

**GENETIC EVALUATION FOR YIELD AND RESISTANCE TO PHOMOPSIS
BLIGHT IN BRINJAL (*Solanum melongena* L.)**

By
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(2011-11-158)

THESIS

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DECLARATION

I hereby declare that this thesis entitled “**Genetic evaluation for yield and resistance to phomopsis blight in brinjal (*Solanum melongena* L.)**” is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

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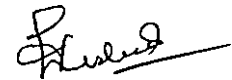
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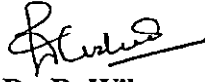
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Dedicated to

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LIST OF ABBREVIATIONS

%	-	per cent
$^{\circ}\text{C}$	-	Degree Celsius
CD	-	Critical difference
cm	-	centimeter
DAT	-	Days After Transplanting
<i>et al.</i>	-	and others
Fig.	-	Figure
g	-	gram
GA	-	Genetic Advance
GAM	-	Genetic Advance as percentage of Mean
GCV	-	Genotypic Coefficient of Variation
H^2	-	Heritability
ha	-	hectare
<i>i.e.</i>	-	that is
KAU	-	Kerala Agricultural University
kg	-	kilogram
m	-	metre
mg	-	milligram
ml	-	millilitre

mm	-	millimeter
nm	-	nanometer
PCV	-	Phenotypic Coefficient of Variation
PDI	-	Percentage Disease Index
RH	-	Relative Humidity
SE	-	Standard error
SFB	-	Shoot and Fruit Borer
t	-	tons
q	-	quintal
<i>viz.</i>	-	namely

Introduction

1. INTRODUCTION

Solanum is a large and important genus of the family Solanaceae. Eggplant or brinjal or aubergine (*Solanum melongena* L.) represents the non-tuberous group of *Solanum* species (Narasimha, 1979). Brinjal is the most common, popular and widely grown vegetable crop of both tropics and sub-tropics of the world (Roychowdhury and Tah, 2011). India and China are its primary centers of diversity (Kashyap *et al.*, 2003). It is being grown extensively in India, Bangladesh, Pakistan, China, Philippines, France, Italy and United States. Brinjal is highly productive and usually finds its place as the poor man's vegetable (Som and Maity, 2002). Brinjal is major vegetable crop of our country and since ancient time the human society has social and economic relationship with this crop. India ranks second after China in area and production of brinjal. Brinjal shares 8.1 percent of production in total vegetable production in India. The cultivated area of brinjal in India is about 6.80 lakh hectares with production of 118.96 lakh tonnes and productivity of 17.5 tonnes per hectare, while West Bengal is leading state in area, production and productivity of 1.58 lakh hectares as well as production of 28.70 lakh tonnes and productivity of 18.1 tonnes per hectare (Anon., 2011).

Brinjal (*Solanum melongena* L.) is indigenous to a vast area stretching from northeast India and Burma to northern Thailand, Laos, Vietnam and southwest 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 indications that it was cultivated in antiquity. Several Sanskrit documents, dated from as early as 300 BCE, mention this plant with various descriptive words, which suggest its wide popularity as food and medicine (Nadkarni, 1927). In the Ayurvedic, white types were recommended for diabetic patients and roots for the treatment of asthma.

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 (Chaudhary, 1976) and fruits are rich source of minerals like Ca, Mg and 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.

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

The crop is known to suffer from 12 diseases and among them phomopsis blight and fruit rot caused by *Phomopsis vexans* are the major constraints to eggplant cultivation (Khan, 1999; Das, 1998). These diseases cause crop loss up to 30-50 per cent affecting eight million farm families involved in eggplant cultivation (Masuduzzaman *et al.*, 2008). Phomopsis blight not only harms eggplants but also makes fruits inedible and unmarketable.

Fruit and shoot borer (*Leucinodes orbonalis* Guen.) is most serious insect pest of brinjal throughout the country. It attacks the plant in 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 not only is 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.

Improvement in fruit yield, colour and insect and pest resistance will certainly enhance the production and consumption of the crop. For improvement programme, the information about variability is a prerequisite. Genetic variability of brinjal has been studied by various workers in India (Misra, 1961; Thakur *et al.*, 1968; Chowdhury, 2005). The phenotypic variability among a collection of genetic stocks gives an indication of potential genotypic variability; however, the

quantitative characters are greatly influenced by the environment. Therefore, information of the extent of variability available in some important economic traits and their heritability will be helpful to the breeders to formulate sound breeding programmes. The knowledge of the extent to which the desirable characters with economic values are heritable is a prerequisite for any crop improvement programme (Roychowdhury and Tah, 2011a). Breeders have continually retained their interest in the grouping of the germplasm and the pedigree of selected cultivars since the information might be particularly helpful in effective breeding strategy determination (Ali *et al.*, 2011).

In the formulation of a selection programme for improvement of yield, a study on the interrelationship of yield with other traits would be of great value. Correlation studies enable researchers to determine association between yield and other yield contributing components. The genotypic and phenotypic correlations existing between yield and other characters and among the characters themselves are important in the breeding programme.

Yield being a complex character, is dependent upon a number of attributes. Before initiating an effective selection programme, it is necessary to know the importance and association of various components with yield and among each other. Studies on this aspect were made earlier by several workers. A simple measure of correlation of characters does not quantify the relative contribution of causal factors to the ultimate yield. Since the component traits themselves are inter-dependent, they often affect their direct relationship with yield and consequently restrict the reliability of selection indices based upon correlation coefficients. The path coefficient analysis permits the separation of direct effects from indirect effects through other related traits by partitioning the genotypic correlation coefficients.

Information concerning the extent and nature of genetic diversity within a crop species is essential. 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 the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization program. Genetically diverse parents are likely to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1 s and broad spectrum of variability in segregating generations (Arunachalam, 1981).

Hence the present investigation was undertaken with the following objectives:

- To study variability and heritability for yield and yield components in the genotypes.
- To estimate the *genotypic correlations and direct and indirect effects of component characters on yield by path analysis*
- To estimate the genetic divergence in available germplasm using D^2 analysis.
- To identify genotypes with high yield and tolerance to phomopsis blight

Review of Literature

2. REVIEW OF LITERATURE

2.1 Germplasm evaluation

Brinjal (*Solanum melongena* L.) is an important solanaceous vegetable in many countries of Asia and Africa. It is a good source of minerals and vitamins in the tropical diets. Assessment of genetic resources is the starting point of any crop improvement programme. In India, the National Bureau of Plant Genetic Resources is the nodal institute for management of germplasm resources of crop plants and holds more than 2500 accessions of brinjal in its gene bank (Kumar *et al.*, 2008)

2.2 Variability

A study of yield and seven yield related characters in nineteen varieties gave high genotypic coefficient of variation (GCV) and heritability values for fruits per plant, fruit length : circumference ratio and average fruit weight (Sinha, 1983)

Vadivel and Bapu (1990) evaluated nineteen brinjal genotypes, including seven from foreign sources and reported that plant height, branches per plant, fruit weight and fruits per plant exhibited high genotypic and phenotypic variance. High GCV and PCV for fruit length, girth and weight, fruits per plant and fruit yield per plant were shown.

Evaluation of 15 genotypes by Mohanty (1999) revealed considerable genotype environment interaction for yield, average fruit weight, number of fruits and branches per plant. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the traits.

Negi *et al.* (2000) studied genetic variability in forty genotypes of brinjal for 21 characters. Significant differences were found among the genotypes for all the traits, indicating wide range of variation. High genotypic coefficients of

variation were found for number of fruits per plant, fruit yield per plant and fruit set.

Fifteen cultivars of brinjal were evaluated for six economic characters by Mohanty and Prusti (2002) and reported that PCV was greater than GCV for all the traits. High GCV was observed for yield, average fruit weight, number of fruits and branches per plant while plant height and days to first harvest showed low GCV.

Genetic variability for different yield contributing characters was studied in twenty two diverse germplasms of brinjal by Patel *et al.* (2004). The study indicated existence of considerable amount of genetic variability for all the characters studied except plant spread, plant height and days to 50 per cent flowering. Fruit length, yield per plant and fruit weight exhibited highest values of genotypic and phenotypic coefficient of variation.

Among the 25 diverse brinjal genotypes, Singh and Kumar (2005) reported that average fruit weight showed the highest phenotypic and genotypic coefficient of variation, closely followed by number of fruits per plant. The lowest values were recorded for days to first fruit set followed by days to first flowering. All the characters exhibited less difference between GCV and PCV values, and traits like average fruit weight, days to first fruit harvest, fruit index and yield per plant showed nearly equal GCV and PCV values, indicating the low influence of environment on their expression

Naliyadhara *et al.* (2007) evaluated twenty one genotypes of brinjal during late kharif season and reported that PCV was slightly greater than GCV for all the traits. High heritability with moderate to high GCV and genetic gain was observed for all the characters except fruit yield indicating scope for improvement by simple selection methods. Kamani and Monpara (2007) accounted both GCV and PCV were low for days to first picking, moderate for days to first flower, plant height and fruit girth and high for branches per plant, fruit length, fruit shape index, fruits per plant, fruit weight and fruit yield per plant.

Mishra *et al.* (2008) studied brinjal genotypes for genetic variability for yield and yield components (number of days to 50% flowering, number of days to maturity, number of primary branches, plant height, plant spread, length of fruit, girth of fruit, fruit shape index, average weight of fruits, number of fruits per plant and yield per plant). The analysis of variance revealed significant differences for all characters except number of primary branches. The estimates of the genetic coefficient of variation were higher than the estimates of phenotypic coefficient of variation. The highest estimates of GCV and PCV were recorded for fruit shape index.

Sixteen genotypes of local and exotic germplasm were studied by Islam and Uddin (2009) to estimate variability. High genotypic and phenotypic coefficients of variation were reported for number of fruits per plant, individual fruit weight, and yield per plant.

An investigation was carried out to study genetic variability in twenty genotypes of brinjal by Nair and Mehta (2009) and reported that phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters. Both phenotypic coefficient of variation as well as genotypic coefficient of variation was high for seed pulp ratio, weight of fruit and number of fruits per plant.

Eight morphological characters in thirty four brinjal genotypes were studied by Muniappan *et al.* (2010). High PCV and GCV were recorded by the characters viz., number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight, and fruit yield per plant.

Roychowdhury *et al.* (2011) revealed significant differences among the genotypes for all the characters studied indicating the presence of substantial genetic variability. The magnitude of PCV was higher than GCV, indicating the greater influence of environment. High GCV and PCV have been obtained for number of fruits per plant and average fruit weight.

Kumar *et al.* (2011) studied sixty-two genotypes of brinjal to estimate the extent of variability present in the experimental material. Analysis of variance indicated presence of large variability for different characters under study. Genotypes PCPGR No. 7030 and KS-331 for earliness, SMB 115 for maximum number of fruits, BARI for maximum length of fruit, PCPGR No.7041 and 7028 for maximum number of fruit per plant, and sel- 6 for yield were found promising, hence can be utilized for improvement for these traits in brinjal.

Ansari *et al.* (2011) estimated mean performance and genetic variability parameters in seven parents and twenty one hybrids of brinjal to identify suitable parents and F_1 s for brinjal cultivation. The study revealed highly significant differences for most of the traits. The moderate estimates of Genotypic coefficient of variation and Phenotypic coefficient of variation were observed for number of fruits per cluster, average fruit weight, total number of fruits per plant, fruit length. Maximum GCV and PCV were observed for number of flowers per inflorescence, number of fruits per picking and fruit girth, indicating scope for selection to improve these characters.

Different parameters were estimated to assess the magnitude of genetic variability in forty diverse genotypes of brinjal by Kafyullah *et al.* (2011). The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes from all the characters studied except total chlorophyll content. The high phenotypic coefficient of variation and genotypic coefficient of variation were observed 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 pre plot, fruit set per cent and fruit yield per hectare.

Kumar *et al.* (2011) reported that PCV was higher than their corresponding GCV for all the characters. Phenotypic coefficient of variation followed by number of fruits per cluster and number of flowers per cluster while, diameter of fruit, length of fruit, number of primary branches per plant, plant height and days to fifty per cent flowering showed minimum phenotypic

coefficient of variation. The genotypic coefficient of variation among the parents was recorded high for total yield per plant, weight of fruit, number of flowers per cluster and diameter of fruit. Whereas, it was moderate for length of fruit and number of fruits per cluster, however, it was showed low rate for plant height, number of primary branches per plant and it was lowest for days to fifty per cent flowering. The highest genotypic and phenotypic coefficient of variation was recorded for total yield per plants and lowest for days to fifty per cent flowering.

Chourasia and Shree (2012) reported highest range of variation for fruit weight followed by fruit length, number of fruits per cluster and number of fruits per plant. The highest PCV and GCV were estimated for number of fruits per cluster in all the four seasons indicating its widest range of variability in all the situations under study.

Danquah and Ofori (2012) assessed ten accessions of garden eggplants for variance and reported high phenotypic and genotypic coefficient of variances were observed for fruit length, number of seeds per fruit, fruit weight and height at flowering. In addition, genetic and phenotypic variances were higher in fruit weight, height at flowering, days to flowering and number of seeds per fruits.

Mean performance and genetic variability parameters were estimated by Kumar *et al.* (2012) in 33 local types of brinjal to identify suitable parents for hybridization. The study revealed that highly significant differences were observed for most of the traits. Mean performance showed that EP 27 registered highest fruit yield per plant followed by EP 3. High estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed 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.

