GENERATION MEAN ANALYSIS IN BRINJAL (*Solanum melongena* L.) FOR YIELD AND YIELD ATTRIBUTES.

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KERALA, INDIA

2015

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by

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THESIS

Submitted in partial fulfillment of the requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS

COLLEGE OF AGRICULTURE

VELLAYANI, THIRUVANANTHAPURAM- 695 522

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DECLARATION

I, hereby declare that this thesis entitled **"GENERATION MEAN ANALYSIS IN BRINJAL (*Solanum melongena* L.) FOR YIELD AND YIELD ATTRIBUTES"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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CERTIFICATE

Certified that this thesis entitled **"GENERATION MEAN ANALYSIS IN BRINJAL (*Solanum melongena* L.) FOR YIELD AND YIELD ATTRIBUTES"** is a record of bonafide research work done independently by Mrs. Soumya B. Nair (2013-11-147) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

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EXTERNAL EXAMINER

Acknowledgement

I feel immense pleasure to express my profound and heartfelt thankfulness to ***Dr. D. Wilson,*** *Professor and Head, Department of Plant Breeding and Genetics and Chairman of the advisory committee, for his guidance, suggestions, constant encouragement, support, unfailing patience and above all the kind of understanding throughout the course of this research work and preparation of the thesis.*

My sincere thanks to ***Dr. P. Manju****, Professor, Department of Plant Breeding and Genetics and member of advisory committee, for the critical evaluation of thesis and.timely help during the course of this research.*

I am grateful to ***Dr. Sunny. K, Oommen****, Professor, Department of Plant Breeding and Genetics and member of advisory committee for his valuable suggestions, timely support and critical evaluation during the course of this work.*

My profound gratitude to ***Dr. Vijayaraghavakumar****, Professor and Head, Department of Agricultural Statistics, for his valuable suggestion, encouragement and co-operation rendered throughout the study, as a member of advisory committee.*

I wish to express my heartfelt thanks to ***Dr. Sverup John****, Dean, College of Agriculture, Vellayani for providing me all the necessary facilities from the University during the whole course of study.*

I express my sincere thanks to all the teachers of the Department of of Plant Breeding and Genetics for their entire well wishes, help and support.

I earnestly express my profound gratitude to my dear classmates ***Anju and Srinivas*** *for their valuable guidance, moral support, encouragement during the entire period of study.*

My loving and wholehearted thanks to my friends ***Sruthy, Anamika, Divya, Darsana, Surya, Anju, Ardra, Silpa, Anila, Aswathy, Nitya, Litty and Lishma*** *for their help, good company, positive criticism and moral support throughout my P.G. programme.*

I also express my sincere thanks to part time labourers ***Vijayamma chechi, Beena chechi, Jose, Prasanth chetan, Rajendra prasad and Jayadevan*** *for their help during the field work. I am deeply obliged to* ***Rajsekhar chetan, Narmada chechi and Srinivas chetan*** *for their advice and support. I wish to express my gratefulness to my seniors and juniors for their timely help and support. I take this opportunity to acknowledge them for all the inspiring words, unconditional love, care and support they offered to me.*

. I am most indebted to Abhi chetan, Amma, Achan, vava, Chetan's amma for their affection, patience, constant encouragement, moral support and blessings that have enabled me to finish this work, without which I would not have completed this research. My immortal love to my dear kid Karthi who suffered the most during the field work.

Above all, I believe it is the unbound love and blessings of God, which is the prime factor that led to the successful completion of my entire work. I humbly bow my head before that almighty for the numberless blessings that he shower upon my life.

Soumya B. Nair

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Per cent
CD	Critical difference
cm	Centimeter
F_1	First filial generation
F_2	Second filial generation
et al.	And other co workers
Fig.	Figure
g	Gram
i.e.	that is
kg	Kilo gram
m	Meter
viz.	Namely
No.	Number
S.E	Standard error
NBPGR	National Bureau of Plant Genetic Resources

DEDICATED TO

MY FAMILY

INTRODUCTION

1. INTRODUCTION

Brinjal (*Solanum melongena* L.) is an important solanaceous vegetable crop widely grown in the tropics and subtropics in the world. The crop has a somatic chromosome number of 2n=24 and comprises of three botanical varieties viz., var *esculentum*, with round or egg shaped fruits, var. *serpentinum* with long slender fruits and var. *depressum* having dwarf stature. India and China are the primary centers of diversity (Kashyap *et al*., 2003). It is being grown extensively in India, Bangladesh, Pakistan, China, Philippines, France, Italy and the United States.

Brinjal is referred by various names in different parts of the country as Baigan (Hindi), Badanekai (Kannada), Vangi (Marathi), Katharikai (Tamil), Vankai (Telugu) etc. Internationally, it is referred as Eggplant (England) or Aubergine (France). Further, in various other countries it is referred as Alberenjina (Arab Countries).

Brinjal is a major vegetable crop of our country since ancient times and the human society has social and economic relationship with this crop. India ranks second after China in area and production of brinjal. Brinjal shares 8.3 percent of total vegetable production in India. The cultivated area of brinjal in India is about 7.22 lakh hectares with production of 134.43 lakh tonnes and the productivity of 18.6 tonnes per hectare. West Bengal is the leading state with an area of 1.61 lakh hectares and annual production of 29.65 lakh tonnes. The productivity is 18.4 tonnes per hectare (Anon., 2013).

Brinjal (*Solanum melongena* L.) is indigenous to a vast area stretching from northeast India and Burma to northern Thailand, Laos, Vietnam and south west China and wild plants can still be found in these locations (Daunay and Janick, 2007). Eggplant was domesticated from wild forms in the Indo-Burma region with indication that it was cultivated with antiquity. Several sanskrit documents, dated as early as 300 BC, mention this plant with various descriptive words, which suggest its wide popularity as food and medicine (Nadkarni, 1927). In the

Ayurveda, white types were recommended for diabetic patients and roots for the treatment of asthma.

Though brinjal is a self pollinated crop, cross pollination occurs to an extent of 30-40 per cent (Daskalov, 1955 and Agrawal, 1980). Brinjal is highly productive and usually finds its place as the poor man's vegetable (Som and Maity, 2002). It is popular among people of all social strata and hence it is rightly called as 'vegetable of masses' (Patel and Sarnaik, 2003).

In India the average vegetable consumption is only 185 g per capita per day which is less than the required amount of 300 g (125 g leafy vegetable, 100 g root and tubers and 75 g other vegetables) per day per head as per ICMR recommendation. Therefore, production of vegetables has to be increased considerably to mitigate prevailing chronic malnutrition against the ICMR recommendation of 300 g per head per day (Kalloo, 2006).

In India, immature fruits of brinjal are consumed as cooked vegetable in various ways (Rai *et al*., 1995). The nutritive value of brinjal is comparable to tomato (Chaudary, 1976) and fruits are rich source of minerals like Ca, Mg, P and fatty acids. Besides, it is used as fresh vegetable and known to have some medicinal properties in curing diabetes, asthma, cholera, bronchitis, diarrhoea and liver complaints (Tomar and Kalda, 1998). Its fruits and leaves are reported to lower the blood cholesterol.

Eggplant is threatened by many insect pests and diseases from the time of planting till its harvest. Among these, bacterial wilt caused by *Ralstonia solanacearum* is the most important. The incidence of this disease is increasing further by cultivation of other solanaceous crops in the same land. Most of the commercial brinjal varieties are susceptible to bacterial wilt (Madalageri *et al*., 1983). Therefore, efforts must be put to exploit regional genetic resources without losing consumer's preferences.

Fruit and shoot borer (*Leucinodes orbonalis* Guen.) is the most serious insect pest of brinjal throughout the country. It attacks the plant at any season and

stage of growth, causing dead shoot in vegetative stage and fruit boring later rendering them unmarketable. This pest may cause fruit damage as high as 100 per cent (Panda, 1999). Insecticidal control is not only uneconomical but also invites environmental pollution. Consequently, host plant resistance would be useful either as a complete control measure or as a part of the integrated pest management programme with limited dependence on pesticides. Development of hybrids resistant to major pests and diseases is an ideal choice to overcome such situation.

Many local cultivars are popular in different locations for their qualitative traits though they are poor yielders and susceptible to various pest and diseases. It is high time to develop genotypes with high yield potential. Strategies are also developed to boost vegetable production by some national institutions like NBPGR (Dharwad *et al*., 2009).

Efficiency of selection for the improvement of both quantitative and qualitative traits depends upon the nature and interaction of the genes involved in the inheritance of a particular character. Knowledge of gene action helps in the selection of parents for use in the hybridization programmes and also in the choice of appropriate breeding procedure for the genetic improvement of various quantitative characters. Hence insight into the nature of gene action involved in the expression of various quantitative characters is essential to a plant breeder for starting a judicious breeding programme. Since components of genetic variances are used as measures of gene action, all those factors which affect estimates of genetic variances also affect gene action. Such factors include type of genetic material, mode of pollination, mode of inheritance, existence of linkage, sample size, sampling method and method of calculation. Generation mean analysis helps to understand the nature and magnitude of gene action using the means of different generations.

The success of breeding programme depends on the availability of genetic variation in a population. Improvement in fruit yield, colour and insect pest

resistance will certainly enhance the production and consumption of the crop. For improvement programme, the information about variability is a prerequiste. Genetic variability of brinjal has been studied by various workers in India (Misra, 1961; Thakur *et al*., 1968; Chowdhury, 2005). It is particularly useful for characterizing individual accessions and cultivars and as a general guide in the selection of the parents for hybridization (Furini and Wunder, 2004). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in nature or by hybridization.

The present study was undertaken with the following objectives

- Estimation of genetic variability among the F_2 population.
- Estimation of genetic variability within the F_2 progenies.
- To study the genetic basis and inheritance pattern of yield and yield attributes.
- To formulate an appropriate breeding programme for developing high yielding varieties in brinjal.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Brinjal, being a crop of Indian orgin has also developed some secondary variability in China (Vavilov, 1931). Brinjal has a rich diversity in the form of plant and fruit morphological characteristics. During the last few decades, work on enrichment of germplasm through indigenous and exotic sources has been in progress at NBPGR. The magnitude of success to be obtained lies in the selection of the base material and its creative manipulation. The progress in plant breeding depends on the genetic information available from the parents and their combinations on the inheritance and behavior of quantitative characters associated with yield or any economical trait of concern to the breeder. To generate such genetic information it is necessary to conceive a genetic model in relation to the material that is proposed to be utilized and to design suitable mating system that can fit into the chosen genetic model.

To enhance the pace of genetic improvement in eggplant detailed investigation regarding gene action and genetic variability is essential.

The knowledge of gene effects for different traits in brinjal is of prime importance in breeding programme. The present study was therefore undertaken to study the mode of inheritance for yield and yield attributes in brinjal through generation mean analysis.

Keeping in view the objectives of the present investigation relevant literature is reviewed and presented in the following headings.

2.1 GENETIC PARAMETERS

2.1.1 Gene Action

Gene action refers to the behaviour or mode of expression of genes in a genetic population. Major genes, which govern the inheritance of qualitative characters, have large effects. The effects of these genes can be separated by usual mendelian techniques even in the presence of segregation. Therefore, decision regarding the best breeding procedure can be easily taken. Action of the genes

controlling quantitative characters can be described by the use of gene models. First attempt to contruct a gene model was that of Fisher (1918). In this model he included dominance at a single locus. Fisher, Immer and Tedin (1932) used this gene model to describe gene action of any number of genes on a given character. Gene models were also developed by Comstock and Robinson (1948) and Mather (1949) to evaluate the relative importance of additive and dominance gene effects. Epistatic effects were assumed to be negligible in these gene models. Anderson and Kempthorne (1954), Hayman (1958) and Gamble (1962) believed that epistatic effects could be of significance for quantitative characters. Hayman and Mather developed a gene model based on theory developed by Fisher *et al*. (1932) and Mather (1949). Hayman (1958) described a general procedure to estimate parameters referring to the additive, dominance, additive x additive, additive x dominance and dominance x dominance effects in addition to mean. Gamble (1962), on the other hand, proposed a perfect fit solution to estimate additive, dominance, additive x additive, additive x dominance and dominance x dominance effects from the mean measurements of six generations *viz*. P_1, P_2, F_1, F_2, BC_1 and BC_2.

Gene action is measured in terms of components of genetic variance or combining ability variances and effects. Gene action is of two types, *viz*., additive gene action, and non-additive gene action. Additive gene action includes additive genetic variance and additive x additive type of epistatic variance. Non additive gene action includes dominance variance, additive x dominance and dominance x dominance types of epistatic variances.

Peter and Singh (1973) studied five varieties of *Solanum melongena* and reported that number of days to flowering and number of primary branches were controlled by over dominant genes; fruit weight per plant by dominant genes; height by additive gene action with some over dominance; and number of flowers per inflorescence, number of long-styled and medium-styled flowers, number of short-styled and pseudostyled flowers, fruit length and equatorial perimeter of

fruit by additive gene action. Additive gene action was observed for number of fruits per plant and dominant gene action for weight of fruits per plant.

Singh *et al*. (1974) evaluated seven varieties and revealed additive gene action for the days to flowering, plant height, number of fruits per plant and fruit length, and non additive-gene action for yield per plant and fruit girth except for number of fruits per plant, which showed more pronounced epistatic gene action.

Gill *et al.* (1976) reported additive gene action for number of days to flowering, plant height, number of fruits per plant, yield, fruit size index, number of branches. Mital *et al.* (1976) reported additive gene action for number of days to flowering and fruit weight and dominance gene action for yield. Bajpai (1977) reported additive gene action for number of days to flowering and plant height and dominance effect for number of branches and plant spread.

Hani (1977) reported over dominance for number of days to flowering. Dharmagowda (1977) reported additive and dominance gene action for fruit weight, additive and non-additive gene action for plant height and over dominance for seeds per fruit. Singh *et al*. (1979) reported additive gene action for number of fruits per plant, fruit length and plant height and non-additive gene effect for number of days to flowering.

Sidhu *et al.* (1980) crossed Pusa Purple Long, BR112, Aushey, R 34 and Sel 26 in all possible combinations, excluding reciprocals. For yield, length of fruit, number of flowers and days to flowering both additive and dominant gene effects were significant, the latter being larger. Additive gene effects were more important than dominant gene effects for fruit number, weight and girth.

Singh *et al.* (1982) reported additive gene action for fruit weight. Dixit *et al.* (1984) reported the importance of both additive and non-additive gene action for yield per plant, fruits per plant and plant height. Additive gene action was important for length, circumference and weight of fruit. There was partial

dominance for all characters except yield per plant and plant height, which were controlled by over dominance and complete dominance.

Additive gene action was reported for yield by Sharma (1985). Kumar and Ram (1987) reported additive gene action for early yield and yield. Randhawa (1987) reported additive gene action for fruit weight, yield and number of fruits per plant.

Singh and Mital (1988) reported additive gene action for number of fruits per plant, fruit length and non-additive gene action for number of days to flowering while additive and non-additive gene action for fruit width and plant height. Chandha and Sharma (1989) reported additive gene action for number of fruits per plant and yield. Singh and Mital (1988) reported that days to flowering, plant height and yield per plant were controlled chiefly by non-additive gene action.

Vaidvel and Babu (1993) studied seven yield components in the F_2 population of three intervarietal crosses of *Solanum melongena* and reported the role of additive gene action in the control of plant height, fruit yield per plant, number of fruits per plants and fruit length. Patel *et al*. (1994) studied 7 diverse *Solanum melongena* varieties and their hybrids and observed that gene action of the non-additive type was predominant for fruit yield and some yield components.

Chaudhary and Kumar (1999) reported that both additive and non-additive gene actions were important in the inheritance of different characters. The superior performance of F_1 hybrids was largely due to the presence of additive

and additive × additive type of epistatic interactions. Patil et al.(2000) reported that additive gene as well as non.additive gene effects were predominant for fruit weight, fruits per plant and yield per plant.

Chaudhary and Pathania (2001) reported that dominant components of genetic variance played a key role in the inheritance of days to 50% flowering, days to first picking, fruit length, fruits per plant, branches per plant, plant height, yield per plant, TSS, leaf area, crop growth rate, leaf growth rate, net assimilation rate, leaf area ratio, leaf weight ratio and specific leaf weight. Both additive and non-additive components were equally important in fruit diameter, average fruit diameter and pedicel length. However, fruit weight was under the control of additive genes.

Das and Barua (2001) reported significant differences among genotypes for characters *viz*., days to first flowering, days to 50% flowering, plant height, primary branches per plant, fruit length, fruit girth, number of fruits per plant, fruit weight and yield.

Singh *et al*. (2002) reported the predominance of additive gene effects for days to first flowering, plant height, number of branches per plant, fruit length, fruit diameter, number of fruits per plant, and fruit weight. They suggested that single plant selection in the early segregating generation of crosses would be highly effective in aubergine.

Chezhian *et al*. (2005) reported additive × additive gene action for plant height, number of fruits per plant, fruit weight and fruit yield per plant. Bendale *et al*. (2005) studied 28 F_1 hybrids of aubergine and their parents and observed that non-additive gene action was predominant over the additive gene effect for the expression of the traits plant height, leaf area per plant, number of branches per plant, number of days to 50% flowering, number of days to first picking, and fruit yield per plant.

Suneetha *et al*. (2005) reported that non-additive gene action was preponderant for the traits fruit yield, yield components, quality and physiological characters of brinjal (aubergine). Suneetha *et al.* (2006) studied 45 aubergine hybrids and reported preponderant non-additive gene action for fruit yield per plant, days to first picking, plant height, and the quality traits studied, during all the cropping seasons.

Kamalakkannan *et al*. (2007) reported additive gene action for earliness, number of fruits, and fruit yield per plant, while the non-additive gene action was predominant for plant height, number of branches per plant, fruit weight, fruit length and fruit girth, indicating the potential of heterosis breeding for the improvement of aubergine.

Umareitya (2008) reported that both additive and non additive gene action were important in the expression of fruit yield and attributing characters. The magnitude of non-additive gene action was higher than that of additive component in respect of days to flowering, fruit length, fruit girth, fruit weight, number of fruits per plant, number of branches per plant, plant height and total fruit yield per plant and for days to first picking additive type of gene action was important.

Shanmugapriya *et al*. (2009) reported the predominance of non-additive gene action for eight traits namely days to first flowering, number of branches per plant, plant height, number of fruits per plant, fruit weight, fruit length, fruit girth, fruit yield per plant in brinjal.

Kumar *et al*. (2009) reported that additive x dominance (j) gene effect was more frequent for most of the characters. Characters like days to first flower, number of branches per plant, length of fruits, width of fruits, fruits per plant and yield per plant had significant and high values of dominance (h) and additive x dominance (j) and dominance x dominance (l) reflecting preponderance of non-additive gene action in the inheritance of these traits. Duplicate type of epistasis was more prevalent for most of traits in comparison to complementary type.

Prasad *et al.* (2010) studied 28 cross combinations along with their eight parents and observed that additive and dominance genetic variance were important in the expression of characters. Dominance genetic variance was greater than additive genetic variance for all traits except fruit length, fruit breadth and average fruit weight, which could be exploited through heterosis breeding, nevertheless fruit size and weight could be improved through hybridization followed by selection.

Das *et al.* (2010) studied brinjal shoot and fruit borer (*Leucinodes orbonalis* Guen.) and observed prevalence of additive variance for most of the traits, plant height, number of primary branches per plant, days to 50% flowering, fruits per plant, fruit length, fruit girth, fruit weight and percentage fruit and shoot infested. So, conventional breeding approaches like pedigree, single seed descent and recurrent selection methods can be used to improve these characters.

Kafytullah *et al*. (2011) reported additive gene action for fruit volume, fruit weight, leaf area index, fruit length, fruit diameter and number of fruits per plant. Rai and Asati (2011) reported preponderance of both additive and non-additive genes for yield and its contributing characters. Shafeeq *et al*. (2013) reported both additive and non-additive gene actions were observed for characters like average fruit weight, fruit length, number of fruits per clusters, number of leaves, number of branches at one month after transplanting, plant height at final harvest and seedling height at transplanting.

Reddy and Patel (2014) studied the gene action in brinjal (*Solanum melongena* L.) for fourteen characters including fruit yield and its component characters and revealed that both additive as well as non-additive effects were important in the inheritance of all the traits studied.

Deshmukh *et al*. (2014) reported the importance of non-additive systems operating in inheritance of yield and its important components. Degree of dominance was in range of over dominance range for all the characters and close to complete dominance for plant height. The traits *viz*. plant height, plant spread, days to first flower, days to 50% flower, number of branches per plant, fruit

length and yield exhibited significant environmental effect. For fruit diameter, chlorophyll content, days to 50% flower, number of fruits per plant, fruit weight and fruit length dominant genes were more frequently distributed in the parents.

Sharafuddin *et al*. (2015) evaluated eighteen eggplant genotypes and reported the importance of both additive and non additive gene actions for fruit weight, fruit length, fruit breadth, number of fruits per plant and yield per plant.

Gene action in brinjal with respect to various characters is given in Table 1.

2.1.2 Generation Mean Analysis

Generation mean analysis is one of the biometrical technique which is used for the study of gene action in plant breeding. The concept of generation mean analysis was developed by Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation. Analysis of this technique is based on six different generations of a cross, *viz*., parents (P_1, P_2), their F_1, F_2 and backcrosses (B_1, B_2). The mean values over replications are used for the estimation of gene effects. Six parameter model was first suggested by Hayman (1958) for the estimation of various genetic componens from the generation means. This method is used when non- allelic interactions are present.

