for yield involved high × high, high × low and low × low gca parents and could be exploited for hybrid vigour. In their experiment, the range of heterobeltiosis expressed by different crosses was from 8.23 to 25.78 per cent and -0.22 to -8.31 per cent for grain yield and days to silking, respectively. They suggested that the better performing four crosses ($P_1 \times P_7$, $P_6 \times P_7$, $P_1 \times P_4$ and $P_4 \times P_5$) can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

Singh and Singh (2007) worked on the inheritance of seed yield and its components in lentil (*Lens culinaris* Medic.) through a set of 8-parent diallel cross technique. They observed that earlyness and 1000-seed weight were conditioned primarily by additive gene action with a very low incidence of dominance and seed yield, primary and secondary branches per plant and seed weight conditioned by both the additive and non-additive gene action. Partial dominance was observed for days to flower, days to maturity and 1000-seed weight, while over dominance for remaining studied characters. Heritability estimates were over high for 1000-seed weight, days to flower and maturity than other characters. They suggested that biparental mating there after pedigree method of selection can do to isolate desirable recombinations and transgressive segregants.

Ajmal *et al.* (2007) worked on gene action and genetic parameters for yield and its components in an 8 parent diallel cross of mungbean. The estimates of components of genetic variation showed that additive genetic effects appeared to be important for pod length and 100 seed weight and the non-additive effects were more pronounced in the genetic control of pods per plant, seeds per pod and grain yield per plant. Directional dominance was observed for pods per plant, seeds per pod and grain yield per plant. The parental lines contained equal number of dominant and recessive genes for all the characters except 100 seed weight for which the genes were distributed asymmetrically among the parents. The graphic analysis revealed that partial dominance was present for all of the characters studied and pod length and 100 seed weight being controlled by additive genetic effects with partial dominance.

Zubair *et al.* (2007) worked on combining ability analysis in an 8 × 8 complete diallel of mungbean. They observed that significant differences were present for gca and sca among parents and hybrids for all the characters under study. Estimates of variances due to gca and sca suggested predominance of additive gene action for plant height, days to maturity, pod length and 100 seed weight. High sca variance for pods per plant, seeds per pod and grain yield per plant showed the importance of non additive gene action for these characters in their study. They suggested that for the improvement of grain yield in mungbean, the parents, NM 121-25, NM 51, VC 3902 and VC 4152 need special consideration. The cross combination, NM 121-25 × VC 4152, was the best for high grain yield on the basis of sca and the specific crosses, NM 51 × VC 4982, NM 20-21 × VC 1163 and NM 51 × VC 3902 revealed high number of pods coupled with high grain yield.

Forty two hybrids generated by crossing three testers with fourteen lines of okra were studied along with parents by Mehta *et al.* (2007) for studying heterosis and gene action for days to first flowering, days to 50 percent flowering, fruit weight, fruit length, plant height, number of seeds per fruit, 100-seed weight and fruit yield per plant during rainy season and summer season of 2002-03 at the Department of Horticulture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, India. The most heterotic combinations found were VRO-6 × Parbhani Kranti, VRO-4 × Parbhani Kranti, Daftari-1 × Arka Abhaya and Kaveri Selection × Ankur Abhaya for fruit yield per plant. They found that the sca variances for days to fruit flower, days to 50 percent flowering, fruit weight, fruit length, plant height, number of seeds per fruit and 100-seed weight were higher than gca variances and for these reason a preponderance of non-additive gene action was found. The gca variances were greater than sca variances for fruit yield per plant indicating preponderance of additive gene action for this trait. Their results were quite indicative of the fact that hybrid okra has great potentialities of maximizing fruit yield in Chhattisgarh plains.

Panday (2007) worked on combining ability, heterosis and inbreeding depression in *Amaranthus* for ten characters. Non- additive genetic variance was predominant for majority of characters in both F_1 and F_2 generations. The parent AG-21 was good general combiner for yield per plant also showed high gca effects for panicles per plant and harvest index in both F_1 and F_2 generations. He observed that the hybrids exhibited highest heterosis also showed high inbreeding depression. Heterosis over better parent was highest for economic grain yield (145.047%), followed by panicles per plant (113.675%), panicle length (33.656%) and grain weight per panicle (23.566%).

Eshghi and Akhundova (2009) worked on an eight-parent diallel, involving hulless barley varieties ICNBF-582, ICB-102607, ICNBF93-328, SB91925, ICNBF8-613, BBSC congana, Petuina2 and ICNBF93-369 and that was evaluated to determine the genetic parameters contributing to plant height, days to maturity, number of tillers, number of grains per spike and grain yield per plant. In their investigation, generation mean and variance analysis was carried out on six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from the cross ICNBF93-369 × ICNBF-582 and SB91925 × ICB-102607 to complement the genetic information obtained from the diallel analysis. Wr/Vr graph in diallel analysis and average degree of dominance together with narrow-sense heritability values in both experiments revalued additive gene effects for plant height, number of tillers and days to maturity and over-dominance gene action were observed for number of grains per spike.

Genetic analysis was studied by Khan *et al.* (2009) in a 6 × 6 diallel cross following Hayman's diallel approach and Mather's concept of D (additive), H (dominance) genetic components of variation in F_1 and F_2 hybrids in a randomized complete block design in upland cotton during 2003-2005 at the Agricultural Research Institute, Dera Ismail Khan, Pakistan. Additive-dominance model was used in their experiment for validation of data. Design with the intention to decipher the inheritance pattern; gene action and correlation involved in seed cotton yield and yield contributing characters (boll weight and bolls number) and staple length. Genotypes mean values differed significantly ($p \leq 0.01$) for all the characters and the scaling tests used fully satisfy the pre-requisites of additive-dominance model and the characters i.e., boll weight and staple length in F_1 generations showed complete adequacy in their experiment. All other characters in both generations did not satisfy the assumptions and made the additive-dominance model partially adequate for the data. It was found that additive component (D) was found significant for boll weight and staple length in both generations and in F_1s bolls per plant. Dominance components (H_1, H_2) were also found significant for all the characters in F_1s and non-significant in F_2 generations in their study. In their experiment, in case of F_1s, the additive gene action was somewhat partial, while in F_2s most of characters were controlled by additive gene action with some contradictions between genetic components of variance revealed by the results.

Amiri-Oghana *et al.* (2009) worked on twenty one F_2 progenies derived from a 7 × 7 diallel crosses and along with parents to evaluate the inheritance pattern for the characters namely grain yield, flowering and maturity time in oilseed rape (*Brassica napus* L.). The genotypic effects were significant for all characters and analyses of combining ability and genetic components were performed on F_2 progenies. The analysis of variance revealed that both additive and non-additive genetic effects were involved in controlling these characters. The gca/sca ratios were 0.91, 0.95 and 0.83 for days to flowering, for days to maturity and for grain yield respectively indicating that the additive gene effects were more important than non-additive gene effects for all these characters. Narrow-sense heritability was high for days to maturity (81.99%) followed by days to flowering (73.12%) and low for grain yield (30.15%). Heterosis in hybrids seemed to be largely determined by complementary epistasis as well as genetic distance between the parents revealed by the results. In their experiment, the spring-type varieties, Tower and Regent appeared as the best parents for earliness, whereas winter-type varieties like D.R. and Ceres were the best parents for high grain yield.

Heterosis in bottle gourd was studied in a set of 13 F_1 with 26 parents by Quamruzzaman *et al.* (2009). Results showed highly significant differences for all the characters among the materials studied. Heterosis was higher for yield per plant, number of fruits per plant and individual fruit weight, medium in fruit length and fruit diameter, and lower in days to 1st harvest.

Combining ability analysis of 10 × 10 diallel set of crosses in Indian mustard for ten quantitative characters was studied by Singh *et al.* (2010) and the results revealed preponderance of non-additive gene effects for plant height, number of primary branches per plant and seed yield per plant, whereas additive gene effect was found to be predominant for the inheritance of rest of the characters. In their investigation, the parent Durgamani, RLM-198 and Varuna were the good general combiners for seed yield and oil content and Varuna and Durgamani also exhibited desirable general combining ability effect for earliness and dwarfness. Among the cross combinations, cross Kanti × Pusa Agrani exhibited superior specific combining ability effects for seed yield, oil content and other yield attributing characters and most of the crosses involving high × low general combining parents, exhibited high sca effects for various characters.

Al-Hamdany (2010) worked on inheritance of yield, combining ability and inbreeding depression in durum wheat of F_2 half diallel crossing among the 7 varieties viz., Leeds, Waha, Azeghar1, Um-Rabie3, Brashua, Cyprus1 and Korfila. Genotypes, general and specific combining ability mean square were highly significant. The durum wheat yield was under the dominance gene effect and the parents Leeds and Um-Rabie3 were considered suitable according to their yield capacities and general combining ability effects revealed by the results. The two hybrids (Leeds × Brashua) and (Waha × Brashua) had significantly higher yield (2.943 and 2.955 ton per hectare, respectively) as compared with others, and also possessed significant positive specific combining ability effects, highly significant positive inbreeding depression values and deviation from local variety Um-Rabei5. Therefore they were considered to be promising hybrids.

Six morphological and agronomic characters of Snap bean (*Phaseolus vulgaris* L.) were studied by Arunga *et al.* (2010) to investigate their gene action, and to estimate the general combining abilities (gca) and specific combining abilities (sca) of parents and crosses. Three snap bean varieties viz., Amy, Monel and Morlane and two dry bean varieties viz., GLP 20 and GLPX 92 were used as parents in a complete diallel cross. Their experiment was laid out in a randomized complete block design in a greenhouse. Significant ($p < 0.01$) additive and dominance effects were identified for days to flowering, plant height at flowering, number of pods per plant, pod weight per plant, pod length and pod diameter in their experiment. Additive gene effects were predominant for all characters apart from pod weight. Significant ($p < 0.01$) maternal and non-maternal reciprocal effects were also detected on plant height and days to flowering. Estimates of gca, sca and reciprocal effects suggested that Amy, Morlane and GLP 20 were generally the best combiners for incorporation into snap bean breeding programmes and this basic information was valuable for snap bean breeding programmes.

Khatun *et al.* (2010) worked on estimation of heterosis in a set of 7 × 7 diallel crosses of spring wheat (*Triticum aestivum* L.). The varieties were Gaurab, Kanchan, Balaka, Sonora, Protiva, Pavon, and Anza used as parent materials. Their work on the diallel trial for seven parental material and their 21 F_2 progenies under two contrasting cultural conditions for different yield and yield contributing characters were carried out. In their study, cultural conditions I was provided by the BARI recommended doses of fertilizer and irrigation, and 2 have no fertilizer but two irrigations once at crown root initiation stage and twice at panicle initiation stage. In their experiment, heterosis was measured as i) relative heterosis and ii) heterobeltiosis. The result of relative heterosis revealed that cross Sonora × Anza exhibited superior performance for grain yield per plot in environment-I and desirable negative heterosis was observed in cross Balaka × Anza in environment-I and Pavon × Anza in environment-2 for days to 50% heading character. For the character days to maturity, desirable negative heterosis was found in cross Pavon × Anza in both cultural environments. The estimation of heterobeltiosis for different yield contributing characters showed that cross Sonora × Anza exhibited the highest heterosis for grain yield per plant in environment-1 and Kanchan × Balaka in environment-2. Cross Pavon × Anza exhibited superior relative heterosis and heterobeltiosis for 100-grain weight in both cultural environments. By comparing two cultural conditions, it was found that 1 is better than 2 for all the characters in their observation.

Heterosis in lentil was studied for yield and component characters in 48 hybrids involving 16 parents comprise 4 females and 12 males by Milan *et al.* (2010). In their study, analysis of variance showed significant differences in parents *vs* crosses for all the characters except days to maturity revealed by the result. Greater variability in the parents indicated the possibility of getting higher heterosis in the crosses. The high manifestation of heterosis for yield per plant was evident by significant superiority of hybrids over better parent ranging from 6.58 to 118.76% and over standard variety (PL 406) ranging from 8.05 to 94.21% in several crosses. The high heterobeltiosis for yield per plant was evident in the cross of (Globe × KL 86-2) × Precoz Sel (118.76%) and this cross had also high heterobeltiosis for days to 50% flowering, plant height, days to maturity, biological yield per plant and harvest index. Similarly, the cross PL 406 × Ranjan which displayed superiority over standard variety for yield per plant also showed significant heterosis for days to 50% flowering, number of pods per plant, biological yield per plant and harvest index in their study. The crosses exhibiting good heterotic expression in F_1 were likely to give better segregants in later generations where additive gene effects were high.

Heterotic effects were studied over mid parent and better parent values for yield and its components in 8 parental diallel involving 5 exotic and 3 local mungbean genotypes by Zubair *et al.* (2010). Hybrids were evaluated along with their parents in the field of National Agricultural Research Centre, Islamabad, Pakistan. High level of hybrid vigour was observed for plant height, number of pods per plant and grain yield per plant in their study. By considering overall performance, they observed that the superior F_1s were NM 51 × VC 3902, NM 51 × VC 4982, NM 20-21 × VC 1163, NM 51 × VC 3301 and VC 3301 × VC 1163 revealing strong heterotic effects for number of pods per plant, number of grain per pod and grain yield per plant. These hybrids were, therefore, suggested to be utilized for developing high yielding mungbean cultivars.

Tchiagam *et al.* (2011) conducted a study at Dang (Soudano-Guinean zone of Cameroon) to determine the variability of 100-seed weight, geometric surface, porosity and sphericity of the seeds of 10 cowpea (*Vigna unguiculata*) genotypes and investigate the genetic basis of these characters through a 5 × 5 half-diallel cross mating. Knowledge of the physical properties of the seed of cowpea was necessary for the design of equipment for transporting, sorting, cleaning, separating, smashing and processing it into different foods. A randomized complete block design was included for their experiment with three replicates. The results showed that these genotypes presented a significant variability for the four physical properties and the average properties of seed were found to be a hundred seed mass of 20.46g, a surface area of 0.84 cm^2, a sphericity of 35.50% and a porosity of 0.65. Genetic analysis revealed that the parents differed for their general combining ability (gca). The crosses showed specific combining ability (sca). In their study, these physical parameters were highly heritable with broad-sense heritability (h^2) values that ranged from 0.76 to 0.96. Both dominant and additive gene effects were significant for all characters with a predominance of additive genes for seed mass and dominant genes for degree of sphericity. The alleles for seed weight, degree of porosity and sphericity were mostly recessive, whereas the higher performances for seed surface were due to the presence of dominant alleles revealed by the result. Heterosis in F_1 over best parent was recorded for some combinations in their experiment. They suggested that recurrent selection might be a useful breeding strategy for these characters.

A 5 × 5 half-diallel cross set of chickpea (Arman, Hashem, ILC588, ICCV2 and ILC3279) was studied by Karami (2011) to estimate the gene effects and genetic parameters of twenty characters including days to 50% flowering, days to podding, days to maturity, plant height, basal pod height, plant ordinate, root length, number of primary branches, number of secondary branches, biomass, pods weight per plant, straw yield per plant, 100- Seed weight, number of pods per plant, number of empty pods per plant, number of double seed pods per plant, number of single seed pods per plant, number of seeds per plant, seed yield per plant, seed size and harvest index. This study was carried out at the experimental farm of the Sara-rood Dry Land Research Sub institutes, in Kerman Shah Province (West Iran) during the spring of 2007. His study revealed that according to analysis of variance for diallel, only additive genes effects were found significant for plant height (cm), pod height (cm), number of primary branches, empty pods and straw yield (gm) per plant. In addition to the significant additive gene effects, dominant gene effects were significant for days to

50% flowering, days to podding, days to maturity, biological yield (gm), 100-seed weight (gm), seed size, harvest index, pod weight (gm), number of pods, single seed pods, seeds number and seed yield per plant (gm), but about plant ordinate and number of double seed pods per plant only dominant gene effects were significant. Additive and dominant gene effects were not found significant for root length and number of secondary branches. Estimates of genetic parameters also revealed that additive and dominance variance were significant for most studied characters in that research. However, both the additive and dominance gene affects together had the importance to control of the most quantitative characters in the chickpea (*Cicer arietinum* L.). The degree of dominance average $(H_1/D)^{1/2}$ (H_1 = dominance variance, D= additive variance) was higher than one indicating over dominance for all the characters except for PHT, BPHT and HI. The narrow-sense heritability was high for HI (67%), 100-seed weight (56%), SS (55%), basal pod height (47%), PHT (42%) and SY/P (37%) indicating that great genetic gain could be achieved for these characters.

Nature of gene action and combining ability is valuable in determining whether heterosis is fixable or predictable. Thus, to know the inheritance pattern of some morphological characters and to evaluate the best heterotic combinations, Tiwari *et al.* (2011) conducted an experiment with sixty F_1 hybrids along with their parents (3 CMS lines and 20 restorer variety) of rice. The results of their study revealed that the male lines i.e., IR35454-18-1-1-2R, IET201108 and IR52256-9-2-2-1R were good general combiner for grain yield and almost all major components. The higher magnitude of sca than gca variance, greater values of average degree of dominance and lower predictability ratio was observed in all characters suggesting significant role of non-additive gene action. Out of 60 crosses, about 30% crosses showed significant and desirable sca effects for grain yield along with its important characters, viz., number of fertile spikelets, number of spikelets per panicle and biological yield. High sca effects were observed by them in the crosses NMS4A × IR633-76-1R, IR58025A × IR19058-107-1R, IR58025A × IR32419-28-3-1-3-3R, NMS4A × IR35454-18-1-1-2R and NMS4A × IR5226-9-2-2-1R. Heterobeltiosis for grain yield was observed significant of 43 hybrids ranging from 11.63 to 113.04%. Better parent heterosis was observed also for 46 hybrids over standard check (Sarjoo-52) ranging from 10.48 to 71.56%.

Most of the crosses which exhibited superiority over better parent or standard variety for grain yield also showed significant heterosis for number of fertile spikelets and number of spikelets per panicle. They found that the best cross combination IR58025A × IR48749-53-2-2-2R, NMS4A × IR633-76-1R, IR58025A × IR54853-43-1-3R, IR58025A × IR19058-107-1R, PMS10A × IR54853-43-1-3R, NMS4A × IR52256-9-2-2-1R, NMS4A × IET9352 and IR58025A × IET201102 having more than 50% heterosis in order of merit grain yield.

Seven genotypes of faba bean (*Vicia faba* L.) were used in carrying out half diallel cross, 21 F_1 hybrids and 21 F_2 progenies by Farag and Afiah (2012) to evaluate under well watered and rainfed conditions at the Maryout Agriculture Experimental Station of Desert Research Center. Mean squares of genotypes in F_1 and F_2 generations revealed that the differences due to genotypes were significant for all of the characters studied under well watered and rainfed conditions. The parental genotype P_2 recorded the highest number of branches per plant i.e., 7.85 and 6.94 branches under well watered and rainfed treatments, respectively. While, the two crosses; $P_2 \times P_4$ and $P_2 \times P_6$ showed the highest number of pods per plant in both generations under well watered and rainfed treatments. For 100-seed weight, the parent Aquadulce (P_4) recorded the highest values under well watered and rainfed conditions (95.62 and 71.72 g, respectively) and the two crosses, $P_2 \times P_5$ and $P_2 \times P_6$ recorded the highest values for seed yield per plant. Significant positive heterosis and heterobeltiosis were recorded for different characters and in case of seed yield per plant, the seven crosses namely $P_1 \times P_7$, $P_2 \times P_5$, $P_2 \times P_6$, $P_4 \times P_6$, $P_5 \times P_6$, $P_5 \times P_7$ and $P_6 \times P_7$ had significant positive heterotic effects relative to mid and better parents under the two irrigation treatments. Mean squares due to both gca and sca estimates were highly significant or significant in both generations for all the studied characters under well watered and rainfed conditions and variances due to gca were larger than those for sca. General combining ability results showed that the three parental genotypes namely P_1 (G.461), P_2 (NBL2) and P_4 (Aquadulce) were good combiners for improving most studied characters in the experiment.

Sattar *et al.* (2012) conducted an experiment to study combining ability effects and gene action for seed yield and their components in faba bean. Seven faba bean genotypes and the resultant twenty one hybrid combinations were evaluated using the diallel cross analysis according to Griffing (1956) as method 2 model 1 and significant mean squares were detected for genotypes, general and specific combining ability effects for all characters. The ratio of gca/sca exceeded unity for all characters except no. of branches per plant indicating that additive gene action was more important than non-additive gene action in these characters' inheritance. The best general combining ability effects for seed yield per plant and one or more of its attributes were found in the parents P_5, P_7 and P_3. The hybrid combination $P_1 \times P_2$, $P_1 \times P_4$, $P_2 \times P_3$, $P_4 \times P_6$ and $P_5 \times P_7$ showed highly significant desirable sca effects for yield and most components in their study. Estimates of broad sense heritability varied from 0.57 for plant height to 0.91 for both of seed yield per plant and 100 – seed weight. The best five selected genotypes as detected by general selection criterion were $P_1 \times P_3$, $P_5 \times P_7$, $P_3 \times P_5$, $P_1 \times P_2$ and $P_1 \times P_4$ and these crosses were the highest in most of the characters and these characters showed high significant and positive correlation among each other and also between them and seed yield per plant.

In order to estimate heritability and gene action for grain yield and its related characters in lentil, six basic generations were evaluated in a randomized complete block design with three replications in a field experiment by Khodambashi *et al.* (2012). Besides seed yield per plant, plant height, pod length, and 100-seed weight, the number of pods per plant, primary branches, clusters per plant, nodes per main stem, secondary branches, and the number of seeds per pod were recorded in the experiment. Generation mean analysis using A, B, C and joint scaling tests revealed that additive [a], dominance [d] and at least one of the epistatic effect (additive × additive [aa], additive × dominance [ad] and dominance × dominance [dd]) were involved in the inheritance of the studied characters. However, simple additive-dominance model was sufficient only for pod length studied by them. It was found that significant dominance [d] and dominance × dominance [dd] interactions with opposite sign indicated duplicate epistasis for all characters except pod length. Narrow-sense heritability was low for seed yield per plant, pod length, number of seeds per pod and 100-seed weight and moderate for other characters. Average dominance ratio was more than unity for seed yield per plant, number of primary and secondary branches, pod length, and 100-seed weight, which showed the high importance of dominance gene effect in control of these characters. But due to the presence of greater non-additive gene effects combined with low narrow-sense heritability, selection for almost all of the studied characters in the specific cross in the study, especially in early generations, would be complex in conventional methods.

Biabani *et al.* (2012) worked on estimating genetic parameters and recognizing superior *Jatropha curcas L.*combinations. Ten superior plants were selected based on seed yield and oil content, and were crossed among them in a 10 × 10 half-diallel mating design to produce 45 F_1-hybrids. Their experiment was conducted in nursery stage using a randomized complete block design (RCBD) with three replications. In the experiment, analysis of variance for the combining ability revealed that gca and sca variance were significant at 1% probability for plant height, collar diameter and number of leaves in nursery stage and the non-additive effects were indicated by the low ratio of gca/sca. Values of broad sense heritability were high for plant height, collar diameter and number of leaves and values of narrow sense heritability of the characters, plant height, collar diameter and number of leaves were low. Percentages of heterosis and heterobeltiosis values for plant height, collar diameter and number of leaves ranged from negative to positive in their study. This result showed the existence of dominance or non-additive gene actions might be present in the hybrids. On the basis of gca and sca effects, they suggested that parents, Ph1.2 and In2.1 and hybrids Ph1.2 (3) × In1.2 (8), Ph1.1 (9) × My2.2 (10) and My2.1 (1)× My2.2 (10) could be used for future breeding programme.

Hasanuzzaman *et al.* (2012) conducted an experiment with six different homozygous divergent parents, CCA 2, CCA 5, BARI Morich 1, CCA 11, CCA 15 and CCA 19 of chilli (*Capsicum annuum*) to evaluate combining ability using 6 × 6 diallel cross excluding reciprocals. The results revealed that the general combining ability (gca) was significant for days to 50% flowering, fruit length, fruit width, fruit weight, days to fruit maturity (green), days to maturity (ripe), plant height, plant canopy width, number of seeds per plant, number of fruits per plant and yield per plant. Significant specific combining ability (sca) was observed for all the measured variables except fruit width. Both additive and non-additive effects influenced the performance of the hybrid for all of the characters revealed by the results. The non-additive effects played a more important role than additive effects for all the characters. They identified that the parents CCA 5, BARI Morich 1 and CCA 19 were the reliable general combiners. Considering the sca effects and mean performance, hybrids $P_3 \times P_6$ and $P_2 \times P_3$ were the best genotypes. Top two yield were obtained for hybrids $P_3 \times P_6$ (BARI Morich 1× CCA 19) with the value of 898.87g of yield per plant and $P_2 \times P_3$ (CCA 5× BARI Morich) with the value of 833.63g of yield per plant. No parent and cross had significant gca and sca effects, respectively in all the characters studied. The broad sense heritability of all the 11 characters was above 90% indicating that all characters are highly heritable and narrow sense heritability of days to 50% flowering, fruit length, fruit width, fruit weight, days to fruit maturity (green), days to maturity (ripe), plant height, plant canopy width were high (37.34-81.26), whereas the number of seeds per plant, number of fruits per plant and yield per plant were in medium range of narrow sense heritability (18.42-29.19) in their study. Estimates of heritability by mid parent-offspring regression indicated that all the studied characters were highly heritable.

MATERIALS AND METHODS

MATERIALS

For the present investigation, the materials were obtained from ILL 6002, Bari Masur-2, Bari Masur-3 and Bari Masur-4. Co^{60} source in the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, Bangladesh was used to put irradiation on these lines.

Table 2: Different radiated and non radiated lentil lines chosen for the experiment are shown in the table.

1.	P_1	Bari Masur - 4
2.	P_2	Bari Masur - 3 (20 Kr)
3.	P_3	Bari Masur - 2 (20 Kr)
4.	P_4	Bari Masur - 4 (30 Kr)
5.	P_5	Bari Masur - 4 (20 Kr)
6.	P_6	ILL 6002 (20 Kr)

METHODS

1. Description of the experimental site

The experimental field was at the agricultural land located west region of the 3rd science building of University of Rajshahi.

2. Methods of producing seeds used for different experiments

The study was conducted during the period of December, 2005 to March, 2009. The crops were grown during winter seasons of the above years except 2009. For obtaining necessary amount of seeds to conduct crossing programmes and for trial of parents, F_1 and F_2s, works were done under following title and sub heads.

a. Trial of irradiated lines

- *i) Irradiation of the materials*
- *ii) Preparation of the experimental field*
- *iii) Layout of the experimental field*
- *iv) Sowing of irradiated and non irradiated seeds*
- *v) Maintenance of the experimental plants*
- *vi) Collection of seeds*

i) Irradiation of the materials

To conduct the present investigation, 12 lines of lentil were collected from ICARDA, Syria and 4 lines were from RARS, Ishurdi, Pabna, Bangladesh. Radiation of different doses i.e., 20 Kr, 25 Kr and 30 Kr were put to the lines from the Co^{60} source in the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, Bangladesh in the first week of December, 2005.

Table 3: Lentil lines used to conduct the experiment.

NO	ILL/SEL.	Source of Collection
1	4404	From ICARDA, Syria
2	4605	From ICARDA, Syria
3	5888	From ICARDA, Syria
4	6002	From ICARDA, Syria
5	6024	From ICARDA, Syria
6	7543	From ICARDA, Syria
7	7979	From ICARDA, Syria
8	8006	From ICARDA, Syria
9	8008	From ICARDA, Syria
10	8009	From ICARDA, Syria
11	8010	From ICARDA, Syria
12	L-4147	From ICARDA, Syria
13	Bari Masur-1	From RARS, Ishurdi, Pabna, Bangladesh
14	Bari Masur-2	From RARS, Ishurdi, Pabna, Bangladesh
15	Bari Masur-3	From RARS, Ishurdi, Pabna, Bangladesh
16	Bari Masur-4	From RARS, Ishurdi, Pabna, Bangladesh

ii) Preparation of the experimental field

The field was opened in the month of November, 2005 with the help of a plough. Then the land was prepared by several ploughings and cross ploughings followed by laddering. After removal of weeds and trashes, the land was finally brought into a good tilth by breaking large clods into fine particles. Manure was added for fertility of the soil.

iii) Layout of the experimental field

The experiment was laid down in randomized complete block design. The irradiated and non irradiated types of lentil lines mentioned above were sown in two replications. Each replication had sixty four plots. The size of each plot was 120cm×150cm. The space between rows was 30 cm and between plants was 25 cm. The materials were distributed at random in each replication.

iii) Sowing of irradiated and non irradiated seeds

Seeds were sown in December 14, 2005. The seeds were germinated after 3-7 days.

iv) Maintenance of the experimental plants

The crop was always kept under careful observation. Suitable cultural practice such as weeding, watering and applying of fertilizers were done and also for crop protection, fungicides and insecticides etc. were sprayed regularly to obtain healthy plants.

v) Collection of seeds

After maturation of plants, seeds were collected separately in packets. They were dried in the sunlight and put in the desiccators.

b. Screening of the materials and production of F_1 seeds

i) Preparation of the experimental field
ii) Layout of the experimental field
iii) Sowing of irradiated and non irradiated seeds
iv) Maintenance of the experimental plants
vi) Selfing and crossing
v) Collection of seeds

i) Preparation of the experimental field

The field was prepared as the previous year of this investigation.

ii) Layout of the experimental field

Field layout was also same as the previous year. Six parents were crossed in all possible combinations. The cross combinations were as follows:

Table 4: Crossing pattern of diallel fashion of this experiment.

♂ ♀	P_1	P_2	P_3	P_4	P_5	P_6
P_1	$P_1\times P_1$	$P_1\times P_2$	$P_1\times P_3$	$P_1\times P_4$	$P_1\times P_5$	$P_1\times P_6$
P_2		$P_2\times P_2$	$P_2\times P_3$	$P_2\times P_4$	$P_2\times P_5$	$P_2\times P_6$
P_3			$P_3\times P_3$	$P_3\times P_4$	$P_3\times P_5$	$P_3\times P_6$
P_4				$P_4\times P_4$	$P_4\times P_5$	$P_4\times P_6$
P_5					$P_5\times P_5$	$P_5\times P_6$
P_6						$P_6\times P_6$

Where, Parent 1 (P_1) is Bari Masur-4, Parent 2 (P_2) is Bari Masur-3 (20 Kr), Parent 3 (P_3) is Bari Masur-2 (20 Kr), Parent 4 (P_4) is Bari Masur-4 (30 Kr), Parent 5 (P_5) is Bari Masur-4 (20 Kr) and Parent 6 (P_6) is ILL 6002 (20 Kr).

iii) Sowing of irradiated and non irradiated seeds

Seeds were shown on 7 and 8 November, 2006.

iv) Maintenance of the experimental plants

Proper care was taken for raising healthy plants. Suitable agronomic and cultural practices such weeding, watering, applying of fertilizers and fungicides and insecticides etc. were done as and when necessary as in the 1st year of the experiment.

v) Selfing and crossing

Screening of the mutant lines was maintained on the basis of survibility and maturity for flowering and crossing was done in this year.

As lentil is a self pollinated plant, selfing was not necessary. For crossing, emasculation of flowers was done. Previous day of crossing, emasculation was done of the selected flowers by excluding anther from the flower. After removing anther, bagging was completed of the flowers. Every apparatus were sterilized by ethanol after emasculation of each plot.

Crossing was done by collecting pollen of the expected plants and by touching of pollen to the expected stigma of the flowers. After crossing, further bagging of the flowers was done. Fruits were observed by 3-4 days of crossing. Precautions were taken when crossing was done for every cross.

vi) Collection of seeds

F_1 and parental seeds were collected separately. Seeds of other plants were collected separately and maintained well.

c. Production of F_1 and F_2 and parental seeds

To obtain F_1s, F_2s and parental seeds, works were done by following sub heads:

i) Preparation of the experimental field,
ii) Layout of the experimental field,
iii) Sowing of F_1 and parental seeds,
iv) Maintenance of the experimental plants,
v) Selfing and crossing in crossing plots,
vi) Collection of seeds.

i) Preparation of the experimental field

The experimental field was prepared as the previous years.

ii) Layout of the experimental field

The experiment was laid down in a randomized complete block design with two replications. In total there were 42 plots. The size of each plot was 50cm×30cm. The space between rows was 30cm and between plants was 25cm. The cross and parental materials were distributed at random in each of the replications.

iii) Sowing of F_1 and parental seeds

Seeds of F_1 generation and their parents were sown in 7th November, 2007. In each plot, each type of F_1s or parents was sown. As F_1 seeds were limited and less than estimated hills, gaps were filled by Bari Masur-4.

iv) Maintenance of the experimental plants

For the healthy experimental plants, all necessary cultural practices were done. In these practices, weeding, watering, applying of fungicides and insecticides were done.

v) Selfing and Crossing in crossing plots

Besides the above works, crossing was done in the crossing plots to produce F_1 seeds.

vi) Collection of seeds

Seeds of F_1, F_2 progenies and parents were collected in separate packets. After collection of seeds, packets with seeds were dried by sunlight and preserved in desiccators.

3. Experiment I: Combining ability and gene action of twelve yield and yield contributing characters by half diallel

The methods to conduct the experiment are described under the following sub heads:

i) Preparation of the experimental field
ii) Layout of the main field
iii) Seed sowing
iv) Maintenance of the experimental plants
v) Harvesting of plants
vi) Collection of Data
vii) Techniques of analysis of data

i) Preparation of the experimental field

Preparation of the experimental field and maintenance of the plants were the same as described earlier.

ii) Layout of the main field

Field trial of F_1, F_2 generations and parents was conducted under randomized complete block design with two replications having forty eight plots. The plot size was about 50cm × 30cm with two rows and each row had three hills. In each hill, one plant was maintained. The gap between plants in the row was 25cm and gap between rows was 30 cm and the gap between plots was 40 cm. Gap between replication was 100cm. In this experiment, single plant randomization was done. After completing seed sowing with experimental seeds, gap was filled with Bari Masur - 3 (20Kr).

iii) Seed sowing

Seeds were sown in 12th and 13th November, 2008. Seedlings were maintained well.

iv) Maintenance of the experimental plants

Plants were maintained with carefull observations. All cultural practices were done.

v) Harvesting of plants

The plants were harvested when pods became mature.

vi) Collection of data

Data on twelve yield and yield contributing characters were recorded. They were as follows:

1. *Days to flower (DF)*: This data was counted by counting days from the date of sowing to the date of first flower.
2. *Plant height at first flower (PHFF)*: Plant height was measured in cm at the date of first flower.
3. *Number of primary branches at first flower (NPBFF)*: Number of primary branches at first flowering date was counted.
4. *Number of secondary branches at first flower (NSBFF)*: Number of secondary branches at first flowering date was counted.
5. *Canopy area at maximum flower (CAMF)*: Canopy area was measured in cm by the formula πr^2.
6. *Number of secondary branches at maximum flower (NSBMF)*: Number of secondary branches at maximum flowering time was counted.
7. *Number of pods per plant (NPdPP)*: Total number of pods per plant were counted and recorded.

8. *Pod weight per plant (PdWPP)*: All pods per plant were weighted in gram and recorded.
9. *Number of seeds per plant (NSPP)*: All seeds from each pod per plant were counted and recorded.
10. *Seed weight per plant (SWPP)*: Total seeds per plant were weighted in gram and recorded.
11. *Individual plant weight (IPlW)*: Total weight of each plant without root was taken in gram and recorded.
12. *Root weight (RW)*: Root weight was measured in gram.

vii) Techniques of analysis of data

The collected data were analyzed following the biometrical techniques. "The diallel techniques of analysis" according to the Method 2 (Parents+F_1's = Half diallel) given by Griffing (1956) was followed for testing the significance of genotypic differences and for combining ability analysis. With 'n' lines, the total entries to be analysed in this method is thus n(n+1)/2. In this study, n = 6, there were 21 total entries, i.e., 15 crosses and 6 parents. Techniques of analyses of the data are described under the following sub-heads.

a. Testing the significance of genotypic differences

The data were first analyzed to test the significance of genotypic differences. The total variability was partitioned into treatments, replications and error.

The sums of squares are calculated as follows:

$$\text{Correction factor} = \frac{(\text{Grand total})^2}{r \times \frac{1}{2} n(n+1)}$$

$$\text{Total S.S.} = \Sigma Yij^2 - \text{C.F.}$$

$$\text{Treatments S.S.} = \frac{\Sigma Yi.^2}{r} - \text{C.F.}$$

$$\text{Replications S.S.} = \frac{\Sigma Y.j^2}{\frac{1}{2} n(n+1)} - \text{C.F.}$$

Error S.S. = Total S.S. - Treatment S.S. - Replication S.S.

Here,

Yi. = Treatment total

Y.j = Replication total

Yij = Individual mean data

r = Number of replication

n = Number of parents

Table 5: Preparation of Anova

Source	df	S.S.	M.S.	F
Treatments	{n(n+1)/2}-1	SS_1	= SS_1/ df	= M.S./E. M.S.
Replications	r-1	SS_2	= SS_2/ df	= M.S./E. M.S.
Error	[{n(n+1)/2}-1] (r-1)	SS_3	= SS_3/ df	
Total	{n(n+1)/2}r-1			

b. Combining ability analysis

In the combining ability analysis, the data are rearranged in Table 20. In this table, each value is the mean square value. The total variability of the population was partitioned into components like variance due to general combining ability (gca), specific combining ability (sca) and error. Using replicate mean, the various sum of squares were obtained as follows:

$$\text{S.S. due to gca} = \frac{1}{n+2}\left[\sum(Y_{i.} + Y_{ii})^2 - \frac{4}{n}Y^2..\right]$$

$$\text{S.S. due to sca} = \sum \sum Y_{ij}^2 - \frac{1}{n+2}\sum(Y_{i.} + Y_{ii})^2 + \frac{2}{(n+1)(n+2)}Y^2.$$

Table 6: Anova for combining ability analysis in Method 2

Source	d.f.	S.S.	M.S.	E(M.S.)
gca	5	SS_1	MS_g	$\sigma^2_e + \sigma^2_s + (n+2)\,\sigma^2_g$
sca	15	SS_2	MS_s	$\sigma^2_e + \sigma^2_s$
Error	20	SS_3	MS_e	σ^2_e

Where,

gca = General combining ability,

sca = Specific combining ability,

Yij = Mean of i×j th cross

MSg = Mean square of gca effects,

MSs = Mean square of sca effects,

MSe = Mean square of error.

The mean of sum of squares due to error was divided by the number of replications. Mean error variance, MSg and MSs have been calculated from the mean data, mean error variance is, therefore, required for F-test.

$$\text{Thus, MS}' \text{ (error)} = \frac{\text{MS (error)}}{\text{Number of replications}}$$

Estimation of component variances and their genetic interpretations:

From the E(M.S.) given in the table it is obvious that:

$$\sigma^2_g = \frac{1}{n+2}(M_g - M_s)$$

$$\sigma^2_s = M_s - M'_e$$

$$\sigma^2_e = M'_e$$

where σ^2_g, σ^2_s and σ^2_e are the estimates.

These components may be translated into genetic components using following equations:

$$\sigma^2_g = 1/2\ \sigma^2_A$$

$$\sigma^2_s = \sigma^2_D$$

Accordingly,

$$\sigma^2_A = 2\ \sigma^2_g$$

$$\sigma^2_D = \sigma^2_s$$

The general combining ability effects are defined as follows:

$$g_i = \frac{1}{n+2}\ [\Sigma(Y_{i.} + Y_{ii}) - \frac{2}{n}\ Y_{..}]$$

The specific combining ability effects are defined as follows:

$$S_{ij} = Y_{ij} - \frac{1}{n+2}\ (Y_{i.} + Y_{ii} + Y_{.j} + Y_{jj}) + \frac{2}{(n+1)(n+2)}\ Y_{..}$$

Standard Errors are as follows:

$$S.E.(g_i)=[(n-1)\ \sigma^2_e/n(n+2)]^{1/2}$$

$$S.E.(s_{ij})=[n(n-1)\sigma^2_e\ /\ (n + 1)\ (n+2)]^{1/2}$$

c. Estimation of variances and covariances in F_1 **and** *F_2 generations*

A number of first and second degree statistics (Mather, 1949) were calculated from the mean data. With the environmental expectation (E) included, the statistics of the above parameters may be shown as follows (Hayman, 1954 b):

Parental mean $= \dfrac{\text{Sum of all the diagonal values}}{\text{Number of parents}}$, where

$$V_{0L0} = \frac{1}{n-1}\left[\sum \text{Diagonal values}^2 - \frac{\left(\sum \text{Diagonal values}\right)^2}{\text{Number of parents}}\right]$$

$$V_r = \frac{1}{n-1}\left[\sum \text{Crosses involving a particular parent}^2 - \frac{(\sum \text{Crosses involving a particular parent})^2}{\text{Number of parents}}\right.$$

$$V_{1L1} = \frac{1}{n}\sum V_{ri}$$

$$W_{0L01} = \frac{1}{n}\sum W_{ri}$$

$$V_{0L1} = \frac{1}{n-1}\left[\sum \text{Array mean}^2 - \frac{\left(\sum \text{Arrays mean}\right)^2}{\text{Number of arrays}}\right] \text{ and}$$

$$(ML_1 - ML_0)^2 = [\frac{1}{n}\ \{\frac{1}{n}\ (\text{Grand total - Diagonal values})\}]^2.$$

The above statistics may be defined as follows:

V_{0L0} = Variance of parents.

V_r = Variance of each array.

V_{1L1} = Mean variance of the arrays.

W_r = Covariance between parents and their offsprings.

W_{0L01} = Mean covariance between the parents and the arrays.

V_{0L1} = Variance of the mean arrays.

$(ML_1 - ML_0)^2$ = The difference between the mean of the parents and the mean of their n^2 progeny.

The environmental variation (E) was calculated by using the following formula:

$$E = 1/r \left\{ \frac{\text{Error ss} + \text{Replication ss}}{\text{Error df} + \text{Replication df}} \right\} \text{ and}$$

E=The expected environmental component of variation.

d. Testing the validity of the hypothesis

The probable fulfillment of the hypothesis (Hayman, 1954b) was tested by using the following formula:

$$t^2 = \frac{n - 2}{4} \left[\frac{(\text{VarVr - VarWr})^2}{\text{VarVr} \times \text{VarWr} - \text{Cov}^2(\text{Vr, Wr})} \right]$$

which is an F with 4 and (n - 2) degrees of freedom.

When,

$$\text{Var }(W_r) = \frac{1}{n-1} \left[\{\sum W_{ri}^2 - \frac{(\sum W_{ri})^2}{n} \right],$$

$$\text{Var }(V_r) = \frac{1}{n-1} \left[\{\sum Vr_{ri}^2 - \frac{(\sum V_{ri})^2}{n} \} \right] \text{ and}$$

$$\text{Cov }(V_r, W_r) = \frac{1}{n-1} \left[\{\sum V_r W_r - \frac{\sum V_r \sum W_r}{n} \right].$$

Were,

$\text{Var}(W_r)$ = Variance of W_r,

$\text{Var}(V_r)$ = Variance of V_r and

$\text{Cov}(V_r, W_r)$ = Covariance between V_r and W_r.

This is tested against the table value of "F" with 4 and (n - 2) degrees of freedom. Its significance indicates failure of the hypothesis. Another way of testing the hypothesis is through the regression coefficient, calculated by using the following formula:

$$b = \frac{\text{Cov}(V_r, W_r)}{\text{Var}(V_r)},$$

where,

$$\text{Cov}(W_r, V_r) = \left[\sum V_r W_r - \frac{\sum V_r \sum W_r}{n}\right] / (n-1)$$

and $$\text{Var}(V_r) = \left[\sum V_{ri}^2 - \frac{\left(\sum V_{ri}\right)^2}{n}\right] / (n-1).$$

Therefore,

$$b = \frac{\text{Cov}(V_r, W_r)}{\text{Var}(V_r)} \text{ and}$$

Standard error (b) = $[(\text{Var } W_r - b \text{ Cov } W_r V_r)/\text{Var } V_r (n - 2)]^{½}$.

Now the significance of b from zero and unity can be tested as follows:

$H_0 : b = 0$

$= (b - 0)/\text{S.E.}(b)$ and

$H_0 : b = 1$

$= (1 - b)/\text{S.E.}(b)$

These values are tested against table value of "t" for (n-2) degrees of freedom.

e. Components of variation and their proportions

For F_1 generation, the expected values of the components of variation obtained by least square computations were as follows:

Hayman (1954) derived the expectations for the statistics calculated from F_1 diallel table:

$D = V_{oLo}-E$,

$F=2\ V_{oLo}-4\ W_{oLo1}-2(n-2)E/n$,

$H_1= V_{oLo}-4\ W_{oLo1}+4\ V_{1L1}-(3n-2)E/n$,

$H_2=4\ V_{1L1}-4\ V_{oL1}-2E$,

$h^2=4(M_{L1}-M_{L0})^2-4(n-1)E/n^2$ and

$Fr=2(V_{oLo}-\ W_{oLo1}+\ V_{1L1}-Wr-Vr)-2(n-2)E/n$.

The above components are genetic parameters:

D=Variation due to additive effect,

F=The mean of 'Fr' over the arrays,

H_1=Component of variation due to the dominance effect of the genes and

$H_2= H_1[1-(u-v)^2]$.

where,

u=proportion of positive genes in the parents,

v= proportion of negative genes in the parents,

h^2= Dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses) and

Fr = The covariance of additive and dominance effects in a single array.

To test the significance of each of these components, respective standard error were calculated. Here, the common multiplier or variance (s^2) was calculated using the following formula:

$$s^2= \frac{1}{2}\,[\mathrm{Var}(Wr-Vr)]$$

$$=\frac{1}{2}\left[\frac{1}{n-1}\left\{\Sigma(Wri-Vri)^2-\frac{\Sigma\,(Wri-Vri)^2}{n}\right\}\right]$$

The specific multipliers for each component were calculated with the following formula:

$D= (n^5+n^4)/ n^5$,

$F= (4 n^5+20 n^4-16n^3+16n^2)/n^5$,

$H_1=(n^5+41 n^4-12 n^3+4n^2)/n^5$,

$H_2= (36n^4)/n^5$,

$h^2= (16 n^4+16n^2-32n+16)/n^5$ and

$E= n^4/ n^5$.

The standard errors for different estimates were then calculated using the specific multiplier and common multiplier which are as follows:

$SE (D) = \{\text{Specific multiplier} \times \text{Common multiplier } (s^2)\}^{1/2}$.

If the value of a parameter divided by its standard error exceeds 1.96, then it is significant.

Other parameters for F_1 generation, the proportional values were measured as follows:

i) Mean degree of dominance= $(H_1/D)^{1/2}$,

ii) Proportion of genes with positive and negative effects in the parents = $H_2/4 H_1$,

iii) Proportion of dominant and recessive genes in the parents $= [4 D H_1)^{1/2}+F]/[4 D H_1)^{1/2}-F]$ and

iv) The coefficient of correlation (r) between the parental order of dominance (Wr+Vr) and parental measurement Yr.

By comparing Wr+Vr values for each array with the mean of the common parent, i.e., comparing (Wri+Vri) with $\overline{Y}ri$, the direction of dominance can be seen. If the correlation is negative, it means parents containing most increasing genes have the lowest values of Wri+Vri, and thus, contain most dominant genes and correlation will be positive if the case is reverse. Thus, on the basis of this one can conclude whether or not the increasing or decreasing genes are the dominant ones.

v) Prediction for measurement of completely dominant and recessive parents,

$= r^2$,

vi) The number of groups of genes which control the character and exhibit dominance

$= h^2/H_2$,

vii) Fr = The covariance of additive and dominance effects in a single array

$Fri = 2[V_{oLo} - W_{oLo1} + V_{1L1} - (Wri + Vri)] - 2(n-2)E/n$

Mean of Fri= F.

In case of unequal gene frequencies the sign and amount of F will determine the relative frequency of dominant and recessive alleles. F is positive where dominant alleles are more frequent than recessive, irrespective of whether or not the dominant alleles have increasing or decreasing effects (Mather and Jinks, 1971).

viii) $h^2_{(ns)}$ = Heritability in narrow sense

$$= \frac{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{2}H_2 - \frac{1}{2}F}{\frac{1}{2}D + \frac{1}{2}H_1 - \frac{1}{4}H_2 - \frac{1}{2}F + E}$$

The components of variation of F_2 generation were estimated by the formulae given by Jinks (1956).

The composition of F_2 variances and covariances are as follows:

$$\overline{Vr} = V_{oL2} = \frac{1}{4}D + \frac{1}{16}H_1 - \frac{1}{8}F + E_2,$$

$$\overline{Wr} = W_{oLo2} = \frac{1}{2}D - \frac{1}{8}F + \frac{1}{n}E_2,$$

$$V_m = V_{oL2} = \frac{1}{4}D + \frac{1}{16}H_1 - \frac{1}{16}H_2 - \frac{1}{8}F + \frac{1}{n}E_2 \text{ and}$$

$$V_p = V_{oLo} = D + E.$$

where,

$E_2 = VE/r = Me'$ of F_2 and

N = Number of parents.

Components of variation in F_2 generations were measured as follows:

$D = V_{oLo}-E$,

$H_1 = 16\ V_{1L2} - 16\ W_{oLo2} + 4\ V_{oLo} - 4(5n-4)/n \times E_2$,

$H_2 = 16V_{1L2} - 16\ V_{oL2} - 16(n-1)/n \times E_2$,

$h^2 = (4M_{L2}-4M_{L0})^2 - 16(n-1)/n \times E_2$ and

$F = 4\ V_{oLo} - 8\ W_{oLo2} - 4(n-2)/n \times E_2$.

The standard errors, to test the significance of components listed above, were calculated as follows:

S.E. of $D = \sqrt{S^2(n^5+n^4)/n^5}$,

S.E. of $H_1 = \sqrt{S^2\ (16n^5+656\ n^4-192\ n^3+64n^2)/n^5}$,

S.E. of $H_2 = \sqrt{S^2(576n^4)/n^5}$,

S.E. of $F = \sqrt{S^2\ (16\ n^5+80\ n^4-64n^3+6n^2)/n^5}$,

S.E. of $h^2 = \sqrt{S^2\ (256\ n^4+256n^2-512n+256)/n^5}$ and

S.E. of $E_2 = \sqrt{S^2\ n^4/n^5}$.

where, n= Number of parents and $S^2 = 1/2$ Var.(Wr-Vr).

The significance of the various statistics was tested by '*t*' test at n-2 degrees of freedom as *t* = Parameter/S.E. of parameter.

In F_2 generation, the different proportions of the genetic components are worked out according to the procedure given below:

(i) Degree of dominance: The mean degree of dominance in F_2 is $[1/4(H_1/D)]^{1/2}$ following Verhalen *et al.* (1971) and when

$[1/4(H_1/D)]^{1/2}=1$, it is complete dominance, it is more than 1 then it is overdominance, it is less than 1 then it is partial dominance.

(ii) Proportion of genes with positive and negative effects in the parents: It is calculated as the ratio ($H_2/4\ H_1$). It denotes the mean product of u_i and v_i averaged over all the parents of a diallel set of crosses. When u and v are symmetrically distributed, i.e., u=v=0.5, the ratio will give the value of

$$H_2/4\ H_1=0.25.$$

(iii) Proportion of dominant and recessive genes in the parents: It is calculated as:

$$=\frac{\frac{1}{4}(4\ D\ H_1)^{1/2}+\frac{1}{2}F}{\frac{1}{4}(4\ D\ H_1)^{1/2}-\frac{1}{2}F}$$

(iv) Number of groups of genes which control the character and exhibit dominance: It is calculated as h^2/H_2. It is an approximate measure of sets of genes exhibiting dominance and

(v) Estimation of heritability: Heritability in narrow sense is defined as the ratio of additive and/or additive×additive genetic variance to the total phenotypic variance. In F_2, it is calculated following Verhalen and Murray (1969) as:

$$\text{Heritability}=\frac{\frac{1}{4}D}{\frac{1}{4}D+\frac{1}{16}H_1-\frac{1}{8}F+E}$$

f. Graphical analysis

The relationship of Wr with Vr provides some useful information. Therefore, the Wr values are plotted against the corresponding values of Vr. Corresponding values of Wri against Vr values are calculated following formulae given below. These values are called parabola limits which help to draw parabola.

$\mathrm{Wri} = (\ \mathrm{Vri} \times \mathrm{V}_{\mathrm{oLo}})^{1/2}$ and

Initial value $\mathrm{Wr} = [\ \mathrm{V}_{\mathrm{1L1}} . \mathrm{V}_{\mathrm{oLo}}]^{1/2}$

Using these *Wr* values against *Vr* values, the external limits of parabola are determined.

For drawing regression line, the expected *Wrei* values are required. These are calculated as below:

$$\mathrm{Wrei} = \overline{\mathrm{Wr}} - \mathrm{b}\ \overline{\mathrm{Vr}} + \mathrm{b}\ \mathrm{Vri}$$

The point of interception of the regression line with *Wr* ordinate i.e. 'a' is obtained by the following equation:

$$\mathrm{a} = \overline{\mathrm{Wr}} - \mathrm{b}\ \overline{\mathrm{Vr}}$$

From Wr, Vr- graph, the following information are observed:

1. In the absence of non-allelic interaction and with independent distribution of genes among the parents, *Wr* is related to *Vr* by a straight regression line of unit slope.

2. The distance between the origin and the point where the regression line cuts the *Wr*-axis provides a measure of average degree of dominance:

    (i) $D>H_1$ (partial dominance), when the intercept is positive;
    (ii) $D=H_1$ (complete dominance), when the line passes through origin;
    (iii) $D<H_1$ (overdominance), when the intercept is negative, and
    (iv) No dominance, when the regression line touches parabola limit.

3. The order of the array points along the regression line throws light on the distribution of dominant and recessive genes amomg the parents. The parents with most dominant genes have their points nearest to the origin, while the parents with most recessive genes fall furtherest from origin. Evidently, the parents with equal frequencies of dominant and recessive genes fall in the middle.

The Vr/Wr graph in F_2 generation was also done.

Experiment II:

In experiment II, materials were same of experiment I. Data on twelve quantitative traits (described in Experiment I) were analyzed following the techniques given below.

Techniques of the analysis of data

a. Estimation of heterosis over mid-parent and better-parent

For estimation of heterosis in each parameter the mean values of the 15 F_1s have been compared with better-parents (BP) for heterobeltoisis and with mid-parent (MP) for heterosis over mid parent value. Percent heterosis was calculated as

$$\text{Heterosis (MP)} = \frac{\overline{F}_1 - MP}{MP} \times 100$$

and

$$\text{Heterosis (BP)} = \frac{\overline{F}_1 - BP}{BP} \times 100.$$

Overall heterosis was calculated. Significant tests were done by using standard error of mean described below.

Mid-parent = $\frac{1}{2}(P_1+P_2)$,

Variance of $F_1 = VF_1$,

Variance of MP and $F_1 = VF_1 - 1/4(VP_1+VP_2)$,

Standard error of MP and $F_1 = \sqrt{1/4VP_1+1/4VP_2+VF_1}$,

Standard error of mean = Standard error of MP and $F_1/\sqrt{n}$,

$$\text{Variance of } F_1 = \frac{\Sigma x_i^2 - \frac{(\Sigma x_i)^2}{n}}{n-1},$$

$$\text{Variance of } P_1 = \frac{\Sigma x_i^2 - \frac{(\Sigma x_i)^2}{n}}{n-1},$$

and

$$\text{Variance of } P_2 = \frac{\Sigma x_i^2 - \frac{(\Sigma x_i)^2}{n}}{n-1}.$$

Here, variances were within variances between observations for respective generation and

t = Estimated value of mid parent heterosis/Standard error of mean,

Variance=Variance of F_1- Variance of better parent

=VF_1+ VP_i and

t = Estimated value of better parent heterosis/standard error of mean.

The variances were within variances of F_1s and parents.

b. Model fitting: Generation mean analysis

Model fitting is a procedure known as the joint scaling test proposed by Cavalli (1952). It consists of estimating parameters, $\hat{m}$, [d] and [h] from means of the available types of generations followed by a comparison of the observed generation means with expected values derived from the estimates of the three parameters.

In the present study, the model was fitted consisting of $\hat{m}$, [d] and [h] by weighted least squares techniques and testing its goodness of fit using χ^2 for 4-3=1 df from observed and expected values. When potence absent, $\hat{m}$ and [d] parameters were considered. The model was considered as given in Table 7.

Table 7: Generation mean, weights and co-efficient in 3-parameter model

Generation	Mean	Weight	Coefficients of parameters		
			$\hat{m}$	[d]	[h]
P_1			1	1	0
P_2			1	-1	0
F_1			1	0	1
F_2			1	0	½

Here, '$\hat{m}$' measures mean, [d] measures the additive gene effects and [h] measures the dominance gene effects.

The four equations and their weights were combined to three or two equations. A general approach for the solution was followed by matrix inversion. The formula is $M = J^{-1} S$, where M is the estimation of the parameters, S is the matrix of score and J is the information matrix. J^{-1} is the inverse of the information matrix and is a variance-covariance matrix.

Calculation of Score Matrix is as follows:

$\sum[\text{Coef.m.Yi.wi}]$

$\sum[\text{Coef.d.Yi.wi}]$

$\sum[\text{Coef.h.Yi.wi}]$

Information Matrix is estimated by the following formulae:

$\sum[\text{Coef.m}^2\text{.wi}]$

$\sum[\text{Coef.m. Coef d.wi}]$

$\sum[\text{Coef.m. Coef h.wi}]$

$\sum[\text{Coef.d}^2\text{.wi}]$

$\sum[\text{Coef.d. Coef h.wi}]$

$\sum[\text{Coef.h}^2\text{.wi}]$

When potence absent, the calculation are as follows:

Calculation of Score Matrix is like

$\sum[\text{Coef.m.Yi.wi}]$

$\sum[\text{Coef.d.Yi.wi}]$

and Information matrix is given by

$\sum[\text{Coef.m}^2\text{.wi}]$

$\sum[\text{Coef.m. Coef d.wi}]$

$\sum[\text{Coef.d}^2\text{.wi}]$.