2.3 Heritability and genetic advance

Mohanty (1999) evaluated 15 genotypes and reported that high heritability accompanied by moderate to high genetic gain was recorded for average fruit weight, number of fruits and branches per plant. Negi *et al.* (2000) found that most of the traits showed high estimates of heritability (>70 %). High genetic advance coupled with high heritability was exhibited by number of fruits per plant, fruit yield per plant and weight per fruit suggesting predominance of additive gene action. Days to fifty per cent flowering and picking had high heritability and low genetic advance.

Patel *et al.* (2004) detailed high estimates of heritability (broad sense) and genetic advance for fruit length, yield per plant and fruit weight. These characters can be effectively improved through selection.

Singh and Kumar (2005) studied 25 brinjal genotypes and reported that the heritability estimates were high (above 87 per cent) for all the characters. The highest heritability was observed for average fruit weight, closely followed by fruit index and yield per plant. The genetic advance as percentage of mean was high for average fruit weight, number of fruits per plant and yield per plant. High heritability coupled with high genetic advance was observed for number of fruits per plant, average fruit weight and yield per plant, indicating that they are governed by additive genes.

Kamani and Monpara (2007) reported high heritability along with high genetic advance and GCV for fruit length, fruit shape index, fruits per plant, fruit weight and fruit yield per plant in all the crosses suggesting preponderance of additive gene actions for these traits.

High heritability combined with high genetic advance as percentage of mean was observed for fruit length, fruit girth and 10-fruits weight (Golani *et al.*, 2007). This indicated that these three characters are under the control of additive gene action and would respond very well to continuous selection.

Kafyullah *et al.* (2011) found high heritability coupled with high genetic advance for fruit volume, fruit weight, leaf area index, fruit length, fruit diameter and number of fruits per plant indicating these characters are governed by additive gene action. Hence, direct selection may be followed for the improvement of brinjal for these characters. High heritability with moderate to genetic gain was observed for all the characters except fruit yield which could be improved by simple selection methods (Naliyadhara *et al.*, 2007).

Mishra *et al.* (2008) reported that heritability estimates were highest for fruit shape index. High level of genetic advance was registered for fruit shape index and average weight of fruit. Plant height, plant spread, girth of fruit and number of fruits per plant exhibited high levels of heritability and genetic advance, indicating the importance of additive gene effect for these traits. Thus, simple selection will be effective for these traits.

Nair and Mehta (2009) reported high heritability accompanied by high genetic advance for weight of fruit indicating negligible environment effect and this trait will be more amenable to improvement through mass selection, progeny selection etc., aiming at exploiting the additive variance. High heritability and moderate genetic advance were observed for plant height, fruiting span and number of fruits per plant suggesting that selection based on phenotypic performance of these traits is possible.

Heritability and genetic advance were high for number of fruits per plant, individual fruit weight and yield per plant indicating the possibility of selection to improve these characters (Islam and Uddin, 2009).

All the characters were accompanied by high heritability and high genetic advance excepting days to 50 per cent flowering (Muniappan *et al.*, 2010). The heritability values ranged from 72.18 per cent for fruit yield per plant to 99.83 per cent for fruit length. All the estimates for heritability had very high value. The maximum genetic advance was observed in fruit yield per plant whereas the characters fruit breadth and fruit length recorded the minimum genetic advance

value of 1.88 and 2.26 respectively. The genetic advance as per cent of mean was noted maximum for fruit yield per plant.

Ansari *et al.* (2011) estimated high estimates of heritability coupled with high genetic advance for the average fruit weight and number of fruits per plant revealing the effectiveness of simple selection for improvement of these characters.

Roychowdhury *et al.* (2011) reported high heritability estimates for number of fruits and leaves per plant, days to first harvest, average fruit weight; moderate for plant height, number of branches per plant, fruit length, total yield; lower for days to seed germination and internodal length. High heritability with high genetic advance over the mean (GAM) was observed for number of fruits and average fruit weight. Other characters like number of branches and fruit length exhibited moderate; while number of leaves and days to first harvest showed lowest value.

Kumar *et al.* (2011) assessed 15 genotypes and reported that heritability estimate was highest for weight of fruits followed by plant height, total yield per plant, length of fruits, days to fifty per cent flowering, number of primary branches per plant and number of fruits per cluster. Rest of the characters exhibited moderate to low heritability among the parents. The highest genetic gain was observed for total yield per plant followed weight of fruit and length of fruit, but it was low for diameter of fruit, number of fruits per cluster and plant height.

Chourasia and Shree (2012) reported highest heritability (in broad sense) for fruit length followed by fruit weight, number of fruits per cluster, fruit width and number of fruits per plant. The characters namely leaf area, number of days to first harvest and number of days to fifty per cent flowering were found to have lower heritability estimates. High heritability with high genetic advance were found for total yield (q/ha), fruit weight and number of leaves per plant.

Danquah and Ofori (2012) reported high heritability estimates for fruit length, days to flowering, fruit weight and height at flowering. However, number of seeds per fruit exhibited moderately high heritability. Kumar *et al.* (2012) reported high estimates of heritability coupled with high genetic advance as per cent of mean for number of primary branches per plant, internodal length, fruit length, average fruit weight, ascorbic acid content, number of fruits per plant and fruit yield per plant indicated that selection will be effective for improvement of these characters.

Variability was assessed 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 in thirty one genotypes by Shekar *et al.* (2012) and reported that almost all the characters exhibited high heritability except for plant height and moderate to low heritability was recorded for average fruit weight. Highest genetic advance as percentage of mean was observed for almost all the characters except for days to first flowering, days to first picking, plant height and average fruit weight recorded moderate to low genetic advance as per cent of mean.

Sixty brinjal germplasm lines were evaluated for fourteen quantitative characters by Lokesh *et al.* (2013) and reported that genetic advance as percentage of mean were high (above 20.0) for plant height, plant spread, average fruit weight and shoot and fruit borer incidence on shoots. High heritability accompanied with high genetic advance was noticed for plant height, plant spread, average fruit weight and shoot and fruit borer incidence on shoot indicating that simple selection may be effective to fix and improve such traits.

2.4 Correlation and path analysis

Yield is a complex character; its direct improvement is difficult. Knowledge in respect of the nature and magnitude of associations of yield with various component characters is a pre-requisite to bring improvement in the desired direction. A crop breeding programme, aimed at increasing the plant

productivity requires consideration not only of yield but also of its components that have a direct or indirect bearing on yield. The necessity of coefficient of correlation is to describe the degree of association between independent and dependent variables. Path coefficient analysis measures the direct influence of one variable upon another and permits the separation of correlation coefficient into components of direct and indirect effects.

Sinha (1983) reported that yield was positively correlated with fruits per plant, plant height and branches per plant at the phenotypic and genotypic levels, and with fruit length : circumference ratio at the genotypic level. Path analysis indicated that fruits per plant and fruit length: circumference ratio had the maximum direct effect on yield combined with high GCV and heritability values.

Mohanty (1999) evaluated 15 genotypes and found that the genotypic correlation coefficients were higher than corresponding phenotypic one for most character combinations. Yield displayed positive and significant genotypic and phenotypic association with plant height and number of fruits per plant. Path coefficient studies explained that number of fruits per plant and plant height exerted maximum positive direct effect on yield.

Naliyadhara *et al.* (2007) reported that the genotypic correlation coefficients were higher than corresponding phenotypic one for most characters reflecting predominant role of heritable factors. Fruit yield displayed significant and positive genotypic and phenotypic correlations only with ten-fruit weight. Path coefficient studies explained that fruit length, ten-fruit weight and plant spread exerted higher positive direct effect on fruit yield suggesting to give emphasis on such fruits while imposing selection for fruit yield of brinjal.

Correlation and path analyses by Lohakare *et al.* (2008) in twenty three genotypes of green fruited brinjal indicated that yield per plant was closely associated with number of fruits per cluster, fruit index, average fruit weight and number of fruits per plant. Path analysis revealed positive direct effect on yield per plant through number of fruits per plant, average fruit weight, fruit index, days

to first fruit harvest, number of primary branches and plant spread. Hence, these characters may be given consideration while making selection for the improvement of brinjal.

Bansal and Mehta (2008) carried out studies on correlation and path analysis in twenty six genotypes of brinjal and disclosed that yield per plant had strong positive association with plant height, plant spread, branches per plant, leaves per plant and fruits per plant at the genotypic level. Path analysis revealed that fruits per plant had maximum direct positive effect on yield, followed by fruit weight, days to fifty per cent flowering, leaves per plant and per cent fruit set. These traits were considered important in the selection programme for yield improvement in brinjal. Islam and Uddin, (2009) reported that yield showed highly significant and positive association with number of fruits per plant and individual fruit weight, which indicate the importance of these characters during selection for high yielding genotypes in brinjal.

Nalini *et al.*, (2009) conducted correlation studies in thirty-six brinjal genotypes comprising eight parents and twenty-eight F₁ hybrids during summer season of 2006. Results indicated strong correlation of number of branches per plant, fruit weight and flowers per inflorescence with fruit yield. However, it exhibited weak association with days to flowering and fruits per cluster. Path analysis revealed high direct contribution of fruits per plant, fruit weight and flowers per inflorescence on fruit yield, while fruits per cluster and days to flowering exhibited negative direct effect. However, indirect positive contributions of branches per plant and fruits per cluster were appreciable.

Dahatonde *et al.* (2010) conducted correlation and path analysis in twenty genotypes of purple fruited brinjal and indicated that fruit yield per plant was closely associated with diameter of fruit, number of fruits per plant and average fruit weight. Path analysis revealed positive direct effect on fruit yield per plant through average fruit weight and number of fruits per plant. Hence, these

characters may be given consideration while making selection for improvement of brinjal.

Muniappan *et al.*, (2010) stated that characters such as number of branches per plant, fruit breadth, number of fruits per plant and average fruit weight exhibited positive and significant association with fruit yield per plant. Path analysis indicated that number of fruits per plant and average fruit weight had high direct effects and were the major factors that determine fruit yield per plant. The indirect effects on fruit yield per plant via average fruit weight was expressed by number of branches per plant and fruit breadth.

Kafyullah *et al.* (2011) assessed forty brinjal genotypes, genotypic and phenotypic correlations and path coefficient analysis were worked out for twelve important yield attributing characters including fruit yield per plant. The fruit yield per hectare exhibited highly significant and positive correlation with days to first flowering, number of flowers per cluster, fruit set per cent, fruit yield per plant, number of fruits per cluster and fruit length at both genotypic and phenotypic levels and with number of clusters per plant only at genotypic level. These results indicate that simultaneous selection for these characters would be rewarding in improving the fruit yield. Direct and indirect effects showed that during the selection of superior genotypes in brinjal emphasis should be given for parameters like days to first flowering, number of flowers per cluster, fruit set percentage, fruit yield per plant, number of clusters per plant, number of fruits per cluster and fruit length.

Eighty one brinjal genotypes (nine parents and seventy two hybrids) were evaluated for 14 characters and results showed that marketable yield per plant had significant positive association for both at genotypic and phenotypic level with all the characters studied viz., plant height, number of branches per plant, fruit girth, calyx length, number of fruits per plant, single fruit weight, protein content and total phenol content (Praneetha *et al.*, 2011). The earliness showed positive association with fruit borer infestation both at genotypic and phenotypic level.

The marketable yield per plant had significant negative association both at genotypic and phenotypic level with shoot and fruit borer infestation. Neither positive nor negative significant correlation was registered by shoot borer infestation with other characters. The shoot borer infestation showed negative relation with ascorbic acid content, protein content of fruit and total phenol content at vegetable maturity.

Thangamani and Jansirani (2012) studied twenty five F_1 hybrids in brinjal and revealed that yield per plant showed positive correlation with number of branches per plant, percentage of long styled flowers, number of fruits per plant, fruit dry matter content and ascorbic acid content. A significant negative correlation of yield was observed with days to first flowering. Fruit borer incidence had a significant positive association with calyx length and fruit girth however, significant negative correlation with total phenols, ascorbic acid content and dry matter content. The path analysis study revealed that the number of fruits per plant is the most important yield determinant, because of its high direct effect and indirectly influence the yield through number of branches per plant and fruit weight. Moderate effects exerted by fruit girth, fruit length and dry matter content were also influences the yield via many other yield improving characters. Emphasis must be given characters having high direct effect like number of fruits per plant, while exercising selection to improve the yield.

Danquah and Ofori (2012) reported that fruit weight showed significant positive association with fruit diameter and fruit length. Days to flowering registered significant positive correlations with height at flowering and fruit length at both phenotypic and genotypic levels. The most striking result was significant negative correlation between number of seeds per fruit and fruit length. Thus suggesting that selection for accessions with long fruits characteristics will lead to reduction in seed content of the fruits

The genotypic path coefficient analysis by Ahmed *et al.*, (2013) revealed that highest positive direct effect on fruit yield followed by number of fruits per

plant, plant spread, fruit width and fruit length whereas, plant height showed negative direct effects on fruit yield per plant. Overall the path analysis confined that direct effect of fruit weight, number of fruits per plant, plant spread, fruit width, fruit length and number of primary branches, whereas indirect effect of plant height should be considered simultaneously for amenability in fruit yield of brinjal.