Nualsri *et al.* (1986) conducted generation means analysis of data on yield per plant and five related characters from six crosses (involving 4 parental lines) suggested that additive gene action was important for all of them except yield per plant, which appeared to be largely conditioned by dominance x dominance interaction effects.

Lawande *et al*. (1992) reported that additive gene effects were observed for fruit number and fruit weight while yield per plant exhibited non additive gene effects.The components of additive x dominance and dominance x dominance also played important role for this character

Table 1. Gene action studies in brinjal

Characters	Additive	Non Additive	Dominance
1. Days to first flowering	Mital *et al*.(1976) Gill *et al.* (1976) Bajpai (1977) Kamalakkannan *et al.* (2007) Das *et al.* (2010)	Patil *et al.* (2000) Singh *et al.* (1979) Singh and Mital (1988) Umareitya *et al*. (2008) Kumar *et al*. (2009) Bendale *et al*. (2005)	Kumar *et al.* (2009) Sindhu *et al*.(1980), Peter and Singh (1973,1976) Hani (1977 Chaudhary and Pathania (2001)
2. Number of primary branches	Patil *et al.* (2003) Gill *et al.* (1976) Das *et al.* (2010)	Patil *et al.* (2003) Umareitya *et al*. (2008) Kamalakkannan *et al.* (2007) Bendale *et al.* (2005)	Kumar *et al*. (2009) Bajpai (1977)
3. Days to first harvest	Vaghasiya *et al.* (2009)	Vaghasiya *et al.* (2009) Suneetha *et al*. (2005) Bendale *et al.* (2005)	
4. Number of fruits per plant	Lawande *et al*.(1992) Patil *et al.* (2000) Patil *et al.* (2003) Singh *et al.* (1979) Das *et al*. (2010) Singh and Mital (1988) Gill *et al.* (1976) Dixit *et al.* (1984) Randhawa (1987) Randhawa (1987) Shanmugapriya *et al. (*2009) Chandha and Sharma (1989)	Patil *et al.* (2000) Vaghasiya *et al.* (2009) Patil *et al.* (2003) Dixit *et a.l* (1984) Umareitya *et al.(*2008) Kumar *et al.* (2009) Chezhian *et al*. (2005)	Kumar *et al. (*2009) Chaudhary and Pathania (2001)

Table 1. Gene action studies in brinjal. contd.....

	Patil *et al.* (2000) Patil *et al.* (2003) Kumar and Ram (1987) Sharma (1985) Gill *et al* (1976) Das *et al.* (2010) Madalageri (1986) Dixit *et al.* (1984) Shanmugapriya *et al.* (2009) Kamalakkannan *et al.* (2007) Randhawa (1987) Chandha and Sharma(1989)	Lawande *et al.* (1992) Patil *et al.* (2000) Vaghasiya *et al.* (2009) Patil *et al.* (2003) Chezhian *et al.* (2005) Dixit *et al.* (1984) Umareitya *et al.*(2008) Kumar *et al.* (2009) Suneetha *et al.* (2005) Suneetha *et al.* (2006) Bendale *et al.* (2005)	Kumar *et al.* (2009) Mital *et al.* (1976) Chaudhary and Pathania (2001)
6. Number of fruits per cluster	Shafeeq *et al.* (2013)	Shafeeq *et al.* (2013)	
7. Length of fruit (cm)	Singh *et al.* (1979) Singh and Mital (1988) Peter and Singh (1973,1976) Sindhu *et al.* (1980) Das *et al.* (2010) Dixit *et al.* (1984) Kafytullah *et al.* (2011)	Umareitya *et al.* (2008) Kumar *et al.* (2009)	Kumar *et al.* (2009) Prasad *et al.* (2010)
8. Girth of fruit (cm)	Singh and Mital (1988) Dixit *et al.* (1984) Das *et al.* (2010) Kafytullah *et al.* (2011)	Vaghasiya *et al.* (2009) Singh and Mital (1988) Umareitya *et al.* (2008) Kumar *et al.* (2009)	Kumar *et al.* (2009) Prasad *et al.* (2010)
9. Weight of fruit (g)	Lawande *et al.* (1992) Patil *et al.* (2000) Das *et al.* (2010) Vaghasiya *et al.* (2009 Kafytullah *et al.* (2011) Shanmugapriya *et al.* (2009)	Patil *et al.* (2000) Vaghasiya *et al.* (2009) Patil *et al.* (2003) Umareitya (2008) Kamalakkannan *et al.* (2007) Chezhian *et al.* (2005)	Dharmagowda (1977) Prasad *et al.* (2010)

Table 1. Gene action studies in brinjal. contd...

	Patil *et al.* (2003) Chaudhary and Pathania (2001) Mital *et al* (1976) Peter and Singh (1973, 1976) Singh *et al.* (1982) Dixit *et al.* (1984) Randhawa(1987) Dharmagowda (1977)		
10.Volume of fruit (cm^3)	Kafytullah *et al.* (2011)		
11. Calyx length (cm)	Shinde *et al.* (2009		
12. Plant height (cm)	Singh *et al.* (1979) Singh and Mital (1988) Gill *et al.* (1976) Dixit *et al.* (1984) Shanmugapriya *et al.* (2009) Dharmagowda (1977) Das *et al.* (2010)	Vaghasiya *et al.* (2009 Singh and Mital (1988) Bendale *et al.* (2005) Dixit *et al.* (1984) Dharmagowda (1977) Umareitya *et al.* (2008) Suneetha *et al.* (2006)	
13. Incidence of pests and diseases	Das *et al.* (2010)		Singh and Kalda (1997) Chaudhary and Pathania (2001)

Patil *et al.* (2003) studied gene effects through generation mean analysis on aubergine and six crosses were utilized for the study. The predominance of additive as well as non-additive gene effects (additive × additive (i), additive × dominance (j), and dominance × dominance (l)) were recorded for primary branches per plant, fruit size index, fruit weight, fruits per plant, and yield per plant.

Hazra and Roy (2004) studied the inheritance of fruit yield and its components in brinjal through generation means analysis

Indiresh *et al.* (2005) conducted generation mean analysis of 5 generations (P_1, P_2, F_1, F_2 and F_3) of 5 crosses, *i.e*., West Coast Green Round (WCGR) × Arka Keshav (AK), WCGR × BB-1, Hissar Jamun × AK, WCGR × Arka Nidhi and WCGR × BB-11. Both additive and non-additive gene actions were involved in the inheritance of most of the characters. Duplicate type of gene action was involved in the expression of plant height, days to first flowering, fruit length, fruit diameter, fruit weight, fruit number per plant and fruit yield per plant. Fruit

yield per plant and days to first flowering was found to be predominantly under the control of dominance effect.

Two crosses *viz*., Pusa Ankur x Udaipur local and IC-112358 x Pusa Uttam with six generations *viz*., P_1, P_2 ,F_1, F_2, B_1 and B_2 in brinjal were studied by Aravindakshan *et al.* (2005) inorder to know the nature of genetic control for yield. In both the crosses, fruit yield and fruit number per plant showed additive and non additive type of gene action. These traits also indicated duplicate type of gene action.

Shinde (2007) analysed the nature and magnitude of gene action in a six parameter model for ten chemical characters in brinjal shoots involving four crosses. Study indicated that magnitude of additive and dominance effects were significant mostly in all the crosses. Epistatic components *viz*., additive × additive (i), additive × dominance (j) and dominance × dominance (l) were involved in the

expression of most of the chemical characters in brinjal shoots. Duplicate type of epistasis was observed for most of the characters in most of the crosses.

Shinde *et al.* (2009) analysed the nature and magnitude of gene action in six generation mean for resistance to shoot and fruit borer related characters of four crosses in brinjal. Study indicated that magnitude of dominance effect was higher for almost all the characters except per cent infested shoots, fruit length, pedicel length, days to 50% flowering and fruit skin thickness. Epistatic component additive x additive (i) and dominance x dominance (l) were involved in the expression of most of the characters. Duplicate type of epistasis was observed for most of the crosses. Significant epistatic gene effects coupled with duplicate epistasis indicated that through effective selection, transgressive segregants could be obtained in the subsequent generations.

Vaghasiya *et al*. (2000) studied six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of brinjal [*Solanum melongena*] crosses KS233 × PLR1 and Green Round × PLR1 and results showed that in KS233 × PLR1, additive as well as non-additive gene effects were important for fruit weight and days to first picking, while only non-additive effects were important for fruit yield per plant, fruits per plant, fruit girth and plant height. In Green Round × PLR1, all characters were under the control of both additive and non-additive gene effects.

Dhameliya *et al.* (2009) studied the gene effects through five generations namely P_1, P_2, F_1, F_2, and F_3 of two intervarietal crosses *viz*., PLR1 x Green Round and GBL1 x GCL 99-1 was studied in brinjal. Both additive and non-additive gene effects were important for most of the characters in both the crosses. The complimentary type of interaction was detected for number of primary branches per plant in cross 1 and single fruit weight in cross II, while duplicate type of epistasis was important for almost all the remaining characters in both the crosses. Simple pedigree selection as well as intermating among the elite segregants in the early generations followed by delayed selection might be useful in improving the yield levels in brinjal.

Thangavel *et al*. (2011) studied six families *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 for fruit yield and its component characters in brinjal and reported that additive, dominance and epistatic gene effects were found to contribute significantly in the inheritance of various characters of interest. The epistasis was of duplicate dominant type.

2.1.3 Variability

The effectiveness of selection in crop improvement programmes depends on the extent of genetic variability present in the population. In the past, very little efforts have been taken for development of inbred lines of brinjal through the exploitation of genetic variability present in the exotic hybrids. F_2 generation obtained from the selfing of F_1 hybrid provides all possible variations. So, selection with particular objectives in F_2 generation is very much effective and selfing of those selected genotypes generation after generation helps to develop inbred lines (similar to the parental lines of the exotic hybrids). These inbreds with desired characters including high yield potential can be used as High Yielding Variety (HYV) as well as the parents for hybrid variety. To increase the genetic yield potential, the maximum utilization of the desirable characters for developing any ideal genotypes is essential. Variability in brinjal is expected to be immense as the fruits vary greatly in shape and size (Kumar *et al*., 2013).

Doshi *et al*. (1999) studied 41 genotypes of brinjal (*Solanum melongena*) and reported wide variation for yield and quality characters like anthocyanin content, glycoalkaloid content. High heritability was observed for all the characters studied for brinjal. Further, anthocyanin content, total phenols, polyphenol oxidase activity, total soluble sugars and reducing sugars had high genetic advance coupled with high heritability, which suggested that these traits are under the control of additive gene action and can be improved through simple selection procedures.

Patel *et al*. (1999) studied fourty one genotypes of brinjal (*Solanum melongena*) and observed large variation for fruit volume followed by seed to pulp ratio, fruit weight, fruit volume, plant height. Negi *et al.* (2000) was studied genetic variability in 40 genotypes of brinjal [aubergine] for 21 characters. Significant differences were found among the genotypes for all the traits, indicating wide range of variation for number of fruits per plant, fruit yield per plant and fruit set.

Twenty three genotypes of brinjal (aubergine) were assessed by Golani *et al*. (2007) to determine the nature and magnitude of genetic divergence and genetic variability and reported significant variability for fruit yield and its contributing characters: plant height, plant spread, fruit length, fruit girth and 10-fruit weight. Prabhu and Natarajan (2007) studied two interspecific crosses of brinjal in BC_3F_3 generation and observed large variability for shoot and fruit borer infestation.

Ram and Singh (2007) evaluated sixty crosses and analysis of variance revealed significant differences among female and male genotypes for the characters like days to flowering, plant height, number of branches per plant, number of fruits per plant. Monpara *et al.* (2007) studied F_1, F_2 and their three parents of two crosses *viz*, H7 x green round and H7 x GCL 99 -1 observed wide range of variation for fruit yield per plant.

Kamani *et al.* (2007) studied F_2 generation of four crosses along with their five parents reported large variability for number of branches per plant, fruit length, fruit shape index, fruits per plant, fruit weight and fruit yield per plant, low variability for days to first picking and moderate for days to first flower, plant height and fruit girth. Prabhu *et al*. (2007) conducted a study on four interspecific crosses of aubergine in F_4 generation: and recorded significant variation on plant height, number of branches per plant, mean fruit weight, fruit length, fruit girth, number of fruits per plant, fruit and shoot borer (*Leucinodes orbonalis*) infestation, calyx length and marketable yield per plant.

Ravishankar (2007) compared the single cross and double cross F_1 hybrids, assessed the magnitude of variability in F_2 generation and reported wide variability for yield and yield attributing traits in segregating single and double cross F_2 populations.

Dhameliya *et al*. (2008) assessed genetic variability created through biparental mating and selfing in the F_2 of GBL 1 x GCL 99 -1 cross of brinjal and reported that biparental mating created more variability for days to first flowering, days to first picking, fruit length, single fruit weight, plant height, number of fruits per plant and fruit yield per plant.

Muniappan *et al.* (2010) studied genetic divergence in thirty four eggplant (*Solanum melongena* L.) genotypes and recorded wide variability for characters *viz*., number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight and fruit yield per plant.

Prasad *et al.* (2010) found that estimates of additive genetic variance (D) were significant for plant height at last picking, days to first fruit picking, fruit setting flowers, fruit volume, fruit length, fruit breadth, seed to pulp ratio, number of marketable fruits per plant, yield of marketable fruits per plant and average fruit weight. Dominance genetic variance (H1 and H2) were significant for all traits under study except plant height at first flowering, days to 50 %flowering and moisture content in fruits. The significance of additive and dominance variance components suggests that both these gene actions are important in the expression of their characters.

Dharwad *et al*. (2011) reported predominant non-additive gene action for number of branches per plant, days to flowering, number of fruits per plant, number of flowers per cluster, number of fruits per cluster and fruit weight (g).

Chattopadhyay *et al.* (2011) evaluated 35 diverse genotypes of brinjal for their morphological and yield component characters showed highly significant

variations and wide range of days to 50% of flowering, fruit length, fruit girth, fruit weight, number of marketable fruits per plant among the genotypes

Kafytullah *et al*. (2011) estimated the magnitude of genetic variability in 40 diverse genotypes of brinjal (*Solanum melongena* L.). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for fruit volume, fruit weight, fruit length, leaf area index, number of fruits per plant, fruit borer incidence, fruit diameter, number of fruits per cluster, yield per plot, fruit set per cent and fruit yield per hectare.

Shekar *et al.* (2011) evaluated 31 accessions and wide variation was observed for number of leaves per plant, leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant, fruit yield per plot, fruit yield per hectare. Thangavel *et al*. (2011) studied F_2, B_1 and B_2 segregating generations of four crosses of brinjal and reported wide range of variation for fruit length and number of fruits per plant and low for days to first flowering and number of branches per pant.

Kumar *et al*. (2012) reported wide variation for number of primary branches per plant, internodal length, average fruit weight, number of fruits per plant and fruit yield per plant indicating that selection can be predicted to improve the brinjal genotypes for these characters. Dhaka and Soni (2012) reported that highly significant differences were observed among the 20 diverse brinjal genotypes for different characters like average fruit weight, number of fruits per plant and fruit yield per plant.

Kumar *et al*. (2013) determined variability in segregants of eggplant (*Solanum melongena* L.). The crosses L_5 x T_4 (Palamedu Local x EP 65) and L_4 x T_1 (Alagarkovil Local x Annamalai) had the highest mean with high variability for individual fruit weight and fruit yield per plant. Favorable low mean with high variability occurred for days to first flowering (earliness) in the crosses L_5 x T_2 (Palamedu Local x KKM 1) and L_4 x T_2 (Alagarkovil Local x KKM 1). Direct

selection may be executed considering these genotypes for selection towards the development of early in flowering and high yielding brinjal varieties.

Sixty three genotypes of eggplant were studied by Manpreet *et al*. (2013) to estimate variability and wide variation was observed for traits like fruits per plant, fruit weight, pseudo style flowers, long style flowers, short style flowers, medium style flowers, flowers per inflorescence, fruit setting and fruit length.

Nayak and Nagre (2013) studied variability among 20 genotypes which revealed highly significant differences among the varieties for characters like fruit length, diameter, weight and fruit yield per plant. Singh *et al*. (2013) reported wide variation for characters *viz*., plant height, primary branches per plant, plant spread, days to first flowering, days to first fruit set, days to first harvest, average fruit weight, fruit length, fruit diameter, fruit index, fruits per plant and yield per plant.

Lokesh *et al*. (2013) studied 60 brinjal germplasm lines and reported wide variability for plant height, plant spread, number of branches per plant, number of fruits per cluster, average fruit diameter, average fruit weight, shoot and fruit borer incidence on shoot and fruit and fruit yield per plant. Prabakaran *et al.* (2013) evaluated 33 eggplant genotypes and reported wide variation for number of primary branches per plant, internodal length, leaf area index, number of long styled flowers per plant, fruit length, number of fruit per plant, average fruit weight, fruit yield per plant, total number of harvests, little leaf incidence and fruit borer infestation.

Kumar *et al.* (2013) reported large variation for calyx length, fruit pedicel length, shoot borer infestation, fruit borer infestation, little leaf incidence, ascorbic acid content, total phenols content, number of fruit per plant and fruit yield per plant. Yadav *et al.* (2014) evaluated 75 genotypes of eggplant and revealed large variability for average fruit weight, number of fruits per plant, plant spread, plant height, days to 50% flowering and days to first fruit set.

Kumar *et al.* (2014) assessed variability in 34 brinjal genotypes and recorded large variability for characters number of branches per plant, fruit length,

fruit breadth, number of fruits per plant, average fruit weight and fruit yield per plant.

Sabolu *et al.* (2014) conducted generation mean analysis in six populations, namely P_1, P_2, F_1, F_2, B_1 and B_2 and found significant digenic interactions for all the characters in majority of the crosses. Character and cross combination revealed the adequacy of simple additive dominance model for anthocyanin content (in crosses 2 and 3), glycolalkaloid content (in crosses 2, 3 and 4), dry matter content (in cross 4) and reducing sugars (in cross 2) indicating the absence of non-allelic interactions.

Genetic characters were studied in 36 different genotypes of brinjal by Mili *et al.* (2014). The genotypes showed significant differences for characters, single fruit weight, fruit diameter, seed yield per fruit, pulp seed ratio, total fruit yield per plot, fruits per plant, fruit yield per plant and fruit length.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The study entitled "Generation mean analysis in brinjal (*Solanum melongena* L.) for yield and yield attributes" was conducted in the Department of Plant Breeding and Genetics, College of Agricuture, Vellayani, during the period 2013-15.

The study comprised of two experiments.

Experiment I : Generation mean analysis

Experiment II : Study of F_2 population

3.1 EXPERIMENT I: GENERATION MEAN ANALYSIS

3.1.1 Materials

The materials for the study comprised of three F_1 hybrids, their respective parents (Wardha local, Surya, NBR-38, Swetha, Haritha), back cross generations B_1 and B_2 and F_2 produced from these F_1 hybrids. The detailed description of parental lines is given in Table 2.

3.1.2 Methods

3.1.2.1 Building up of Generations

Three superior F_1 hybrids selected from the 28 F_1 hybrids from the PG project entitled, 'Diallel analysis in brinjal (*Solanum melongena* L.)' were back crossed to their respective parents to produce B_1 and B_2 generations. Simultaneously, the F_1 hybrids were selfed to develop F_2 generation. The detailed list of F_1 hybrids and back crosses are given in Table 3 and F_2 population in Table 4.

3.1.2.2 Evaluation of Generations

The six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of each hybrid combination were evaluated in a randomised block design with three replications. Five plants were selected at random from each replication for recording observations in P_1,

Table 2. List of parental lines

Sl. No	Accession number	Name of parents	Source
1	P1	Wardha local	Wardha, Maharashtra
2	P2	Surya	KAU, Vellanikkara
3	P3	NBR-38	Nagpur, Maharashra
4	P4	Swetha	KAU, Vellanikkara
5	P5	Haritha	KAU, Vellanikkara

Table 3. List of hybrids and back crosses

List of hybrids		
Cross 1	P1×P2	Wardha local × Surya
Cross 2	P1×P3	Wardha local × NBR-38
Cross 3	P4×P5	Swetha × Haritha
List of back crosses		
Cross 1	(Wardha local × Surya) x Wardha local	(Wardha local × Surya) × Surya
Cross 2	(Wardha local × NBR-38) × Wardha local	(Wardha local × NBR-38) × NBR-38
Cross 3	Swetha x Haritha	(Swetha × Haritha) × Haritha

Table 4. List of F_2 population

Sl. No.	Cross combinations
1	Wardha local x Palakurthi local
2	Wardha local x Surya
3	Wardha local x NBR-38
4	Wardha local x Swetha
5	Swetha x Haritha
6	Surya x Haritha
7	Wardha local x Selection Pooja
8	Wardha local x Gopulapur local

Plate 1. Hand Emasculation

P_2, B_1, B_2 and F_1 and ten plants in F_2. Thirty five days old seedlings having 8-10 cm height were transplanted into the main field at a spacing of 60 × 60 cm. The crop received timely management practices as per Package of Practices Recommendations of Kerala Agricultural University (KAU, 2011).

3.1.2.3 Selfing and Crossing Technique

In brinjal anthesis occurs between 8 a.m. to 12 noon. Mature flower buds likely to open next morning were emasculated during previous evening hours and bagged. On the next day morning (between 7 to 10 a.m.) emasculated buds were pollinated by the pollen of the respective male parents. The pollinated buds were again bagged with paper bags and labeled. The mature crossed fruits were harvested and the seeds were collected separately from each cross. For the maintenance of parental lines and production of F_2 population flower buds of different parents and hybrids respectively were selfed by bagging the individual buds and properly tagged and later the seeds were collected from the mature fruits accordingly.