Test of potence:

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

Potence = $\overline{F}_1 - \overline{F}_2$ with

Standard error = $\sqrt{VF_1+VF_2}$

Test of significance are done by't' test, where

t = Estimated value of $\overline{F}_1 - \overline{F}_2$ / Standard error of mean

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

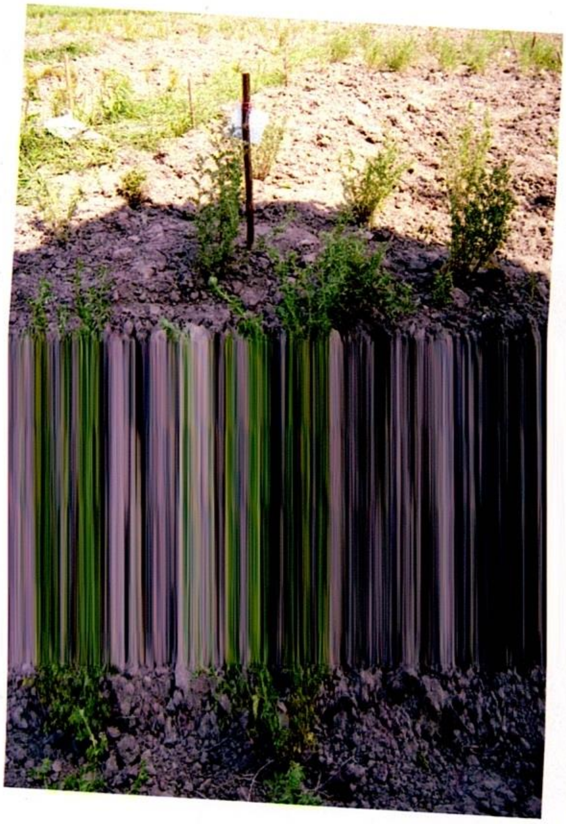

Plate 1: Plants of M_1 generation

Plate 2: Plants of M_2 generation

Plate 3: Crossing pattern in M_2 generation

Plate 4: Cross pod in the bag

Plate 5: Layout of experimental field for F_1 generation and parents trial

Plate 6: Plants of F_1 generation and

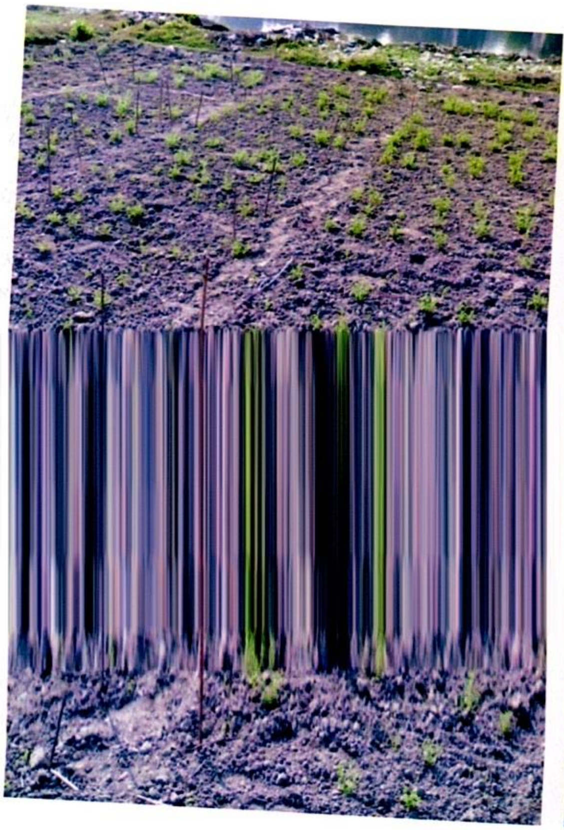

Plate 7: Plants of crossing plots

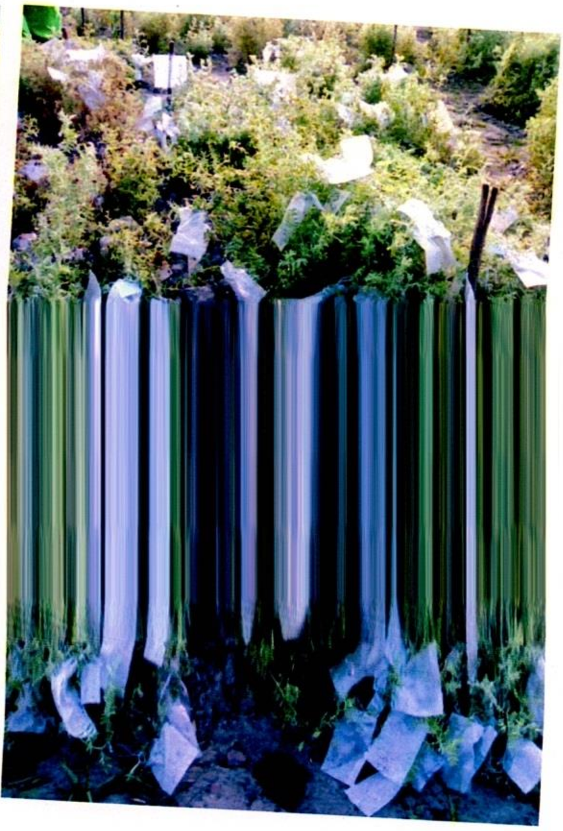

Plate 8: Crossing plots

Plate 9: Field trial of F_1, F_2 progenies and parents

Plate 10: Plant of F_1 (24)

Plate 11: Plant of F_2 (36)

Plate 12: Plant of F (15)

RESULTS

Experiment-wise results are discussed as follows:

Experiment I: Combining ability and gene action of twelve yield and yield contributing characters through half diallel

The present investigation involved diallel analysis of yield and some of the yield contributing characters viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), number of secondary branches at maximum flower (NSBMF), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) in lentil using Griffing's (1956) and Hayman's (1954) approach and by using the formulae given by Jinks (1956).

a. Testing the significance of genotypic differences

According to Griffing (1956), analyses of variance of six parental half diallel analysis and test of significance were done. The results are shown in Table 8-19. This analysis involves the partitioning of the total variance into treatments, replications and error.

b. Combining ability analysis

For the combining ability analysis, the total variability of the population was partitioned into components like variance due to general combining ability (gca), specific combining ability (sca) and error. These results are shown in Table 20.

From analysis of variance, the variation due to gca was found to be significant for the characters viz., DF, PHFF, CAMF and RW indicating that additive gene actions played significant role for the expression of these characters. In the present investigation, variance due to sca was non significant for all of the characters. The relative magnitude of gca was higher than sca for all twelve characters studied indicating the predominance of the additive gene effects for the characters. Component variance due to gca (σ^2g) was higher than that of due to sca (σ^2s) for DF, NPBFF, CAMF, PdWPP, SWPP and IPlW (Table-21). Additive genetic component (σ^2A) was greater than dominance component (σ^2D) for DF, PHFF, NPBFF, CAMF, PdWPP, SWPP, IPlW and RW.

For DF (Table 22), the negative and significant gca effect was obtained by P_3, positive and significant value was obtained by P_4. The highest value of gca effect was obtained by P_3 followed by P_6, P_1 and P_2, respectively.

For PHFF, positive and significant gca effects was obtained by P_2 and P_3. Negative and significant gca effect was obtained by P_1. The highest positive value of gca effect was obtained by P_2 followed by P_3. P_1, P_4, P_5 and P_6, respectively showing negative and non significant gca effects.

For NPBFF, the highest positive gca effect was shown by P_5 followed by P_4 and P_1.

For NSBFF, the highest positive gca effect was obtained by P_4 followed by P_5. P_4 also obtained significant gca effect.

For CAMF, the highest positive gca effect was shown by P_2 followed by P_3. These two parents showed significant gca effects for this trait.

For NSBMF, the highest positive gca effect was shown by P_5 followed by P_1 and P_2.

For NPdPP, the highest positive and non significant gca effect was shown by P_4 followed by P_5, P_3, P_2 and P_1, respectively.

The highest positive gca effect was obtained by P_2 followed by P_4, P_3 and P_5, respectively for PdWPP.

For NSPP, P_4 showed the highest positive gca effect followed by P_3 and P_2.

The highest positive gca effect was shown by P_2 followed by P_4 and P_3 for SWPP.

For IPlW, the highest positive gca effect was shown by P_2 followed by P_3 and P_4.

For RW, parent P_4 showed the highest positive gca effect followed P_2 and P_1.

The parent 4 (P_4) showed the highest gca effects for NSBFF, NPdPP, NSPP and RW, parent 2 (P_2) showed the highest values for PHFF, CAMF, PdWPP SWPP and IPlW, parent 5 (P_5) showed the highest values for NPBFF and NSBMF and parent 3 (P_3) showed the highest value for DF, P_4, P_2, P_5 and P_3. These performed better combiner for the respective traits. P_6 showed significant and negative gca effects for all of the characters except DF, PHFF, NSBFF and NSBMF.

The specific combining ability effects of fifteen crosses for twelve characters studied are presented in Table 23 to Table 34. Of the F_1s, different cross combinations showed significant and non significant sca effects for different characters. The highest positive and significant sca effects were obtained for NSBFF, PdWPP, SWPP and RW in $P_1 \times P_2$. For CAMF, NSBMF, NPdPP and IPlW, the highest positive and significant sca effects were obtained in $P_1 \times P_3$. The cross combinations of $P_1 \times P_2$ and $P_1 \times P_3$ are very consistent regarding specific combining ability for the improvement of the respective characters. The highest negative and significant sca effect was recorded in $P_2 \times P_4$ for DF and for PHFF, the highest positive sca effect was obtained in $P_4 \times P_5$. The highest positive and significant sca effect was obtained in $P_4 \times P_6$ for NPBFF and the highest positive sca effect was obtained in $P_5 \times P_6$ for NSPP. These results indicated that above crosses were also good specific combiners for the respective characters.

Table 8: Analysis of variance for the character, days to flower (DF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	306.0297	15.30148	1.933915^{NS}
Replications	1	1.805459	1.805459	0.228187^{NS}
Error	20	158.2436	7.912178	
Total	41	466.0787		

'NS' indicates non significant.

Table 9: Analysis of variance for the character, plant height at first flower (PHFF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	116.3951	5.819757	1.527512^{NS}
Replications	1	3.456456	3.456456	0.907216^{NS}
Error	20	76.19918	3.809959	
Total	41	196.0508		

'NS' indicates non significant.

Table 10: Analysis of variance for the character, number of primary branches at first flower (NPBFF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	32.68805	1.634403	1.082022^{NS}
Replications	1	4.12798	4.12798	2.732844^{NS}
Error	20	30.21014	1.510507	
Total	41	67.02618		

'NS' indicates non significant.

Table 11: Analysis of variance for the character, number of secondary branches at first flower (NSBFF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	275.9459	13.79729	1.763552^{NS}
Replications	1	21.27456	21.27456	2.719287^{NS}
Error	20	156.4717	7.823583	
Total	41	453.6921		

'NS' indicates non significant.

Table 12: Analysis of variance for the character, canopy area at maximum flower (CAMF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	615707.9	30785.39	2.198621*
Replications	1	53159.12	53159.12	3.796501 ^{NS}
Error	20	280042.7	14002.14	
Total	41	948909.7		

'*' indicates significant at 5% level and 'NS' indicates non significant.

Table 13: Analysis of variance for the character, number of secondary branches at maximum flower (NSBMF) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	850.2306	42.51153	0.907628 ^{NS}
Replications	1	192.6425	192.6425	4.112948 ^{NS}
Error	20	936.761	46.83805	
Total	41	1979.634		

'NS' indicates non significant.

Table 14: Analysis of variance for the character, number of pods per plant (NPdPP) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	40993.26	2049.663	0.913344 ^{NS}
Replications	1	771.8546	771.8546	0.343944 ^{NS}
Error	20	44882.61	2244.13	
Total	41	86647.72		

'NS' indicates non significant.

Table 15: Analysis of variance for the character, pod weight per plant (PdWPP) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	52.38616	2.619308	1.067213 ^{NS}
Replications	1	4.414372	4.414372	1.798596 ^{NS}
Error	20	49.08687	2.454343	
Total	41	105.8874		

'NS' indicates non significant.

Table 16: Analysis of variance for the character, number of seeds per plant (NSPP) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	51713.26	2585.663	0.890375 ^{NS}
Replications	1	971.2526	971.2526	0.334452 ^{NS}
Error	20	58080.32	2904.016	
Total	41	110764.8		

'NS' indicates non significant.

Table 17: Analysis of variance for the character, seed weight per plant (SWPP) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	30.72092	1.536046	1.144696 ^{NS}
Replications	1	1.240705	1.240705	0.924601 ^{NS}
Error	20	26.83763	1.341882	
Total	41	58.79926		

'NS' indicates non significant.

Table 18: Analysis of variance for the character, individual plant weight (IPlW) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	31.63814	1.581907	1.318264 ^{NS}
Replications	1	8.704243	8.704243	7.253584*
Error	20	23.99984	1.199992	
Total	41	64.34222		

'*' indicates significant at 5% level and 'NS' indicates non significant.

Table 19: Analysis of variance for the character, root weight (RW) is shown in the table.

Source	d.f.	S.S.	M.S.	F.
Treatments	20	0.16385	0.008192	1.973445 ^{NS}
Replications	1	0.032365	0.032365	7.796201*
Error	20	0.083027	0.004151	
Total	41	0.279242		

'*' indicates significant at 5% level and 'NS' indicates non significant.

Table 20: Anova of combining ability for different characters

Sources	df	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
gca	5	19.79922**	9.10334**	1.077917^{NS}	10.26172^{NS}	36381.6*	21.53223^{NS}	1121.474^{NS}	1.743968^{NS}	1588.537^{NS}	0.991245^{NS}	1.367646^{NS}	0.007409**
sca	15	3.601248^{NS}	0.845391^{NS}	0.730296^{NS}	5.777624^{NS}	8396.396^{NS}	21.16361^{NS}	992.6176^{NS}	1.164883^{NS}	1194.263^{NS}	0.693616^{NS}	0.598723^{NS}	0.002992^{NS}
Error	20	3.956089	1.90498	0.755254	3.911791	7001.068	23.41903	1122.065	1.227172	1452.008	0.670941	0.599996	0.002076

N.B. ** Significant at 1% level of probability

* Significant at 5% level of probability

^{NS} Non-significant

Table 21: Component variances due to general combining ability, specific combining ability, additive gene effects and dominant gene effects are shown in the table for the twelve characters.

	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
$\sigma^2 g$	2.024746	1.032244	0.043453	0.560512	3498.151	0.046077	16.107	0.072386	49.28419	0.037204	0.096115	0.000552
$\sigma^2 s$	-0.35484	-1.05959	-0.02496	1.865832	1395.328	-2.25542	-129.448	-0.06229	-257.745	0.022675	-0.00127	0.000916
$\sigma^2 e$	3.956089	1.90498	0.755254	3.911791	7001.068	23.41903	1122.065	1.227172	1452.008	0.670941	0.599996	0.002076
$\sigma^2 A$	4.049493	2.064487	0.086905	1.121023	6996.302	0.092155	32.21401	0.144771	98.56838	0.074407	0.192231	0.001104
$\sigma^2 D$	-0.35484	-1.05959	-0.02496	1.865832	1395.328	-2.25542	-129.448	-0.06229	-257.745	0.022675	-0.00127	0.000916

Table 22: Estimates of gca effects of parents for different characters.

	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
P_1	-0.48507^{NS}	-0.98951*	0.140625^{NS}	-0.96632^{NS}	-36.8722^{NS}	0.63125^{NS}	1.640973^{NS}	-0.01717^{NS}	-0.41118^{NS}	-0.02756^{NS}	-0.05858^{NS}	0.016121^{NS}
P_2	-0.07153^{NS}	1.690585*	-0.03855^{NS}	-0.36529^{NS}	83.23422*	0.379169^{NS}	1.746179^{NS}	0.431035^{NS}	1.030487^{NS}	0.39309^{NS}	0.579375*	0.03014*
P_3	-2.29757*	0.946629*	-0.07188^{NS}	-0.40539^{NS}	79.6638*	-0.00469^{NS}	2.937842^{NS}	0.051367^{NS}	12.07632^{NS}	0.087371^{NS}	0.3109^{NS}	-0.01277^{NS}
P_4	2.265969*	-0.38013^{NS}	0.25105^{NS}	1.805027*	-9.79882^{NS}	-0.09219^{NS}	11.52325^{NS}	0.384329^{NS}	14.29508^{NS}	0.194833^{NS}	0.055719^{NS}	0.031308*
P_5	1.173781^{NS}	-0.569^{NS}	0.381244^{NS}	0.946183^{NS}	-33.0705^{NS}	2.042188^{NS}	5.120142^{NS}	0.018317^{NS}	-1.72316^{NS}	-0.0007^{NS}	-0.33845^{NS}	-0.02191^{NS}
P_6	-0.58558^{NS}	-0.69858^{NS}	-0.66249*	-1.01422^{NS}	-83.1566*	-2.95573^{NS}	-22.9684*	-0.86788*	-25.2675*	-0.64704*	-0.54896*	-0.04289*

N.B. ** Significant at 1% level of probability

* Significant at 5% level of probability

^{NS} Non-significant

Table 23: Estimates of sca effects for days to flower (DF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	1.307586^{NS}	-2.35388^{NS}	0.165936^{NS}	-1.26273^{NS}	2.350836^{NS}
P_2		-0.37991^{NS}	-3.1101*	-0.16376^{NS}	-0.8419^{NS}
P_3			-0.20906^{NS}	4.049773*	-2.39916^{NS}
P_4				0.361236^{NS}	0.920598^{NS}
P_5					-0.14136^{NS}

Table 24: Estimates of sca effects for plant height at first flower (PHFF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	0.599598^{NS}	0.343554^{NS}	0.549511^{NS}	0.400829^{NS}	-0.12789^{NS}
P_2		-0.03905^{NS}	-1.08309^{NS}	1.076579^{NS}	-0.96634^{NS}
P_3			0.150867^{NS}	-2.06446*	0.610967^{NS}
P_4				1.174792^{NS}	-0.40563^{NS}
P_5					0.809942^{NS}

Table 25: Estimates of sca effects for number of primary branches at first flower (NPBFF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	0.914582^{NS}	-0.50209^{NS}	0.966682^{NS}	-0.45521^{NS}	-0.49477^{NS}
P_2		-0.69792^{NS}	-0.72914^{NS}	0.973963^{NS}	-0.0823^{NS}
P_3			0.054182^{NS}	1.257288^{NS}	-0.53227^{NS}
P_4				-0.56564^{NS}	1.728101*
P_5					0.181257^{NS}

Table 26: Estimates of sca effects for number of secondary branches at first flower (NSBFF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	4.999254*	-0.26065^{NS}	-0.13771^{NS}	-0.09136^{NS}	-2.11011^{NS}
P_2		-2.01168^{NS}	-4.13874*	1.824254^{NS}	-0.60284^{NS}
P_3			-0.44864^{NS}	-3.04815*	0.078961^{NS}
P_4				2.616442^{NS}	1.426848^{NS}
P_5					1.498242^{NS}

Table 27: Estimates of sca effects for canopy area at maximum flower (CAMF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	117.2787^{NS}	138.7746*	-9.46407^{NS}	-15.8468^{NS}	-25.4296^{NS}
P_2		-115.943^{NS}	-75.1116^{NS}	-21.8127^{NS}	15.23168^{NS}
P_3			22.06223^{NS}	-128.179*	61.31005^{NS}
P4				120.7686^{NS}	-130.121*
P5					78.242^{NS}

Table 28: Estimates of sca effects for number of secondary branches at maximum flower (NSBMF).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	4.390774^{NS}	11.66213*	0.99963^{NS}	0.156905^{NS}	-4.88683^{NS}
P_2		-4.37329^{NS}	0.714212^{NS}	5.454837^{NS}	1.127755^{NS}
P_3			-0.63528^{NS}	-4.93631^{NS}	-0.93839^{NS}
P_4				-0.59881^{NS}	0.949112^{NS}
P_5					2.389737^{NS}

Table 29: Estimates of sca effects for number of pods per plant (NPdPP).

Parents	P2	P3	P4	P5	P6
P1	45.88229^{NS}	68.64063*	20.43021^{NS}	-5.54167^{NS}	-22.0364^{NS}
P2		-33.5396^{NS}	3.250007^{NS}	-15.3885^{NS}	11.14165^{NS}
P3			3.299995^{NS}	-25.8385^{NS}	-8.08331^{NS}
P4				14.07604^{NS}	7.264576^{NS}
P5					32.23439^{NS}

Table 30: Estimates of sca effects for pod weight per plant (PdWPP).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	2.533476*	1.535395^{NS}	-0.90757^{NS}	-0.72216^{NS}	-0.00451^{NS}
P_2		-0.95906^{NS}	-0.03952^{NS}	-0.92411^{NS}	-0.08932^{NS}
P_3			0.180145^{NS}	-0.83009^{NS}	-0.0443^{NS}
P_4				0.790695^{NS}	-1.14811^{NS}
P_5					0.924751^{NS}

Table 31: Estimates of sca effects for number of seeds per plant (NSPP).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	27.58279^{NS}	49.99946^{NS}	11.11406^{NS}	11.77809^{NS}	7.426669^{NS}
P_2		-31.7547^{NS}	-7.39011^{NS}	-26.8094^{NS}	2.68915^{NS}
P_3			22.64741^{NS}	-48.7511^{NS}	-15.8733^{NS}
P_4				40.03019^{NS}	-23.4254^{NS}
P_5					54.9053^{NS}

Table 32: Estimates of sca effects for seed weight per plant (SWPP).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	1.966702*	0.913571^{NS}	-0.82224^{NS}	-0.67876^{NS}	-0.04247^{NS}
P_2		-0.78523^{NS}	-0.10849^{NS}	-0.66676^{NS}	-0.09732^{NS}
P_3			0.333877^{NS}	-0.56269^{NS}	-0.1055^{NS}
P_4				0.851096^{NS}	-1.00707^{NS}
P_5					0.777164^{NS}

Table 33: Estimates of sca effects for individual plant weight (IPIW).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	1.011328^{NS}	1.353553*	0.579984^{NS}	-0.13105^{NS}	-0.40488^{NS}
P_2		-1.1104^{NS}	1.033528^{NS}	0.094996^{NS}	0.123809^{NS}
P_3			-0.2291^{NS}	-0.66908^{NS}	0.229384^{NS}
P_4				-0.00515^{NS}	-0.49063^{NS}
P_5					0.677234^{NS}

Table 34: Estimates of sca effects for root weight (RW).

Parents	P_2	P_3	P_4	P_5	P_6
P_1	0.146471*	0.029383^{NS}	-0.0522^{NS}	0.002521^{NS}	0.045346^{NS}
P_2		-0.03764^{NS}	-0.00422^{NS}	-0.012^{NS}	0.012477^{NS}
P_3			4.55E-05^{NS}	-0.02759^{NS}	-0.00076^{NS}
P_4				0.025833^{NS}	-0.04969^{NS}
P_5					-0.00437^{NS}

c. Estimation of variances and covariances in F_1 and F_2 generations

Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown in Table 35 and 38 for twelve characters of F_1 and F_2 generations, respectively. Above estimates of twelve characters for replication 1 and 2 are shown in Table 36 and for replication total are shown in Table 37 of F_1 generation and all the above estimates for these characters of replication 1 and 2 of F_2 generation are shown in Table 39 and for replication total of F_2 generation, the above estimates are presented in Table 40.

d. Testing the validity of the hypothesis

The validity of the postulated hypothesis for diallel was tested by t^2 and the values were obtained as 1.217789, 0.187565, 0.016454, 2.69364, 2.5545595, 4.853816, 0.604256, 0.920536, 0.686233, 1.900917, 0.009248 and 2.116959 for DF, PHFF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW, respectively in F_1 generation. The above non significant values suggested the probable fulfillment of the postulated hypothesis.

Values of testing the significance difference of regression coefficient (b) from zero and unity are shown in Table 41 for twelve characters of replication 1 and in Table 42 of replication 2 in F_1 generation. The values of above estimations for these characters are presented in Table 43 for replication 1 and in Table 44 for replication 2 in F_2 generation and these estimates are presented in Table 45 for replication total of F_1 generation and in Table 46 for replication total of F_2 generation.

e. Components of variation and their proportions

The components of variation and their proportions of twelve characters namely days to first flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF) number of secondary branches at maximum flower (NSBMF), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), seed weight per plant

(SWPP), individual plant weight (IPlW) and root weight (RW) are shown in Table 47 and Table 48 for F_1 and F_2 generations, respectively.

In F_1 generation, the component D which measures variation due to additive effects was significant for DF, PHFF, NPBFF and CAMF indicating that there was a significant role of additive gene effects on their inheritance.

The F values were non significant for all the characters except NPBFF indicating equal amount of dominant and recessive genes were present in the parents. The significant F values of NPBFF suggested the presence of dominant genes in the parents.

Component of variation H_1 which is due to the dominance effect of the genes was significant for the character CAMF revealing that there was a significant role of dominant gene effects in the expression of this character.

The H_2 component was significant for DF, NPBFF and CAMF indicating dominance with asymmetry of positive and negative effects was present for the respective traits. H_1 was greater than H_2 for PHFF, NSBFF, NPdPP, NSPP and RW indicating that dominance effect was important in controlling these characters. H_2 was greater than H_1 for DF, NPBFF, CAMF, NSBMF, PdWPP, SWPP and IPlW.

The h^2, the dominance effect as the algebraic sum over heterozygous phase in all crosses was non significant for all the characters under studied. It was negative for DF, PHFF, NSBFF, CAMF, PdWPP, SWPP and RW indicated that decreasing alleles are dominant in the loci in heterozygous phase in all crosses. Rest of all traits showed positive value of h^2 suggesting that increasing alleles are dominant in the loci in heterozygous phase in all crosses.

E, the expected environmental variation was significant for all of the characters indicating that environment play an important in the expression of these characters.

In the present study, the ratios of $[(H_1/D)]^{1/2}$ suggested over dominance for NSBFF, NSPP, SWPP, IPlW and RW, whereas partial dominance was recorded for the remaining characters except NPBFF, NPdPP and PdWPP. For NPBFF, NPdPP and PdWPP, this ratio showed negative values which were more than one.

The ratio of $H_2/4H_1$ provides an estimate of the average frequency of positive and negative alleles in the parents. In the present study, the values of this ratio were less than 0.25 for PHFF, NSBFF, NSPP and RW indicating asymmetry in gene distribution. Symmetrical distribution was found for all other characters.

The ratio of $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ estimates the relative proportion of dominant and recessive genes in the parents. In this study, the values of the ratio were more than one recorded in CAMF, NSBMF, NPdPP, NSPP, SWPP and RW indicating the presence of an excess of dominant genes in the parents. Excessive of recessive genes was found for all other traits except NSBFF. Nearly equal distribution of dominant and recessive genes was found for NSBFF. Negative values, which were more than one, were observed for NPBFF and PdWPP.

The ratio of h^2/H_2 indicates the number of groups of genes which control the character exhibiting dominance. Only one group of genes controlled the characters namely DF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW and two group of genes controlled PHFF.

The coefficient of correlation (r) was negative for DF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP and IPlW indicating that parents containing most increasing genes have the lowest values of Wr_i+Vr_i and thus contain most dominant genes. For the characters, PHFF, SWPP and RW, the coefficient of correlation (r) was positive indicating that parents containing most increasing genes having the highest values of Wr_i+Vr_i.

The value of heritability in narrow sense was 0.462991, 0.495144, 0.135144, 0.218407, 0.36782, 0.07324, 0.092914, 0.127152, 0.089877, 0.137807, 0.218579 and 0.318706 for DF, PHFF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW, respectively. The highest value of heritability was obtained by PHFF.

Value of Fr_1 was negative for all of the traits indicating that parent 1 possessed more recessive genes for all of the characters. Value of Fr_2 was positive for DF, PHFF, NSBFF, CAMF, NPdPP, NSPP and IPlW indicating dominant genes were more frequent than recessive genes in parent 2 for these traits. Value of Fr_3 was positive for NSBFF, CAMF, PdWPP, SWPP, IPlW and RW indicaing that parent 3 possessed more dominant genes for these traits. Value of Fr_4 was positive for PHFF, NPBFF, NSBMF and NPdPP indicating that parent 4 possessed more dominant genes for these traits. Value of Fr_5 was positive for DF, PHFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW indicating more dominant genes were possessed by parent 5 for these traits. Value of Fr_6 was positive for PHFF, PdWPP, NSPP, SWPP and RW suggesting more dominant genes were possessed by parent 6 for these traits.

In F_2 generation, additive component (D) was significant for PHFF, CAMF, IPlW and RW indicating the importance of the additive gene effects in controlling of these characters.

The H_1 component was significant for NPdPP, PdWPP, NSPP and SWPP indicating dominant genes had a significant role in these characters inheritance.

H_2 component was significant for PdWPP, NSPP and SWPP. The value of H_1 was greater than H_2 for DF, PHFF, NSBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP and IPlW, suggesting that asymmetry of gene distribution was present for these characters.

The h^2 was significant for NPBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW indicating that significant dominance effect as the algebraic sum over all loci in heterozygous phase in all crosses was present in the parents for these characters.

F was significant for NSPP suggesting the presence of dominant genes in the parents. F was non significant for rest of the characters indicating equal amount of dominant and recessive genes was present in the parents for these traits.

E_2 was significant for all the character except DF and NSBFF indicating that environment play an important in the expression of these characters.

In the present study, the ratio of $[1/4(H_1/D)]^{1/2}$ suggested over dominance for DF, NPBFF, NSBFF, NSBMF, NPdPP, NSPP and SWPP, whereas partial dominance was shown by PHFF, CAMF, IPlW and RW. The PdWPP showed negative value, which was more than one.

The ratio $H_2/4H_1$ indicates proportion of genes with positive and negative effects in the parents. The values of the ratio were less than 0.25 for the characters viz., DF, PHFF, NSBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP and IPlW indicating unequal distribution of genes with positive and negative effects. NSBMF and RW showed more value than 0.25 indicating symmetrical distribution of genes with positive and negative effects in the parents.

$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$ is the calculation of proportion of dominant and recessive genes in the parents. This value was more than one for the characters viz., DF, NSBFF, CAMF and IPlW indicating the presence of an excess of dominant genes in the parents. Rest of the characters except PdWPP showed excess of recessive genes in the parents and PdWPP showed more than one but negative value.

The h^2/H_2 indicates the number of groups of genes which control the character and exhibit dominance. Only one group of genes controlled DF, PHFF and NSBFF characters. Six groups of genes controlled the character, NPBFF with negative effect. Four groups of genes controlled the characters viz., CAMF and NSBMF and for later with negative effects. There were three groups of genes that controlled NPdPP and two groups of genes controlled PdWPP, NSPP and SWPP. Ten groups of genes controlled IPlW and RW was controlled by seven groups of genes.

The highest value of heritability was obtained for RW (1.118606) and others showed moderate heritability except NPBFF, NSBFF, NSBMF and NPdPP. Negative value were shown by NPBFF, NPdPP and SWPP. SWPP showed the value -4.12541.

Table 35: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters in the F_1 generation.

Days to flower (DF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	6.40202	6.509406	-0.10739	12.91143	65.625	V_{oLo} = 10.07315
2	2.052967	2.702082	-0.64912	4.755049	68.15	V_{1L1}=5.923189
3	5.702526	10.26924	-4.56671	15.97176	62.75	V_{oL1}=2.580079
4	4.88884	5.816221	-0.92738	10.70506	72.16665	W_{oLo1}=4.619814
5	1.831651	2.667123	-0.83547	4.498774	67.625	
6	6.840878	7.575063	-0.73418	14.41594	65.58335	

Plant height at first flower (PHFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.616289	2.205042	1.411247	5.821331	16.6625	V_{oLo}=6.5463
2	2.555825	1.94737	0.608456	4.503195	23.11165	V_{1L1}=1.7786
3	3.264171	2.437741	0.82643	5.701912	21.91665	V_{oL1}=1.0033
4	1.406066	0.735184	0.670882	2.14125	18.57085	W_{oLo1}=2.5135
5	2.095419	2.284642	-0.18922	4.380061	17.6875	
6	2.143378	1.06177	1.081607	3.205148	18.16665	

Number of primary branches at first flower (NPBFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.302535	0.784456	-0.48192	1.086991	7.75	V_{oLo}=0.486565,
2	0.325252	0.874395	-0.54914	1.199647	7.41665	V_{1L1}=0.829235,
3	0.442468	0.978056	-0.53559	1.420524	7.75	V_{oL1}=0.152912,
4	-0.24432	0.624764	-0.86908	0.380446	7.45835	W_{oLo1}=0.21933
5	0.18448	0.545598	-0.36112	0.730078	7.75	
6	0.305561	1.168141	-0.86258	1.473702	5.95835	

Number of secondary branches at first flower (NSBFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.120279	7.928237	-4.80796	11.04852	9.25	V_{oLo}=7.017565,
2	-4.31708	7.600666	-11.9177	3.283583	11.61665	V_{1L1}=6.644175,
3	3.435113	3.778227	-0.34311	7.213341	14.41665	V_{oL1}=1.383359,
4	2.905833	7.936531	-5.0307	10.84236	16.3333	W_{oLo1}=2.106271
5	2.253802	6.967395	-4.71359	9.221197	12.875	
6	5.239683	5.653997	-0.41431	10.89368	10.20835	

Table 35 continued

Canopy area at maximum flower (CAMF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	25108.974	24037.5	1071.47	49146.48	302.2075	V_{oLo}=27460.507, V_{1L1}=11861.268, V_{oL1}=4079.0392, W_{oLo1}=9728.9081
2	3870.305	7515.748	-3645.44	11386.05	685.255	
3	1562.2643	9256.114	-7693.85	10818.38	648.9234	
4	11109.704	13241.44	-2131.74	24351.14	494.9434	
5	4110.6533	4732.797	-622.144	8843.451	395.8813	
6	12611.548	12384	227.5429	24995.55	312.6784	

Number of secondary branches at maximum flower (NSBMF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	13.37742	50.01361	-36.6362	63.39104	18	V_{oLo}=9.384513, V_{1L1}=22.40486, V_{oL1}=3.518444, W_{oLo1}=3.017445
2	4.804383	22.56744	-17.7631	27.37182	20	
3	-6.99317	38.25591	-45.2491	31.26274	22.5	
4	1.16043	2.18805	-1.02762	3.34848	22	
5	-2.11088	12.05382	-14.1647	9.94294	25.75	
6	7.866488	9.350323	-1.48383	17.21681	17.66665	

Number of pods per plant (NPdPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1225.224	2533.407	-1308.18	3758.631	122.875	V_{oLo}=859.6662, V_{1L1}=1002.211, V_{oL1}=161.4792, W_{oLo1}=191.5727
2	-373.381	733.7086	-1107.09	360.3275	171.1	
3	-384.673	1512.633	-1897.31	1127.96	176.9167	
4	76.51296	245.7047	-169.192	322.2176	172.1667	
5	-70.7594	299.1121	-369.871	228.3527	183.75	
6	676.5127	688.6998	-12.1871	1365.213	117.0834	

Pod weight per plant (PdWPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.802212	2.822671	-2.02046	3.624883	3.125	V_{oLo}=1.260597, V_{1L1}=1.304767, V_{oL1}=0.230772, W_{oLo1}=0.36528
2	-0.32231	1.80579	-2.1281	1.483484	4.978	
3	-0.07436	0.881017	-0.95538	0.806655	4.53835	
4	1.226917	1.324788	-0.09787	2.551705	5.7075	
5	0.425174	0.582991	-0.15782	1.008165	4.79375	
6	0.134046	0.411347	-0.2773	0.545394	2.82165	

Table 35 continued

Number of seeds per plant (NSPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1514.009	1641.446	-127.437	3155.455	154.125	V_{oLo}=1641.613, V_{1L1}=1212.725, V_{oL1}=201.7928, W_{oLo1}=316.8447
2	-3.76423	560.038	-563.802	556.2738	228.8	
3	243.767	1911.543	-1667.78	2155.309	244.9167	
4	622.1377	1034.79	-412.652	1656.928	216	
5	-685.618	1245.454	-1931.07	559.8357	189.875	
6	210.5368	883.0808	-672.544	1093.618	145.5017	

Number of seeds per plant (NSPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1514.009	1641.446	-127.437	3155.455	154.125	V_{oLo}=1641.613, V_{1L1}=1212.725, V_{oL1}=201.7928, W_{oLo1}=316.8447
2	-3.76423	560.038	-563.802	556.2738	228.8	
3	243.767	1911.543	-1667.78	2155.309	244.9167	
4	622.1377	1034.79	-412.652	1656.928	216	
5	-685.618	1245.454	-1931.07	559.8357	189.875	
6	210.5368	883.0808	-672.544	1093.618	145.5017	
Total	1901.068	7276.351	-5375.28	9177.419	1179.218	
Mean	316.8447	1212.725			196.5364	

Seed weight per plant (SWPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.484424	1.662225	-1.1778	2.146649	2.24875	V_{oLo}=0.544343, V_{1L1}= 0.797926, V_{oL1}= 0.135374, W_{oLo1}=0.209347
2	-0.13738	1.061455	-1.19884	0.924074	3.604	
3	0.057335	0.427303	-0.36997	0.484639	3.25	
4	0.64335	0.94851	-0.30516	1.59186	3.73835	
5	0.178005	0.38535	-0.20734	0.563355	3.11085	
6	0.03035	0.302712	-0.27236	0.333063	1.9158	

Individual plant weight (IPlW)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.121743	1.637721	-0.51598	2.759465	1.86125	V_{oLo}=0.795498, V_{1L1}=0.703416, V_{oL1}=0.191007, W_{oLo1}=0.272452
2	-0.28658	0.583601	-0.87018	0.297022	3.765	
3	-0.11224	0.674596	-0.78683	0.56236	4.0175	
4	0.407735	0.839387	-0.43165	1.247121	2.85	
5	0.076967	0.148326	-0.07136	0.225293	2.5225	
6	0.427081	0.336862	0.090219	0.763944	2.0175	

Table 35 continued

Root weight (RW)						
Array	**Wr**	**Vr**	**Wr-Vr**	**Wr+Vr**	**Yr**	
1	0.000872	0.007182	-0.00631	0.008054	0.13875	V_{oLo}=0.004308, V_{1L1}=0.003583, V_{oL1}=0.001125, W_{oLo1}=0.001205
2	-0.00024	0.006365	-0.00661	0.006124	0.2	
3	0.001211	0.001488	-0.00028	0.002699	0.185	
4	0.003401	0.003111	0.00029	0.006512	0.295	
5	0.001969	0.001599	0.00037	0.003567	0.15625	
6	1.76E-05	0.001755	-0.00174	0.001773	0.105	

Table 36: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters of replication 1 and 2 in the F_1 generation.

Days to flower (DF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	7.533333333	16.36666667	-8.833333333	23.9	65	V_{oLo} =11.74166667
2	1.969166667	16.14041667	-14.17125	18.10958333	70.5	V_{IL1} =12.67133177
3	8.495833333	10.76041667	-2.264583333	19.25625	64.5	V_{oL1} =3.802161714
4	3.169166667	11.73041667	-8.56125	14.89958333	72	W_{oLo1} =5.29787
5	5.831961667	3.451156482	2.380805185	9.283118148	71	
6	4.787758333	17.57891748	-12.79115915	22.36667582	65.5	

Days to flower (DF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	6.857656778	3.882516223	2.975140555	10.740173	66.25	
2	6.621867889	4.582442482	2.039425407	11.20431037	65.8	V_{oLo} =13.66102222
3	3.686406778	15.71119122	-12.02478444	19.397598	61	V_{IL1} =7.331576035
4	6.229077445	3.352981427	2.876096018	9.582058871	72.3333	V_{oL1} =2.503107855
5	-0.366147611	11.04888193	-11.41502954	10.68273432	64.25	W_{oLo1} = 5.185810009
6	8.085998778	5.411442927	2.674555851	13.49744171	65.6667	

Plant height at first flower (PHFF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	5.556312157	6.009235482	-0.452923324	11.56554764	15.975	
2	1.408057969	7.685850682	-6.277792713	9.09390865	22.1833	V_{oLo} =7.240506871
3	2.942076102	2.020268815	0.921807287	4.962344917	21.3833	V_{IL1} =4.426841375
4	-0.883437767	4.152416667	-5.035854433	3.2689789	16.175	V_{oL1} =0.502308479
5	0.890850833	4.826895723	-3.936044889	5.717746556	16.925	W_{oLo1} =1.583448856
6	-0.413166157	1.866380882	-2.279547039	1.453214724	18.25	

Plant height at first flower (PHFF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.853944145	0.92889289	0.925051255	2.782837034	17.35	
2	4.454574423	3.898621527	0.555952896	8.353195949	24.04	V_{oLo} =7.211616223
3	4.465860811	3.64307709	0.822783722	8.108937901	22.45	V_{IL1} =3.297129996
4	5.598186778	5.522332927	0.075853851	11.1205197	20.9667	V_{oL1} =2.031832687
5	2.197530622	1.830531215	0.366999407	4.028061837	18.45	W_{oLo1} =3.765714282
6	4.024188911	3.959324327	0.064864585	7.983513238	18.0833	

Table 36 continued

Number of primary branches at first flower (NPBFF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	-0.16946	2.766666667	-2.936126667	2.597206667	7	V_{oLo} =0.585184815
2	0.179356315	3.412277815	-3.2329215	3.59163413	6.8333	V_{1L1} =1.969629241
3	0.4000075	1.19375	-0.7937425	1.5937575	8	V_{oL1} =0.342527926
4	0.4514	2.391666667	-1.940266667	2.843066667	6.25	W_{oLo1} =0.132917148
5	-0.080095463	1.434496482	-1.514591945	1.354401019	7	
6	0.016294537	0.618917815	-0.602623278	0.635212352	5.75	

Number of primary branches at first flower (NPBFF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.429245408	0.325596816	0.103648592	0.754842224	8.5	V_{oLo} =0.896283704
2	0.304083704	0.209309927	0.094773777	0.513393631	8	V_{1L1} =1.483676779
3	0.692572408	1.135154816	-0.442582408	1.827727224	7.5	V_{oL1} =0.073450473
4	-1.101823704	2.543512594	-3.645336298	1.44168889	8.6667	W_{oLo1} =0.203822803
5	-0.109301296	1.790025927	-1.899327223	1.680724631	8.5	
6	1.008160296	2.898460594	-1.890300298	3.90662089	6.1667	

Number of secondary branches at first flower (NSBFF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	9.455508056	19.04076148	-9.585253426	28.49626954	6.5	V_{oLo} =16.26030833
2	-12.39577261	23.39350882	-35.78928143	10.9977362	11.8333	V_{1L1} =19.44550435
3	6.795798056	8.404571482	-1.608773426	15.20036954	13.8333	V_{oL1} =4.651994131
4	5.466667056	27.32957748	-21.86291043	32.79624454	18.3333	W_{oLo1} =5.108476482
5	9.136031111	22.35183037	-13.21579926	31.48786148	12	
6	12.19262722	16.15277648	-3.960149259	28.3454037	9.25	

Number of secondary branches at first flower (NSBFF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.121572278	1.994508223	-1.872935945	2.116080501	12	V_{oLo} =2.648152223
2	0.335184055	2.107399482	-1.772215426	2.442583537	11.4	V_{1L1} =1.291711257
3	0.899697278	1.386114223	-0.486416945	2.285811501	15	V_{oL1} =0.262485411
4	0.873596778	0.47572326	0.397873518	1.349320038	14.3333	W_{oLo1} =0.652154676
5	0.231841056	0.71124976	-0.479408704	0.943090816	13.75	
6	1.451036611	1.075272594	0.375764018	2.526309205	11.1667	

Table 36 continued

Canopy area at maximum flower (CAMF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	57563.95672	71870.14835	-14306.19163	129434.1051	296.8725
2	7967.588689	45391.1328	-37423.54411	53358.72149	824.732
3	-11836.56972	23990.49336	-35827.06308	12153.92364	685.1117
4	5057.449745	8709.381994	-3651.932249	13766.83174	451.6067
5	3463.644625	5251.88787	-1788.243245	8715.532494	403.25
6	15540.30958	14150.792	1389.517588	29691.10158	276.62

$V_{oLo}=48388.48133$

$V_{1L1}=28227.30606$

$V_{oL1}=5666.169267$

$W_{oLo1}=12959.39661$

Canopy area at maximum flower (CAMF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	6925.562111	3408.97858	3516.583531	10334.54069	307.5425
2	6715.978741	5625.086691	1090.89205	12341.06543	545.778
3	9681.216784	9129.783032	551.4337523	18810.99982	612.735
4	12929.20123	23929.93099	-11000.72975	36859.13222	538.28
5	4381.391253	5098.347047	-716.9557938	9479.7383	388.5125
6	5186.655665	18496.39621	-13309.74055	23683.05188	348.7367

$V_{oLo}=15498.07145$

$V_{1L1}=10948.08709$

$V_{oL1}=4042.410563$

$W_{oLo1}=7636.667631$

Number of secondary branches at maximum flower (NSBMF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	54.81986304	191.3122798	-136.4924168	246.1321429	19.25
2	-3.535737333	53.13066667	-56.666404	49.59492933	20.4
3	-0.006414463	172.1519148	-172.1583293	172.1455004	29
4	5.182712204	23.37630948	-18.19359728	28.55902169	18
5	-13.4983978	37.13795148	-50.63634928	23.63955369	22
6	6.342224648	13.72343748	-7.381212833	20.06566213	17.3333

$V_{oLo}=18.17342848$

$V_{1L1}=81.80542662$

$V_{oL1}=12.00950118$

$W_{oLo1}=8.217375049$

Number of secondary branches at maximum flower (NSBMF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	13.36	12.67666667	0.683333333	26.03666667	16.75
2	7.02025	7.784416667	-0.764166667	14.80466667	19.6
3	8.733125	3.5134375	5.2196875	12.2465625	16
4	-2.606875	8.540104167	-11.14697917	5.933229167	26
5	8.054375	19.40760417	-11.35322917	27.46197917	29.5
6	12.884375	9.162604167	3.721770833	22.04697917	18

$V_{oLo}=30.25375$

$V_{1L1}=10.18080556$

$V_{oL1}=3.240256944$

$W_{oLo1}=7.907541667$

Table 36 continued

Number of pods per plant (NPdPP) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4092.834445	10317.89375	-6225.059305	14410.7282	95.25	V_{oLo} =2128.58405 V_{1L1} =4069.131151 V_{oL1} =480.6763479 W_{oLo1} =238.7207124
2	-1837.116989	4186.720217	-6023.837207	2349.603228	190	
3	-1613.294261	6094.537844	-7707.832105	4481.243582	186.3333	
4	149.2852847	1160.936936	-1011.651651	1310.22222	134.3333	
5	-904.6547232	660.1154915	-1564.770215	-244.5392318	172	
6	1545.270519	1994.582667	-449.312148	3539.853185	85	

Number of pods per plant (NPdPP) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	423.0472571	340.1243033	82.92295387	763.1715604	150.5	V_{oLo} =676.7337855 V_{1L1} =236.9736688 V_{oL1} =204.2029946 W_{oLo1} =370.7313691
2	448.4588193	362.1216667	86.33715267	810.580486	152.2	
3	298.864463	140.3477099	158.516753	439.2121729	167.5	
4	382.913221	224.14	158.773221	607.053221	210	
5	369.1372371	214.1142233	155.0230139	583.2514604	195.5	
6	301.967217	140.9941099	160.9731071	442.961327	149.1667	

Pod weight per plant (PdWPP) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.8913182	11.14125667	-9.249938467	13.03257487	2.795	V_{oLo} =3.674556735 V_{1L1} =4.581670673 V_{oL1} =0.628734297 W_{oLo1} =0.690958797
2	-1.22460632	8.667601867	-9.892208187	7.442995547	5.716	
3	-0.694049225	3.561455482	-4.255504707	2.867406257	4.1867	
4	2.10021785	1.494154167	0.606063683	3.594372017	6.635	
5	0.489443253	1.333629882	-0.844186629	1.823073135	6.16	
6	1.583429023	1.291925975	0.291503048	2.875354998	1.93	

Pod weight per plant (PdWPP) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.199481812	0.121310958	0.078170854	0.32079277	3.455	V_{oLo} =0.42448784 V_{1L1} =0.739369436 V_{oL1} =0.150716165 W_{oLo1} =0.195068298
2	0.262860652	0.185050967	0.077809685	0.447911619	4.24	
3	0.19795481	0.093803582	0.104151228	0.291758392	4.89	
4	0.12064795	2.115314375	-1.994666425	2.235962325	4.78	
5	0.521435384	1.13444935	-0.613013966	1.655884734	3.4275	
6	-0.131970818	0.786287384	-0.918258202	0.654316566	3.7133	

Table 36 continued

Number of seeds per plant (NSPP) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4499.98901	6797.249171	-2297.260161	11297.23818	118	V_{oLo} =3404.907446
2	-1167.3375	5570.433679	-6737.771179	4403.096179	252.6	V_{1L1} =4093.492789
3	-1065.855784	4965.053002	-6030.908787	3899.197218	230.8333	V_{oL1} =338.3089092
4	313.5328294	1302.84887	-989.316041	1616.3817	154.6667	W_{oLo1} =35.07349363
5	-2638.873824	2748.972017	-5387.845841	110.0981935	162.5	
6	268.9862303	3176.399995	-2907.413765	3445.386226	110.67	

Number of seeds per plant (NSPP) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	978.0056815	1407.052501	-429.0468194	2385.058182	190.25	V_{oLo} =1497.03499
2	1302.822919	1699.814792	-396.9918735	3002.637711	205	V_{1L1} =1294.84737
3	793.1133588	871.6908962	-78.57753741	1664.804255	259	V_{oL1} =514.5331492
4	1273.416104	2108.412473	-834.9963696	3381.828577	277.3333	W_{oLo1} =864.6649833
5	801.0581806	1280.414105	-479.3559242	2081.472285	217.25	
6	39.57365596	401.6994499	-362.125794	441.2731059	180.3333	

Seed weight per plant (SWPP) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.119364708	6.364763082	-5.245398374	7.48412779	2.145	V_{oLo} =1.547475856
2	-0.414295428	4.977184895	-5.391480323	4.562889467	4.118	V_{1L1} =2.573399056
3	-0.04649823	1.638863482	-1.685361712	1.592365252	2.97	V_{oL1} =0.322723799
4	0.98228583	0.880411695	0.101874135	1.862697525	4.14	W_{oLo1} =0.440311563
5	0.16359404	0.730286627	-0.566692587	0.893880667	4.1467	
6	0.837418456	0.848884556	-0.0114661	1.686303012	1.2033	

Seed weight per plant (SWPP) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.153207661	0.079946355	0.073261307	0.233154016	2.3525	V_{oLo} =0.330576598
2	0.188835271	0.115371855	0.073463416	0.304207126	3.09	V_{1L1} =0.533226921
3	0.150838495	0.069697563	0.081140932	0.220536057	3.53	V_{oL1} =0.094462019
4	0.002886936	1.500150514	-1.497263577	1.50303745	3.3367	W_{oLo1} =0.130129943
5	0.347325747	0.728234491	-0.380908744	1.075560238	2.075	
6	-0.062314455	0.705960751	-0.768275206	0.643646295	2.6283	

Table 36 continued

Individual plant weight (IPlW) replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2.932215589	5.560368307	-2.628152718	8.492583895	1.6825	V_{oLo} =1.801362102 V_{1L1} =2.506690422 V_{oL1} =0.468674608 W_{oLo1} =0.440585171
2	-1.38113966	2.901153162	-4.282292821	1.520013502	4.094	
3	-0.314159536	3.098786082	-3.412945618	2.784626545	5.06	
4	0.721267664	2.444040122	-1.722772458	3.165307785	2.36	
5	-0.100828866	0.451233392	-0.552062258	0.350404526	2.3325	
6	0.786155839	0.584561471	0.201594368	1.370717309	1.9933	

Individual plant weight (IPlW) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.149887208	0.068960947	0.080926261	0.218848155	2.04	V_{oLo} =0.375235127 V_{1L1} =0.154028182 V_{oL1} =0.09663028 W_{oLo1} =0.185532552
2	0.132542358	0.137245916	-0.004703558	0.269788274	3.436	
3	0.188747497	0.097595647	0.09115185	0.286343143	2.975	
4	0.285608613	0.264929042	0.020679572	0.550537655	3.34	
5	0.156934456	0.071758375	0.085176081	0.228692831	2.7125	
6	0.199475183	0.283679166	-0.084203983	0.483154348	2.0417	

Root weight (RW) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	-0.000288218	0.023713507	-0.024001725	0.023425289	0.1275	V_{oLo} =0.00770788 V_{1L1} =0.01062404 V_{oL1} =0.002447227 W_{oLo1} =0.000874087
2	-0.002453998	0.022417335	-0.024871333	0.019963337	0.212	
3	0.000517582	0.004260882	-0.0037433	0.004778464	0.2	
4	0.006090882	0.005203122	0.00088776	0.011294004	0.35	
5	0.002097334	0.003444638	-0.001347304	0.005541972	0.2	
6	-0.000719062	0.004704756	-0.005423818	0.003985694	0.0967	

Root weight (RW) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.001337292	0.000907783	0.000429509	0.002245075	0.15	V_{oLo} =0.00235788 V_{1L1} =0.001018729 V_{oL1} =0.000573356 W_{oLo1} =0.001117257
2	0.000716552	0.000463762	0.00025279	0.001180314	0.188	
3	0.0010913	0.000514562	0.000576738	0.001605862	0.17	
4	0.00149596	0.001986667	-0.000490707	0.003482627	0.24	
5	0.001717024	0.001310188	0.000406836	0.003027212	0.1125	
6	0.000345412	0.000929411	-0.000583999	0.001274823	0.1133	

Table 37: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters of replication total in the F_1 generation.

Days to flower (DF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	25.60808	26.03762	-0.42954	51.6457	131.25	V_{oLo} =40.2926 V_{1L1} =23.69276 V_{oL1} =10.32032 W_{oLo1} = 18.47925
2	8.211867	10.80833	-2.59646	19.0202	136.3	
3	22.8101	41.07695	-18.2668	63.88706	125.5	
4	19.55536	23.26489	-3.70952	42.82025	144.3333	
5	7.326603	10.66849	-3.34189	17.9951	135.25	
6	27.36351	30.30025	-2.93674	57.66377	131.1667	

Plant height at first flower (PHFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	14.46516	8.820169	5.644987	23.28532	33.325	V_{oLo} =26.18529 V_{1L1} =7.1145 V_{oL1} =4.013123 W_{oLo1} =10.0541
2	10.2233	7.789479	2.433823	18.01278	46.2233	
3	13.05668	9.750964	3.30572	22.80765	43.8333	
4	5.624264	2.940736	2.683528	8.565	37.1417	
5	8.381675	9.138569	-0.75689	17.52024	35.375	
6	8.573511	4.247082	4.32643	12.82059	36.3333	

Number of primary branches at first flower (NPBFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1	1.21014	3.137823	-1.92768	4.347963	15.5
2	2	1.301007	3.497582	-2.19657	4.798588	14.8333
3	3	1.769872	3.912225	-2.14235	5.682097	15.5
4	4	-0.97727	2.499056	-3.47633	1.521782	14.9167
5	5	0.73792	2.182391	-1.44447	2.920311	15.5
6	6	1.222243	4.672564	-3.45032	5.894807	11.9167

Number of secondary branches at first flower (NSBFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	12.48112	31.71295	-19.2318	44.19406	18.5	V_{oLo} =28.07026 V_{1L1} =26.5767 V_{oL1} =5.533434 W_{oLo1} =8.425085
2	-17.2683	30.40266	-47.671	13.13433	23.2333	
3	13.74045	15.11291	-1.37246	28.85336	28.8333	
4	11.62333	31.74612	-20.1228	43.36945	32.6666	
5	9.015209	27.86958	-18.8544	36.88479	25.75	
6	20.95873	22.61599	-1.65726	43.57472	20.4167	

Table 37 continued

Canopy area at maximum flower (CAMF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	100435.9	96150.02	4285.88	196585.9	604.415	V_{oLo} =109842 V_{1L1} =47445.07 V_{oL1} =16316.16 W_{oLo1} =38915.63
2	15481.22	30062.99	-14581.8	45544.21	1370.51	
3	6249.057	37024.46	-30775.4	43273.51	1297.847	
4	44438.82	52965.76	-8526.94	97404.57	989.8867	
5	16442.61	18931.19	-2488.58	35373.8	791.7625	
6	50446.19	49536.02	910.1714	99982.21	625.3567	

Number of secondary branches at maximum flower (NSBMF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	53.50968	200.0545	-146.545	253.5641	36	V_{oLo} =37.53805 V_{1L1} =89.61944 V_{oL1} =14.07378 W_{oLo1} =12.06978
2	19.21753	90.26975	-71.0522	109.4873	40	
3	-27.9727	153.0236	-180.996	125.051	45	
4	4.641721	8.752198	-4.11048	13.39392	44	
5	-8.44351	48.21527	-56.6588	39.77176	51.5	
6	31.46595	37.40129	-5.93534	68.86724	35.3333	

Number of pods per plant (NPdPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4900.896	10133.63	-5232.73	15034.52	245.75	V_{oLo} =3438.665 V_{1L1} =4008.843 V_{oL1} =645.9167 W_{oLo1} = 766.2908
2	-1493.52	2934.835	-4428.36	1441.31	342.2	
3	-1538.69	6050.531	-7589.22	4511.84	353.8333	
4	306.0518	982.8187	-676.767	1288.871	344.3333	
5	-283.038	1196.448	-1479.49	913.4107	367.5	
6	2706.051	2754.799	-48.7483	5460.85	234.1667	

Pod weight per plant (PdWPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.208848	11.29068	-8.08183	14.49953	6.25	V_{oLo} =5.04239 V_{1L1} =5.219069 V_{oL1} =0.923087 W_{oLo1} =1.461121
2	-1.28923	7.223162	-8.51239	5.933936	9.956	
3	-0.29745	3.524067	-3.82151	3.226621	9.0767	
4	4.907667	5.299151	-0.39148	10.20682	11.415	
5	1.700696	2.331963	-0.63127	4.032658	9.5875	
6	0.536186	1.64539	-1.1092	2.181575	5.6433	

Table 37 continued

Number of seeds per plant (NSPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	6056.035	6565.785	-509.749	12621.82	308.25
2	-15.0569	2240.152	-2255.21	2225.095	457.6
3	975.0679	7646.17	-6671.1	8621.238	489.8333
4	2488.551	4139.16	-1650.61	6627.711	432
5	-2742.47	4981.814	-7724.29	2239.343	379.75
6	842.1473	3532.323	-2690.18	4374.47	291.0033

V_{oLo} =6566.454

V_{1L1} =4850.901

V_{oL1} =807.1714

W_{oLo1} =1267.379

Seed weight per plant (SWPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	1.937697	6.648901	-4.7112	8.586597	4.4975
2	-0.54952	4.24582	-4.79534	3.696296	7.208
3	0.229342	1.709212	-1.47987	1.938554	6.5
4	2.573401	3.79404	-1.22064	6.367441	7.4767
5	0.712021	1.541399	-0.82938	2.25342	6.2217
6	0.121401	1.210849	-1.08945	1.332251	3.8316

V_{oLo} =2.177373

V_{1L1} =3.191704

V_{oL1} =0.541494

W_{oLo1} =0.83739

Individual plant weight (IPIW) replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	4.486974	6.550885	-2.06391	11.03786	3.7225
2	-1.14632	2.334404	-3.48072	1.188087	7.53
3	-0.44895	2.698386	-3.14733	2.249438	8.035
4	1.630938	3.357547	-1.72661	4.988485	5.7
5	0.307868	0.593305	-0.28544	0.901173	5.045
6	1.708325	1.34745	0.360875	3.055775	4.035

V_{oLo} =3.181991

V_{1L1} =2.813663

V_{oL1} =0.764028

W_{oLo1} = 1.089807

Root weight (RW) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr
1	0.003489	0.028727	-0.02524	0.032217	0.2775
2	-0.00096	0.025462	-0.02643	0.024497	0.4
3	0.004844	0.005951	-0.00111	0.010796	0.37
4	0.013605	0.012444	0.001162	0.026049	0.59
5	0.007874	0.006394	0.00148	0.014269	0.3125
6	7.05E-05	0.007021	-0.00695	0.007091	0.21

V_{oLo} =0.017233

V_{1L1} =0.014333

V_{oL1} =0.004501

W_{oLo1} = 0.00482

Table 38: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters in F_2 generation.