Correlation and path coefficient analyses were carried out by Shekar *et al.* (2013) for 14 characters of yield and its components. Differences were observed among genotypes. Character association indicated that fruit yield per plant was positively and significantly associated with number of leaves per plant, number of fruits per plant, average fruit weight and total number of harvests at phenotypic and genotypic correlation levels. Path analysis indicated that number of fruits per plant and average fruit weight had direct effects on fruit yield per plant; the remaining characters had negligible to low indirect effects through other component characters. Number of fruits per plant and average fruit weight are reliable characters to use for improvement of eggplant.

2.5 Divergence analysis (D^2 Analysis)

The multivariate analysis provides valuable information on the extent of variation present in the crop under improvement. Selection of parents/lines based on individual attribute may not be as advantageous as the one based on a number of important traits collectively. In any breeding programme inclusion of such genetically diverse parents is important to get desirable recombinants.

There are several criteria by which a breeder can choose suitable parents for successful hybridization, of which the two important are: combining ability of the parents and genetic diversity between the parents. The great interest in genetic diversity arises from the possibility of demonstrating that phenotypic mean values express, in a larger or smaller degree, the genotypic value of an individual. Thus, while evaluating the divergence among populations, based on average phenotypic values, the divergence among genotypic values associated with gene frequency in

different sample units (populations, varieties, clones, etc.) is also evaluated. Among the several techniques used to express divergence between samples' genetic base, the Mahalanobis' generalized distance (D^2) stands out as one of the most robust (Rao, 1952). The cluster analysis based on D^2 data is used for grouping samples in such a way that a high level of homogeneity within each group and high heterogeneity between groups is obtained (Johnson and Wichern, 1982).

Kumar *et al.* (2007) assessed 57 genotypes in brinjal for genetic diversity using D^2 statistics under subtropical conditions of Jammu. They were grouped into eight clusters based on magnitude of yield and yield related characters. Cluster I accommodated maximum number of genotypes and in sequence clusters were having 12, 11, 9, 6, 6, 5, 5 and 3 genotypes respectively. Intra-cluster distance was quite high in clusters VIII, VII, VI and III inferring that variability within these clusters can be crossed to get some improvements, while the inter-cluster distance was maximum between cluster VIII and VII (6.57) followed by cluster VIII and III (5.53); cluster VII and IV (5.33); cluster VII and VI (5.22) and cluster VII and I (5.11) respectively. The characters like fruit length, fruit width, average fruit weight and fruit yield per plant contributed maximum to genetic divergence indicating that diversity in brinjal has resulted mostly from fruit characters.

Twenty three genotypes of brinjal were assessed to know the nature and magnitude of genetic divergence by Golani *et al.* (2007). The population was grouped into six clusters. The cluster I comprised of six genotypes followed by cluster II and III each with five genotypes, while the cluster VI was solitary cluster. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. However, the shape and colour of fruits of genotypes played major role in grouping of genotypes into various clusters. Maximum intra cluster D^2 value was observed in cluster IV (8.45) followed by cluster I (8.24) indicating that genotypes included in both these clusters are very much diverse as compared genotypes of other clusters.

Inter cluster D^2 was minimum (14.01) between cluster IV and VI indicating close relationship among the genotypes included in these clusters. While, it was maximum (151.84) between cluster I and III. The large inter cluster distance (D^2) was also observed between cluster II and III, cluster III and V, cluster II and IV and cluster II and V. This indicated that the genotypes included in these clusters had greater genetic divergence.

Dutta *et al.* (2009) grouped seventy entries into six distinct clusters based on the divergence between the entries, as measured by the D^2 statistic. Cluster I, the largest one contained 39 genotypes followed by cluster II with 22 genotypes and cluster V and VI, the smallest with one genotype each in them. The data suggested medium and consistent level of intra-cluster divergence in all the clusters (D^2 19.36 to 24.07). Low intra-cluster divergence also suggested the proposition that common character constellation was expressed in the genotypes. Maximum inter-cluster distance existed between cluster IV and V (D^2 104.70) followed by between III and IV (D^2 95.44) and between I and V (D^2 83.33).

Muniappan *et al.* (2010) grouped thirty four genotypes of eggplant into seven clusters using clustering technique. The intra cluster distance ranged from 0.00 to 144.95. Cluster II showed minimum intra-cluster distance (49.18) and maximum intra-cluster distance was exhibited by cluster III (144.95) followed by cluster V (144.14). Maximum inter cluster distance was found between clusters II and VII (255.42). This was followed by clusters VI and VII (237.29). Minimum inter cluster distance was observed between clusters II and V (116.77).

Shekar *et al.* (2012) grouped accessions into 6 groups. Groups IV and VI were the largest consisting of seven accessions each followed by group II consisting of six accessions, groups I and III consisting of four accessions each and group V consisting of three accessions. The accessions exhibited random pattern of distribution into various groups and the magnitude of D^2 values suggested that there was considerable amount of diversity in the accessions of brinjal under investigation indicating that forces such as genetic drift, natural and

artificial selection and exchange of genetic material might have played an important role in the diversity of accessions.

Morphological diversity in ninety-two brinjal genotypes based on twenty one characters was estimated using Mahalanobis' D^2 statistics by Begum *et al.* (2013). The highest intra-cluster distance was observed in cluster VIII (2.13), containing seven genotypes and the lowest intra-cluster distance (1.18) was observed in cluster IV having four genotypes. Ninety two eggplant genotypes were grouped into ten different clusters by non-hierarchical clustering. The cluster X had the maximum number (17) of genotypes and cluster II and III had minimum number (3) of genotypes. The highest inter-cluster distance was observed between cluster II and VIII (30.86) indicated the genotypes in these clusters were more diverged than those of other clusters. The lowest inter-cluster distance was observed between the clusters V and X (3.72) suggesting a close relationship among the genotypes included within these clusters. Cluster II constitute three genotypes and produced the highest mean value for number of flowers per inflorescence (4.67) and yield per plant (812.33) and the lowest mean value for days to 1st flowering (108.22). Cluster IV constitute three genotypes produced fruits for longer duration (82.33). Cluster VIII constitute seven genotypes and showed the lowest mean value for number of infected shoots per plant (1.57). Cluster X established with 17 genotypes produced the lowest mean value for number of infected fruit per plant (8.26)

2.6 Phomopsis blight:

2.6.1 Symptomatology, economic importance and perpetuation

Brinjal crop suffers from many biotic stresses, out of which leaf blight/fruit rot caused by *Phomopsis vexans* (Sacc. & Syd.) Harter, is of great economic value. Halsted first described the organism in the United States in 1892 as *Phoma solani* Halst. Since the name had been used for another fungus it was changed to *Phoma vexans* by Saccardo and Sydow in 1899. Harter transferred it to *Phomopsis vexans* (Sacc. and Syd.) Harter (Walker, 1952).

The only economic host of *Phomopsis vexans* is brinjal and the disease is variously known as tip over, stem blight or canker, leaf blight or spot and fruit rot; damping-off can also take place (Punithalingam *et al.*, 1972). Leaf spots (up to 3 cm diam.) are conspicuous, irregular in outline and may coalesce; lower leaves may be affected first. In stem lesions the cortex dries and cracks, plants become stunted and girdling cankers cause death. Fruit spots are pale, sunken, and conspicuous and may affect the whole fruit; fruit may drop or remain attached, becoming mummified after a soft decay. Pycnidia are abundant.

Brinjal leaf blight and fruit rot caused by *Phomopsis vexans* (Sacc. & Syd.) Harter, (perfect stage: *Diaporthe vexans* Gratz) is a major constraint in producing the profitable crop and is one of the major limitations for limited productivity of brinjal throughout the world. In India, phomopsis blight of brinjal was first reported from Gujarat in 1914 and thereafter from many other parts of the country (Harter, 1914). In India yield loss due to fruit rot, ranges from 10 to 20 per cent (Panwar *et al.*, 1970). It is more destructive in subtropical and tropical regions where 50 per cent losses have been recorded (Sherf and Macnab, 1986).

Thippeswamy *et al.* (2012) reported phomopsis blight by *Phomopsis vexans* and leaf spots by *Alternaria solani*, reduce the seed germination and yield upto 30-50 per cent.

Akhtar and Chaube (2012) reported substantial differences in radial growth of the isolates on PDA. Similarly biomass production ranged between 20.0 mg to 353.0 mg. The morphological characters notably type of colony, colour, texture, zonation too differed significantly. The variation in stylospore morphology was relatively higher. The germinability of pycnidiospore from different isolates differed significantly and it ranged from 31.0 to 72.0 per cent. Pycnidia were black in some isolates while in some brown pycnidia developed.

Sharma and Razdan (2012) isolated a total of ten fungal species from the brinjal seed samples collected from different locations using standard blotter and agar plate methods. *Aspergillus flavus*, *A. fumigatus*, *A. niger* and *P. vexans* were

isolated from all the seed samples, whereas, spores of only four fungal genera *Alternaria* spp., *Curvularia* spp., *Fusarium* spp. and *P. vexans* were detected during seed washing method. *P. vexans* was found to perpetuate through infected plant debris (leaf and fruit). Pathogen survived at all the six depths tested in the infected leaf debris till 240 days, though, there was a decrease in per cent survival over the period of time, however, after 300 days the pathogen was not recovered at any depth, except from the surface. Survival of *P. vexans* recorded in infected fruit debris was cent per cent till 60 days after their burial in soil and a considerable decrease in the survival was observed with an increase in time period, the pathogen was recovered till 270 days.

A total of 145 seed samples were collected from farmers, agro agencies and seeds extracted from fruits were subjected for standard blotter method (SBM) by Thippeswamy *et al.* (2012). Five samples showing higher incidence of seed borne fungi in SBM were selected for studying the location and transmission of the pathogen. The results revealed the presence of *P. vexans* (0-10 per cent) and *A. solani* (3-10 per cent) in the SBM method. *Phomopsis vexans* ranged from 0-2 per cent in seed coat, 0-4 per cent in cotyledons and 0-4 per cent in embryonic axis. Their distribution varied in different seed parts.

Vishunavat and Kumar (1994) reported that component plating of infected seeds of the aubergine cv. PBR-5 yielded 22 per cent and 12 per cent infection in seed coats and cotyledons respectively. Pycnidia and mycelium were seen on seed coats and in the embryo. Host debris and seed from infected fruit are primary sources of inoculum. Naturally infected seed germinates less well and more slowly (Punithalingam *et al.*,1972).

Pawar and Patel (1958) reported that the minimum temperature for growth of the pathogen (*P. vexans*) lies between 7⁰ C and 11⁰ C., the optimum near 28°C, and the maximum between 35 and 40°C. Effect of temperature, relative humidity, fruit age, inoculum age, inoculum load and repeated sub-cultured inoculum was ascertained by Sugha *et al.*(2002) on the development of phomopsis fruit rot of

brinjal incited by *Phomopsis vexans* and reported that the temperature of 25°C, RH~90%, fruits of younger age (5-10 day old), higher inoculum load (>120 spores/ml) and inoculum of younger age (14-day old) were found conducive for the development and progress of phomopsis fruit rot. Repeated sub-culturing of inoculum resulted in loss of aggressiveness of the pathogen.

Thippeswamy *et al.* (2012) reported that the seeds harvested during kharif and rabi season favoured the more number of pathogens in the seed coat than in the other components. The transmission of *P. vexans* and *A. solani* was 10.6 per cent in kharif. In rabi, the transmission was 16.8 per cent in all the five seed samples.

2.6.2 Germplasm evaluation for phomopsis blight resistance

Eighty four genotypes of brinjal were evaluated against phomopsis leaf blight and fruit rot disease (*Phomopsis vexans* (Sacc. & Syd.) Harter) by Sugha *et al.* (2002). Out of 84 genotypes screened against leaf blight, 7, 34, 33 and 10 had a resistant, moderately susceptible (MS), susceptible (S) and highly susceptible (HS) reaction to the pathogen, respectively.

Thirty six eggplant cultivars were evaluated by Patil *et al.* (2002) for resistance to phomopsis blight (caused by *Phomopsis vexans* [*Diaporthe vexans*]) under natural and artificial inoculum pressure in the field. The per cent disease intensity on leaves, stems, and fruits was recorded during winter 1996-97 and 1997-98. Of the 36 cultivars, none was immune to the disease. Only KS-202-9 and Nurki were found resistant, while CHBR-1, CHBR-3, JB-64, Bhagyanath, PBR-7, T-3 and Brinjal Long were determined to be moderately susceptible. Highly susceptible cultivars were PLR-1, Pusa Purple Cluster, Pusa Kranti, PBR-129-5, AC-Sel-1, and H-5.

Twenty eggplant cultivars were evaluated in Akola, Maharashtra, India, during 1997-98 and 1998-99 for resistance to phomopsis rot by Patil *et al.* (2003) and reported four cultivars (CHBR-1, CHBR-2, KS-233 and KS-229) were

resistant (0-10% infection), whereas eight cultivars (CHBR-3, ABV-1, DSBR-8, Pusa Purple Cluster, JB-64-1-2, Mahabeej hybrid, Jalgaon local and Manjrigota) were moderately resistant (11-25% infection).