3.2 EXPERIMENT 2: STUDY OF F_2 POPULATION

The materials for the study comprised of eight F_2 population which were obtained by selfing eight superior F_1 hybrids selected from the 28 F_1 hybrids from the PG project entitled, 'Diallel analysis in brinjal (*Solanum melongena* L.)' and were evaluated in a field experiment. For selfing, mature flower buds that would open on the following day were covered with butter paper covers in the previous evening hours, labeled and the covers were retained till fruit set. The detailed list of hybrids used for developing F_2 population is given in Table 4.

3.2.1 Design and Layout

The experiment was laid out in compact family block design with eight families in three replications. There were five progenies within each family and ten plants within each progeny. Five randomly selected plants were tagged in

Plate 2. Overall view of the field

each progeny to record the observations and the average from these five plants was worked out for statistical analysis. Thirty five days old seedlings having 8-10 cm height were transplanted into the mainfield at a spacing of 60 × 60 cm. The crop received timely management practices as per Package of Practices Recommendations of Kerala Agricultural University (KAU, 2011).

3.3 BIOMETRIC OBSERVATIONS FOR EXPERIMENTS I AND II

Following were the observations recorded in this experiment.

3.3.1 Days to First Flowering

Number of days from the date of transplanting to the first flowering of observational plants was recorded and the average obtained.

3.3.2 Days to First Harvest

Number of days from the date of transplanting to the first fruit harvest of observational plants was recorded and the average obtained.

3.3.3 Fruit Length(cm)

Five fruits were selected at random from the observational plants. Fruit length was measured as the distance from peduncle attachment of fruit to the apex using twine and scale. Average was taken and expressed in centimeters.

3.3.4 Fruit Girth (cm)

Fruit girth was taken at the broadest part from the fruits used for recording the fruit length. Average was taken and expressed in centimeters.

3.3.5 Fruit Weight (g)

Weight of fruits used for recording fruit length was measured and average was found out and expressed in grams.

3.3.6 Calyx Length (cm)

The length of calyx was recorded for each fruit selected at random from the observational plants and expressed in centimeters.

3.3.7 Number of Fruits per Cluster

Number of fruits at each cluster in each observational plant was recorded and average was worked out.

3.3.8 Number of Primary Branches per Plant

Primary branches per plant were recorded from all the sample plants at the peak harvest stage and average was worked out.

3.3.9 Plant Height (cm)

Plant height was recorded from the ground level to the top most bud leaf of the plants at the time of peak harvest and presented in centimeters.

3.3.10 Yield per Plant (kg)

Weight of all fruits harvested from selected plants was recorded,average worked out and expressed in kilograms per plant

3.3.11 Number of Fruits per Plant

Number of fruits in each observational plant was recorded and average was worked out.

3.3.12 Volume of Fruit (cm^3)

Volume was recorded for each fruit selected at random from the observational plants using water displacement method and expressed in cubic centimeters.

3.3.13 Fruit and Shoot Borer (*Leucinodes orbonalis* Guen.)

Characterization of shoot and fruit borer incidence was done as suggested by Tewari and Krishnamoorthy (1985).

The incidence of shoot and fruit borer on plants was assessed in terms of percentage of infested plants out of total number of plants available in each plot.

$$Percentage\ of\ plants\ \text{inf}ested = \frac{Number\ of\ plants\ showing\ damage\ symptom \times 100}{Total\ number\ of\ plants}$$

Incidence on fruits was assessed by calculating percentage of infested fruits at different pickings and pooled data was subjected to statistical analysis.

$$Percentage\ of\ damaged\ fruits = \frac{Number\ of\ fruits\ with\ bore\ hole \times 100}{Total\ number\ of\ fruits\ on\ sample\ plants}$$

Total number of fruits with bore hole was recorded and percentage of damaged fruits was worked out.

Pest rating was done as per the scale suggested by Mukhopadhyay and Mandal (1994).

Percentage of fruit infestation	Rating
0 %	Immune
1-10 %	Highly resistant
11-20 %	Fairly resistant
21-30 %	Tolerant
31-40 %	Suceptible
41 % and above	Highly suceptible

3.4 STATISTICAL ANALYSIS

3.4.1 Experiment 1: Generation Mean Analysis

The concept of generation mean analysis was developed by Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation. Analysis of this technique was based on six different generations of a cross, *viz.*, parents (P_1, P_2), their F_1, F_2 and backcrosses (B_1, B_2). The mean values over replications were used for the estimation of gene effects.

The biometrical analysis consisted of two main steps, *viz., (i)* testing for epistasis *(ii)* estimation of gene effects and variances.

3.4.1.1 Development of Scales

Using the scaling test proposed by Mather (1949), estimation of additive (d) and dominance (h) components of genetic variance were made using the mean and variance of six generations *viz*., P_1, P_2, F_1, F_2, B_1, B_2.

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

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

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

$$D = 2\overline{F}_2 - \overline{B}_1 - \overline{B}_2$$

$$V(A) = 4V(\overline{B}_1) + V(\overline{P}_1) + V(\overline{F}_1)$$

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

$$V(C) = 16V(\overline{F}_2) + 4V(\overline{F}_1) + V(\overline{P}_{2)})$$

$$V(D) = 4V(\overline{F}_2) + V(\overline{B}_1) + V(\overline{B}_2)$$

Where, $\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{B}_1$ and $\overline{B}_2$ are the means of respective generations over all replications and $V(\overline{P}_1)$,$V(\overline{P}_2)$, $V(\overline{F}_1)$, $V(\overline{F}_2)$, $V(\overline{B}_1)$ and $V(\overline{B}_2)$ are the

respective variances. The standard errors of A, B, C and D were obtained as square root of V(A),V(B), V(C) and V(D) respectively.

$$S.E.(A) = \sqrt{V(A)}$$

$$S.E.(B) = \sqrt{V(B)}$$

$$S.E.(C) = \sqrt{V(C)}$$

$$S.E.(D) = \sqrt{V(D)}$$

3.4.1.2 Testing of Epistasis

Significance of any of the four scales indicates the inadequacy of additive-dominance model and presence of epistasis. For testing the significance of A, B, C and D scales, t test was employed.

$$\text{t (A)} = \frac{|A|}{S.E.(A)}$$

$$\text{t (B)} = \frac{|B|}{S.E.(B)}$$

$$\text{t (C)} = \frac{|C|}{S.E.(C)}$$

$$\text{t (D)} = \frac{|D|}{S.E(C|}$$

If the calculated 't' value of these scales is higher than 1.96, it is considered as significant. Significance of each of these scales reveals the presence of specific type of epistasis as detailed below:

a. The significance of either one or both of A and B scales indicates the presence of all the three types digenic interactions *viz*., additive x additive (i), additive x dominance (j) and dominance x dominance (l).

b. The significance of scale C denotes dominance x dominance type of non allelic interactions.

c. The significance of scale D reveals additive x additive type of gene interactions.

d. The significance of both C and D scales depicts dominance x dominance and additive x additive type of epistasis.

Variance of various generations was calculated by analysis of variance

3.4.1.3 Analysis of Variance

The biometric observations recorded were subjected to ANOVA for the estimation of variance of six generations (P_1, P_2, B_1, B_2, F_1 and F_2) used.

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replication	(r-1)	SS_R	MSR	MSR/MSE
Error	(n-r)	SS_E	MSE	
Total	(n-1)	SS_T		

r - Number of replications, n - Total number of observation

Error mean sum of squares (MSE) is the estimate of variance.

Estimate of variance of mean $= \frac{MSE}{r}$

Standard error of mean $= \sqrt{\frac{MSE}{r}}$

3.4.1.4 Estimation of Genetic Components

When the scales A, B, C and D were significantly different from zero, a digenic interaction model was assumed. Hayman (1958) and Jinks and Jones (1958) gave six parameter model for the estimation of various genetic components.

$$m = \overline{F}_2$$

$$d = \overline{B}_1 - \overline{B}_2$$

$$h = \overline{F}_1 - 4\overline{F}_2 - (1/2)\overline{P}_1 - (1/2)\overline{P}_2 + 2\overline{B}_1 + 2\overline{B}_2$$

$$i = 2\overline{B}_1 + 2\overline{B}_2 - 4\overline{F}_2$$

$$j = \overline{B}_{1-}(1/2)\overline{P}_1 - \overline{B}_2 + (1/2)\overline{P}_2$$

$$l = \overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$$

where,

m = mean

d = Additive effect

h = Dominance effect

i = Additive x Additive type of gene interaction

j = Additive x dominance type of gene interaction

l = Dominance x dominance type of gene interaction

The variance of these six genetic parameters were computed as follows:

$$V(m) = V(\overline{F}_2)$$

$$V(d) = V(\overline{B}_1) + V(\overline{B}_2)$$

$$V(h) = V(\overline{F}_1) + 16\,V(\overline{F}_2) + \tfrac{1}{4}\,V(\overline{P}_1) + \tfrac{1}{4}\,V(\overline{P}_2) + 4\,V(\overline{B}_1) + 4\,V(\overline{B}_2)$$

$$V(i) = 4\,V(\overline{B}_1) + 4\,V(\overline{B}_2) + 16\,V(\overline{F}_2)$$

$$V(j) = V(\overline{B}_1) + \tfrac{1}{4}V(\overline{P}_1) + V(\overline{B}_2) + \tfrac{1}{4}V(\overline{P}_2)$$

$$V(l) = V(\overline{P}_1) + V(\overline{P}_2) + 4\,V(\overline{F}_1) + 16\,V(\overline{F}_2) + 16\,V(\overline{B}_1) + 16\,V(\overline{B}_2)$$

The above genetic parameters were tested for significance using 't' test as in the case of scaling test.

3.4.1.5 Transgressive Segregants (%)

$$Transgressive\ segregants\ (\%) = \frac{Number\ of\ \ plants\ better\ than\ superior\ \ parent \times 100}{Total\ number\ of\ \ F_2\ \ plants}$$

3.4.2 Experiment No: 2

Study of F_2 population was done using compact family block design which utilizes the principle of local control more fully than a randomized block design.

3.4.2.1 Analysis of Variance

The analysis of variance was carried out for all the traits to find out whether there is any significant difference among the families and the progenies within the family.

Analysis of Variance for Families

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replication	(r-1)	SSR	MSR	MSR/MSE
Families	(f-1)	SSF	MSF	MSF/MSE
Error	(r-1)(f-1)	SSE	MSE	

Analysis of Variance for Progenies within the Family

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replication	(r-1)	SSR	MSR	MSR/MSE
Progenies	(p-1)	SSP	MSP	MSP/MSE
Error	(r-1) (p-1)	SSE	MSE	

Pooled Analysis of Variance

Source	df	Sum of squares	Mean squares	F
Replication	(r-1)	SSR	MSR	MSR/MSE
Families	(f-1)	SSF	MSF	MSF/MSE
Error	(r-1) (f-1)	SSE	MSE	
Progenies in i^{th} family	(p-1)	SSP_i	MSP_i	MSP_i/ MSE
Pooled error	f(r-1)(p-1)	SSE	MSE	

Where,

r = Number of replication, f = Number of treatments

p = Number of progenies, SSR = Replication sum of squares

MSR = Replication mean square SSF = Family sum of square

MSPi = Progeny mean square and i range from 1 to 8

MSF = Family mean square

Test of significance for various components was carried out by 'F' test. The F values were calculated as under

Replication = MSR/MSE

Treatments = MST/MSE

MSR - Mean square of replication

MST - Mean square of treatments

When the treatments differed significantly by the F test, the pair wise comparison of the treatment means are made by using critical difference as

$$Critical\ difference\,(CD) = t_{\propto} \times \sqrt{\frac{2MSE}{r}}$$

Where, $t_{\propto}$ is the students 't' table value for $\propto$ (5 per cent or 1 per cent) level of significance corresponding to the error degree of freedom.

RESULTS

4. RESULTS

4.1 GENERATION MEAN ANALYSIS

Generation mean analysis was done for the three selected crosses Wardha local x Surya, Wardha local x NBR-38 and Swetha x Haritha with respect to 13 characters. The results of generation mean analysis are presented in Table 5. The fruits of six generations P_1, P_2, F_1, F_2, B_1 and B_2 of the selected crosses are presented in Plates 3, 4 and 5. The results obtained from the present investigation are given below.

4.1.1 Days to First Flowering

Among the generations, F_2 in crosses 1 (28.56) and 2 (37.00) and B_2 in cross 3 (28.56) were earlier to flower while B_1 and P_2 (44.13) in cross 1, F_1 (48.06) in cross 2and P_1 (45.00) in cross 3 were late to flower.

Presence of non allelic interactions in all the crosses were indicated by the significant values of scales A, B, C and D.

Among the genetic components additive effect was significant and positive in cross 1 and non significant in crosses 2 and 3 while dominance effect was significant and positive in crosses 1 and 2 but negative in cross 3.

Of the interaction effects, additive x additive (i) was significant and positive in crosses 1 and 2 but negative in cross 3. Additive x dominance (j) type of interaction was positively significant in crosses 1 and 2 and non significant in cross 3. Dominance x dominance (l) type of interaction was significant, negative and greater than all other genetic components in cross 1 while in cross 3, it was positively significant.

Opposite signs of dominance (h) and dominance x dominance (l) indicated the duplicate nature of epistasis in all the crosses.

Table 5. Generation means (±SE), Scale values (±SE) and estimates of genetic components (±SE) in three selected crosses of brinjal.

	Days to first flowering			Days to first harvest		
	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Generation means						
P_1	38.26±0.21	38.26± 0.21	45.00±0.21	71.26± 0.42	71.26± 0.42	69.86±0.40
P_2	44.13±0.14	45.33±0.26	40.4±0.44	64.13±0.48	72.80± 0.36	59.66±0.34
F_1	41.60±0.17	48.06±0.16	36.46±0.39	65.00±0.50	64.60±0.31	61.60±0.33
F_2	28.56±0.14	37.00±0.15	33.26±0.19	63.00±0.24	71.00±0.30	59.43±0.26
B_1	44.13±0.14	41.00±0.17	29.73±0.40	63.60±0.42	68.00±0.49	64.33±0.34
B_2	40.60±0.13	41.60±0.16	28.56±0.36	50.00±0.45	58.00±0.46	59.13±0.26
Scale values						
A	8.40*±0.39	-4.32* ±0.43	-22.00*±0.91	-4.86*±1.07	-10.06*±1.11	-2.80*±1.04
B	-4.53*±0.35	-10.19*±0.44	-19.74*±0.93	-1.73±1.14	1.20±1.04	-3.00*±0.88
C	-51.35*±0.70	-31.71*±0.84	-25.28*±1.21	-62.59*±1.53	-48.06*±1.47	-15.00*±1.35
D	-27.61*±0.34	-8.60*±0.39	8.23*±0.66	-28.00*±0.78	-19.60*±0.90	-4.60*±0.78
Genetic components						
m	28.56*±0.77	37.00*±0.86	33.26*±1.07	50.00*±0.15	58.00*±0.15	59.43*±0.26
d	3.53*±0.19	-0.60±0.90	3.53±2.09	2.00*±0.61	-6.40*±0.67	5.20*±0.58
h	55.62*±0.72	23.46*±4.02	-51.26*±5.78	51.90*±1.86	35.17*±1.86	6.04*±1.63
i	55.22*±0.68	17.2*±3.91	-16.46*±6.01	56.00*±1.56	39.20*±2.03	9.20*±1.57
j	6.46* ±0.23	2.935*±1.12	-1.13±2.30	-1.56*±0.69	-5.63*±1.69	0.10*±0.64
l	-59.09*±1.05	-2.69*±8.49	58.20*±10.08	-49.41*±9.68	-30.34*±2.50	-3.40*±2.70
Epistasis	D	D	D	D	D	D

D : Duplicate type of epistasis C : Complimentary type of epistasis

Cross 1: Wardha local x Surya Cross 2: Wardha local x NBR-38 Cross 3: Swetha x Haritha

*Significant at 5 % level

4.1.2 Days to First Harvest

The generations B_2 in crosses 1 (50.00) and 2 (58.00) and F_2 and B_1 in cross 3 (59.13) were found earlier to harvest and P_1 in crosses 1 (71.20) and 3 (69.86) and P_2 in cross 2 (72.80) were noticed late to harvest.

Scales A, C and D were significant and negative in all the three crosses denoting the presence of non allelic interaction. Negative significance could be observed for scale B in cross 3 while it was absent in crosses 1 and 2.

Additive effect was significant and positive in crosses 1 and 3 and negative in cross 2 where as dominance effect and additive x additive (i) type of interaction were significant and positive in all the crosses. Crosses 1 and 2 displayed negatively significant values for additive x dominance (j) and dominance x dominance (l) type of interactions.

Duplicate nature of epistasis was prevalent in all the three crosses which was indicated by the opposite signs of dominance (h) and dominance x dominance (l) effects.

4.1.3 Length of Fruit (cm)

The longest fruits were observed in B_2, P_1 and F_2 in crosses 1 (18.33 cm), 2 (16.13 cm) and 3 (23.50 cm) respectively while the shortest fruits were recorded by P_2 in crosses 1 (9.26 cm) and 2 (7.33 cm) and B_2 in cross 3 (14.49 cm).

Significance could be noticed for the scales B, C and D in crosses 1 and 3 and scales A, C and D in cross 2 indicating the presence of all the types of epistatic interactions in all the crosses.

Additive (d) effect, additive x dominance (j) and dominance x dominance (l) type of interactions were significant and positive in crosses 1 and 2 and

Table 5. Generation means (±SE), Scale values (±SE) and estimates of genetic components (±SE) in three selected crosses of brinjal. Contd...

	Length of fruit (cm)			Girth of fruit (cm)		
	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Generation means						
P_1	16.13±0.41	16.13±0.41	18.00±0.37	14.20±0.32	14.20±0.32	16.70±0.29
P_2	9.26±0.38	7.33±0.47	20.06±0.41	14.90±0.33	14.13±0.30	17.30±0.30
F_1	14.80±0.49	14.66±0.48	16.13±0.47	12.06±0.34	12.00±0.34	15.8±0.31
F_2	10.13±0.31	9.40±0.28	23.50±0.28	15.04±0.22	13.73±0.24	14.30±0.21
B_1	14.86±0.43	13.20±0.439	21.79±0.43	13.7±0.36	16.8±0.30	12.9±0.34
B_2	18.33±0.46	14.93±0.42	14.49±0.46	13.1±0.30	15±0.33	13.6±0.33
Scale values						
A	-1.39±1.09	-0.01±1.08	-7.53*±1.06	-3.78*±0.86	-7.00*±0.76	2.00*±0.81
B	-3.86*±1.11	-1.73±1.08	5.14*±1.11	2.2*±0.77	-3.47*±0.811	-1.6±0.80
C	18.21*±1.70	9.86*±1.64	-23.68*±1.58	-4.1*±1.216	-1.93±1.29	-5.4*±1.16
D	11.73*±0.89	5.80*±0.84	-10.65*±0.85	-1.26±0.64	4.27*±0.67	-2.9*±0.64
Genetic components						
m	18.33*±0.27	14.93*±0.25	14.49*±0.18	13.93*±0.23	13.93*±0.23	10.03*±0.28
d	4.67*±0.63	5.26*±0.61	-7.37*±0.63	-3.34*±0.47	-1.73*±0.44	1.50*±0.47
h	-21.29*±1.77	-10.13*±1.77	24.05*±1.79	1.67*±1.40	-5.90*±1.40	1.70*±1.35
i	-23.46*±1.79	-11.60*±2.02	21.30*±1.70	2.52±1.29	-8.54*±1.56	5.80*±1.29
j	1.23*±0.69	0.86*±2.07	-6.33*±0.69	-2.99*±0.52	-1.76±1.54	1.80*±0.52
l	28.71*±10.02	13.34*±2.44	-18.91*±3.00	-0.94±7.41	19.01*±1.79	-6.20*±2.23
Epistasis	D	D	D	D	D	D

negative in cross 3 whereas dominance effect (h) and additive x additive (i) type of interaction were negatively significant in crosses 1 and 2 and positively significant in cross 3.

Presence of duplicate nature of epistasis for this trait was indicated by the opposite signs of dominance (h) and dominance x dominance (l) in all the crosses.

4.1.4 Girth of Fruit (cm)

The maximum values of fruit girth were observed for F_2 in cross 1 (15.04 cm), B_1 in cross 2 (16.8 cm) and P_2 in cross 3 (17.30 cm) and the minimum values were recorded by F_1 in crosses 1 (12.06 cm) and 2 (12.00 cm) and B_1 in cross 3 (12.90 cm).

Scales A, B and C exhibited significance in cross 1, scales A, B and D in cross 2 and scales A, C and D in cross 3 were significant indicating the presence of all the three types of digenic interactions.

Among the genetic components additive effect was significant and negative in crosses 1 and 2 and positive in cross 3 while dominance effect was significant and positive in crosses 1 and 3 and negative in cross 2.

Additive x additive (i) interaction was not significant in cross 1, significant and negative in cross 2 but positive in cross 3. Negatively significant additive x dominance (j) type of interaction was noticed in cross 1 while it was positive in cross 3 and absent in cross 2. Dominance x dominance (l) effect was not significant in cross 1, significant but positive in cross 2 and negative in cross 3. Epistasis was revealed to be duplicate in all the three crosses.

Table 5. Generation means (±SE), Scale values (±SE) and estimates of genetic components (±SE) in three selected crosses of brinjal. Contd...