Days to flower (DF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.393844	1.840113	1.553731	5.233957	65.625	V_{oLo}=10.07315
2	0.113252	6.558735	-6.44548	6.671987	68.15	V_{1L1}=8.27461
3	-0.13063	14.02862	-14.1593	13.898	62.75	V_{oL1}=0.229571
4	8.965293	12.08783	-3.12254	21.05313	72.16665	W_{oLo1}=0.691756
5	-8.76788	12.17441	-20.9423	3.406528	67.625	
6	0.576658	2.957949	-2.38129	3.534606	65.58335	

Plant height at first flower(PHFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.914399	3.052732	0.861668	6.967131	16.6625	
2	5.425172	6.945843	-1.52067	12.37102	23.11165	V_{oLo}=6.546323
3	3.504209	3.560843	-0.05663	7.065052	21.91665	V_{1L1}=3.291257
4	2.04373	2.907703	-0.86397	4.951433	18.57085	V_{oL1}=1.919364
5	2.82891	1.802604	1.026306	4.631514	17.6875	W_{oLo1}=3.09895
6	0.877277	1.477818	-0.60054	2.355095	18.16665	

Number of primary branches at first flower(NPBFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.635844	1.419528	-0.78368	2.055372	7.75	V_{oLo}=0.486565
2	-0.12248	0.211837	-0.33432	0.089358	7.41665	V_{1L1}=0.942307
3	0.390949	1.667897	-1.27695	2.058846	7.75	V_{oL1}=0.137151
4	-0.19998	1.097732	-1.29772	0.897749	7.45835	W_{oLo1}=0.156268
5	0.141144	0.719659	-0.57851	0.860803	7.75	
6	0.09213	0.537193	-0.44506	0.629323	5.95835	

Number of secondary branches at first flower(NSBFF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	6.775986	14.44008	-7.6641	21.21607	9.25	V_{oLo}=7.017565
2	0.777816	0.643485	0.134331	1.421301	11.61665	V_{1L1}=8.703289
3	-7.61275	16.16591	-23.7787	8.553163	14.41665	V_{oL1}=0.478793
4	-0.27028	14.33498	-14.6053	14.06471	16.3333	W_{oLo1}=0.553172
5	-0.68664	3.109044	-3.79569	2.4224	12.875	
6	4.334901	3.526227	0.808674	7.861128	10.20835	

Table 38 continued

Canopy area at maximum flower (CAMF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	17341.85	12057.13	5284.723	29398.98	302.2075	V_{oLo}=27460.51
2	21304.07	30010.03	-8705.96	51314.1	685.255	V_{1L1}=13018.53
3	18348.33	18614.93	-266.6	36963.26	648.9234	V_{oL1}=6062.775
4	2403.173	6561.438	-4158.26	8964.61	494.9434	W_{oLo1}=11943.49
5	11445.82	7394.152	4051.673	18839.98	395.8813	
6	817.6904	3473.523	-2655.83	4291.214	312.6784	

Number of secondary branches at maximum flower (NSBMF)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	5.791483	17.38468	-11.5932	23.17617	18	V_{oLo}=9.384513
2	-0.85321	4.049499	-4.90271	3.196288	20	V_{1L1}=15.33105
3	-7.06519	31.9588	-39.024	24.89361	22.5	V_{oL1}=1.249555
4	-7.36497	19.34845	-26.7134	11.98348	22	W_{oLo1}=0.144424
5	6.746144	13.78825	-7.04211	20.53439	25.75	
6	3.612285	5.45663	-1.84434	9.068915	17.66665	

Number of pods per plant (NPdPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	844.741	2117.068	-1272.33	2961.809	122.875	V_{oLo}=859.6662
2	103.9391	370.195	-266.256	474.1341	171.1	V_{1L1}=1092.919
3	-421.617	1287.035	-1708.65	865.4182	176.9167	V_{oL1}=124.1754
4	-584.91	916.4991	-1501.41	331.5889	172.1667	W_{oLo1}=162.8394
5	465.2134	632.6842	-167.471	1097.898	183.75	
6	569.6695	1234.035	-664.365	1803.704	117.0834	

Pod weight per plant (PdWPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.891732	1.693697	-0.80196	2.585429	3.125	V_{oLo}=1.260597
2	0.059194	0.682872	-0.62368	0.742066	4.978	V_{1L1}=0.919379
3	-0.50829	0.797058	-1.30535	0.288763	4.53835	V_{oL1}=0.153189
4	-0.00278	1.115415	-1.11819	1.112637	5.7075	W_{oLo1}=0.238724
5	0.330801	0.61761	-0.28681	0.948411	4.79375	
6	0.661692	0.60962	0.052072	1.271312	2.82165	

Table 38 continued

Number of seeds per plant (NSPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1914.014	2619.826	-705.812	4533.839	154.125	V_{oLo}=1641.613
2	786.8073	1081.882	-295.075	1868.689	228.8	V_{1L1}=1416.742
3	433.8713	1638.366	-1204.49	2072.238	244.9167	V_{oL1}=388.3286
4	-480.155	1111.32	-1591.48	631.1651	216	W_{oLo1}=674.5143
5	438.7868	465.8632	-27.0764	904.65	189.875	
6	953.7617	1583.196	-629.434	2536.957	145.5017	

Seed weight per plant (SWPP)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.521479	0.995523	-0.47404	1.517003	2.24875	V_{oLo}=0.544343
2	0.087493	0.421313	-0.33382	0.508806	3.604	V_{1L1}=0.489842
3	-0.17843	0.433425	-0.61185	0.254996	3.25	V_{oL1}=0.091086
4	-0.09406	0.453418	-0.54748	0.35936	3.73835	W_{oLo1}=0.137624
5	0.14746	0.253757	-0.1063	0.401217	3.11085	
6	0.341797	0.381616	-0.03982	0.723413	1.9158	

Individual plant weight(IPlW)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.719237	0.750587	-0.03135	1.469824	1.86125	V_{oLo}=0.795498
2	0.530283	0.67439	-0.14411	1.204673	3.765	V_{1L1}=0.466007
3	0.342989	0.697861	-0.35487	1.04085	4.0175	V_{oL1}=0.173707
4	-0.18012	0.185089	-0.36521	0.004967	2.85	W_{oLo1}=0.33983
5	0.334206	0.237428	0.096779	0.571634	2.5225	
6	0.292385	0.250689	0.041696	0.543074	2.0175	

Root weight (RW)

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.001905	0.001026	0.00088	0.002931	0.13875	V_{oLo}=0.004308
2	-2.5E-05	0.000359	-0.00038	0.000335	0.2	V_{1L1}=0.001269
3	-0.00144	0.000894	-0.00234	-0.00055	0.185	V_{oL1}=0.000198
4	0.002216	0.004007	-0.00179	0.006223	0.295	W_{oLo1}=0.000767
5	0.000177	0.000118	5.87E-05	0.000296	0.15625	
6	0.001772	0.001209	0.000563	0.002981	0.105	

Table-39: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters of replication 1 and 2 in the F_2 generation.

Days to flower (DF) of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4.511135	2.685214815	1.825920185	7.196349815	65	V_{oLo} =11.74166667
2	-1.27014	4.175658812	-5.445798812	2.905518812	70.5	V_{1L1} =8.950704024
3	3.463216667	15.28579837	-11.8225817	18.74901504	64.5	V_{oL1}=0.479331703
4	5.289833333	14.62527794	-9.335444609	19.91511128	72	W_{oLo1} =1.342773889
5	-7.01857	14.86559952	-21.88416952	7.847029524	71	
6	3.081168333	2.066674682	1.014493652	5.147843015	65.5	

Days to flower (DF) of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.096032055	2.492328143	-1.396296087	3.588360198	66.25	V_{oLo} =13.66102222
2	5.819210185	13.81183006	-7.992619872	19.63104024	65.8	V_{1L1} =11.0856552
3	-0.157654667	17.98841667	-18.14607133	17.830762	61	V_{oL1}=0.538629527
4	10.86292144	11.35034786	-0.487426418	22.21326931	72.3333	W_{oLo1} =1.498050855
5	-5.981492667	15.30541667	-21.28690933	9.323924	64.25	
6	-2.650711222	5.565591815	-8.216303037	2.914880593	65.6667	

Plant height at first flower of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4.013305367	2.992132827	1.021172541	7.005438194	15.975	V_{oLo} =7.240506871
2	4.507658865	4.992364011	-0.484705145	9.500022876	22.1833	V_{1L1} =3.038024098
3	2.763910841	3.258657978	-0.494747136	6.022568819	21.3833	V_{oL1}=1.640461493
4	3.507428303	3.875452931	-0.368024628	7.382881233	16.175	W_{oLo1} =3.161980251
5	3.562604488	1.793419472	1.769185016	5.35602396	16.925	
6	0.616973639	1.31611737	-0.699143731	1.933091008	18.25	

Plant height at first flower of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4.338636189	4.054269946	0.284366244	8.392906135	17.35	V_{oLo} =7.211616223
2	6.715200021	9.521317618	-2.806117597	16.23651764	24.04	V_{1L1} =4.544429767
3	4.319042933	4.491613082	-0.172570148	8.810656015	22.45	V_{oL1}=2.598021056
4	1.878137445	3.567104946	-1.688967501	5.44524239	20.9667	W_{oLo1} =3.551123661
5	2.935997467	3.165866307	-0.22986884	6.101863773	18.45	
6	1.119727911	2.466406707	-1.346678795	3.586134618	18.0833	

Table 39 continued

Number of primary branches at first flower of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.881092813	2.152459282	-1.271366469	3.033552095	7	
2	-0.25184664	0.792188535	-1.044035175	0.540341895	6.8333	V_{oLo} =0.585184815
3	0.549234581	0.764699411	-0.21546483	1.313933992	8	V_{1L1} =1.214181332
4	-0.313656065	0.535027038	-0.848683103	0.221370973	6.25	V_{oL1} =0.174508002
5	0.452063177	0.606115414	-0.154052237	1.058178591	7	W_{oLo1} =0.216107994
6	-0.020239903	2.434598311	-2.454838214	2.414358408	5.75	

Number of primary branches at first flower of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.035193704	2.046949927	-2.011756223	2.082143631	8.5	
2	0.0777725	0.291666667	-0.213894167	0.369439167	8	V_{oLo} =0.896283704
3	0.318865	3.380416667	-3.061551667	3.699281667	7.5	V_{1L1} =1.576521189
4	0.462803	2.52492989	-2.06212689	2.98773289	8.6667	V_{oL1} =0.222612441
5	-0.1683435	1.0634375	-1.231781	0.895094	8.5	W_{oLo1} =0.176756009
6	0.334245352	0.151726482	0.18251887	0.485971834	6.1667	

Number of secondary branches at first flower of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	11.09418952	14.6488168	-3.554627278	25.74300631	6.5	
2	0.653108195	0.941932871	-0.288824676	1.595041065	11.8333	V_{oLo} =16.26030833
3	-10.05093745	13.21861909	-23.26955654	3.167681636	13.8333	V_{1L1} =10.33608405
4	4.481027732	19.97230075	-15.49127302	24.45332848	18.3333	V_{oL1} =0.672841603
5	0.310910946	7.009055186	-6.69814424	7.319966131	12	W_{oLo1} =2.549401971
6	8.808112888	6.225779586	2.582333303	15.03389247	9.25	

Number of secondary branches at first flower of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	4.956541889	15.94749064	-10.99094875	20.90403253	12	
2	0.625807259	1.475348035	-0.849540775	2.101155294	11.4	V_{oLo} =2.648152223
3	-3.2305855	24.11555581	-27.34614132	20.88497031	15	V_{1L1} =9.910585505
4	-2.953560055	10.66237076	-13.61593081	7.708810702	14.3333	V_{oL1} =1.135354037
5	-0.007271778	3.993195556	-4.000467334	3.985923778	13.75	W_{oLo1} =0.13600721
6	1.425111445	3.269552223	-1.844440778	4.694663667	11.1667	

Table 39 continued

Canopy area at maximum flower of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	23378.04	15812.6	7565.439	39190.64	296.8725	
2	41121.25	59303.64	-18182.4	100424.9	824.732	V_{oLo} =48388.48
3	39054.09	33546.25	5507.844	72600.34	685.1117	V_{1L1} =21979.07
4	1166.624	10582.88	-9416.25	11749.5	451.6067	V_{oL1} =8622.013
5	15149.8	7616.178	7533.618	22765.97	403.25	W_{oLo1} =19836.19
6	-852.686	5012.901	-5865.59	4160.215	276.62	

Canopy area at maximum flower of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	16718.45942	30604.18529	-13885.72587	47322.64471	307.5425	
2	9790.519428	12235.01075	-2444.491319	22025.53017	545.778	V_{oLo} =15498.07145
3	3072.376142	23239.72401	-20167.34787	26312.10016	612.735	V_{1L1} =14261.95806
4	3534.432979	4438.046509	-903.6135296	7972.479488	538.28	V_{oL1} =5128.694381
5	8832.23037	9751.801699	-919.5713283	18584.03207	388.5125	W_{oLo1} =7350.284011
6	2153.685726	5302.980109	-3149.294384	7456.665835	348.7367	

Number of secondary branches at maximum flower of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	-10.518865	32.01658766	-42.53545266	21.49772266	16.75	
2	-1.9441975	5.054233026	-6.998430526	3.110035526	19.6	V_{oLo} =30.25375
3	-23.0935	54.436	-77.5295	31.3425	16	V_{1L1} =29.30961304
4	7.5589275	42.3721492	-34.8132217	49.9310767	26	V_{oL1} =0.97000024
5	21.832375	36.19560417	-14.36322917	58.02797917	29.5	W_{oLo1} =-1.661939167
6	-3.806375	5.783104167	-9.589479167	1.976729167	18	

Number of secondary branches at maximum flower of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	12.35715734	15.87095704	-3.513799695	28.22811438	19.25	
2	8.109168323	8.483717455	-0.374549132	16.59288578	20.4	V_{oLo} =18.17342848
3	15.24143432	28.581211	-13.33977668	43.82264533	29	V_{1L1} =13.05862217
4	-11.37812791	8.412945122	-19.79107303	-2.965182786	18	V_{oL1} =3.241202752
5	5.761147502	7.163750798	-1.402603296	12.9248983	22	W_{oLo1} =6.277066452
6	7.571619129	9.839151583	-2.267532454	17.41077071	17.3333	

Table 39 continued

Number of pods per plant of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1760.611603	2150.756529	-390.144926	3911.368131	95.25	V_{oLo} =2128.58405 V_{lL1} =1372.923453 V_{oL1} =275.7353171 W_{oLol} =692.1541227
2	418.4745731	1349.736193	-931.2616199	1768.210766	190	
3	678.1487152	377.7525796	300.3961356	1055.901295	186.3333	
4	-698.5606773	1184.764418	-1883.325096	486.2037412	134.3333	
5	514.3197095	688.006787	-173.6870776	1202.326497	172	
6	1479.930813	2486.524212	-1006.593399	3966.455025	85	

Number of pods per plant of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	198.7537112	5195.412417	-4996.658705	5394.166128	150.5	V_{oLo} =676.7337855 V_{lL1} =2874.436965 V_{oL1} =301.8195205 W_{oLol} =-15.1609754
2	253.0497321	337.2378547	-84.18812264	590.2875868	152.2	
3	-1295.110353	6278.754417	-7573.86477	4983.644063	167.5	
4	-17.80519158	2314.373604	-2332.178796	2296.568413	210	
5	547.5158282	1596.364438	-1048.848609	2143.880266	195.5	
6	222.6304209	1524.479063	-1301.848642	1747.109484	149.1667	

Pod weight per plant of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.996730327	2.579530998	-0.582800671	4.576261325	2.795	V_{oLo} =3.674556735 V_{lL1} =1.741312781 V_{oL1} =0.196872872 W_{oLol} =0.750072578
2	-0.343081705	2.982754358	-3.325836063	2.639672653	5.716	
3	1.133227447	0.524228307	0.60899914	1.657455754	4.1867	
4	-0.200683156	2.117189776	-2.317872932	1.91650662	6.635	
5	0.332128259	1.139664222	-0.807535963	1.471792481	6.16	
6	1.582114297	1.104509026	0.477605271	2.686623323	1.93	

Pod weight per plant of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.184419426	6.014498175	-4.830078749	7.198917601	3.455	V_{oLo} =0.42448784 V_{lL1} =2.387522332 V_{oL1} =0.378080213 W_{oLol} =0.287632873
2	0.351645658	0.394965066	-0.043319408	0.746610724	4.24	
3	-0.49802284	5.0492923	-5.54731514	4.55126946	4.89	
4	-0.05214094	0.997377067	-1.049518007	0.945236127	4.78	
5	0.079841492	0.538114402	-0.45827291	0.617955894	3.4275	
6	0.660054444	1.330886983	-0.670832539	1.990941427	3.7133	

Table 39 continued

Number of seeds per plant of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2900.540597	4707.125475	-1806.584878	7607.666071	118	
2	1200.085094	3008.532926	-1808.447833	4208.61802	252.6	V_{oLo} =3404.907446
3	1912.293759	1859.971773	52.32198662	3772.265532	230.8333	V_{1L1} =2583.588234
4	-156.9107432	1703.748527	-1860.65927	1546.837784	154.6667	V_{oL1} =563.8716276
5	1021.022376	1030.161097	-9.138720676	2051.183472	162.5	W_{oLo1} =1343.576364
6	1184.427102	3191.989604	-2007.562502	4376.416706	110.67	

Number of seeds per plant of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2495.924236	8318.067714	-5822.143478	10813.99195	190.25	
2	1065.156009	1250.495014	-185.3390046	2315.651023	205	V_{oLo} =1497.03499
3	-1221.564531	9374.889667	-10596.4542	8153.325135	259	V_{1L1} =4418.753022
4	-174.5806497	3672.635468	-3847.216118	3498.054818	277.3333	V_{oL1} =785.5303623
5	378.6819212	1790.733604	-1412.051683	2169.415525	217.25	W_{oLo1} =542.2784768
6	710.0538761	2105.696664	-1395.642788	2815.750541	180.3333	

Seed weight per plant of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.062508768	1.607269494	-0.544760726	2.669778262	2.145	
2	0.071613166	1.982941296	-1.91132813	2.054554462	4.118	V_{oLo} =1.547475856
3	0.598857858	0.314112575	0.284745283	0.912970433	2.97	V_{1L1} =0.97899334
4	-0.394643692	0.80243803	-1.197081722	0.407794338	4.14	V_{oL1} =0.11894123
5	0.134812394	0.453457547	-0.318645153	0.588269941	4.1467	W_{oLo1} =0.373327148
6	0.766814392	0.713741098	0.053073294	1.48055549	1.2033	

Seed weight per plant of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.789645079	3.779113999	-2.98946892	4.568759078	2.3525	
2	0.230334122	0.30317927	-0.072845148	0.533513391	3.09	V_{oLo} =0.330576598
3	-0.216772993	2.856461467	-3.07323446	2.639688473	3.53	V_{1L1} =1.415013361
4	0.021923031	0.495634663	-0.473711631	0.517557694	3.3367	V_{oL1} =0.241171674
5	0.090542282	0.265028322	-0.17448604	0.355570603	2.075	W_{oLo1} =0.231112246
6	0.471001958	0.790662444	-0.319660486	1.261664402	2.6283	

Table 39 continued

Individual plant weight of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	1.035719747	0.739211611	0.296508136	1.774931358	1.6825	V_{oLo} =1.801362102 V_{IL1} =0.685715075 V_{oL1} =0.281102439 W_{oLo1} =0.693828064
2	1.115486287	1.355648475	-0.240162187	2.471134762	4.094	
3	1.381458624	1.199649178	0.181809446	2.581107801	5.06	
4	-0.008401437	0.280103867	-0.288505304	0.271702429	2.36	
5	0.469819684	0.231480078	0.238339607	0.701299762	2.3325	
6	0.168885478	0.308197244	-0.139311766	0.477082722	1.9933	

Individual plant weight of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.300048891	1.229041515	-0.928992624	1.529090405	2.04	V_{oLo} =0.375235127 V_{IL1} =0.613109161 V_{oL1} =0.102579944 W_{oLo1} =0.113714141
2	0.217344187	0.336375574	-0.119031387	0.55371976	3.436	
3	-0.317021473	0.939091867	-1.25611334	0.622070393	2.975	
4	-0.001570925	0.438823883	-0.440394807	0.437252958	3.34	
5	0.273308062	0.388845115	-0.115537053	0.662153177	2.7125	
6	0.210176106	0.346477012	-0.136300906	0.556653118	2.0417	

Root weight of replication 1

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.002535776	0.002371811	0.000163965	0.004907587	0.1275	V_{oLo} =0.00770788 V_{IL1} =0.00256101 V_{oL1} =0.000135973 W_{oLo1} =0.000906583
2	-0.00237478	0.001896843	-0.004271619	-0.000477933	0.212	
3	-0.00048514	0.001284895	-0.001770031	0.000799759	0.2	
4	0.003910834	0.007664759	-0.003753925	0.011575593	0.35	
5	-3.701E-05	0.00067863	-0.00071564	0.00064162	0.2	
6	0.001889812	0.001469124	0.000420688	0.003358936	0.0967	

Root weight of replication 2

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.001539572	0.00189893	-0.000359358	0.003438502	0.15	V_{oLo} = 0.00235788 V_{IL1} = 0.001622463 V_{oL1} = 0.000327803 W_{oLo1} =0.000776255
2	0.001047412	0.000643319	0.000404093	0.001690731	0.188	
3	-0.001025602	0.002464615	-0.003490217	0.001439013	0.17	
4	0.001196694	0.002969927	-0.001773233	0.004166621	0.24	
5	0.000493866	0.000336884	0.000156982	0.00083075	0.1125	
6	0.00140559	0.001421104	-1.5514E-05	0.002826694	0.1133	

Table 40: Array variance (Vr), array covariance (Wr), variance of parents (V_{oLo}), mean variance (V_{1L1}), variance of mean of arrays (V_{oL1}), mean covariance (W_{oLo1}) and diagonal values (Yr) are shown for twelve characters of replication total in the F_2 generation.

Days to flower (DF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	13.57538	7.360452	6.214926	20.93583	131.25	
2	0.453007	26.23494	-25.7819	26.68795	136.3	V_{oLo} =40.2926
3	-0.52251	56.1145	-56.637	55.59198	125.5	V_{1L1} =33.09844
4	35.86117	48.35133	-12.4902	84.2125	144.3333	V_{oL1} =0.918286
5	-35.0715	48.69763	-83.7692	13.62611	135.25	W_{oLo1} =2.767026
6	2.30663	11.8318	-9.52517	14.13843	131.1667	

Plant height at first flower (PHFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	15.6576	12.21093	3.44667	27.86852	33.325	
2	21.70069	27.78337	-6.08268	49.48406	46.2233	V_{oLo} =26.18529
3	14.01684	14.24337	-0.22654	28.26021	43.8333	V_{1L1} =13.16503
4	8.174919	11.63081	-3.45589	19.80573	37.1417	V_{oL1} =7.677455
5	11.31564	7.210417	4.105225	18.52606	35.375	W_{oLo1} = 12.3958
6	3.509107	5.911271	-2.40216	9.420378	36.3333	

Number of primary branches at first flower (NPBFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2.543376	5.67811	-3.13473	8.221486	15.5	
2	-0.48992	0.847347	-1.33726	0.357432	14.8333	V_{oLo} =1.94626
3	1.563795	6.671587	-5.10779	8.235383	15.5	V_{1L1} =3.76923
4	-0.79993	4.390929	-5.19086	3.590998	14.9167	V_{oL1} =0.548602
5	0.564576	2.878634	-2.31406	3.44321	15.5	W_{oLo1} = 0.62507
6	0.368522	2.148771	-1.78025	2.517293	11.9167	

Number of secondary branches at first flower (NSBFF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	27.10394	57.76033	-30.6564	84.86427	18.5	
2	3.111265	2.57394	0.537325	5.685205	23.2333	V_{oLo} =28.07026
3	-30.451	64.66365	-95.1146	34.21265	28.8333	V_{1L1} =34.81316
4	-1.08111	57.33994	-58.421	56.25883	32.6666	V_{oL1} =1.915171
5	-2.74658	12.43618	-15.1828	9.689601	25.75	W_{oLo1} =2.212689
6	17.3396	14.10491	3.234695	31.44451	20.4167	

Table 40 continued

Canopy area at maximum flower (CAMF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	69367.41	48228.52	21138.89	117595.9	604.415	
2	85216.27	120040.1	-34823.9	205256.4	1370.51	V_{oLo} =109842
3	73393.32	74459.73	-1066.4	147853	1297.847	V_{1L1} =52074.14
4	9612.691	26245.75	-16633.1	35858.44	989.8867	V_{oL1} =24251.1
5	45783.3	29576.61	16206.69	75359.9	791.7625	W_{oLo1} = 47773.96
6	3270.762	13894.09	-10623.3	17164.86	625.3567	

Number of secondary branches at maximum flower (NSBMF) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	23.16593	69.53873	-46.3728	92.70466	36	
2	-3.41284	16.19799	-19.6108	12.78515	40	V_{oLo} =37.53805
3	-28.2607	127.8352	-156.096	99.57445	45	V_{1L1} =61.32421
4	-29.4599	77.39381	-106.854	47.93392	44	V_{oL1} =4.998218
5	26.98458	55.153	-28.1684	82.13757	51.5	W_{oLo1} =0.577694
6	14.44914	21.82652	-7.37738	36.27566	35.3333	

Number of pods per plant (NPdPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3378.964	8468.271	-5089.31	11847.24	245.75	
2	415.7564	1480.78	-1065.02	1896.536	342.2	V_{oLo} =3438.665
3	-1686.47	5148.139	-6834.61	3461.673	353.8333	V_{1L1} =4371.677
4	-2339.64	3665.996	-6005.64	1326.356	344.3333	V_{oL1} =496.7016
5	1860.854	2530.737	-669.883	4391.59	367.5	W_{oLo1} =651.3575
6	2278.678	4936.139	-2657.46	7214.817	234.1667	

Pod weight per plant (PdWPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	3.56693	6.774787	-3.20786	10.34172	6.25	
2	0.236774	2.73149	-2.49472	2.968264	9.956	V_{oLo} =5.04239
3	-2.03318	3.18823	-5.22141	1.155053	9.0767	V_{1L1} =3.677515
4	-0.01111	4.461662	-4.47278	4.450548	11.415	V_{oL1} =0.612757
5	1.323203	2.470441	-1.14724	3.793644	9.5875	W_{oLo1} =0.954898
6	2.646769	2.43848	0.208289	5.08525	5.6433	

Table 40 continued

Number of seeds per plant (NSPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	7656.055	10479.3	-2823.25	18135.36	308.25	
2	3147.229	4327.528	-1180.3	7474.757	457.6	V_{oLo} =6566.454
3	1735.485	6553.465	-4817.98	8288.95	489.8333	V_{1L1} =5666.969
4	-1920.62	4445.281	-6365.9	2524.66	432	V_{oL1} =1553.314
5	1755.147	1863.453	-108.305	3618.6	379.75	W_{oLo1} =2698.057
6	3815.047	6332.783	-2517.74	10147.83	291.0033	

Seed weight per plant (SWPP) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2.085918	3.982093	-1.89617	6.06801	4.4975	
2	0.349973	1.68525	-1.33528	2.035223	7.208	V_{oLo} =2.177373
3	-0.71372	1.733702	-2.44742	1.019985	6.5	V_{1L1} =1.959368
4	-0.37623	1.813671	-2.1899	1.43744	7.4767	V_{oL1} =0.364343
5	0.589841	1.015027	-0.42519	1.604868	6.2217	W_{oLo1} =0.550495
6	1.367188	1.526466	-0.15928	2.893653	3.8316	

Individual plant weight (IPlW) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	2.876949	3.002346	-0.1254	5.879295	3.7225	
2	2.121131	2.697559	-0.57643	4.81869	7.53	V_{oLo} =3.181991
3	1.371957	2.791445	-1.41949	4.163402	8.035	V_{1L1} =1.864029
4	-0.72049	0.740355	-1.46084	0.019866	5.7	V_{oL1} =0.694829
5	1.336825	0.94971	0.387115	2.286535	5.045	W_{oLo1} = 1.359319
6	1.169541	1.002756	0.166785	2.172297	4.035	

Root weight (RW) of replication total

Array	Wr	Vr	Wr-Vr	Wr+Vr	Yr	
1	0.007622	0.004103	0.003519	0.011724	0.2775	
2	-9.8E-05	0.001437	-0.00154	0.001339	0.4	V_{oLo} =0.017233
3	-0.00578	0.003578	-0.00935	-0.0022	0.37	V_{1L1} =0.005076
4	0.008865	0.016027	-0.00716	0.024892	0.59	V_{oL1} =0.000794
5	0.000709	0.000474	0.000235	0.001183	0.3125	W_{oLo1} = 0.003068
6	0.007089	0.004837	0.002252	0.011925	0.21	

Table 41: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication 1 in the F_1 generation for different characters.

Character / Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	-0.10639099± 0.231258979	0.309535826± 0.500396645	0.004402192± 0.120414961	-0.448619867± 0.632474358	0.692529501± 0.299698614	0.192525262± 0.117462958	0.318829901± 0.263429621	-0.056426833± 0.161466536	0.5771628± 0.527020093	-0.003871504± 0.12711502	0.387179393± 0.334080714	-0.170980336± 0.127071775
H_0 : b=0	-0.460051281^{NS}	0.618580939^{NS}	0.036558518^{NS}	-0.709309178^{NS}	2.310753099^{NS}	1.639029566^{NS}	1.210303912^{NS}	-0.349464565^{NS}	1.095143823^{NS}	-0.030456701^{NS}	1.158939673^{NS}	-1.345541413^{NS}
H_0 : b=1	4.7842077**	1.379833738^{NS}	8.268057401**	2.290400944^{NS}	1.025932337^{NS}	6.874292532**	2.585776406^{NS}	6.542698327**	0.802317038^{NS}	7.897347678**	1.834348951^{NS}	9.21510959**

Table 42: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication 2 in the F_1 generation for different characters.

Character / Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	-0.42791707± 0.224984153	0.860743642± 0.086149629	-0.142878692± 0.322350137	-0.323608607± 0.348094928	0.217689519± 0.155417597	0.163597594± 0.529036773	0.626907788± 0.071291053	-0.00980861± 0.132974332	0.711019324± 0.140839552	-0.099210095± 0.11806245	0.407885717± 0.198845354	0.511970921± 0.371995259
H_0 : b=0	-1.901987607^{NS}	9.991263485**	-0.443240673^{NS}	-0.929656199^{NS}	1.400674842^{NS}	0.309236716^{NS}	8.793639046**	-0.07376318^{NS}	5.048435003**	-0.840318783^{NS}	2.05127104^{NS}	1.376283457^{NS}
H_0 : b=1	6.346745108**	1.616447564^{NS}	3.545457441*	3.802435777*	5.03360298**	1.580991054^{NS}	5.233366545**	7.594011551**	2.051843195^{NS}	9.31041234**	2.977762723*	1.311922844^{NS}

Table 43: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication 1 in the F_2 generation for different characters.

Character / Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	-0.152085082± 0.347761367	0.734790149± 0.353661336	0.167430998± 0.272544505	0.079161304± 0.546403399	0.742814± 0.220486	-0.111555127± 0.380036334	0.632264839± 0.429731863	-0.305189437± 0.478011272	0.519687622± 0.281501222	0.061511218± 0.398253323	1.007939527± 0.262048649	0.598454429± 0.331555345
H_0 : b=0	-0.437325984^{NS}	2.077666043^{NS}	0.614325348^{NS}	0.144877035^{NS}	3.368986*	-0.293538056^{NS}	1.471300814^{NS}	-0.638456571^{NS}	1.846129185^{NS}	0.154452492^{NS}	3.846383224*	1.804991046^{NS}
H_0 : b=1	3.312861032*	0.749897782^{NS}	3.054800178*	1.685272636^{NS}	1.166448^{NS}	2.924865407*	0.855731662^{NS}	2.730457448^{NS}	1.706253257^{NS}	2.356512121^{NS}	-0.030297912^{NS}	1.21109666^{NS}

Table 44: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication 2 in the F_2 generation for different characters.

Character / Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	-0.013401213± 0.507179112	0.710124118± 0.178006363	0.065019923± 0.085029109	-0.084533061± 0.16672408	0.340875463± 0.204701898	0.679853573± 0.455133076	-0.205275108± 0.095114521	0.048793136± 0.115949515	-0.035194569± 0.175246864	0.076776327± 0.111123333	-0.134092063± 0.305314664	-0.146397698± 0.459817056
H_0 : b=0	-0.026423038^{NS}	3.989318738*	0.764678395^{NS}	-0.507023707^{NS}	1.66522864^{NS}	1.493746793^{NS}	-2.158188959^{NS}	0.42081363^{NS}	-0.200828522^{NS}	0.690910942^{NS}	-0.439192999^{NS}	-0.318382486^{NS}
H_0 : b=1	1.99811307^{NS}	1.628457985^{NS}	10.9959999**	6.50495755**	3.219923912*	0.70341279^{NS}	12.67183077**	8.203629541**	5.907064723**	8.308099161**	3.714502437*	2.493160448^{NS}

Table 45: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication total in the F_1 generation for different characters.

Character Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	0.622522± 0.202894	0.871391± 0.376399	0.638708± 0.418128	-0.78861± 0.923021	1.222732± 0.210123	0.091164± 0.191702	0.405958± 0.302219	0.169117± 0.308211	0.49966± 0.687175	0.265556± 0.247918	0.698095± 0.334767	-0.17233± 0.248534
H_0:b=0	3.068206*	2.315075^{NS}	1.527543^{NS}	-0.85438^{NS}	5.819116**	0.475553^{NS}	1.343257^{NS}	0.548706^{NS}	0.727121^{NS}	1.071145^{NS}	2.085314^{NS}	-0.6934^{NS}
H_0 : b=1	1.860466^{NS}	0.341682^{NS}	0.864072^{NS}	1.93778^{NS}	-1.06^{NS}	4.740883**	1.965602^{NS}	2.695825^{NS}	0.728111^{NS}	2.96245*	0.901836^{NS}	4.716982**

Table 46: Regression coefficient (b) with standard error (S.E.) and significancy of b from zero and unity are shown in the table for replication total in the F_2 generation for different characters.

Character Estimated value	DF	PHFF	NPBFF	NSBFF	CAMF	NSBMF	NPdPP	PdWPP	NSPP	SWPP	IPIW	RW
b±S.E.	-0.19086± 0.545631	0.692454± 0.204027	0.378029± 0.212665	-0.18215± 0.34205	0.742294± 0.232976	-0.32753± 0.259046	0.362042± 0.429446	0.48367± 0.542015	0.379708± 2.023411	0.59992± 0.411924	0.860175± 0.365136	0.594692± 0.415055
H_0 : b=0	-0.34979^{NS}	3.393927*	1.77758^{NS}	-0.53252^{NS}	3.186139*	-1.26437^{NS}	0.843043^{NS}	0.892355^{NS}	2.02341^{NS}	1.456385^{NS}	2.355766^{NS}	1.432801^{NS}
H_0 : b=1	2.182533^{NS}	1.507376^{NS}	2.924648*	3.45607*	1.106149^{NS}	5.124685**	1.485536^{NS}	0.952612^{NS}	0.61019^{NS}	0.971247^{NS}	0.382939^{NS}	0.976515^{NS}

Table 47: Components of variation and their proportional values are shown for twelve characters in F_1 generation.

Days to flower (DF)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	$6.26246 \pm 1.240596^*$	$[(H_1/D)]^{1/2}$	0.90462
H_1	$5.12481 \pm 3.149365^{NS}$	$H_2/4H_1$	0.28055
H_2	$5.751058 \pm 2.813407^*$	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	0.536919
h^2	$-1.67694 \pm 1.893609^{NS}$	h^2/H_2	-0.29159
F	$-3.41387 \pm 3.030777^{NS}$	h^2 (Heritability)	0.462991
E	$3.810691 \pm 0.468901^*$	r	-0.53237
Fr_1	-8.15072	r^2	0.283418
Fr_2	8.162032		
Fr_3	-14.2714		
Fr_4	-3.73799		
Fr_5	8.674583		
Fr_6	-11.1598		

Plant height at first flower (PHFF)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	$4.64976 \pm 0.412731^*$	$[(H_1/D)]^{1/2}$	-0.558579
H_1	$-1.45078 \pm 1.047756^{NS}$	$H_2/4H_1$	0.119203
H_2	$-0.69175 \pm 0.935987^{NS}$	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	0.821259
h^2	$-0.89314 \pm 0.629981^{NS}$	h^2/H_2	1.291139
F	$0.509797 \pm 1.008303^{NS}$	h^2 (Heritability)	0.495144
E	$1.896563 \pm 0.155998^*$	r	0.170794
Fr_1	-2.54857	r^2	0.029171
Fr_2	0.087706		
Fr_3	-2.30973		
Fr_4	4.811596		
Fr_5	0.333974		
Fr_6	2.6838		

Table 47 continued

Number of primary branches at first flower (NPBFF)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	-0.33101±0.159664*	$[(H_1/D)]^{1/2}$	-1.50122
H_1	0.745989±0.405321 ^{NS}	$H_2/4H_1$	0.358633
H_2	1.070145±0.362084*	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	-4424.65
h^2	0.160879±0.243706 ^{NS}	h^2/H_2	0.150334
F	-0.99429±0.390059*	h^2 (Heritability)	0.135144
E	0.817574±0.060347*	r	-0.41916
Fr_1	-1.07114	r^2	0.175697
Fr_2	-1.29645		
Fr_3	-1.73821		
Fr_4	0.341951		
Fr_5	-0.35731		
Fr_6	-1.84456		

Number of secondary branches at first flower (NSBFF)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	2.785512±3.229714 ^{NS}	$[(H_1/D)]^{1/2}$	2.232545
H_1	13.88371±8.198922 ^{NS}	$H_2/4H_1$	0.226509
H_2	12.57916±7.324302 ^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	0.994757
h^2	-2.32623±4.929739 ^{NS}	h^2/H_2	-0.18493
F	-0.03269±7.890194 ^{NS}	h^2 (Heritability)	0.218407
E	4.232053±1.220717*	r	-0.05685
Fr_1	-4.62883	r^2	0.003232
Fr_2	10.90103		
Fr_3	3.041519		
Fr4	-4.21653		
Fr5	-0.97419		
Fr6	-4.31916		

Table 47 continued

Canopy area at maximum flower (CAMF)			
Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	19527.131±2447.2368*	$[(H_1/D)]^{1/2}$	0.8715935
H_1	14834.276±6212.5334*	$H_2/4H_1$	0.2572111
H_2	15262.162±5549.8114*	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	1.379391
h^2	-4254.878±3735.3893 ^{NS}	h^2/H_2	-0.278786
F	5427.5468±5978.602 ^{NS}	h^2 (Heritability)	0.36782
E	7933.3767±924.96857*	r	-0.654928
Fr_1	-49685.06	r^2	0.4289313
Fr_2	25835.793		
Fr_3	26971.142		
Fr_4	-94.38753		
Fr_5	30920.998		
Fr_6	-1383.206		

Number of secondary branches at maximum flower (NSBMF)			
Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	-17.506±13.89075 ^{NS}	$[(H_1/D)]^{1/2}$	-0.932609
H_1	15.22601±35.26293 ^{NS}	$H_2/4H_1$	0.357358
H_2	21.76454±31.50126 ^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	17.67081
h^2	4.978847±21.20242 ^{NS}	h^2/H_2	0.22876
F	-29.1548±33.93511 ^{NS}	h^2 (Heritability)	0.07324
E	26.89056±5.250209*	r	-0.53682
Fr_1	-105.092	r^2	0.288178
Fr_2	-33.0539		
Fr_3	-40.8357		
Fr_4	14.99281		
Fr_5	1.803894		
Fr_6	-12.7438		

Table 47 continued

Number of pods per plant (NPdPP)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	-227.345±567.4025 ^{NS}	$[(H_1/D)]^{1/2}$	-2.30083
H_1	1203.523±1440.403 ^{NS}	$H_2/4H_1$	0.246963
H_2	1188.905±1286.748 ^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	2.805214
h^2	783.8411±866.0663 ^{NS}	h^2/H_2	0.659297
F	-496.306±1386.165 ^{NS}	h^2 (Heritability)	0.092914
E	1087.011±214.458*	r	-0.74478
Fr_1	-5626	r^2	0.554699
Fr_2	1170.606		
Fr_3	-364.659		
Fr_4	1246.825		
Fr_5	1434.555		
Fr_6	-839.164		

Pod weight per plant (PdWPP)

Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	-0.01324±0.711519 ^{NS}	$[(H_1/D)]^{1/2}$	-11.06709
H_1	1.621642±1.806255 ^{NS}	$H_2/4H_1$	0.269527
H_2	1.748304±1.613573 ^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	-2.69729
h^2	-0.69446±1.086041 ^{NS}	h^2/H_2	-0.39722
F	-0.63838±1.738241 ^{NS}	h^2 (Heritability)	0.127152
E	1.273839±0.268929*	r	-0.00785
Fr_1	-4.54805	r^2	6.16E-05
Fr_2	-0.26525		
Fr_3	1.088406		
Fr_4	-2.40169		
Fr_5	0.685388		
Fr_6	1.610929		

Table 47 continued

Number of seeds per plant (NSPP)

Components of variation	Estimated values with standard error	Other parameters	Estimated values
D	235.6235±556.1966^{NS}	$[(H_1/D)]^{1/2}$	2.502699
H_1	1475.829±1411.956^{NS}	$H_2/4H_1$	0.208654
H_2	1231.75±1261.335^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	1.272
h^2	50.84424±848.962^{NS}	h^2/H_2	0.041278
F	141.1947±1358.789^{NS}	h^2 (Heritability)	0.089877
E	1405.99±210.2226*	r	-0.18958
Fr_1	-3110.58	r^2	0.035939
Fr_2	2087.787		
Fr_3	-1110.28		
Fr_4	-113.521		
Fr_5	2080.663		
Fr_6	1013.099		

Seed weight per plant (SWPP)

Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	-0.12419±0.357102^{NS}	$[(H_1/D)]^{1/2}$	2.997578
H_1	1.115906±0.906537^{NS}	$H_2/4H_1$	0.294188
H_2	1.313146±0.809832^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	13.25521
h^2	-0.37123±0.54507^{NS}	h^2/H_2	-0.2827
F	-0.64008±0.872401^{NS}	h^2 (Heritability)	0.137807
E	0.668532±0.134972*	r	0.028929
Fr_1	-2.91883	r^2	0.000837
Fr_2	-0.47368		
Fr_3	0.40519		
Fr_4	-1.80925		
Fr_5	0.247757		
Fr_6	0.708342		

Table 47 continued

Individual plant weight (IPlW)

Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	0.016829 ± 0.291379^{NS}	$[(H_1/D)]^{1/2}$	5.130089
H_1	0.442904 ± 0.739692^{NS}	$H_2/4H_1$	0.27788
H_2	0.492298 ± 0.660785^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	-0.51341
h^2	0.211381 ± 0.444752^{NS}	h^2/H_2	0.429377
F	-0.53704 ± 0.711839^{NS}	h^2 (Heritability)	0.218579
E	0.778669 ± 0.110131*	r	-0.5783
Fr_1	-4.10423	r^2	0.334428
Fr_2	0.820655		
Fr_3	0.28998		
Fr_4	-1.07954		
Fr_5	0.964112		
Fr_6	-0.11319		

Root weight (RW)

Components of variation	**Estimated values with standard error**	**Other parameters**	**Estimated values**
D	0.001561 ± 0.002483^{NS}	$[(H_1/D)]^{1/2}$	2.040004
H_1	0.006495 ± 0.006303^{NS}	$H_2/4H_1$	0.166956
H_2	0.004338 ± 0.00563^{NS}	$(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$	1.04272
h^2	-0.00071 ± 0.00379^{NS}	h^2/H_2	-0.16295
F	0.000133 ± 0.006065^{NS}	h^2 (Heritability)	0.318706
E	0.002747 ± 0.000938*	r	0.414136
Fr_1	-0.0064	r^2	0.171508
Fr_2	-0.00254		
Fr_3	0.004312		
Fr_4	-0.00331		
Fr_5	0.002575		
Fr_6	0.006164		

Table 48: Components of variation and their proportional values are shown for twelve characters in F_2 generation.

Days to flower (DF)

Components of variation	Estimated values	Proportions	Estimated values
D	8.131666±6.421467^{NS}	$[1/4(H_1/D)]^{1/2}$	1.693473390608
H_1	93.28166±65.20592^{NS}	$H_2/4H_1$	0.204097
H_2	76.154±58.25008^{NS}	$1/4(4DH_1)^{1/2}+1/2F/$ $1/4(4DH_1)^{1/2}-1/2F$	15.7106055142379
h^2	-51.7943±39.20615^{NS}	h^2/H_2	-0.68013
F	24.24523±31.22369^{NS}	Heritability	0.300112
E_2	3.942496±2.427087^{NS}		

Plant height at first flower (PHFF)

Components of variation	Estimated values	Proportions	Estimated values
D	5.739938±0.763505**	$[1/4(H_1/D)]^{1/2}$	0.55226851965869
H_1	7.002736±7.752909^{NS}	$H_2/4H_1$	0.172348
H_2	4.82762±6.925868^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/$ $4(4DH_1)^{1/2}-1/2F$	0.514780903462146
h^2	-4.27276±4.661566^{NS}	h^2/H_2	-0.88507
F	-2.03084±3.712461^{NS}	Heritability	0.489272
E_2	1.284201±0.288578*		

Number of primary branches at first flower (NPBFF)

Components of variation	Estimated values	Proportions	Estimated values
D	-0.01525±0.317893^{NS}	$[1/4(H_1/D)]^{1/2}$	2.16156919398165
H_1	-0.28492±3.228003^{NS}	$H_2/4H_1$	-1.30902
H_2	1.491879±2.883656^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/$ $4(4DH_1)^{1/2}-1/2F$	-0.920011937825084
h^2	-8.61461±1.940891*	h^2/H_2	-5.77434
F	-1.58201±1.545721^{NS}	Heritability	-0.00562
E_2	0.854297±0.120152**		

Table 48 continued

Number of secondary branches at first flower (NSBFF)

Components of variation	Estimated values	Proportions	Estimated values
D	5.279718±7.277897^{NS}	$[1/4(H_1/D)]^{1/2}$	2.17409221637265
H_1	99.82209±73.90241^{NS}	$H_2/4H_1$	0.216577
H_2	86.47652±66.01887^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	4.50836538638934
h^2	-22.6496±44.43506^{NS}	h^2/H_2	-0.26192
F	14.6218±35.38799^{NS}	Heritability	0.176723
E_2	3.383656±2.750786^{NS}		

Canopy area at maximum flower (CAMF)

Components of variation	Estimated values	Proportions	Estimated values
D	22660.73±4006.945**	$[1/4(H_1/D)]^{1/2}$	-0.720826
H_1	-47096.9±40687.98^{NS}	$H_2/4H_1$	0.120292
H_2	-22661.4±36347.59^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	2.23176270649356
h^2	-72725.1±24464.33*	h^2/H_2	3.209202
F	-12496.6±19483.34^{NS}	Heritability	0.62368
E_2	10046.52±1514.483**		

Number of secondary branches at maximum flower (NSBMF)

Components of variation	Estimated values	Proportions	Estimated values
D	1.41068±11.14208^{NS}	$[1/4(H_1/D)]^{1/2}$	2.47589647964316
H_1	34.59023±113.1407^{NS}	$H_2/4H_1$	0.261086
H_2	36.12406±101.0715^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	0.655559127924558
h^2	-125.552±68.02776^{NS}	h^2/H_2	-3.47558
F	-1.45332±54.17717^{NS}	Heritability	0.033052
E_2	14.18849±4.211311*		

Table 48 continued

Number of pods per plant (NPdPP)

Components of variation	**Estimated values**	**Proportions**	**Estimated values**
D	-84.8437 ± 499.9657^{NS}	$[1/4(H_1/D)]^{1/2}$	6.85370967553923
H_1	$-15941.6\pm5076.834^{*}$	$H_2/4H_1$	0.170233
H_2	-10855.1 ± 4535.262^{NS}	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	-0.458828624866598
h^2	$-24904.9\pm3052.531^{**}$	h^2/H_2	2.294302
F	-3135.05 ± 2431.029^{NS}	Heritability	-0.06653
E_2	$1976.625\pm188.9693^{**}$		

Pod weight per plant (PdWPP)

Components of variation	**Estimated values**	**Proportions**	**Estimated values**
D	0.195711 ± 0.388192^{NS}	$[1/4(H_1/D)]^{1/2}$	-5.148184
H_1	$-20.7484\pm3.941839^{**}$	$H_2/4H_1$	0.192272
H_2	$-15.9573\pm3.521344^{*}$	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	-9.13275607750104
h^2	$-24.8857\pm2.370097^{**}$	h^2/H_2	1.559514
F	-2.51067 ± 1.88754^{NS}	Heritability	0.373854
E_2	$2.116226\pm0.146723^{**}$		

Number of seeds per plant (NSPP)

Components of variation	**Estimated values**	**Proportions**	**Estimated values**
D	-240.245 ± 440.1219^{NS}	$[1/4(H_1/D)]^{1/2}$	7.1479
H_1	$-49098.2\pm4469.158^{**}$	$H_2/4H_1$	0.180757
H_2	$-35499.4\pm3992.41^{**}$	$1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$	-0.4572
h^2	$-48670.8\pm2687.156^{**}$	h^2/H_2	1.3710
F	$-9220.47\pm2140.045^{*}$	Heritability	0.6371
E_2	$3896.553\pm166.3504^{**}$		

Table 48 continued

Seed weight per plant (SWPP)

Components of variation	Estimated values	Proportions	Estimated values
D	-0.10436±0.180347 ^{NS}	$[1/4(H_1/D)]^{1/2}$	5.91529342829717
H_1	-14.6059±1.831313**	$H_2/4H_1$	0.185971
H_2	-10.8651±1.635957**	$1/4(4DH_1)^{1/2}+1/2F/$ $1/4(4DH_1)^{1/2}-1/2F$	-0.315495673153254
h^2	-16.3651±1.101107**	h^2/H_2	1.506212
F	-2.37266±0.876919 ^{NS}	Heritability	-4.12541
E_2	1.293389±0.068165**		

Individual plant weight (IPlW)

Components of variation	Estimated values	Proportions	Estimated values
D	0.60253±0.151465*	$[1/4(H_1/D)]^{1/2}$	-0.738972
H_1	-1.31611±1.538032 ^{NS}	$H_2/4H_1$	0.063869
H_2	-0.33624±1.373963 ^{NS}	$1/4(4DH_1)^{1/2}+1/2F/$ $1/4(4DH_1)^{1/2}-1/2F$	4.07047972440337
h^2	-3.29939±0.924768*	h^2/H_2	9.812736
F	-0.53925±0.736483 ^{NS}	Heritability	0.458197
E_2	0.375977±0.057248**		

Root weight (RW)

Components of variation	Estimated values	Proportions	Estimated values
D	0.003482±0.00099*	$[1/4(H_1/D)]^{1/2}$	-0.171289
H_1	-0.00041±0.010055 ^{NS}	$H_2/4H_1$	1.603114
H_2	-0.00262±0.008983 ^{NS}	$1/4(4DH_1)^{1/2}+1/2F/$ $1/4(4DH_1)^{1/2}-1/2F$	-0.713796420511149
h^2	-0.01681±0.006046*	h^2/H_2	6.414524
F	0.007147±0.004815 ^{NS}	Heritability	1.118606
E_2	0.001481±0.000374*		

f. Graphical Analysis

Wr/Vr graphs drawn on the basis of array variance (Vr) and co-variance (Wr) are presented in Figures 1 to 72 of twelve yield and yield contributing characters of F_1s and F_2 generations for replication 1 and 2 and for total values of replications. In figures, Series1 indicates the array points obtained by plotting Wr values against Vri values. These array points indicate an excess of dominant or recessive genes and or equal amount of dominant and recessive genes in the respective parents by their positions along the regression line. Series2 denotes the array points obtained by plotting Wrei values against Vri values. Through these points regression line was drawn and Series3 represents the array points obtained by plotting Wri values against Vri values. Through these array points, parabola limit was drawn.

For DF of replication 1 of F_1 generation, the Wr/Vr graph along with regression line and limiting parabola were drawn in Fig. 1, which showed negative association ($b= -0.10639 \pm 0.231259$). The regression line deviated significantly from unity indicating presence of non allelic interaction. Array 5 possessed complete heterozygosity as it touched the parabola limit.

For DF of replication 2 of F_1 generation (Fig. 2), the Wr/Vr graph showed negative relation. The regression coefficient ($b = -0.42792 \pm 0.224984$) was negative. The regression line deviated significantly from unity indicating presence of non allelic interaction. Array 1, 4 and 6 showed complete heterozygosity.

The Wr/Vr graph for PHFF of replication 1 of F_1 generation (Fig. 3) showed partial dominance. The regression line was present with the value of 0.309536 ± 0.500397 deviating non significantly from zero and unity indicated absence of non allelic interaction.

The recurrent parent for the array no. 6 possessed the most dominant genes. The positions of the arrays 3, 4 and 5 are intermediate; containing more or less equal frequencies of dominant and recessive genes. The arrays 1 and 2 being far away from the point of origin and hence the recurrent parents of these arrays possessed an excess of recessive genes. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for PHFF of replication 2 of F_1 generation (Fig. 4) showed partial dominance. The regression line was present with the value of 0.860744 ± 0.08615 deviating significantly from zero.

The recurrent parents for the array no. 1 and 5 possessed an excess of dominant genes. The positions of the arrays 2, 3, 4 and 6 are intermediate which contain more or less equal frequencies of dominant and recessive genes. The array 4 being far away from the point of origin and hence, the recurrent parent of this array possessed an excess of recessive genes.

For NPBFF of replication 1 of F_1 generation (Fig. 5), the Wr/Vr graph showed partial dominance. The regression line with the value of 0.004402 ± 0.120415 deviated significantly from unity indicating the presence of non allelic interaction.

By plotting the paired values of Wr and Vr, the position of arrays was obtained in the Wr/Vr graph. Array 6 is near to the point of origin and hence the recurrent parent for this array possessed the most dominant genes. The positions of the arrays 3, 4, 5 and 1 are intermediate that contain more or less equal frequencies of dominant and recessive genes. The recurrent parent of the array 2 possessed an excess of recessive genes as it is far away from the point of origin.

The Wr/Vr graph for NPBFF of replication 2 of F_1 generation (Fig. 6) showed negative relation. The regression line was present with the value of -0.14288 ± 0.32235. It deviated significantly from unity indicating the presence of non allelic interaction. Array 1 and 2 indicated complete heterozygous condition in the respective recurrent parents.

In the Wr/Vr graph for NSBFF of replication 1 of F_1 generation (Fig. 7), relation of Wr and Vr was negative. The regression line with the value of -0.44862 ± 0.632474 was not deviated significantly from zero and unity suggesting the absence of non allelic interaction.

The Wr/Vr graph for NSBFF of replication 2 of F_1 generation (Fig. 8) indicated negative association. The regression line with a slope of -0.32361 ± 0.348095 deviated significantly from unity indicating the presence of non allelic interaction.

For CAMF of replication 1 of F_1 generation, the Wr/Vr graph along with the regression line and limiting parabola drawn (Fig. 9). The graph showed that the regression line passed below the origin, which indicated the presence of over dominant genes in all arrays.

The regression line was present with the value of 0.69253 ± 0.299699 that did not deviated significantly from zero and unity suggesting the absence of non allelic interaction.

By plotting the paired values of Wr and Vr, the position of arrays was obtained in the Wr/Vr graph. Array 5 and 4 are near to the point of origin and hence the recurrent parents for these arrays possessed an excess of dominant genes. The positions of the arrays 6, 3 and 2 are intermediate that contain more or less equal frequencies of dominant and recessive genes. The array 1, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes.

The regression line of the Wr/Vr graph intersected the Wr axis above the origin indicated partial dominance in all arrays for CAMF of replication 2 of F_1 generation (Fig. 10).

The regression line with the value of 0.21769 ± 0.155418 deviated significantly from unity which indicated presence of non allelic interaction. Furthermore, all the Wr and Vr points were within the boundary of the limiting parabola.

By plotting the paired values of Wr and Vr, the positions of arrays were obtained in the Wr/Vr graph. Array no. 1, 2 and 5 are near to the point of origin and hence, the recurrent parents for the possessed an excess of dominant genes. The positions of the arrays 3 and 6 are intermediate containing more or less equal frequencies of dominant and recessive genes. The array 4, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes. Array 1 possessed complete heterozygosity, because it touched the parabola limit.

The regression line of the Wr/Vr graph intersected the Wr axis below the origin indicating over dominance in all arrays for NSBMF of replication 1 of F_1 generation (Fig. 11). The regression line with the value of 0.192525 ± 0.117463 deviated significantly from unity indicating presence of non allelic interaction.

By plotting the paired values of Wr and Vr, the positions of arrays were obtained in the Wr/Vr graph. The recurrent parents for the array no. 6, 4, 5 and 2 possessed an excess of dominant genes. The position of the array 3 is intermediate that contain more or less equal frequencies of dominant and recessive genes. The array 1, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes. Array 1 possessed complete heterozygosity.

For NSBMF of replication 2 of F_1 generation, the Wr/Vr graph along with the regression line and limiting parabola was drawn (Fig. 12). The graph showed that the regression line passed above the origin, which indicated the presence of partial dominant genes in all arrays.

The regression line with the value of 0.163598 ± 0.529037 deviated non significantly from zero and unity suggesting absence of non allelic interaction. All the Wr and Vr points were within the boundary of the limiting parabola.

It was observed that the array 3 had lower Wr, Vr values fall nearest to the origin and hence, its recurrent parent had the most dominant genes; whilst array 5 with larger value of Wr and Vr fall furthest from the origin and hence it had mostly recessive genes. The positions of the arrays 4, 2, 6 and 1 are intermediate containing more or less equal frequencies of dominant and recessive genes. Array 3 indicated the presence of complete heterozygous condition in its respective recurrent parent.

For NPdPP of replication 1 of F_1 generation, the Wr/Vr graph along with the regression line and limiting parabola was drawn (Fig. 13). The graph showed that the regression line passed below the origin indicating the presence of over dominant genes in all arrays. The regression line was present with the value of 0.31883 ±

0.26343. This line was not deviated significantly from zero and unity indicating absence of non allelic interaction.

The relative positions of Wr and Vr points on the Wr/Vr graph suggest the dominance order of the arrays. Here, the recurrent parents for the array no. 5 and 4 possessed an excess of dominant genes. The positions of the arrays 6, 2 and 3 are intermediate and hence, contain more or less equal frequencies of dominant and recessive genes. The array 1, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes.

The Wr/Vr graph for NPdPP of replication 2 of F_1 generation (Fig. 14) showed that the regression line intersected the Wr axis above the origin indicating partial dominance in all arrays. The regression line had a slope of 0.626908 ± 0.071291, which was deviated significantly from unity indicating presence of non allelic interaction. The regression line deviated significantly from zero also.

Here, it was observed that the recurrent parents for the array 3 and 6 possessed an excess of dominant genes. The positions of the arrays 5 and 4 are intermediate that contain more or less equal frequencies of dominant and recessive genes. The array 1 and 2, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Parents of array 3, 6, 4 and 5 possessed completely heterozygosity.

The Wr/Vr graph for PdWPP of replication 1 of F_1 generation (Fig. 15) showed negative relation. The regression line with the value of -0.05643 ± 0.161467 deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for PdWPP of replication 2 of F_1 generation (Fig. 16) showed negative relation. The regression line was present with the value of -0.00981 ± 0.132974 deviating significantly from unity that indicated presence of non allelic interaction. Array 1, 2 and 3 possessed complete heterozygosity.

The Wr/Vr graph for NSPP of replication 1 of F_1 generation (Fig. 17) indicated over dominance. The regression line was present with the value of 0.577163

± 0.52702. This line deviated significantly from unity indicating presence of non allelic interaction.

By plotting the paired values of Wr and Vr, the positions of arrays are obtained in the Wr/Vr graph. The recurrent parent for the array no. 4 possessed the most dominant genes. The positions of the arrays 6, 5, 3 and 2 are intermediate containing more or less equal frequencies of dominant and recessive genes. The array 1, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes.

The Wr/Vr graph for NSPP of replication 2 of F_1 generation (Fig. 18) showed over dominance. The regression line was present with the value of 0.711019 ± 0.14084. This line deviated significantly from zero. The graph shows that the array 6 lies near the point of origin. The recurrent parent for this array possessed the most dominant genes. The array 2 and 4, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. The positions of the arrays 3, 5 and 1 are intermediate and contain more or less equal frequencies of dominant and recessive genes.

The Wr/Vr graph for SWPP of replication 1 of F_1 generation (Fig. 19) indicated that array variances (Vr) and covariances (Wr) were negatively related. The regression line was with the value of -0.00387 ± 0.127115, which deviated significantly from unity indicating presence of non allelic interaction. Array 4 possessed complete heterozygosity.

The Wr/Vr graph for SWPP of relication 2 of F_1 generation (Fig. 20) indicated that array variances (Vr) and covariances (Wr) were negatively related and the regression line was with the value of -0.09921 ± 0.118062. The regression line deviated significantly from unity indicating presence of non allelic interaction. Array 1, 2 and 3 possessed complete heterozygosity.

The Wr/Vr graph for IPlW of replication 1 of F_1 generation (Fig. 21) showed over dominance. The regression line was present with the value of 0.387179 ± 0.334081. This line was not deviated significantly from zero and unity.

By plotting the paired values of Wr and Vr, the positions of arrays are obtained in the Wr/Vr graph. The recurrent parents for the array 5 and 6 possessed an excess of dominant genes. The positions of the arrays 4, 3 and 2 are intermediate and these contain more or less equal frequencies of dominant and recessive genes. The array 1 being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes. Array 1 and 6 indicated the presence of complete heterozygosity in their respective recurrent parents.