Five isolates of *Phomopsis vexans* evaluated against 25 genotypes of brinjal showed substantial differences in their aggressiveness (Akhtar, 2006). Disease severity ranged from moderately susceptible to highly susceptible and resistant to moderately resistant. Aggressiveness of five isolates of *Phomopsis vexans* on the basis of responses shown by 25 host genotypes revealed that mean aggressiveness response value in terms of incubation period was 0.57 (range 0.48-0.68) and in terms of lesion area, it was 0.56 (range 0.42-0.70). The mean response values for isolates against the genotypes ranged from 0.42 to 0.70.

2.7 Shoot and fruit borer

2.7.1 About the pest and its symptoms

The brinjal shoot and fruit borer, *Leucinodes orbonalis* Guenee (Pyralidae: Lepidoptera) one of the major pests of brinjal causing considerable damage to this crop (Pugalendhi *et al.*, 2010). It is a serious pest of brinjal all over the country causing yield loss up to 100 per cent if no control measures are applied (Rahman, 2007). The percentage of fruit damage due to this pest was reported to vary from 25.82 to as high as 92.50 (Atwal and Verma, 1972). At the vegetative phase, the newly hatched larvae bore into the petioles and midribs of large leaves and young tender shoots. They feed on the internal tissue causing the shoot droop down and withered at the reproductive phase, the larva prefers to bore into flower buds and also enter into the tender fruits through the calyx (Hossain *et al.*, 2002). Observing the boring holes, the infested fruits can easily be identified. Besides, the dark coloured excreta can easily be seen on the hole of infested fruits. Secondary infections by certain microorganisms may cause further deterioration of the fruits and make them ultimately unfit for human consumption.

Hossain *et al.* (2002) stated that plant age had significant effect on the incidence of brinjal shoot and fruit borer. Highest percentage (32.891) of brinjal shoot and fruit borer infestation was observed at 70 DAT and lowest (5.181) was found at 40 DAT. The rate of infestation gradually increased with the increase of plant age and then decreased in 100 DAT. Highest percentage of infestation was observed in 70 DAT, which was significantly different from 40 DAT but identical with 100 DAT.

Dhankhar (1988) reviewed the progress made in the study of resistance in aubergines to the *Leucinodes orbonalis*. Resistance exists at a low level in the cultivars screened. Screening of large numbers of cultivars and breeding lines with broad genetic base is emphasized. The possibility of transferring resistance from wild relatives needs thorough investigation. The use of tolerant cultivars with less insecticide is suggested as the most acceptable control method.

2.7.2 Screening for shoot and fruit borer resistance

Darekar *et al.* (1991) screened nine varieties of brinjal for resistance to *Leucinodes orbonalis* and found PBR-129-5, Arka Kusumakar and Wild Brinjal were resistant. Biochemical characters, such as total sugars and free amino acids, were positively correlated with fruit infestation, whereas polyphenol content was negatively correlated with attack.

Twenty-seven germplasms and two wild species of brinjal were tested for resistance against *Leucinodes orbonalis* by Gangopadhyay *et al.* (1996) and accounted *Solanum melongena* cultivars Arka Kusumakar, Nischintapur, Brinjal Long Green, Altapati, Arka Shirish, Manipur, Makra and Chikon long were relatively resistant to the pest, whereas Green Brinjal Round, Suphal, Gourkaji, Brinjal No. 3 and Light Purple Round were highly susceptible. *S. macrocarpon* resisted shoot infestation completely, performing better than *S. incanum* which is known to be pest resistant. Physical characters of the germplasms indicated that resistance is not conferred by any single character like spininess, shape and size of fruits or arrangement of seeds.

Ten varieties and twenty five lines of brinjal and *S. gilo* and *S. anomalum* were screened for resistance to shoot and fruit borer (*Leucinodes orbonalis*) at IARI, New Delhi in 1988-89 by Singh and Kalda (1997). Annamalai, Aushey and Pusa Purple Cluster were resistant at seedling stage, and Annamalai and Aushey were also moderately resistant at the vegetative and bearing stages. Among 20 F₁ hybrids and six pure lines screened, only 5 F₁ hybrids and 5 pure lines were resistant at seedling stage. However, none of the hybrids and pure lines showed resistance at the vegetative and bearing stages. The incidence of infestation in hybrids varied from 30.5 to 39.3 per cent, indicating that susceptibility is a dominant character. In pure lines, incidence of infestation ranged between 34 to 42 per cent. *S. gilo* and *S. anomalum* showed a high degree of resistance to fruit borer at all three stages. Since *S. gilo* is compatible with *S. melongena*, it can be used in breeding brinjal resistant to shoot and fruit borer.

Forty brinjal accessions were evaluated for resistance to fruit and shoot borer by Kumar *et al.* (1998) and reported that Pusa Purple Cluster and BB-13 were resistant to brinjal shoot and fruit borer. Pant Samrat, KT-4, BB-26, PB-29, PB-34, BB-46, Composite-2, NDBH-7, NDB-25, Pusa Hybrid-5, PB-38, PB-39, PB-41, PB-42, PB-44 and ARBH-527 were tolerant to this insect pest. Based on simple correlations assuming non-damaged fruit number (%) and non-damaged fruit weight (%) as the dependent variables, fruit diameter, fruit weight and fruit volume were effective for selection for resistance/tolerance. Since fruit size was negatively correlated to borer resistance, it was suggested to select for fruit number rather than size to increase yield and resistance simultaneously.

The screening of selected genotypes of brinjal (Pusa Purple Cluster, Bhagyamathi, Annamalai, APAU-4, Aushey, Nurki, Singnath, Pusa Kranti, *Solanum gilo*, *S. anomalum*, *S. indicum* and *S. incanum*) was carried out under field conditions by Behera *et al.* (1999) during 1995-96 and 1996-97 in New Delhi, India and reported considerable variability in relation to infestation by shoot and fruit borer. Pusa Kranti and Aushey showed the highest degree of susceptibility whereas *S. indicum*, *S. gilo* and *S. incanum* were resistant.

Forty-one diverse *Solanum melongena* genotypes were screened under conditions of natural infection and infestation by Doshi *et al.* (2002). Banaras Giant, CHBR1, PLR1 and Local Alwar were the highest yielders of fruit (4.63, 4.59, 4.45, 4.17 kg/plant). Fruit borer (*Leucinodes orbonalis*) damage was lowest in BB102 and little leaf (caused by a phytoplasma) incidence was least in Banaras Giant.

Hossain *et al.* (2002) screened out twenty varieties and lines of brinjal to observe their resistance level to brinjal shoot and fruit borer infestation in the field conditions and reported that the infestation varied significantly among the lines. The brinjal shoot and fruit borer infestations for different varieties/lines were found in the following order of intensity: Nayankajal > BL095 > BL085 > BL098 > BLO114 > Khotkhotia-2 Borka > Laffa > Islampuri > BL045 > Ohohazari- 2 > BL0101 > Ohohazari-1 > Khotkhotia-1 > BL096 > Sada ball > Singnath > Uttara > Baromashi > Jhumki. Varietal resistance of brinjal against brinjal shoot and fruit borer indicated significant variation among different brinjal varieties/lines.

Jat *et al.* (2003) evaluated ten brinjal cultivars (Pusa Kranti, Unnati, Pusa Purple Round, Pusa Purple Long, SM-10, Neelum Long, Pant Rituraj, Arka Kusumakar, Daftari, and Black Round) in Jobner, Rajasthan, India, during kharif 1999 and 2000 for resistance to *L. orbonalis*. Shoot infestation varied from 3.28 to 12.71 per cent. Shoot damage was lowest in Arka Kusumakar (3.28 per cent). Neelum Long (5.71 per cent), Pusa Purple Long (6.28 per cent), Pusa Kranti (6.51 per cent) and Pant Rituraj (7.42 per cent) were moderately susceptible to the shoot borer. Arka Kusumakar (18.33 per cent) and SM-10 (20.23 per cent) showed the lowest fruit infestation. Neelum Long (30.72 per cent) and Pusa Purple Long (31.60 per cent) were moderately susceptible to the fruit borer. Fruit infestation was greatest in Pusa Purple Round (46.51 per cent). Pant Rituraj and Arka Kusumakar had the highest yield (23.74 and 22.94 t/ha, respectively). Arka Kusumakar and SM-10 were resistant to shoot and fruit borer.

Materials & Methods

3. MATERIALS AND METHODS

The experiment entitled “Genetic evaluation for yield and resistance to phomopsis blight in brinjal (*Solanum melongena* L.)” was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during the period 2012-13. The experimental site was located at 8° 25' N latitude and 76° 59' E longitude at an altitude of 29 m above mean sea level. Predominant soil type of the experimental site was red loam belonging to Vellayani series, texturally classified as sandy clay loam.

The study comprised of two experiments.

Experiment 1: Screening of brinjal genotypes for yield and phomopsis blight resistance in pot culture.

Experiment 2: Evaluation of genotypes for genetic variability, yield and tolerance to major pests and diseases under field conditions.

3.1 Experiment 1

3.1.1 Materials

The experimental material comprised of 32 accessions of brinjal collected from different parts of the country. The details of genotypes used in the experiment are given in Table 1.

3.1.2 Methods

3.1.2.1 Design and layout

The experiment was laid out in a completely randomized block design with 32 treatments and three replications. Thirty five days old seedlings having 8-10 cm height were transplanted into the pots. The crop received timely management practices.

Table 1. Brinjal accessions used for evaluation

Sl. No.	Accession Number	IC No. / accession name	Source
1	SM 1	Surya	KAU, Vellanikkara
2	SM 2	Haritha	KAU, Vellanikkara
3	SM 3	Swetha	KAU, Vellanikkara
4	SM 4	Local	Vellanikkara, Kerala
5	SM 5	Local	Akola, Maharastra
6	SM 6	Local	Akola, Maharastra
7	SM 7	NBR-15	Nagpur, Maharastra
8	SM 8	NBR-38	Nagpur, Maharastra
9	SM 9	Local	Vellayani, Kerala
10	SM 10	Local-2	Thakkallapalli, Andhra Pradesh
11	SM 11	Local-3	Thakkallapalli, Andhra Pradesh
12	SM 12	Local-1	Palakurthi, Andhra Pradesh
13	SM 13	Local	Palakurthi, Andhra Pradesh
14	SM 14	Local	Gopulapur, Andhra Pradesh
15	SM 15	Local	Gopulapur, Andhra Pradesh
16	SM 16	Local	Gopulapur, Andhra Pradesh
17	SM 17	Local	Pattipaka, Andhra Pradesh
18	SM 18	Local	Pattipaka, Andhra Pradesh
19	SM 19	Selection Pooja	Bharat Seed Company, Jodhpur.
20	SM 20	Suketh-111	Bharat Seed Company, Jodhpur
21	SM 21	Local	Vellanikkara, Kerala
22	SM 22	Local	Kakamoola, Kerala
23	SM 23	Local	Charlapalli, Andhra Pradesh
24	SM 24	Mukta Jhuri	Bkhra Seeds, W.B
25	SM 25	Local	Kakamoola, Kerala
26	SM 26	Local	Wardha, Maharastra
27	SM 27	Local (SM-44)	Vellayani, Kerala
28	SM 28	Local	Thakkallapalli, Andhra Pradesh
29	SM 29	Local	Yavatmal, Maharastra
30	SM 30	Kaveri-901	Bharat Seed Company, Jodhpur
31	SM 31	Vijay SGS-548	Sardar Seed Company, Jodhpur
32	SM 32	Gaurav SGS-538	Sardar Seed Company, Jodhpur

3.1.2.2 Biometric observations

Observational plants in each replication were tagged for recording the biometric observations.

3.1.2.2.1. 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.

3.1.2.2.2 Number of primary branches

Number of branches arising from the main stem was recorded from all the sample plants at the peak harvest stage and average was worked out.

3.1.2.2.3 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.

3.1.2.2.4 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.

3.1.2.2.5 Fruit length

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

3.1.2.2.6 Calyx length

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

3.1.2.2.7 Fruit girth

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

3.1.2.2.8 Fruit weight

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

3.1.2.2.9 Number of fruits per cluster

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

3.1.2.2.10 Fruits per plant

Total number of fruits produced per plant till last harvest was counted.

3.1.2.2.11 Yield per plant

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

3.1.2.2.12 Colour of fruit

Dominant pigmentation on fruits of each variety was recorded.

3.1.2.2.13 Leaf spininess

Based on the presence of spines on the leaves, accessions were categorized in to spiny and spineless.

3.1.2.3 Screening for phomopsis blight

3.1.2.3.1 Isolation and multiplication of the pathogen

Phomopsis vexans, the casual organism of phomopsis blight was isolated from naturally infected brinjal fruit showing characteristic symptoms of the disease and conducted Koch's postulate to prove the pathogenicity. Once the pathogen was identified, it was multiplied for spore suspension in Czapek's Dox broth in conical flasks. Five mm disc of culture was inoculated in 150 ml of broth in 250 ml conical flasks.

3.1.2.3.2 Inoculation on plants







The spore load in the suspension was adjusted to 10^6 using haemocytometer. This suspension was inoculated on observational plant leaves and fruits through a fine spray delivered from an atomizer. The inoculation was carried out twice *i.e.*, at 30 DAT on leaves and after first fruit set.