	Number of primary branches			Fruits per cluster		
	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Generation means						
P_1	7.80±0.16	7.80±0.16	5.30±0.16	2.20±0.18	2.20±0.18	1.40±0.21
P_2	4.60±0.15	5.30±0.16	6.20±0.17	1.06±0.14	0.60±0.14	1.00±0.10
F_1	6.06±0.13	4.10±0.13	4.93±0.17	1.86±0.08	1.70±0.07	2.60±0.07
F_2	4.93±0.10	6.70±0.11	4.20±0.10	0.93±0.05	1.13±0.09	3.80±0.08
B_1	5.2±0.16	6.2±0.14	6.9±0.15	3.10±0.14	2.93±0.12	0.93±0.12
B_2	5.36±0.17	4.7±0.13	7.50±0.13	2.50±0.12	3.80±0.09	2.10±0.12
Scale values						
A	-0.88*±0.39	-5.80*±0.35	-2.34*±0.39	-1.56*±0.35	-1.73*±0.32	2.87*±0.33
B	0.06±0.40	1.9*±0.34	-4.7*±0.37	-2.3*±0.30	-1.27*±0.24	5.67*±0.28
C	3.84*±0.53	-6.7*±0.57	4.7*±0.59	0.53*±0.37	6.54*±0.48	4.14*±0.43
D	-0.27±0.31	-1.4*±0.29	5.87*±0.28	2.201*±0.228	4.77*±0.25	-2.2*±0.24
Genetic components						
m	5.36*±0.19	6.03*±0.20	6.90*±0.25	0.93*±0.05	1.83*±0.09	1.00*±0.08
d	1.13*±0.24	-2.60*±0.19	0.73*±0.20	0.93*±0.19	0.57*±0.15	-1.2*±0.17
h	-0.46±0.61	2.45*±0.61	-10.59*±0.61	-2.93*±0.52	-8.01*±0.52	4.13*±0.50
i	0.54±0.63	2.80*±0.78	-11.74*±0.57	-4.40*±0.45	-9.54*±0.90	4.40*±0.48
j	-0.47±0.26	-3.85*±0.80	1.18*±0.23	0.36*±0.22	-0.23*±0.54	-1.40*±0.21
l	0.28±3.80	1.10±0.82	18.78*±1.01	8.27±3.06	12.54±0.71	-12.94±0.83
Epistasis	D	C	D	D	D	D

4.1.5 Number of Primary Branches

Number of primary branches were the highest for P_1 in crosses 1 (7.80) and 2 (7.80) and B_2 in cross 3 (7.50) andthe lowest for P_2 in cross 1 (4.60), F_1 in cross 2 (4.10) and F_2 in cross 3 (4.20).

Significance was noticed for scales A and C in all the three crosses while scales B and D exhibited significance in crosses 2 and 3.

All the crosses exhibited positively significant additive (d) effect whereas dominance (h) effect was significant and positive in cross 2, negative in cross 3 and non significant in cross 1.

All the interactions were not significant in cross 1 and significant in cross 3. Additive x additive (i) interaction was significant and positive and additive x dominance (j) interaction was negative in cross 2.

Opposite signs of dominance (h) and dominance x dominance (l) indicated the duplicate nature of epistasis in crosses 1 and 3 and similar sign showed the complementary nature of epistasis in cross 2.

4.1.6 Number of Fruits per Cluster

The maximum number of fruits per cluster were recorded by B_1 (3.10), B_2 (3.80) and F_2 (3.80) in crosses1, 2 and 3 respectively and the minimum values were recorded by F_2 in cross 1 (0.93), P_2 in cross 2 (0.60) and B_1 in cross 3 (0.93).

Crosses 2 and 3 exhibited significance for all the scales and cross 1 showed significance for all the scales except C.

For number of fruits per cluster additive effect was found to be significant and positive in crosses 1 and 2 but dominance effect was negatively significant. Additive and dominance effects were significant in cross 3. Additive x additive

interaction was significant in cross 3 and the other two crosses had significant negative additive effect. Additive x dominance (j) effect and dominance x Table dominance (l) effect were significant in crosses 1 and 2 where as in cross 3 it was significant and negative. Duplicate nature of epistasis was revealed in all the three crosses.

4.1.7 Plant Height (cm)

Maximum values for plant height were exhibited by F_1 (131.08 cm), P_1 (123.24 cm) and P_2 (137.50 cm) generations in crosses 1, 2 and 3 respectively whereas minimum values were displayed by the generations B_1 (77.47 cm) in cross 1, P_2 (70.47 cm) in cross 2 and P_1 (103.10 cm) in cross 3.

All the four scales displayed significance in all the crosses except scale D in cross 3 denoting the presence of all the epistatic interaction.

Among the genetic components additive (d) effect was significant and positive in cross 1, negative in cross 2 and non significant in cross 3 while dominance (h) effect was significant and positive in cross 1 and negativein crosses 2 and 3.

Among the interactions additive x additive (i) effect was significant and positive in cross 1, negative in cross 2 and non significant in cross 3 while additive x dominance (j) interaction was significant but positive in crosses 1 and 3 and negative in cross 2. Dominance x dominance (l) interaction was significant but negative in cross 1 and positivein crosses 2 and 3.

In all the crosses duplicate nature of epistasis was seen for this trait which is evident from the opposite signs of dominance (h) and dominance x dominance (l).

Plate 3. Fruits characteristics of six generations (P_1, P_2, B_1, B_2, F_1 and F_2) in cross 1.

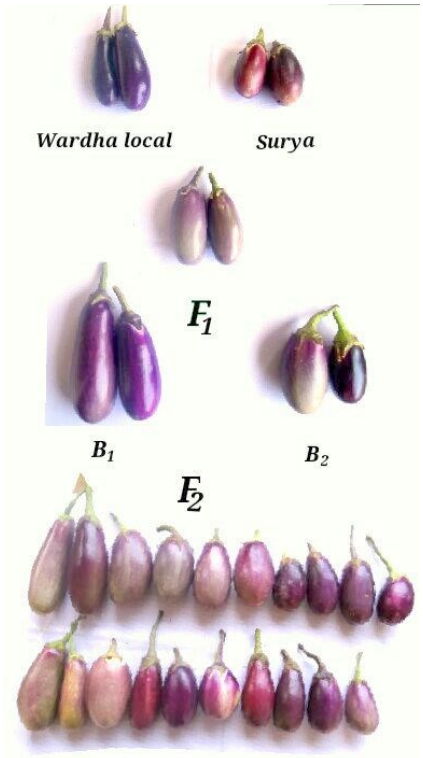
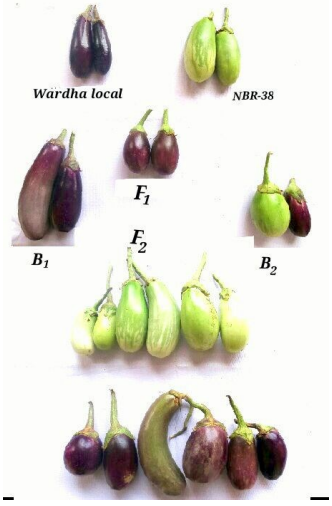
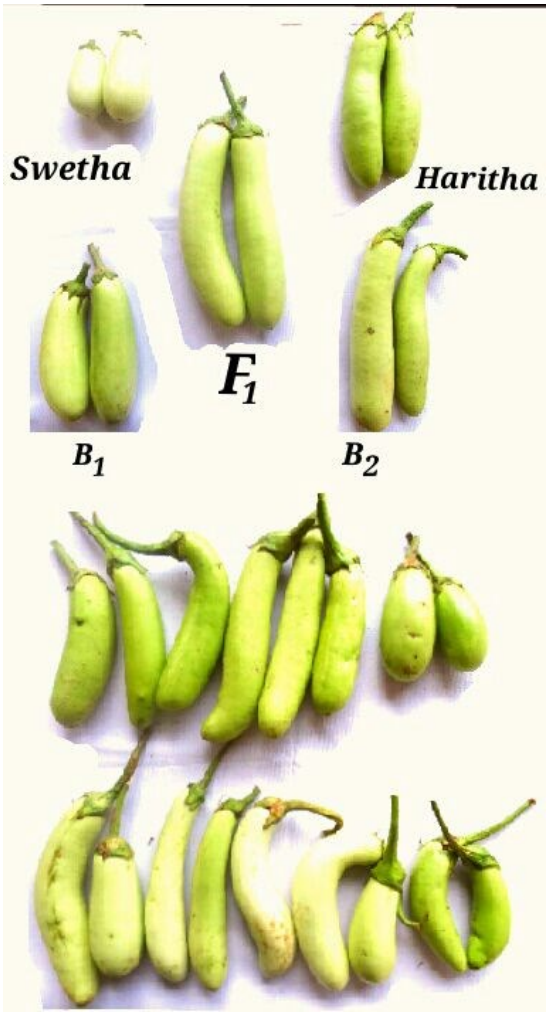


Plate 2. Fruits characteristics of six generations (P_1, P_2, B_1, B_2, F_1 and F_2) in cross 2.



F_2

Plate 3. Fruits characteristics of six generations (P_1, P_2, B_1, B_2, F_1 and F_2) in cross 3.



F_2

4.1.8 Calyx Length (cm)

The highest mean values for calyx length were recorded by F_1 (3.74 cm), B_2 (4.15 cm) and P_2 (5.06 cm) in crosses 1, 2 and 3 respectively and the lowest values by were recorded by P_2 (2.92 cm), F_2 (2.39 cm) and P_1 (3.13 cm) in crosses 1, 2 and 3 respectively.

All the scales were significant in all the crosses indicating the presence of all the epistatic interaction.

Among the genetic components additive effect was significant and positive in crosses 1 and 2 and negative in cross 3 while dominance effect was negatively significant in crosses 1 and 2 and non significant in cross 3.

Additive x additive (i) interaction was significant and negative in all the crosses while dominance x dominance (l) interaction was positivein crosses 2 and 3. Additive x dominance (j) type of interaction was significant but positive in crosses 1 and 2 while non significant in cross 3.

Dominance (h) and dominance x dominance (l) with opposite signs showed duplicate nature of epistasis in all crosses.

4.1.9 Volume of Fruit (cm^3)

The maximum values for fruit volume were recorded by B_1 in cross 1 (180.40 cm^3) and 2 (180.40 cm^3) and P_2 (190.83 cm^3) and B_1 (190.83 cm^3) in cross 3 and the minimum values were recorded by P_1 (80.17 cm^3), P_2 (60.18 cm^3) and B_2 (60.35 cm^3) in crosses 1, 2 and 3 respectively.

Significance was reported for all the scales in all the crosses indicating the presence of all the epistatic interaction.

Additive (d) effect was significant but positive in crosses 1 and 2 and negative in cross 3 while dominance (h) effect was positive in all crosses.

Table 5. Generation means (±SE), Scale values (±SE) and estimates of genetic components (±SE) in three selected crosses of brinjal. Contd..

	Weight of fruit (g)			Volume of fruit (cm^3)		
	Cross 1	Cross 2	Cross 3	Cross 1	Cross 2	Cross 3
Generation means						
P_1	90.04±0.37	90.04±0.37	81.30±0.42	80.17±0.33	80.17±0.33	121.33±0.36
P_2	54.46±0.4	44.81±0.38	121.21±0.41	151.34±0.37	60.18± 0.30	190.83±0.26
F_1	100.74±0.40	95.48±0.37	75.84±0.43	150.94±0.55	140.81±0.35	140.81±0.26
F_2	65.35±0.43	54.46±0.36	114.57±0.4	100.21±0.33	90.01± 0.22	170.73± 0.21
B_1	115.96±0.40	125.73±0.4	130.86±0.40	180.40±0.43	180.40±0.36	190.83±0.36
B_2	60.68±0.43	51.61±0.32	55.19±0.26	80.58±0.35	70.29±0.35	60.35±0.30
Scale values						
A	-4.50*±0.98	-24.81*±0.92	-60.48*±1.05	41.31*±1.08	21.04*±0.89	-30.54*±0.85
B	-39.71*±1.02	-61.62*±0.91	-22.92*±0.98	131.32*±0.97	-60.57*±0.87	-40.20*±0.71
C	-133.7*±1.44	-179.84*±1.62	-243.45*±1.46	-269.99*±1.81	-220.00*±1.30	-452.39*±1.11
D	-44.74*±0.80	-46.70*±0.83	-80.02*±0.79	-89.99*±0.87	-90.24*±0.67	-190.82±0.63
Genetic components						
m	60.68*±0.25	51.61*±0.38	55.19*±0.31	80.58*±0.21	70.29*±0.22	60.35*±0.21
d	35.39*±0.59	41.02*±0.52	-38.73*±0.59	50.73*±0.56	50.80*±0.50	-29.92*±0.47
h	133.19*±1.74	151.71*±1.74	189.64*±1.66	244.63*±1.43	290.71*±1.43	416.40*±1.32
i	89.48*±1.60	93.41*±2.05	160.04*±1.59	179.98*±1.75	180.48*±1.85	381.65*±1.27
j	17.60*±0.65	18.40*±2.02	-18.77*±0.66	86.32*±0.61	40.81*±1.50	4.83*±0.52
l	-45.26*±9.32	-6.98*±2.23	-76.63*±2.79	-89.97*±8.92	-140.95*±1.98	-310.91*±2.19
Epistasis	D	D	D	D	D	D

Positively significant additive x additive (i) and additive x dominance (j) and negatively significant dominance x dominance (l) interactions were noticed in all the crosses.

Opposite signs of dominance (h) and dominance x dominance (l) showed duplicate nature of epistasis in all crosses.

4.1.10 Weight of Fruit (g)

The maximum values for fruit weight were observed for B_1 in cross 1 (115.96 g), cross 2 (125.73 g) and cross 3 (130.86 g) while the minimum values were recorded by P_2 in cross 1 (54.46 g) and cross 2 (44.81 g) and B_2 in cross 3 (55.19 g).

Presence of epistatic interaction was indicated by the significance of all the scales in all the crosses.

Among the genetic components additive (d) effect was significant and positive in crosses 1 and 2 and negativein cross 3 while dominance (h) effect was positively significant in all the crosses.

Positive significance of additive x additive (i) and negative significance of dominance x dominance (l) effects were reported in all the crosses. Additive x dominance (j) effect was significant and positive in crosses 1 and 2 and negative in cross 3.

Opposite signs of dominance (h) and dominance x dominance (l) showed duplicate nature of epistasis in all crosses.

4.1.11 Number of Fruits per Plant

The highest means for number of fruits per plant were recorded by B_2 in crosses 1 (50.26) and 2 (42.93) and F_1 in cross 3 (50.26) while the lowest means were recorded by F_2 in crosses 1(18.20) and 3 (18.20) and B_1 in cross 2(14.26).

Scales A, B, C and D were significant but positive in all the crosses except scale B in crosses 1 and 3 and scale A in cross 2 where they were negatively significant.

Among the genetic components additive effect was significant and positive in crosses 1 and 3 and negativein cross 2 while dominance effect was negatively significant in all crosses.

Additive x additive (i) effect was significant and negative in all the crosses. Additive x dominance (j) effect was significant and negative in cross 2 and positive in crosses 1 and 3 while dominance x dominance (l) effect was positively significant in crosses 1 and 2 and non significant in cross 3.

Duplicate nature of epistasis was reported in all the crosses which was indicated by the opposite signs of dominance (h) and dominance x dominance(l).

4.1.12 Yield per Plant (kg)

The highest and the lowest fruit yield per plant were exhibited by F_1 (3.65 kg) and F_2 (1.18 kg) in cross 1, P_1 (3.08 kg) and P_2 (0.96 kg) in cross 2 and B_1 (3.66 kg) and B_2 (1.18 kg) in cross 3 respectively.

Significance was exhibited by all the scales in all the crosses indicating the presence of non allelic interaction.

Significance was observed for additive (d) effect which was positive in cross 1 and negative in crosses 2 and 3 whereas dominance (h) effect was negative in cross 1 and positive in other two crosses.

Additive x additive (i) effect was significant but negative in cross 1 and positive in crosses 2 and 3, additive x dominance (j) effect was negative in cross 2 and positive in crosses 1 and 3 and dominance x dominance (l) effect was positive in crosses 1 and 3 and non significant in cross 2.

Table 5. Generation means (±SE), Scale values (±SE) and estimates of genetic components (±SE) in three selected crosses of brinjal. Contd....

	Fruit and shoot borer incidence (%)		
	Cross 1	Cross 2	Cross 3
Generation means			
P_1	54.00±0.33	54.00±0.29	34.00±0.33
P_2	21.00±0.29	65.00±0.30	29.00±0.31
F_1	42.00±0.32	78.00±0.32	42.00±0.30
F_2	16.00±0.20	18.00±0.23	15.00±0.21
B_1	73.00±0.33	89.00±0.28	36.00±0.29
B_2	28.00±0.31	92.00±0.29	45.00±0.30
Scale values			
A	50.00*±0.82	46.00*±0.72	-4.00*±0.73
B	-7.00*±0.77	41.00*±0.74	19.00*±0.75
C	-95.00*±1.14	-203.00*±1.20	-0.21±1.14
D	-69.00*±0.62	-145.00*±0.62	-51.00*±0.47
Genetic components			
m	16.00*±0.20	18.00*±0.23	15.00*±0.21
d	45.00*±0.46	-3.00*±0.41	-9.00*±0.42
h	142.5.00*±1.30	308.50*±1.30	112.50*±1.26
i	138.00*±1.24	290.00*±1.24	102.00*±1.20
j	28.50*±0.51	2.50*±0.46	-11.50*±0.48
l	-181.00*±2.18	-377.00*±2.05	-117.00*±2.04
Epistasis	D	D	D

Table 6. Fruit infestation percentage (Mukhopadhya and Mandel (1994)) and Scoring rate.

Sl. No.	Fruit infestation %	Grade	Rating	Genotype
1	0%	1	Immune	Nil
2	1-10 %	2	Highly resistant	Nil
3	11-20%	3	Fairly resistant	F_2 in crosses 1, 2 and 3
4	21-30 %	4	Tolerant	P_2 in crosses 1 and 3, B_2 in cross 1
5	31-40 %	5	Suceptible	P_1, B_1 in cross 3
6	41 % and above	6	Highly suceptible	P_1, F_1 and B_1 in cross 1 P_1, P_2, B_1, B_2, F_1 in cross 2 F_1 and B_2 in cross 3

Crosses 1 and 2 exhibited duplicate epistasis whereas complementary epistasis was displayed in cross 3.

4.1.13 Fruit and Shoot Borer Incidence (%)

Incidence of fruit and shoot borer was the lowest in F_2 in all the crosses. Cross 3 has the minimum value of 15.00 % followed by cross 1 (73.00 %) and cross 2 (92.00 %).

All the scales were significant in all the crosses except scale C in cross 3 indicating the presence of all the epistatic interaction.

Among the genetic components additive (d) effect was significant and positive in cross 1 while negative in crosses 2 and 3. Dominance (h) effect was positively significant in all the three crosses.

Additive x additive (i) interaction was significant but positive and dominance x dominance (l) interaction was negative in all the crosses and additive x dominance (j) interaction was positive in crosses 1 and 2 and negatively significant in cross 3. Epistasis was duplicate in all the crosses.

Pest rating was done as per the scale suggested by Mukhopadhyay and Mandel (1994) is presented in Table 6. None of the crosses were in the range of immune or highly resistant. F_2 in cross 1, 2 and 3 were fairly resistant and P_2 in crosses 1 and 3, B_2 in cross 1 were tolerant while P_1 and B_1 in cross 3 were susceptible.

Results showed that in cross 1, additive gene effects (additive, additive x additive) were important for fruit girth, number of primary branches, calyx length and plant height while non-additive gene actions (dominance, additive x dominance and dominance x dominance) were recorded for fruit weight, fruit volume, fruit length, yield per plant, days to first flowering, days to first harvest, number of fruits per plant, number of fruits per cluster, plant height and low

Table 7. Transgressive segregants in three crosses of brinjal.

Sl. No.	Characters	Transgressive Segregants (%)		
		Cross 1	Cross 2	Cross 3
1	Days to first flowering	Nil	Nil	Nil
2	Number of primary branches	76.6 %	63.3 %	60 %
3	Days to first harvest	Nil	Nil	Nil
4	Number of fruits per plant	53.3 %	Nil	Nil
5	Yield per plant (kg)	Nil	Nil	Nil
6	Number of fruits per cluster	Nil	Nil	Nil
7	Length of fruit (cm)	20 %	Nil	Nil
8	Girth of fruit (cm	40 %	40 %	3.3 %
9	Weight of fruit (g)	Nil	Nil	Nil
10	Volume of fruit (cm^3)	Nil	Nil	Nil
11	Calyx length (cm)	36.6 %	93.3 %	Nil
12	Plant height (cm)	Nil	Nil	Nil
13	Incidence of pests and diseases (%)	Nil	Nil	Nil

incidence of fruit and shoot borer. In cross 2, additive gene effects were predominant for yield per plant and number of primary branches and non additive gene actions were important for all other traits. In cross 3, additive gene action was reported for fruit girth and number of fruits per cluster and all other characters were under the control of non-additive gene action. Duplicate type of epistasis was observed for most of the crosses.

4.2 TRANSGRESSIVE SEGREGANTS

Transgressive segregants were observed in all the three crosses for number of primary branches and girth of fruit (Table 7). The highest percentage of segregants (76.6%) was observed in cross 1 followed by cross 2 (66.3%) and cross 3 (60%). Crosses 1 and 2 recorded the highest percentage of segregants for girth of fruit (40%) followed by cross 3 (3.3 %). Transgressive segregants for number of fruits per plant (53.3 %) and length of fruit (20 %) were observed in cross 1. Crosses 1 and 2 recorded transgressive segregants for calyx length.