The Wr/Vr graph for IPlW of replication 2 of F_1 generation (Fig. 22) indicated partial dominance. The regression line with the value of 0.407886 ± 0.198845 deviated significantly from unity indicating presence of non allelic interaction. Array 1 and 5 are near the point of origin. Hence the recurrent parents for these arrays possessed an excess of dominant genes. The positions of the arrays 3 and 2 are intermediate and contain more or less equal frequencies of dominant and recessive genes. The array 4 and 6 being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Array 1, 3 and 5 possessed complete heterozygosity

The Wr/Vr graph for RW of replication 1 of F_1 generation (Fig. 23) indicated negative relation between Wr and Vr values for this character. The regression line was present with the value of -0.17098 ± 0.127072. The regression line deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for RW of replication 2 of F_1 generation (Fig. 24) indicated partial dominance. The regression line was present with the value of 0.511971 ± 0.371995. It was not deviated significantly from zero and unity indicating absence of non allelic interaction. The corresponding parent for the array no. 2 possessed the most dominant genes.

The positions of the arrays 3, 6 and 1 are intermediate containing more or less equal frequencies of dominant and recessive genes. The array 4 and 5, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Array 1, 3 and 5 possessed complete heterozygosity.

The Wr/Vr graph for DF of replication 1 of F_2 generation (Fig. 25) indicated negative relation of variances (Vr) and covariances (Wr). The regression line was present with the value of -0.15209 ± 0.347761. The regression line deviated significantly from unity indicating presence of non allelic interaction. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for DF of replication 2 of F_2 generation (Fig. 26) indicated negative relation of variances (Vr) and covariances (Wr). The regression line was present with the value of -0.0134 ± 0.006367. The regression line was not deviated significantly from zero and unity indicating absence of non allelic interaction in this case.

The Wr/Vr graph for PHFF of replication 1 of F_2 generation (Fig. 27) indicated partial dominance. The regression line with the value of 0.73479 ± 0.353661 was not deviated significantly from zero and unity indicating absence of non allelic interaction.

By plotting the paired values of Wr and Vr, the positions of arrays are obtained in the Wr/Vr graph. The array 6 is near the point of origin and hence the recurrent parent of this array possessed the most dominant genes. The positions of the arrays 5, 3, 1 and 4 are intermediate that contain more or less equal frequencies of dominant and recessive genes. The array 2 being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes.

The Wr/Vr graph for PHFF of replication 2 of F_2 generation (Fig. 28) indicated complete or slightly partial dominance. The regression line with the value of 0.710124 ± 0.178006 deviated significantly from zero. The Wr/Vr graph showed that the recurrent parent for the array 6 possessed the most dominant genes. The positions of the arrays 5, 4, 3 and 1 are intermediate and hence, contain more or less equal frequencies of dominant and recessive genes. The array 2, being far away from the point of origin, the recurrent parent of this array possessed an excess of recessive genes.

The Wr/Vr graph for NPBFF of replication 1 of F_2 generation (Fig. 29) indicated complete or slightly partial dominance. The regression line with the value of 0.167431 ± 0.272545 deviated significantly from unity indicating presence of non allelic interaction. The recurrent parents for the arrays 4 and 2 are near to the point of origin and hence the recurrent parents of these arrays possessed an excess of dominant genes. The positions of the arrays 5 and 3 are intermediate that contain more or less equal frequencies of dominant and recessive genes. The array 1 and 6, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. The regression line deviated significantly from unity.

The Wr/Vr graph for NPBFF of replication 2 of F_2 generation (Fig. 30) indicated partial dominance. The regression line was present with the value of 0.06502 ± 0.085029. This line deviated significantly from unity indicating presence of non allelic interaction.

The recurrent parents for the array no. 2 and 6 possessed an excess of dominant genes. The positions of the arrays 5 and 1 are intermediate indicating more or less equal frequencies of dominant and recessive genes. The array 3 and 4 being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for NSBFF of replication 1 of F_2 generation (Fig. 31) indicated partial dominance. The regression line with the value of 0.079161 ± 0.546403 was not deviated significantly from zero and unity. The recurrent parent for the array 2 possessed the most dominant genes. The positions of the arrays 5, 6 and 3 are intermediate containing more or less equal frequencies of dominant and recessive genes. The array 4 and 1, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for NSBFF of replication 2 of F_2 generation (Fig. 32) indicated negative relation between variances (Vr) and covariances (Wr). The regression line was present with the value of -0.08453 ± 0.166724. The regression line deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for CAMF of replication 1 of F_2 generation (Fig. 33) indicated partial dominance. The regression line with the value of 0.742814 ± 0.220486 deviated significantly from zero. The recurrent parents for the array 6 and 4 possessed an excess of dominant genes. The positions of the arrays 5 and 1 are intermediate which contain more or less equal frequencies of dominant and recessive genes. The array 3 and 2 being far away from the point of origin, parents of these arrays possessed an excess of recessive genes. Arrays 1, 3 and 5 possessed complete heterozygosity in this case.

The Wr/Vr graph for CAMF of replication 2 of F_2 generation (Fig. 34) indicated partial dominance. The regression line with the value of 0.340875 ± 0.204702 deviated significantly from unity indicating presence of non allelic interaction. The recurrent parents for the array no. 4 and 6 possessed an excess of dominant genes. The positions of the arrays 5, 2 and 3 are intermediate indicating more or less equal frequencies of dominant and recessive genes. The array 1, being far away from the point of origin, the recurrent parent of it possessed an excess of recessive genes.

The Wr/Vr graph for NSBMF of replication 1 of F_2 generation (Fig. 35) showed that array variances (Vr) and covariances (Wr) were negatively related. The regression coefficient ($b = -0.11156 \pm 0.380036$) was negative. The regression line deviated significantly from unity.

The Wr/Vr graph for NSBMF of replication 2 of F_2 generation (Fig. 36) indicated over dominance. The regression line with the value of 0.679854 ± 0.455133 was not deviated significantly from zero and unity.

The corresponding parent for the array 5 possessed the most dominant genes. The positions of the arrays 2, 6, 4 and 1 are intermediate containing more or less equal frequencies of dominant and recessive genes. The array 3, being far away from the point of origin, the recurrent parent of it possessed an excess of recessive genes.

The Wr/Vr graph for NPdPP of replication 1 of F_2 generation (Fig. 37) indicated over dominance. The regression line with the value of 0.632265 ± 0.429732 was not deviated significantly from zero and unity indicating absence of non allelic interaction. Array 3 and 5 are near the origin and hence the recurrent parents of these arrays possessed an excess of dominant genes. The parent 6 and 1 possessed an excess of recessive genes as the array points for these parents being far from the origin. Array 4 and 2 possessed more or less equal proportion of dominant and recessive genes. Array 6 possessed complete heterozygosity.

In case of NPdPP of replication 2 of F_2 generation (Fig. 38), the Wr/Vr graph revealed the negative relation between variances (Vr) and covariances (Wr). The regression line with the value of -0.20528±0.095115 deviated significantly from unity.

In case of PdWPP of replication 1 of F_2 generation (Fig. 39), the Wr/Vr graph indicated negative relation between variances (Vr) and covariances (Wr). The regression line with value of -0.30519 ± 0.478011 was not deviated significantly from zero and unity indicating absence of non allelic interaction.

The Wr/Vr graph for PdWPP of replication 2 of F_2 generation (Fig. 40) indicated partial dominance. The regression with the value of 0.048793 ± 0.11595 deviated significantly from unity indicating presence of non allelic interaction. The recurrent parents of array 2, 5 and 4 possessed an excess of dominant genes and the parents of array 1 and 3 had more recessive genes as the arrays fall furthest from the origin. Parent of array 6 had more or less equal proportion of dominant and recessive genes. Array 2 and 6 indicated the presence of complete heterozygous in their respective recurrent parents.

The Wr/Vr graph for NSPP of replication 1 of F_2 generation (Fig. 41) indicated complete or slightly over dominance. The regression coefficient ($b = 0.519688 \pm 0.281501$) was positive and was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents of array 5 and 4 possessed an excess of dominant genes and the parent 1 possessed an excess of recessive genes as the array point for this parent fall the furthest from the point of origin. Recurrent parents of array 6, 2 and 3 had more or less equal proportion of dominant and recessive genes.

For NSPP of replication 2 of F_2 generation (Fig. 42), the regression coefficient (b = -0.03519±0.175247) was negative. The regression line deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for SWPP of replication 1 of F_2 generation (Fig. 43) indicated partial dominance. The regression line with the value of 0.061511 ± 0.398253 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents for the array 3 and 5 possessed an excess of dominant genes. The positions of the arrays 6 and 4 are intermediate and hence, contain more or less equal frequencies of dominant and recessive genes. The array 1 and 2, being far away from the point of origin, the recurrent parents possessed an excess of recessive genes. Array 3 possessed complete heterozygosity as it touched the parabola limit.

The Wr/Vr graph for SWPP of replication 2 of F_2 generation (Fig. 44) indicated partial dominance. The regression line was present with the value of 0.076776 ± 0.111123. It deviated significantly from unity indicating presence of non allelic interaction. Array 5, 2 and 4 are near the point of origin and hence, the recurrent parents for these arrays possessed more dominant genes. The position of the array 6 is intermediate and contains more or less equal frequencies of dominant and recessive genes. The array 1 and 3, being far away from the point of origin, the recurrent parents of these arrays possessed an excess of recessive genes. Array 2 and 6 possessed complete heterozygosity.

The Wr/Vr graph for IPlW of replication 1 of F_2 generation (Fig. 45) indicated complete or slightly over dominance. The regression coefficient (b = 1.00794 ±0.262049) was positive and deviated significantly from zero. Array 5, 4 and 6 are near the point of origin and hence the recurrent parents of these arrays possessed more dominant genes. The recurrent parents of array 2 and 3 obtained more recessive genes as the array points for these parents being far from the origin. Array 1 showed more or less equal proportion of dominant and recessive genes. Array 3 possessed complete heterozygosity and array 1 possessed less heterozygosity than 3.

The Wr/Vr graph for IPlW of replication 2 of F_2 generation (Fig. 46) showed negative association of Wr and Vr. The regression line with the value of -0.13409±0.305315 deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for RW of replication 1 of F_2 generation (Fig. 47) showed over dominance and the regression line with the value of 0.598454 ± 0.331555 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents of array 5 and 3 possessed more dominant genes as the array points were near the origin and the parent of array 4 possessed more recessive genes because the array point was far from the origin. The positions of the array 2, 6 and 1 are intermediate and the recurrent parents of the arrays contain more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for RW of replication 2 of F_2 generation (Fig. 48) indicated that array variances (Vr) and covariances (Wr) were negatively related. The regression line with the value of -0.1464 ± 0.459817 was not deviated significantly from zero and unity indicating absence of non allelic interaction. Array 2 possessed complete heterozygosity.

The Wr/Vr graph for DF of replication total of F_1 generation (Fig. 49) showed partial dominance. The regression line with the value of 0.622522 ± 0.202894 deviated significantly from zero. From the Wr/Vr graph, it was shown that the recurrent parents of array 2 and 5 possessed more dominant genes as the array points were near the origin and the parent 3 possessed more recessive genes as the array points were far from the origin. Array 4, 1 and 6 showed more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for PHFF of replication total of F_1 generation (Fig. 50) showed partial dominance. The regression line had a slope of 0.871391 ± 0.376399, which was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents of array 4 and 6 possessed more dominant genes and the parents of array 1 and 3 possessed more recessive genes as the array points for these parents being far from the origin. Array 2 and 5 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for NPBFF of replication total of F_1 generation (Fig. 51) showed over dominance. The regression line had a slope of 0.638708 ± 0.418128 and was not deviated significantly from zero and unity indicating absence of non allelic interaction. From the Wr/Vr graph, it was shown that the recurrent parents of array 5 and 4 possessed more dominant genes as the array points near the origin and parents of array 6 and 3 possessed more recessive genes as the array points were far from the origin. Array 1 and 2 showed more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for NSBFF of replication total of F_1 generation (Fig. 52) indicated that array variances (Vr) and covariances (Wr) were negatively related and the regression coefficient (b = -0.78861 ±0.923021) was negative. The regression line was not deviated significantly from zero and unity indicating absence of non allelic interaction.

The Wr/Vr graph for CAMF of replication total of F_1 generation (Fig. 53) showed over dominance. The regression line had a slope of 1.222732 ±0.210123 and deviated significantly from zero. The recurrent parents of array 5, 3 and 2 possessed more dominant genes and the parent of array 1 possessed more recessive genes. Array 6 and 4 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for NSBMF of replication total of F_1 generation (Fig. 54) showed partial dominance. The regression line with the value of 0.091164 ± 0.191702 deviated significantly from unity indicating presence of non allelic interaction. The recurrent parents of array 4, 6 and 5 possessed an excess of dominant genes and the parent 1 possessed an excess of recessive genes as the array point for this parent was situated far from the origin. Array 2 and 3 showed more or less equal proportion of dominant and recessive genes. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for NPdPP of replication total of F_1 generation (Fig. 55) showed over dominance. The regression line with the value of 0.405958 ±0.302219 was not deviated significantly from zero and unity. The recurrent parents of array no. 4 and 5 possessed more dominant genes and the parent 1 possessed more recessive genes as the array point of this parent was situated far away from the origin. Array 6, 2 and 3 showed more or less equal proportion of dominant and recessive genes. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for PdWPP of replication total of F_1 generation (Fig. 56) showed partial dominance. The regression line with the value of 0.169117 ± 0.308211 was not deviated significantly from unity indicating absence of non allelic interaction. The parents of array 6, 5 and 3 possessed an excess of dominant genes because the array points were near the origin and the parent 1 possessed an excess of recessive genes as the array point for this parent lied far from the origin. Array 4 and 2 showed more or less equal proportion of dominant and recessive genes as these arrays were situated at the middle of the regression line. Array 4 possessed complete heterozygosity.

The Wr/Vr graph for NSPP of replication total of F_1 generation (Fig. 57) showed over dominance. The regression line with the value of 0.49966 ± 0.687175 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parent of array 2 possessed the most dominant genes and the parent 3 and 1 possessed an excess of recessive genes as the array points for these parents being far away from the origin. Array 6, 4 and 5 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for SWPP of replication total of F_1 generation (Fig. 58) showed complete or slightly partial dominance. The regression line had a slope of 0.265556 ± 0.247918 and deviated significantly from unity indicating presence of non allelic interaction. The Wr/Vr graph showed that the recurrent parents of array 6, 3 and 5 contain an excess of dominant genes and the parent 1 posses an excess of recessive genes. Array 4 and 2 showed more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for IPlW of replication total of F_1 generation (Fig. 59) showed over dominance. The regression line with the value of 0.698095 ± 0.334767 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The Wr/Vr graph showed that the recurrent parent of array 5 had the most dominant genes and the parent 1 had the most recessive genes. Array 6, 2, 3 and 4 showed more or less equal proportion of dominant and recessive genes. Array 1 and 6 possessed complete heterozygosity in this case.

The Wr/Vr graph for RW of replication total of F_1 generation (Fig. 60) indicated that array variances (Vr) and covariances (Wr) were negatively related. The regression line with the value of -0.17233 ± 0.248534 was deviated significantly from unity indicating presence of non allelic interaction. Array 4 and 6 possessed complete heterozygosity in this case.

The Wr/Vr graph for DF of replication total of F_2 generation (Fig. 61) indicated that array variances (Vr) and covariances (Wr) were negatively related. The regression line with the value of -0.19086 ± 0.545631 was present. The regression line was not deviated significantly from zero and unity. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for PHFF of replication total of F_2 generation (Fig. 62) showed partial dominance. The regression line with the value of 0.692454 ± 0.204027 was deviated significantly from zero. The recurrent parent of array 6 possessed the most dominant genes and the parent 2 possessed the most recessive genes. Array 5, 4, 1 and 3 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for NPBFF of replication total of F_2 generation (Fig. 63) showed over dominance. The regression line had a slope of 0.378029 ± 0.212665 and significantly deviated from unity indicating presence of non allelic interaction. The recurrent parent of array 2 possessed the most dominant genes as the array point situated near the origin. The parent 3 and 1 possessed an excess of recessive genes as the array points were far from the origin for this character. Array 6, 5 and 4 showed more or less equal proportion of dominant and recessive genes as their positions were at the middle along the regression line.

The Wr/Vr graph for NSBFF of replication total of F_2 generation (Fig. 64) indicated that array variances (Vr) and covariances (Wr) were negatively related. The regression line with the value of -0.18215 ± 0.34205 was present. The regression line deviated significantly from unity indicating presence of non allelic interaction. Array 6 possessed complete heterozygosity.

The Wr/Vr graph for CAMF of replication total of F_2 generation (Fig. 65) showed partial dominance. The regression line with the value of 0.742294 ± 0.232976 was present. The recurrent parents of array 6 and 4 possessed mostly dominant genes and the parent 2 possessed an excess of recessive genes. Array 5, 1 and 3 showed more or less equal proportion of dominant and recessive genes. The regression line deviated significantly from zero. Array 1 and 5 possessed complete heterozygosity.

The Wr/Vr graph for NSBMF of replication total of F_2 generation (Fig. 66) indicated that array variances (Vr) and covariances (Wr) were negatively related and the value of regression coefficient was -0.32753 ±0.259046. The regression line deviated significantly from unity indicating presence of non allelic interaction.

The Wr/Vr graph for NPdPP of replication total of F_2 generation (Fig. 67) showed over dominance. The regression line had a slope of 0.362042 ± 0.429446. It was not deviated significantly from zero and unity indicating absence of non allelic interaction. From the Wr/Vr graph, it was observed that the recurrent parent of array 2 possessed an excess of dominant genes and the parent 1 had the most recessive genes. Array 5, 6, 4 and 3 showed more or less equal proportion of dominant and recessive genes as they were at the middle along the regression line.

The Wr/Vr graph for PdWPP of replication total of F_2 generation (Fig. 68) showed over dominance. The regression line with value of 0.48367 ± 0.542015 was present. The regression line was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents of array 2, 5, 6 and 3 possessed an excess of dominant genes and the parent of array 1 had more recessive genes as the array point for this parent was situated far away from the origin. Array 4 showed more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for NSPP of replication total of F_2 generation (Fig. 69) showed over dominance. The regression line with the value of 0.768306 ± 0.379708 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parents of array 5 and 4 possessed an excess of dominant genes and the parent of array 1 had the most recessive genes. Array 2, 3 and 6 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity.

The Wr/Vr graph for SWPP of replication total of F_2 generation (Fig. 70) showed over dominance. The regression line with the value of 0.59992 ±0.411924 was not deviated significantly from zero and unity indicating absence of non allelic interaction. The recurrent parent of array 5 possessed the most dominant genes and the parent of array 1 possessed the most recessive genes. Array 6, 2, 4 and 3 showed more or less equal proportion of dominant and recessive genes.

The Wr/Vr graph for IPlW of replication total of F_2 generation (Fig. 71) showed over dominance. The regression line had a slope of 0.860175 ± 0.365136 and was not deviated significantly from zero and unity indicating absence of non allelic interation. The recurrent parents of array 4, 5 and 6 possessed an excess of dominant genes and the parents of array 1and 2 possessed an excess of recessive genes as the array points for these parents occured far away from the origin. Array 3 showed more or less equal proportion of dominant and recessive genes. Array 1 possessed complete heterozygosity in this case.

The Wr/Vr graph for RW of replication total of F_2 generation (Fig. 72) showed complete dominance. The regression had a slope of 0.594692 ± 0.415055 and was not deviated significantly from zero and unity suggesting absence of non allelic interaction. The recurrent parents of array 5 and 2 possessed an excess of dominant genes and the recurrent parent of array 4 possessed an excess of recessive genes. Array 3, 1 and 6 showed more or less equal proportion of dominant and recessive genes. Array 1 and 5 possessed complete heterozygosity in this case.

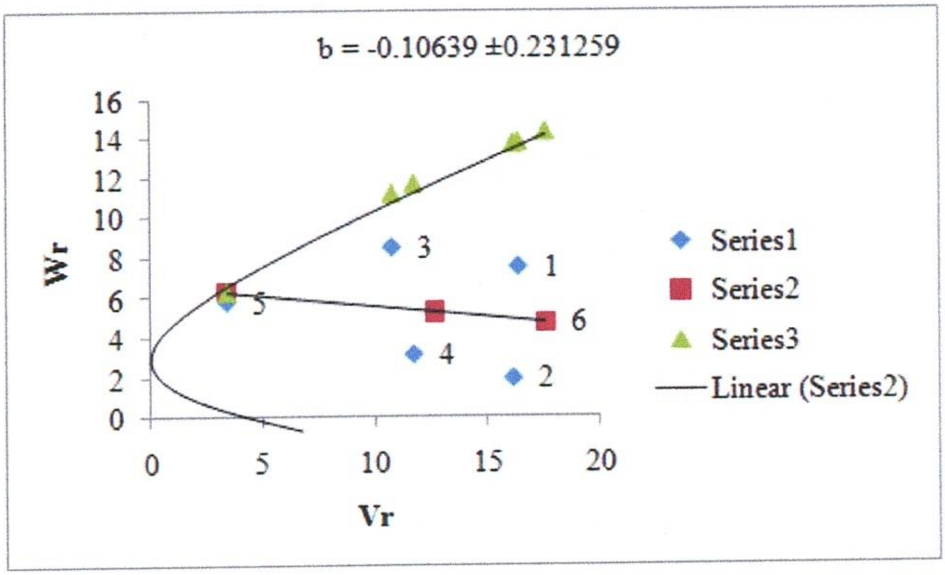

Fig 1: Wr/Vr graph for days to flower of F_1 generation for replication 1.

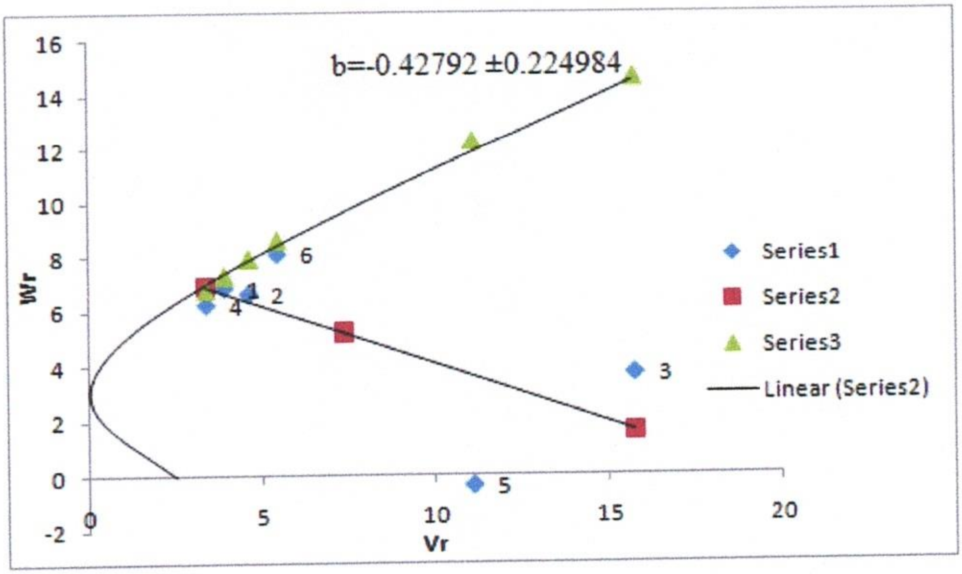

Fig 2: Wr/Vr graph for days to flower of F_1 generation for replication 2.

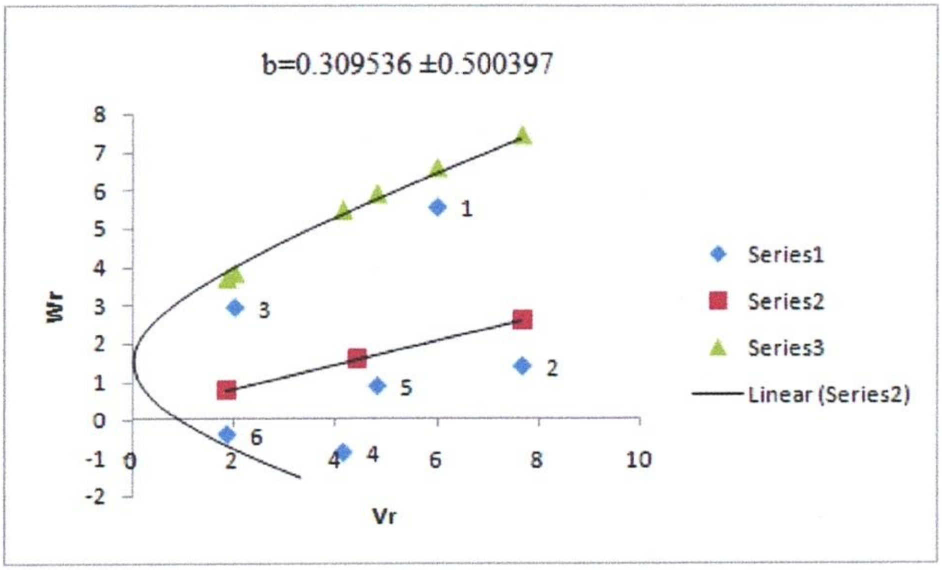

Fig 3: Wr/Vr graph for plant height at first flower of F_1 generation for replication 1.

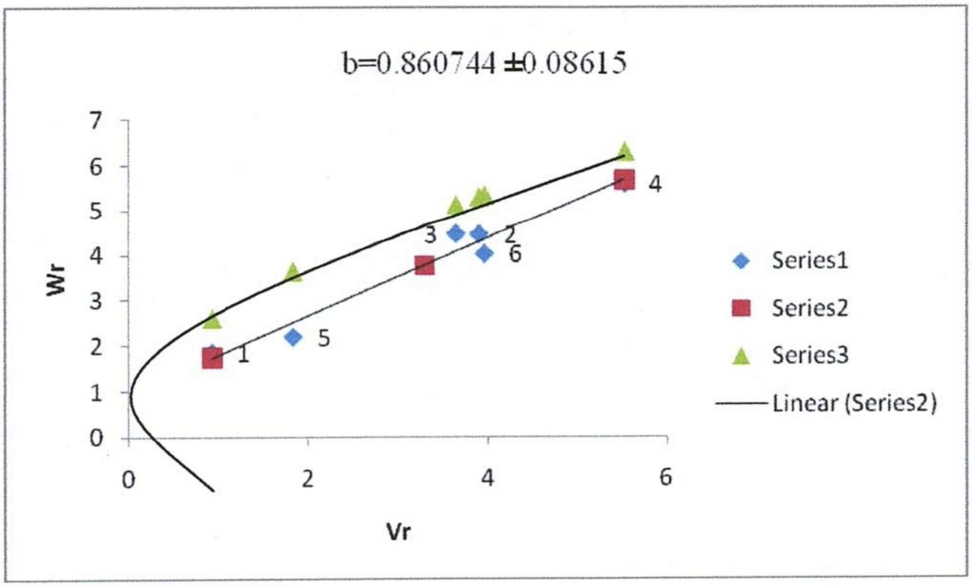

Fig 4: Wr/Vr graph for plant height at first flower of F_1 generation for replication 2.

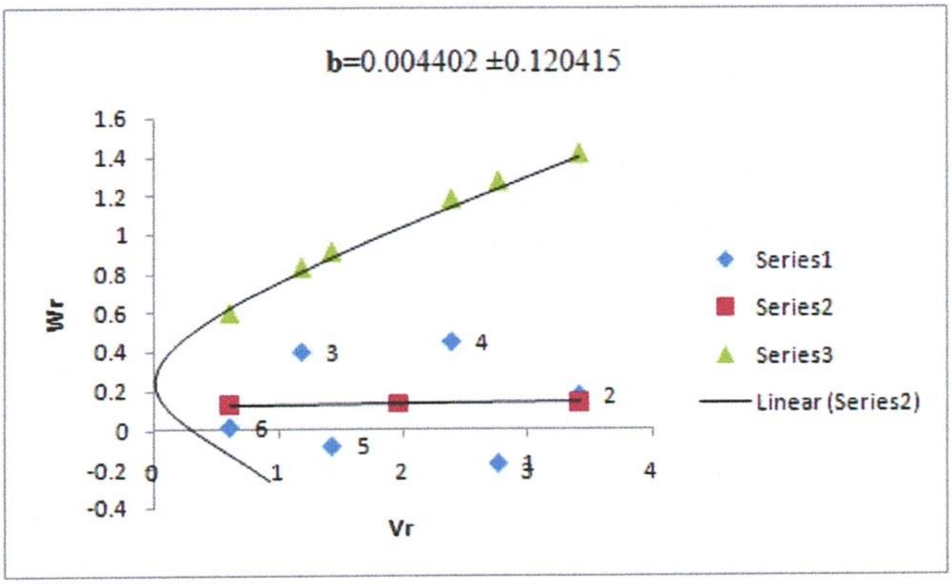

Fig 5: Wr/Vr graph for number of primary branches at first flower of F_1 generation for replication 1.

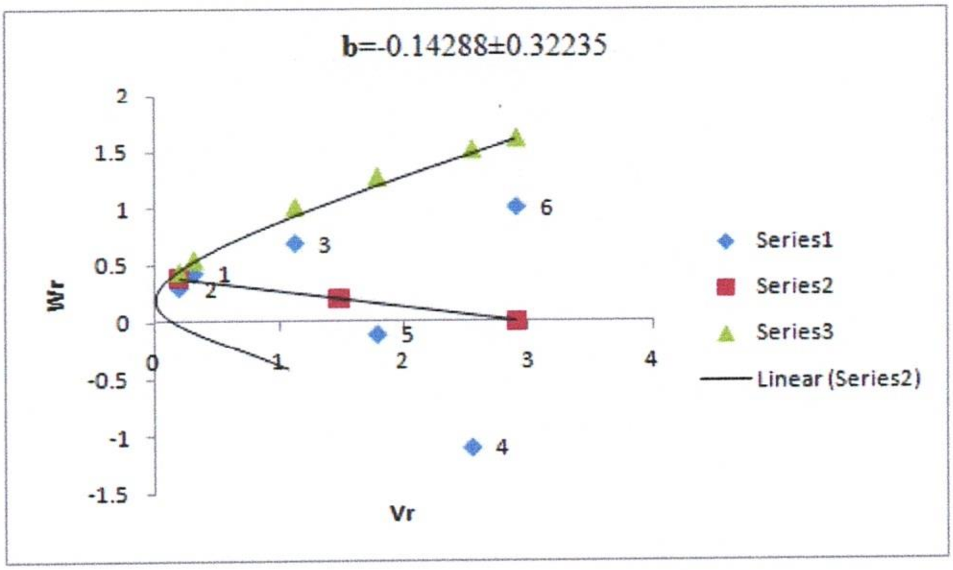

Fig 6: Wr/Vr graph for number of primary branches at first flower of F_1 generation for replication 2.

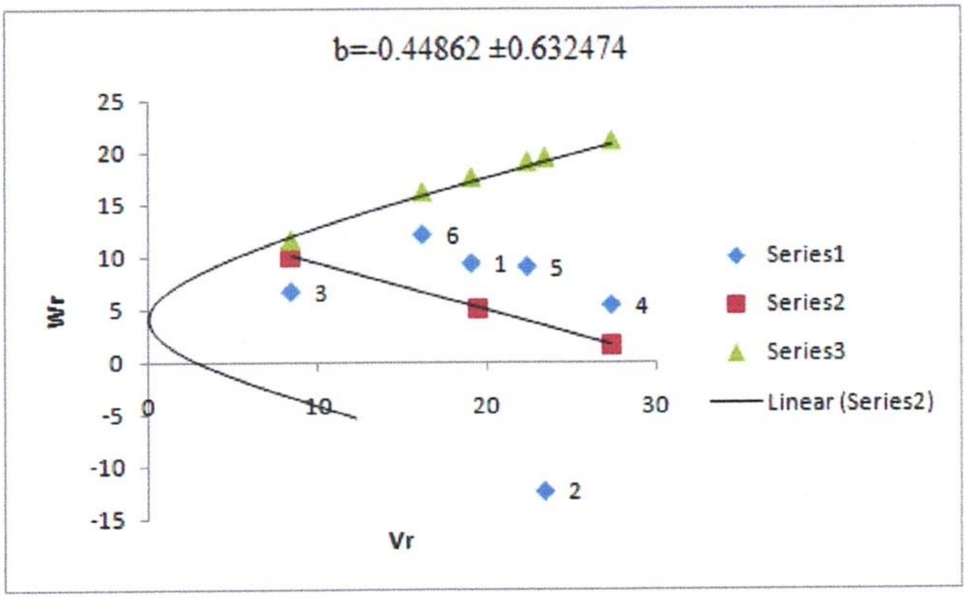

Fig 7: Wr/Vr graph for number of secondary branches at first flower of F_1generation for replication 1.

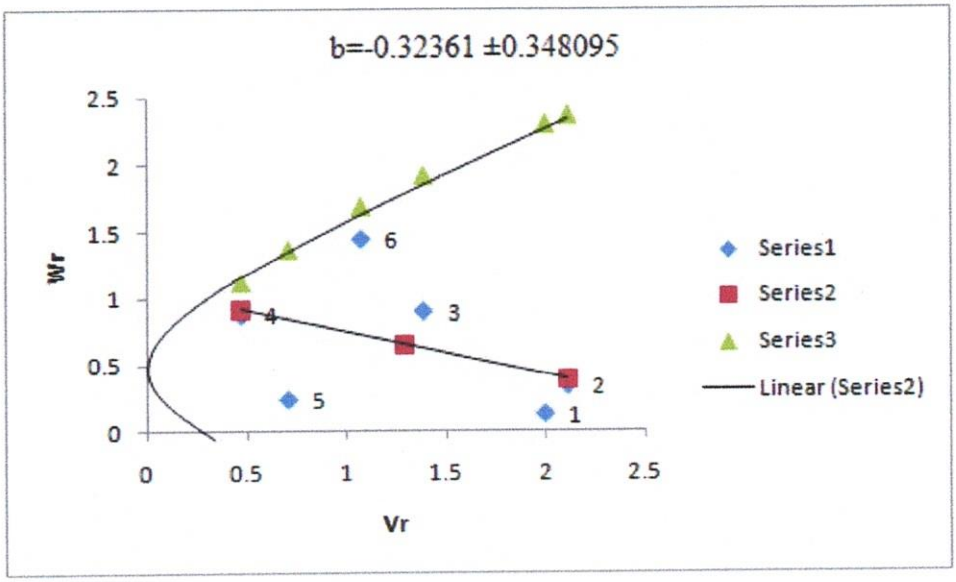

Fig 8: Wr/Vr graph for number of secondary branches at first flower of F_1 generation for replication 2.

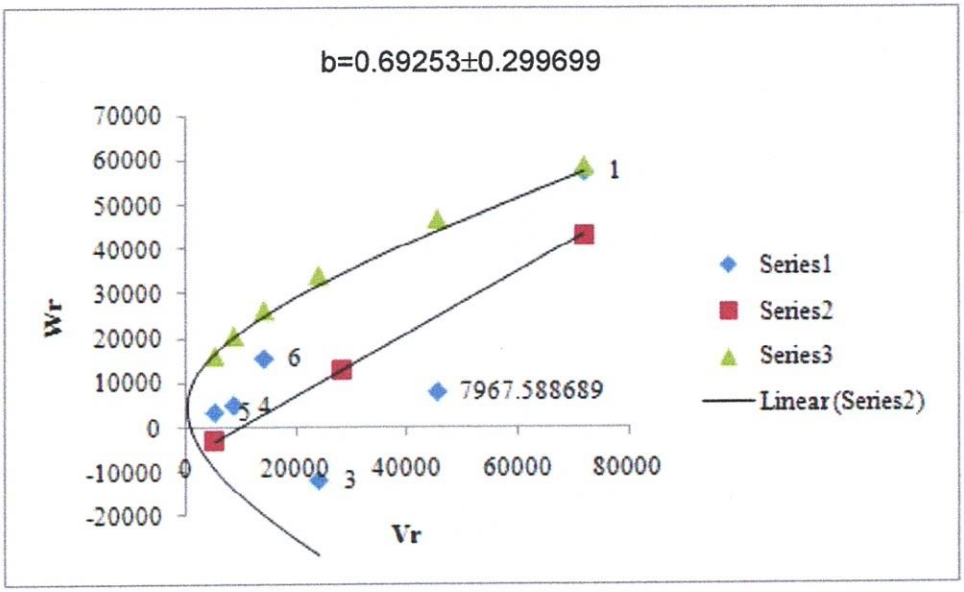

Fig 9: Wr/Vr graph for canopy area at maximum flower of F_1 generation for replication 1.

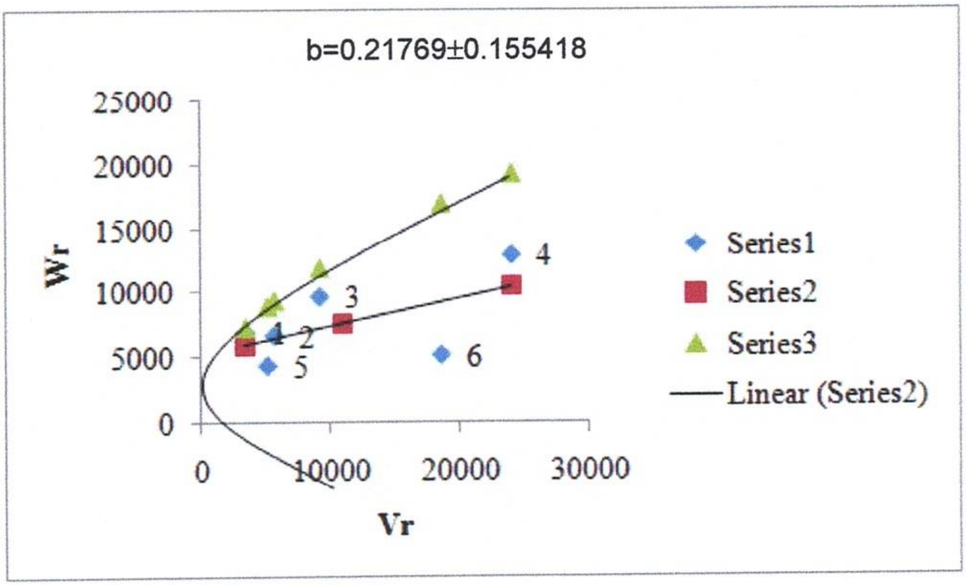

Fig 10: Wr/Vr graph for canopy area at maximum flower of F_1 generation for replication 2.

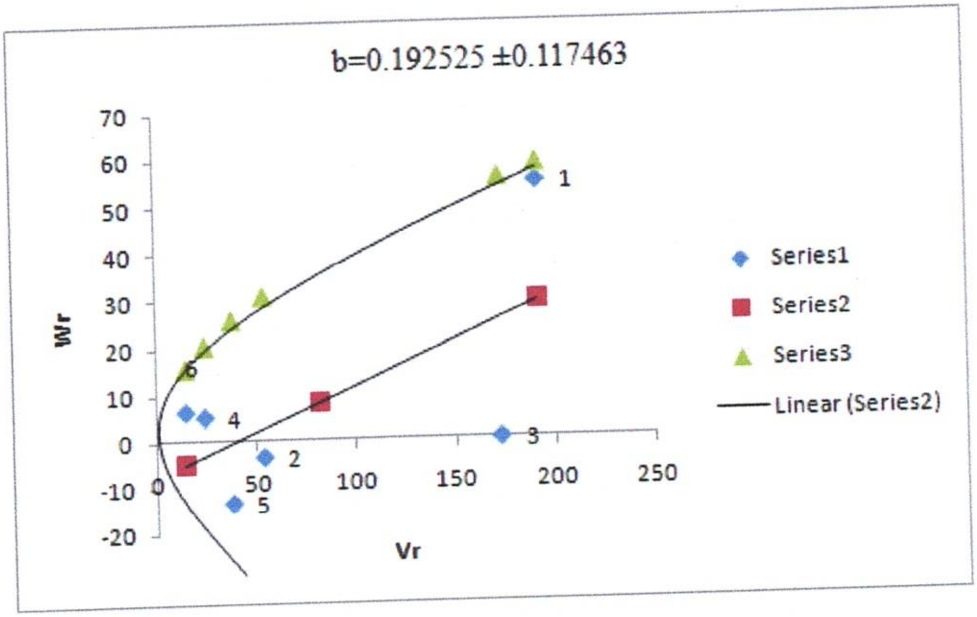

Fig 11: Wr/Vr graph for number of secondary branches at maximum flower of F_1 generation for replication 1.

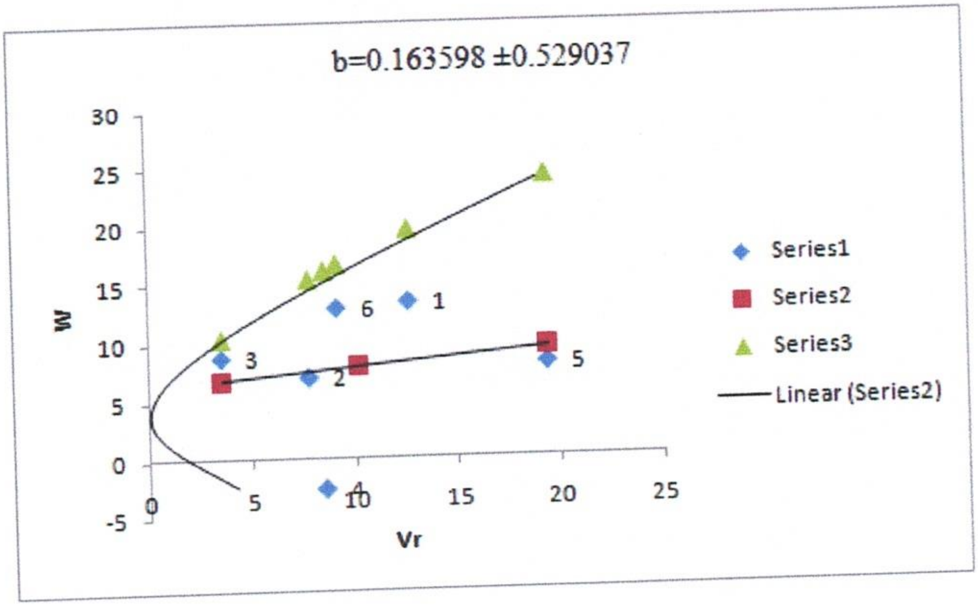

Fig 12: Wr/Vr graph for number of secondary branches at maximum flower of F_1 generation for replication 2.

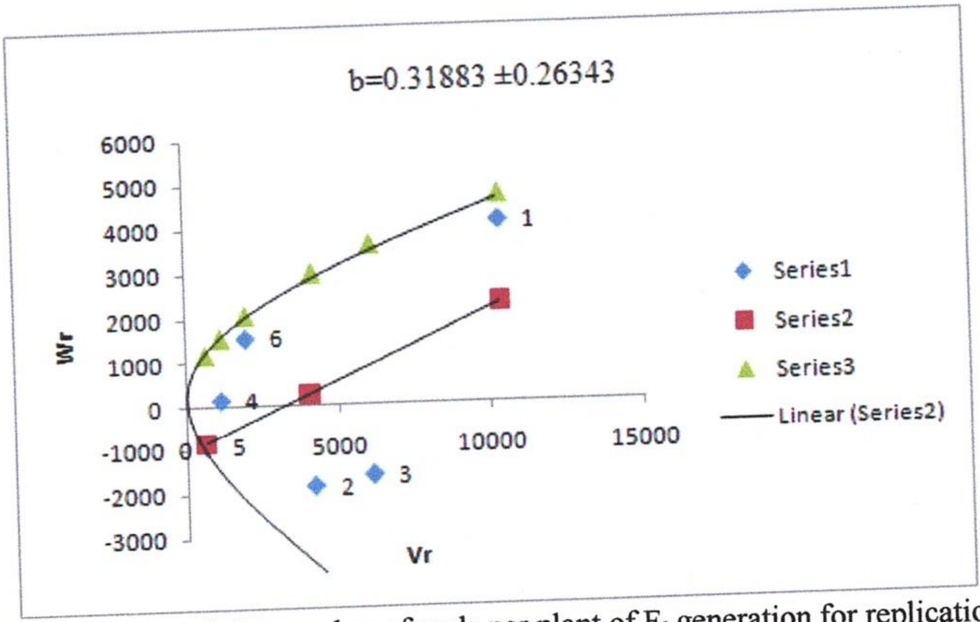

Fig 13: Wr/Vr graph for number of pods per plant of F_1 generation for replication 1.

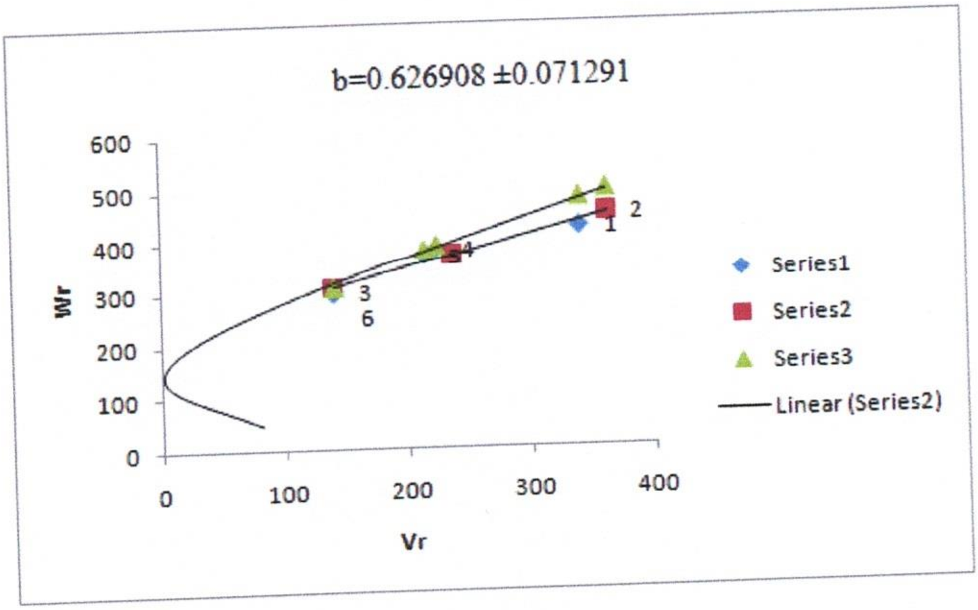

Fig 14: Wr/Vr graph for number of pods per plant of F_1 generation for replication 2.

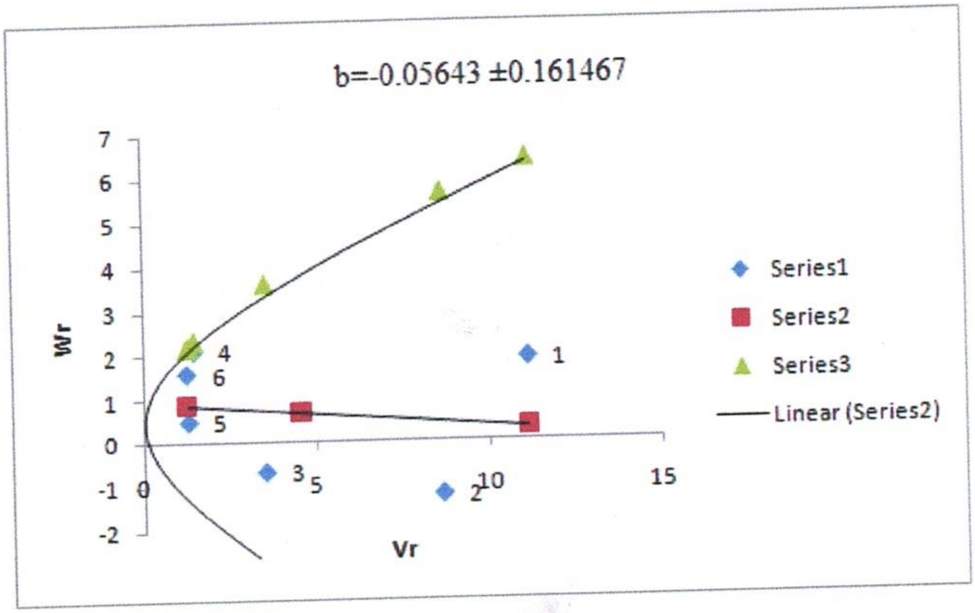

Fig 15: Wr/Vr graph for pod weight per plant of F_1 generation for replication 1.

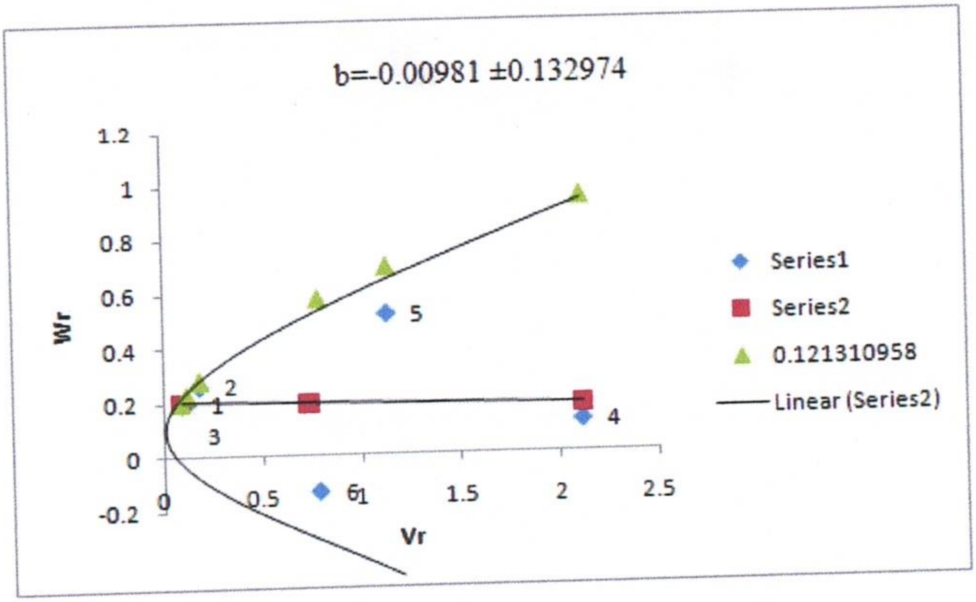

Fig 16: Wr/Vr graph for pod weight per plant of F_1 generation for replication 2.

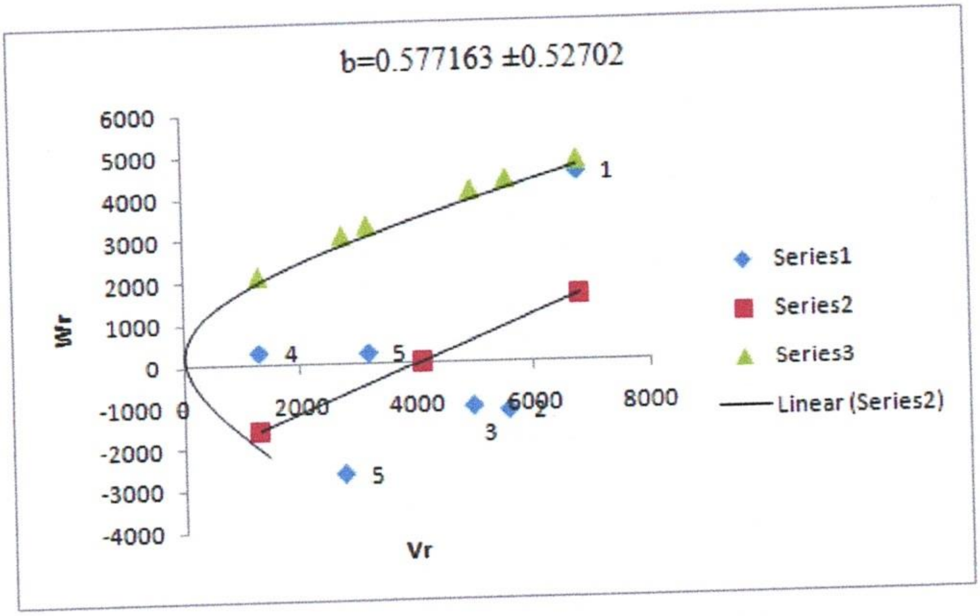

Fig 17: Wr/Vr graph for number of seeds per plant of F_1 generation for replication 1.

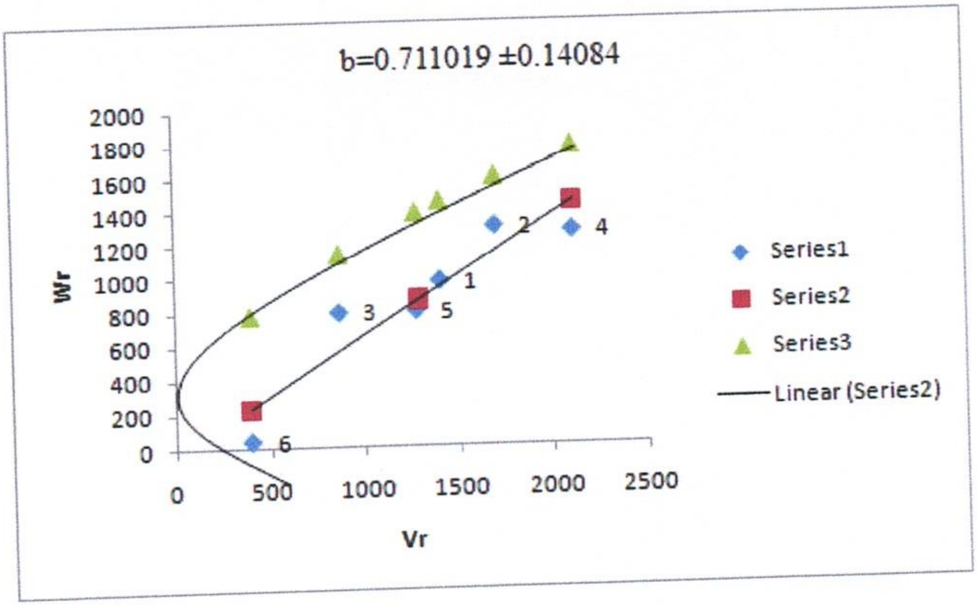

Fig 18: Wr/Vr graph for number of seeds per plant of F_1 generation for replication 2.

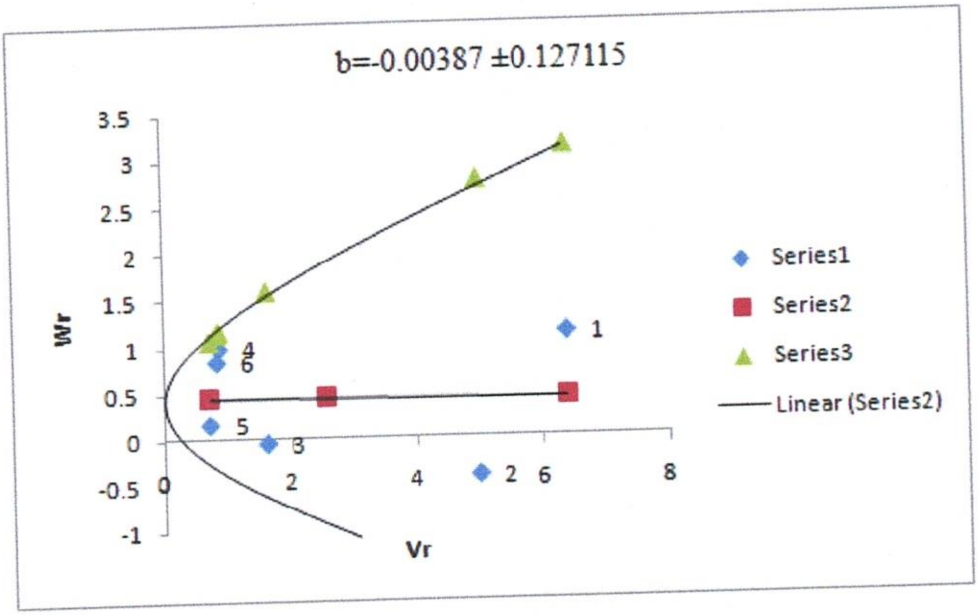

Fig 19: Wr/Vr graph for seed weight per plant of F_1 generation for replication 1.

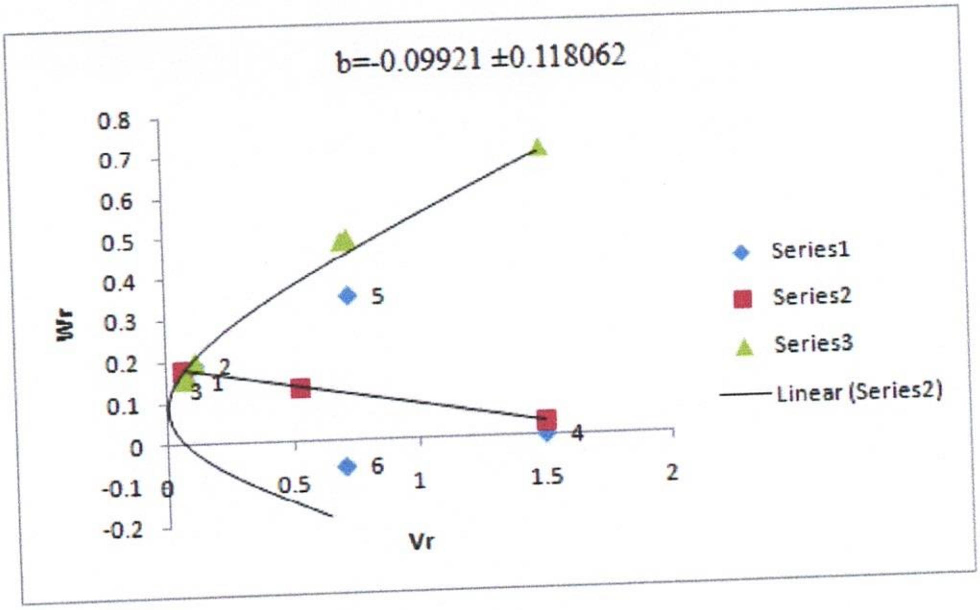

Fig 20: Wr/Vr graph for seed weight per plant of F_1 generation for replication 2.

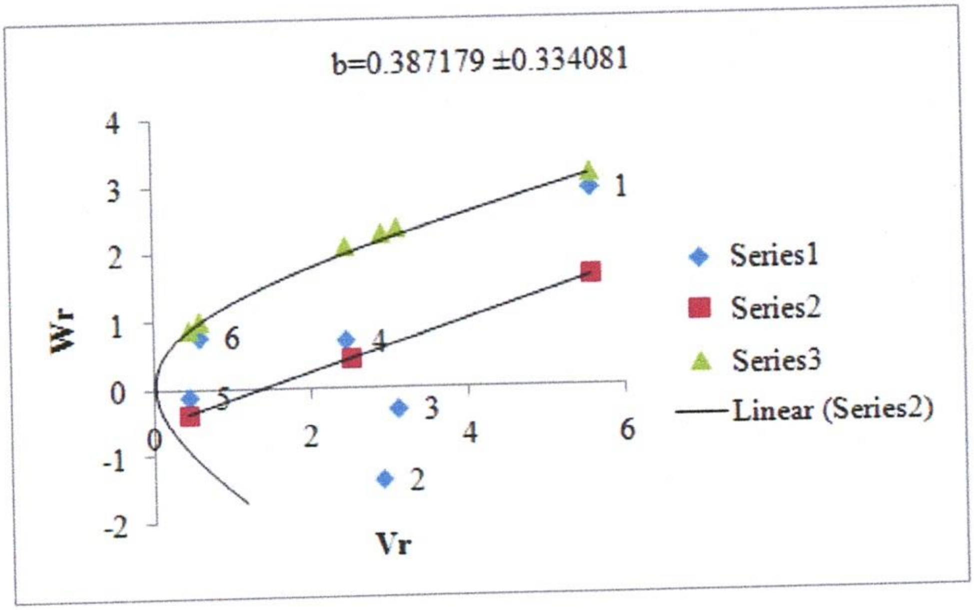

Fig 21: Wr/Vr graph for individual plant weight of F_1 generation for replication 1.