3.1.2.3.3 Scoring of the disease

After the onset of infection, disease severity (the area or proportion of plant tissue affected) was estimated utilizing the standard area diagram (Fig. 1). According to Islam and Pan (1993) the infection grades used for visually estimated spot areas were:

Sl. No.	Score	Fruit area affected (%)
1	0	No infection
2	1	> 0 - ≤ 1.0
3	2	> 1 - ≤ 10.0
4	3	> 10.0 - ≤ 25.0
5	4	> 25.0 - ≤ 50.0
6	5	> 50.0

Fig 1. Disease score chart of blight and fruit rot in brinjal incited by *Phomopsis vexans* (Islam and Pan, 1993)

					
0	1	2	3	4	5
NO INFECTION	≤ 0 to 1%	>1 to ≤ 10	>10 to ≤ 25	>25 to ≤ 50	> 50

3.1.2.3.4 Disease intensity

From the scores obtained using standard scoring chart developed by Islam and Pan (1993), percentage disease index (PDI) of fruit rot was calculated using the formula developed by Mc Kinney (1923).

$$\text{PDI} = \frac{\text{Sum of individual ratings} \times 100}{\text{Total number of fruits assessed} \times \text{Maximum disease category}}$$

3.1.2.3.5 Categorization of host-pathogen reaction

Category	PDI range
Resistant	0
Moderately resistant	1 - 20
Moderately susceptible	21 - 40
Susceptible	41 - 60
Highly susceptible	>61

3.2 Experiment 2

3.2.1 Materials

Thirty two accessions used in pot culture were used in field experiment for yield assessment.

3.2.2 Methods

3.2.2.1 Design and Layout

The experiment was laid out in a randomized block design with 32 treatments and three replications. Thirty five days old seedlings having 8-10 cm height were transplanted into the main field at a spacing of 60 cm x 60 cm. The

crop received timely management practices as per package of practices recommendations of Kerala Agricultural University (KAU, 2007).

3.2.2.2 Biometric observations

All the observations recorded in pot culture were also recorded in the field experiment according to the procedures discussed in section 3.1.2.2. In addition to them, data on 100 seed weight was taken according to the procedure given below. Five plants were selected randomly from each plot and tagged for recording the biometric observations.

3.2.2.2.1 Hundred seed weight

Hundred seeds were counted for each genotype and weight has been recorded using electronic balance.

3.2.2.3 Fruit and shoot borer (*Leucinodes orbonalis* Guen.)

3.2.2.3.1 Percentage of plants infested

Number of plants showing damage symptoms (on shoots/ on fruits or on both) were recorded and from this percentage of plants infested was calculated. Observations were recorded 15 days interval from 30 DAT (Days After Transplanting) to 90 days.

$$\text{Percentage of plants infested} = \frac{\text{No. plants showing damage symptoms}}{\text{Total number of plants}} \times 100$$

3.2.2.3.2 Percentage of damaged fruits

The total number of fruits with bore holes was recorded and the percentage of damaged fruits was worked out. Observations were taken at 10 days interval from 80 DAT to 100 DAT.

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

3.2.2.3.3 Scoring for shoot and fruit borer

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

The incidence of *L. orbonalis* on plants was assessed in terms of the percentage of infested plants out of the total number of plants available in each plot. Incidence on fruits was assessed by calculating percentage of infested fruits at different pickings and pooled data was subjected for statistical analysis. Pest rating was done as per the scale suggested by Mukhopadhyay and Mandal (1994).

Percentage of fruit infestation	Rating
<15	: Tolerant (T)
16-25	: Moderately resistant (MR)
26-40	: Susceptible (S)
>40	: Highly Susceptible (HS)

3.3 Statistical Analysis

Data recorded from experimental plants were statistically analysed.

Analysis of variance and covariance were done:

- a) To test significant difference among the genotypes and
- b) To estimate variance components and other genetic parameters like correlation coefficients, heritability, genetic advance etc.

3.3.1 Variance and covariance

The variance and covariance components were calculated as:

For the character X_i ,

$$\text{Environmental variance } (\sigma_{ei}^2) = \text{MSE}$$

$$\text{Genotypic variance } (\sigma_{gi}^2) = \frac{\text{MST}-\text{MSE}}{r}$$

$$\text{Phenotypic variance } (\sigma_{pi}^2) = \sigma_{gi}^2 + \sigma_{ei}^2$$

where, MST and MSE are the mean sum of squares for treatment and error respectively from ANNOVA and r is the number of replications and \bar{x}_i is the overall mean of the i^{th} trait calculated from all varieties. For two characters X_i and Y_j , the covariances were worked out from the ANCOVA as:

$$\text{Environmental covariance } \sigma_{eij}^2 = \text{MSPE}$$

$$\text{Genotypic covariance } \sigma_{gij}^2 = \frac{\text{MSPT}-\text{MSPE}}{r}$$

$$\text{Phenotypic covariance } \sigma_{pij}^2 = \sigma_{gij}^2 + \sigma_{eij}^2$$

where MSPT and MSPE are the mean sum of products for treatment and error respectively between i^{th} and j^{th} characters.

3.3.2 Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were estimated as

$$\text{GCV} = \frac{\sigma_{gi}}{\bar{X}} \times 100$$

$$\text{PCV} = \frac{\sigma_{pi}}{\bar{X}} \times 100$$

Where,

σ_{gi} - genotypic standard deviation

σ_{pi} - phenotypic standard deviation

\bar{X} - Mean of the character under study

Categorization of range of variation was followed as proposed by Sivasubramanian and Menon (1973).

Less than 10 % \longrightarrow Low

10 to 20 % \longrightarrow Moderate

More than 20 % \longrightarrow High

3.3.3 Heritability

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where, H^2 is the heritability expressed in percentage (Jain, 1982). Heritability estimates were categorized as suggested by Johnson *et al.* (1955).

0 – 30 per cent	→	Low
31 – 60 per cent	→	Moderate
> 60 per cent	→	High

3.3.4 Genetic advance under selection

$$GA = \frac{k H^2 \sigma_p}{\bar{x}} \times 100$$

Where, k is the standard selection differential.

k = 2.06 at 5% selection intensity (Miller *et al.*, 1958)

3.3.5 Genetic Advance as percentage of mean

$$GAM = \frac{GA}{\text{Mean}} \times 100$$

The range of genetic advance as per cent of mean was classified according to Johnson *et al.* (1955).

0- 10 per cent	→	Low
11- 20 per cent	→	Moderate
> 20 per cent	→	High

3.3.6 Correlation

The correlation coefficients (phenotypic, genotypic and environmental) between two characters denoted as i and j were worked out as

$$\text{Genotypic correlation coefficient } (r_{gij}) = \frac{\sigma_{gij}}{\sigma_{gi} \times \sigma_{gj}}$$

$$\text{Phenotypic correlation coefficient } (r_{pij}) = \frac{\sigma_{pij}}{\sigma_{pi} \times \sigma_{pj}}$$

$$\text{Environmental correlation coefficient } (r_{eij}) = \frac{\sigma_{eij}}{\sigma_{ei} \times \sigma_{ej}}$$

3.3.7 Path analysis

The direct and indirect effects of yield contributing factors were estimated through path analysis technique (Wright, 1954; Dewey and Lu, 1959).

3.3.8 Divergence analysis

Genetic divergence was studied based on 13 characters taken together using D^2 statistic. The genotypes were clustered by Tocher's method as described by Rao (1952).

3.3.8 Selection Index

The selection index developed by Smith (1937) using discriminate function of Fisher (1936) was used to discriminate the genotypes based on all the characters.

The selection index is described by the function, $I = b_1 x_1 + b_2 x_2 + \dots + b_k x_k$ and the merit of a plant is described by the function, $H = a_1 G_1 + a_2 G_2 + \dots + b_k G_k$ where x_1, x_2, \dots, x_k are the phenotypic values and

G_1, G_2, \dots, G_k are the genotypic values of the plants with respect to characters, x_1, x_2, \dots, x_k and H is the genetic worth of the plant. It is assumed that the economic weight assigned to each character is equal to unity *i.e.*, $a_1, a_2, \dots, a_k = 1$

The regression coefficients (b) are determined such that the correlation between H and I is maximum. The procedure will reduce to an equation of the form, $b = P^{-1}Ga$ where, P is the phenotypic variance-covariance matrix and G is the genotypic variance-covariance matrix x .

Results

4. RESULTS

The results of the present study entitled "Genetic evaluation for yield and resistance to phomopsis blight in brinjal (*Solanum melongena* L.)" are presented below.

4.1 Screening of brinjal genotypes for yield and phomopsis blight resistance in pot culture

4.1.1 Analysis of variance

Analysis of variance has been carried out for all the characters studied and it revealed significant variation among the thirty two genotypes used in the experiment (Table 2).

4.1.2 Mean performance of accessions

The mean values of the genotypes for growth and yield characters and phomopsis blight incidence are given in Table 3.

4.1.2.1 Biometric characters

Among the thirty two genotypes evaluated in pot culture experiment, a considerable variation for all the characters studied was noticed. *SM* 15 (46.60) was the earliest to flower and no genotype was on par with it. The latest genotype to attain flowering was *SM* 23 (69.50). The range for first harvest of fruit was 56.50 to 80.33 days. *SM* 15 (56.50) was the earliest to produce harvestable fruits while *SM* 23 (80.33) was the latest. *SM* 2, *SM* 13 and *SM* 29 were on par with the earliest type.

Regarding length of calyx, the range was between 1.43 and 2.93 cm. *SM* 9 produced the longest calyx and *SM* 13, *SM* 25 and *SM* 28 were on par with it while *SM* 5 produced the shortest calyx.

The variation for fruit weight ranged from 39.67 to 76.20 g. *SM* 19 produced heaviest fruits and it was followed by *SM* 15 (74.47), *SM* 1 (74.00),

Table 2. Analysis of variance of 12 characters in 32 brinjal genotypes under pot experiment

Sl. No.	Character	Mean squares	
		Genotypes	Error
	Degrees of freedom	31	64
1.	Calyx length	0.67**	0.01
2.	Days to first flower	89.01**	0.28
3.	Days to first harvest	152.06**	0.34
4.	Fruit girth (cm)	11.45**	0.02
5.	Fruit length (cm)	17.49**	0.02
6.	Fruit weight (g)	308.23**	0.90
7.	Fruits per cluster	1.68**	0.01
8.	Fruits per plant	118.75**	0.93
9.	Plant height (cm)	103.89**	1.27
10.	Primary branches	0.55**	0.20
11.	Yield per plant (g)	449678.50**	82.25
12.	Percentage disease index (PDI)	794.60**	16.06

** Significant at 1 % level

Table 3. Mean performance of brinjal (*Solanum melongena* L.) genotypes under pot culture

Accessions	Calyx length (cm)	Days to first flower	Days to first harvest	Plant height (cm)	Number of 1 ^o branches	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Fruits per cluster	Fruits per plant	Yield per plant (g)	Phomopsis disease score	PDI
SM 1	2.46	54.00	69.50	52.17	2.33	8.61	13.46	74.00	2.18	18.83	1498.00	2.67	53.33
SM 2	1.82	49.50	56.83	55.00	2.83	7.48	10.58	56.47	1.73	15.67	1226.67	3.11	62.22
SM 3	1.73	49.80	59.50	55.17	2.83	9.76	9.77	45.20	3.27	19.33	1316.00	3.11	62.22
SM 4	1.91	52.33	60.17	59.33	2.83	10.37	10.81	68.07	2.18	18.67	1530.67	1.56	31.11
SM 5	1.43	54.67	66.33	51.00	2.50	6.39	13.02	50.40	1.88	13.50	864.67	2.00	40.00
SM 6	1.68	52.83	61.17	60.17	2.17	5.45	13.77	40.60	2.58	14.00	795.33	2.94	58.89
SM 7	1.96	49.67	65.17	56.33	3.17	5.95	13.03	59.47	1.82	14.50	1055.50	2.06	41.11
SM 8	1.70	54.67	63.67	56.33	3.00	7.07	14.32	50.20	2.82	31.83	1874.33	2.44	48.89
SM 9	2.93	65.67	77.33	56.33	3.33	10.94	10.57	63.27	1.03	10.17	749.83	0.61	12.22
SM 10	1.61	51.33	59.50	60.17	3.17	5.73	9.73	51.60	2.17	21.67	1252.17	3.17	63.33
SM 11	1.87	51.50	58.17	64.00	3.67	11.25	8.12	56.40	3.67	33.00	1671.50	2.94	58.89
SM 12	2.06	53.17	62.33	50.17	2.67	6.09	13.79	58.73	1.65	14.00	785.83	2.17	43.33
SM 13	2.87	48.13	56.67	63.83	3.33	11.77	8.91	48.93	3.60	28.33	1540.50	3.28	65.56
SM 14	1.77	59.33	74.33	60.17	2.83	8.69	12.62	58.27	2.10	20.50	1297.33	1.39	27.78
SM 15	1.82	46.60	56.50	54.17	3.33	10.38	9.09	74.47	3.63	32.00	2095.50	1.83	36.67
SM 16	2.09	59.50	71.33	54.67	2.67	10.02	8.03	43.33	2.92	21.00	1002.17	3.39	67.78
SM 17	1.87	63.17	69.83	65.00	2.50	5.31	11.84	57.47	1.87	13.33	970.50	2.11	42.22
SM 18	2.53	54.73	63.83	61.00	3.33	10.40	9.92	47.27	2.82	24.33	1261.67	2.00	40.00
SM 19	2.81	60.83	73.50	51.67	3.17	13.37	14.36	76.20	3.08	26.33	1946.33	1.75	35.00
SM 20	1.71	56.20	65.67	48.50	3.00	4.96	10.19	57.93	1.70	17.00	1053.00	3.17	63.33
SM 21	1.83	49.87	57.67	45.67	2.17	6.76	10.04	47.80	2.00	20.17	1050.50	3.06	61.11
SM 22	1.71	53.67	77.50	49.83	2.50	5.82	11.11	45.20	1.35	15.33	759.17	1.83	36.67
SM 23	2.66	69.50	80.33	55.33	3.33	8.69	10.15	67.07	1.20	20.17	1244.00	0.83	16.67
SM 24	2.47	57.67	69.50	49.00	3.00	5.57	13.80	57.67	2.03	24.00	1450.33	2.00	40.00
SM 25	2.89	68.67	78.83	64.17	4.00	5.92	10.05	61.80	1.05	8.33	603.17	0.61	12.22
SM 26	2.45	58.67	66.83	64.50	3.00	8.71	9.36	72.87	2.80	25.67	2019.00	1.06	21.11
SM 27	1.79	52.83	69.17	50.50	2.83	6.59	8.70	56.87	1.70	19.50	1121.33	1.94	38.89
SM 28	2.90	52.50	59.00	51.67	3.00	10.78	13.34	68.93	1.12	10.33	845.00	1.17	23.33
SM 29	2.72	48.43	56.67	65.50	3.00	11.13	10.09	66.40	1.57	14.83	1195.33	2.11	42.22
SM 30	1.59	50.97	59.67	51.00	2.33	5.63	13.27	50.47	1.95	19.33	1106.67	2.94	58.89
SM 31	1.70	53.50	66.67	53.83	3.50	5.27	12.73	39.67	2.13	20.33	965.83	2.00	40.00
SM 32	2.45	51.00	63.00	44.83	2.67	6.09	12.49	56.07	2.05	17.50	1147.33	1.33	26.67
CD at 5 %	0.09	0.95	0.95	1.84	0.73	0.23	0.23	1.55	0.19	1.57	14.81	0.33	6.54