4.3 STUDY OF F_2 POPULATION

The eight F_2 families and each family consisting of five progenies were evaluated in the field for 13 biometric characters namely days to first flowering, number of primary branches, days to first harvest, number of fruits per plant, yield per plant (kg), number of fruits per cluster, length of fruit (cm), girth of fruit (cm), weight of fruit (g), volume of fruit (cm^3), calyx length (cm), plant height (cm) and fruit and shoot borer incidence (%).

4.3.1 Variability among the Families

The analysis of variance conducted for different characters showed significant differences for all the characters among the different families. Mean square values of thirteen characters in eight families of brinjal is presented in Table 8.

Table 8. Mean square values of twelve characters in eight families of brinjal.

Sources	**df**	**Days to first flowering**	**Length of fruit (cm)**	**Girth of fruit (cm)**	**Number of fruits per cluster**	**Number of primary branches**	**Days to first harvest**	**Volume of fruit (cm^3)**
Replication	2	313.72	21.47	40.01	0.0050	39.51	230.33	311.82
Families	7	356.06	149.07	52.96	25.73	14.47	547.42	2412.14
Error	14	0.48	2.27	0.003	0.0051	0.02	1.11	6.34
Progeny in Family1	4	1.47	0.69	0.19	0.0057	0.85	4.73	1.51
Family 2	4	2.17	0.62	0.37	0.0040	0.74	2.40	2.69
Family 3	4	1.74	0.77	0.41	0.0107	1.03	2.46	0.67
Family 4	4	1.20	0.72	0.42	0.0107	1.17	3.20	1.96
Family 5	4	1.16	0.63	0.45	0.0173	1.05	4.30	1.12
Family 6	4	1.34	0.71	0.32	0.0160	0.83	2.46	2.56
Family 7	4	1.07	0.66	0.49	0.0493	0.56	1.86	1.33
Family8	4	1.09	0.52	0.41	0.0040	1.05	1.24	2.86
Pooled error	64	0.042	0.03	0.02	0.017	0.013	0.029	0.548

Table 8. Mean square values of twelve characters in eight families of brinjal. Contd…

Sources	**df**	**Plant height (cm)**	**Number of fruits per plant**	**Weight of fruit (g)**	**Yield per plant (kg)**	**Calyx length (cm)**	**% of plants infested with shoot and fruit borer**
Replication	2	251.62	262.39	489.99	1.95	41.01	15407.50
Families	7	4939.87	83.9	858.36	1.06	4.55	3037.61
Error	14	2.15	1.37	1.65	0.008	0.014	26.54
Progeny in Family1	4	5.02	2.16	1.58	0.007	0.75	166.66
Family 2	4	4.31	3.63	2.40	0.020	0.38	123.33
Family 3	4	5.12	2.30	2.78	0.012	0.54	156.66
Family 4	4	6.09	2.44	2.46	0.016	0.51	176.66
Family 5	4	6.61	2.34	1.70	0.011	0.65	176.66
Family 6	4	4.69	2.56	3.29	0.021	0.30	159.99
Family 7	4	6.17	2.55	3.60	0.015	0.35	150.00
Family 8	4	5.60	2.324	3.60	0.018	0.55	156.66
Pooled error	64	0.033	0.026	0.03	0.0001	0.010	47.08

4.3.2 Mean Performance of the Families and Progenies within Families

Mean performance of 8 F_2 families for thirteen biometric characters studied are given in Table 9 and mean performance of progenies in 8 families for different characters is presented in Table 10 (Plates 6-13).

4.3.2.1 Days to First Flowering

Days to first flowering showed significant differences among the families. Mean values for this character ranged from 28.02 to 42.06 days. Family 2 (28.02 days) was the earliest to flower and other families were significantly different from family 1 for days to first flowering and family 8 (42.06) was found late to flower.

There were significant differences among the progenies for days to first flowering in all the families except family 6. Mean values for this trait ranged from 35.66 to 37.46 days in family 1. Progeny 4 (35.66) was the earliest to flower and progeny 2 (37.46) was late to flower (Fig 1).

In family 2 mean values for days to first flowering ranged from 27.00 to 29.16 days. Progeny 1 (27.00) exhibited early flowering and other progenies were significantly different from progeny 1 for days to first flowering and progeny 4 (29.16) was found late to flower.

For days to first flowering mean values ranged from 38.10 to 39.76 days in family 3. Minimum number of days to first flowering was taken by progeny 3 (38.10) and progeny 1 (39.76) took the maximum days to first flowering which was on par with progeny 5 (39.26).

Mean values for days to first flowering ranged from 36.16 to 38.16 days in family 4. Early flowering was reported in progeny 5 (36.16 days) and progeny 3 (38.16 days) took maximum days to first flowering.

Table 9. Mean values of thirteen characters in eight families of brinjal

Families	Days to first flowering	Length of fruit (cm)	Girth of fruit (cm)	Number of fruits per cluster	Number of primary branches	Days to first harvest	Volume of fruit (cm^3)
1	36.50 [a]	13.1 [ab]	9.94	2.36	6.15 [a]	62.47	60.05
2	28.02	9.16	13.00	1.40 [a]	5.07 [b]	49.67	82.23 [a]
3	37.00 [a]	6.95	14.03	1.64	6.03 [a]	58.03	70.38 [b]
4	38.91	13.06 [ab]	11.08	2.80	4.80	65.53	80.56
5	35.66	14.08 [a]	10.05	1.22 [a]	7.08	59.81	63.39
6	29.78	14.15 [a]	11.03	1.22 [a]	5.05 [b]	55.12	100.16
7	40.15	17.13	8.05	4.75	4.00	64.04	72.16 [b]
8	42.06	12.11[b]	12.00	1.26 [a]	6.17 [a]	68.32	80.81 [a]
CD @ 5 %	0.546	1.180	0.045	0.193	0.127	0.827	1.97

Families	Plant height (cm)	Number of fruits per plant	Weight of fruit (g)	Yield per plant (kg)	Calyx length (cm)	% of plants infested with shoot and fruit borer
1	132.02	21.80 [cd]	39.90	0.87	3.01	51.34[a]
2	86.82	25.79 [a]	60.13 [a]	1.55 [a]	3.35 [b]	64.07
3	108.94	20.68 [e]	50.14 [c]	1.04	3.92	58.85
4	102.78	27.10	54.43 [b]	1.48	3.70 [a]	50.39 [a]
5	124.78	21.09 [de]	54.22 [b]	1.15 [b]	4.20	33.60
6	139.60	25.23 [a]	64.00	1.62 [a]	2.46	45.76 [b]
7	96.13	22.52 [bc]	50.68 [c]	1.14 [b]	3.36 [b]	45.04 [b]
8	110.36	22.78 [b]	60.18 [a]	1.37	3.72 [a]	58.95
CD @ 5 %	1.150	0.918	1.007	0.071	0.093	4.020

Table 10. Mean values of progenies for different characters

Family	progenies	Days to first flowering	Length of fruit (cm)	Girth of fruit (cm)	Number of fruits per cluster	Number of primary branches	Days to first harvest	Volume of fruit (cm^3)	Plant height (cm)	Number of fruits per plant	Weight of fruit (g)	Calyx length (cm)	Yield (Kg)	% of plants infested with shoot and fruit borer
1	1	36.93	13.46	10.00 [a]	2.36	6.36	62.33	59.20	131.80 [a]	21.66	39.76	2.80	0.86	51.14
	2	37.46	13.80	10.06[a]	2.30	6.13	63.53	60.13	132.90	23.06	40.86	2.30	0.94	45.00
	3	36.30[a]	13.10[a]	10.26	2.40	6.90	63.83	60.26	133.73	22.03	40.4	3.00	0.89	57.78
	4	35.66	13.00[a]	9.80	2.26	5.90	61.93	61.06	131.16 [ab]	21.53	39.33	3.43[a]	0.85	53.85
	5	36.16[a]	12.53	9.60	2.46	5.46	60.73	59.60	130.53 [b]	20.73	39.13	3.53[a]	0.81	48.92
CD @ 5 %		0.354	0.129	0.103	NS	0.091	0.827	NS	0.798	0.102	0.162	0.119	0.009	NS
Family mean		36.50	13.10	9.94	2.36	6.15	62.47	60.05	132.02	21.80	39.90	0.87	3.01	51.34
2	1	27.00	8.93	12.56	1.36	4.80	48.70 [b]	81.43 [b]	85.20	26.56[ab]	60.90[a]	3.20	1.62[a]	57.78
	2	27.76	8.56	13.00	1.40	4.50	49.66	81.13 [b]	87.16	27.03[a]	60.00	3.50	1.62[a]	68.06
	3	28.56	9.20	13.13	1.50	5.03	50.50[a]	82.53[a]	87.36	26.00 [b]	61.20[a]	3.30	1.59 [a]	72.78
	4	29.16	9.30	13.50	1.43	5.20	50.63 [a]	82.60	88.30	25.00	59.36[b]	3.86	1.49	60.00
	5	27.60	9.80	12.80	1.30	5.83	48.86b	83.46[a]	86.10	24.36	59.20[b]	2.90	1.44	61.71
CD @ 5 %		0.108	0.087	0.077	NS	0.059	0.121	0.964	0.107	0.616	0.441	0.087	0.039	NS
Family mean		28.02	9.16	13.00	1.40	5.07	49.67	82.23	86.82	25.79	60.13	1.55	3.35	64.07
3	1	37.03[a]	7.06[a]	14.06	1.70	6.70	57.26	70.23	108.13	20.33	49.43[a]	4.50	1.00	61.92
	2	37.13 [a]	7.16[a]	14.33	1.66	5.80	57.03	70.63	107.23	19.53	49.10[a]	3.63	0 .96	51.14
	3	38.16	7.60	14.43	1.53	5.20	58.00	71.06	109.26	20.53	50.10	3.40	1.03	57.78
	4	36.50	6.66	13.80	1.60	6.00	58.73	70.16	109.46	21.13	50.56	4.00	1.07	68.06
	5	36.16	6.26	13.53	1.73	6.46	59.13	69.83	110.63	21.86	51.53	4.10	1.13	55.36
CD @ 5 %		0.118	0.114	0.064	NS	0.106	0.171	NS	0.093	0.051	0.336	0.087	0.013	NS
Family mean		37.00	6.95	14.03	1.64	6.03	58.03	70.38	108.94	20.68	50.14	1.04	3.92	58.85
4	1	39.76[a]	12.40	10.90	2.83	5.53[a]	66.80	80.90	104.60	27.50	55.16	3.46	1.52	45.00[a]
	2	38.66[c]	13.16	10.66	2.76	4.50	65.06[a]	81.73	101.93	28.30	55.53	3.16	1.57	51.14[a]
	3	38.10	13.26	11.00	2.80	3.90	64.10	79.70	100.90	26.56	53.66	3.76	1.43	57.78
	4	38.73 [bc]	13.70	11.16	2.70	5.10[a]	65.53 [a]	79.93	103.00	25.93	53.46	3.86	1.39	46.92 [a]
	5	39.26 [ab]	12.80	11.66	2.93	5.00[ab]	66.16	80.56	103.50	27.20	54.33	4.26	1.48	51.14[a]
CD @ 5 %		0.561	0.060	0.084	NS	0.557	0.128	NS	0.162	0.066	0.105	NS	0.013	6.458

Table 10. Mean values of progenies for different characters. Contd.....

Family mean		38.91	13.06	11.08	2.80	4.80	65.53	80.56	102.78	27.10	54.43	1.48	3.70	50.39
5	1	35.86[a]	14.70	10.6333	1.1667	7.0000	60.20[a]	63.53	126.03	21.50	54.60	4.43	1.18	38.85[a]
	2	36.56	13.80	9.9000	1.3000	7.4333	61.50	64.16	126.33	22.40	55.23	4.83	1.24	30.00[bc]
	3	35.20	13.50	9.56	1.16	7.83	58.96[b]	63.03	123.83	20.80[a]	53.53	3.90	1.12[a]	28.07[c]
	4	34.93	14.16	10.03	1.23	6.86	58.40[b]	63.66	122.80	20.10	53.43	3.63	1.08	32.21[b]
	5	35.66a	14.26	10.13	1.23	6.26	60.00[a]	62.56	124.93	20.66[a]	54.33	4.23	1.13[a]	38.85[a]
CD @ 5 %		0.245	0.060	0.097	NS	0.108	0.475	NS	0.119	0.557	0.063	0.087	0.032	3.717
Family mean		35.66	14.08	10.05	1.22	7.08	59.81	63.39	124.78	21.09	54.22	1.15	4.20	33.60
6	1	29.56[a]	14.10	10.90	1.23	4.50	54.36[a]	100.23	139.83[a]	25.66	64.90[a]	2.50	1.67	46.92
	2	28.93	14.60	11.50	1.30	5.00	54.16[a]	100.70	140.16[a]	25.00	64.00	2.60	1.60	38.85
	3	29.66[a]	13.90	10.60	1.20	5.20	55.00	101.30	141.20	26.56	65.16[a]	2.90	1.73	45.00
	4	30.00	13.50	11.13	1.10	5.86	55.86	99.66	138.93	24.80	63.26	2.20	1.57	51.14
	5	30.76	14.66	11.03	1.26	4.70	56.23	98.90	137.90	24.13	62.70	2.10	1.51	46.92
CD @ 5 %		NS	NS	0.061	NS	0.048	0.670	NS	.3867	0.098	0.365	NS	.0129	NS
Family mean		29.78	14.15	11.03	1.22	5.05	55.12	100.16	139.60	25.23	64.00	1.62	2.46	45.76
7	1	40.60[ab]	16.83	7.60	4.73	3.83	63.03	72.40	97.36	22.30	50.36[b]	3.23[bc]	1.12[a]	51.14
	2	40.00[b]	16.60	8.10	4.76	3.40	64.00	72.93	96.2	23.06	51.53[a]	3.00[c]	1.19	38.85
	3	40.86[a]	17.13[a]	8.00	4.70	4.00	64.33	71.70	97.60	23.76	52.00[a]	3.20[c]	1.24	45.29
	4	39.96[b]	17.26[a]	8.70	4.80	4.20	65.16	71.26	95.23	21.36	49.36	3.46[ab]	1.05	44.91
	5	39.33	17.83	7.86	4.76	4.56	63.70	72.50	94.20	22.10	50.13b	3.90[a]	1.11[a]	45.00
CD @ 5 %		0.788	0.159	0.047	NS	0.097	0.209	NS	0.153	0.146	0.560	0.471	.0239	NS
Family mean		40.15	17.13	8.05	4.75	4.00	64.04	72.16	96.13	22.52	50.68	1.14	3.36	45.04
8	1	42.00	12.20	12.00	1.20	6.60	68.10	79.53	112.10	22.63	60.20	3.16	1.36	57.78
	2	42.90	12.26	12.50	1.33	6.93	67.43	80.43	110.90	23.23	61.06	3.46	1.42	68.06
	3	41.76	12.66	12.10	1.26	6.00	68.33	80.63	110.70	24.00	61.46	3.80[a]	1.48	51.14
	4	41.30	11.86	11.46	1.16	5.90	68.53	81.33	109.60	22.40	59.23	3.90[a]	1.33	61.92
	5	42.36	11.56	11.93	1.36	5.43	69.20	82.13	108.50	21.66	58.96	4.30	1.28	55.86
CD @ 5 %		0.049	NS	NS	0.073	0.139	0.078	0.091	0.065	0.231	.119	0.015	NS	NS
Family mean		42.06	12.11	12.00	1.26	6.17	68.32	80.81	110.36	22.78	60.18	1.37	3.72	58.95
CD @ 5 % progenies in same families		0.336	0.309	0.243	0.184	NS	0.277	1.209	0.297	0.264	0.286	0.160	0.019	8.957
CD @ 5 % progenies in different families		0.623	1.212	0.222	0.208	NS	0.863	2.249	1.180	0.948	1.039	0.171	0.073	8.960

Range of mean values for days to first flowering was from 34.93 to 36.56 days in family 5. Progeny 4 (34.93) took minimum number of days to first flowering and progeny 2 (36.56) took the maximum days to first flowering.

Mean values for days to first flowering ranged from 39.33 to 40.86 days in family 7. Minimum number of days to first flowering was displayed by progeny 5 (39.33) and progeny 3 (40.86) took the maximum days to first flowering.

For days to first flowering mean values ranged from 41.30 to 42.90 daysin family 8. Progeny 4 (41.30) was found late to flower and progeny 2 (42.90) was earliest to flower.

4.3.2.2 Length of Fruit (cm)

Significant differences were observed among the families for length of fruit ranged from 6.95 to 17.13 cm. Maximum fruit length was recorded in family 7 (17.13 cm) followed by family 6 (14.15 cm) which is on par with family 5 (14.08 cm) and the minimum fruit length was recorded in family 3 (6.95 cm) followed by family 2 (9.160 cm) (Fig 2). There were significant differences among the progenies for length of fruit except families 6 and 8.

For length of fruit, mean values ranged from 12.53 to 13.80 cm in family 1. Minimum fruit length was recorded in progeny 2 (12.53 cm) and the maximum fruit length was recorded in progeny 5 (13.80 cm).

There were significant differences among the progenies for length of fruit in family 2. Mean values for this character ranged from 8.56 to 9.80 cm. Maximum fruit length was recorded in progeny 5 (9.80 cm) and the minimum fruit length was recorded in progeny 2 (8.56 cm).

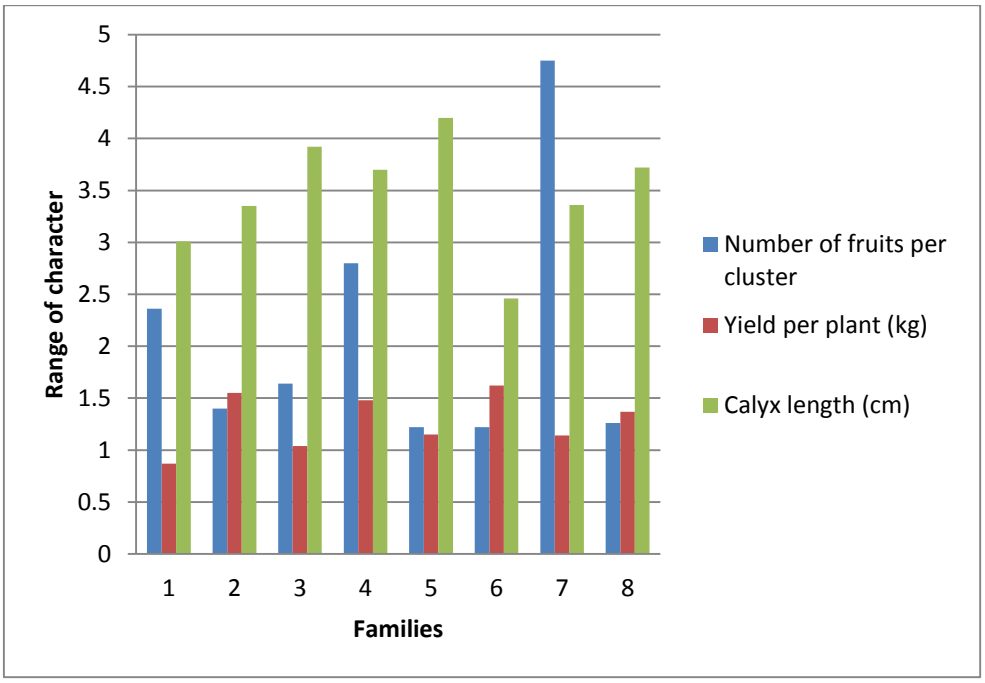


Fig.3 Performance of families based on number of fruits per cluster, yield per plant and calyx length

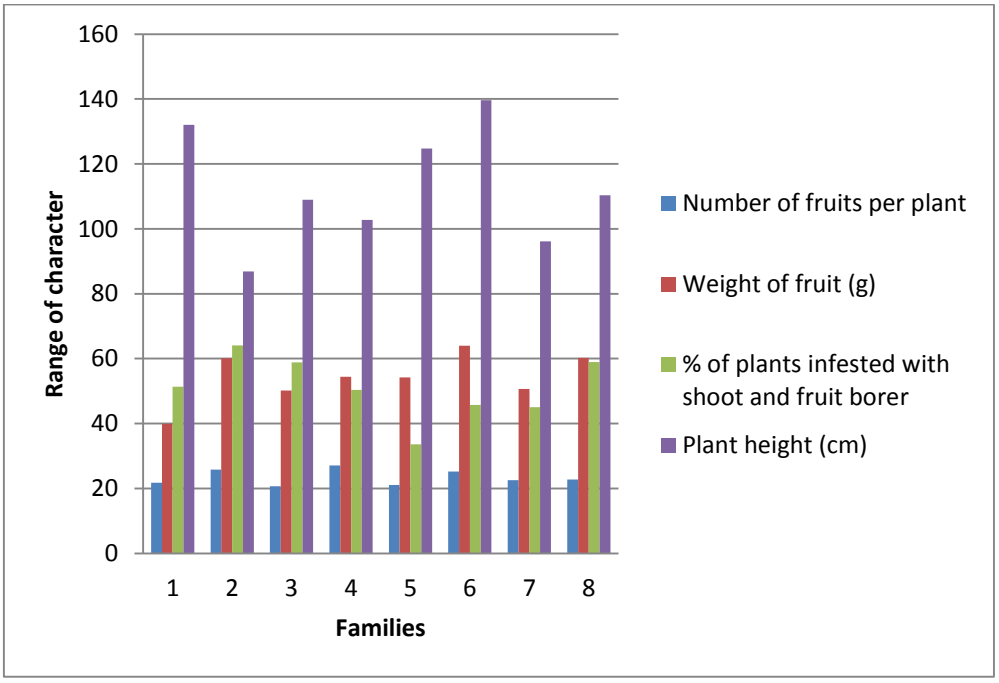


Fig.4 Performance of families based on weight of fruit, plant height, number of fruits per plant and % of plants infested with shoot and fruit borer

Mean values for this character ranged from 6.26 to 7.60 cm in family 3. Maximum fruit length was recorded in progeny 3 (7.60 cm) and the minimum fruit length was recorded in progeny 5 (6.26 cm).