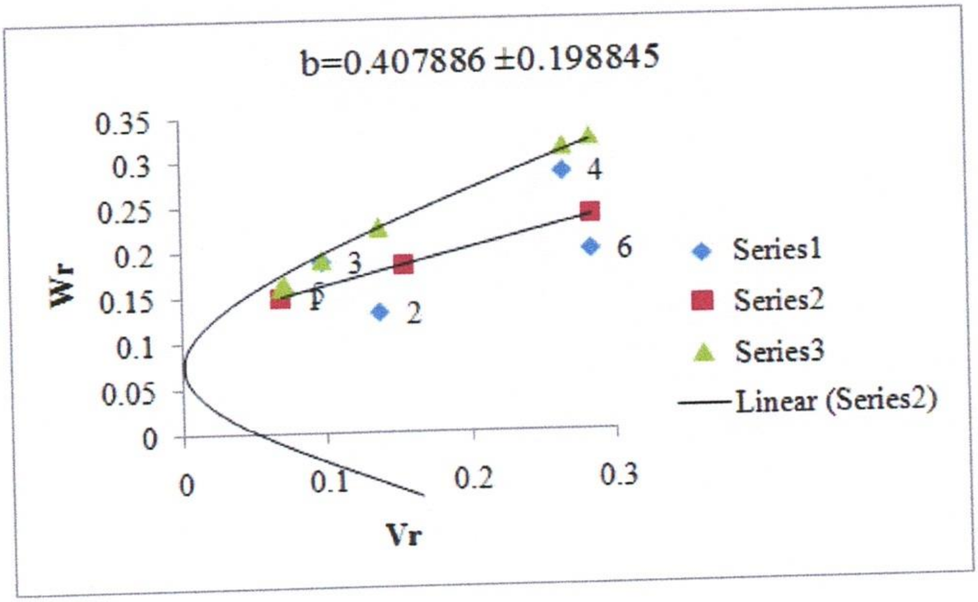

Fig 22: Wr/Vr graph for individual plant weight of F_1 generation for replication 2.

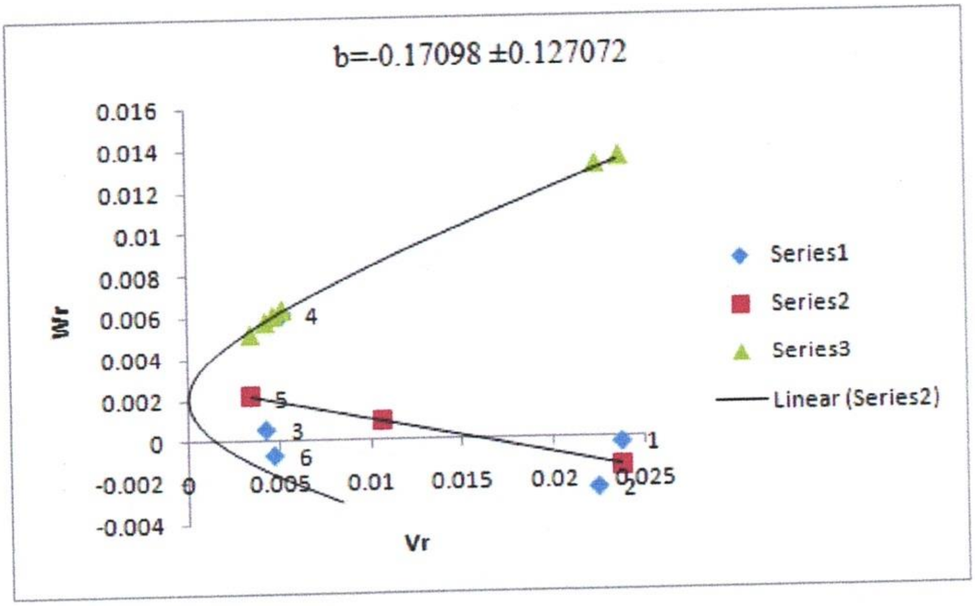

Fig 23: Wr/Vr graph for root weight of F_1 generation for replication 1.

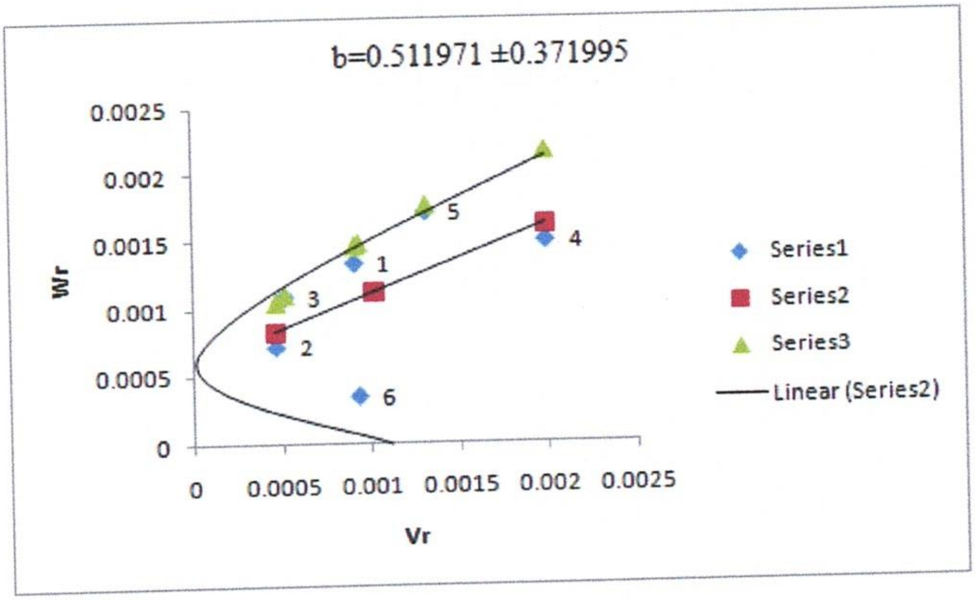

Fig 24: Wr/Vr graph for root weight of F_1 generation for replication 2.

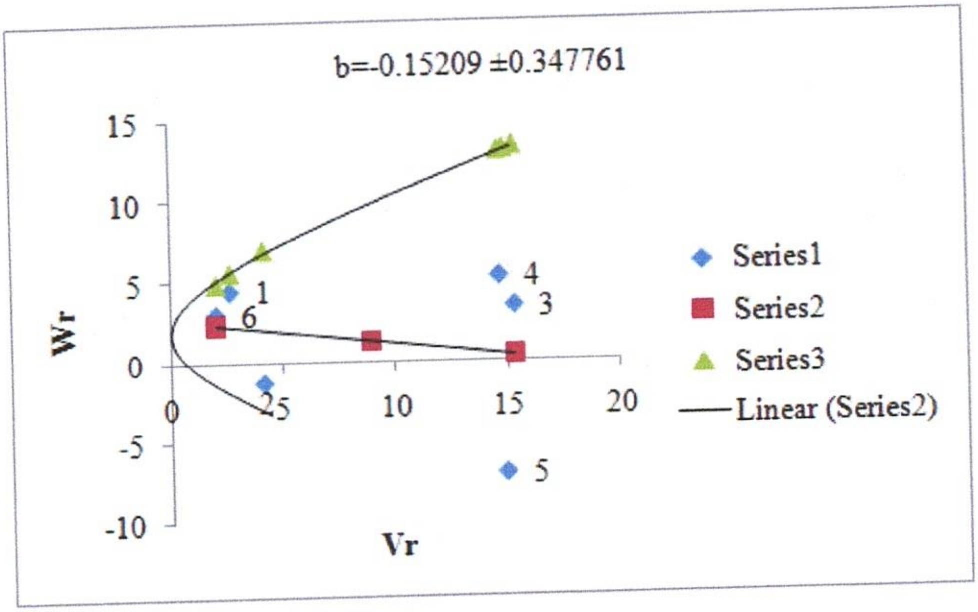

Fig 25: Wr/Vr graph for days to flower of F_2 generation for replication 1.

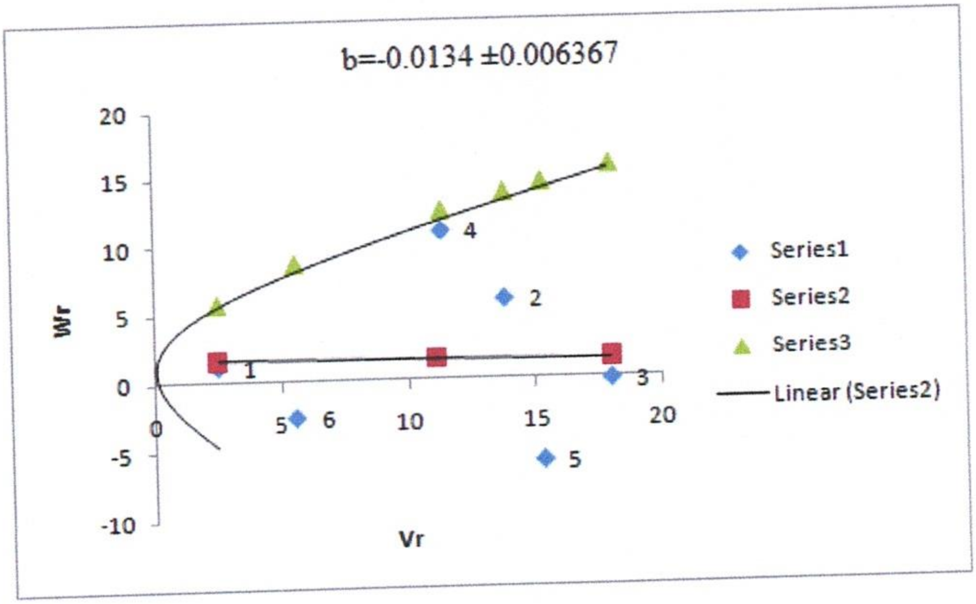

Fig 26: Wr/Vr graph for days to flower of F_2 generation for replication 2.

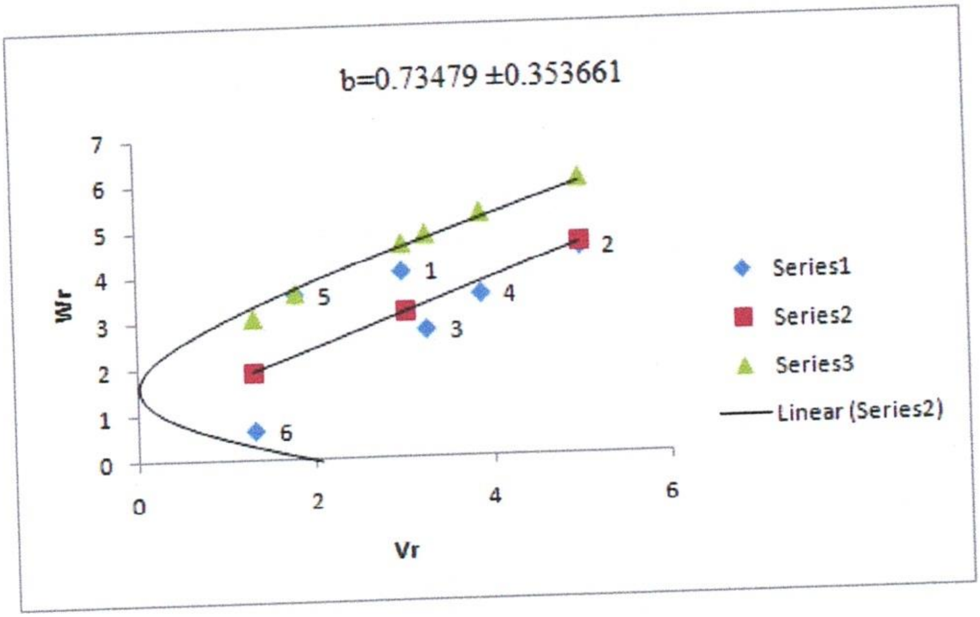

Fig 27: Wr/Vr graph for plant height at first flower of F_2 generation for replication 1.

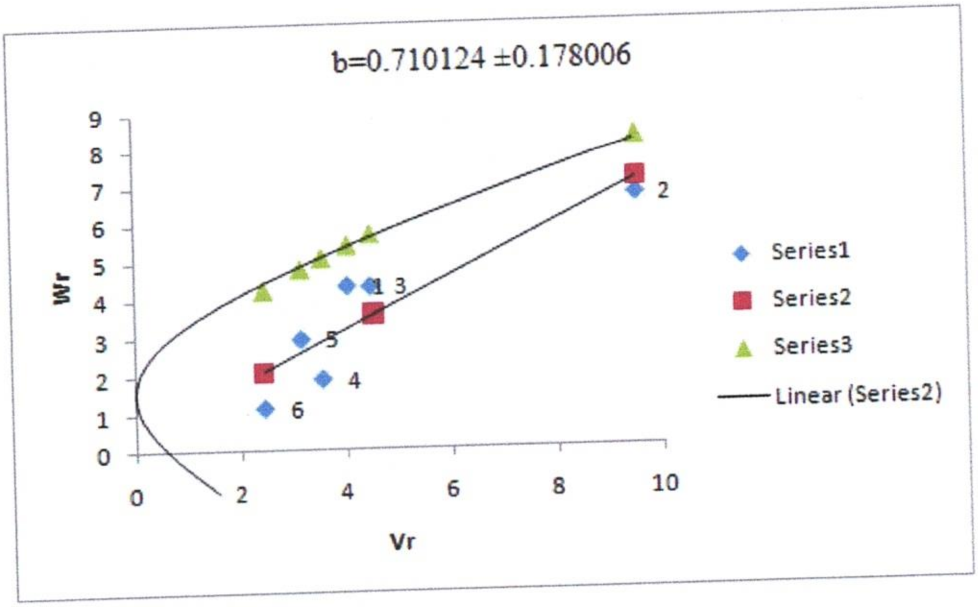

Fig 28: Wr/Vr graph for plant height at first flower of F_2 generation for replication 2.

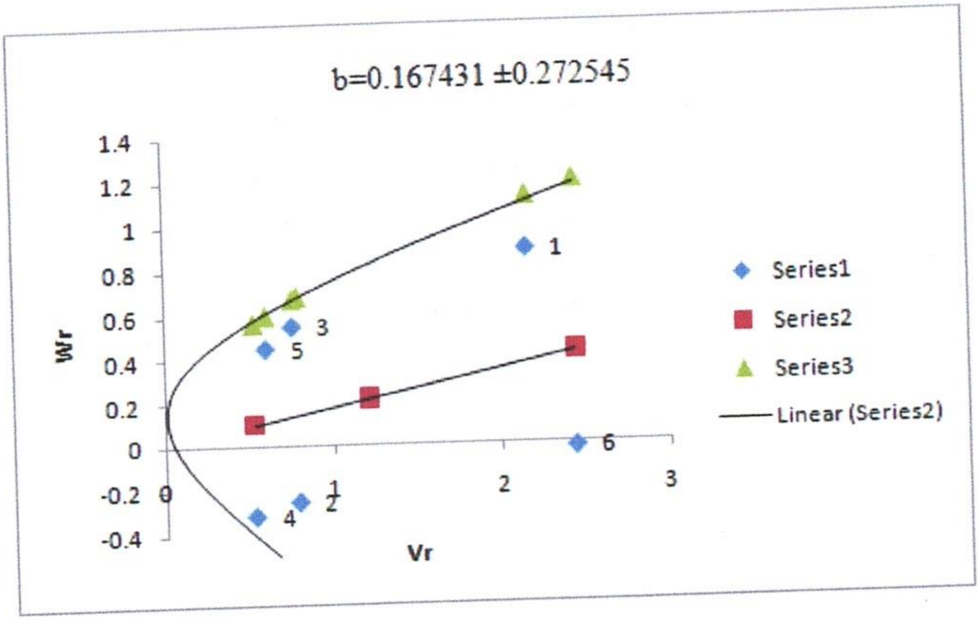

Fig 29: Wr/Vr graph for number of primary branches at first flower of F_2 generation for replication 1.

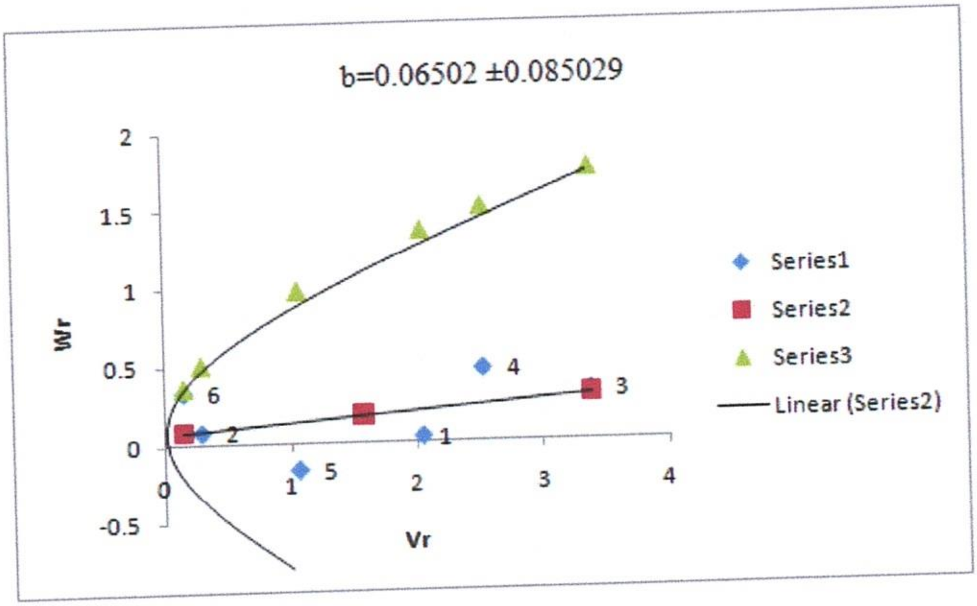

Fig 30: Wr/Vr graph for number of primary branches at first flower of F_2 generation for replication 2.

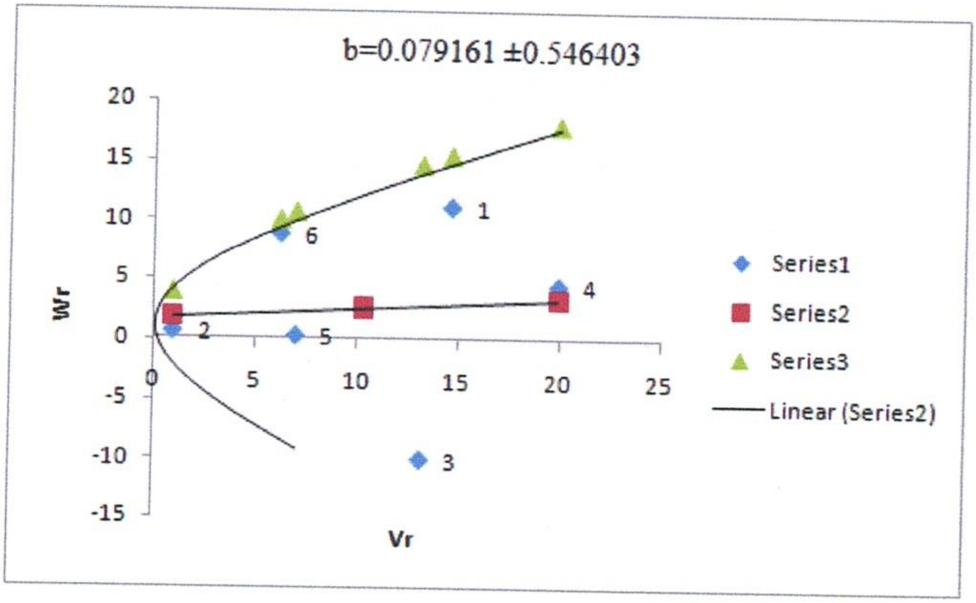

Fig 31: Wr/Vr graph for number of secondary branches at first flower of F_2 generation for replication 1.

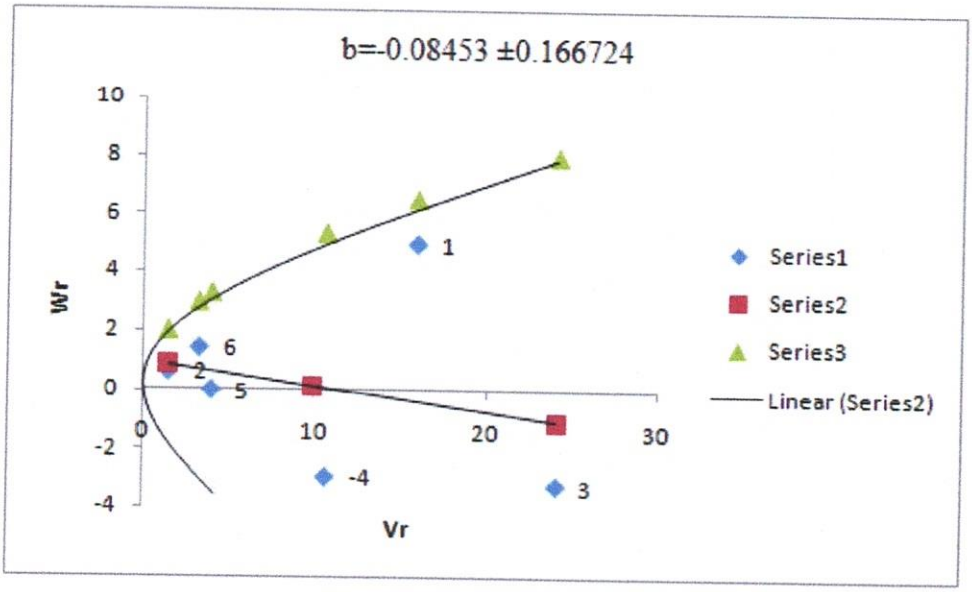

Fig 32: Wr/Vr graph for number of secondary branches at first flower of F_2 generation for replication 2.

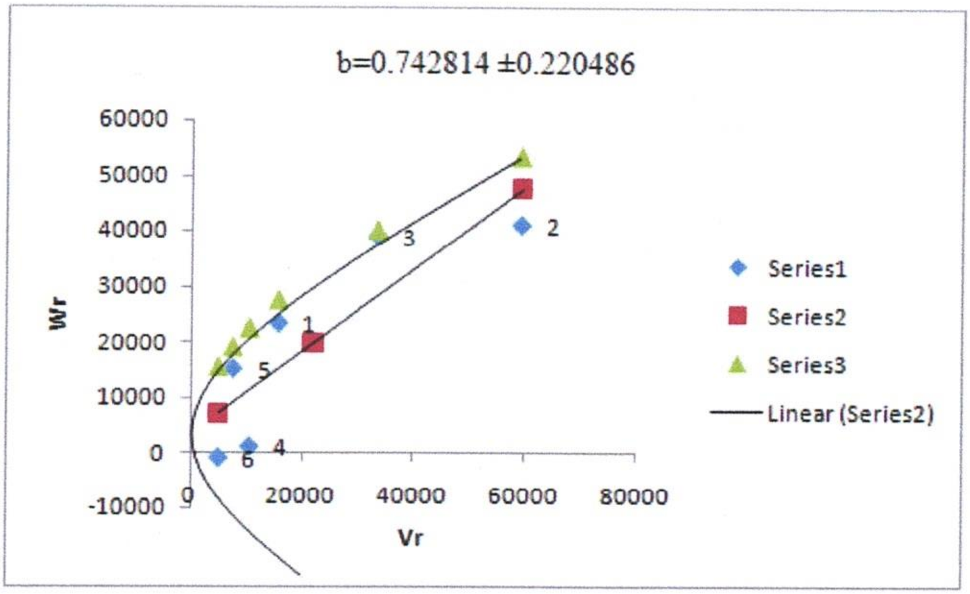

Fig 33: Wr/Vr graph for canopy area at maximum flower of F_2 generation for replication 1.

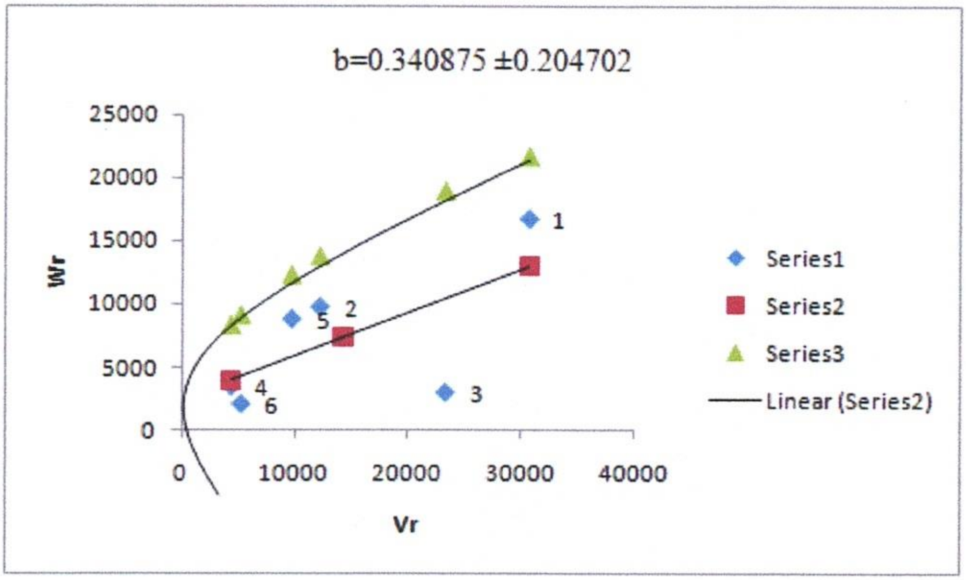

Fig 34: Wr/Vr graph for canopy area at maximum flower of F_2 generation for replication 2.

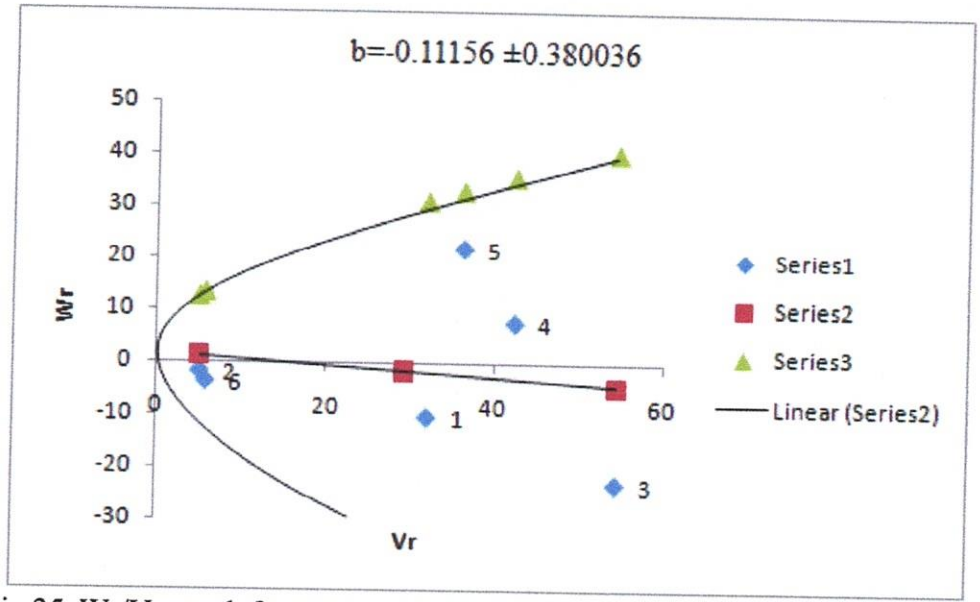

Fig 35: Wr/Vr graph for number of secondary branches at maximum flower of F_2 generation for replication 1.

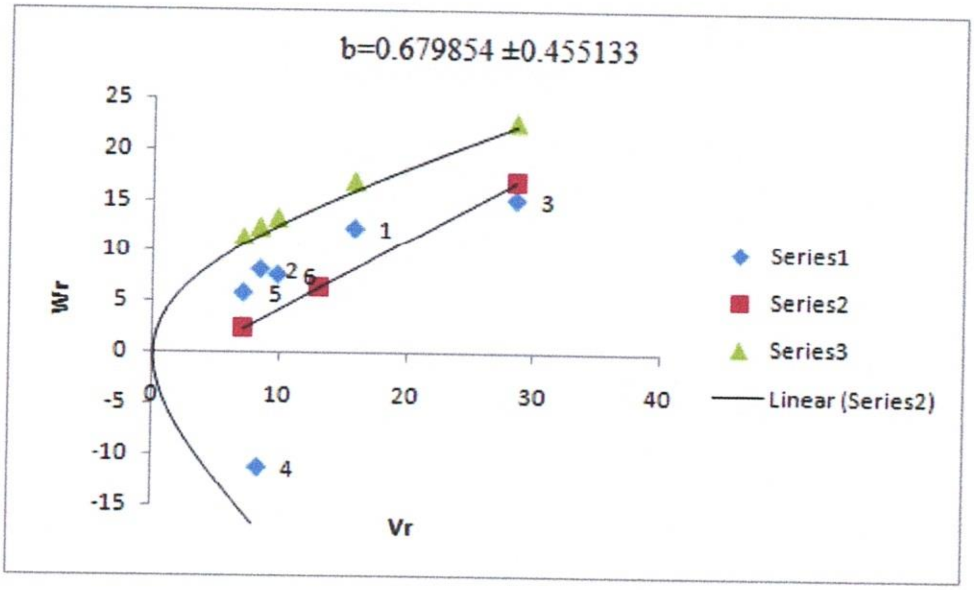

Fig 36: Wr/Vr graph for number of secondary branches at maximum flower of F_2 generation for replication 2.

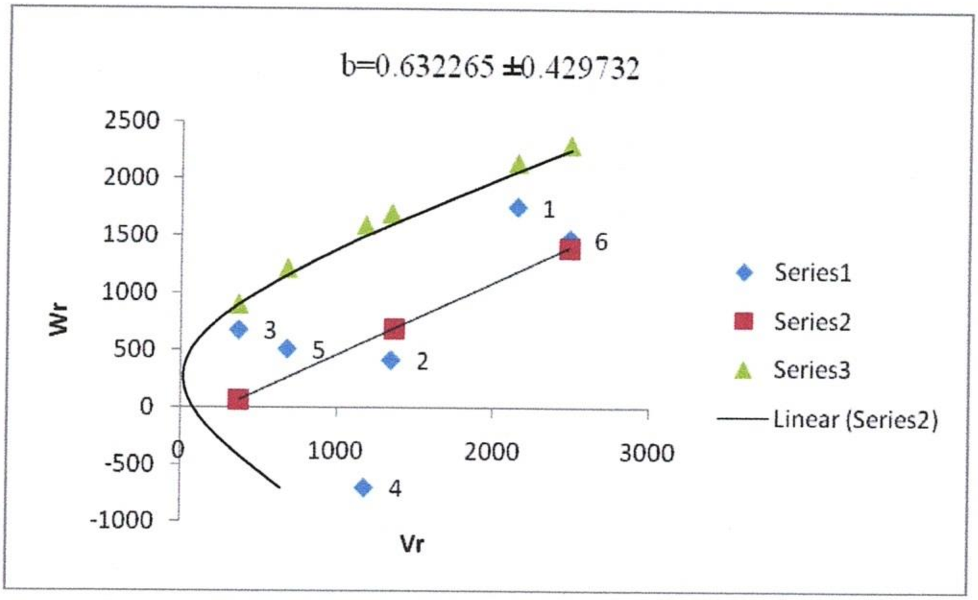

Fig 37: Wr/Vr graph for number of pods per plant of F_2 generation for replication 1.

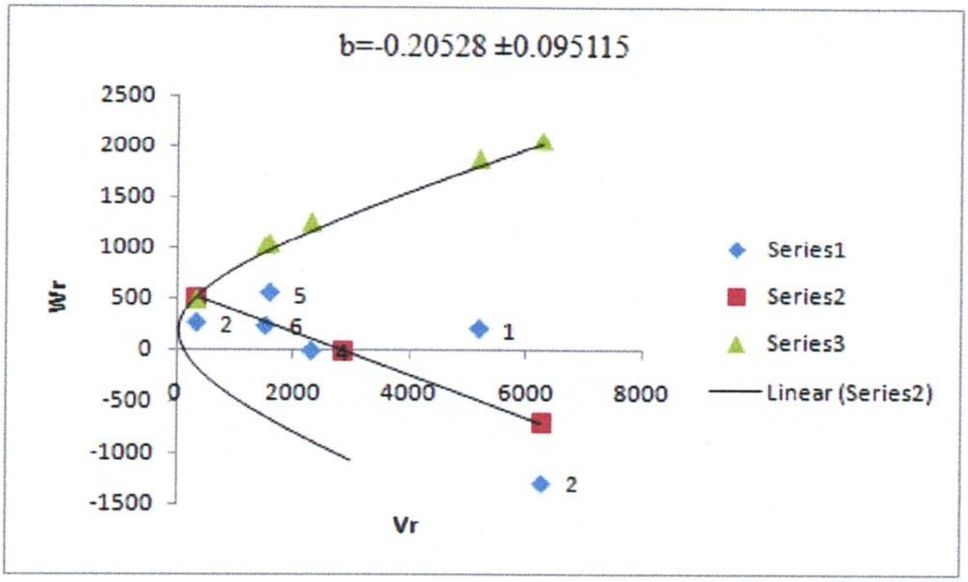

Fig 38: Wr/Vr graph for number of pods per plant of F_2 generation for replication 2.

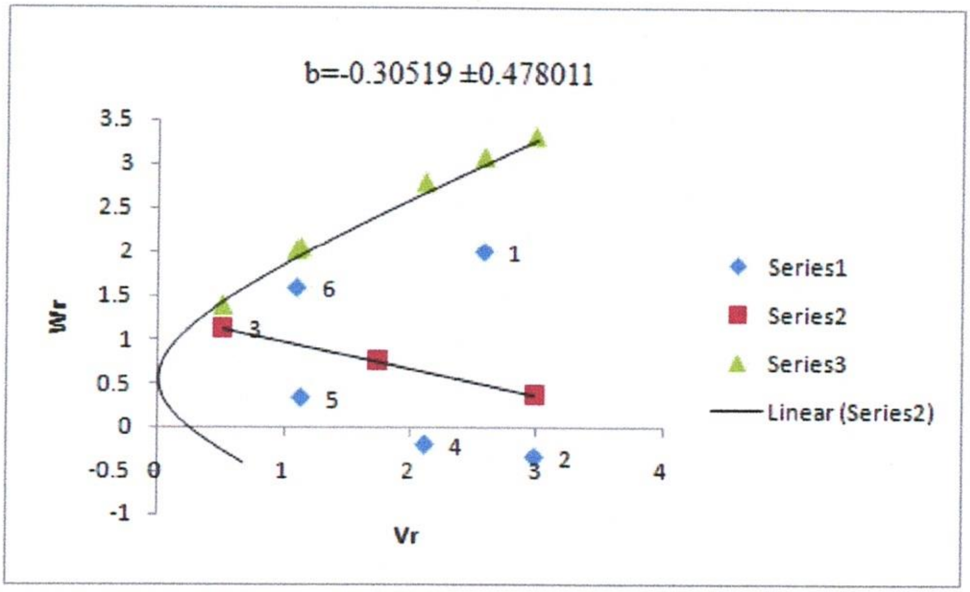

Fig 39: Wr/Vr graph for pod weight per plant of F_2 generation for replication 1.

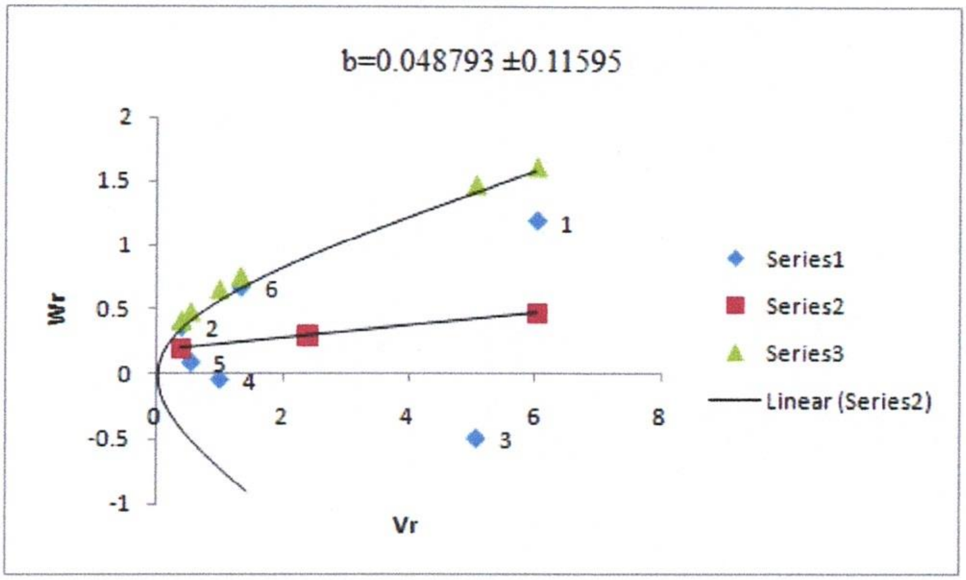

Fig 40: Wr/Vr graph for pod weight per plant of F_2 generation for replication 2.

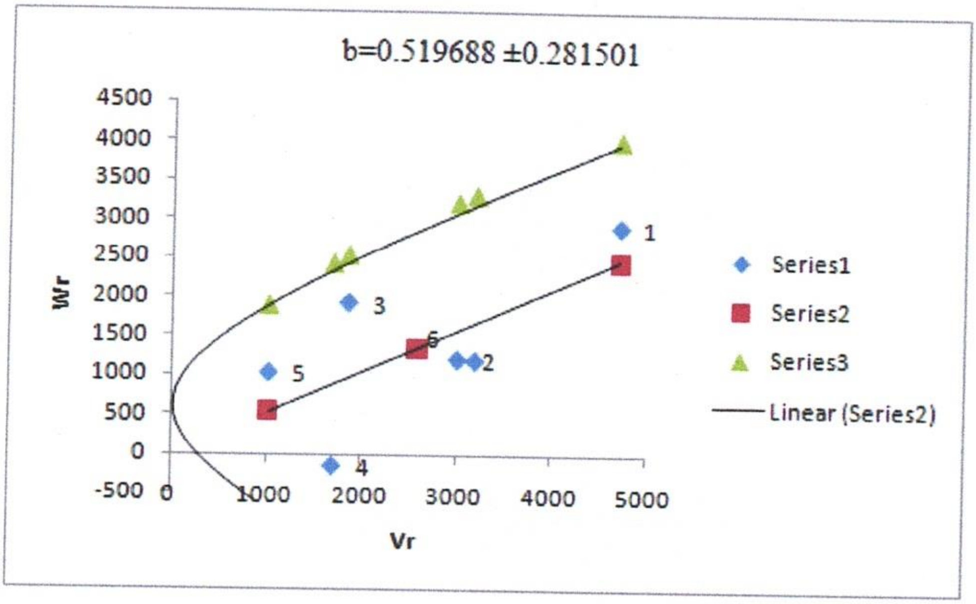

Fig 41: Wr/Vr graph for number of seeds per plant of F_2 generation for replication 1.

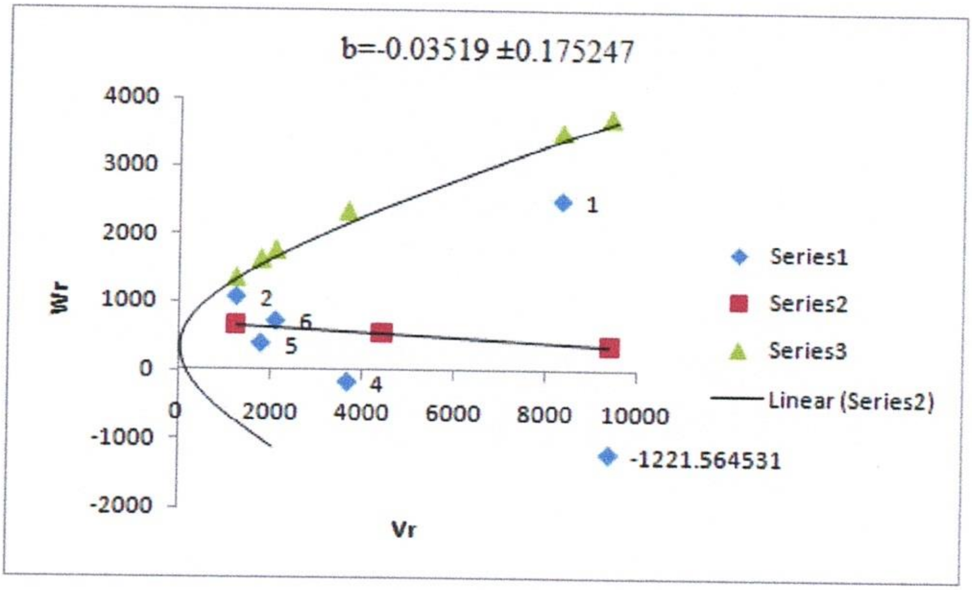

Fig 42: Wr/Vr graph for number of seeds per plant of F_2 generation for replication 2.

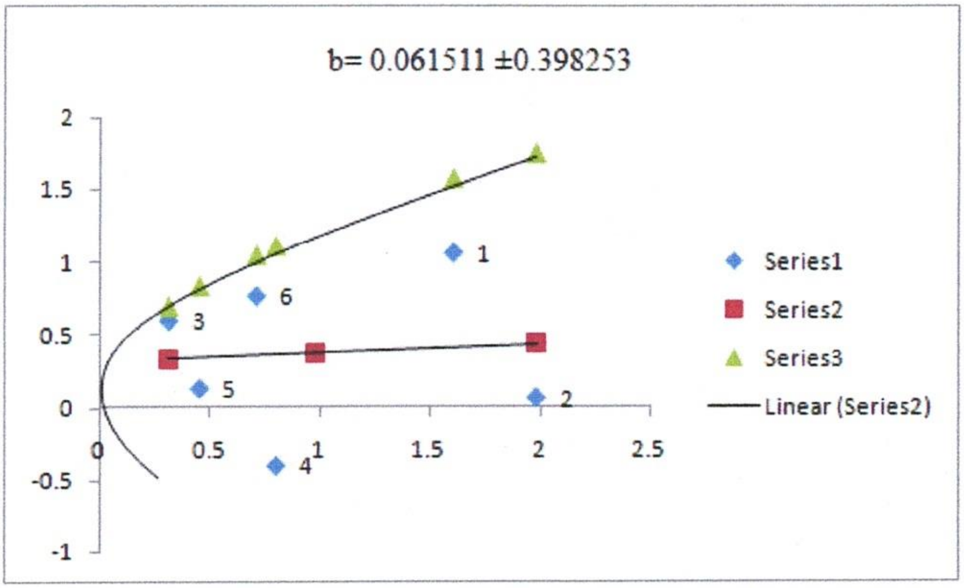

Fig 43: Wr/Vr graph for seed weight per plant of F_2 generation for replication 1.

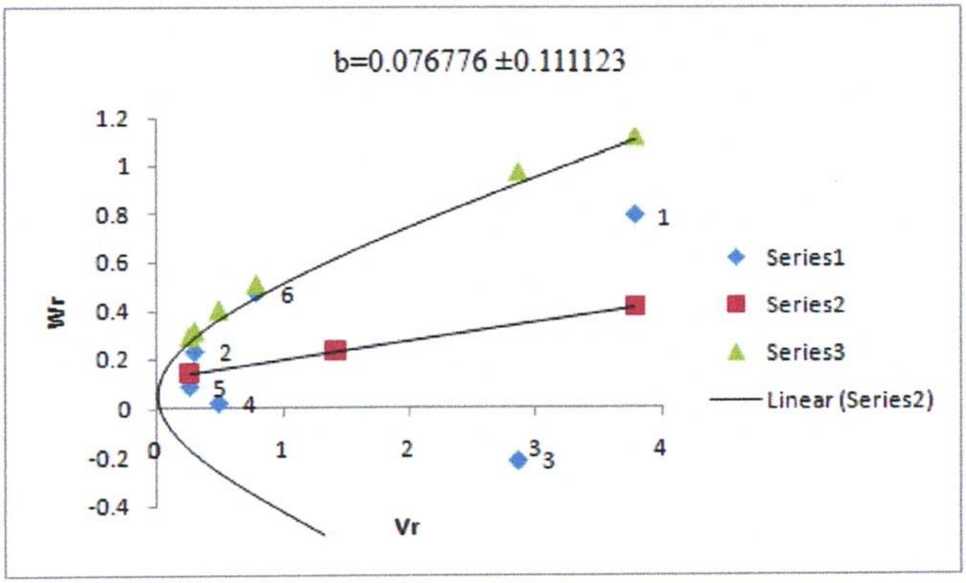

Fig 44: Wr/Vr graph for seed weight per plant of F_2 generation for replication 2.

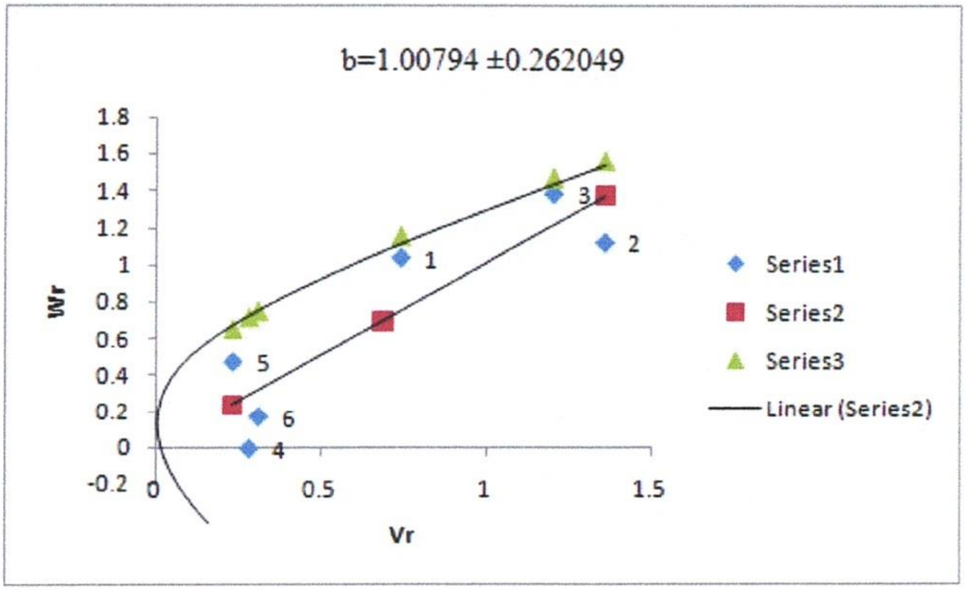

Fig 45: Wr/Vr graph for individual plant weight of F_2 generation for replication 1.

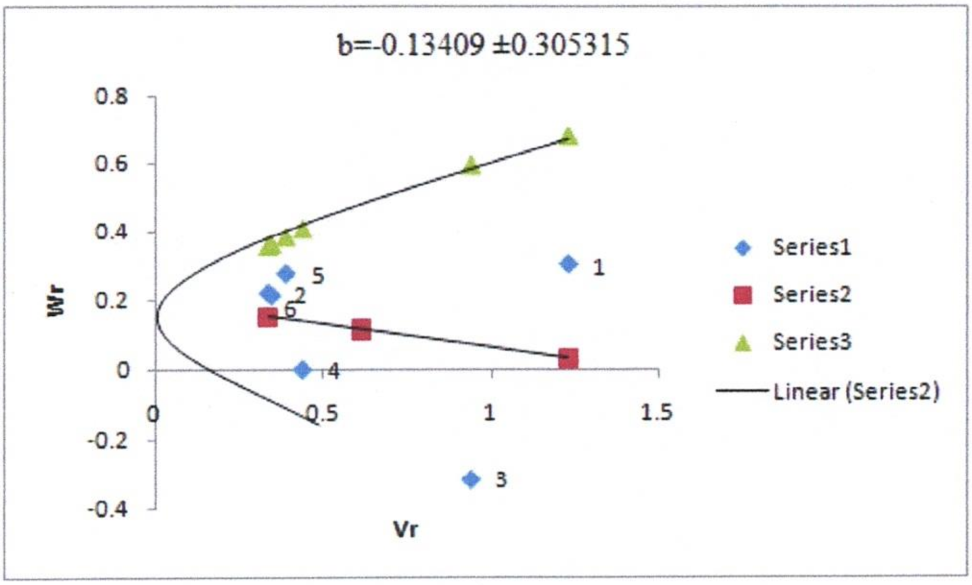

Fig 46: Wr/Vr graph for individual plant weight of F_2 generation for replication 2.

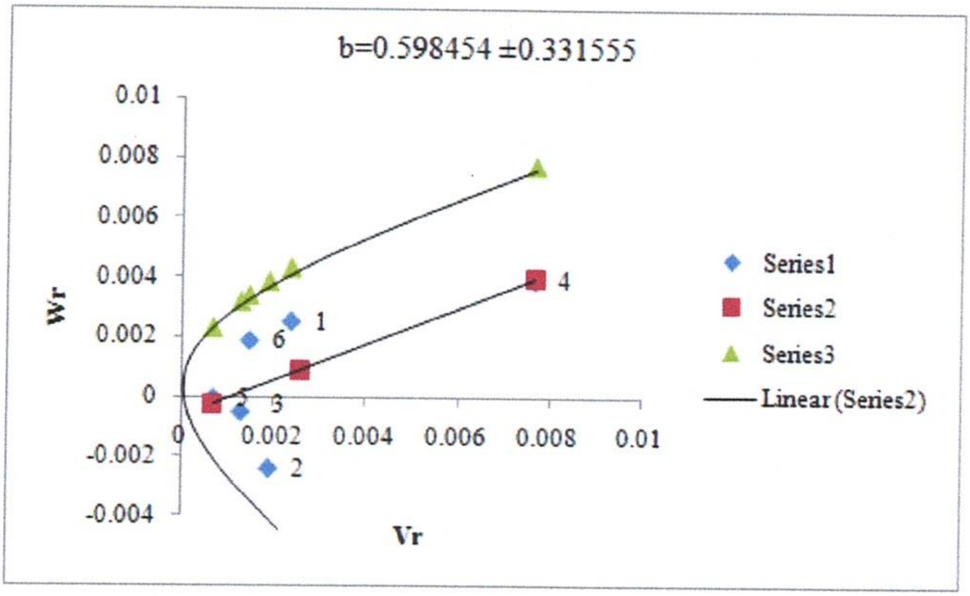

Fig 47: Wr/Vr graph for root weight of F_2 generation for replication 1.

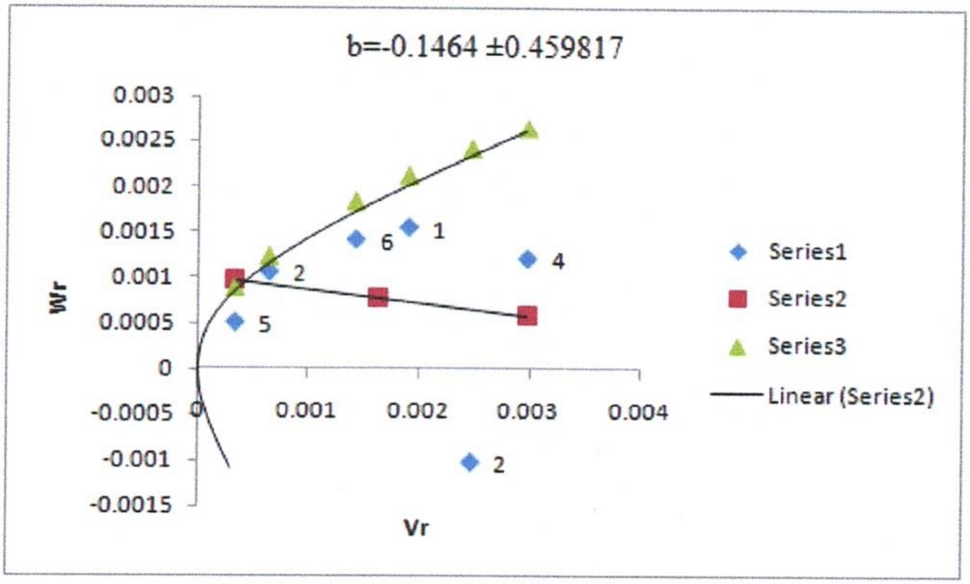

Fig 48: Wr/Vr graph for root weight of F_2 generation for replication 2.

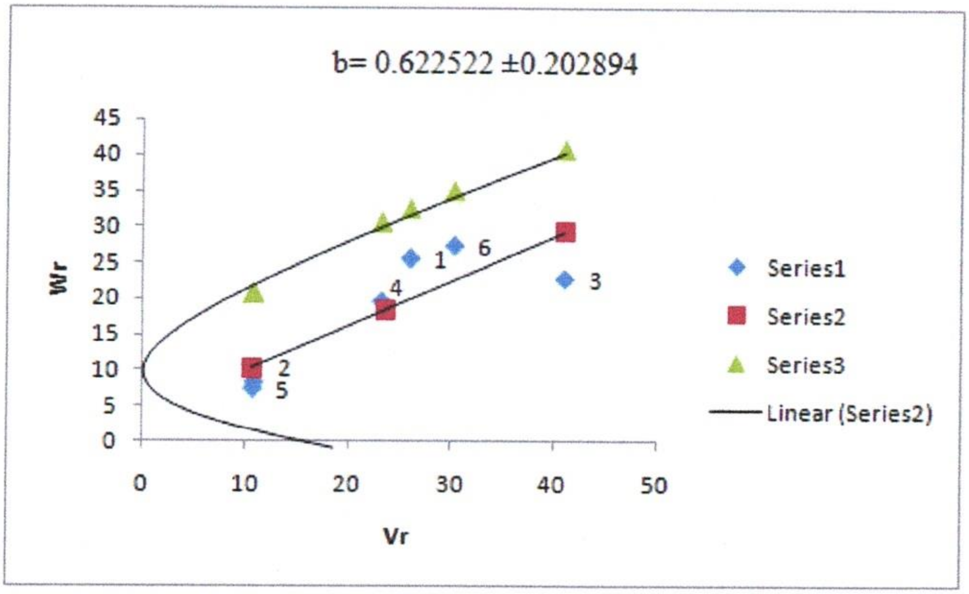

Fig 49: Wr/Vr graph for days to flower of F_1 generation for replication total.

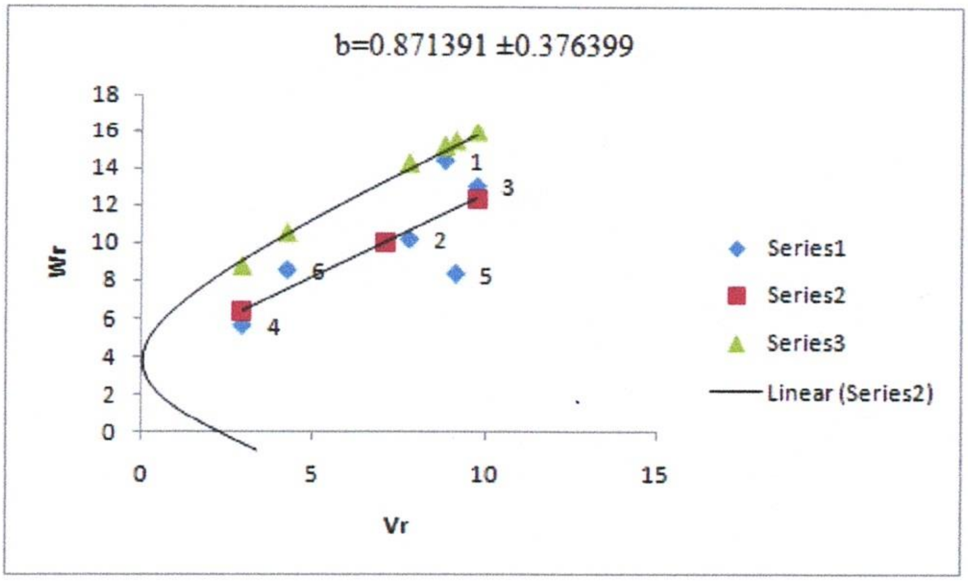

Fig 50: Wr/Vr graph for plant height at first flower of F_1 generation for replication total.

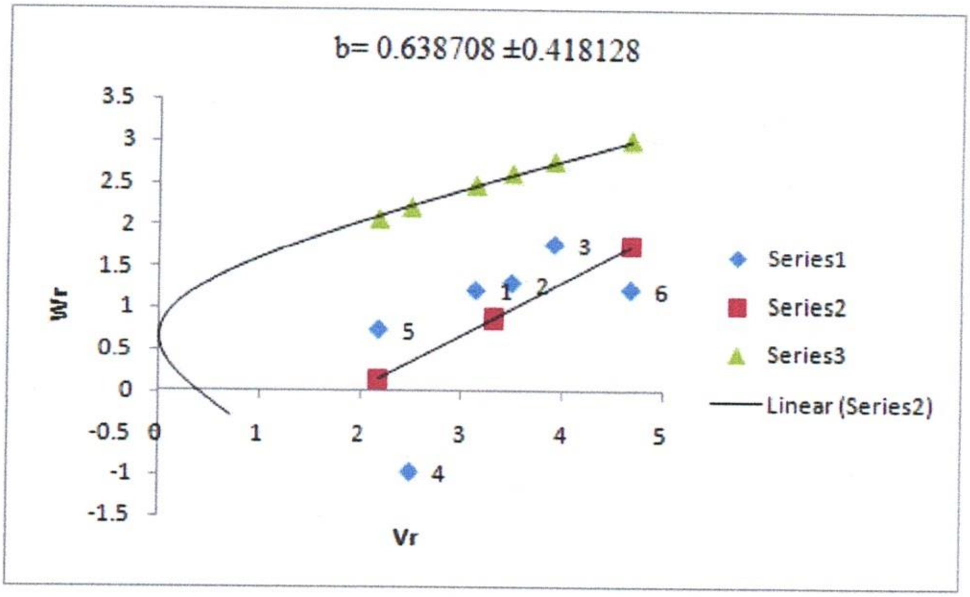

Fig 51: Wr/Vr graph for number of primary branches at first flower of F_1 generation for replication total.

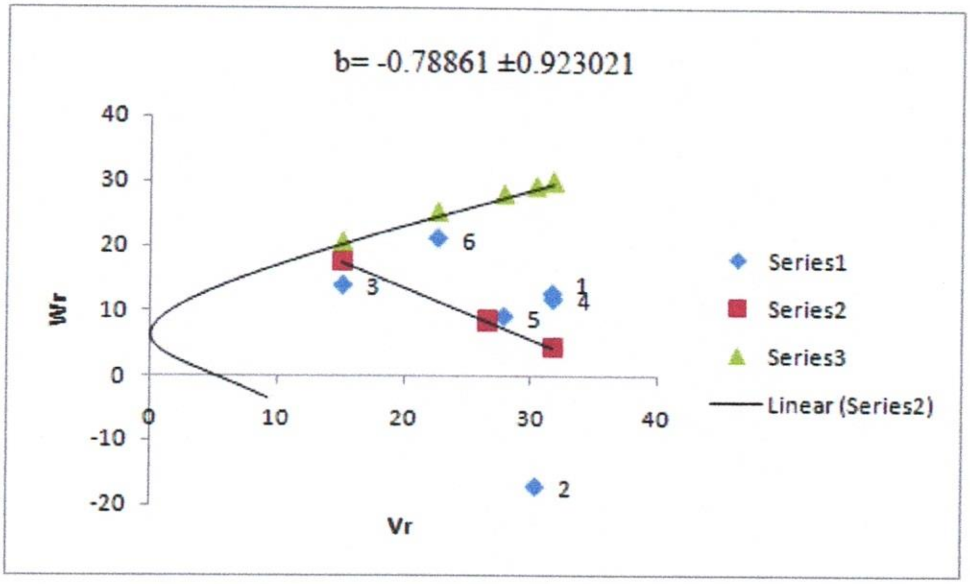

Fig 52: Wr/Vr graph for number of secondary branches at first flower of F_1 generation for replication total.