Plate 1. General view of pot culture experiment



Plate 2. Phomopsis fruit rot symptoms in SM 3



SM 26 (72.87) and *SM 4*(68.07). The lightest fruits were produced by the genotype *SM 31*.

Fruit length and girth also have shown considerable variation among the genotypes. *SM 19* (14.36 cm) had the thickest fruits and was on par with *SM 8*. *SM 16* (8.03 cm) had leaner fruits. The longest fruits were observed in *SM 19* (13.37 cm) while the shortest fruits observed in genotype *SM 20* (4.96 cm) and no genotype was on par with either of the extremes for the character.

The number of fruits per cluster ranged between 1.03 and 3.67. The highest number of fruits per cluster was recorded in *SM 11* which was on par with *SM 13* and *SM 15*. The lowest number of fruits per cluster was observed in *SM 9*.

The tallest genotype was *SM 29* (65.50cm) and *SM 26*, *SM 25*, *SM 17*, *SM 13* and *SM 11* were on par with it. The shortest genotype was *SM 32* (44.83).

Maximum number of primary branches was recorded in *SM 25* (4), on par with it are *SM 9*, *SM 11*, *SM 13*, *SM 15*, *SM 19* and *SM 31*. Minimum number of primary branches was recorded in *SM 6* and *SM 21* (2.17).

SM 11 (33) produced the highest number of fruits per plant and *SM 8* and *SM 13* were on par with it. *SM 25* (8.33) recorded the lowest number of fruits per plant.

The highest yield per plant was recorded by *SM 15* (2095.50 g) followed by *SM 26* (2019.00 g), *SM 19* (1946.33 g) and *SM 8* (1874.33 g). The lowest yield per plant was observed in *SM 25* (603.17 g) and none of the genotype was on par with it.

4.1.2.2 Screening for phomopsis blight

Out of the 32 genotypes screened against phomopsis blight based on the percentage disease index, none was found to be resistant to the disease. *SM 9* (12.22), *SM 23* (16.67) and *SM 25* (12.22) were moderately resistant to the disease. On the other hand, *SM 2* (62.22), *SM 3* (62.22), *SM 10* (63.33), *SM 13*

(65.56), *SM* 16 (67.78), *SM* 20 (63.33) and *SM* 21 (61.11) were the susceptible genotypes to the phomopsis blight disease. Remaining categories *ie.*, moderately susceptible and susceptible comprised 13 and 9 genotypes respectively (Table 4).

4.2 Evaluation of genotypes for genetic variation, yield and tolerance to pests and diseases under field conditions

The thirty two genotypes were subjected to detailed study on variability, heritability, genetic advance, correlation, path analysis, genetic divergence and screening for pests and diseases.

4.2.1 Analysis of variance

The analysis of variance revealed significant variation among the thirty two genotypes for all the characters studied (Table 5).

4.2.2 Mean performance of accessions

The mean values of the genotypes for growth, yield and incidence of pest and diseases are presented below.

4.2.2.1 Biometric characters

The mean values for the twelve biometric characters are furnished in Table 6.

In the present investigation, biometric characters *viz.*, plant height, days to first flowering, days to first harvest, fruit length, fruit weight, fruits per plant and yield per plant showed wide variation among the genotypes.

Significant variation was noticed for plant height which ranged between 58.8 cm (*SM* 32) and 119 cm (*SM* 17). None of the genotypes was on par with the highest value of plant height, while *SM* 30 (60.07) was on par with the shortest plant.

The number of primary branches was highest in *SM* 15 (3.93) and *SM* 30 (2.27) produced the lowest number of primary branches.

Table 4. Rating of brinjal (*Solanum melongena* L.) genotypes against phomopsis blight disease based on PDI

Sl. No.	PDI	Category	Genotypes
1.	0	Resistant	–
2.	1 – 20	Moderately resistant	<i>SM 9, SM 23 and SM 25</i>
3.	21 -40	Moderately susceptible	<i>SM 4, SM 5, SM 14, SM 15, SM 18, SM 19, SM 22, SM 24, SM 26, SM 27, SM 28, SM 31 and SM 32</i>
4.	41 -60	Susceptible	<i>SM 1, SM 6, SM 7, SM 8, SM 11, SM 12, SM 17, SM 29 and SM 30</i>
5.	> 60	Highly susceptible	<i>SM 2, SM 3, SM 10, SM 13, SM 16, SM 20 and SM 21</i>

Table 5. Analysis of variance of 13 characters in 32 brinjal genotypes under field experiment

Sl. No.	Character	Mean squares		
		Genotypes	Replication	Error
	Degrees of freedom	31	2	62
1.	Calyx length	0.69**	0.04	0.02
2.	Days to first flower	66.69**	0.21	0.74
3.	Days to first harvest	143.42**	0.12	0.73
4.	Fruit girth (cm)	10.08**	0.08	0.16
5.	Fruit length (cm)	21.38**	0.49	0.18
6.	Fruit weight (g)	267.05**	2.45	1.32
7.	Fruits per cluster	1.35**	0.04	0.02
8.	Fruits per plant	171.21**	0.69	0.26
9.	Plant height (cm)	821.59**	2.32	5.33
10.	Primary branches	0.51**	0.07	0.02
11.	Yield per plant (g)	759016.19**	81.32	52.31
12.	100 seed weight (g)	0.01**	0.00	0.00
13.	SFB infestation (%)	1043.34**	0.54	0.68

** Significant at 1 % level

Table 6. Mean performance of brinjal (*Solanum melongena* L.) genotypes under field evaluation

Accessions	Calyx length (cm)	Days to first flower	Days to first harvest	Plant height (cm)	Number of 1 ^o branches	Fruit length(cm)	Fruit girth(cm)	Fruit weight(g)	Fruits per cluster	Fruits per plant	100 Seed weight(g)	Yield per plant(g)
SM 1	2.43	43.27	68.80	83.47	3.07	7.79	14.81	70.13	2.10	22.00	0.223	1947.93
SM 2	1.71	40.47	58.73	80.87	2.53	7.03	11.08	58.60	1.67	17.60	0.263	1249.80
SM 3	1.61	43.67	59.13	76.73	2.87	9.39	9.94	44.47	3.10	24.07	0.257	1132.87
SM 4	1.81	44.40	60.33	114.33	2.87	10.09	9.91	65.47	1.53	17.27	0.203	1293.13
SM 5	1.35	43.60	64.40	65.53	2.40	5.93	13.14	50.80	1.70	11.20	0.230	609.40
SM 6	1.59	38.73	58.67	90.93	2.73	5.19	12.27	35.60	2.37	16.00	0.363	603.00
SM 7	2.51	40.13	65.60	73.07	3.33	5.89	12.78	54.67	1.53	15.60	0.277	966.67
SM 8	2.09	43.80	63.80	98.53	3.07	6.44	13.91	49.40	2.67	34.60	0.247	1838.33
SM 9	2.98	52.13	79.87	77.47	3.67	10.85	11.08	60.73	1.33	9.80	0.267	599.13
SM 10	1.70	43.40	61.73	68.00	2.93	6.24	10.83	52.67	2.09	19.20	0.167	1072.13
SM 11	1.80	41.73	59.60	79.00	3.53	13.81	7.96	56.00	3.43	43.80	0.330	2509.73
SM 12	2.07	48.27	63.27	71.33	2.73	6.66	13.46	58.60	1.37	11.07	0.363	661.60
SM 13	2.47	40.27	58.60	89.13	3.53	14.18	8.23	48.00	2.97	26.27	0.327	1300.73
SM 14	1.86	46.60	78.20	105.20	3.53	9.69	12.42	56.40	1.47	17.87	0.327	1074.27
SM 15	1.83	47.33	59.87	102.40	3.93	9.41	8.73	69.47	3.43	29.40	0.290	2181.33
SM 16	1.91	41.07	73.40	106.40	2.87	9.49	8.95	41.40	2.40	18.33	0.210	802.07
SM 17	2.09	49.40	73.00	119.00	2.67	5.13	12.25	53.33	1.33	12.80	0.210	739.13
SM 18	2.53	47.60	68.20	110.00	3.33	10.06	9.23	47.13	2.63	23.67	0.183	1068.53
SM 19	2.63	44.87	71.27	85.40	3.67	14.95	12.19	71.13	2.87	30.33	0.120	2189.40
SM 20	1.43	48.47	68.07	63.07	2.87	8.37	10.66	59.47	1.73	15.33	0.250	937.60
SM 21	1.98	40.40	58.73	64.80	2.67	7.51	10.30	51.53	1.80	20.47	0.307	1176.53
SM 22	1.77	42.60	78.33	82.33	2.73	6.48	10.52	48.40	1.30	14.93	0.140	762.40
SM 23	2.71	60.33	78.47	91.93	3.53	8.96	10.99	63.07	1.83	21.87	0.263	1416.20
SM 24	2.94	43.33	72.40	88.07	2.93	6.67	14.07	56.40	1.93	24.80	0.330	1507.60
SM 25	2.93	56.40	78.27	110.00	3.67	6.82	10.29	60.13	1.30	9.47	0.243	607.93
SM 26	2.27	42.93	69.67	84.20	3.00	9.37	9.73	72.93	2.76	23.27	0.257	1700.27
SM 27	1.85	49.40	71.47	70.60	2.87	6.46	8.92	60.80	1.78	20.33	0.190	1262.40
SM 28	2.81	46.87	61.87	84.40	2.87	11.19	13.13	68.20	1.10	9.87	0.190	778.67
SM 29	2.77	47.93	70.67	87.20	2.93	11.83	11.56	64.07	1.27	14.07	0.147	943.73
SM 30	1.66	49.00	75.20	60.07	2.27	4.93	12.55	51.93	1.40	18.40	0.177	990.20
SM 31	1.81	43.87	69.27	72.07	3.40	6.98	13.21	37.80	1.93	23.67	0.253	938.67
SM 32	2.47	45.60	66.73	58.80	2.87	6.63	12.81	56.13	1.73	21.33	0.223	1250.20
CD at 5%	0.20	1.40	1.40	3.77	0.25	0.69	0.65	1.88	0.25	0.83	0.016	11.82

Plate 3. General view of the field experiment



Plate 4. SM 11 – the highest yielder under field experiment



Days to first flower ranged from 38.73 to 60.33 days. *SM 6* was the earliest to flower and on par with it was *SM 7* (40.13). *SM 23* took the maximum number of days to flower.

SM 13 (58.60) took the minimum number of days to first harvest and was on par with *SM 6* (58.67), *SM 21* (58.73), *SM 2* (58.73), *SM 3* (59.13), *SM 11* (59.60) and *SM 15* (59.87). *SM 9* (79.87 days) recorded the longest duration to attain first harvest.

SM 9 (2.98 cm) produced the longest calyx and the shortest was observed in *SM 5* (1.35 cm). *SM 24* (2.94), *SM 25* (2.93) and *SM 28* (2.81) were on par with the longest calyx length.

Fruit length exhibited significant variation among the genotypes with a range of 4.93 - 14.95 cm. The longest fruits were produced by *SM 19* (14.95 cm) whereas *SM 30* (4.93 cm) had the smallest fruits. Fruit girth ranged from 7.96 cm (*SM 11*) to 14.81 cm (*SM 1*).