Progenies of family 4 reported mean values for length of fruit ranged from 12.40 to 13.70 cm. Maximum fruit length was recorded in progeny 4 (13.70 cm) and the minimum fruit length was recorded in progeny 1 (12.40 cm).

Significant differences were observed among the progenies for length of fruit in family 5 ranged from 13.50 to 14.70 cm. Maximum fruit length was recorded in progeny 1 (14.70 cm) and the minimum fruit length was recorded in progeny 3 (13.50 cm).

Among the progenies of family 7 significant differences were observed for length of fruit and the mean values ranged from 16.60 to 17.83 cm. Maximum fruit length was recorded in progeny 5 (17.83 cm) and the minimum length of fruit was recorded in progeny 2 (16.60 cm)**.**

4.3.2.3 Girth of Fruit (cm)

Girth of fruit exhibited significant differences between families which ranged from 8.05 to 14.03 cm. Maximum fruit girth was recorded in the family 3 (14.03 cm) followed by family 2 (13.00 cm) and the minimum fruit girth was recorded in the family 7 (8.05 cm) (Fig 2). There were significant differences among the progenies for girth of fruit in families except family 8.

Mean values for girth of fruit ranged from 9.60 to 10.26 cm among the progenies of family 1. Minimum fruit girth was recorded in progeny 5 (9.60 cm) and the maximum girth of fruit was recorded in progeny 3 (10.26 cm)**.** Significant differences were observed among the progenies for girth of fruit in family 2 and mean values for this character ranged from 12.56 to 13.50 cm.

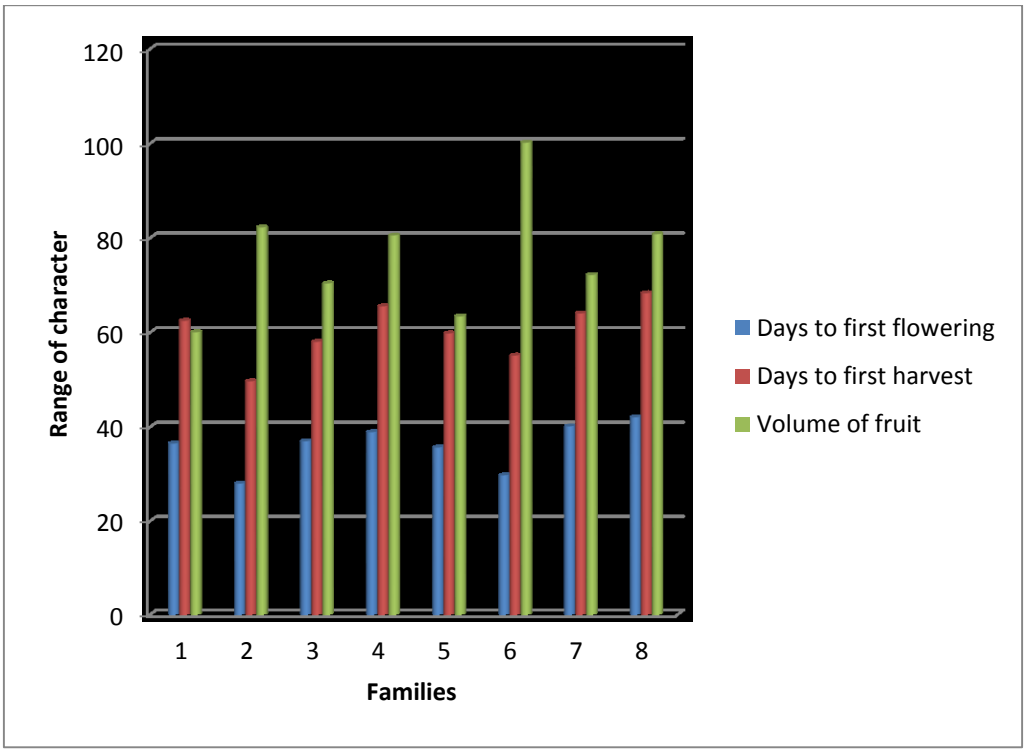


Fig.1 Performance of families based on days to first flowering, days to first harvest and volume of fruit (cm^3)

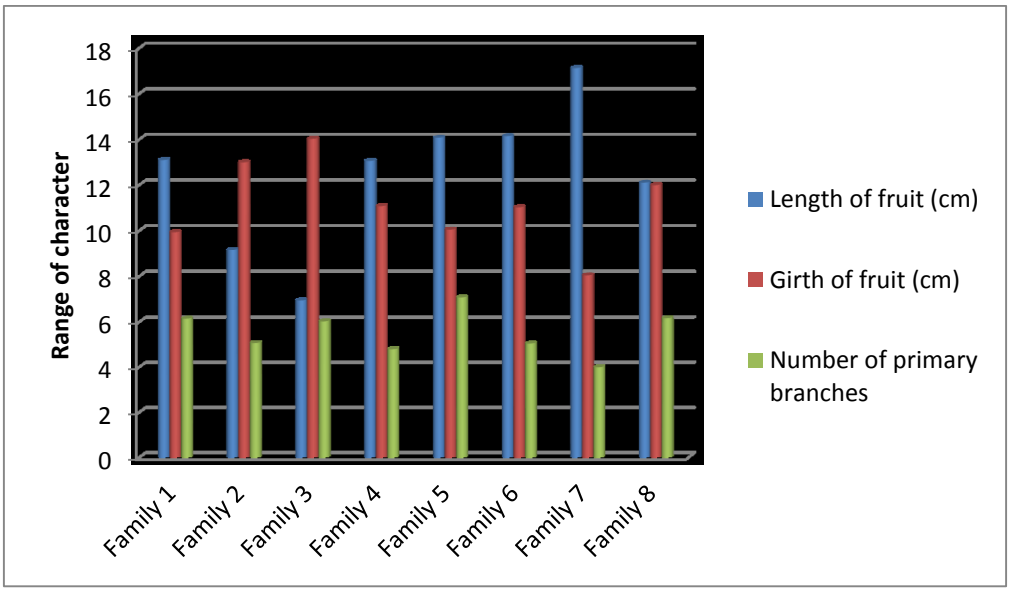


Fig.2 Performance of families based on length of fruit, girth of fruit and number of primary branches

Progeny 4 (13.50 cm) recorded maximum fruit girth and the minimum fruit length was recorded in progeny 1 (12.56 cm)**.**

For girth of fruit, mean values ranged from 13.53 to 14.43 cm. Maximum fruit girth was reported in progeny 3 (14.43 cm) and the minimum girth of fruit was recorded in progeny 5 (13.53 cm)**.**

Among the progenies of family 4, the mean values for girth of fruit ranged from 10.66 to 11.66 cm. Maximum fruit girth was exhibited by progeny 2 (11.66 cm) and the minimum girth of fruit was recorded in progeny 5 (10.66 cm)**.**

Significant differences were observed among the progenies for girth of fruit in family 5. Mean values for this character ranged from 9.56 to 10.63 cm. Maximum fruit girth was recorded in progeny 1 (10.63 cm) and minimum girth of fruit was recorded in progeny 3 (9.56 cm)**.**

Mean values ranged from 10.60 to 11.50 cm in family 6. Maximum fruit girth was recorded in progeny 2 (11.50 cm) and the minimum girth of fruit was recorded in progeny 3 (10.60 cm).

Significant differences were observed among the progenies for girth of fruit in family 7. Mean values for this character ranged from 7.60 to 8.70 cm. Maximum fruit girth was recorded in progeny 4 (8.70 cm) and the minimum girth of fruit was recorded in progeny 1 (7.60 cm)**.**

4.3.2.4 Number of Fruits per Cluster

Number of fruits per cluster exhibited significant differences among the families and mean values ranged from 1.22 to 4.75. Maximum number of fruits per cluster was recorded in family 7 (4.75) followed by family 4 (2.80) and the minimum number of fruits per cluster was recorded in the family 5 and family 6 (1.22) (Fig 4).

Plate 6. Variation in fruit characters in family 1

Plate 7. Variation in fruit characters in family 2.

Plate 8. Variation in fruit characters in family 3.

Plate 9. Variation in fruit characters in family 4.

Plate 10. Variation in fruit characters in family 5

Plate 11. Variation in fruit characters in family 6

Plate 12. Variation in fruit characters in family 7.

Plate 13. Variation in fruit characters in family 8.

There were significant differences among the progenies of family 8 fornumber of fruits per cluster. Mean values for this character ranged from 1.16 to 1.36. Maximum number of fruits per clusterwas recorded in progeny 5 (1.36) and the minimum was recorded by progeny 4 (1.16).

There were significant differences among the progenies for number of fruits per cluster in all families except family 8.

4.3.2.5 Number of Primary Branches

Mean values for number of primary branches ranged from 4.00 to 7.08. Maximum number of primary branches was recorded in family 5 (7.08) followed by family 8 (6.17) which is on par with family 1 (6.15) and family 3 (6.03) and the minimum number of primary branches was recorded in family 7 (4.00) (Fig 2).

In family 1, maximum number of primary branches was recorded in progeny 3 (6.90) and the minimum number of primary branches was recorded in progeny 5 (5.46).

Significant differences were observed among the progenies for number of primary branches in family 2. Mean value for number of primary branches ranged from 4.50 to 5.83. Progeny 5 (5.83) exhibited maximum number of primary branches and the minimum number of primary branches was recorded in progeny 2 (4.50).

Among the progenies of family 3 number of primary branches exhibited significant differences and mean values ranged from to 5.20 to 6.70. Maximum number of primary branches was recorded in progeny 1 (6.70) and the minimum number of primary branches was recorded in progeny 3 (5.20).

For number of primary branches in family 4 significant differences were observed among the progenies and mean values ranged from to 3.90 to 5.53.

Maximum number of primary branches was recorded in progeny 1 (5.53) which was on par with progeny 4 (5.10) and the minimum number of primary branches was recorded in progeny 3 (3.90).

Significant differences were observed among the progenies for number of primary branches in family 5. Mean values for this character ranged from to 6.26 to 7.83. Maximum number of primary branches was recorded in progeny 3 (7.83) and the minimum number of primary branches was recorded in progeny 5 (6.26).

In family 6 significant differences were observed among the progenies for number of primary branches and the mean values ranged from 4.50 to 5.86. Highest number of primary branches was recorded in the progeny 4 (5.86) and the lowest number of primary branches was recorded in progeny 1 (4.50).

Significant differences were observed among the progenies for number of primary branches in family 7. Mean values for this character ranged from 3.40 to 4.56. Maximum number of primary branches was recorded in progeny 5 (4.56) and the minimum number of primary branches was recorded in progeny 2 (3.40).

There is large variation among the progenies for number of primary branches in family 8 and mean values ranged from 5.43 to 6.93. Maximum number of primary branches was recorded in progeny 5 (5.43) and the minimum number of primary branches was recorded in progeny 2 (6.93).

4.3.2.6 Days to First Harvest

Wide variation could be observed between the families for days to first harvest and mean values ranged from 49.67 to 68.32 days. Maximum days to first harvest was recorded in family 8 (68.32) followed by family 4 (65.53) and the minimum days to first harvest was recorded in family 2 (49.67 days) (Fig 1).

Days to first harvest exhibited significant differences among the progenies of family 1 which ranged from 60.73 to 63.83 days. Early harvest was observed in progeny 5 (60.73 days) and progeny 3 (63.83 days) was found late to harvest.

Significant differences were observed among the progenies for days to first harvest in family 2. Mean values for this character ranged from 48.70 to 50.63 days. Maximum days to first harvest was recorded in progeny 4 (50.63) which was on par with progeny 3 (50.50) and the minimum days to first harvest was recorded in progeny 1 (48.70) which was on par with progeny 5 (48.87).

Among the progenies of family 3 mean values ranged from 57.03 to 59.13 days. Maximum days to first harvest was recorded in progeny 5 (59.13) and the minimum days to first harvest were recorded in progeny 2 (57.03).

In family 4 mean values ranged from 64.10 to 66.80 days. For days to first harvest the minimum values were displayed by progeny 3 (64.10 days) and the maximum value was recorded in progeny 1 (66.80 days).

Mean values for days to first harvest ranged from 58.40 to 61.50 days in family 5. Progeny 2 (61.50) exhibited the maximum days to first harvest and the minimum days to first harvest was recorded in progeny 4 (58.40) which was on par with progeny 3 (58.96).

Progeny 2 (54.16 days) was the earliest to harvest and progeny 5 (56.23) was found late to harvest among the progenies of family 6. Among the progenies of family 7, progeny 1 (63.03 days) was found earliest to harvest and progeny 4 (65.16 days) was late to harvest. In family 8 progeny 2 (67.43 days) took the minimum and progeny 5 (69.20 days) took the maximum days to first harvest.

4.3.2.7 Volume of Fruit (cm^3)

Volume of fruit exhibited wide variation and the mean values ranged from 60.05 cm^3 to 100.16 cm^3. Maximum volume of fruit was recorded in family 6 (100.16 cm^3) followed by family 2 (82.23 cm^3) which was on par with family 8 (80.81 cm^3) and the minimum volume of fruit was recorded in family 1 (60.05 cm^3) (Fig 1). There were no significant differences among the progenies for volume of fruit except in family 8.

There were significant differences among the progenies for fruit volume in family 2. Mean values for this character ranged from 81.13 to 83.47cm^3. Maximum plant height was recorded in progeny 5 (83.47 cm^3) which was on par with progeny 3 (82.53 cm^3) and the minimum plant height was recorded in progeny 2 (81.13 cm^3) which was on par with progeny 1 (81.43 cm^3).

Significant differences were observed among the progenies for volume of fruit in family 8. Mean values for this character ranged from 79.53 to 82.13 cm^3. Maximum volume of fruit was recorded in progeny 5 (82.13 cm^3) and the minimum volume of fruit was recorded in progeny 1 (79.53 cm^3).

4.3.2.8 Plant Height (cm)

Plant height exhibited significant difference between the families and mean values ranged from 86.82 cm to 139.60 cm. Maximum plant height was recorded in family 6 (139.60 cm) followed by family 1 (132.02 cm) and the minimum plant height was recorded in family 2 (86.82 cm) (Fig 3).

Mean values for plant height ranged from 130.53 to 133.73 cm in family 1. Minimum plant height was recorded in progeny 5 (130.53 cm) and the maximum plant height was recorded in progeny 3 (133.73 cm) which was on par with progeny 4 (131.17 cm).

There were significant differences among the progenies for plant height in family 2. Mean values for this character ranged from 85.20 to 88.30 cm. Maximum plant height was recorded in progeny 4 (88.30 cm) and the minimum plant height was recorded in progeny 1 (85.20 cm).

Variability among the progenies of family 3 for plant height were prominent with mean values ranged from 107.23 to 110.63 cm. Maximum plant height was recorded in progeny 5 (110.63 cm) and the minimum plant height was recorded in progeny 2 (107.23 cm).

There were wide variations among the progenies of family 4 for plant height ranged 100.90 to 104.60 cm. Maximum plant height was recorded in progeny 3 (104.60 cm) and the minimum plant height was recorded in progeny 5 (100.90 cm).

Mean values for progenies of family 5 for plant height ranged from 122.80 to 126.33 cm. Maximum plant height was recorded in progeny 2 (126.33 cm) and the minimum plant height was recorded in progeny 4 (122.80 cm).

There were significant differences among the progenies of family 6 for plant height and mean values ranged from 137.90 to 141.20 cm. Maximum plant height was recorded in progeny 3 (141.20 cm) and the minimum plant height was recorded in progeny 5 (137.90 cm).

There were significant differences among the progenies for plant height in family 7. Mean values for this character ranged from 94.20 to 97.60 cm. Maximum plant height was recorded in progeny 3 (97.60 cm) and the minimum plant height was recorded in progeny 5 (94.20 cm).

Significant differences were observed among the progenies for plant height in family 8. Mean values for this character ranged from 108.50 to 112.10 cm. Minimum plant height was recorded in the progeny 5 (108.50 cm) and the maximum plant height was recorded in progeny 1 (112.10 cm).

4.3.2.9 Number of Fruits per Plant

Number of fruits per plant with mean values ranged 20.68 to 27.10 exhibited large variation between families. Maximum number of fruits per plant was recorded in family 4 (27.10) followed by family 2 (25.79) and the minimum number of fruits per plant was recorded in family 3 (20.68) (Fig 3).

Significant differences were observed among the progenies for number of fruits per plant in family 1. Mean values for this character ranged from 20.73 to 23.06. Maximum number of fruits per plant was recorded in progeny 2 (23.06) and the minimum number of fruits per plant was recorded in progeny 5 (20.73).

Among the progenies of family 2, number of fruits per plant with mean values ranged from 24.37 to 27.03. Maximum number of fruits per plant was recorded in progeny 2 (27.03) which was on par with progeny 1 (26.57) and the minimum number of fruits per plant was recorded in progeny 5 (24.37).

Significant differences were observed among the progenies for number of fruits per plant in family 3. Mean values for this character ranged from 19.53 to 21.86. Maximum number of fruits per plant was recorded in progeny 5 (21.86) and the minimum number of fruits per plant was recorded in progeny 2 (19.53).

In family 4 significant differences were observed among the progenies for number of fruits per plant and mean values ranged from 25.93 to 28.30. Maximum number of fruits per plant was recorded in progeny 2 (28.30) and the minimum number of fruits per plant was recorded in progeny 4 (25.93).

Among the progenies of family 5 significant difference were observed and mean values ranged from 20.10 to 22.40. Maximum number of fruits per plant was recorded in progeny 2 (22.40) and the minimum number of fruits per plant was recorded in progeny 4 (20.10).

Significant differences wereobserved among the progenies for number of fruits per plant in family 6. Mean values for this character ranged from 24.13 to 26.56. Maximum number of fruits per plant was recorded in progeny 3 (26.56) and the minimum number of fruits per plant was recorded in progeny 5 (24.13).

For number of fruits per plant, mean values ranged from 21.36 to 23.76 among the progenies of family 7. Maximum number of fruits per plant was recorded in the progeny 3 (23.76) and the minimum number of fruits per plant was recorded in progeny 4 (21.36).

Significant differences were observed among the progenies for number of fruits per plant in family 8. Mean values for this character ranged from 21.66 to 24.00. Maximum number of fruits per plant was recorded in progeny 3 (24.00) and the minimum number of fruits per plant was recorded in progeny 5 (21.66).

4.3.2.10 Weight of Fruit (g)

Weight of fruit exhibited wide variation between families ranged from 39.90 to 64.00 g. Maximum weight of fruit was recorded in the family 6 (64.00 g) followed by family 8 (60.18 g) and the minimum weight of fruit was recorded in the family 1 (39.90 g) (Fig 3.)

Significant differences were observed among the progenies for weight of fruit in family 1. Mean values for this character ranged from 39.13 to 40.86 (g). Maximum weight of fruit was recorded in progeny 2 (40.86 g) and the minimum weight of fruit was recorded in progeny 5 (39.13 g).

Among the progenies of family 2, the mean values for weight of fruit ranged from 59.20 to 61.20 (g). Maximum fruit weight was recorded in progeny 3 (61.20 g) which was on par with progeny 1 (60.90 g) and the minimum fruit weight was recorded in progeny 5 (59.20 g) which was on par with progeny 4 (59.37).

For fruit weight significant differences were observed among the progenies of family 3 and mean values ranged from 49.10 to 51.53 g. Maximum fruit weight was recorded in progeny 5 (51.53 g) and the minimum weight of fruit was recorded in progeny 2 (49.10 g) which is on par with progeny 1 (49.43 g).

Significant differences were observed among the progenies for weight of fruit 4. Mean values for this character ranged from 53.46 to 55.53 g. Progeny 2 (55.53 g) recorded the maximum fruit weight and the minimum fruit weight was recorded in progeny 4 (53.46 g).

Mean values for weight of fruit ranged from 53.43 to 55.23 g in family 5. Maximum weight of fruit was recorded in progeny 2 (55.23 g) and the minimum weight of fruit was recorded in progeny 4 (53.43 g).

Significant differences were observed among the progenies for weight of fruit in family 7. Mean values for this character ranged from 49.36 to 52.00 g which was on par with progeny 2 (51.53 g). Maximum weight of fruit was recorded in progeny 3 (52.00 g) and the minimum weight of fruit was recorded in progeny 4 (49.36 g).

In family 8 mean values for weight of fruit ranged from 58.96 to 61.46 g. Maximum weight of fruit was recorded in progeny 3 (61.46 g) and the minimum weight of fruit was recorded in progeny 5 (58.96 g).

There were no significant differences among the progenies for weight of fruit in family 6.

4.3.2.11 Fruit Yield per Plant (kg)

Mean values for fruit yield per plant ranged 0.87 kg to 1.62 kg exhibited wide variation between families. The maximum yield per plant was recorded in

the family 6 (1.62 kg) which was on par with family 2 and the minimum yield per plant was recorded in the family 1 (0.87 kg) (Fig 4).