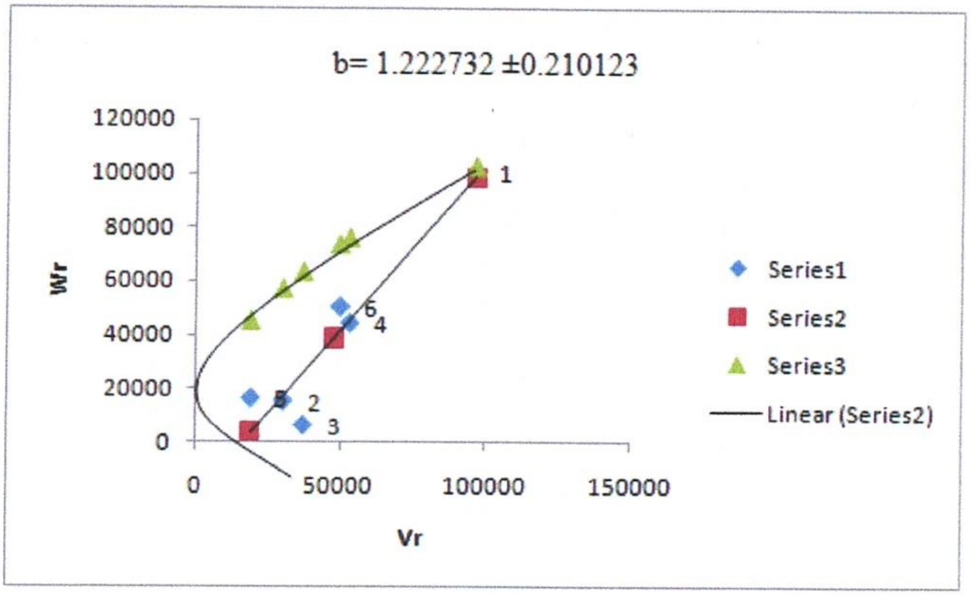

Fig 53: Wr/Vr graph for canopy area at maximum flower of F_1 generation for replication total.

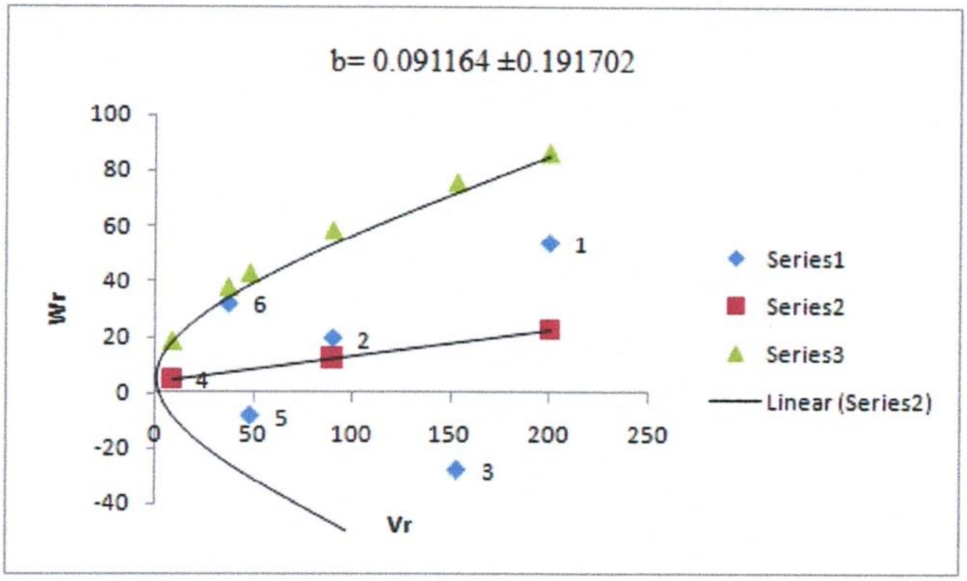

Fig 54: Wr/Vr graph for number of secondary branches at maximum flower of F_1 generation for replication total.

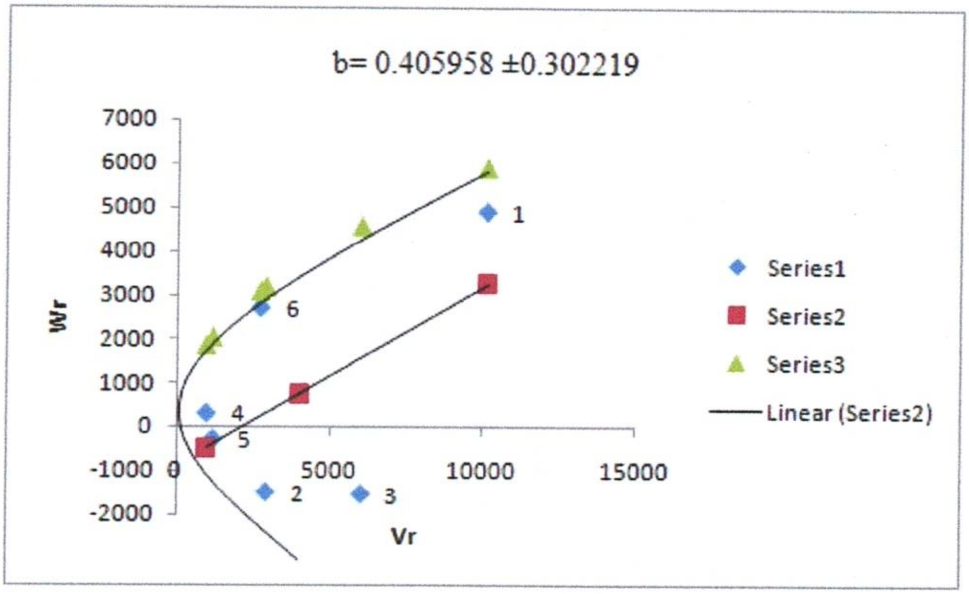

Fig 55: Wr/Vr graph for number of pods per plant of F_1 generation for replication total.

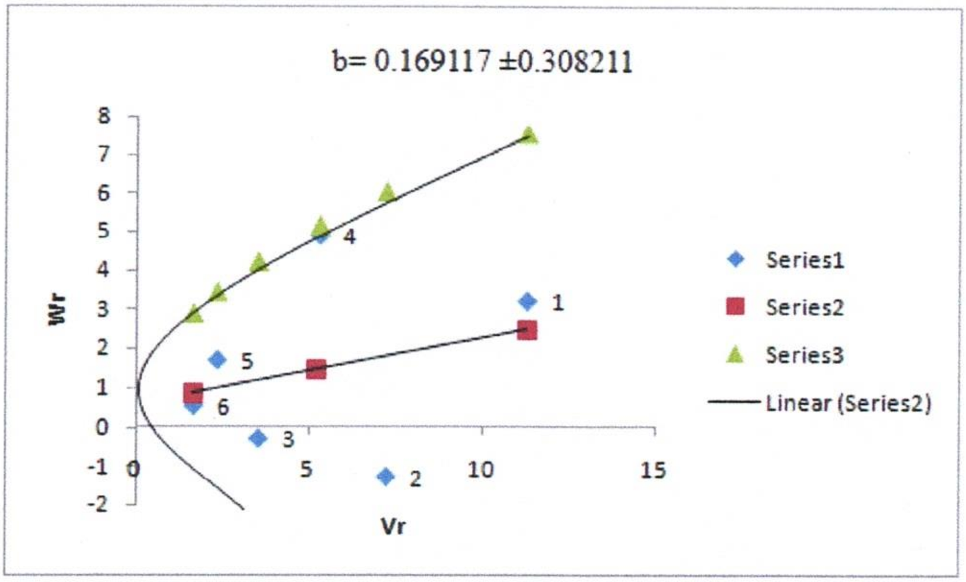

Fig 56: Wr/Vr graph for pod weight per plant of F_1 generation for replication total.

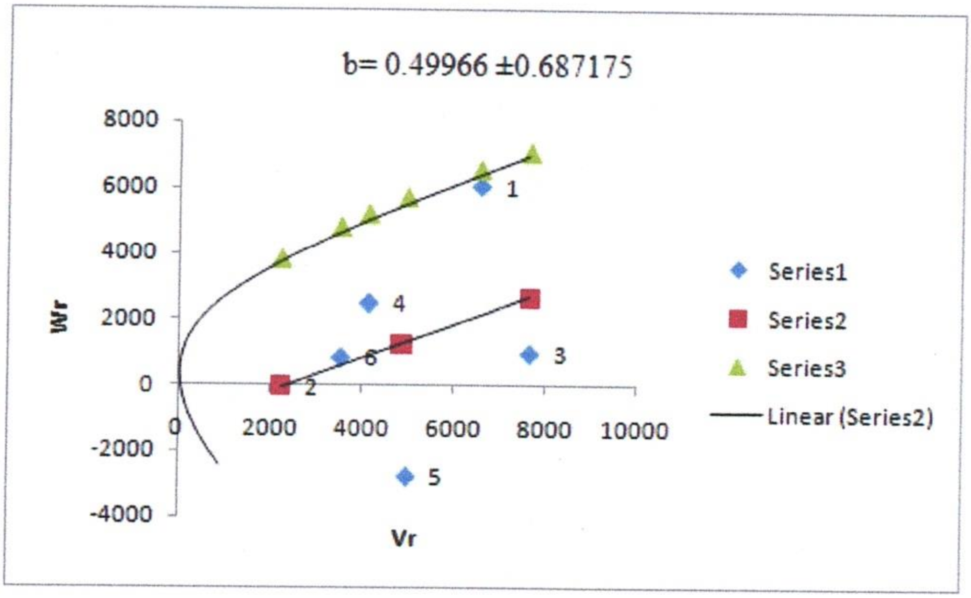

Fig 57: Wr/Vr graph for number of seeds per plant of F_1 generation for replication total.

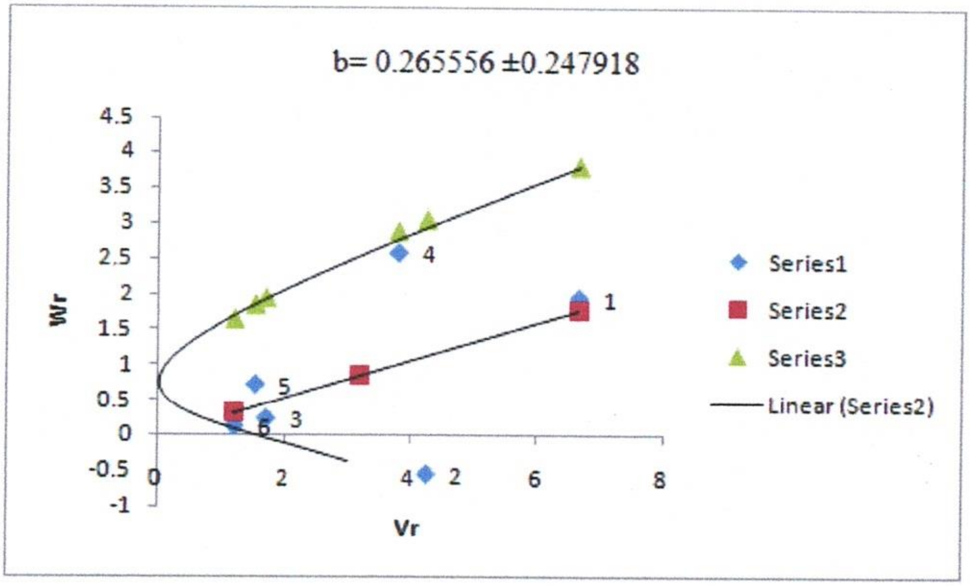

Fig 58: Wr/Vr graph for seed weight per plant of F_1 generation for replication total.

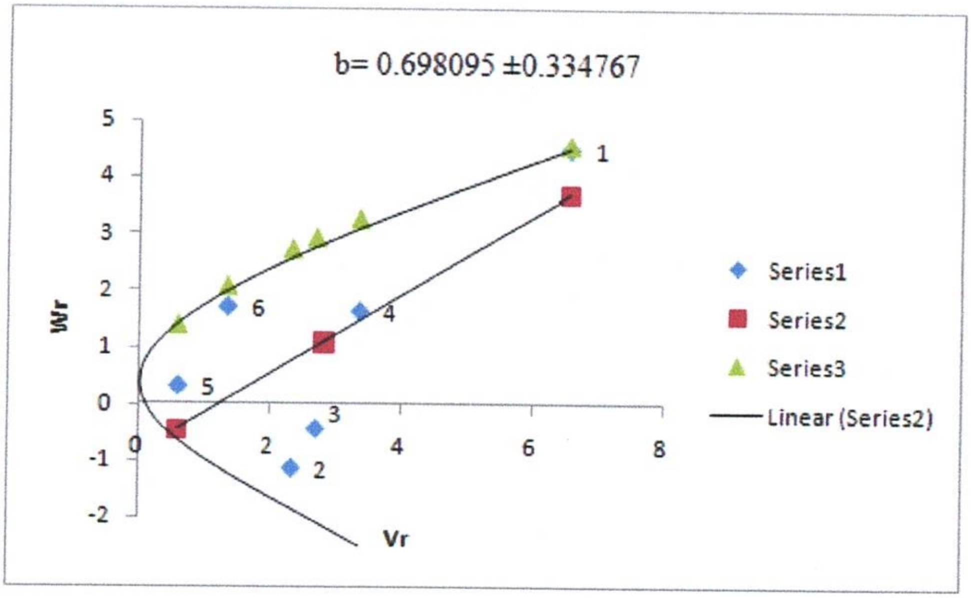

Fig 59: Wr/Vr graph for individual plant weight of F_1 generation for replication total.

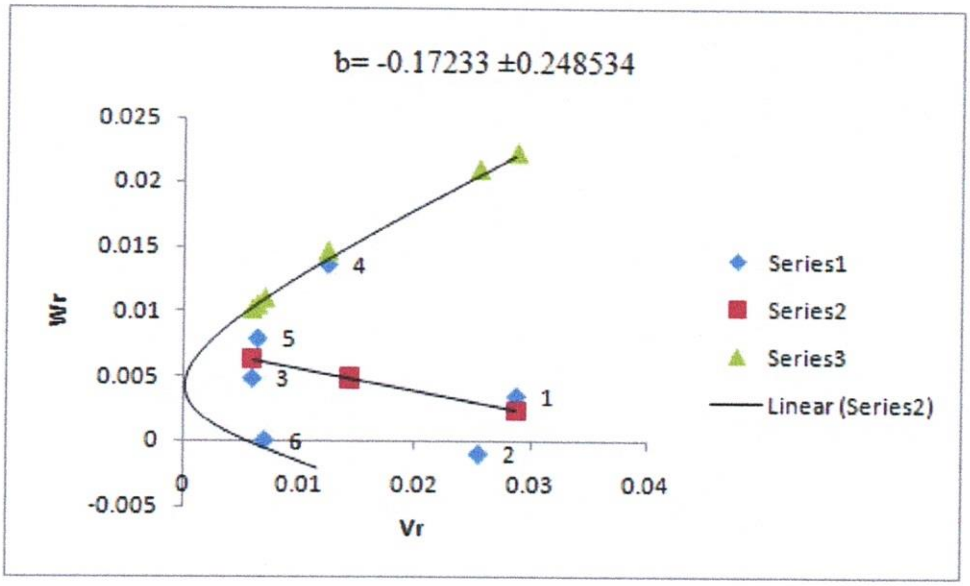

Fig 60: Wr/Vr graph for root weight of F_1 generation for replication total.

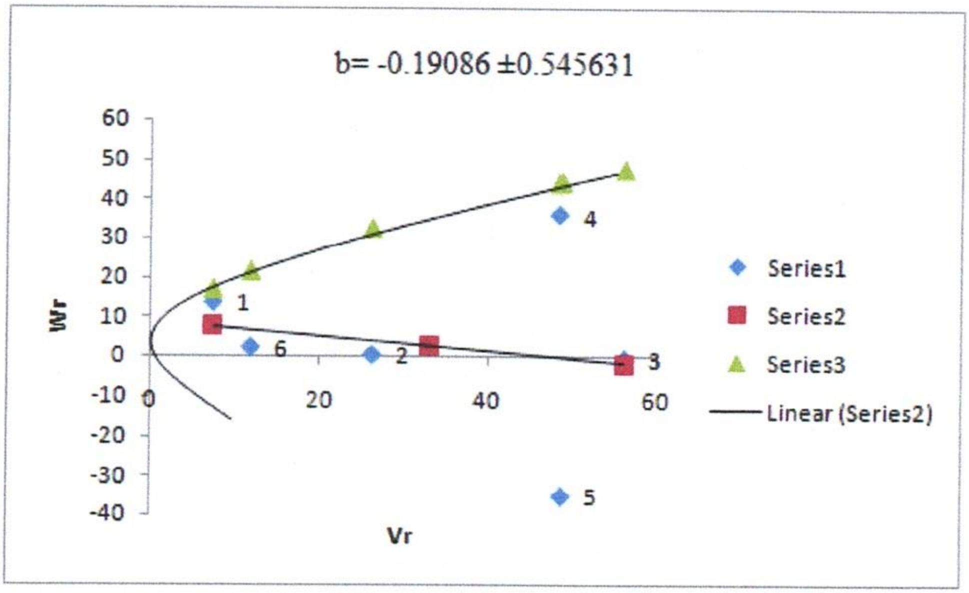

Fig 61: Wr/Vr graph for days to flower of F_2 generation for replication total.

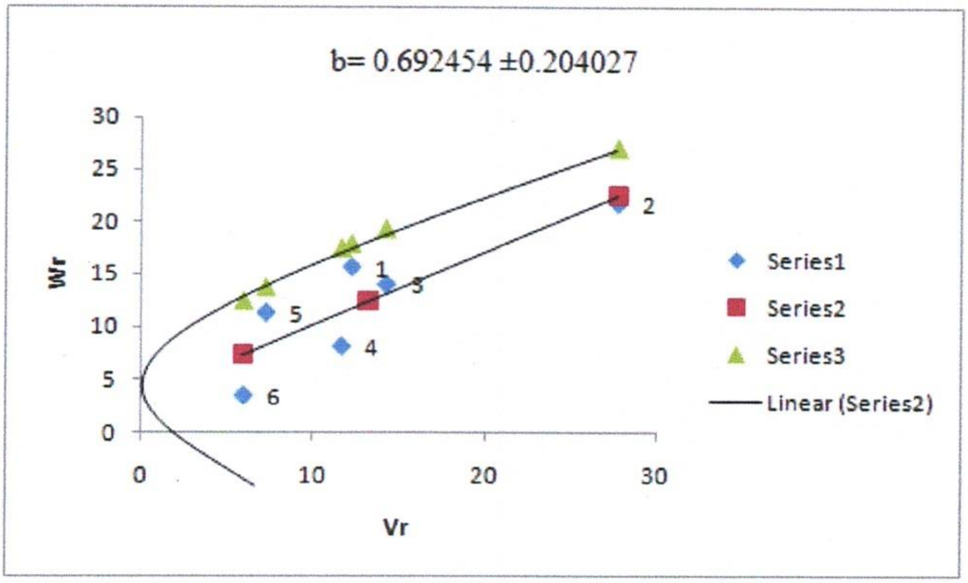

Fig 62: Wr/Vr graph for plant height at first flower of F_2 generation for replication total.

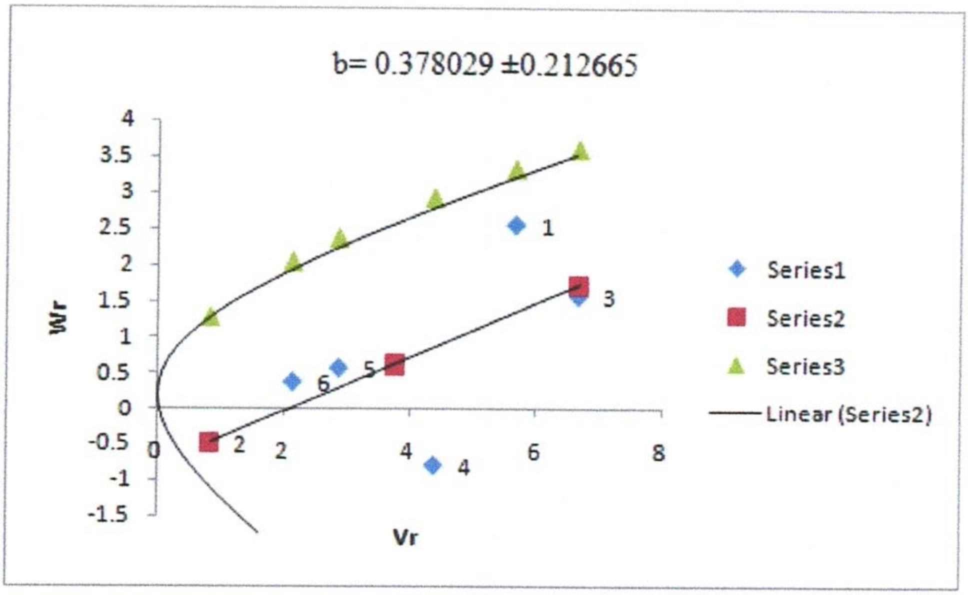

Fig 63: Wr/Vr graph for number of primary branches at first flower of F_2 generation for replication total.

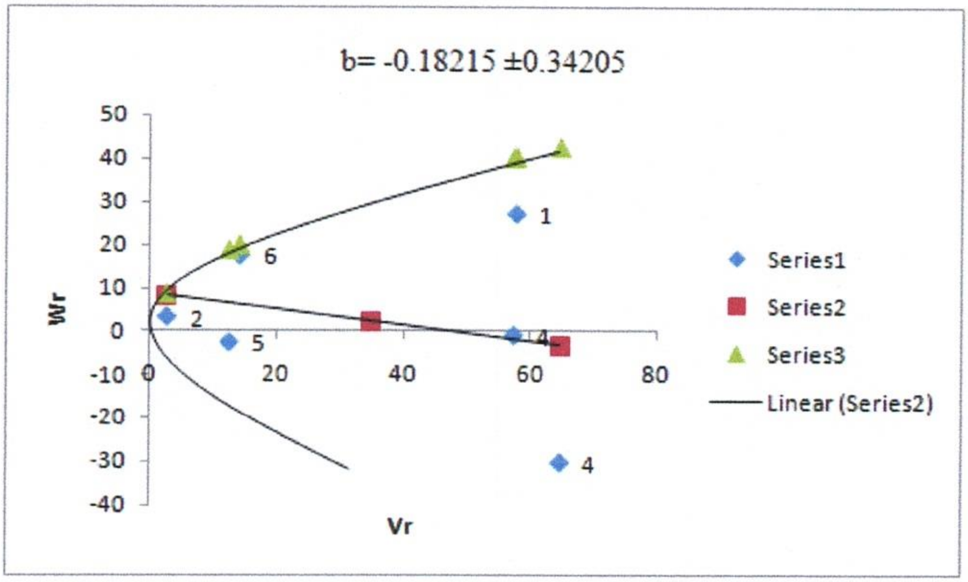

Fig 64: Wr/Vr graph for number of secondary branches at first flower of F_2 generation for replication total.

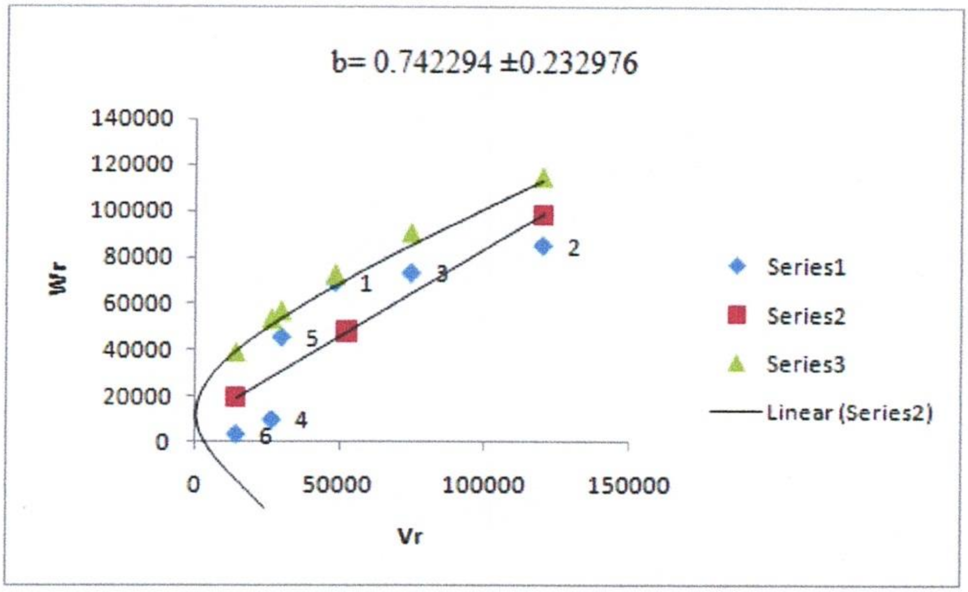

Fig 65: Wr/Vr graph for canopy area per plant at maximum flower of F_2 generation for replication total.

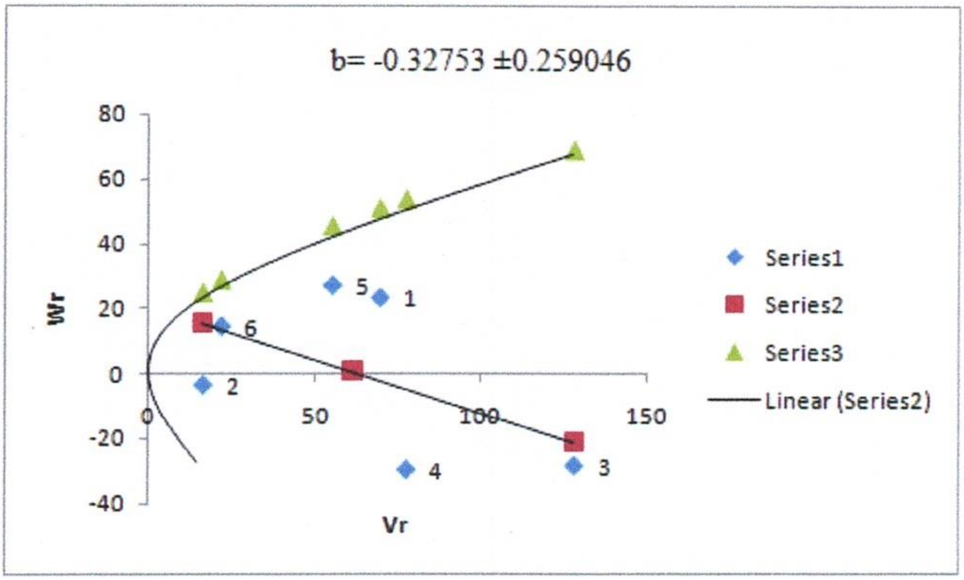

Fig 66: Wr/Vr graph for number of secondary branches per plant at maximum flower of F_2 generation for replication total.

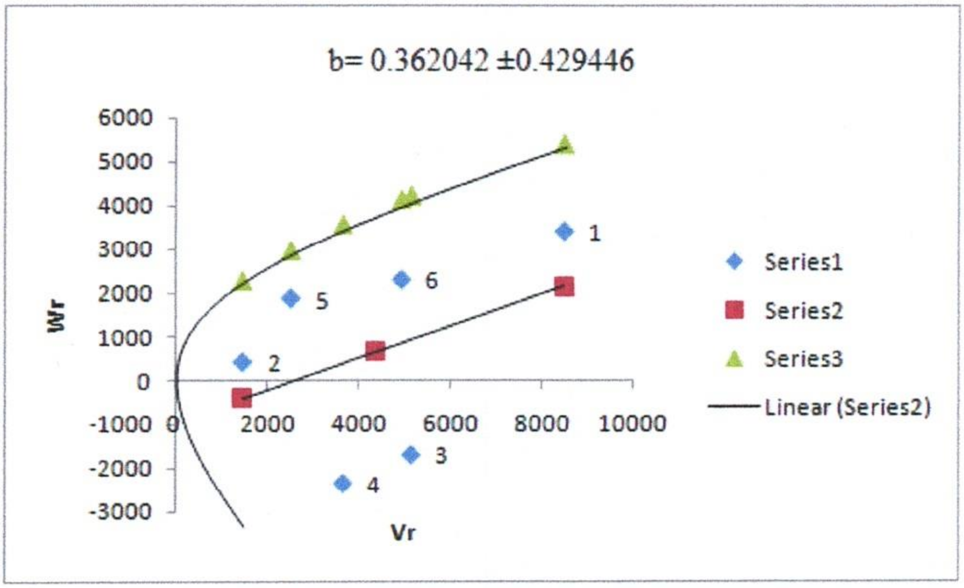

Fig 67: Wr/Vr graph for number of pods per plant of F_2 generation for replication total.

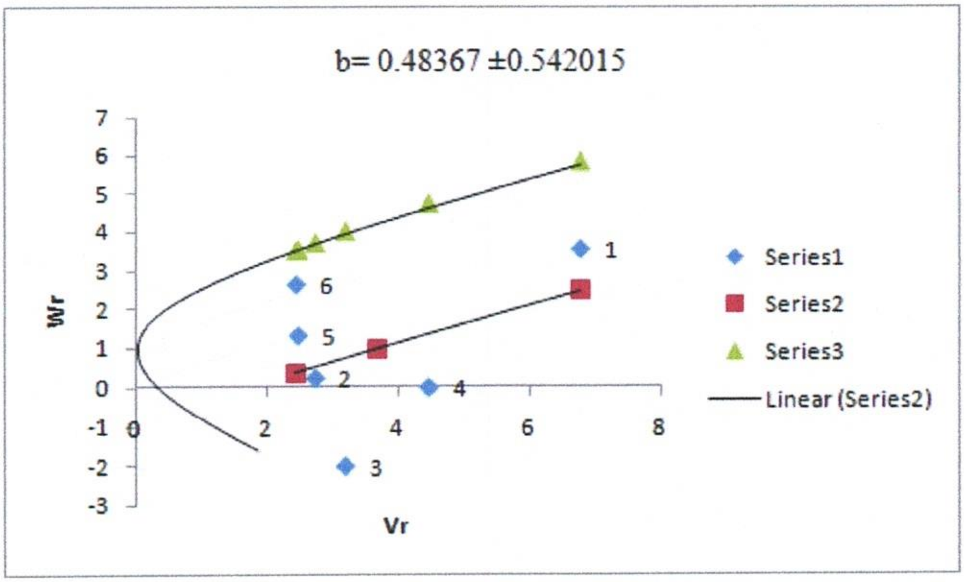

Fig 68: Wr/Vr graph for pod weight per plant of F_2 generation for replication total.

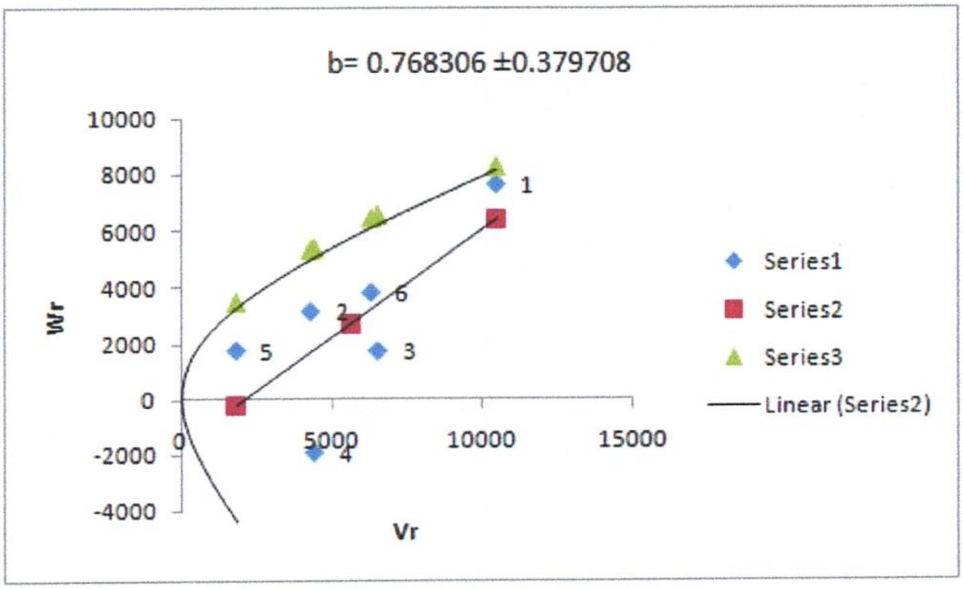

Fig 69: Wr/Vr graph for number of seeds per plant of F_2 generation for replication total.

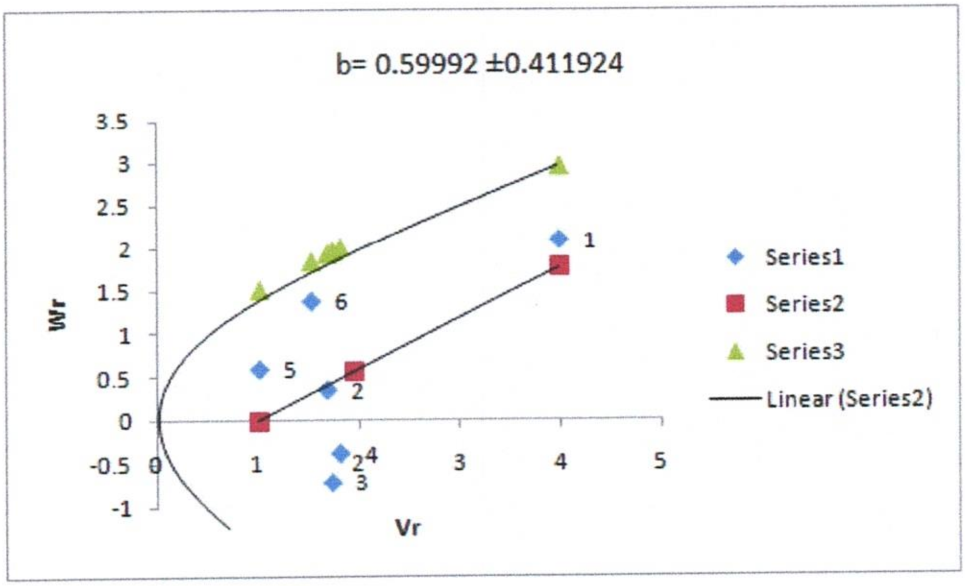

Fig 70: Wr/Vr graph for seed weight per plant of F_2 generation for replication total.

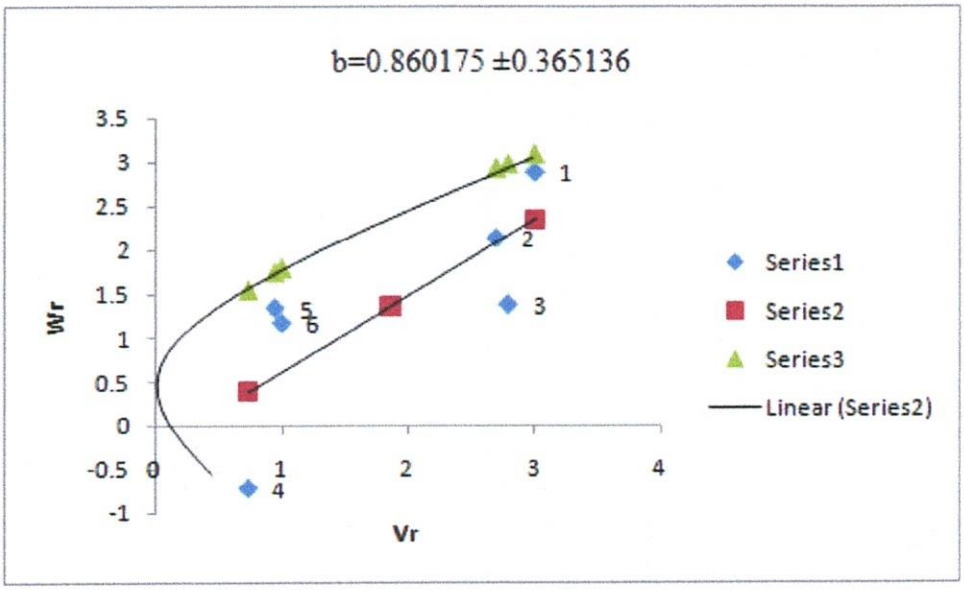

Fig 71: Wr/Vr graph for individual plant weight of F_2 generation for replication total.

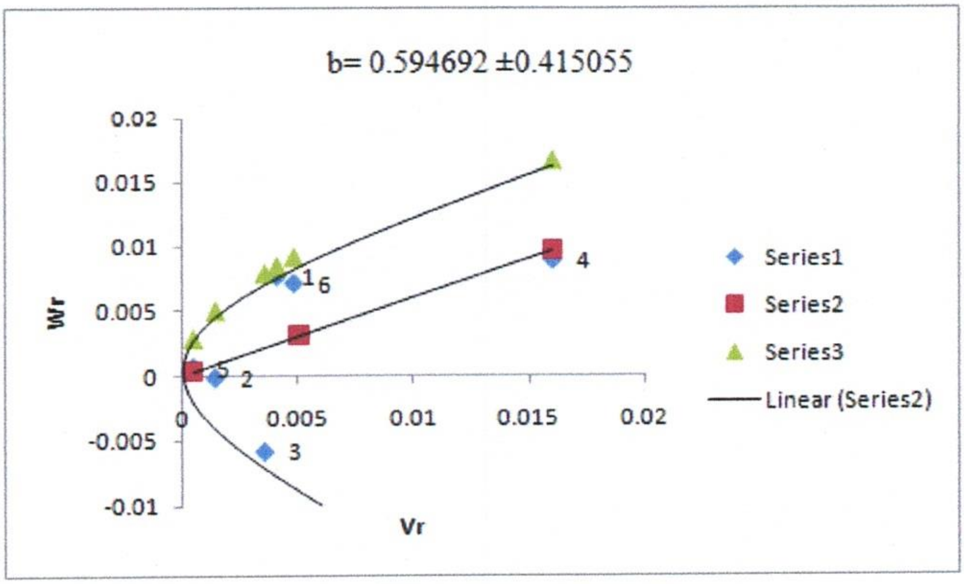

Fig 72: Wr/Vr graph for root weight of F_2 generation for replication total.

Experiment II

a. Estimation of heterosis over mid parent and better parent

The estimation of percent heterosis observed in F_1 generations over mid parent and better parent for diffenent characters are presented in Table 49 and 50.

Heterosis over mid parent for different crosses was recorded non significant in all crosses for DF. The highest percent of heterosis over mid parent was recorded to be -6.23586 in $P_2 \times P_4$ (Table 49) for this character. Both negative and positive heterosis over mid parent and better parent was recorded (Table 49 and 50, respectively) and The highest heterobeltotic effect for this character was observed also in $P_2 \times P_4$ with -8.84522.

The highest heterosis over mid parent and better parent was recorded in $P_4 \times P_5$ with 8.940423 and 6.349467, respectively for PHFF.

For NPBFF, the highest heterosis over mid parent and better parent was recorded in $P_4 \times P_6$ with 34.16116 and 20.67012, respectively.

For NSBFF, the highest heterosis over mid parent and better parent was recorded in $P_1 \times P_2$ with 53.83399 and 38.16376, respectively.

For CAMF, the highest positive heterosis over mid parent was recorded in $P_1 \times P_3$ with the value of about 38.81884 and that of over better parent was recorded 12.43863 in $P_4 \times P_5$. Different crosses for this character exhibited non significant, negative to positive heterosis over better parent and mid parent.

For NSBMF, the highest positive heterosis over mid parent and better parent was recorded in $P_1 \times P_3$ of 73.76543 and 56.38889, respectively.

The highest heterosis over mid parent and better parent was recorded in $P_1 \times P_3$ with value of 64.44754 and 39.33115, respectively for NPdPP. Both positive and negative non significant heterosis were recorded for this trait in different crosses.

For PdWPP, the highest heterosis over mid parent and better parent was recorded 80.77255 and 47.12736, respectively in $P_1 \times P_2$.

For NSPP, the highest heterosis over mid parent and better parent was recorded in $P_5 \times P_6$ with value of 41.22182 and 24.72021, respectively.

Regarding SWPP, the highest heterosis over mid parent and better parent was recorded 81.26522 and 47.18368, respectively, in $P_1 \times P_2$. Out of fifteen cross combinations, six F_1s showed positive mid parent heterosis, whereas three F_1s showed positive better parent heterosis.

For IPlW, the highest heterosis over mid parent was recorded 67.6072 in $P_1 \times P_2$ and that of over better parent was recorded in $P_1 \times P_4$ with a value of 31.92982. Both positive and negative heterosis was recorded over mid parent and better parent for this trait.

For RW, the highest heterosis over mid parent and better parent was recorded 127.3063 and 92.5, respectively in $P_1 \times P_2$. All the crosses showed significant heterosis over mid parent and better parent for this character.

b. Model fitting: Generation mean analysis

Through joint scaling test, the adequacy of additive-dominance model can observed. The values of m, [d] and [h] were calculated in term of 3- parameters model are shown in Table 51 to 62 for different characters. From these parameters with their co-efficient, the expected generation means were calculated. The χ^2 test was done to test the goodness of fit of the observed means with that of the expected means based on the 3 and 2 parameters. The χ^2 values with [h] and without [h] are shown (d.f. = 1 and 2, respectively) in Table 51 to Table 62 for different characters.

The $\hat{m}$ was significant for all of the characters in all cross combinations as all the studied characters were quantitative in nature.

For DF (Table 51), χ^2 value was found to be significant in the crosses $P_1 \times P_3$, $P_2 \times P_5$, $P_3 \times P_4$, $P_3 \times P_5$, $P_4 \times P_5$ and $P_4 \times P_6$. Significant χ^2 value indicated the presence of non allelic interaction and /or epistasis. [d] was significant for $P_1 \times P_4$ and $P_3 \times P_4$ crosses indicating that additive gene components played an important role in these crosses for this character inheritance. [h] was significant for $P_4 \times P_5$ indicating that dominance gene components played an important role in this cross for the character inheritance.

For PHFF (Table 52), χ^2 value was found to be non significant in all combinations except $P_1 \times P_6$, $P_2 \times P_6$, $P_3 \times P_6$ and $P_5 \times P_6$. [d] was significant for $P_1 \times P_2$, $P_1 \times P_3$, $P_2 \times P_4$, $P_2 \times P_5$, $P_2 \times P_6$, $P_3 \times P_5$ and $P_3 \times P_6$ and [h] was significant for $P_1 \times P_6$.

For NPBFF (Table 53), χ^2 value was found to be non significant in all the crosses except $P_2 \times P_5$, $P_3 \times P_4$ and $P_4 \times P_5$. [d] was non significant for all the crosses.

For NSBFF (Table 54), χ^2 value was found to be non significant in all the crosses except $P_1 \times P_3$, $P_3 \times P_4$ and $P_4 \times P_5$. [d] was significant for $P_1 \times P_4$ and $P_4 \times P_6$ combinations.

In case of CAMF (Table 55), χ^2 value was non significant for all of the character except $P_2 \times P_6$ and $P_3 \times P_6$. [d] was significant for $P_1 \times P_2$, $P_1 \times P_3$, $P_3 \times P_5$ and $P_3 \times P_6$.

For NSBMF (Table 56), χ^2 value was significant in $P_2 \times P_5$, $P_3 \times P_4$ and $P_4 \times P_5$ crosses. All other crosses combinations showed non significant χ^2 values. [d] was significant for $P_1 \times P_3$ combination.

For NPdPP (Table 57), χ^2 value was significant in $P_1 \times P_4$ and $P_4 \times P_5$. Rest of all crosses showed non significant χ^2 values. [d] was non significant for all crosses and [h] was significant for $P_4 \times P_5$.

For PdWPP (Table 58), χ^2 value was found non significant in all of the crosses except $P_4 \times P_5$ indicating that additive-dominance model was adequate in these crosses for this character. The [d] was significant for $P_1 \times P_4$, $P_4 \times P_5$ and $P_4 \times P_6$ whereas [h] was significant for $P_1 \times P_6$.

For NSPP (Table 59), χ^2 value was found non significant in all of the crosses except $P_1 \times P_6$ and $P_4 \times P_5$ and [d] was non significant for all of the crosses. [h] was significant for $P_1 \times P_6$ and $P_4 \times P_5$ indicating that dominance gene components played an important role in this character inheritance for these crosses.

For SWPP (Table 60), non significant χ^2 values were obtained by all of the crosses. [d] was significant only for $P_4 \times P_6$.

For IPIW, χ^2 value was significant for $P_1 \times P_6$ and $P_4 \times P_5$. [d] was significant for $P_1 \times P_2$, $P_1 \times P_3$ and $P_3 \times P_6$ and [h] was significant for $P_1 \times P_6$ and $P_4 \times P_5$ (Table 61).

In case of RW (Table 62), χ^2 value was non significant for all of the crosses except $P_4 \times P_5$. [d] was significant for $P_1 \times P_4$, $P_2 \times P_6$, $P_3 \times P_4$, $P_3 \times P_6$, $P_4 \times P_5$ and $P_4 \times P_6$.

Table 49: Percent heterosis over mid parent for different yield contributing characters in different crosses of lentil

Crosses Characters	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
DF	0.840964^{NS}	-4.08958^{NS}	-0.36283^{NS}	-0.75047^{NS}	3.620235^{NS}	-2.29183^{NS}	-6.23586^{NS}	-0.36826^{NS}	-2.49253^{NS}	-1.48236^{NS}	6.807287^{NS}	-4.28567^{NS}	0.864394^{NS}	0.61706^{NS}	0.813275^{NS}
PHFF	4.716254^{NS}	2.775722^{NS}	6.17327^{NS}	6.938282^{NS}	1.686949^{NS}	-1.73957^{NS}	-5.22785^{NS}	6.485062^{NS}	-5.27711^{NS}	-0.01013^{NS}	-9.92106^{NS}	1.704949^{NS}	8.940423^{NS}	-1.78972^{NS}	6.357005^{NS}
NPBFF	14.7254^{NS}	-6.45161^{NS}	18.90442^{NS}	0	-2.73519^{NS}	-9.34056^{NS}	-3.64101^{NS}	18.68145^{NS}	3.17757^{NS}	4.109913^{NS}	19.35484^{NS}	-6.38261^{NS}	1.917697^{NS}	34.16116^{NS}	10.63841^{NS}
NSBFF	53.83399^{NS}	-9.15487^{NS}	2.280394^{NS}	10.92294^{NS}	-14.7749^{NS}	-26.2483^{NS}	-30.7094^{NS}	20.75544^{NS}	-4.69645^{NS}	-13.2789^{NS}	-27.6335^{NS}	-10.3212^{NS}	21.54079^{NS}	10.01577^{NS}	19.67544^{NS}
CAMF	30.08069^{NS}	38.81884^{NS}	5.995785^{NS}	12.54121^{NS}	8.361511^{NS}	-21.2154^{NS}	-19.1777^{NS}	-6.21732^{NS}	-1.01193^{NS}	-0.24443^{NS}	-24.0006^{NS}	11.56916^{NS}	24.9421^{NS}	-36.7199^{NS}	24.37151^{NS}
NSBMF	48.94737^{NS}	73.76543^{NS}	22.1875^{NS}	17.61897^{NS}	-12.0327^{NS}	-11.0588^{NS}	13.80952^{NS}	34.53552^{NS}	13.89386^{NS}	-0.37461^{NS}	-17.0984^{NS}	-5.39415^{NS}	1.570681^{NS}	4.873994^{NS}	12.28411^{NS}
NPdPP	51.40743^{NS}	64.44754^{NS}	40.23444^{NS}	13.81981^{NS}	8.282708^{NS}	-17.0011^{NS}	10.58458^{NS}	-7.13916^{NS}	13.26123^{NS}	9.453331^{NS}	-13.7708^{NS}	-1.24714^{NS}	14.63358^{NS}	16.92308^{NS}	24.76456^{NS}
PdWPP	80.77255^{NS}	55.1867^{NS}	-13.1333^{NS}	-7.67103^{NS}	17.27948^{NS}	-18.0358^{NS}	-3.5609^{NS}	-20.1392^{NS}	-1.2648^{NS}	-2.54591^{NS}	-22.4987^{NS}	-4.4606^{NS}	6.082609^{NS}	-35.6325^{NS}	16.91704^{NS}
NSPP	23.83626^{NS}	35.60615^{NS}	26.38749^{NS}	27.0591^{NS}	27.2556^{NS}	-19.6777^{NS}	-2.50299^{NS}	-13.3477^{NS}	0.106425^{NS}	11.91468^{NS}	-21.5716^{NS}	-7.87658^{NS}	28.85741^{NS}	-3.45826^{NS}	41.22182^{NS}
SWPP	81.26522^{NS}	43.5108^{NS}	-22.5902^{NS}	-15.4694^{NS}	8.304619^{NS}	-22.1622^{NS}	-5.97833^{NS}	-19.6438^{NS}	-5.03279^{NS}	2.6952^{NS}	-21.5121^{NS}	-10.6779^{NS}	17.31297^{NS}	-46.4818^{NS}	23.41022^{NS}
IPlW	67.6072^{NS}	62.91729^{NS}	59.61794^{NS}	21.12005^{NS}	11.91492^{NS}	-23.8612^{NS}	46.68178^{NS}	11.93002^{NS}	15.42067^{NS}	-3.30106^{NS}	-23.9679^{NS}	5.193041^{NS}	7.771056^{NS}	-9.64561^{NS}	30.95595^{NS}
RW	127.3063**	38.99614**	-13.5447**	28.13559**	73.00513**	-10.6494**	0.808081**	5.824561**	25.90164**	-12.1458**	-23.8095**	-6.31034**	0.831025**	-34.5**	-5.76077**

N.B. ** Significant at 1% level of probability

* Significant at 5% level of probability

^{NS} Non-significant

Table 50: Percent heterosis over better parent for different yield contributing characters in different crosses of lentil

Crosses Characters	$P_1\times P_2$	$P_1\times P_3$	$P_1\times P_4$	$P_1\times P_5$	$P_1\times P_6$	$P_2\times P_3$	$P_2\times P_4$	$P_2\times P_5$	$P_2\times P_6$	$P_3\times P_4$	$P_3\times P_5$	$P_3\times P_6$	$P_4\times P_5$	$P_4\times P_6$	$P_5\times P_6$
DF	-1.02715^{NS}	-6.19048^{NS}	-4.87871^{NS}	-2.21811^{NS}	3.587352^{NS}	-6.16288^{NS}	-8.84522^{NS}	-0.75202^{NS}	-4.32869^{NS}	-7.90989^{NS}	2.957486^{NS}	-6.35321^{NS}	-2.30945^{NS}	-3.97226^{NS}	-0.70854^{NS}
PHFF	-9.89393^{NS}	-9.54366^{NS}	0.718061^{NS}	3.839717^{NS}	-2.52275^{NS}	-4.27988^{NS}	-14.5379^{NS}	-6.01061^{NS}	-15.4106^{NS}	-7.64236^{NS}	-18.6121^{NS}	-6.99605^{NS}	6.349467^{NS}	-2.85851^{NS}	4.954408^{NS}
NPBFF	12.25806^{NS}	-6.45161^{NS}	16.6671^{NS}	0	-13.9781^{NS}	-11.2903^{NS}	-3.91038^{NS}	16.12903^{NS}	15.80387^{NS}	2.150968^{NS}	19.35484^{NS}	-17.2039^{NS}	0	20.67012^{NS}	-2.15032^{NS}
NSBFF	38.16376^{NS}	-25.4334^{NS}	-19.8977^{NS}	-4.69243^{NS}	-18.7753^{NS}	-33.4103^{NS}	-40.7141^{NS}	14.85437^{NS}	-10.4733^{NS}	-18.3671^{NS}	-31.5028^{NS}	-23.4101^{NS}	8.673691^{NS}	-10.6121^{NS}	7.281942^{NS}
CAMF	-6.27591^{NS}	1.733803^{NS}	-14.6421^{NS}	-0.77359^{NS}	6.547127^{NS}	-23.304^{NS}	-30.4008^{NS}	-26.0189^{NS}	-27.9221^{NS}	-12.0797^{NS}	-38.8183^{NS}	-17.3361^{NS}	12.43863^{NS}	-48.3715^{NS}	11.30185^{NS}
NSBMF	41.5^{NS}	56.38889^{NS}	11.07955^{NS}	-0.08097^{NS}	-12.8472^{NS}	-16^{NS}	8.636364^{NS}	19.51456^{NS}	7.25^{NS}	-1.48156^{NS}	-22.3301^{NS}	-15.5556^{NS}	-5.82524^{NS}	-5.45455^{NS}	-5.33981^{NS}
NPdPP	30.07013^{NS}	39.33115^{NS}	20.15974^{NS}	-5.03401^{NS}	5.730783^{NS}	-18.3655^{NS}	10.24202^{NS}	-10.3356^{NS}	-4.61718^{NS}	7.983986^{NS}	-15.3741^{NS}	-17.9463^{NS}	11.02041^{NS}	-1.78121^{NS}	2.131537^{NS}
PdWPP	47.12736^{NS}	31.02229^{NS}	-32.7858^{NS}	-23.7413^{NS}	11.5872^{NS}	-21.6553^{NS}	-9.72405^{NS}	-21.6171^{NS}	-22.6497^{NS}	-12.5274^{NS}	-24.5632^{NS}	-22.5302^{NS}	-2.40911^{NS}	-51.9054^{NS}	-7.1322^{NS}
NSPP	3.627622^{NS}	10.47126^{NS}	8.285116^{NS}	15.09764^{NS}	23.6956^{NS}	-22.3205^{NS}	-5.23018^{NS}	-20.7186^{NS}	-18.1163^{NS}	5.307949^{NS}	-30.3845^{NS}	-26.5737^{NS}	21.06481^{NS}	-19.213^{NS}	24.72021^{NS}
SWPP	47.18368^{NS}	21.40462^{NS}	-38.0128^{NS}	-27.1823^{NS}	0.286826^{NS}	-25.985^{NS}	-7.66782^{NS}	-25.1415^{NS}	-27.2752^{NS}	-4.01247^{NS}	-23.1923^{NS}	-29.0123^{NS}	7.467198^{NS}	-59.5276^{NS}	-0.29413^{NS}
IPlW	25.2324^{NS}	19.19726^{NS}	31.92982^{NS}	5.244797^{NS}	7.581165^{NS}	-26.2539^{NS}	28.8579^{NS}	-6.53918^{NS}	-11.3652^{NS}	-17.3516^{NS}	-38.1145^{NS}	-20.9907^{NS}	1.578947^{NS}	-22.8421^{NS}	17.84737^{NS}
RW	92.5**	21.62162**	-36.4407**	20.96**	51.96396**	-14**	-15.4237**	-5.75**	-4**	-28.5254**	-29.7297**	-26.5676**	-22.8814**	-55.5932**	-21.216**

N.B. ** Significant at 1% level of probability

* Significant at 5% level of probability

^{NS} Non-significant

Table 51: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for days to flower (DF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	67.22509± 0.797181*	66.55698± 1.252209*	68.69059± 0.28565*	66.77909± 0.93417*	66.06102± 0.671985*	65.57857± 1.154987*	67.84692± 0.780848*	65.2937± 0.89916*	67.54954± 0.715804*	64.36639± 1.445795*	69.29085± 1.105401*	63.55289± 0.885247*	64.75085± 1.23222*	66.92533± 0.741956*	67.63298± 0.809479*
[d]	-1.42761± 1.106639^{NS}	0.061101± 1.391942^{NS}	-3.15325± 1.219176*	-1.06439± 1.221766^{NS}	-0.17317± 0.815244^{NS}	-2.5125± 1.512672^{NS}	-1.06886± 1.481758^{NS}	-0.86831± 1.380084^{NS}	-1.69982± 0.926082^{NS}	-4.27218± 1.799075*	-1.37502± 1.652425^{NS}	-1.79097± 1.111729^{NS}	-1.4026± 1.651914^{NS}	-1.79889± 1.048724^{NS}	-1.70137± 1.023123^{NS}
[h]		-3.86344± 2.017234^{NS}								0.179813 ±2.145626^{NS}			5.709434± 1.314377*		
Potence	-2.94805^{NS}	-5.70395*	-0.46528^{NS}	-0.5625^{NS}	1.590311^{NS}	-1.31667^{NS}	-2.57777^{NS}	6.738333^{NS}	-3.37083^{NS}	4.190483*	-2.28947^{NS}	-4.65077^{NS}	6.087719*	3.833333^{NS}	0.308343^{NS}
χ^2	1.76602^{NS}	7.054957**	0.651509^{NS}	0.066609^{NS}	1.247337^{NS}	0.279877^{NS}	3.906275^{NS}	10.23299**	3.250915^{NS}	10.79333**	9.121117*	4.948534^{NS}	21.16166**	6.753453*	1.46667^{NS}

Table 52: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for plant height at first flower (PHFF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	19.63269± 0.450775*	19.77498± 0.145891*	18.13494± 0.605607*	17.08688± 0.542634	16.52653± 0.599798*	22.3428± 0.497471*	18.61077± 0.70266*	19.68781± 0.596828*	19.41777± 0.732193*	20.31044± 0.565732*	18.92226± 0.554024*	19.174± 0.59375*	17.56738± 0.466766*	18.14167± 0.493991*	16.93904± 0.907113*
[d]	3.125963± 0.786938*	2.435162± 0.657867*	1.250653± 0.985241^{NS}	0.464757± 0.907277^{NS}	0.788614± 0.674101^{NS}	0.6901± 0.751527^{NS}	3.414242± 1.167722*	2.885687± 1.061406*	2.072555± 0.786627*	1.441134± 0.922525^{NS}	2.433174± 0.864244*	1.781875± 0.642813*	0.18622± 1.401753^{NS}	0.005722± 0.925674^{NS}	0.796372± 0.976804^{NS}
[h]					1.181688± 0.59988*				-0.89375± 1.2685^{NS}			-0.07975± 1.061876^{NS}			1.486371± 1.506842^{NS}
Potence	0.34026^{NS}	-0.16316^{NS}	0.9361^{NS}	1.9125^{NS}	2.25835*	-0.76582^{NS}	1.1478^{NS}	2.969^{NS}	3.92625*	-2.29546^{NS}	-1.13684^{NS}	2.729376*	3.289474^{NS}	0.970175^{NS}	3.3981*
χ^2	0.177313^{NS}	0.968831^{NS}	0.718043^{NS}	1.386131^{NS}	8.154858**	0.241646^{NS}	3.599477^{NS}	2.431955^{NS}	14.96111**	3.304993^{NS}	1.497655^{NS}	8.670913**	3.87666^{NS}	0.464054^{NS}	4.87814*

Table 53: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for number of primary branches at first flower (NPBFF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	7.463416± 0.360854*	8.254655± 0.391936*	8.037884± 0.500244*	6.840045± 0.280917*	6.482535± 0.373799*	7.552533± 0.153536*	7.15173± 0.383604*	7.147838± 0.516018*	6.975334± 0.233416*	6.031287± 0.346512*	7.286555± 0.521615*	6.740706± 0.369375*	5.959191± 0.349063*	6.95127± 0.307989*	7.097659± 0.377786*
[d]	0.142726± 0.515603^{NS}	-0.07702± 0.595368^{NS}	0.167567± 0.748952^{NS}	-0.052± 0.683723^{NS}	0.689784± 0.541107^{NS}	0.237596± 0.435573^{NS}	0.146639± 0.545052^{NS}	-0.01067± 0.536493^{NS}	0.654924± 0.402425^{NS}	0.950136± 0.623222^{NS}	0.200907± 0.586941^{NS}	0.901341± 0.463733^{NS}	0.51277± 0.724905^{NS}	0.816528± 0.554946^{NS}	0.969916± 0.528675^{NS}
[h]								1.293401± 0.980193^{NS}			1.33659± 0.947938^{NS}				
Potence	0.87013^{NS}	-2.10526^{NS}	1.590267^{NS}	0.75^{NS}	1.000033^{NS}	-1.00002^{NS}	-0.28887^{NS}	3.05*	-0.5625^{NS}	2.459537^{NS}	2.026316*	-0.15077^{NS}	2.964912^{NS}	0.719298^{NS}	1.361914^{NS}
χ^2	0.477505^{NS}	4.158875^{NS}	2.260271^{NS}	2.357781^{NS}	1.822983^{NS}	1.450677^{NS}	0.143795^{NS}	5.833234*	1.454822^{NS}	8.848627*	3.555219^{NS}	0.482536^{NS}	8.259192*	0.795584^{NS}	1.887493^{NS}