The highest fruit weight was recorded in *SM 26* (72.93 g) which was on par with *SM 19* (71.13 g) and the lowest was recorded in *SM 6* (35.6 g). The genotypes *SM 11* and *SM 15* (3.43) had the maximum number of fruits per cluster and *SM 28* (1.10) had the minimum.

The genotypes differed significantly with respect to number of fruits per plant which ranged from 9.47 (*SM 25*) to 43.8 (*SM 11*). *SM 11* was followed by *SM 8* (34.60), *SM 19* (30.33), *SM 15* (29.40), *SM 13* (26.27) and *SM 24* (24.80).

The weight of 100 seeds ranged between 0.363 g (*SM 6* and *SM 12*) and 0.120 g (*SM 19*) with an overall mean of 0.240 g.

Fruit yield per plant ranged from 2509.73 g (*SM 11*) to 599.13 g (*SM 9*). The highest fruit yield was recorded in *SM 11* and it was followed by *SM 19* (2989.40), *SM 15* (2181.33), *SM 1* (1947.93) and *SM 8* (1838.33).

4.2.2.3 Morphological characters

Phenotypic expression of fruit colour and spininess on leaves is given in Table 7. The variation for fruit colour among the genotypes is illustrated in Plates 1 and 2.

4.2.2.4 Incidence of phomopsis blight

There was no incidence of phomopsis blight under field conditions during the season.

4.2.2.5 Screening for shoot and fruit borer

Evaluation of genotypes for resistance to shoot and fruit borer (SFB) was carried out based on percentage of infestation.

4.2.2.5.1 Plant infestation percentage

The percentage of infestation of SFB on all the genotypes at different intervals after transplanting is furnished in Table 8.

A wide variation for plant infestation by SFB was observed among the genotypes. The least plant infestation percentage by SFB was recorded in *SM 30* (2.43) and the highest was in *SM 13* (90.33) at 30 DAT. It was the lowest in *SM 27* at 45 DAT, 60 DAT, 75 DAT and 90 DAT (11.9, 14.73, 16.3 and 17.3 respectively). The highest plant infestation was in *SM 7* (85.53) at 45 DAT; at 60 DAT, 75 DAT and 90 DAT, highest infestation was recorded in *SM 13* (85.9, 77.5 and 75.4 respectively). The overall plant infestation was minimum in *SM 27* (12.87)

4.2.2.5.1 Fruit infestation percentage

The fruit infestation percentage in thirty two genotypes at 10 days interval is provided in Table 9.

Differential response to the fruit infestation by SFB was noticed in the germplasm. The minimum fruit infestation at all 80 DAT, 90 DAT and 100 DAT

Plate 5. Variation of fruit colour and shape 1



SM 1



SM 3



SM 4



SM 5



SM 7



SM 8



SM 9



SM 11

Plate 6. Variation of fruit colour and shape 2

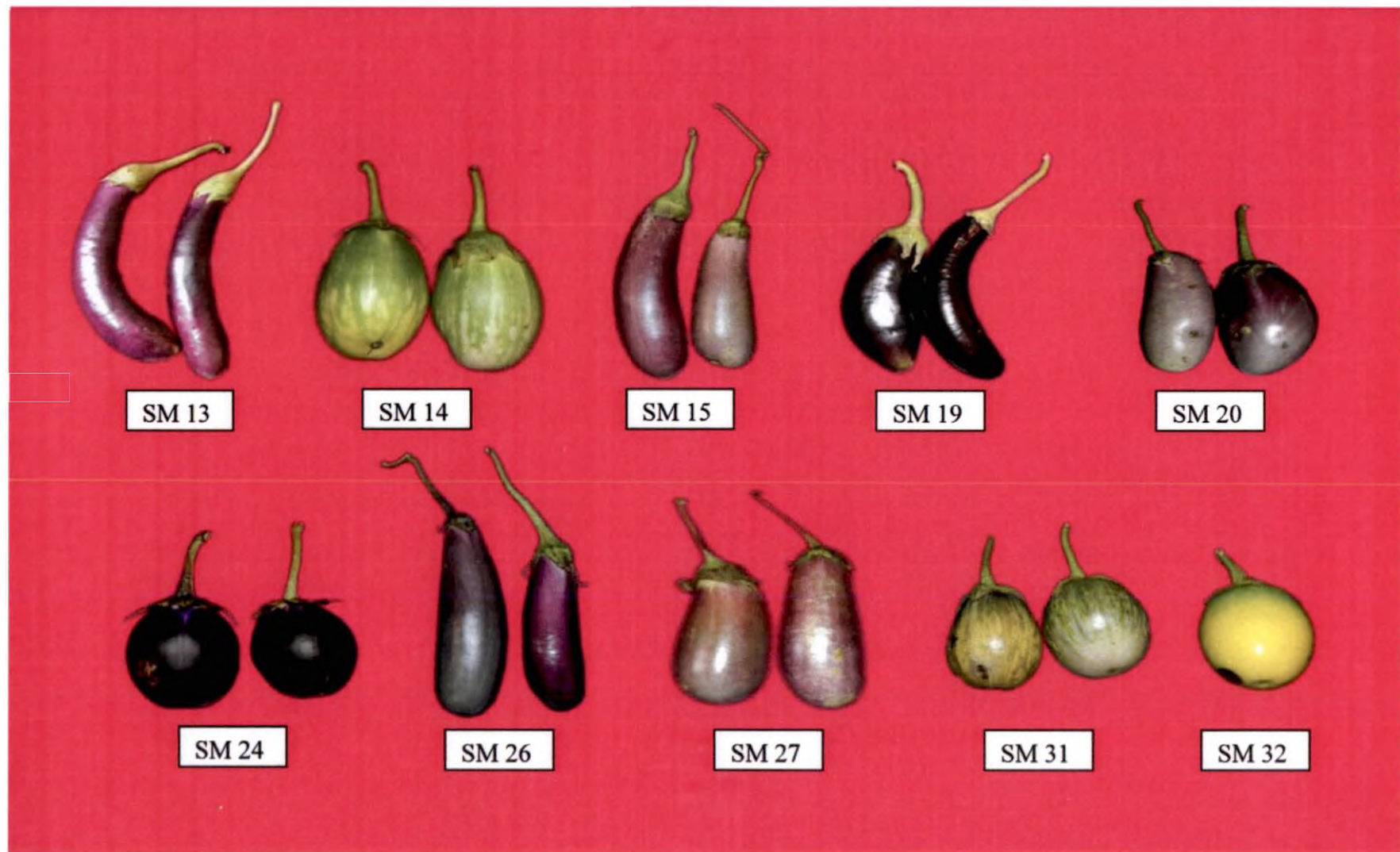


Table 7. Phenotypic expression of fruit colour, fruit shape and spinness on leaves in 32 brinjal genotypes

Genotype	Fruit colour	Fruit shape	Spinness on leaf
<i>SM 1</i>	Purple	Oval	Spineless
<i>SM 2</i>	Light green	Medium long	Spineless
<i>SM 3</i>	White	Long	Spineless
<i>SM 4</i>	Violet black	Oval	Spineless
<i>SM 5</i>	Green with white strips	Round small	Spineless
<i>SM 6</i>	Green	Round small	Spineless
<i>SM 7</i>	Green	Round	Spineless
<i>SM 8</i>	Green	Round	Spiny
<i>SM 9</i>	Light green	Medium long	Spineless
<i>SM 10</i>	Green with white strips	Round	Spineless
<i>SM 11</i>	Violet	Long	Spineless
<i>SM 12</i>	Green	Round	Spineless
<i>SM 13</i>	Violet	Long	Spineless
<i>SM 14</i>	Green with white strips	Round	Spineless
<i>SM 15</i>	Violet	Medium long	Spineless
<i>SM 16</i>	Green	Long	Spineless
<i>SM 17</i>	Green with white strips	Round	Spiny
<i>SM 18</i>	Green with white strips	Medium long	Spineless
<i>SM 19</i>	Black	Long	Spineless
<i>SM 20</i>	Violet	Round	Spiny
<i>SM 21</i>	Light green with white strips	Round	Spineless
<i>SM 22</i>	Green	Round	Spineless
<i>SM 23</i>	Light green	Medium long	Spineless
<i>SM 24</i>	Violet	Round	Spineless
<i>SM 25</i>	Light green	Medium long	Spineless
<i>SM 26</i>	Purple	Medium long	Spineless
<i>SM 27</i>	Purple	Round	Spiny
<i>SM 28</i>	Green	Medium long	Spineless
<i>SM 29</i>	Light green	Medium long	Spineless
<i>SM 30</i>	Purple with white strips	Round	Spiny
<i>SM 31</i>	White with purple strips	Round	Spineless
<i>SM 32</i>	Green with white strips	Round	Spineless

Table 8. Percentage of plants infested by shoot and fruit borer in 32 brinjal genotypes at 15 days interval

Genotypes	30 DAT	45 DAT	60 DAT	75 DAT	90 DAT	Pooled mean
SM 1	18.07	26.23	27.73	33.83	31.63	27.50
SM 2	14.00	26.13	24.43	26.37	26.83	23.55
SM 3	16.90	33.93	37.00	31.30	31.97	30.22
SM 4	64.93	39.57	33.50	34.33	24.87	39.44
SM 5	65.43	50.50	48.27	43.97	39.43	49.52
SM 6	50.03	81.63	59.87	54.43	43.97	57.99
SM 7	73.53	85.53	62.03	49.83	42.03	62.59
SM 8	67.30	61.43	60.37	52.77	55.47	59.47
SM 9	59.50	49.13	62.20	56.50	54.90	56.45
SM 10	42.07	51.27	43.60	36.70	32.10	41.15
SM 11	70.93	76.73	69.10	53.67	49.07	63.90
SM 12	26.13	37.43	28.13	26.43	24.23	28.47
SM 13	90.33	84.47	85.90	77.50	75.40	82.72
SM 14	35.63	38.83	43.63	42.13	39.30	39.91
SM 15	84.10	56.87	60.83	57.43	55.00	62.85
SM 16	59.40	62.63	42.30	36.20	32.10	46.53
SM 17	2.67	17.87	25.33	30.90	33.87	22.13
SM 18	49.67	45.00	51.33	47.37	44.70	47.61
SM 19	84.17	67.10	73.20	68.67	66.40	71.91
SM 20	49.10	49.77	43.67	40.17	37.23	43.99
SM 21	5.10	18.83	32.53	29.40	26.57	22.49
SM 22	56.47	64.13	48.93	46.33	42.33	51.64
SM 23	37.40	35.57	39.80	36.33	33.33	36.49
SM 24	16.57	27.63	37.53	33.33	30.63	29.14
SM 25	15.27	26.80	19.07	19.30	18.47	19.78
SM 26	17.47	18.93	27.87	20.50	19.97	20.95
SM 27	4.27	11.90	14.73	16.13	17.30	12.87
SM 28	67.73	61.47	48.23	44.63	43.03	53.02
SM 29	82.00	62.70	68.97	63.33	59.47	67.29
SM 30	2.43	15.60	27.07	24.43	21.37	18.18
SM 31	15.57	17.77	21.93	23.37	22.17	20.16
SM 32	14.50	14.53	24.60	24.33	23.07	20.21
CD at 5%	3.49	2.40	2.33	1.60	1.49	1.09

Table 9. Fruit infestation percentage by shoot and fruit borer in 32 brinjal genotypes at 10 days interval

Genotypes	80 DAT	90 DAT	100 DAT	Pooled mean	Rating
<i>SM 1</i>	27.33	30.14	32.44	29.97	S
<i>SM 2</i>	25.73	25.88	26.36	25.99	S
<i>SM 3</i>	36.03	35.57	32.33	34.64	S
<i>SM 4</i>	38.93	34.87	23.90	32.57	S
<i>SM 5</i>	49.40	49.46	39.13	46.00	HS
<i>SM 6</i>	74.63	60.19	42.80	59.21	HS
<i>SM 7</i>	77.00	61.44	42.10	60.18	HS
<i>SM 8</i>	61.47	57.62	54.52	57.87	HS
<i>SM 9</i>	52.53	62.13	55.33	56.67	HS
<i>SM 10</i>	48.93	44.03	32.17	41.71	HS
<i>SM 11</i>	74.60	68.90	49.03	64.18	HS
<i>SM 12</i>	34.63	29.31	24.61	29.52	S
<i>SM 13</i>	84.43	83.23	74.77	80.81	HS
<i>SM 14</i>	41.37	43.01	40.21	41.53	HS
<i>SM 15</i>	57.97	60.34	56.34	58.22	HS
<i>SM 16</i>	56.23	41.60	31.90	43.24	HS
<i>SM 17</i>	21.07	27.68	32.77	27.17	S
<i>SM 18</i>	48.20	52.28	46.09	48.86	HS
<i>SM 19</i>	69.80	71.27	66.79	69.29	HS
<i>SM 20</i>	47.43	44.16	36.43	42.67	HS
<i>SM 21</i>	23.10	31.08	27.97	27.38	S
<i>SM 22</i>	59.70	47.91	42.57	50.06	HS
<i>SM 23</i>	37.43	37.53	34.68	36.55	S
<i>SM 24</i>	32.30	34.81	30.77	32.63	S
<i>SM 25</i>	25.07	19.99	18.67	21.24	MR
<i>SM 26</i>	22.93	27.66	20.10	23.56	MR
<i>SM 27</i>	12.80	17.04	16.64	15.50	MR
<i>SM 28</i>	56.80	47.98	42.33	49.04	HS
<i>SM 29</i>	64.60	66.59	59.53	63.57	HS
<i>SM 30</i>	19.33	27.09	22.74	23.06	MR
<i>SM 31</i>	18.23	22.61	22.49	21.11	MR
<i>SM 32</i>	18.40	25.17	23.68	22.41	MR
CD at 5%	7.98	2.44	1.86	1.09	

MR- Moderately Resistant

S - Susceptible

HS - Highly Susceptible

was observed in *SM 27* (12.80, 17.04 and 16.64 respectively) followed by *SM 31* (18.23, 22.61 and 22.49 respectively). The maximum fruit infestation was recorded in *SM 13* at all intervals *ie.*, 80 DAT, 90 DAT and 100 DAT (84.43, 83.23 and 74.47 respectively). The overall fruit damage by SFB was least in *SM 27* (15.50).