Significant differences were observed among the progenies for fruit yield per plant in family 1. Mean values for this character ranged from 0.82 to 0.95 kg. Maximum yield was recorded in the progeny 2 (0.95 kg) and the minimum yield was recorded in progeny 5 (0.82 kg)**.**

Among the progenies of family 2 significant differences were observed for fruit yield per plant. Mean values ranged from 1.45 to1.63 kg. Progenies 1 and 2 (1.63 kg) which was on par with progeny 3 (1.59 kg) exhibited maximum yield and the minimum yield was recorded in progeny 5 (1.45 kg).

Significant differences were observed among the progenies for yield in family 3. Mean values for this character ranged from 0.96 to 1.13 kg. Maximum fruit yield per plant was recorded in the progeny 5 (1.13 kg) and the minimum fruit yield per plant was recorded in progeny 2 (0.96 kg).

For fruit yield per plant significant differences were observed among the progenies of family 4. Mean values for this character ranged from 1.39 to 1.57 kg. Progeny 4 (1.39 kg) displayed maximum fruit yield per plant and the maximum fruit yield per plant was recorded in progeny 2 (1.57 kg).

Mean values for fruit yield per plant ranged from 1.08 to 1.24 kg in family 5. Minimum fruit yield per plant was recorded in progeny 4 (1.08 kg) and the maximum fruit yield per plant was recorded in progeny 2 (1.24 kg).

Among the progenies of family 6 mean values for fruit yield per plant ranged from 1.51 to 1.73 kg. Minimum fruit yield per plant was recorded in progeny 5 (1.51 kg) and the maximum fruit yield per plant was recorded in progeny 3 (1.73 kg).

Significant differences were observed among the progenies for fruit yield per plant in family 7. Mean values for this character ranged from 1.05 to 1.24 kg. Minimum fruit yield per plant was recorded in progeny 4 (1.05 kg) and the maximum fruit yield per plant was recorded in progeny 3 (1.24 kg).

4.3.2.12 Calyx Length (cm)

Calyx length exhibited wide variation between families with mean values ranged from 2.46 to 4.20 cm. Maximum calyx length was recorded in the family 5 (4.20 cm) followed by family 3 (3.92 cm) and the minimum calyx length was recorded in the family 6 (2.46) (fig 4). There were significant differences among the progenies for calyx length in all families except families 4 and 5.

In family 1 significant differences were observed among the progenies for calyx length. Mean values for this character ranged from 2.30 to 3.53 cm. Maximum calyx length was recorded in the progeny 5 (3.53 cm) which was on par with progeny 4 (3.43 cm) and the minimum calyx length was recorded in progeny 2 (2.30 cm)**.**

Among the progenies of family 2 mean values ranged from 2.90 to 3.87cm. Maximum calyx length was recorded in the progeny 4 (3.87 cm) and the minimum calyx length was recorded in progeny 5 (2.90 cm).

In family 3 significant differences were observed among the progenies for calyx length. Mean values for this character ranged from 3.40 to 4.50 cm. Maximum calyx length was recorded in progeny 1 (4.50 cm) and the minimum calyx length was recorded in progeny 3 (3.40 cm).

Significant differences were observed among the progenies for calyx length in family 5. Mean values for this character ranged from 3.63 to 4.83 cm. Maximum calyx length was recorded in progeny 2 (4.83 cm) and the minimum calyx length was recorded in progeny 4 (3.63 cm).

For calyx length the mean values ranged from 3.00 to 3.90 cm in family 7. Maximum calyx length was recorded in progeny 5 (3.90 cm) and the minimum calyx length was recorded in progeny 2 (3.00 cm).

Significant differences were observed among the progenies for calyx length in family 8. Mean values for this character ranged from 3.16 to 4.30 cm. Maximum calyx length was recorded in progeny 5 (4.30 cm) and the minimum calyx length was recorded in progeny 1 (3.16 cm).

4.3.2.13 Fruit and Shoot Borer Incidence (%)

There were significant difference among the families for plants infested with fruit and shoot borer. Mean values for this character ranged from family 5 (33.60 %) to family 2 (64.07 %). Fruit and shoot borer incidence was recorded maximum in family 2 (64.07 %) followed by family 8 (58.95 %) and the minimum was recorded in family 5 (33.60 %) (Fig 3).

Mean values for percentage of plants infested with fruit and shoot borerranged from 45.00 to 57.78 % in family 4. Maximum percentage of plants infested with fruit and shoot borer was recorded in the progeny 3 (57.78%) and the minimum was recorded in progeny 1 (45.00 %).

Percentage of plants infested with shoot and fruit borer ranged from 28.07 to 38.85 among the progenies of family 5. Progenies 1 and 5 (38.85 %) exhibited maximum percentage of plants infested with shoot and fruit borer and the minimum was recorded in progeny 3 (28.07 %) which was on par with progeny 2 (30.00 %).

There were no significant differences observed among the progenies for percentage of plants infested with shoot and fruit borer in families 1, 2, 3, 6, 7 and 8.

4.3.3 Variability Among the Progenies of 8 Different Families (Pooled Analysis)

The pooled analysis of the data showed significant difference among the progenies for all the characters. Variations for days to first flowering ranged from 27.00 to 42.90. Minimum days to flowering were recorded in progeny 1 of family 2 (27.60) followed by progeny 5 of same family. Maximum time for flowering was taken by progeny 2 of family 8 (42.90).

Days to first harvest was found to be highly variable from 48.70 to 69.20 days. The progeny 1 of family 2 (48.70) which is on par with progeny 5 (48.86) of the same family was found to be earliest to harvest. Maximum duration was taken by progeny 5 of family 8 (69.20).

Significant variation for fruit length was observed among the progenies. Progeny 5 of family 7 recorded the longest fruits having the length of 17.83 cm. Progenies 3 and 4 of the same family also produced fruits having more than 17 cm. Shortest fruits having an average length of 6.26 cm were produced by progeny 5 of family 3.

Fruit girth recorded a wide range of variation from 7.60 to 14.43 cm. Progeny 1 of family 7 recorded the lowest fruit girth (7.60 cm). Highest fruit girth was observed in progeny 3 of family 3 (14.43 cm).

Fruit weight was found to be highly variable from 39.13 to 65.16 g among the progenies. Progeny 3 of family 6 produced fruits having the maximum fruit weight (65.16 g) which is on par with progeny 1 of family 6 (64.90 g).

Analysis of the pooled data revealed significant differences among the progenies for number of fruits. Mean values ranged from 19.53 to 28.30. Maximum number of fruits was produced by progeny 2 of family 4 (28.30) and the minimum was recorded by progeny 2 of family 3.

Significant differences were observed among the progenies for number of fruits per cluster. Progeny 4 of family 7 produced the maximum number of fruits per cluster (4.80) and the minimum was recorded by progeny 4 of family 6 (1.10).

Analysis of the pooled data revealed significant differences among the progenies for number of primary branches. Mean values for this character ranged from 3.40 to 7.83. Maximum number of primary branches was produced by progeny 2 of family 7 (7.83) and the minimum was recorded by progeny 2 of family 3 (3.40).

Volume of fruit recorded a wide range of variation from 59.20 to 101.30 cm^3. Progeny 1 of family 1 (59.20 cm^3) produced fruits with the minimum volume and the maximum (101.30 cm^3) were recorded by progeny 3 of family 6.

Plant height recorded a wide range of variation from 85.20 to 141.20 cm. Progeny 1 of family 2 (85.20 cm) had the minimum plant height and the maximum was recorded by progeny 3 of family 6 (141.20 cm).

Calyx length recorded a wide range of variation from 2.10 to 4.83 cm. Progeny 5 of family 6 (2.10 cm) recorded the minimum plant height and the maximum (4.83 cm) was recorded by progeny 2 of family 5. Significant variation for yield was observed among the progenies. Progeny 3 of family 6 recorded the highest yield of 1.73 kg and the minimum was recorded by progeny 5 of family 1 (0.81 kg).

Plants infested with shoot and fruit borer revealed significant difference among the progenies of families 4 and 5. The minimum percentage of infestation was recorded by progeny 3 of family 5 (28.07 %) and maximum by progeny 3 of family 2 (72.78 %).

DISCUSSION

5. DISCUSSION

The present investigation was conducted at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani to understand the nature and magnitude of gene action using the means of different generations and also to study the extent of genetic variability between families and between progenies within these families.

The study was carried out in two experiments *viz.*,

1. Generation mean analysis
2. Study of F_2 population

The salient results gathered in the light of the present investigation are discussed here under the following sub headings.

1. Generation mean analysis
2. Study of F_2 population
3. Variability among the F_2 families
4. Variability among the progenies

5.1 GENERATION MEAN ANALYSIS

A sound knowledge of the genetic makeup of genotypes and their behaviour in different genetic backgrounds is of utmost importance in formulating the most suited breeding strategy. Generation mean analysis is of great importance in this context as it derives additional knowledge on epistasis (additive x additive, additive x dominance and dominance x dominance interactions). In generation mean analysis, mean values of various generations for 13 characters were utilized for conducting scaling test and estimation of components of genetic variance.

5.1.1 Days to First Flowering

Earliness is considered as an important character in any crop improvement programme and preferred for commercial cultivation when high yield is coupled with earliness.

Mean values of F_1 were higher than those of F_2 in all the three crosses. Significance was observed for all the scales during scaling test in cross 1 among which scales B, C and D were acting in the favourable negative direction of which scale C had the highest magnitude which implies that F_2 is better than the parents.

All the genetic components were significant among which dominance x dominance effect had the highest magnitude and was in the favourable negative direction. Cheah *et al*. (1981), Umareitya *et al*. (2008), Kumar *et al*. (2009) and Bendale *et al*. (2005) had reported the importance of dominance x dominance gene action in controlling the inheritance of this trait. Hence hybridization followed by selection would improve this trait in cross 1.

In cross 2, negative significance was observed for the scales A, B, C and D of which scale C had the highest magnitude which implies that F_2 is better than the parents. Dominance, additive x additive and additive x dominance effects were significant among which dominance effect had the highest magnitude.

Significance was observed for all the scales in cross 3 among which scales A and C were in the favourable negative direction of which scale C had the highest magnitude which implies that F_2 is better than the parents. Significance was observed for dominance, additive x additive and dominance x dominance effects. But dominance and additive x additive effects were in the favourable negative direction of which dominance effect had the highest magnitude. The role of dominance effect for this trait had been reported by Kumar *et al*. (2009), Sindhu *et al.* (1980), Peter and Singh (1973, 1976), Hani (1977) and Chaudhary

and Pathania (2001). Since dominance variance was predominant heterosis breeding would improve the trait in crosses 2 and 3.

Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.1.2 Days to First Harvest

Significance observed for the scales A, C and D in crosses 1 and 2 and all the scales in cross 3 revealed the inadequacy of simple additive-dominance model and the presence of all the three types of epistatic interactions. Among the scales, scale C had the highest magnitude which implies that F_2 is better than parents in all the crosses.

Further analysis showed the significance of additive and dominance gene action and the three types of digenic interactions in all the three crosses. Additive x dominance (j) interaction was absent in cross 3.

Since epistatic variance dominance x dominance is relatively high, more reliance should be placed on hybridization followed by selection in all the crosses. The findings are in accordance with Vaghasiya *et al.* (2009), Suneetha *et al.* (2005) and Bendale *et al.* (2005) who reported the role of non additive (dominance, additive x dominance and dominance x dominance) gene effects in the inheritance of this trait. All the three crosses displayed duplicate epistasis which is evident from the opposite signs of dominance (h) and dominance x dominance (l) gene effects.

5.1.3 Length of Fruit (cm)

Fruit length is an important parameter in deciding consumer preference. In cross 1 significance was observed for scales B, C and D among which scales C and D were in the favourable positive direction of which scale D had the highest magnitude which implies that F_2 is better than back crosses. Significance of additive, dominance, additive x additive and dominance x

dominance effects were reported of which additive gene action and dominance x dominance type of interaction were in the favourable positive direction. Dominance x dominance effect had the highest magnitude.

Significant values of C and D scales in cross 2 pointed out the presence of dominance x dominance and additive x additive type of interactions respectively. Additive and dominance gene actions were also significant. Predominance of dominance x dominance interaction is evident from the highest magnitude of scale C. Predominance of dominance x dominance effect was suggested earlier by Umareitya *et al.* (2008) and Kumar *et al.* (2009). This pointed out the possibility of obtaining early harvesting types through hybridization and selection in crosses 1 and 2.

Cross 3 witnessed significance for all the scales among which scale B was in the positive direction which implies that F_1 is better than P_2. Though all the genetic components were significant, dominance and additive x additive effects were in the favourable positive direction of which dominance effect had the highest magnitude. Hence heterosis breeding would improve the trait. The role of dominance, dominance x dominance had been reported earlier by Kumar *et al*. (2009) and Prasad *et al*. (2010). Duplicate nature of epistasis is prevalent in all the three crosses.

5.1.4 Girth of Fruit (cm)

Fruit girth is an important character as that of fruit length. In cross 1, significance was observed for scales A, B and C among which scale B was in the positive direction which implies that F_1 is better than P_2. Negative significance of additive and additive x dominance effects were observed on further assessment. Singh and Mital (1988), Das *et al. (*2010), Kafytullah *et al.* (2011) and Dixit *et al.* (1984) had reported the significance of additive effects in controlling the inheritance of this character. Hence direct selection would improve the trait.

Scales A, B and D were significant among which scale D was in the positive direction which implies that F_2 is better than back crosses in cross 2. Further analysis showed the significance of additive, dominance, additive x additive and dominance x dominance effects of which only dominance x dominance effect was in the favourable positive direction and had the highest magnitude. Hence resorting to recombination breeding would improve the trait.

In cross 3, significance was observed for scales A, C and D among which scale A was in the positive direction which implies that F_1 is better than P_1. Positive significance of additive, additive x additive and additive x dominance effect was reported among which additive x additive effect had the highest magnitude. Hence hybridization followed selection would improve the trait. Presence of non additive gene actions were suggested earlier by Vaghasiya *et al.* (2009), Singh and Mital (1988), Umareitya *et al*. (2008) and Kumar *et al.* (2009). Duplicate nature of epistasis in all the three crosses were indicated by the opposite signs of dominance (h) and dominance x dominance (l) effects.

5.1.5 Number of Primary Branches

Number of primary branches per plant is one of the major parameter contributing total yield per plant. Significant values of scales A and C denoted that all types of digenic interactions are present in cross 1 though positive significance of only additive effect was revealed on further analysis.

Superiority of F_1 over the second parent was witnessed by the significance with highest magnitude of scale B over all other scales in cross 2. Eventhough significance was observed for additive, dominance and all the three types of digenic interactions except dominance x dominance interaction, additive effect was predominant. Predominance of additive variance suggested that direct selection would improve the trait in crosses 1 and 2. Significance of additive effect was also suggested in accordance with the earlier reports of Patil *et al*. (2003) and Gill *et al.* (1976) and Das *et al*. (2010).

All the three kinds of digenic interactions along with additive and dominance effects were significant in cross 3. Scale D had the highest magnitude which implies that F_2 is better than backcrosses. However, additive, additive x dominance and dominance x dominance effects possessed the positive value of which dominance x dominance effect had the highest magnitude. Significance of dominance x dominance effect was in accordance with the earlier reports of Umareitya *et al.* (2008), Kamalakkannan *et al*. (2007), Bendale *et al.* (2005)). Hence hybridization and selection could improve the trait in both crosses 2 and 3.

Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in crosses 1 and 3 and similar sign showed the complementary nature of epistasis in cross 2.

5.1.6 Number of Fruits per Cluster

Significance was observed for the scales A, B and D of which scale D was in the favourable positive direction which implies that F_2 is better than backcrosses in cross 1.

Though all the scales were significant scale C had the highest magnitude in cross 2 which implies that which implies that F_2 is better than parents in all the crosses. All the scales were significant among which scale B had the highest magnitude in cross 3 indicating that F_1 is better than second parent.

In all the three crosses, though various components displayed significance, only dominance x dominance effect was found to act in positive direction with highest magnitude.

Predominance of epistatic variance suggested that hybridization followed by selection would improve the trait in all crosses. Shafeeq *et al.* (2013) also obtained similar results. Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.1.7 Plant Height (cm)

In cross 1, significance was observed for all the scales among which scales A and B were in the positive direction of which scale A had the highest magnitude which implies that F_1 is better than P_1. Significance of additive and non additive gene actions were observed of which additive x additive effect had the highest magnitude.

Significance was observed for all the scales among which scales B, C and D were in the positive direction and scale B had the highest magnitude in cross 2 which implies that F_1 is better than P_2. Further analysis showed the significance of additive and non additive gene actions among which dominance x dominance effect was in the positive direction.

All the scales were significant among which scales A, C and D were in the positive direction of which scale C had the highest magnitude in cross 3 which implies that F_2 is better than parents. Eventhough dominance and all other epistatic effects were significant additive x dominance and dominance x dominance effects were in the positive direction and dominance x dominance effect had the highest magnitude.

Predominance of epistatic variance suggested that recombination breeding would improve the trait in all crosses. The role of dominance x dominance and additive x dominance in controlling the inheritance of plant height had been reported by Vaghasiya *et al.* (2009), Singh and Mital (1988), Umareitya *et al.* (2008), Suneetha *et al.* (2006), Dixit *et al.* (1984) and Dharmagowda (1977). Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.1.8 Calyx Length (cm)

All the three crosses witnessed the presence of all the kinds of epistatic interactions as indicated by the significance of all the four scales except scale B in crosses 1 and 2. F_2 is better than parents in crosses 1 and 2 which is evident

from the significance with high magnitude values of scale C whereas scale A had the highest magnitude which implies that F_1 is better than P_1.

Detailed analysis of cross 1 revealed the significance of additive, additive x additive effects and additive x dominance effects of which dominance and additive x additive effects were in the positive direction.

Eventhough significance was observed for additive, dominance and all the three types of interaction only additive, additive x dominance and dominance x dominance effects were in the positive direction and dominance x dominance effect had the highest magnitude in cross 2. Predominance of epistatic variance suggested that hybridisation and selection would improve the trait in crosses 1 and 2.

In cross 3 additive, additive x additive and dominance x dominance effects were significant among which dominance effect was in the positive direction and had the highest magnitude. Hence heterosis breeding would improve the trait. This is contradictory to the findings of Shinde *et al.* (2009) who reported that additive gene action is responsible for the trait. In all the crosses duplicate nature of epistasis was prevalent.

5.1.9 Volume of Fruit (cm^3)

Inadequacy of additive- dominance model and presence of epistasis in all the three crosses were suggested by the significance of scales. Scale A was positively significant which implies that F_1 is better than P_1 in crosses 1 and 2 and in cross 3 scale C had the highest magnitude which implies that F_2 is better than parents. Eventhough additive and non additive gene actions were significant, the relative assessment of magnitude indicated the predominance of dominance gene action there by suggesting the usefulness of heterosis breeding in improving this trait..

This is contradictory to the findings of Kafytullah *et al*. (2011) who suggested that additive gene action is responsible for the trait.

5.1.10 Weight of Fruit (g)

Fruit weight is one of the component character directly influencing the fruit yield. In cross 1, significance was observed for scale A, B, C and D among which scale C had the highest magnitude which implies that F_2 is better than parents. Further analysis showed the significance of all types of gene action of which dominance effect had the highest magnitude.

Significance was observed for scale A, B, C and D among which scale C had the highest magnitude in cross 2 which implies that F_2 is better than parents. Additive, additive x dominance and dominance x dominance effects were significant of which dominance effect had the highest magnitude.

In cross 3, negative significance was observed for scale A, B, C and D among which scale C had the highest magnitude. Further analysis showed the significance of additive and non additive gene actions among which dominance effect had the highest magnitude. Significance of dominance effect was in accordance with earlier report of Dharmagowda (1977) and Prasad *et al.* (2010).

Heterosis breeding would improve the trait in all crosses since dominance effect was predominant. Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.1.11 Number of Fruits per Plant

Number of fruits per plant is a commercially important trait which gain high market value through high productivity.

In all the crosses significance was observed for all the scales among which scale C had the highest magnitude which implies that F_2 is better than parents. Further analysis showed the significance of all the effects of which positive significance was observed for additive x dominance interaction in crosses 1 and 3

and dominance x dominance interaction in all the three crosses. Additive x additive interaction was negative in all the three crosses.

Highest magnitude was recorded for dominance x dominance effect in crosses 1 and 2 and additive x dominance effect in cross 3. Presence of non additive gene action for this trait was suggested earlier by Patil *et al.* (2003), Dixit *et al*. (1984), Umareitya *et al.* (2008), Kumar *et al.* (2009) and Chezhian *et al.* (2005). Predominance of epistatic variance indicated that recombination breeding could improve the trait in all the crosses. Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.1.12 Yield per Plant (kg)

Yield per plant is the ultimate and the most important trait. It is dependent mainly on the fruits per plant and fruit weight. In cross 1, significance was observed for scales A, B, C and D among which scales A and C were in the favourable positive direction of which scale C had the highest magnitude which implies that F_2 is better than the parents. Further analysis showed the significance of all the components among which additive, additive x dominance and dominance x dominance effects was in the favourable positive direction of which dominance x dominance effect had the highest magnitude.

Significance was observed for scales A, B and C among which scale B was in the positive direction which implies that F_1 is better than P_1 in cross 2. Further analysis showed the significance of all the genetic components of which only dominance and additive x additive effect was in the favourable positive direction and additive x additive effect had the highest magnitude. Predominance of non additive gene action was suggested earlier by Chezhian *et al.* (2005), Dixit *et al*. (1984), Umareitya *et al.* (2008), Suneetha *et al*. (2005, 2006), and Bendale *et al*. (2005).

Predominance of epistatic variance suggested that hybridization followed by selection would improve the trait in crosses 1 and 2.