Table 54: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for number of secondary branches at first flower (NSBFF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	11.31158± 0.691186*	13.20936± 1.338148*	12.81572± 0.34883*	10.31604± 0.902523*	8.557171± 0.852843*	13.00006± 0.181078*	11.87487± 0.930878*	12.31637± 0.947876*	11.05791± 0.68276*	7.53871± 0.603541*	11.76835± 0.761249*	11.51622± 0.906554*	10.25894± 0.885322*	13.44083± 0.959016*	11.96333± 1.010301*
[d]	0.970804± 1.334741^{NS}	2.162619± 1.409309^{NS}	3.545419± 1.650029*	1.920527± 1.424521^{NS}	0.939387± 1.317792^{NS}	1.253763± 1.226309^{NS}	1.512454± 1.442751^{NS}	0.626336± 1.251617^{NS}	0.619526± 1.160516^{NS}	-1.41349± 1.485393^{NS}	0.688839± 1.301459^{NS}	1.778443± 1.208026^{NS}	0.451427± 1.530517^{NS}	2.998138± 1.421429*	1.286011± 1.232367^{NS}
[h]		-0.55458± 2.35368^{NS}													
Potence	4.675325^{NS}	-8.42982*	0.263867^{NS}	2.65625^{NS}	0.644641^{NS}	-4.61665^{NS}	-2.84443^{NS}	5.448333^{NS}	-0.37917^{NS}	6.610263^{NS}	-0.55263^{NS}	-0.49601^{NS}	11.15789^{NS}	1.894737^{NS}	3.879771^{NS}
χ^2	3.369628^{NS}	11.45968**	0.047356^{NS}	1.264521^{NS}	1.495194^{NS}	1.925107^{NS}	4.319213^{NS}	3.082582^{NS}	0.049509^{NS}	32.48769**	2.764322^{NS}	0.894493^{NS}	15.01552**	0.380144^{NS}	1.419408^{NS}

Table 55: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for canopy area at maximum flower (CAMF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	487.0645±64.29194*	537.1821±46.79136*	399.5594±22.76329*	320.8851±42.68319*	332.8409±4.981873*	659.4647±62.18135*	404.3151±48.84822*	523.6182±66.4495*	326.3389±69.80395*	544.0326±32.04684*	436.6384±39.50822*	428.5831±47.00148*	368.9541±31.97789*	393.3258±37.17502*	360.7622±37.62984*
[d]	188.8437±94.77619*	173.5237±70.64706*	96.41±78.64496^{NS}	53.00284±68.69645^{NS}	-1.88917±43.86404^{NS}	0.205462±87.03791^{NS}	27.24755±95.60671^{NS}	135.0129±86.06296^{NS}	28.71773±74.93296^{NS}	93.80341±71.74836^{NS}	130.6431±63.25671*	132.5254±50.23461*	29.70453±69.67002^{NS}	73.576±51.1412^{NS}	35.84538±46.52417^{NS}
[h]									110.6376±100.0124^{NS}			21.87102±81.82802^{NS}			
Potence	75.09649^{NS}	179.295^{NS}	23.75165^{NS}	132.4237^{NS}	40.08355^{NS}	-159.424^{NS}	117.757^{NS}	26.08033^{NS}	258.8914*	36.47168^{NS}	10.67021^{NS}	221.6232*	234.0754^{NS}	-97.5232^{NS}	197.904^{NS}
χ^2	0.192089^{NS}	2.106652^{NS}	0.043232^{NS}	1.071285^{NS}	0.381379^{NS}	0.467562^{NS}	4.772324^{NS}	0.078374^{NS}	12.0441**	0.410931^{NS}	3.680987^{NS}	9.648781**	4.406611^{NS}	1.048427^{NS}	2.648059^{NS}

Table 56: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for number of secondary branches at maximum flower (NSBMF)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	21.01809±1.542872*	25.90776±1.608337*	20.2315±1.20528*	20.44702±1.698903*	15.9869±1.085703*	22.35314±2.01397*	20.01727±1.79922*	20.41687±2.574271*	18.44838±1.253276*	19.25582±2.704807*	20.94918±1.586483*	20.60765±1.139129*	16.26371±1.220525*	20.08313±1.184653*	22.12277±1.771868*
[d]	0.942704±2.37867^{NS}	5.284522±2.68027*	2.055964±2.704369^{NS}	3.537554±2.712613^{NS}	-0.46685±2.039928^{NS}	3.278226±2.656802^{NS}	0.736341±2.684888^{NS}	2.228665±2.721087^{NS}	0.988705±2.023106^{NS}	2.728413±3.042724^{NS}	0.827127±3.033393^{NS}	3.782069±2.219277^{NS}	1.918854±3.07871^{NS}	2.209837±2.247293^{NS}	4.166982±2.339209^{NS}
[h]								0.890941±5.611561^{NS}		-7.63997±5.130944^{NS}					
Potence	6.168831^{NS}	14.08991^{NS}	5.458333^{NS}	8.459821^{NS}	0.875^{NS}	-1.98333^{NS}	6^{NS}	16.4875*	5.504167^{NS}	11.75*	0.979167^{NS}	-2^{NS}	12.14035^{NS}	0.77193^{NS}	5.265873^{NS}
χ^2	3.237089^{NS}	3.455847^{NS}	0.832944^{NS}	2.044021^{NS}	1.218551^{NS}	0.540236^{NS}	1.110103^{NS}	7.234837**	2.626702^{NS}	14.53573**	4.562087^{NS}	1.134606^{NS}	9.379458**	0.079053^{NS}	1.129161^{NS}

Table 57: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for number of pods per plant (NPdPP)

	$P_1×P_2$	$P_1×P_3$	$P_1×P_4$	$P_1×P_5$	$P_1×P_6$	$P_2×P_3$	$P_2×P_4$	$P_2×P_5$	$P_2×P_6$	$P_3×P_4$	$P_3×P_5$	$P_3×P_6$	$P_4×P_5$	$P_4×P_6$	$P_5×P_6$
$\hat{m}$	158.5424± 17.3854*	187.008± 18.56619*	183.132± 13.42175*	137.9856± 15.68491*	110.8808± 9.91176*	173.1219± 12.10395*	164.6544± 18.95139*	164.4558± 19.74643*	144.3596± 13.19753*	151.2248± 15.16937*	154.7428± 18.38067*	148.2331± 12.55422*	110.2271± 20.49158*	171.3872± 14.00116*	161.8463± 19.43945*
[d]	25.01987± 24.21083 ^{NS}	32.53662± 24.36983 ^{NS}	27.06838± 24.07169 ^{NS}	26.27719± 26.58831 ^{NS}	6.406302± 20.01996 ^{NS}	5.221916± 25.33886 ^{NS}	0.607± 25.04877 ^{NS}	3.768595± 27.82503 ^{NS}	19.90931± 20.88343 ^{NS}	4.136781± 25.20509 ^{NS}	-4.10858± 27.96533 ^{NS}	24.6217± 20.94646 ^{NS}	-8.24482± 27.70459 ^{NS}	29.38042± 20.84682 ^{NS}	31.07296± 23.7267 ^{NS}
[h]													78.99936 ±26.80612*		
Potence	16.19481 ^{NS}	53.29825 ^{NS}	68.22915 ^{NS}	54.46429 ^{NS}	34.4792 ^{NS}	-34.725 ^{NS}	41.84286 ^{NS}	16.2125 ^{NS}	28.06667 ^{NS}	64.64904 ^{NS}	32.63333 ^{NS}	-11.3651 ^{NS}	85.70175*	-28.5 ^{NS}	52.73017 ^{NS}
χ^2	0.553966 ^{NS}	5.425754 ^{NS}	6.448005*	1.645694 ^{NS}	2.669766 ^{NS}	0.34068 ^{NS}	0.379857 ^{NS}	0.505867 ^{NS}	0.781438 ^{NS}	3.028861 ^{NS}	1.946863 ^{NS}	0.259231 ^{NS}	12.62946**	2.189611 ^{NS}	0.878034 ^{NS}

Table 58: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for pod weight per plant (PdWPP)

	$P_1×P_2$	$P_1×P_3$	$P_1×P_4$	$P_1×P_5$	$P_1×P_6$	$P_2×P_3$	$P_2×P_4$	$P_2×P_5$	$P_2×P_6$	$P_3×P_4$	$P_3×P_5$	$P_3×P_6$	$P_4×P_5$	$P_4×P_6$	$P_5×P_6$
$\hat{m}$	4.377009± 0.699287*	4.965205± 0.569953*	4.200448± 0.227037*	3.41844± 0.509669*	2.216569± 0.560354*	4.741836± 0.187941*	4.327087± 0.534304*	4.398287± 0.671606*	3.628468± 0.450544*	4.374935± 0.422053*	3.904678± 0.553106*	3.620962± 0.40487*	3.809531± 0.369545*	4.228659± 0.375765*	4.074451± 0.594775*
[d]	0.989112± 0.957595 ^{NS}	0.449785± 0.809824 ^{NS}	1.288663± 0.478715*	0.751126± 0.854266 ^{NS}	-0.34164± 0.7155 ^{NS}	0.330809± 0.870712 ^{NS}	1.0203± 0.631069 ^{NS}	0.102624± 0.941771 ^{NS}	0.705856± 0.758896 ^{NS}	0.954993± 0.520706 ^{NS}	0.056729± 0.796793 ^{NS}	0.591757± 0.659489 ^{NS}	1.358984± 0.519606*	1.24658± 0.454442*	0.81687± 0.70782 ^{NS}
[h]					1.254897± 0.575641*										
Potence	1.371299 ^{NS}	0.650132 ^{NS}	-0.67375 ^{NS}	0.991396 ^{NS}	1.248433*	-1.07987 ^{NS}	1.944524 ^{NS}	-0.14605 ^{NS}	0.867333 ^{NS}	1.519712 ^{NS}	0.57 ^{NS}	-0.57824 ^{NS}	2.498421 ^{NS}	-1.09289 ^{NS}	1.371486 ^{NS}
χ^2	0.641103 ^{NS}	4.579337 ^{NS}	1.793385 ^{NS}	1.005547 ^{NS}	3.533832 ^{NS}	0.389077 ^{NS}	2.948399 ^{NS}	0.33747 ^{NS}	1.00399 ^{NS}	2.696384 ^{NS}	1.083935 ^{NS}	0.374367 ^{NS}	9.160993*	0.845657 ^{NS}	0.690261 ^{NS}

Table 59: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for number of seeds per plant (NSPP)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	196.4165± 25.60207*	245.8074± 20.867*	233.9303± 0.069433*	165.231± 21.13555*	108.3052± 24.23046*	236.5589± 4.811362*	210.6863± 27.14741*	188.7086± 25.35971*	176.2167± 18.92145*	200.7653± 21.77378*	188.3782± 23.60073*	180.5929± 17.76138*	139.6142± 25.40869*	201.8891± 19.70008*	190.2337± 24.21801*
[d]	38.11422± 38.39329^{NS}	43.0246± 35.91171^{NS}	25.72001± 33.55245^{NS}	18.6384± 33.52422^{NS}	14.05482± 31.09813^{NS}	4.105218± 38.69647^{NS}	3.363631± 36.47398^{NS}	13.99828± 36.27888^{NS}	29.05826± 32.96809^{NS}	7.547431± 34.01285^{NS}	20.54502± 33.93019^{NS}	35.53452± 31.10077^{NS}	12.67725± 31.79626^{NS}	31.94945± 29.3488^{NS}	19.01759± 29.34616^{NS}
[h]					80.97877± 25.278*								93.59366± 33.97542*		
Potence	-17.3896^{NS}	33.45395^{NS}	48.86802^{NS}	85.00893^{NS}	75.14585*	-60.525^{NS}	14.1508^{NS}	-9.13542^{NS}	29.93333^{NS}	81.71475^{NS}	15.2^{NS}	-13.5159^{NS}	112.6316*	-45.8158^{NS}	87.41469^{NS}
χ^2	0.092845^{NS}	3.321988^{NS}	3.102805^{NS}	1.8229^{NS}	5.475857*	0.647452^{NS}	0.234262^{NS}	0.604673^{NS}	0.764816^{NS}	2.021991^{NS}	1.118599^{NS}	0.502278^{NS}	10.9734**	1.150129^{NS}	2.038777^{NS}

Table 60: The estimated values of $\hat{m}$,[d] and [h] of 3-parameter model for seed weight per plant (SWPP)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	3.168656± 0.552363*	3.591438± 0.425603*	2.870156± 0.132856*	2.281951± 0.382638*	1.49039± 0.433067*	3.415336± 0.114948*	2.856071± 0.392085*	3.077535± 0.518539*	2.548133± 0.346878*	3.042683± 0.338593*	2.728927± 0.429246*	2.494357± 0.323698*	2.556289± 0.301939*	2.816442± 0.30386*	2.78923± 0.464525*
[d]	0.729866± 0.756887^{NS}	0.324315± 0.639129^{NS}	0.756937± 0.421502^{NS}	0.371688± 0.662666^{NS}	-0.2104± 0.563393^{NS}	0.265903± 0.69488^{NS}	0.603128± 0.517396^{NS}	0.267391± 0.739079^{NS}	0.54791± 0.603829^{NS}	0.462589± 0.444654^{NS}	0.095634± 0.625043^{NS}	0.442971± 0.526249^{NS}	0.800415± 0.447899^{NS}	0.783021± 0.389584*	0.479491± 0.553774^{NS}
[h]					0.648206± 0.536592^{NS}										
Potence	1.072987^{NS}	-0.05167^{NS}	-0.85202^{NS}	0.355236^{NS}	0.827867*	-0.97367^{NS}	1.216848^{NS}	-0.26037^{NS}	0.564667^{NS}	1.101235^{NS}	0.231333^{NS}	-0.68527^{NS}	1.921439^{NS}	-1.18833^{NS}	0.936275^{NS}
χ^2	0.635692^{NS}	3.611309^{NS}	4.978133^{NS}	0.501081^{NS}	3.375878^{NS}	0.731627^{NS}	2.70096^{NS}	0.175682^{NS}	0.806588^{NS}	1.612594^{NS}	0.484343^{NS}	0.813188^{NS}	5.596405^{NS}	1.716157^{NS}	0.832863^{NS}

Table 61: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for individual plant weight (IPIW)

	$P_1\times P_2$	$P_1\times P_3$	$P_1\times P_4$	$P_1\times P_5$	$P_1\times P_6$	$P_2\times P_3$	$P_2\times P_4$	$P_2\times P_5$	$P_2\times P_6$	$P_3\times P_4$	$P_3\times P_5$	$P_3\times P_6$	$P_4\times P_5$	$P_4\times P_6$	$P_5\times P_6$
$\hat{m}$	2.848466± 0.342726*	3.513677± 0.360904*	2.399707± 0.25961*	2.032933± 0.249015*	1.356307± 0.270811*	3.923272± 0.400802*	2.386677± 0.268957*	3.150273± 0.379871*	2.597844± 0.258464*	2.952546± 0.302362*	2.886118± 0.277906*	2.939859± 0.25485*	1.729362± 0.305345*	2.522934± 0.221116*	2.421985± 0.29295*
[d]	0.481453*	1.409508± 0.470102*	0.495889± 0.425441^{NS}	0.331489± 0.417089^{NS}	0.331902± 0.337307^{NS}	0.402137± 0.540103^{NS}	0.231526± 0.486878^{NS}	0.620552± 0.48237^{NS}	0.681992± 0.375429^{NS}	0.701411± 0.476297^{NS}	0.859419± 0.46589^{NS}	1.053282± 0.367839*	0.125685± 0.424324^{NS}	0.450809± 0.335408^{NS}	0.310753± 0.3397^{NS}
[h]					0.733846± 0.320474*								1.142224± 0.334859*		
Potence	1.087662^{NS}	1.769167^{NS}	1.761017^{NS}	1.026932^{NS}	0.843117*	-1.00942^{NS}	3.364^{NS}	0.783742^{NS}	1.289048^{NS}	1.169375^{NS}	0.017083^{NS}	0.811848^{NS}	1.11*	-0.37851^{NS}	1.143871^{NS}
χ^2	0.858133^{NS}	1.870624^{NS}	1.122609^{NS}	1.792285^{NS}	6.981314**	0.907406^{NS}	5.856786^{NS}	0.33235^{NS}	3.99982^{NS}	5.381361^{NS}	2.813037^{NS}	2.039918^{NS}	10.53023**	0.487756^{NS}	1.726717^{NS}

Table 62: The estimated values of $\hat{m}$, [d] and [h] of 3-parameter model for root weight (RW)

	$P_1 \times P_2$	$P_1 \times P_3$	$P_1 \times P_4$	$P_1 \times P_5$	$P_1 \times P_6$	$P_2 \times P_3$	$P_2 \times P_4$	$P_2 \times P_5$	$P_2 \times P_6$	$P_3 \times P_4$	$P_3 \times P_5$	$P_3 \times P_6$	$P_4 \times P_5$	$P_4 \times P_6$	$P_5 \times P_6$
$\hat{m}$	0.177611± 0.022125*	0.180451± 0.017862*	0.204778± 0.014742*	0.136091± 0.016662*	0.130246± 0.015836*	0.191897± 0.0132*	0.204997± 0.016647*	0.180997± 0.015847*	0.164554± 0.014932*	0.136151± 0.016875*	0.139877± 0.022267*	0.174146± 0.02095*	0.170329± 0.020508*	0.174819± 0.012375*	0.143291± 0.016114*
[d]	0.028074± 0.027701^{NS}	0.040311± 0.047505^{NS}	0.063697± 0.025536*	0.007367± 0.028921^{NS}	0.019286± 0.023451^{NS}	0.007917± 0.035084^{NS}	0.037059± 0.022144^{NS}	0.024362± 0.024726^{NS}	0.049119± 0.020313*	0.127722± 0.033452*	-0.00827± 0.041943^{NS}	0.065691± 0.031977*	0.06715± 0.023497*	0.077649± 0.019124*	0.026542± 0.021473^{NS}
[h]													0.039318± 0.029713^{NS}		
Potence	0.136623^{NS}	0.07614^{NS}	-0.0319^{NS}	0.090682^{NS}	0.081683^{NS}	-0.02283^{NS}	0.099026^{NS}	0.052908^{NS}	0.028762^{NS}	0.085417^{NS}	-0.00256^{NS}	-0.0661^{NS}	0.09*	-0.045^{NS}	0.03851^{NS}
χ^2	2.181087^{NS}	2.098263^{NS}	0.765803^{NS}	1.166582^{NS}	1.111947^{NS}	0.084343^{NS}	4.6828^{NS}	1.710646^{NS}	0.995569^{NS}	2.271729^{NS}	0.090245^{NS}	2.299929^{NS}	10.6877**	2.685371^{NS}	1.540585^{NS}

DISCUSSION

Experiment-wise discussions are given as follows:

Experiment I: Combining ability and gene action of twelve yield and yield contributing characters through half diallel

Majority of the quantitative characters are controlled by polygenes. Each gene has small effect, which is cumulative in nature. Quantitative characters show a continuous variations and it is not possible to classify them into distinct classes. The inheritance studies of quantitative characters have to employ through biometry by construction of special models and procedures. Parents have to be chosen on the basis of the genetic values. Diallel analysis is one of the important techniques for the evaluation of varieties in terms of their genetic make-up. The present investigation was carried out in obtaining genetic information following six parent half diallel analysis.

In this investigation, diallel analysis was studied with different yield contributing characters in lentil (*Lens culinaris* Medic.). Testing the significance of genotypic difference showed that the crosses including parents were used in this study, which were non significantly different from each other for all the characters except CAMF. The t^2 tests indicated probable fulfillment for all the postulated assumptions for all the yield contributing characters under study.

Genetic parameters like additive variance (D) was significant for DF, PHFF, NPBFF and CAMF and two dominant components of variance i.e., H_1 and H_2 were significant for CAMF, and DF, NPBFF and CAMF, respectively and another dominant component h^2 was non significant for all of the characters in F_1 generation. Significant values of D, H_1 and H_2 components indicated additive variation and dominant variation were greater in magnitude for the respective characters. Singh and Singh (2007) observed that earlyness and 1000-seed weight were conditioned primarily by additive gene action with a very low incidence of dominance in lentil. In F_2 generation, D was significant for PHFF, CAMF, IPlW and RW. H_1, H_2 and h^2 component were significant for PdWPP, NSPP and SWPP in the present investigation. Besides these, H_1 was significant for NPdPP and h^2 was significant for NPBFF, CAMF, NPdPP, IPlW and RW. In the present study, the non additive component, H_1 was greater than D (additive) for NPBFF, NSBFF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW and D was greater than H_1 and H_2 for DF, PHFF and CAMF in the present investigation in F_1 generation. Component, H_1 and H_2 were greater than D for DF, NPBFF, NSBFF, NSBMF, NPdPP, NSPP, and SWPP in F_2 generation. H_1 was greater than D for PHFF and IPlW in this generation. D was greater than H_1 and H_2 for CAMF, PdWPP and RW in F_2 generation of the present investigation. Syamal and Joshi (1997) in a study on the genetics of number of seeds in tomato showed that the non additive components (H_1 and H_2) were highly significant and large in magnitude than additive (D) component in both F_1 and F_2 generations of 7 parent diallel analysis. Swarup *et al.* (1991) worked on lentil and they found that time to flowering and plant height had the additive gene effects. For days to flowering and plant height at flowering in snap bean, investigated by Arunga *et al.* (2010) and for plant height in maize, observed by Subramanian and Subbaraman (2006) got the same results. The dominance effect is also estimated by the component, h^2. In the present investigation, the significant value of h^2 suggested that dominance effect over all loci in heterozygous phase was important for NPBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW in F_2 generation. Mandal *et al.* (1998) estimated both additive and dominant gene actions for submerged tolerance in rice.

The parameter F is a measure of dominant and recessive genes present in the parents. In this study, significant and non significant F values for different characters indicated the presence of dominant alleles and both dominant and recessive alleles contributed equally in the parents, respectively. The ratio $(4DH_1)^{1/2}+F / (4DH_1)^{1/2}-F$ in F_1 generation and $1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$ in F_2 generation determines the proportion of dominant and recessive genes in the parents. In this present investigation, the ratios greater than one and less than one were recorded for different characters indicating the presence of dominant genes and equal proportion of dominant and recessive genes in the parents, respectively. The sign of the Fri value was an indicator of relative frequencies of dominant and recessive alleles.

The environmental components (E and E_2 in F_1 and F_2 generations, respectively) were significant for all of the characters and for all of the characters except DF and NSBFF in F_1 and F_2 generations, respectively. Milkova and Petkova (1979) reported that plant height was controlled by environmental factors up to 77% in red pepper.

The regression lines drawn in Wr/Vr graphs indicated partial dominance for DF, PHFF, NSBMF and PdWPP and complete or slightly partial dominance for SWPP in case of replication total in F_1 generation. On the other hand, over dominance was shown by NPBFF, CAMF, NPdPP, NSPP and IPlW in case of replication total in F_1 generation. In F_2 generation, partial dominance was shown by PHFF and CAMF of replication total. Over dominance was shown by NPBFF, NPdPP, PdWPP, NSPP, SWPP and IPlW for replication total in F_2 generation. The ratio of $(H_1/D)^{1/2}$ indicated the over and partial dominance for different characters in both F_1 and F_2 generations in the present investigation. Khaleque (1975) in six parent diallel cross in rice reported that partial dominance was present for most of the characters. Graph in Fig. 72 indicated complete dominance for RW. Tabassum and Saleem (1993) observed in their study that grain yield per plant and 100 grain weight showed partial dominance in F_1 generation in maize. These findings were similar with the present study.

The proportion, $H_2/4H_1$ measures average value of positive and negative genes i.e., uv over all loci in the parents. In case of unequal allelic frequencies i.e., $u \neq v$ at all loci estimated from the ratio $H_2/4H_1$was less than its maximum value 0.25, which happens when $u = v = 0.5$ at all loci. Both symmetrical and asymmetrical distribution of genes with positive and negative effects were recorded for different characters in F_1 and F_2 generations. Findings of both equal and unequal gene frequencies were also obtained by Ahmed (2002) in eight- parent diallel cross for tomato and that of unequal gene frequencies for submerged tolerance in rice was observed by Mandal *et al.* (1998). Swarup *et al.* (1991), Subramanian and Subbaraman (2006) and Ara (2010) also found the similar results in lentil, maize and onion, respectively.

In this investigation, the ratios of h^2/H_2 indicated only one group of genes controlled the characters namedly DF, NPBFF, NSBFF, CAMF, NSBMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW and two group of genes controlled PHFF in F_1 generation having dominance. In F_2 generation, only one group of genes controlled the characters viz. DF, PHFF and NSBFF. NPBFF was controlled by six groups of genes and four groups of genes were involved in controlling the characters viz., CAMF and NSBMF. There were three groups of genes controlling NPdPP and two groups of genes controlling PdWPP, NSPP and SWPP. Ten groups of genes were involved in controlling IPlW and seven groups of genes were involved in controlling RW in F_2 generations in the present investigation. Paul *et al.* (1976a) estimated 1-18 effective factors for the control of different quantitative traits in jute. Ahmed (2002) estimated 1-4 gene or gene groups in the inheritance of five characters as per their own ratio in tomato. Ara (2010) found two to one group of genes for bulb length, neck diameter, leaf length, bulb volume and number of leaves in onion.

The location of array points along the regression line in Wr/Vr graph depends on the relative proportion of dominant and recessive genes present in the recurrent parents of each array (Jinks, 1954 and Hayman, 1954b). With an excess of dominant genes, the parent shows a low array variance and covariance and its position will be near the point of origin on regression line. In this way, array 1 possessed dominant gene in excess for PHFF of replication 2, for CAMF of replication 2 and for IPlW of replication 2 in F_1 generation. Array 2 possessed dominant gene in excess for RW of replication 2, for DF and NSPP of replication total in F_1 generation and for NPBFF of replication 2, for NSBFF of replication 1, for PdWPP of replication 2, for NPBFF, NPdPP and PdWPP of replication total. Array 2 possessed dominant gene in excess in F_2 generation. Array 3 possessed dominant gene in excess for NSBMF of replication 2 and for NPdPP of replication 2 in F_1 generation and for NPdPP of replication 1 and for SWPP of replication 1 in F_2 generation. Array 4 possessed dominant gene in excess for NSPP of replication 1, for PHFF, NSBMF and NPdPP of replication total in F_1 generation and for NPBFF of replication 1, for CAMF of replication 2 and for IPlW of replication 1 in F_2 generation. Array 5 possessed dominant gene in excess for CAMF of replication 1, for NPdPP of replication 1, for IPlW of replication 1, for NPBFF, CAMF and IPlW of replication total in F_1 generation and for NSBMF of replication 2, for NSPP of replication 1, for SWPP of replication 2, for IPlW of replication 1, for RW of replication 1, for NSPP, SWPP and RW of replication total in F_2 generation. Array 6 possessed dominant gene in excess for PHFF of replication 1, for NPBFF of replication 1, for NSBMF replication 1, for NSPP of replication 2, for PdWPP and SWPP of replication total in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for CAMF of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 1 possessed recessive gene in excess for PHFF of replication 1, for CAMF of replication 1, for NSBMF of replication 1, for NPdPP of replication 1, for NPdPP of replication 2, for NSPP of replication 1, for IPlW of replication 1, for PHFF, CAMF, NSBMF, NPdPP, PdWPP, SWPP and IPlW of replication total in F_1 generation. Array 1 possessed recessive gene in excess for NPBFF of replication 1, for CAMF of replication 2, for PdWPP of replication 2, for NSPP of replication 1, for SWPP of replication 1, for SWPP of replication 2, for NPdPP, PdWPP, NSPP, SWPP and IPlW of replication total in F_2 generation. Array 2 possessed recessive gene in excess for NPBFF of replication 1 and for NSPP of replication 2 in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for IPlW of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 3 possessed recessive gene in excess for DF and NSPP of replication total in F_1 generation. This array possessed excess of recessive genes for NPBFF of replication 2, for CAMF of replication 1, for NSBMF of replication 2 and for NPBFF of replication total in F_2 generation. Array 4 possessed recessive gene in excess for PHFF of replication 2, for CAMF replication 2, for IPlW of replication 2 and for RW of replication 2 in F_1 generation. This array possessed recessive in excess for NSBFF of replication 1, for RW of replication 1 and for RW of replication total in F_2 generation. Array 5 possessed recessive gene in excess for NSBMF of replication 2 in F_1 generation. Array 6 possessed recessive gene in excess for NPBFF in F_1 and for NPdPP of replication 1 in F_2 generation. Array 3 possessed more or less equal proportion of dominant and recessive genes for most of the characters in both generations.

The combining ability analysis revealed that the gca variances were significant for DF, PHFF, CAMF and RW and sca variances were non significant for all the characters in this investigation. The relative magnitude of gca was higher than sca for all the twelve characters studied indicating the predominance of the additive, additive × additive gene effects for the characters. Gowda and Bahl (1978) found that mean squares due to general combining ability were significant for plant height and flowering time.

Comparison of gca effects of individual parents for twelve characters showed both positive and negative effects except P_1 and P_6. Significant effects were obtained by P_1 for PHFF , P_2 for PHFF, CAMF, IPlW and RW, P_3 for PHFF, DF and CAMF , P_4 for DF, NSBFF and RW and P_6 for NPBFF, CAMF, NPdPP, PdWPP, NSPP, SWPP, IPlW and RW.

In this study, the highly positive sca estimations were recorded in the cross, $P_1 \times P_2$ for the characters namedly NSBFF, PdWPP, SWPP and RW and for CAMF, NSBMF, NPdPP and IPlW, the cross $P_1 \times P_3$ were indicated as good specific combiners.

Experiment II:

a. Estimation of heterosis over mid parent and better parent

Heterosis is the amount of which the mean of an F_1 exceeds its parents (Mather and Jinks, 1971). In the present investigation, all of the crosses showed non significant heterosis over mid parent for all the characters except RW. Both positive and negative heterosis was found over mid parent for different characters in the present study. Non significant high heterotic values were found over mid parent. Heterosis over mid parent for SWPP was recorded as 81.26522, being highest in $P_1 \times P_2$.

Most of the crosses exhibited heterosis over mid parents and better parents for most of the characters. All of the crosses showed non significant heterosis over better parent for all of the characters except RW. Positive and negative heterosis were found over better parent for different characters in the present study. Non significant high heterotic values were found over better parent in the present study, which is in agreement with the results of Hosfield *et al.* (1977) in onion. They found non significant high heterosis percent over better parent for some characters.

$P_4 \times P_6$ showed the highest negative heterosis percent (-59.5276) for SWPP, while 47.18368% positive heterosis over better parent was recorded for SWPP in $P_1 \times P_2$. Kumar *et al.* (1994) found that high heterosis value for yield per plant in lentil. Chauhan and Singh (2000) reported that F_1 plants exhibiting heterosis for seed yield also showed high heterotic response for major yield attributes in lentil. Rathi *et al.* (2001) found that heterosis of yield had positive association with vigours of its component characters like test weight and pods per clusters in lentil. Singh and Singh (2006) found moderate value of heterosis for seed yield in lentil. They observed that high heterosis was attributed due to luxuriant plant growth coupled with high frequency of pods seed. This result is supported by the present investigation as high value of heterosis of SWPP for the cross $P_1 \times P_2$ coupled with high heterosis value of NPdPP. Milan *et al.* (2010) also observed that yield per plant showed high heterosis value over better parent in lentil. The presence of heterosis in food legumes for grain yield and its components have been reported by several workers e.g.

Sagar and Chandra (1977), Arora and Pandey (1987), Shinde and Deshmukh (1989), Kunta *et al*. (1997), Patil *et al*. (1998), Gupta *et al*. (2003), Hedge *et al*. (2007) and Adeyanju (2009). Zubair *et al*. (2010) found that heterotic effects were greater for number of pods per plant and grain yield per plant in mungbean (*Vigna radiate* (L.) Wilczek.

Joint scaling test of Cavalli (1952) is more effective than any other test in detecting the adequacy of model. It detects information from all the generations available for each cross at a time. The non significant χ^2 values exhibited the presence of only additive – dominance relationship in the inheritance of the studied characters and crosses in this piece of experiment. Regarding SWPP, all crosses showed non significant χ^2 values

In the inheritance study through diallel and heterosis, it was found that $P_1 \times P_2$ and $P_1 \times P_3$ were the promising crosses in respect of PdWPP, SWPP and RW. These crosses appeared to be important for heterosis study. $P_1 \times P_2$ is leading to show the highest heterosis percent over mid parent and better parent for the above characters. $P_1 \times P_3$ showed the 2nd highest value over mid parent and better parent for the above characters. In combining ability analysis, $P_1 \times P_2$ was found to be the best combination for sca in case of the above characters and showed adequacy of additive-dominance model. $P_1 \times P_3$ also showed the adequacy of additive-dominance model. These two crosses showed good sca as well as P_2 and P_4 were the good general combiner in most of the characters.

SUMMARY

Inheritance of yield and different yield contributing quantitative characters of lentil (*Lens culinaris* Medic.) were studied through half diallel, combining ability, heterosis and joint scaling test in part I under two experiments. Twelve yield contributing characters viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), number of secondary branches at maximum flower (NSBMF), number of pods per plant (NPdPP), pod weight per plant (PdWPP), number of seeds per plant (NSPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) were studied in a six parent half diallel cross of lentil. In experiment II, above characters were considered for both heterosis study and generation mean analysis. The data collected for all of the above characters were analyzed following diallel techniques of Hayman's (1954a and 1954b), and Griffing's (1956) approach and formulae given by Jinks (1956) and following heterosis study and generation mean analysis.

The combining ability analysis in lentil showed that gca variances with each parent played significant role in the choice of parents regarding PHFF, CAMF and RW. The sca variances were non significant for all of the characters in this study. Comparison of gca effects of individual parents for these above characters showed both positive and negative effects except P_1 and P_6. The high positive significant gca effect was recorded for most of the charaters in parent 2 (P_2) followed by P_4. The high positive sca effect was recorded in the cross $P_1 \times P_2$ for NSBFF, PdWPP, SWPP and RW and in the cross $P_1 \times P_3$ for CAMF, NSBMF, NPdPP and IPlW indicating that these crosses were the good specific combiner for the respective characters.

Significant additive (D) component was observed for DF, PHFF, NPBFF and CAMF and significant dominant component of variation, H_1 was observed for CAMF and H_2 for DF, NPBFF and CAMF. Another dominant component h^2 was non significant for all of the characters in F_1 generation. In F_2 generation, significant additive component (D) was observed for PHFF, CAMF, IPlW and RW. Significant dominance variations (H_1, H_2 and h^2) were found for PdWPP, NSPP and SWPP.

Besides these, H_1 was also found significant for NPdPP and h^2 was also significant for NPBFF, CAMF, NPdPP, IPlW and RW.

Over dominance was observed for NSBFF, NSPP, SWPP, IPlW and RW, whereas partial dominance was recorded for the remaining characters except NPBFF, NPdPP and PdWPP in the F_1 generation. In F_2 generation, over dominance was observed for DF, NPBFF, NSBFF, NSBMF, NPdPP, NSPP and SWPP, whereas partial dominance was shown by PHFF, CAMF, IPlW and RW.

The ratio of $(4DH_1)^{1/2}+F/(4DH_1)^{1/2}-F$ estimates the relative proportion of dominant and recessive genes in the parents. In this study, the values of the ratio were more than one recorded in CAMF, NSBMF, NPdPP, NSPP, SWPP and RW. Excessive of recessive genes was found for all other traits except NSBFF in F_1 generation. Nearly equal distribution of dominant and recessive genes was found for NSBFF in F_1 generation. In F_2 generation, the values of the ratio, $1/4(4DH_1)^{1/2}+1/2F/1/4(4DH_1)^{1/2}-1/2F$ were more than one for the characters namedly DF, NSBFF, CAMF and IPlW indicating the presence of an excess of dominant genes in the parents. Rest of the characters except PdWPP showed excess of recessive genes in the parents.

In F_1 generation, only one group of genes were involved in controlling eleven yield contributing characters, whereas in F_2 generation, three characters involved one group of dominant genes which were responsible for their genetical control.

Array 1 possessed dominant gene in excess for PHFF of replication 2, for CAMF replication 2 and for IPlW of replication 2 in F_1 generation. Array 2 possessed dominant gene in excess for RW of replication 2, for DF and NSPP of replication total in F_1 generation and for NPBFF of replication 2, for NSBFF of replication 1, for PdWPP of replication 2, for NPBFF, NPdPP and PdWPP of replication total. Array 2 possessed dominant gene in excess in F_2 generation. Array 3 possessed dominant gene in excess for NSBMF of replication 2 and for NPdPP of replication 2 in F_1 generation and for NPdPP of replication 1 and for SWPP of replication 1 in F_2 generation. Array 4 possessed dominant gene in excess for NSPP of replication 1, for PHFF, NSBMF and NPdPP of replication total in F_1 generation and for NPBFF of replication 1, for CAMF of replication 2 and for IPlW in F_2 generation. Array 5 possessed dominant gene in excess for CAMF of replication 1, for NPdPP of replication 1, for IPlW of replication 1, for NPBFF, CAMF and IPlW of replication total in F_1 generation and for NSBMF of replication 2, for NSPP of replication 1, for SWPP of replication 2, for IPlW of replication 1, for RW of replication 1, for NSPP, SWPP and RW of replication total in F_2 generation. Array 6 possessed dominant gene in excess for PHFF of replication 1, for NPBFF of replication 1, for NSBMF of replication 1, for NSPP of replication 2, for PdWPP and SWPP in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for CAMF of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 1 possessed recessive gene in excess for PHFF of replication 1, for CAMF of replication 1, for NSBMF of replication 1, for NPdPP of replication 1, for NPdPP of replication 2, for NSPP of replication 1, for IPlW of replication 1, for PHFF, CAMF, NSBMF, NPdPP, PdWPP, SWPP and IPlW of replication total in F_1 generation. Array 1 possessed recessive gene in excess for NPBFF of replication 1, for CAMF of replication 2, for PdWPP of replication 2, for NSPP of replication 1, for SWPP of replication 1, for SWPP of replication 2, for NPdPP, PdWPP, NSPP, SWPP and IPlW of replication total in F_2 generation. Array 2 possessed recessive gene in excess for NPBFF of replication 1 and for NSPP of replication 2 in F_1 generation and for PHFF of replication 1, for PHFF of replication 2, for IPlW of replication 1, for PHFF and CAMF of replication total in F_2 generation. Array 3 possessed recessive gene in excess for DF and NSPP of replication total in F_1 generation. This array possessed excess of recessive genes for NPBFF of replication 2, for CAMF of replication 1, for NSBMF of replication 2 and for NPBFF of replication total in F_2 generation. Array 4 possessed recessive gene in excess for PHFF of replication 2, for CAMF replication 2, for IPlW of replication 2 and for RW of replication 2 in F_1 generation. This array possessed recessive in excess for NSBFF of replication 1, for RW of replication 1 and for RW of replication total in F_2 generation. Array 5 possessed recessive gene in excess for NSBMF of replication 2 in F_1 generation. Array 6 possessed recessive gene in excess for NPBFF in F_1 and for NPdPP of replication 1 in F_2 generation. Array 3 possessed more or less equal proportion of dominant and recessive genes for most of the characters in both generations.

Through heterosis study, all of the crosses except $P_1 \times P_5$ for NPBFF, showed non significant heterosis over mid parents for all of the characters except RW. Both positive and negative significant heterosis was estimated in all cross combinations only for RW. All of the crosses exhibited heterosis over better parent for most of the characters. Some of the non-significant heterotic values over better parent were negative and others were positive, but non-significant values were not so much high except PdWPP, SWPP and RW in this study.

The χ^2 values were non-significant in most of the cases.

In the inheritance study through diallel and heterosis, it was found that $P_1 \times P_2$, $P_1 \times P_3$ and $P_4 \times P_6$ were the promising crosses in respect of PdWPP and SWPP.

PART II:
STUDY OF CHARACTER ASSOCIATION AND SELECTION INDEX

INTRODUCTION

As yield is a major objective in plant breeding, the knowledge of genotypic and phenotypic association within and between yield and yield contributing characters has a great importance to plant breeders in their selection practices. It gives them more precision and accuracy in their works. The correlation coefficient estimates the degree of association of these components with yield.

In case of more variables in correlation studies, path analysis permits the partitioning of the correlation coefficient into components of direct and indirect causes of association. Path analysis is a generalization of multiple regression that allows one to estimate the strength and sign of directional relationships for complicated causal schemes with multiple dependent variables (Wright, 1920; Li, 1975). This analysis provides an efficient tool in finding out direct and indirect contributions of different contributing characters towards yield. Selection will be more effective when the simultaneous improvement of the component characters is occurred.

Yield is a quantitative character. It by itself is probably not an adequate criterion of economic worth. It is associated with other component characters which are influenced to varying degree by the fluctuations in the environmental conditions (Chaugale, 1967). For this reason, selection based on that premise could easily lead to develop unsatisfactory plant type (Robinson *et al.*, 1951). So, a complete satisfactory criterion based on discriminant function selection would be more desirable when a combination of two or more characters with yield is studied in a selection index. The characters that show high positive genotypic correlation with yield may serve as basis for selection (Punia *et al.*, 1982). The use of selection index technique would serve a two-fold purpose: (1) to bring about the genetic progress simultaneously in several characters and (2) to improve the yield through selection for relatively more heritable auxiliary characters.

The technique of discriminant function analysis was first evolved by Fisher (1936) and adopted for plant selection by Smith (1936). Later on different workers constructed selection indices for different crops, such as Robinson *et al.* (1951) on corn; Paroda and Joshi (1970) on wheat; Joarder *et al.* (1978) and Samad (1991) on rapeseed and Husain (1997) on chilli etc.

This part of investigation deals with characters association, path-coefficient and construction of suitable selection index using several yield and yield contributing characters from 15 crossing materials in lentil.

REVIEW OF LITERATURE

The correlation coefficient (r) gives the measure of relationship between traits. It provides the degree to which various characters are associated with productivity. It is the result of direct and indirect effects of a number of plant characters. Selection based on these characters rather than seed yield would be more effective. Robinson *et al.* (1951) constructed a number of selection indices on corn. They reported that results showing 14% more expected genetic progress in yield when selection is based entirely on ears per plant compared with selecting for yield alone. They suggested that since yield is a complex character and highly influenced by environmental variations, related characters with high heritability, when properly weighted, may well serve as better indicators of the genetic yield potentialities of a progeny.

Nandan and Pandya (1980) worked on forty nine pure strains of lentil (*Lens culinaris* Medic.) emanating from different sources. These were grown and genotypic and phenotypic correlation and path analysis were done for yield and yield components. Correlation and path studies indicated that number of pods per plant and number of branches per plant have larger effect on grain yield than any other component. The efficiency of index selection over straight selection for grain yield was as high as 22% revealed by the result.

Sharaan *et al.* (2003) worked on eighteen lentil genotypes of diverse origin (including Sinai-1 as check variety) and these were evaluated in two locations differing mainly in soil, water supply and climatic conditions. The climatic conditions were Fayoum (sandy loam soil and surface irrigation) and Maryout (calcareous soil depending on rainfall). During the two experimentation seasons (2000/2001 and 2001/2002), using a randomized complete block design with three replicates, the genotypes were tested for variation, performance and suitability for growing under these stress and control (non stress) environments. Significant genotypic differences were detected for all recorded traits of each season and for combined data over seasons at both locations, which might due to their different genetic background. Combined data revealed that season fluctuations, especially at Maryout, had marked effect on performance of the tested lentil genotypes and mean performance of all traits except number of branches per plant, number of seeds per pod and seed protein content were higher under non-stressed (at Fayoum) than under stressed conditions (at Maryout). Heritability estimates were the highest in seed protein content (96.75%) at Fayoum, number of pods/plant (83.8%) at Maryout and days to 50% flowering (>93%) at both locations and the other traits showed moderate (at Fayoum) to high (at Maryout) estimates. Minor discrepancies between phenotypic and genotypic coefficients of variability were observed. They suggested that the variation due to genetic causes in most studied traits provided a chance for improving these materials by selection. In their study, the tested genotypes were varied in their interaction with the prevailing environmental influences and exhibited different responses. The Argentinean type (no.17) produced the highest yields, 688.1 and 302.3 kg/Fed. at Fayoum and Maryout, respectively and these genotypes followed by no. 16 and 15 as well as no. 5 and 14 (for non-stress) and followed by no. 16, 7 and 8, which were recommended for growing under environmental stress conditions.

Kakde *et al.* (2005) conducted a study, which was carried out in Raipur, Madhya Pradesh, India during rabi 2000-2001 with 25 genotypes of lentil grown under environments: (i) without fertilizer application (E1), with application of recommended dose of NPK of 20:50:20 kg/ha (E2), and with 200% (40:100:40 kg/ha) of the RDF (E3). Characters studied by them were days to 50% flowering, days to maturity, plant height, branches per plant, pods per plant, seeds per plant, 100 seed weight, biological yield, harvest index and seed yield per plant. In their study, correlation analysis revealed that seed yield per plant correlated positively with harvest index in E1 and it would lead to the development of high yielding genotypes such as KLB-321, IPL-134 and LH-97, whereas in E2 and E3 seed yield per plant showed positive correlation with harvest index, biological yield, 100 seed weight and seeds per plant. However, in E1 and E2, seed yield per plant showed negative correlation with plant height. In E3, seed yield per plant was found to be correlated negatively with pods per plant. It leaded to the development of high yielding genotypes such as KLB-148, IPL-133, IPL-125 and L-4076. This type of relationship was further confirmed from path analysis, where harvest index and biological yield showed consistent relationship with seed yield in all the 3 environments. However, it was shown that days to maturity and pods per plant had direct contribution towards seed yield per plant in E1 and E2, whereas days to maturity behaved similarly in E2 only.

A study was conducted to work out the phenotypic and genotypic variance, heritability, genetic advance, correlation coefficients and path analysis for yield and yield contributing traits of wheat (*Triticum aestivum* L.) by Singh and Chaudhary (2006). The results revealed that harvest index and biological yield per meter had direct positive effect both at genotypic and phenotypic level across the entire environment. Higher heritability was found for plant height and its components in their study. The heritability was generally found lower under moisture stress conditions. Plant height, peduncle length and seedling dry weight showed positive correlation with grain yield at genotypic level revealed by their results. They suggested that these traits should be given emphasis while selecting high yielding wheat genotypes under moisture stress conditions.

Thirty one advance lines including six varieties of pea were studied for genetic variability, heritability, genetic advance and character association for seed yield per plant and related attributes by Singh and Singh (2006). The maximum variability was observed by them for seed yield per plant followed by pods per plant, plant height, branches per plant and 100 seed weight. Heritability estimates were found to be high for all characters except days to flower and pod length in broad sense and high expected genetic advance coupled with high heritability estimates were predicted for seed yield per plant, pods per plant and plant height in the study indicating least influence by the environmental variation. Seed yield per plant had significant and positive association with pods per plant, plant height, harvest index and grains per pod.

An experiment was conducted at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad during the years 2006 and 2007 with the objectives: to study the inheritance of seed yield and related traits in both hybridized (F_6) and mutated (M_6) populations of lentil and to determine the best selection criterion for the improvement of seed yield by Ashraf *et al.* (2008). They computed different genetic parameters (variances, heritabilities, genetic gains and correlations) to study the inheritance pattern and interrelationships of different traits. High heritability was observed for days to flower (97.40%), plant height (90.80%), pods per plant (86.20%), hundred seed weight (83.50%) and seed yield per plant (91.80%) in F_6 and for days to flower (96.9%), days to mature (91.8%), hundred seed weight (89.0%) and seed yield per plant (94.0%) in M_6 generation. High heritability coupled with moderate to high genetic advance was noted for plant height (90.8%, 16.29) pods per plant (86.20%, 25.53) hundred seed weight (83.50%, 35.67) and seed yield per plant (91.80%, 35.84) in F_6 generation and for days to flower (96.9%, 25.08), hundred seed weight (89.0%, 25.56) and seed yield per plant (94.0%, 37.01) in M_6 generation. The traits mentioned were found to be under the control of additive genes in their experiment. It was revealed that seed yield had positive and significant correlation with pods per plant in M_6 and with seed weight in both generations. They concluded that seed weight and pods per plant might be used as selection criterion in both hybridized and mutated populations for the improvement of seed yield.

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

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

An experiment was carried out by Karadavut (2009) to investigate relationships between yield and yield components by using a correlation and path coefficient analysis. Path coefficient analysis was done in a population of 24 small seeded lentil varieties (*Lens culinaris* Medic.) and a control varieties, named 'Kışlık kırmızı51'. Biological yield and harvest index had significant direct effect (0.6969 and 0.4947, respectively) on seed yield revealed by the result. According to the results, biological yield and harvest index should be considered in the breeding programmes to increase yield.

Azizi-Chakherchaman *et al.* (2009) conducted an experiment to study relationships between grain yield with yield components, some physiological characters and determine the most effective characters on grain yield of 11 lentil varieties, one advanced line and one selected land race genotype from Ardabil region local population under dry farming conditions in Agricultural and Natural Resources

Research Station of Ardabil. The treatments were arranged in a randomized complete block design with 3 replications. Results revealed that significant variation among studied genotypes for all measured characters was present. Genotypes ILL 8095, ILL 9893 and ILL 6031 produced higher grain yield observed by them. Path analysis of characters revealed that pod numbers per plant and 100 grain weight were the most important effective components on grain yield with direct effect of 2.055 and 1.182, respectively. On the other hand, positive direct effect of harvest index and biological yield on grain yield were non significant. The result showed that the highest positive indirect effects of these traits on yield occurred through number of full pods and 100 grain weight. Direct effects of total pod numbers per plant, lateral branch numbers per plant and the days to maturity on yield were negative. Results of their investigation indicated that characters namely full pod numbers, 100 grain weight, harvest index, number of grains per pod, early flowering and relative water content of leaves can be introduced as selection indices for improving lentil grain yield in dry farming conditions.

Samad *et al.* (2010) conducted an experiment which was carried out in Rabi season (November-March) of 2008-09 at the experimental farm of Bangladesh Institute of Nuclear Agriculture, Mymensingh ($24^{0}75'$ N latitude and $90^{0}50'$ E longitude) to investigate variability and correlation for morpho-physiological, yield attributes and yield in 16 lentil mutants/cultivar. High yielding genotypes, in general, showed taller plant, higher number branches per plant, greater leaf area index (LAI), total dry mass (TDM) per plant and absolute growth rate (AGR) than in the low yielding ones. In terms of seed yield, two mutants, LM-31 and LM-44 produced higher seed yield attributed for higher number of pods per plant and bolder seed sizes. In contrast, LM-135 and LM-201 produced lower seed yield due to production of fewer pods and smaller seed sizes. It was revealed that seed yield and pod number had highly positive and significant correlation with branch number and TDM, and TDM depends on branch number, LAI and AGR indicating yield could be increased by increasing dry matter production through increased LAI and AGR. They suggested that these traits could be used for the improvement of seed yield resulting in the evolution of high yielding varieties of lentil.

The genetic parameters, character association and path coefficient analysis between yield and yield contributing characters of 25 lentil genotypes were studied during 2007 – 2008 by Tyagi and Khan (2010) at Kisan (PG) College, Simbhaoil. The genotypes exhibited a wide range of variability for all the traits studied by them. High heritability accompained by moderate to high GCV and genetic gain were observed for number of pods per plant, number of branches per plant, 100 seed weight, seed yield per plant and harvest index in their study. Correlation studies indicated that number of pods per plant, biological yield and harvest index were positively and significantly correlated with seed yield at both phenotypic and genotypic levels. The path coefficient analysis indicated that harvest index, biological yield and number of pods per plant exhibited maximum and positive direct effect on seed yield.

Gill *et al.* (2010) worked on sixty four bold seeded lines of lentil acquired from the International Centre for Agricultural Research in the Dry Areas (ICARDA), Syria. These lines were evaluated for yield and yield contributing traits under late-sown conditions. Sufficient variability existed in the material under study for all the traits in their experiment. High heritability values were recorded for days to flowering, days to maturity and grain yield. However, economic traits viz., plant height and biological and seed yield showed moderate heritability coupled with high genetic advance. Grain yield showed highly significant positive correlation with biological yield, harvest index, number of pods per plant and plant height in their study. However, days to maturity was negatively correlated to grain yield revealed by the experiment. Biological yield exerted maximum direct effect on grain yield followed by harvest index, days to flowering and days to maturity in this experiment. It was revealed that biological yield, harvest index, number of pods per plant, plant height and days to flowering were identified as important yield components and these should be considered for indirect selection for improving seed yield in lentil under late-sown conditions.

Kotal *et al.* (2010) worked on genetic variability and correlation of different contributing characters associated with grain yield per plant in wheat. The experiment was conducted with fourteen genotypes grown in randomized block design with three replications and evaluated for ten characters. Highly significant differences and adequate genetic variability were observed among the genotypes for all the ten selected characters under study. It was found that number of effective tillers per plant and grain yield per plant were characterized by high GCV, high heritability and high genetic advance and would be effective for selection. Correlation studies and path coefficient analysis revealed that number of effective tillers per plant, number of spikelet per panicle, number of grains per panicle and harvest index were important for improving grain yield per plant as they had positive direct effects on yield and these traits were also significantly and positively correlated with grain yield per plant. They suggested that for increasing grain yield per plant a wheat genotype should have more number of effective tillers per plant, more number of spikelet per panicle, more number of grains per panicle and high harvest index value because these characters were positively associated with grain yield and resemble high estimates of heritability along with high genetic advance. The importance of large panicle length and more 1000 grain weight could not be undermined for yield improvement also noted by them.

A field experiment was conducted with 30 fine rice genotypes for correlation and discriminant function analysis of some selected characters by Akter *et al.* (2010). They observed a remarkable variation in plant characters and yield performance among the fine rice. Genotypic correlation coefficients indicated a fairly strong inherent relationship among the characters. A total of the 31 selection indices along with genetic worths and relative efficiencies over straight selection were estimated and among the five single character selection indices, grain yield offered maximum genetic worth (12.05). The two characters combination did a substantial gain of 171.45%, which was observed when effective tillers per hill were selected together with 1000-grain weight. It was shown that the index I_{245} accounted a profitable efficiency (217.18%) as compared to other three character functions studied and the four character index I_{1245} appeared to be highly beneficial over straight selection. However, they suggested that I_{12345} might be adopted while attention of a breeder is solely engaged for increasing grain yield in fine rice.

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

Saleh (2011) conducted an experiment with seven parents of bread wheat namedly, Giza 168 (P_1), Cham 6 (P_2), Line 1 (P_3), Line 2 (P_4), Sakha 94 (P_5), IB 18 (P_6) and Maryout 5 (P_7) which were crossed in 2008-2009 season in a half diallel pattern. In 2009-2010 season, the 7 parents and their 21 F_1 crosses were grown under two different water regimes, i.e. normal irrigation (plants gave 5 irrigations during growth season) and water stress (plants gave 3 irrigations where the 2nd and 4th irrigations were prevented during vegetative and anthesis stages, respectively) in his experiment. Performance, phenotypic correlation coefficient and path coefficient were evaluated for grain yield per plant and its contributors under target environments. The results revealed that wheat genotypes greatly differed in there responses under both irrigation treatments for the studied traits. The results showed that drought caused great reduction in grain yield and its contributors, i.e. flag leaf area, plant height, spike length, number of spikes per plant, number of spikelets per spike, number of kernels per spike and 1000 kernel weight as well as days to heading and relative water content. The genotypes P_2, P_3, P_4, P_7, $P_1 \times P_4$, $P_2 \times P_7$, $P_4 \times P_7$ and $P_6 \times P_7$ gave the highest values for the most traits under both water regimes and at the same time, the parents P_2, P_6, P_1 and P_3 and the crosses, $P_1 \times P_2$, $P_1 \times P_4$, $P_1 \times P_6$, $P_2 \times P_3$, $P_2 \times P_5$, $P_3 \times P_6$, $P_4 \times P_6$, $P_4 \times P_7$ and $P_5 \times P_7$ were the best drought tolerant according to their drought susceptibility index. Significant and positive phenotypic correlation coefficients were found between grain yield per plant and each of flag leaf area, relative water content, number of kernels per spike, 1000 kernel weight and number of spikes per plant under the two levels of irrigations in his experiment. Results of path coefficient analysis illustrated that flag leaf area, relative water content under both water regimes followed by number of spikes per plant under drought treatment proved to be the major contributors in grain yield variation and these traits should be considered as selection criteria in wheat breeding programmes for yield improvement under the target treatments.

Twenty three promising durum wheat (*Triticum turgidum var. durum*) genotypes were tested by Muhe (2011) in randomized complete block design with three replications. The objective of his experiment was to construct efficient selection indices that could lead to high genetic advance for grain yield. The result indicated that all of the selection indices made up of a single trait were inefficient over direct selection for grain yield at both locations except selection index containing biomass yield per plot which was 17.44% efficient at Ineway. He observed that the relative efficiencies of selection indices constructed in combinations of two or more traits were ranged from 8.89% to 22.27% and 10.64% to 156.47% at Ineway and Keyit, respectively. In his experiment, it was observed that an index composed of grain yield per plot, number of grains per spike and number of grains per spikelet was the most efficient (22.27%) at Ineway and the most efficient (156.47%) selection index at Keyit, which was constructed using plant height and biomass yield per plot. Direct selection for grain yield gave high genetic advance (44.27%) at Ineway than at Keyit (19.55%). The use of selection index improved genetic advance over direct selection for grain yield in both study areas. He suggested that construction and exploration of selection index in practical plant breeding was, therefore, important in wheat breeding programmes.

Barghi *et al.* (2012) studied the evaluation of relationship between grain yield and yield components in lentil under end season heat condition. Their experiment was conducted as a randomized complete block design with three replications under two conditions (planting date) at research station of Ardabil Azad University on May, 2009. In their experiment, first planting date was on 12 May and second was delayed planting time on 3 June in which the lentil genotypes were encountered with heat stress in the reproductive stage and grain-filling period. Data was collected on plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of unfilled pod per plants, 100 seed weight, biomass per unit area and seed yield. Results of their experiment revealed that under both conditions, significant affirmative correlation and direct effect between seed yield and number of filled pods per plant and 100 seeds weight were present.

Two hundred forty five genotypes of lentils were evaluated by Singh *et al.* (2012) for seed yield and its quality traits during 2009–2010. Significant genotypic differences were observed for all the quality traits studied, indicating considerable amount of variation among genotypes in their experiment. PCV was greater than GCV for all the characters. High GCV was observed for seed yield per plant, 100 seed weight, number of pods per plant, biological yield and harvest index. Heritability estimates were high (>80%) for all the characters except number of primary branches and genetic advance were high for seed yield per plant, 100-seed weight, number of pods per plant and biological yield. In their experiment, correlation studies indicated that most of the yield contributing characters were positively and significantly correlated at both phenotypic and genotypic levels and path analysis revealed direct effects of biological yield and harvest index on seed yield. They concluded that these characters expect special attention in formulating selection strategy in lentils for developing high yielding varieties.

MATERIALS AND METHODS

In this part, F_1 materials of half diallel crosses described in part I having yield contributing characters viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), pod weight per plant (PdWPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW).

Techniques of the analyses of data

Techniques of analyses done for the recorded data are described as follows:

1. *Character association*

For the purpose of correlation coefficient, the analysis of both variance and covariance are required (Miller *et al.*, 1958). Therefore, variances and covariances at phenotypic and genotypic level were calculated. These were measured as follows:

a) *Analysis of variation*

Variances due to different sources such as treatments where crosses including parents were involved, replications and error were calculated.

Table 63: Analysis of variance

Sources	d.f.	SS	MS	EMS	F
Treatments	20	SS_1	$SS_1/df = MS_1$	$\sigma^2g+r\,\sigma^2e$	$MS_1/\ MS_3$
Replications	1	SS_2	$SS_2/df = MS_2$		MS_2/MS_3
Error	20	SS_3	$SS_3/df = MS_3$	σ^2e	
Total	41				

Where,

MS_1= Mean square due to treatments

MS_2= Mean square due to replications

MS_3= Mean square due to error

Component of variation: The components of variation were phenotypic (σ^2p), genotypic (σ^2g) and error (σ^2e). These were measured as follows:

$$\sigma^2g = (MS_1\text{-}MS_3)/r$$

and

$$\sigma^2p = \sigma^2g + \sigma^2e.$$

b) Analysis of covariation

Covariances were calculated between all possible pairs of characters. The following formula was followed:

$$\text{Cov.} = \sum_{i=1}^{n} x_i y_i - \left(\sum_{i=1}^{n} x_i\right) \times \left(\sum_{i=1}^{n} y_i\right) / n$$

where,

Cov. = Covariance,

$\sum_{1=1}^{n} x_i y_i$ = Sum of x and y,

$\sum_{1=1}^{n} x_i$ =Grand total of x,

$\sum_{1=1}^{n} y_i$ =Grand total of y,

n = the total number of observations,

$\sum$ = Summation,

n-1 = degrees of freedom and

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

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

Table 64: Analysis of Covariance

Sources	d.f.	SS	MS	EMS	F
Treatments	20	SS_1	$SS_1/df = MCP_1$	$\sigma gigj + r\ \sigma eiej$	$MS_1/\ MS_3$
Replications	1	SS_2	$SS_2/df = MCP_2$	$\sigma rirj + c\ \sigma eiej$	MS_2/MS_3
Error	20	SS_3	$SS_3/df = MCP_3$	$\sigma eiej$	
Total	41				

where,

MCP_1= Mean square due to treatments,

MCP_2= Mean square due to replications,

and

MCP_3= Mean square due to error.