Scales A, B and C were negatively significant among which scale C had the highest magnitude in cross 3. Further analysis showed the significance of additive and non additive gene actions of which dominance, additive x additive, additive x dominance and dominance x dominance effect were in the favourable positive direction. Dominance effect had the highest magnitude. Hence heterosis breeding would improve the trait in cross 3. Kumar *et al*. (2009), Mital *et al.* (1976) and Chaudhary and Pathania (2001) also obtained similar results. Opposite signs of dominance (h) and dominance x dominance (l) indicated the duplicate nature of epistasis in crosses 1 and 2 while similar signs showed complimentary nature of epistasis in cross 3.

5.1.13 Incidence of Fruit and Shoot Borer (Percentage)

Significance was observed for all the scales among which scales B, C and D were in the favourable negative direction of which scale C had the highest magnitude in cross 1. Dominance x dominance effect was in the favourable negative direction and had the highest magnitude eventhough significance was reported for all the genetic components.

In cross 2, significance was observed for all the scales among which scales C and D were in the negative direction of which scale C had the highest magnitude which implies that F_2 is better than parents. Further analysis showed the significance of all the genetic components among which additive and dominance x dominance effects were in the favourable negative direction and dominance x dominance effect had the highest magnitude.

Superiority of F_2 over the backcrosses was evident from the negative significance and the highest magnitude of scale D. Further analysis showed the significance of all the genetic components among which additive and

dominance x dominance were in the favourable negative direction of which dominance x dominance effect had the highest magnitude.

Predominance of epistatic variance suggested that recombination breeding would improve the trait. This is contradictory to the findings of Das *et al*. (2010) who suggested that additive gene action is responsible for the trait. Opposite signs of dominance (h) and dominance x dominance (l) effects indicated the duplicate nature of epistasis in all the crosses.

5.2 TRANSGRESSIVE SEGREGANTS

Estimates of transgressive segregants (percentage) were the highest for number of primary branches in crosses 1 and 3 and calyx length in cross 2. Moreover number of fruits per plant also exhibited high degree of transgressive segregants in cross 1. This indicated the possibility for utilizing these desirable segregants to develop superior varieties. Cross 1 produced the highest level of transgressive segregants for number of primary branches, number of fruits per plant and length of fruit. Cross 2 had the highest level of transgressive segregants for calyx length.

5.3 STUDY OF F_2 POPULATION

Genetic variability for yield and yield contributing traits in the base population is essential for successful crop improvement (Allard, 1960). The larger the variability, the better is the chance of identifying superior genotypes.

5.3.1 Variability Among the F_2 Families

The analysis of variance conducted for eight F_2 families of brinjal showed significant differences among the progenies for the different characters studied. This clearly showed that families were different from each other. Compact family block design used for the conduct of the experiment provides an opportunity to assess the variability among and within the families.

Identification of superior F_2 progenies is useful in further improvement programmes.

There was significant variation among the families for days to first flowering which is evident from the range of variation showed for this character. Early flowering is a desirable attribute. Family 2 was earlier to flower and family 8 took maximum days to first flowering. Significant variation for this trait were reported earlier by Thangavel *et al*. (2011), Ram and Singh (2007), Prabhu *et al*. (2007), Prasad *et al.* (2010) and Chattopadhyay *et al.* (2011).

Length of fruit showed significant variation among the families. Maximum fruit length was recorded in family 7 followed by family 6 and the minimum fruit length was recorded in family 3 followed by family 2. Prabhu *et al*. (2007) and Thangavel *et al*. (2011) also reported significant variations for this trait. There was significant difference among the families for girth of fruit. Maximum fruit girth was recorded in family 3 followed by family 2 and minimum fruit girth was recorded in family 7. This is in accordance with the findings of Shekar *et al.* (2011), Golani *et al*. (2007) and Nayak and Nagre (2013).

Among the families significant differences were observed for number of fruits per cluster. Maximum number of fruits per cluster was recorded in family 7 followed by family 4 and the minimum number of fruits per cluster was recorded in the families 5 and 6. Significant variation for this character was reported earlier by Dharwad *et al*. (2011). There was significant difference among the families for number of primary branches. Maximum number of primary branches was recorded in family 5 followed by family 8 which was on par with families 1 and 3 while minimum number of primary branches was recorded in family 7. Similar findings were obtained by Ram and Singh (2007), Kumar *et al*. (2012), Kamani *et al.* (2007) and Prabhu *et al*. (2007)

Prominent variation was observed among the families for days to first harvest. Family 8 followed by family 4 were found earliest to harvest and family 2 was late to harvest. Singh *et al*. (2013), Prasad *et al.* (2010) and Yadav *et al.* (2014) also reported significant variation for this trait. Significant difference was observed among the families for volume of fruit. Fruit volume was recorded maximum in family 6 followed by family 2 which was on par with family 8 and minimum volume of fruit was recorded in family 1. This was reported earlier by Prasad *et al.* (2010) and Kafytullah *et al*. (2011)

There was significant difference among the families for plant height. Maximum plant height was noticed in family 6 followed by family 1 and minimum plant height was recorded in family 2. Golani *et al*. (2007), Ram and Singh (2007), Kamani *et al.* (2007) and Prabhu *et al*. (2007) also obtained similar results. Calyx length reported significant difference among the families. Family 5 followed by family 3 witnessed maximum calyx length and minimum calyx length was recorded in family 6. Wide variation for calyx length was reported earlier by Prabakaran *et al.* (2013) and Kumar *et al.* (2013)

Among the families significant variation was observed for number of fruits per plant. Maximum number of fruits per plant was recorded in family 4 followed by family 2 and minimum number of fruits per plant was recorded in family 3. Earlier studies by Ram and Singh (2007), Monpara *et al.* (2007), Kamani *et al.* (2007) and Prabhu *et al*. (2007) also reported large variation for number of fruits per plant. For weight of fruit and fruit yield per plant, there was significant difference among the families. Maximum values for these traits were recorded in family 6 while family 1 recorded minimum fruit weight and fruit yield per plant. This is in accordance with the findings of Dhaka and Soni (2012), Kamani *et al.* (2007), Prabhu *et al*. (2007) and Dhameliya *et al*. (2008).

There was significant difference among the families for percentage of plants infested with shoot and fruit borer. Maximum percentage of plants infested with fruit and shoot borer was recorded in family 2 followed by family 8 and

minimum percentage of plants infested with fruit and shoot borer was recorded in family 5. Similar findings were obtained by Prabhu and Natarajan (2007), Kafytullah *et al*. (2011) and Prabhu *et al*. (2007).

5.3.2 Variability Among the Progenies

The mean values of progenies for different characters showed wide variation among the progenies of the same parentage. Compact family block design facilitates the analysis of progenies of different families.

There were significant differences among the progenies of family 1 for different characters studied. Progeny 4 took the minimum number of days to first flowering. Other progenies were significantly different from progeny 4 for days to flowering. Significant difference was observed among the progenies for girth of fruit, plant height and number of primary branches. Maximum fruit girth, plant height and number of primary branches were recorded in progeny 3. Variations were observed for number of fruits per cluster, volume of fruit and percentage of plants infested with fruit and shoot borer were found to be non significant. Hence all the progenies can be selected for getting more number of fruits per cluster, maximum fruit volume and varieties less susceptible to fruit and shoot borer. Progeny 5 was earlier to harvest and have maximum calyx length. Progeny 2 had maximum fruit length, fruit weight, number of fruits per plant and fruit yield per plant.

Progenies of family 2 exhibited significant variation for different characters studied. Progeny 1 was the earliest to flower and to harvest. Other progenies were significantly different from progeny 1 for days to flowering. There was significant difference among the progenies for length of fruit. Progeny 5 was found to have maximum fruit length, more number of primary branches and maximum fruit volume. Significant difference was observed among the progenies for plant height and girth of fruit. Fruit girth and plant height were maximum in progeny 4. Variations shown for the number of fruits per cluster and percentage of plants infested with fruit and shoot borer was found to be not significant.

Hence all the progenies can be selected for getting more number of fruits per cluster and less susceptible varieties. Progeny 2 produced maximum number of fruits per plant and fruit yield per plant while progeny 3 produced fruits with maximum weight. Hence these progenies can be used for further improvement programmes.

Among the progenies of family 3 significant difference was observed for days to first flowering. For fruit length and fruit girth progeny 3 was significantly superior to the other progenies. Maximum plant height, number of fruits per plant, weight of fruit and fruit yield per plant were recorded in progeny 5 which was earliest to flower. Hence progeny 5 can be selected for getting more number of fruits, better fruit yield and early flowering. The maximum number of primary branches and calyx length was recorded in progeny 1. Among the progenies, progeny 2 was earlier to harvest. There were no significant differences observed among the progenies for percentage of plants infested with fruit and shoot borer, volume of fruit and number of fruits per cluster. Hence all the progenies can be utilized for further improvement programmes.

There were significant differences among the progenies of family 4 for different characters studied. Progeny 3 took the minimum number of days to first flowering and the same progeny was the earliest to harvest. Among the different progenies in family 4, progeny 1 had the maximum number of primary branches. The same progeny also recorded the maximum fruit length and plant height. Progeny 2 can be selected from family 4 because of desirable yield attributes for further evaluation. Maximum fruit girth, number of fruits per plant, weight of fruit and fruit yield per plant were recorded in progeny 2. There were statistically no significant differences among the progenies for calyx length, volume of fruit and number of fruits per cluster. Minimum percentage of plants infested with fruit and shoot borer was recorded in progeny 1.

Family 5 recorded significant differences among the progenies for different characters studied. Progeny 4 took minimum number of days to first flowering and first harvest. Regarding fruit length and fruit girth progeny 1 had maximum value. Maximum number of primary branches was recorded in progeny 3. Maximum plant height, calyx length, number of fruits per plant, weight of fruit and fruit yield per plant were recorded in progeny 2. There were no significant differences among the progenies for volume of fruit and number of fruits per cluster. Minimum percentage of plants infested with fruit and shoot borer was recorded in progeny 3 which was on par with progeny 2.

Among the progenies of family 6 significant variations were observed for different characters like girth of fruit, number of primary branches, days to first harvest, plant height, number of fruits per plant, weight of fruit and fruit yield per plant. There were no significant differences among the progenies for different characters like days to first flowering, length of fruit, number of fruits per cluster, volume of fruit, calyx length and percentage of plants infested with fruit and shoot borer. Maximum fruit girth and plant height were recorded in progeny 3. Number of primary branches were recorded maximum in progeny 4. Progeny 2 can be advanced to next generation since it recorded maximum number of fruits per plant, weight of fruit, fruit yield per plant and was the earliest to harvest.

Among the progenies of family 7 progeny 5 had the maximum fruit length and took the minimum number of days to first flowering. Maximum fruit girth and number of primary branches were recorded in progeny 4. Minimum days to first harvest was recorded in progeny 1. Maximum plant height, weight of fruit, fruit yield per plant and number of fruits per plant were recorded in progeny 3. There were no significant differences among the progenies for volume of fruit, number of fruits per cluster and percentage of plants infested with fruit and shoot borer.

There were significant differences among the progenies of family 8 for different characters studied. Progeny 4 took the minimum number of days to first flowering. Maximum number of primary branches and fruit girth were recorded

in progeny 2 which took the minimum days to first harvest. Maximum plant height was recorded in progeny 1. Maximum fruit length, fruit weight, fruit yield per plant and number of fruits per plant were recorded in progeny 3. Maximum calyx length and volume of fruit were recorded in progeny 5. There were no significant differences among the progenies for characters like girth of fruit, number of fruits per cluster and percentage of plants infested with fruit and shoot borer.

The magnitude of variation shown among the progenies of 8 families revealed the heterogenous nature of F_2 families. All families except family 6 showed significant variation among progenies for days to first flowering and fruit length. Variations among the progenies for girth of fruit were expressed by all families except family 8. Number of fruits per cluster showed no significant variation among the progenies. Variations among progenies for number of primary branches, days to first harvest, plant height, number of fruits per plant, weight of fruit and fruit yield per plant were expressed by all families. Variations among progenies were significant for volume of fruit only in families 2 and 8. All families except families 4 and 6 showed significant differences among the progenies for calyx length. For percentage of plants infested with fruit and shoot borer, significant variations were observed among all families except families 4 and 5.

5.3.3 Variability Among the Progenies of 8 Families

The pooled analysis of the data showed significant difference among the progenies for all the characters. Progeny 1 of family 2 was found to be be earliest to flower and harvest. Progeny 5 of family 7 recorded longest fruits and shortest fruits were produced by progeny 5 of family 3. Maximum fruit girth was observed in progeny 3 of family 3 and progeny 3 of family 6 produced fruits having the maximum weight. Maximum number of fruits were produced by progeny 2 of family 4. Progeny 4 of family 7 produced the maximum number of fruits per cluster. Analysis of the pooled data revealed significant differences among the progenies for number of primary branches. Maximum

number of primary branches was produced by progeny 2 of family 7. Progeny 1 of family 1 produced fruits with minimum volume and maximum was recorded by progeny 3 of family 6. Progeny 1 of family 2 was with minimum plant height and maximum was recorded by progeny 3 of family 6. Significant variation for yield was observed among the progenies. Progeny 3 of family 6 recorded the highest yield and the minimum was recorded by progeny 5 of family 1. Percentage of plants infested with shoot and fruit borer revealed significant difference among the progenies for families 4 and 5. Minimum percentage of infestation was recorded in progeny 3 of family 5.

Most of the families showed highly heterogenous nature for different characters. Therefore superior progenies identified for different characters from the F_2 population can be utilized for further improvement.

SUMMARY

6. SUMMARY

Brinjal is a major vegetable crop of our country since ancient time and the human society has social and economic relationship with this crop. To enhance the pace of genetic improvement in eggplant detailed investigation regarding gene action and genetic variability is essential. The project entitled "Generation mean analysis in brinjal (*Solanum melongena* L.) for yield and yield attributes" was carried out at College of Agriculture, Vellayani during 2013-15 to study the gene action and inheritance pattern of yield and yield attributes using generation mean analysis.

In generation mean analysis six generations *viz*. P_1, P_2, F_1, F_2, B_1 and B_2 of three crosses (Wardha local x Surya, Wardha local x NBR-38 and Swetha x Haritha) were evaluated in a field experiment for thirteen yield components. Results showed that in cross 1, additive gene effects (additive, additive x additive) were important for fruit girth, number of primary branches, calyx length and plant height while non additive gene actions (dominance, additive x dominance and dominance x dominance) were recorded for fruit weight, fruit volume, fruit length, yield per plant, days to first flowering, days to first harvest, number of fruits per plant, number of fruits per cluster, fruit and shoot borer incidence and plant height. In cross 2, additive gene effects were predominant for yield per plant and number of primary branches while only non additive gene actions were important for all other traits. In cross 3, additive gene action was reported for fruit girth and number of fruits per cluster and all other characters were under the control of non additive gene action. Duplicate type of epistasis was observed for most of the crosses.

The study suggested that characters governed by predominance of additive component could be improved through selection while dominance component could be improved through heterosis breeding. If the epistatic variance is relatively high, more reliance should be placed on recombination breeding.

The study of F_2 population was undertaken in compact family block design with eight families and five progenies within family to assess the variability between families and among progenies within each family. Eight F_1 hybrids selected were selfed to raise eight F_2 families. Based on the mean values of eight families and their progenies, variability among the families and progenies within families were studied. The analysis of variance conducted for 8 F_2 families showed significant differences among the progenies for different characters. The mean values recorded for eight characters showed wide variation among the families. Family 2 took minimum number of days to first flowering while maximum fruit length and number of fruits per cluster were recorded in family 7. Maximum calyx length, number of primary branches and minimum percentage of plants infested with shoot and fruit borerwere recorded in family 5. Maximum fruit girth was recorded in family 3 and minimum days to first harvest were recorded in family 2. Maximum number of fruits per plant was recorded in the family 4 while maximum volume, plant height, weight of fruit and yield per plant were recorded in the family 6.

The magnitude of variation shown among the progenies of 12 families revealed the heterogenous nature of F_2 families. All families except family 6 showed significant variation among progenies for days to first flowering and fruit length. Variations among progenies for fruit girth was expressed by all families except family 8. None of the families exhibited significant variation among the progenies for number of fruits per cluster. Variations among progenies for number of primary branches, days to first harvest, plant height, number of fruits per plant, fruit weight and yield were expressed by all families. Families 2 and 8 revealed significant variation among the progenies for volume of fruit. All families except family 4 and 6 showed significant difference among progenies for calyx length. Family 4 and 5 showed significant difference among progenies for percentage of plants infested with shoot and fruit borer.

The pooled analysis of the data showed significant difference among the progenies for all the characters. Progeny 1 of family 2 which is on par with

progeny 5 of same family was found to be earliest to flower and harvest while maximum days for first flowering was taken by progeny 1 of family 8. Maximum duration was taken by progeny 5. Progeny 5 of family 7 recorded the longest fruits while the shortest fruits were produced by progeny 5 of family 3. Highest fruit girth was observed in progeny 3 of family 3 and progeny 3 of family 6 produced fruits having the maximum weight. Maximum number of fruits were produced by progeny 2 of family 4. Progeny 4 of family 7 produced maximum number of fruits per cluster while maximum number of primary branches were produced by progeny 2 of family 7. Progeny 1 of family 1 produced fruits with minimum volume and maximum was recorded by progeny 3 of family 6 while progeny 1 of family 2 was with minimum plant height and maximum was recorded by progeny 3 of family 6. Significant variation for yield was observed among the progenies. Progeny 3 of family 6 recorded highest yield and minimum was recorded by progeny 5 of family 1. Percentage of plants infested with shoot and fruit borer revealed no significant difference among the progenies for all families except families 4 and 5 and minimum percentage of infestation was recorded by progeny 3 of family.

Based on the results wide variability among the families and progenies within families revealed the heterogenous nature of F_2 families. The study revealed that among the families studied family 6 recorded maximum fruit weight and yield per plant. Superior F_2 progeny can be used in further improvement programmes. The predominance of additive gene effects as well as non-additive gene effects were recorded for fruit weight, fruits per plant and yield per plant.

FUTURE LINE OF WORK

- Pedigree method of selection can be followed to select superior recombinants from the segregating generations which on attaining uniformity can be released as varieties for cultivation.
- Stability of the superior progenies need to be assessed and the superior ones can be released for cultivation.

- Superior plants can be selected from families and progenies showing wide variability.
- Suitable breeding method can be adopted according to the breeding goal in the light of knowledge on gene action prevalent for each character.

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GENERATION MEAN ANALYSIS IN BRINJAL (*Solanum melongena* L.) FOR YIELD AND YIELD ATTRIBUTES.

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(2013-11-147)

ABSTRACT

of the thesis submitted in the partial fulfilment of

the requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture

Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS

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2015

ABSTRACT

The project entitled "Generation mean analysis in brinjal (*Solanum melongena* L.) for yield and yield attributes" was carried out at College of Agriculture, Vellayani during 2013-15 to study the gene action and inheritance pattern of yield and yield attributes using generation mean analysis. In generation mean analysis six generations *viz.*, P_1, P_2, F_1, F_2, B_1 and B_2 of three crosses (Wardha local x Surya, Wardha local x NBR-38 and Swetha x Haritha) were evaluated in a field experiment for thirteen yield components.

Results showed that in cross 1 additive gene effects (additive, additive x additive) were important for fruit girth, fruit volume, number of fruits per cluster, yield per plant and non additive gene actions (dominance, additive x dominance and dominance x dominance) were recorded for fruit length, days to first flower, days to first harvest, calyx length, fruit volume, number of fruits per plant, number of primary branches and plant height. In cross 2 additive gene effects were predominant for fruit weight, yield per plant and fruit and shoot borer incidence while only non additive gene actions were important for all other traits. In cross 3 additive gene action was reported for fruit and shoot borer incidence and days to first harvest and all other characters were under the control of non additive gene action. Duplicate type of epistasis was observed for most of the crosses.

The study of F_2 population was undertaken in compact family block design with eight families and five progenies within family to assess the variability between families and among progenies within each family. Eight F_1 hybrids selected were selfed to raise eight F_2 families. Based on the mean values of eight families and their progenies, variability among the families and progenies within families were studied.

The analysis of variance conducted for eight F_2 families showed significant differences among the progenies for different characters. Family 2 (Wardha local x Surya) took the minimum number of days to first flowering and first harvest. Maximum fruit length and number of fruits per cluster were recorded in Family 7 (Wardha local x Selection Pooja). Maximum number of fruits per plant was recorded in Family 4 (Wardha local x Swetha) and maximum plant height, fruit volume, fruit weight and yield per plant were recorded in Family 6 (Surya x Haritha).

The magnitude of variation shown among the progenies of eight families revealed the heterogenous nature of F_2 families. All families except family 6 showed significant variation among progenies for days to first flowering and fruit length. Variations among progenies for girth of fruit was expressed by all families except family 8. None of the families exhibited significant variation among the progenies for number of fruits per cluster. All the families possess significant variations among progenies for number of primary branches, days to first harvest, plant height, number of fruits per plant, fruit weight and yield. Families 2 and 8 revealed significant variation among the progenies for volume of fruit. All families except family 4 and 6 showed significant difference among progenies for calyx length. Family 4 and 5 showed significant difference among progenies for percentage of plants infested with shoot and fruit borer.

Based on the results wide variability among the families and progenies within families revealed the heterogenous nature of F_2 families. The study revealed that among the families studied family 6 recorded maximum fruit weight and yield per plant. Superior F_2 progeny can be used in further improvement programmes. The predominance of additive gene effects as well as non-additive gene effects were recorded for fruit weight, fruits per plant and yield per plant. The study suggested that characters governed by predominance of additive component could be improved through selection.