Component of covariation: The components of covariation were phenotypic ($\sigma pipj$), genotypic ($\sigma gigj$) and error ($\sigma eiej$). These were measured as follows:

$$\Sigma g_ig_j = (MCP_1 - MCP_3)/r$$

and

$$\sigma pipj = \sigma gigj + \sigma eiej.$$

c) Correlation coefficient

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

$$r_p = \sigma p_1p_2/[\ \sigma^2 p_{11} \times \sigma^2 p_{22}]^{1/2}$$

and

$$r_g = \sigma g_1g_2/[\ \sigma^2 g_{11} \times \sigma^2 g_{22}]^{1/2}$$

where,

σp_1p_2 and σg_1g_2 represent phenotypic and genotypic covariance of character 1 and 2.

The $\sigma^2 p_{11}$ and $\sigma^2 g_{11}$ represent phenotypic and genotypic variance of character 1 and

$\sigma^2 p_{22}$ and $\sigma^2 g_{22}$ represent phenotypic and genotypic variance of character 2.

2. Path coefficient

The path coefficient analysis was carried out using Wright's (1921 and 1923) formula as illustrated by Dewey and Lu (1959). The path coefficient analysis was done at both phenotypic and genotypic levels by solving the simultaneous equation using matrix algebra.

The form of equation is as follows:

$r_{xy} = p_{xy}+r_{x2}p_{2y}+r_{x3}p_{3y}+\ldots\ldots\ldots\ldots\ldots\ldots r_{xn}p_{ny}$

where, the terms like

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

p_{xy} = Path coefficient between the same component character and yield and

$r_{x2}, r_{x3}\ldots\ldots\ldots\ldots r_{xn}$ = represent correlation coefficient between that character and each of the other yield component in turn.

The above equation was written in a matrix form as:

$$\begin{array}{cccc}
A & & B & & C \\
\begin{pmatrix} r_{1y} \\ r_{2y} \\ r_{3y} \\ r_{iy} \end{pmatrix} & = & \begin{pmatrix} r_{11} & r_{12} & r_{13} & r_{1]} \\ r_{21} & r_{22} & r_{23} & r_{2]} \\ r_{31} & r_{32} & r_{33} & r_{3]} \\ r_{11} & r_{12} & r_{13} & r_{4]} \end{pmatrix} & \times & \begin{pmatrix} p_{1y} \\ p_{2y} \\ p_{3y} \\ p_{iy} \end{pmatrix}
\end{array}$$

when $A = B \times C$; then $C = B^{-1} A$

where,

P_{iy} = direct effect of a particular character I on the dependent trait y (seed weight per plant)

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

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

where,

$i= 1 \ldots\ldots. n$,

$j = 1, \ldots\ldots. n$,

$p_{iy} = p_{1y} \ldots p_{ny}$ and

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

3. Selection index

The coefficients, $b_1, b_2 \ldots\ldots\ldots\ldots b_n$ used in the discriminant function technique were obtained from the genotypic and phenotypic variances and covariances arranged in the matrix form shown as follows:

$$\begin{array}{ccccc} X & b & & G & a \\ \begin{pmatrix} X_{11} & X_{12} & X_{13} & X_{1]} \\ X_{21} & X_{22} & X_{23} & X_{2]} \\ X_{31} & X_{32} & X_{33} & X_{3]} \\ X_{11} & X_{12} & X_{13} & X_{4]} \end{pmatrix} & \begin{pmatrix} b_1 \\ b_2 \\ b_3 \\ b_n \end{pmatrix} & = & \begin{pmatrix} G_{11} & G_{12} & G_{13} & G_{1]} \\ G_{21} & G_{22} & G_{23} & G_{2]} \\ G_{31} & G_{32} & G_{33} & G_{3]} \\ G_{11} & G_{12} & G_{13} & G_{4]} \end{pmatrix} & \begin{pmatrix} a_1 \\ a_2 \\ a_3 \\ a_n \end{pmatrix} \end{array}$$

The solution of these matrices gave the estimates of 'b' values in the following manner (Singh and Chaudhary, 1976).

$b = X^{-1} G_n$

Where 'b' is the column vector, 'X^{-1}' is the inverse of phenotypic variance and covariance matrix. 'G' is the genotypic variance and covariance matrix and 'a' is the column vector for economic weights.

Assuming that all the characters are economically equally Y important i.e., $a_1=a_2=a_3=a_n=1$.

The values obtained for $b_1, b_2 \ldots\ldots b_n$ were used in discriminant function selection technique. The phenotypic and genotypic variances and covariances as obtained were used for constructing the discriminant functions using different character combinations according to the method as developed by Smith (1936). Seed weight per plant (SWPP) was also included as one of the independent characters as suggested by Robinson *et al.* (1951). The expected genetic advance from straight selection {GA (S)} and from discriminant function {GA (D)} was calculated as follows:

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

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

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

In this analysis,

g_{yy} and t_{yy} = the genotypic and phenotypic variances of character,

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

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

The expected gain from the discriminant function over straight selection was calculated for all the functions followsing the formula given below:

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

RESULTS

The present investigation deals with character association and construction of selection index of yield and yield contributing characters in lentil. Nine quantitative characters as used in part I were namedly days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), pod weight per plant (PdWPP), seed weight per plant (SWPP), individual plant weight (IPlW) and root weight (RW) were studied in this investigation to obtain the results which are described under the following sub-heads.

1. Character association:

a) Analysis of variances

Results of the analysis of variance for nine characters done separately are shown in Table 8, 9, 10, 11, 12, 15, 17, 18 and 19. These results were used for the estimation of components of variations as follows:

Components of variation

Results of the estimates of genotypic (σ^2g) and phenotypic (σ^2p) components of variation for all the characters are presented in the Table 65. For all of the characters, the phenotypic component of variation was higher than the genotypic component of variation. The phenotypic component of variation was the joint product of σ^2g and σ^2e. The highest values of σ^2g and σ^2p were recorded for CAMF. The lowest values of σ^2g and σ^2p were recorded for RW.

b) Analysis of covariation

Analysis of covariances for all possible pairs of characters were measured separately and shown in the Appendix 1. Item 'Treatment' was significant when tested against error (E) for few pairs of characters. The replication item was significant for few pairs of characters.

Components of covariation

The components of covariance for all possible pairs of characters, genotypic (σgigj) and phenotypic (σpipj) components were calculated and shown in the Table 66.

These components of total thirty six pairs of characters were measured. The pairs of any character with NSBFF except PHFF and with CAMF except NPBFF showed the maximum genotypic and phenotypic components of covariations. Among the thirty six pairs of characters, PHFF × CAMF showed the highest genotypic and phenotypic covariances (Table 66). The pairs of CAMF × PdWPP, CAMF × IPlW, CAMF × RW and CAMF × SWPP also showed noticeable genotypic and phenotypic covariances. For the purposes of correlation coefficient (r) and path coeeficient analyses, these covariances were measured.

c) Correlation coefficient (r)

The correlation coefficient (r) between pairs of characters was analyzed separately. There were 36 pairs of characters. The results are shown in the Table 67 and 68.

Genotypic correlation co-efficient (r_g)

The highest significant and positive genotypic correlation co-efficient was recorded for NSBFF with PdWPP (Table 67). DF with the association of RW exhibited the lowest but significant genotypic correlation co-efficient. Other pairs of characters showed significant genotypic correlation co-efficient except PHFF × NSBFF, PHFF × RW and NPBFF × RW and NPBFF × SWPP. The highest negative significant value of correlation co-efficient was obtained by DF × PHFF combination.

Phenotypic correlation co-efficient (r_p)

The highest positive and significant phenotypic correlation co-efficient value was obtained by the combination of PdWPP × SWPP (0.984186) followed by PdWPP × RW (0.831182), RW × SWPP (0.801884), PHFF × CAMF (0.75883) and CAMF × SWPP (0.74039). The highest negative value was obtained by DF × IPlW (-0.20752). All pairs with SWPP showed significant phenotypic correlation co-efficient except with DF and NPBFF (Table 68).

2. *Path coefficient*

A path-coefficient analysis that measures the direct as well as the indirect effects of one variable through another on the end product was worked out for eight quantitative characters at both genotypic and phenotypic levels. The direct and indirect effects of the component characters on seed weight per plant (SWPP) were estimated separately for each of the contributing characters.

Path-coefficient at genotypic level

Results of the path-coefficient analysis at genotypic level are presented in the Table 69. It was observed that PdWPP had the highest positive direct effect (0.687275) on SWPP followed by RW (0.2574), PHFF (0.166225) and NPBFF (0.125647). DF, NSBFF, CAMF and IPlW had direct negative effect on SWPP. The highest negative direct effect was obtained by DF on SWPP.

DF had the highest negative direct effect at genotypic level. The character via NPBFF, CAMF and IPlW showed positive indirect effects, while through rest of the characters it showed negative indirect effects on SWPP.

PHFF had positive direct effect of 0.166225. This character via DF, NSBFF, PdWPP and RW showed positive indirect effects and via rest of all characters showed negative indirect effects on SWPP.

The character, NPBFF had positive direct effect on SWPP. The indirect effects of this character via CAMF, PdWPP and IPlW were found to be positive, while negative indirect effects were found via rest of the characters.

NSBFF had negative direct effect on SWPP. It exhibited positive indirect effect through NPBFF, PdWPP and RW. NSBFF through rest of the characters showed negative indirect effect.

The character, CAMF showed negative direct effect (-0.24166). The indirect effect of this character via DF, PHFF, PdWPP and RW was found to be positive. The total effect of this character was 1.203651.

The highest positive direct effect was observed for the character, PdWPP. This character via DF, PHFF, NPBFF and RW possessed positive indirect effects. This trait showed negative indirect effects on SWPP via rest of the characters.

IPlW had negative direct effect on SWPP. It showed positive indirect effects via DF, PHFF, NPBFF and RW. This trait showed negative indirect effects on SWPP via rest of the characters.

RW had positive direct effect on SWPP. This character via DF, PHFF and PdWPP showed positive indirect effects on SWPP.

Path-coefficient at phenotypic level

Results of the path coefficient analysis at phenotypic level are presented in the Table 70. It was observed that PdWPP had the highest positive direct effect (1.05769) on SWPP at phenotypic level.

DF had negative direct effect on SWPP. It showed negative indirect effects via PHFF, NSBFF, CAMF and RW on SWPP. This character through rest of the characters exhibited positive indirect effects.

PHFF showed positive direct effect on SWPP. It had positive indirect effects through DF, NPBFF, CAMF and PdWPP. Negative indirect effects were present via rest of the characters for this character.

NPBFF had positive direct effect. It showed positive indirect effects through the characters viz., PHFF, CAMF and PdWPP. Negative indirect effects were showed through rest of the characters by NPBFF.

NSBFF had negative direct effect on SWPP. It showed positive indirect effects through PHFF, NPBFF, CAMF and PdWPP. Negative indirect effects were showed by this trait via rest of the characters.

The character, CAMF showed positive direct effect. This character via DF, PHFF, NPBFF and PdWPP showed positive indirect effects. It showed indirect negative effects through rest of the characters on SWPP.

PdWPP had the highest positive direct effect on SWPP. It showed indirect positive effects through PHFF, NPBFF and CAMF. Negative indirect effects were showed by this character via rest of the characters.

IPlW had negative direct effect. It showed positive indirect effects on SWPP through DF, PHFF, NPBFF, CAMF and PdWPP. Negative indirect effects were showed by this character via rest of the characters.

RW had negative direct effect. It showed positive indirect effects on SWPP through PHFF, NPBFF, CAMF and PdWPP. Negative indirect effects were showed via rest of the characters by RW.

3. *Selection index*

Results obtained for different indices contributing seed weight per plant and its components with expected gain in percent over straight selection are presented in the Table 71. The maximum expected genetic gain of 4603.196% was found when NPBFF and RW were included in the discriminant function. It was followed by 4556.836% when RW and SWPP were included in the discriminant function.

In the discriminant function analysis of the presnt study, when individual character was considered separately, RW (8) showed the highest expected gain of 1272.823% followed by SWPP (9) of 1054.986% and IPlW (7) of 618.7894%.

The Table 71 revealed that any character associated with RW (8) and SWPP (9) gave the positive high values.

Considering two characters association in discriminant function, NPBFF (3) and RW (8) showed the highest expected genetic gain of 4603.196%. On the other hand, DF (1) in association with RW (8) gave the maximum expected genetic gain of 298.9399% in this series. PHFF (2) associated with RW (8) gave the maximum expected genetic gain of 502.2892% in this series. NSBFF (4) in association with RW (8) gave the maximum expected genetic gain of 427.3018% in this series. IPlW (7) associated with RW (8) showed the maximum expected genetic gain of 1923.761% and RW (8) in association with SWPP (9) had the maximum expected genetic gain of 4556.836%.

In the present study, three characters when associated in different combinations, NPBFF (3), RW (8) and SWPP (9) showed the highest expected genetic gain of 3083.323%. It was found that DF (1) in association with RW (8) and SWPP (9) gave 373.5102%; PHFF (2) in association with RW (8) and SWPP (9) gave 705.441% and NSBFF (4) in association with RW (8) and SWPP (9) showed 494.8328% gain. The PdWPP (6) in association with RW (8) and SWPP (9) exhibited 2020.246% gain and IPlW (7) in association with RW (8) and SWPP (9) had 1820.893% gain.

Considering four characters association in discriminant function, the maximum genetic gain was recorded as 1522.762% for the combination of NPBFF (3), IPlW (7), RW (8) and SWPP (9). DF in association with NPBFF (3), RW (8) and SWPP (9) gave maximum value of 354.7259% in this series. PHFF (2) in association with NPBFF (3), RW (8) and SWPP (9) gave 640.8198%; NPBFF (3) in association with IPlW (7), RW (8) and SWPP (9) gave 1522.762%. NSBFF (4) in association with IPlW (7), RW (8) and SWPP (9) gave 426.5144%; PdWPP (6) in association with IPlW (7) and RW (8) and SWPP (9) gave 1035.431%. All were the highest values for the respective characters when associated with the other characters in four character combinations.

Considering five characters association in discriminant function, the maximum genetic gain was recorded as 884.1068% for the combination of NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), IPlW (7), RW (8) and SWPP (9) gave the highest value of 314.3404% and PHFF (2) in association with NPBFF (3), IPlW (7), RW (8) and SWPP (9) gave the maximum value of this series of 513.1741%. NSBFF (4) in association with PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the highest value of 307.0693% of this series.

In the present study, when six characters associated in different combinations, the maximum genetic gain was recorded of 291.4154% for NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the maximum value of 210.4544% in this series. PHFF (2) in association with NPBFF (3), PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the highest value of 267.5051% in this series.

Considering seven characters association in discriminant function, the maximum genetic gain was recorded of 164.2183% for the combination of PHFF (2), NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9). DF (1) in association with NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9) gave the maximum value of 140.0703% in this series.

Considering eight characters association in discriminant function, the maximum genetic gain was recorded of about 88.21749% for the combination of DF (1), PHFF (2), NPBFF (3), NSBFF (4), PdWPP (6), IPlW (7), RW (8) and SWPP (9).

Table 65: Results of genotypic (σ^2g) and phenotypic (σ^2p) components of variation for nine characters.

Characters	Components	
	σ^2g	σ^2p
Days to flower (DF)	3.694652	11.60683
Plant height at first flower (PHFF)	1.004899	4.814858
Number of primary branches at first flower (NPBFF)	0.061948	1.572455
Number of secondary branches at first flower (NSBFF)	2.986855	10.81044
Canopy area at maximum flower (CAMF)	8391.63	22393.76
Pod weight per plant (PdWPP)	0.082482	2.536826
Individual plant weight (IPlW)	0.190957	1.390949
Root weight (RW)	0.002021	0.006172
Seed weight per plant (SWPP)	0.097082	1.438964

Table 66: Results of genotypic (σgigj) and phenotypic (σpipj) components of covariation for nine characters.

Components	DF × PHFF	DF × PBFF	DF × SBFF	DF × CAMF	DF × PdWPP	DF × IPlW	DF × RW	DF × SWPP
σgigj	-2.60762	0.538625	1.7375	-155.222	-0.40975	-0.74038	-0.00035	-0.45886
σpipj	-0.24958	1.889921	5.033433	-48.0444	1.089017	-0.83383	0.07748	0.852121

Components	PHFF × NPBFF	PHFF × NSBFF	PHFF × CAMF	PHFF × PdWPP	PHFF × IPlW	PHFF × RW	PHFF × SWPP
σgigj	-0.6888	-0.2986	100.4104	0.364716	0.653079	0.00902	0.293677
σpipj	0.538062	2.203047	249.1724	1.12765	1.220898	0.054698	1.021904

Components	NPBFF × NSBFF	NPBFF × CAMF	NPBFF × PdWPP	NPBFF × IPlW	NPBFF × RW	NPBFF × SWPP
σgigj	0.203492	-24.1556	0.053574	-0.11164	-0.00095	-0.00043
σpipj	2.001943	14.05964	0.181847	0.290509	0.017353	0.149539

Components	NSBFF × CAMF	NSBFF × PdWPP	NSBFF × IPlW	NSBFF × RW	NSBFF × SWPP
σgigj	64.48301	1.121326	0.547115	0.057006	0.734607
σpipj	134.4806	1.868239	0.288914	0.082633	1.473221

Components	CAMF × PdWPP	CAMF × IPlW	CAMF × RW	CAMF × SWPP
σgigj	39.01017	42.97545	1.996459	34.36349
σpipj	169.44	128.3616	6.57083	132.9074

Table 66 continued

Components	PdWPP × IPlW	PdWPP × RW	PdWPP × SWPP
σgigj	0.20633	0.01958	0.09343
σpipj	1.220217	0.104005	1.880388

Components	IPlW × RW	IPlW × SWPP
σgigj	0.01549	0.193493
σpipj	0.054332	0.861371

Components	RW × SWPP
σgigj	0.01559
σpipj	0.07557

Table 67: Genotypic correlation co-efficient for quantitative characters in lentil.

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPlW	RW	SWPP
DF	1	-1.35331**	1.125864**	0.523035**	-0.88154**	-0.74225**	-0.88145**	-0.00405**	-0.76617**
PHFF		1	-2.76069**	-0.17235^{NS}	1.093438**	1.266817**	1.49086**	0.200153 ^{NS}	0.940241**
NPBFF			1	0.473071**	-1.05945**	0.749481**	-1.02645**	-0.0849 ^{NS}	-0.00554 ^{NS}
NSBFF				1	0.407301**	2.259151**	0.724442**	0.73372**	1.364202**
CAMF					1	1.482774**	1.073568**	0.48479**	1.20394**
PdWPP						1	1.64405**	1.516526**	1.044089**
IPlW							1	0.788498**	1.421111**
RW								1	1.112996**
SWPP									1

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

Table 68: Phenotypic correlation co-efficient for quantitative characters in lentil

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPIW	RW	SWPP
DF	1	-0.03339^{NS}	0.442382**	0.449351**	-0.09424^{NS}	0.200693^{NS}	-0.20752^{NS}	0.289481^{NS}	0.208506^{NS}
PHFF		1	0.195547^{NS}	0.305359^{NS}	0.75883**	0.322654*	0.471772**	0.317298*	0.388234*
NPBFF			1	0.485558**	0.074924^{NS}	0.091048^{NS}	0.196433^{NS}	0.176146^{NS}	0.099412^{NS}
NSBFF				1	0.273322^{NS}	0.356751*	0.074506^{NS}	0.319903*	0.373526*
CAMF					1	0.710898**	0.727304**	0.558912**	0.74039**
PdWPP						1	0.649585**	0.831182**	0.984186**
IPIW							1	0.586391**	0.608849**
RW								1	0.801884**
SWPP									1

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

Table 69: Path-coefficient analysis showing direct and indirect effects of yield components on seed weight per plant (SWPP) at genotypic level.

Characters	DF	PHFF	NPBFF	NSBFF	CAMF	PdWPP	IPIW	RW	Total effect
DF	**-0.37429**	-0.22495	0.141462	-0.04476	0.213029	-0.51013	0.03472	-0.00104	-0.76597
PHFF	0.50653	**0.166225**	-0.34687	0.014751	-0.26424	0.870652	-0.05872	0.051519	0.939844
NPBFF	-0.4214	-0.4589	**0.125647**	-0.04049	0.256022	0.5151	0.040431	-0.02185	-0.00544
NSBFF	-0.19577	-0.02865	0.05944	**-0.08559**	-0.09843	1.552657	-0.02854	0.18886	1.363994
CAMF	0.329953	0.181757	-0.13312	-0.03486	**-0.24166**	1.019073	-0.04229	0.124785	1.203651
PdWPP	0.277819	0.210577	0.09417	-0.19335	-0.35832	**0.687275**	-0.06476	0.390354	1.043768
IPIW	0.32992	0.247819	-0.12897	-0.062	-0.25943	1.129914	**-0.03939**	0.20296	1.420818
RW	0.001516	0.033271	-0.01067	-0.0628	-0.11715	1.04227	-0.03106	**0.2574**	1.112783

Residual effect 0.132461

N.B. : The bold values denote direct effect.

Table 70: Path-coefficient analysis showing direct and indirect effects of yield components on seed weight per plant (SWPP) at phenotypic level.

Characters	**DF**	**PHFF**	**NPBFF**	**NSBFF**	**CAMF**	**PdWPP**	**IPIW**	**RW**	**Total effect**
DF	**-0.01506**	-0.00298	0.017827	-0.01516	-0.005	0.212271	0.02941	-0.0128	0.208501
PHFF	0.000503	**0.089391**	0.00788	-0.0103	0.040253	0.341268	-0.06686	-0.01403	0.388104
NPBFF	-0.00666	0.01748	**0.040297**	-0.01639	0.003974	0.096301	-0.02784	-0.00779	0.099378
NSBFF	-0.00677	0.027296	0.019567	**-0.03375**	0.014499	0.377332	-0.01056	-0.01414	0.373479
CAMF	0.00142	0.067833	0.003019	-0.00922	**0.053047**	0.75191	-0.10307	-0.02471	0.740222
PdWPP	-0.00302	0.028842	0.003669	-0.01204	0.037711	**1.05769**	-0.09206	-0.03674	0.984047
IPIW	0.003126	0.042172	0.007916	-0.00251	0.038581	0.68706	**-0.14172**	-0.02592	0.608697
RW	-0.00436	0.028364	0.007098	-0.0108	0.029648	0.879133	-0.0831	**-0.04421**	0.801777

Residual effect 0.136646

N.B. : The bold values denote direct effect.

Table 71: Expected genetic gain in percent of seed weight per plant over straight selection from the use of various selection indices in lentil.

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
1	DF	146.4253	43	7+8	1923.761
2	PHFF	-536.038	44	7+9	1448.455
3	NPBFF	103.5193	45	8+9	4556.836
4	NSBFF	277.9674	46	1+2+3	11.74796
5	CAMF	-97.2855	47	1+2+4	57.72797
6	PdWPP	-7164.36	48	1+2+5	-95.9405
7	IPIW	618.7894	49	1+2+6	-300.622
8	RW	1272.823	50	1+2+7	32.49795
9	SWPP	1054.986	51	1+2+8	152.0978
10	1+2	15.14269	52	1+2+9	141.3354
11	1+3	135.8556	53	1+3+4	113.1008
12	1+4	118.325	54	1+3+5	-94.6213
13	1+5	-94.6196	55	1+3+6	-310.546
14	1+6	-319.878	56	1+3+7	132.7679
15	1+7	141.8594	57	1+3+8	282.0425
16	1+8	298.9399	58	1+3+9	262.0726
17	1+9	277.3222	59	1+4+5	-92.062
18	2+3	-493.082	60	1+4+6	15.19263
19	2+4	104.4199	61	1+4+7	112.0412
20	2+5	-102.286	62	1+4+8	177.6178
21	2+6	-917.632	63	1+4+9	169.0213
22	2+7	-330.538	64	1+5+6	-103.463
23	2+8	502.2892	65	1+5+7	-94.1088
24	2+9	431.6049	66	1+5+8	-91.8106
25	3+4	258.6269	67	1+5+9	-91.8708
26	3+5	-97.282	68	1+6+7	-259.671
27	3+6	-3714.07	69	1+6+8	114.8477
28	3+7	561.7619	70	1+6+9	100.4474
29	3+8	4603.196	71	1+7+8	265.0194
30	3+9	2580.477	72	1+7+9	247.5607
31	4+5	-93.409	73	1+8+9	373.5102
32	4+6	-231.491	74	2+3+4	97.41482
33	4+7	246.2488	75	2+3+5	-102.277
34	4+8	427.3018	76	2+3+6	-845.177
35	4+9	395.0003	77	2+3+7	-312.992
36	5+6	-105.927	78	2+3+8	446.8005
37	5+7	-96.3289	79	2+3+9	387.264
38	5+8	-93.1448	80	2+4+5	-94.4623
39	5+9	-93.2166	81	2+4+6	-266.592
40	6+7	-1682.62	82	2+4+7	104.2823
41	6+8	-1330.24	83	2+4+8	223.4569
42	6+9	-921.621	84	2+4+9	208.9656

Table 71 continued

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
85	2+5+6	-106.857	128	6+8+9	2020.246
86	2+5+7	-99.0752	129	7+8+9	1820.893
87	2+5+8	-94.1887	130	1+2+3+4	54.6638
88	2+5+9	-94.27	131	1+2+3+5	-95.9402
89	2+6+7	-684.754	132	1+2+3+6	-294.496
90	2+6+8	-513.258	133	1+2+3+7	28.89317
91	2+6+9	-485.186	134	1+2+3+8	144.4776
92	2+7+8	400.2911	135	1+2+3+9	134.2852
93	2+7+9	354.6596	136	1+2+4+5	-92.9015
94	2+8+9	705.441	137	1+2+4+6	-50.093
95	3+4+5	-93.4124	138	1+2+4+7	57.28958
96	3+4+6	-224.66	139	1+2+4+8	111.4285
97	3+4+7	231.0947	140	1+2+4+9	105.7605
98	3+4+8	400.9213	141	1+2+5+6	-104.877
99	3+4+9	371.5586	142	1+2+5+7	-95.2868
100	3+5+6	-105.919	143	1+2+5+8	-92.6512
101	3+5+7	-96.3278	144	1+2+5+9	-92.7157
102	3+5+8	-93.1484	145	1+2+6+7	-263.895
103	3+5+9	-93.2202	146	1+2+6+8	-7.50989
104	3+6+7	-1384.89	147	1+2+6+9	-16.3161
105	3+6+8	-847.176	148	1+2+7+8	142.3095
106	3+6+9	-696.198	149	1+2+7+9	132.9403
107	3+7+8	1502.55	150	1+2+8+9	219.8593
108	3+7+9	1187.162	151	1+3+4+5	-92.0668
109	3+8+9	3083.323	152	1+3+4+6	12.57756
110	4+5+6	-98.5093	153	1+3+4+7	107.3391
111	4+5+7	-92.9892	154	1+3+4+8	171.0296
112	4+5+8	-90.9567	155	1+3+4+9	162.8047
113	4+5+9	-91.0131	156	1+3+5+6	-103.455
114	4+6+7	-47.1861	157	1+3+5+7	-94.1113
115	4+6+8	234.5534	158	1+3+5+8	-91.8158
116	4+6+9	212.7148	159	1+3+5+9	-91.8759
117	4+7+8	367.0771	160	1+3+6+7	-253.637
118	4+7+9	342.3004	161	1+3+6+8	106.253
119	4+8+9	494.8328	162	1+3+6+9	92.79279
120	5+6+7	-105.365	163	1+3+7+8	251.4564
121	5+6+8	-97.8871	164	1+3+7+9	235.1685
122	5+6+9	-98.1104	165	1+3+8+9	354.7259
123	5+7+8	-92.7289	166	1+4+5+6	-95.1749
124	5+7+9	-92.7969	167	1+4+5+7	-91.7296
125	5+8+9	-90.7538	168	1+4+5+8	-90.0042
126	6+7+8	325.1406	169	1+4+5+9	-90.0552
127	6+7+9	195.1805	170	1+4+6+7	24.05192

Table 71 continued

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
171	1+4+6+8	105.0423	214	2+5+7+8	-93.7051
172	1+4+6+9	98.16097	215	2+5+7+9	-93.7806
173	1+4+7+8	164.8441	216	2+5+8+9	-91.5333
174	1+4+7+9	157.2189	217	2+6+7+8	146.3465
175	1+4+8+9	214.4968	218	2+6+7+9	-338.849
176	1+5+6+7	-102.452	219	2+6+8+9	338.255
177	1+5+6+8	-94.8916	220	2+7+8+9	554.7213
178	1+5+6+9	-94.9807	221	3+4+5+6	-98.5002
179	1+5+7+8	-91.4792	222	3+4+5+7	-92.993
180	1+5+7+9	-91.5374	223	3+4+5+8	-90.9628
181	1+5+8+9	-89.799	224	3+4+5+9	-91.0192
182	1+6+7+8	116.0065	225	3+4+6+7	-48.6903
183	1+6+7+9	103.7822	226	3+4+6+8	218.7383
184	1+6+8+9	245.3727	227	3+4+6+9	198.6913
185	1+7+8+9	329.4043	228	3+4+7+8	347.0194
186	2+3+4+5	-94.4643	229	3+4+7+9	324.1848
187	2+3+4+6	-260.838	230	3+4+8+9	467.3062
188	2+3+4+7	97.98835	231	3+5+6+7	-105.358
189	2+3+4+8	212.4498	232	3+5+6+8	-97.8813
190	2+3+4+9	198.8433	233	3+5+6+9	-98.1037
191	2+3+5+6	-106.848	234	3+5+7+8	-92.733
192	2+3+5+7	-99.0592	235	3+5+7+9	-92.801
193	2+3+5+8	-94.191	236	3+5+8+9	-90.7602
194	2+3+5+9	-94.2722	237	3+6+7+8	254.1386
195	2+3+6+7	-644.513	238	3+6+7+9	154.4775
196	2+3+6+8	-477.961	239	3+6+8+9	1517.018
197	2+3+6+9	-455.11	240	3+7+8+9	1522.762
198	2+3+7+8	364.9551	241	4+5+6+7	-97.1442
199	2+3+7+9	324.9316	242	4+5+6+8	-93.6337
200	2+3+8+9	640.8198	243	4+5+6+9	-93.7076
201	2+4+5+6	-103.143	244	4+5+7+8	-90.6581
202	2+4+5+7	-93.9704	245	4+5+7+9	-90.713
203	2+4+5+8	-91.729	246	4+5+8+9	-89.093
204	2+4+5+9	-91.7883	247	4+6+7+8	211.9972
205	2+4+6+7	-220.684	248	4+6+7+9	194.4161
206	2+4+6+8	81.82416	249	4+6+8+9	350.2515
207	2+4+6+9	71.53775	250	4+7+8+9	426.5144
208	2+4+7+8	203.3384	251	5+6+7+8	-96.7484
209	2+4+7+9	191.0826	252	5+6+7+9	-96.89
210	2+4+8+9	286.8375	253	5+6+8+9	-93.4416
211	2+5+6+7	-106.38	254	5+7+8+9	-90.4539
212	2+5+6+8	-102.837	255	6+7+8+9	1035.431
213	2+5+6+9	-102.984	256	1+2+3+4+5	-92.9054

Table 71 continued

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
257	1+2+3+4+6	-50.9008	300	1+3+4+8+9	207.3027
258	1+2+3+4+7	54.41699	301	1+3+5+6+7	-102.444
259	1+2+3+4+8	107.3318	302	1+3+5+6+8	-94.893
260	1+2+3+4+9	101.8601	303	1+3+5+6+9	-94.982
261	1+2+3+5+6	-95.1298	304	1+3+5+7+8	-91.4848
262	1+2+3+5+7	-95.2876	305	1+3+5+7+9	-91.5429
263	1+2+3+5+8	-92.6554	306	1+3+5+8+9	-89.8063
264	1+2+3+5+9	-92.7198	307	1+3+6+7+8	108.3648
265	1+2+3+6+7	-259.313	308	1+3+6+7+9	96.86077
266	1+2+3+6+8	-10.0451	309	1+3+6+8+9	232.2612
267	1+2+3+6+9	-18.5045	310	1+3+7+8+9	314.3404
268	1+2+3+7+8	135.6503	311	1+4+5+6+7	-94.6261
269	1+2+3+7+9	126.7342	312	1+4+5+6+8	-92.244
270	1+2+3+8+9	210.6124	313	1+4+5+6+9	-92.3049
271	1+2+4+5+6	-96.6387	314	1+4+5+7+8	-89.7485
272	1+2+4+5+7	-92.5328	315	1+4+5+7+9	-89.7984
273	1+2+4+5+8	-90.6871	316	1+4+5+8+9	-88.3523
274	1+2+4+5+9	-90.7398	317	1+4+6+7+8	100.1715
275	1+2+4+6+7	-29.7345	318	1+4+6+7+9	93.96757
276	1+2+4+6+8	48.16791	319	1+4+6+8+9	155.5127
277	1+2+4+6+9	43.54949	320	1+4+7+8+9	198.4229
278	1+2+4+7+8	105.374	321	1+5+6+7+8	-94.3562
279	1+2+4+7+9	100.2045	322	1+5+6+7+9	-94.4373
280	1+2+4+8+9	146.0919	323	1+5+6+8+9	-92.0541
281	1+2+5+6+7	-104.224	324	1+5+7+8+9	-89.5419
282	1+2+5+6+8	-96.2981	325	1+6+7+8+9	221.292
283	1+2+5+6+9	-96.4168	326	2+3+4+5+6	-103.135
284	1+2+5+7+8	-92.2848	327	2+3+4+5+7	-93.973
285	1+2+5+7+9	-92.3465	328	2+3+4+5+8	-91.7343
286	1+2+5+8+9	-90.4895	329	2+3+4+5+9	-91.7935
287	1+2+6+7+8	14.88096	330	2+3+4+6+7	-216.863
288	1+2+6+7+9	7.64501	331	2+3+4+6+8	75.93796
289	1+2+6+8+9	123.4104	332	2+3+4+6+9	66.19217
290	1+2+7+8+9	201.2728	333	2+3+4+7+8	194.0595
291	1+3+4+5+6	-95.1759	334	2+3+4+7+9	182.478
292	1+3+4+5+7	-91.7348	335	2+3+4+8+9	274.3434
293	1+3+4+5+8	-90.0112	336	2+3+5+6+7	-106.372
294	1+3+4+5+9	-90.0621	337	2+3+5+6+8	-102.829
295	1+3+4+6+7	21.41728	338	2+3+5+6+9	-102.976
296	1+3+4+6+8	100.3201	339	2+3+5+7+8	-93.7081
297	1+3+4+6+9	93.7153	340	2+3+5+7+9	-93.7835
298	1+3+4+7+8	159.0161	341	2+3+5+8+9	-91.5388
299	1+3+4+7+9	151.6967	342	2+3+6+7+8	-329.656

Table 71 continued

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
343	2+3+6+7+9	-323.785	386	1+2+3+4+6+7	-30.9141
344	2+3+6+8+9	306.0184	387	1+2+3+4+6+8	45.38071
345	2+3+7+8+9	513.1741	388	1+2+3+4+6+9	40.90789
346	2+4+5+6+7	-101.992	389	1+2+3+4+7+8	101.6341
347	2+4+5+6+8	-94.7241	390	1+2+3+4+7+9	96.63309
348	2+4+5+6+9	-94.8098	391	1+2+3+4+8+9	141.4593
349	2+4+5+7+8	-91.4045	392	1+2+3+5+6+7	-104.217
350	2+4+5+7+9	-91.4618	393	1+2+3+5+6+8	-96.2972
351	2+4+5+8+9	-89.7513	394	1+2+3+5+6+9	-96.4157
352	2+4+6+7+8	85.13121	395	1+2+3+5+7+8	-92.2894
353	2+4+6+7+9	76.12294	396	1+2+3+5+7+9	-92.3511
354	2+4+6+8+9	186.5148	397	1+2+3+5+8+9	-90.4961
355	2+4+7+8+9	258.8172	398	1+2+3+6+7+8	11.9166
356	2+5+6+7+8	-101.403	399	1+2+3+6+7+9	4.961479
357	2+5+6+7+9	-101.682	400	1+2+3+6+8+9	117.1806
358	2+5+6+8+9	-94.5306	401	1+2+3+7+8+9	193.3225
359	2+5+7+8+9	-91.2076	402	1+2+4+5+6+7	-95.8922
360	2+6+7+8+9	290.6178	403	1+2+4+5+6+8	-93.1001
361	3+4+5+6+7	-97.1412	404	1+2+4+5+6+9	-93.1658
362	3+4+5+6+8	-93.6367	405	1+2+4+5+7+8	-90.4138
363	3+4+5+6+9	-93.7106	406	1+2+4+5+7+9	-90.4652
364	3+4+5+7+8	-90.6646	407	1+2+4+5+8+9	-88.9564
365	3+4+5+7+9	-90.7194	408	1+2+4+6+7+8	48.58871
366	3+4+5+8+9	-89.101	409	1+2+4+6+7+9	44.32087
367	3+4+6+7+8	199.2414	410	1+2+4+6+8+9	96.27506
368	3+4+6+7+9	182.9172	411	1+2+4+7+8+9	137.0548
369	3+4+6+8+9	330.4197	412	1+2+5+6+7+8	-95.5911
370	3+4+7+8+9	405.3722	413	1+2+5+6+7+9	-95.691
371	3+5+6+7+8	-96.7464	414	1+2+5+6+8+9	-92.9151
372	3+5+6+7+9	-96.8877	415	1+2+5+7+8+9	-90.2148
373	3+5+6+8+9	-93.4449	416	1+2+6+7+8+9	117.2993
374	3+5+7+8+9	-90.4606	417	1+3+4+5+6+7	-94.6279
375	3+6+7+8+9	884.1068	418	1+3+4+5+6+8	-92.2487
376	4+5+6+7+8	-93.1999	419	1+3+4+5+6+9	-92.3094
377	4+5+6+7+9	-93.2695	420	1+3+4+5+7+8	-89.7557
378	4+5+6+8+9	-91.1818	421	1+3+4+5+7+9	-89.8056
379	4+5+7+8+9	-88.8544	422	1+3+4+5+8+9	-88.3609
380	4+6+7+8+9	307.0693	423	1+3+4+6+7+8	95.88723
381	5+6+7+8+9	-93.0084	424	1+3+4+6+7+9	89.91595
382	1+2+3+4+5+6	-96.6371	425	1+3+4+6+8+9	149.8188
383	1+2+3+4+5+7	-92.5371	426	1+3+4+7+8+9	192.0757
384	1+2+3+4+5+8	-90.6934	427	1+3+5+6+7+8	-94.3583
385	1+2+3+4+5+9	-90.746	428	1+3+5+6+7+9	-94.4393

Table 71 continued

SL No.	Selection indices	Expected gain	SL No.	Selection indices	Expected gain
429	1+3+5+6+8+9	-92.059	472	1+2+3+4+6+7+8	45.95555
430	1+3+5+7+8+9	-89.5494	473	1+2+3+4+6+7+9	41.81555
431	1+3+6+7+8+9	210.4544	474	1+2+3+4+6+8+9	92.6652
432	1+4+5+6+7+8	-91.9041	475	1+2+3+4+7+8+9	132.8536
433	1+4+5+6+7+9	-91.9627	476	1+2+3+5+6+7+8	-95.5914
434	1+4+5+6+8+9	-90.2043	477	1+2+3+5+6+7+9	-95.6912
435	1+4+5+7+8+9	-88.1411	478	1+2+3+5+6+8+9	-92.919
436	1+4+6+7+8+9	145.1587	479	1+2+3+5+7+8+9	-90.2216
437	1+5+6+7+8+9	-91.7133	480	1+2+3+6+7+8+9	111.7506
438	2+3+4+5+6+7	-101.983	481	1+2+4+5+6+7+8	-92.7213
439	2+3+4+5+6+8	-94.7257	482	1+2+4+5+6+7+9	-92.7839
440	2+3+4+5+6+9	-94.8113	483	1+2+4+5+6+8+9	-90.8959
441	2+3+4+5+7+8	-91.4101	484	1+2+4+5+7+8+9	-88.7343
442	2+3+4+5+7+9	-91.4673	485	1+2+4+6+7+8+9	91.5384
443	2+3+4+5+8+9	-89.7586	486	1+2+5+6+7+8+9	-92.5361
444	2+3+4+6+7+8	79.70851	487	1+3+4+5+6+7+8	-91.9091
445	2+3+4+6+7+9	71.13706	488	1+3+4+5+6+7+9	-91.9677
446	2+3+4+6+8+9	177.5972	489	1+3+4+5+6+8+9	-90.2111
447	2+3+4+7+8+9	248.3445	490	1+3+4+5+7+8+9	-88.1499
448	2+3+5+6+7+8	-101.39	491	1+3+4+6+7+8+9	140.0703
449	2+3+5+6+7+9	-101.672	492	1+3+5+6+7+8+9	-91.7185
450	2+3+5+6+8+9	-94.5325	493	1+4+5+6+7+8+9	-89.9437
451	2+3+5+7+8+9	-91.2134	494	2+3+4+5+6+7+8	-94.2122
452	2+3+6+7+8+9	267.5051	495	2+3+4+5+6+7+9	-94.2906
453	2+4+5+6+7+8	-94.2098	496	2+3+4+5+6+8+9	-91.9731
454	2+4+5+6+7+9	-94.2884	497	2+3+4+5+7+8+9	-89.5057
455	2+4+5+6+8+9	-91.9681	498	2+3+4+6+7+8+9	164.2183
456	2+4+5+7+8+9	-89.4981	499	2+3+5+6+7+8+9	-94.0224
457	2+4+6+7+8+9	171.8913	500	2+4+5+6+7+8+9	-91.6346
458	2+5+6+7+8+9	-94.0198	501	3+4+5+6+7+8+9	-90.8823
459	3+4+5+6+7+8	-93.2035	502	1+2+3+4+5+6+7+8	-92.7254
460	3+4+5+6+7+9	-93.273	503	1+2+3+4+5+6+7+9	-92.788
461	3+4+5+6+8+9	-91.1877	504	1+2+3+4+5+6+8+9	-90.9019
462	3+4+5+7+8+9	-88.8626	505	1+2+3+4+5+7+8+9	-88.7424
463	3+4+6+7+8+9	291.4154	506	1+2+3+4+6+7+8+9	88.21749
464	3+5+6+7+8+9	-93.0122	507	1+2+3+5+6+7+8+9	-92.5404
465	4+5+6+7+8+9	-90.8761	508	1+2+4+5+6+7+8+9	-90.6167
466	1+2+3+4+5+6+7	-95.8921	509	1+3+4+5+6+7+8+9	-89.9507
467	1+2+3+4+5+6+8	-93.1038	510	2+3+4+5+6+7+8+9	-91.6399
468	1+2+3+4+5+6+9	-93.1694	511	1+2+3+4+5+6+7+8+9	-90.623
469	1+2+3+4+5+7+8	-90.4204			
470	1+2+3+4+5+7+9	-90.4717			
471	1+2+3+4+5+8+9	-88.9644			

DISCUSSION

In the present investigation, nine quantitative characters of F_1 materials of half diallel crosses, viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), pod weight per plant (PdWPP), individual plant weight (IPlW), root weight (RW) and seed weight per plant (SWPP) were studied for correlation, path-coefficient and selection index.

The different components of variation varied differently for different characters. Phenotypic component of variation (σ^2p) was higher than genotypic (σ^2g) component of variation. These results were in conformity with the findings of Samad (1991) and Nahar (1997). In the present study, the highest genotypic and phenotypic variations were obtained for CAMF. In the present materials, high genotypic values caused high phenotypic values. Larger genotypic values for any character are always helpful for effective selection. These results are in agreement with the findings of Mian and Awal (1979).

It was observed that genotypic correlations were higher than the respective phenotypic correlations for most of the characters as seen in Table 67 and Table 68. The high genotypic correlation indicating the strong inherent associations between characters does not reflect nature and magnitude of phenotypic variation.

Most of the character combinations had highly significant correlation coefficient. SWPP showed highly significant and positive correlation coefficient with other characters except NPBFF at genotypic level and NPBFF and DF at phenotypic level. These results indicated that characters were genetically related with seed weight per plant. These findings were supported by Singh *et al.* (2012) as they observed that most of the yield contributing characters were positively and significantly correlated at both phenotypic and genotypic levels in lentil. Gill *et al.* (2010)

also found that grain yield had highly significant and positive correlation with plant height. Arshad *et al.* (2003) found that grain yield had positive and significant correlation with plant height in chick pea. The present investigation was supported by their result as SWPP showed significant correlation with plant height at genotypic level. Singh and Singh (2006) observed that seed yield per plant had significant and positive association with plant height in pea. Samad *et al.* (2010) found seed yield had highly significant and positive correlation with branch number in lentil which was supported by the present investigation as number of secondary branches at first flower has positive correlation with seed weight per plant. Nandan and Pandya (1980) found number of branches per plant have larger effect on grain yield.

PHFF, NPBFF, PdWPP and RW showed positive direct effect on SWPP at genotypic level and rest of the characters obtained negative direct effect. The negative direct effect of important characters at genotypic level was also supported by Podder (1993) and Nahar (1997) in sugarcane. Direct effect of lateral branch numbers per plant on yield were negative found by Azizi-Chakherchaman *et al.* (2009) in lentil. PHFF, NPBFF, CAMF and PdWPP showed positive direct effect on SWPP at phenotypic level.

In lentil, positive direct effect of number of primary branches on seed yield was found by Rasheed *et al.* (2008) and Tyagi and Khan (2011). Days to flower, plant height, number of primary branches had positive direct effect on seed yield was reported by Younis *et al.* (2008) in lentil. The highest positive direct effect was showed by PdWPP on SWPP at both genotypic and phenotypic level suggesting that through improvement of this character, SWPP can be improved in this crop. Tabasum *et al.* (2010) observed that primary and secondary branches per plant exhibited negative and non significant genotypic correlations with seed yield in mungbean. They found that plant height showed positive non significant and significant genotypic and phenotypic correlation. Total plant weight showed significant genotypic and phenotypic correlation with seed yield. Positive direct effects were exerted through secondary branches and total plant weight.

Yield is a complex character which depends on the action and interaction of a number of factors. For this reason, direct selection for yield may be misleading. To ensure high yield, the multiple selection criteria based on the selection index of most of the yield contributing characters to yield would be most effective. For this purpose, estimation of relative efficiency of the character and character combinations through discriminant function selection is necessary. Many researchers have followed the discriminant function selection in different crops (Joarder *et al.*, 1978 in rape seed; Salehuzzaman and Joarder, 1979 in soybean; Naskar *et al.*, 1982 in sunflower and Kumar *et al.*, 1988 in Indian mustard).

In the present investigation, when RW and SWPP were included with most of the characters, it showed high value of genetic gain. Thus, inclusion of any character noted above, was one of the important component for higher yield. In the present study, the highest value of expected gain was 4603.196% for the association of NPBFF and RW when three character combinations showed the highest value of 3083.323% for the association of NPBFF, RW and SWPP. As the two characters viz., NPBFF and RW had the 4th and 2nd highest direct positive values in path coefficient analysis at genotypic level and as RW had significant association with most of the characters at genotypic level, these two characters were considered as primary yield components. Through improvement of these two characters, yield of this crop can be improved.

SUMMARY

In the present investigation, nine quantitative characters of F_1 materials of half diallel crosses, viz., days to flower (DF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), canopy area at maximum flower (CAMF), pod weight per plant (PdWPP), individual plant weight (IPlW), root weight (RW) and seed weight per plant (SWPP) were studied for correlation, path-coefficient and selection index.

The different components of variation ranged differently for different characters. The highest value of genotypic and phenotypic variation was showed by CAMF. The pairs of any character with NSBFF except PHFF and with CAMF except NPBFF showed the maximum genotypic and phenotypic components of covariations. The pairs of CAMF × PdWPP, CAMF × IPlW, CAMF × RW and CAMF ×SWPP also showed noticeable genotypic and phenotypic covariances indicating wide scope of selection for these pairs of characters.

From the correlation studies, it was revealed that genotypic correlations were higher than phenotypic correlations for most of the characters. This situation was also marked in the path co efficient analysis. Most of the characters associations had highly significant correlation co efficients at genotypic level. SWPP showed highly significant and positive correlation with other character except DF and NPBFF. It had highly significant and negative correlation co efficient with DF at genotypic level. SWPP showed highly significant correlation co efficient with most of the characters. Among all the pairs of character associations, PdWPP × SWPP and NSBFF × SWPP had the strongest correlation co efficient at phenotypic and genotypic level, respectively. PHFF, NPBFF, PdWPP and RW showed positive direct effect on SWPP at genotypic level, whereas PHFF, NPBFF, CAMF and PdWPP showed positive direct effect on SWPP at phenotypic level.

In the present investigation, the maximum expected genetic gain of 4603.196% was found when NPBFF and RW were included in the discriminant function. It was followed by 4556.836% when RW and SWPP were included in the discriminant function. As NPBFF and RW had significant association with most of the characters at genotypic level and had the 4th and 2nd highest direct positive values in path coefficient analysis at genotypic level. These two characters were considered as primary yield components. Through improvement of these two characters, yield of this crop can be improved.

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APPENDIX 01

Appendix 01: Analyses of co variances of different pairs of characters

Days to flower (DF) × Plant height at first flower (PHFF)

Source	df	SS	MS	F
Treatments	20	-57.1439	-2.8572	-1.21168
Replications	1	-2.4981	-2.4981	-1.0594
Error	20	47.1608	2.35804	
Total	41	-12.4812		

Days to flower (DF) × Number of primary branches at first flower (NPBFF)

Source	df	SS	MS	F
Treatments	20	48.57091	2.428545	1.797197^{NS}
Replications	1	-2.73	-2.73	-2.02028
Error	20	27.02593	1.351296	
Total	41	72.86683		

Days to flower (DF) × Number of secondary branches at first flower (NSBFF)

Source	df	SS	MS	F
Treatments	20	135.4187	6.770933	2.05433^{NS}
Replications	1	-6.19761	-6.19761	-1.88038
Error	20	65.91866	3.295933	
Total	41	195.1397		

Days to flower (DF) × Canopy area at maximum flower (CAMF)

Source	df	SS	MS	F
Treatments	20	-4065.32	-203.266	-1.89654
Replications	1	309.8009	309.8009	2.890543^{NS}
Error	20	2143.548	107.1774	
Total	41	-1611.97		

Days to flower (DF) × Pod weight weight per plant (PdWPP)

Source	df	SS	MS	F
Treatments	20	13.58536	0.679268	0.453218 ^{NS}
Replications	1	2.823113	2.823113	1.883624 ^{NS}
Error	20	29.97533	1.498766	
Total	41	46.3838		

Days to flower (DF) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	-31.4841	-1.57421	16.84482**
Replications	1	3.964234	3.964234	-42.4193
Error	20	-1.86907	-0.09345	
Total	41	-29.389		

Days to flower (DF) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	1.542565	0.077128	0.990973 ^{NS}
Replications	1	0.24173	0.24173	3.105838 ^{NS}
Error	20	1.556616	0.077831	
Total	41	3.340912		

Days to flower (DF) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	7.865264	0.393263	0.299977 ^{NS}
Replications	1	1.496677	1.496677	1.141648 ^{NS}
Error	20	26.21958	1.310979	
Total	41	35.58152		

Plant height at first flower (PHFF) × Number of primary branches at first flower (NPBFF)

Source	df	SS	MS	F
Treatments	20	-3.01468	-0.15073	-0.12286
Replications	1	3.777325	3.777325	3.078861 NS
Error	20	24.53716	1.226858	
Total	41	25.2998		

Plant height at first flower (PHFF) × Number of secondary branches at first flower (NSBFF)

Source	df	SS	MS	F
Treatments	20	38.08894	1.904447	0.761277 NS
Replications	1	8.575232	8.575232	3.427834 NS
Error	20	50.03295	2.501647	
Total	41	96.69712		

Plant height at first flower (PHFF) × Canopy area at maximum flower (CAMF)

Source	df	SS	MS	F
Treatments	20	6991.655	349.5828	2.349946*
Replications	1	-428.652	-428.652	-2.88146
Error	20	2975.241	148.762	
Total	41	9538.245		

Plant height at first flower (PHFF) × Pod weight weight per plant (PdWPP)

Source	df	SS	MS	F
Treatments	20	29.84731	1.492366	1.956087 NS
Replications	1	-3.90616	-3.90616	-5.11992
Error	20	15.25868	0.762934	
Total	41	41.19984		

Plant height at first flower (PHFF) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	37.47954	1.873977	3.300307*
Replications	1	-5.48506	-5.48506	-9.65987
Error	20	11.35638	0.567819	
Total	41	43.35086		

Plant height at first flower (PHFF) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	1.27436	0.063718	1.394937^{NS}
Replications	1	-0.33447	-0.33447	-7.32225
Error	20	0.913561	0.045678	
Total	41	1.853454		

Plant height at first flower (PHFF) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	26.31162	1.315581	1.806552^{NS}
Replications	1	-2.07086	-2.07086	-2.84369
Error	20	14.56455	0.728227	
Total	41	38.80531		

Number of primary branches at first flower (NPBFF) × Number of secondary branches at first flower (NSBFF)

Source	df	SS	MS	F
Treatments	20	44.10871	2.205435	1.226298^{NS}
Replications	1	9.371284	9.371284	5.210755*
Error	20	35.96901	1.79845	
Total	41	89.449		

Number of primary branches at first flower (NPBFF) × Canopy area at maximum flower (CAMF)

Source	df	SS	MS	F
Treatments	20	-201.919	-10.096	-0.26419
Replications	1	-468.444	-468.444	-12.258
Error	20	764.3047	38.21523	
Total	41	93.94149		

Number of primary branches at first flower (NPBFF) × Pod weight weight per plant (PdWPP)

Source	df	SS	MS	F
Treatments	20	4.708403	0.23542	1.835306 NS
Replications	1	-4.26877	-4.26877	-33.2788
Error	20	2.56546	0.128273	
Total	41	3.005089		

Number of primary branches at first flower (NPBFF) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	3.577292	0.178865	0.444768 NS
Replications	1	-5.99424	-5.99424	-14.9054
Error	20	8.043054	0.402153	
Total	41	5.626103		

Number of primary branches at first flower (NPBFF) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	0.32797	0.016399	0.895775 NS
Replications	1	-0.36552	-0.36552	-19.9664
Error	20	0.36613	0.018307	
Total	41	0.328585		

Number of primary branches at first flower (NPBFF) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	2.982077	0.149104	0.994201 NS
Replications	1	-2.2631	-2.2631	-15.09
Error	20	2.99947	0.149974	
Total	41	3.71845		

Number of secondary branches at first flower (NSBFF) × Canopy area at maximum flower (CAMF)

Source	df	SS	MS	F
Treatments	20	3979.273	198.9637	2.842434*
Replications	1	-1063.46	-1063.46	-15.1927
Error	20	1399.953	69.99764	
Total	41	4315.771		

Number of secondary branches at first flower (NSBFF) × Pod weight weight per plant (PdWPP)

Source	df	SS	MS	F
Treatments	20	59.79131	2.989565	4.002565**
Replications	1	-9.69092	-9.69092	-12.9746
Error	20	14.93825	0.746912	
Total	41	65.03864		

Number of secondary branches at first flower (NSBFF) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	16.72059	0.83603	-3.2379
Replications	1	-13.608	-13.608	52.7033**
Error	20	-5.16402	-0.2582	
Total	41	-2.05148		

Number of secondary branches at first flower (NSBFF) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	2.792792	0.13964	5.448897**
Replications	1	-0.82979	-0.82979	-32.3793
Error	20	0.512543	0.025627	
Total	41	2.475547		

Number of secondary branches at first flower (NSBFF) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	44.15656	2.207828	2.989153**
Replications	1	-5.13765	-5.13765	-6.95581
Error	20	14.77227	0.738613	
Total	41	53.79118		

Canopy area at maximum flower (CAMF) × Pod weight weight per plant (PdWPP)

Source	df	SS	MS	F
Treatments	20	4169.004	208.4502	1.598178 ^{NS}
Replications	1	484.4214	484.4214	3.714038 ^{NS}
Error	20	2608.597	130.4299	
Total	41	7262.022		

Canopy area at maximum flower (CAMF) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	3426.741	171.337	2.006614 ^{NS}
Replications	1	680.2278	680.2278	7.96649*
Error	20	1707.723	85.38613	
Total	41	5814.691		

Canopy area at maximum flower (CAMF) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	171.3458	8.567289	1.872889 NS
Replications	1	41.47874	41.47874	9.067636**
Error	20	91.48744	4.574372	
Total	41	304.312		

Canopy area at maximum flower (CAMF) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	3345.418	167.2709	1.697425 NS
Replications	1	256.8167	256.8167	2.606114 NS
Error	20	1970.878	98.54391	
Total	41	5573.113		

Pod weight weight per plant (PdWPP) × Individual plant weight (IPlW)

Source	df	SS	MS	F
Treatments	20	28.53094	1.426547	1.407009 NS
Replications	1	6.198691	6.198691	6.113794*
Error	20	20.27772	1.013886	
Total	41	55.00736		

Pod weight weight per plant (PdWPP) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	2.471699	0.123585	1.46383 NS
Replications	1	0.377982	0.377982	4.477093*
Error	20	1.688515	0.084426	
Total	41	4.538196		

Pod weight weight per plant (PdWPP) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	39.47636	1.973818	1.104569^{NS}
Replications	1	2.340285	2.340285	1.309648^{NS}
Error	20	35.73915	1.786957	
Total	41	77.55579		

Individual plant weight (IPlW) × Root weight (RW)

Source	df	SS	MS	F
Treatments	20	1.396438	0.069822	1.797611^{NS}
Replications	1	0.530765	0.530765	13.6649**
Error	20	0.77683	0.038841	
Total	41	2.704032		

Individual plant weight (IPlW) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	21.09728	1.054864	1.579426^{NS}
Replications	1	3.286244	3.286244	4.920424*
Error	20	13.35756	0.667878	
Total	41	37.74109		

Root weight (RW) × Seed weight per plant (SWPP)

Source	df	SS	MS	F
Treatments	20	1.823195	0.09116	1.519839^{NS}
Replications	1	0.200388	0.200388	3.340915^{NS}
Error	20	1.199598	0.05998	
Total	41	3.223181		

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

APPENDIX 02

LIST OF ABBREVIATION

1.	cm	Centimeter
2.	Cov	Covariance
3.	D	Additive variation
4.	d.f.	Degrees of freedom
5.	E	Environmental variation
6.	*et al.*	Et alia (=and others)
7.	etc.	et cetera
8.	F	Fisher's or variance ratio; mean of Fri
9.	F_1	First filial generation
10.	F_2	Second filial generation
11.	Fr	The covariance of additive and dominance effects in a single array
12.	gca	General combining ability
13.	gm	Gram.
14.	H_1	Dominance variation
15.	H_2	Proportion of positive and negative dominant genes
16.	h^2	Dominance effect in heterozygous phase
17.	i.e.	(L. id est) = that is
18.	m	Meter
19.	$(M_{L1}-M_{L0})^2$	The difference between mean of the parents and the mean of their n^2 progeny
20.	M.S.	Mean of squares
21.	sca	Specific combining ability
22.	S.S.	Sum of squares
23.	Var	Variance
24.	viz.	(L. videlicet) = namely; to wit
25.	Vr	Variance of each array
26.	V_{1L1}	Mean variance of the arrays
27.	V_{0L1}	Variance of the mean of arrays
28.	V_{0L0}	Variance of parents
29.	W_{0L01}	Mean covariance between the parents and the arrays
30.	Wr	Covariance between parents and their off-spring