4.2.2.5.2 Rating of genotypes for shoot and fruit borer

Rating of genotypes for shoot and fruit borer was done based on fruit infestation percentage. Out of the thirty two genotypes screened against shoot and fruit borer, none emerged as tolerant to the pest. Based on fruit infestation percentage, genotypes *SM 25*, *SM 27*, *SM 26*, *SM 30*, *SM 31* and *SM 32* were moderately resistant while *SM 5*, *SM 6*, *SM 7*, *SM 8*, *SM 9*, *SM 10*, *SM 11*, *SM 13*, *SM 14*, *SM 15*, *SM 16*, *SM 18*, *SM 19*, *SM 20*, *SM 22*, *SM 28* and *SM 29* were highly susceptible to the pest. Remaining nine genotypes were categorized in susceptible (Table 10).

4.2.3 Genetic variability, heritability and genetic advance as percentage of mean

The population means, range, genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance for all the 13 characters were studied and are presented in Table 11.

For all the characters studied, PCV and GCV corresponded closely, also they exhibited high heritability percentages and genetic advances as percentage of mean. Calyx length, fruit length, fruits per cluster, fruits per plant, yield per plant, 100 seed weight and shoot and fruit borer infestation percentage recorded high estimates of both PCV and GCV, on the other hand, all other characters showed moderate PCV and GCV values.

Calyx length recorded high values of PCV (22.87) and GCV (22.16). It exhibited high heritability and genetic advance as percentage of mean *ie.*, 93.88 and 43.93 per cent.

Table 10. Rating of brinjal genotypes (*Solanum melongena* L.) against shoot and fruit borer based on fruit infestation percentage

Sl. No.	Fruit infestation %	Rating	Genotypes
1.	< 15	Tolerant (T)	--
2.	16 - 25	Moderately Resistant (MR)	<i>SM 25, SM 27, SM 26, SM 30, SM 31 and SM 32</i>
3.	26 - 40	Susceptible (S)	<i>SM 1, SM 2, SM 3, SM 4, SM 12, SM 17, SM 21, SM 23 and SM 24</i>
4.	> 40	Highly Susceptible (HS)	<i>SM 5, SM 6, SM 7, SM 8, SM 9, SM 10, SM 11, SM 13, SM 14, SM 15, SM 16, SM 18, SM 19, SM 20, SM 22, SM 28 and SM 29</i>

Table 11. Genetic parameters for yield and yield contributing characters in brinjal (*Solanum melongena* L.) genotypes

Characters	Range		Mean	GCV	PCV	Heritability	Genetic advance at 5%	Genetic advance as % mean
	Min.	Max.						
Calyx length (cm)	1.34	2.98	2.14	22.16	22.87	93.88	0.94	43.93
Days to first flowering	38.73	60.33	45.56	10.29	10.46	96.76	9.50	20.85
Days to first harvest	58.6	79.87	67.68	10.19	10.27	98.49	14.10	20.83
Fruit girth (cm)	7.96	14.81	11.31	16.08	16.46	95.39	3.66	32.36
Fruit length (cm)	4.93	14.95	8.45	31.46	31.86	97.55	5.41	64.02
Fruit weight (g)	35.6	72.93	56.09	16.77	16.90	98.53	19.25	34.32
Fruits per cluster	1.1	3.43	2.00	33.26	34.15	94.86	1.33	66.50
Fruits per plant	9.47	43.8	19.96	37.82	37.90	99.55	15.51	77.71
Plant height (cm)	58.8	119	84.82	19.45	19.63	98.08	33.65	39.67
Primary branches	2.67	3.93	3.06	13.23	14.13	87.63	0.78	25.49
Yield per plant (g)	599.13	2509.7	1190.99	42.23	42.24	99.97	1036.03	86.99
100 seed weight (g)	0.12	0.36	0.24	26.00	26.34	97.44	0.13	54.17
SFB infestation (%)	12.87	82.72	41.57	44.85	44.90	99.80	38.37	92.30

Days to first flowering recorded moderate values of PCV and GCV viz., 10.46 and 10.29 respectively with high heritability of 96.76 per cent. Its genetic advance as percentage of mean was 20.85.

The PCV and GCV for days to first harvest were 10.27 and 10.19 respectively. Heritability was 98.49 per cent and genetic advance as percentage of mean was 20.83.

The estimates of PCV and GCV for plant height were 19.63 and 19.45 respectively. Heritability was as high as 98.08 per cent while genetic advance as percentage of mean was 39.69.

Number of primary branches per plant recorded moderate PCV (14.13) and GCV (13.23). The heritability was 87.63 per cent while genetic advance as percentage of mean was 25.49.

Fruit girth found to have PCV of 16.46 and GCV of 16.08 which were moderate. High heritability (95.39 per cent) and genetic advance as percentage of mean (32.36) was recorded for this character.

Fruit length recorded high estimates of PCV and GCV values (31.86 and 31.46 respectively). Heritability was as high as 97.55 per cent coupled with high genetic advance as percentage of mean (64.02).

Fruit weight registered moderate values for both PCV and GCV (16.90 and 16.77 respectively). It also recorded high estimates of heritability (98.53) and genetic advance as percentage of mean (34.32).

Number of fruits per cluster recorded high estimates for both PCV and GCV *i.e.*, 34.15 and 33.26 respectively. Also it was found to have high heritability (94.86 per cent) coupled with high genetic advance as percentage of mean (66.50).

The PCV and GCV estimates for number of fruits per plant were 37.90 and 37.82 respectively. Its heritability was 99.55 per cent and genetic advance as percentage of mean was 77.71. Hundred seed weight recorded high values of PCV

(26.34) and GCV (26.00). Its heritability was 97.44 per cent and genetic advance as percentage of mean was 54.17.

Yield per plant showed a PCV of 42.24 and GCV of 42.23. Its heritability was as high as 99.97 per cent coupled with high genetic advance as percentage of mean (86.99).

4.2.4 Correlation studies

The phenotypic, genotypic and environmental correlations among thirteen growth and yield characters were estimated and are presented in Tables 12, 13 and 14 respectively.

4.2.4.1 Phenotypic correlation studies

Yield per plant showed significant positive correlation with number of fruits per plant (0.8752), fruits per cluster (0.6899), fruit length (0.4427), fruit weight (0.4353) and number of primary branches (0.3948). It exhibited significant negative correlation with days to first harvest (-0.2444).

Days to first flowering found to be positively correlated with days to first harvest (0.6006), fruit weight (0.3555) and primary branches (0.2775). It also found to have significant negative correlation with fruits per cluster (-0.3380) and fruits per plant (-0.2826).

Fruit length showed significant positive correlation with borer infestation percentage (0.5960), primary branches (0.5336), fruits per cluster (0.4236) and fruit weight (0.3456). Fruit girth recorded significant negative correlation with fruits per cluster (-0.4377) and fruit length (-0.4292).

Fruits per cluster had shown significant positive correlation with fruits per plant (0.8120), number of primary branches (0.3774) and borer infestation percentage (0.3565).

Fruits per plant had a significant positive correlation with number of primary branches (0.3609).

Table 12. Phenotypic correlation coefficients for growth and yield attributing characters

Character	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1												
X2	0.3794**	1											
X3	0.3716**	0.6006**	1										
X4	0.1670	-0.0068	0.1474	1									
X5	0.3361**	-0.0212	-0.0956	-0.4292**	1								
X6	0.4050**	0.3555**	0.1319	0.0248	0.3456**	1							
X7	-0.1635	-0.3380**	-0.4273**	-0.4377**	0.4236**	-0.0848	1						
X8	-0.0880	-0.2826*	-0.3035*	-0.2618*	0.3940**	-0.0091	0.8120**	1					
X9	0.2368	0.1785	0.1718	-0.1986	0.2027	0.0573	0.1159	0.0367	1				
X10	0.4372**	0.2775*	0.1806	-0.2739*	0.5336**	0.2416*	0.3774**	0.3609**	0.3443**	1			
X11	0.0530	-0.1660	-0.2444	-0.1713	0.4427**	0.4353**	0.6899**	0.8752**	0.0619	0.3948**	1		
X12	-0.0751	-0.1780	-0.3172*	0.0096	-0.0615	-0.2104	0.2102	0.1488	-0.0138	0.1700	0.0489	1	
X13	0.1436	-0.2413*	-0.2202	-0.1829	0.5960**	-0.0100	0.3565**	0.2530*	0.1769	0.4055**	0.2039	0.0110	1

** Significant at 1 % * Significant at 5 %

X1- Calyx length (cm)

X2- Days to first flowering

X3- Days to first harvesting

X4- Fruit girth (cm)

X5- Fruit length (cm)

X6- Fruit weight (g)

X7- Fruits per cluster

X8- Fruits per plant

X9- Plant height (m)

X10-Number of primary branches

X11- Yield per plant (g)

X12- 100 seed weight (g)

X13- Borer infestation (%)

Table 13. Genotypic correlation coefficients for growth and yield attributing characters

Character	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1												
X2	0.3996**	1											
X3	0.3831**	0.6134**	1										
X4	0.1677	-0.0087	0.1522	1									
X5	0.3397**	-0.0086	-0.0993	-0.4501**	1								
X6	0.4168**	0.3686**	0.1329	0.0233	0.3458**	1							
X7	-0.1787	-0.3598**	-0.4511**	-0.4624**	0.4468**	-0.0864	1						
X8	-0.0885	-0.2906*	-0.3067	-0.2715*	0.4003**	-0.0106	0.8372**	1					
X9	0.2431*	0.1801	0.1747	-0.2098	0.2070	0.0560	0.1258	0.0342	1				
X10	0.4803**	0.3013*	0.1906	-0.2921*	0.5783**	0.2653*	0.4150**	0.3880**	0.3620**	1			
X11	0.0544	-0.1688	-0.2462*	-0.1755	0.4484**	0.4385**	0.7090**	0.8774**	0.0624	0.4217**	1		
X12	-0.0786	-0.1801	-0.3211**	0.0069	-0.0649	-0.2136	0.2193	0.1509	-0.0119	0.1811	0.0496	1	
X13	0.1496	-0.2470*	-0.2212	-0.1889	0.6060**	-0.0087	0.3686**	0.2539*	0.1786	0.4351**	0.2040	0.0109	1

** Significant at 1 % * Significant at 5 %

X1- Calyx length (cm)

X2- Days to first flowering

X3- Days to first harvesting

X4- Fruit girth (cm)

X5- Fruit length (cm)

X6- Fruit weight (g)

X7- Fruits per cluster

X8- Fruits per plant

X9- Plant height (m)

X10-Number of primary branches

X11- Yield per plant (g)

X12- 100 seed weight (g)

X13- Borer infestation (%)

Table 14. Environmental correlation coefficients for growth and yield attributing character

Character	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1												
X2	-0.0318	1											
X3	0.1069	0.0825	1										
X4	0.1553	0.0393	-0.0048	1									
X5	0.2867*	-0.4544**	0.0925	0.1509	1								
X6	0.1394	-0.2020	0.0657	0.0851	0.3468**	1							
X7	0.0911	0.1661	0.3133*	0.0434	-0.1772	-0.0472	1						
X8	-0.1482	0.2138	0.0133	0.1934	-0.0437	0.1726	-0.1017	1					
X9	0.1024	0.1191	0.0056	0.1465	0.0087	0.1390	-0.1718	0.3149*	1				
X10	0.0185	0.0014	0.0815	-0.0905	-0.0188	-0.1149	-0.0118	-0.0633	0.1794	1			
X11	0.0919	0.0117	-0.0183	0.0314	-0.0651	0.0000	-0.1623	-0.1259	0.0512	0.0215	1		
X12	0.0034	-0.1083	0.1313	0.0881	0.0739	-0.0558	-0.0181	0.0117	-0.1009	0.0466	-0.0482	1	
X13	-0.1126	0.1698	-0.1722	0.1467	-0.2858	-0.2621*	-0.2208	-0.0300	0.0259	-0.0928	0.2538	0.0423	1

** Significant at 1 % * Significant at 5 %

X1- Calyx length (cm)

X2- Days to first flowering

X3- Days to first harvesting

X4- Fruit girth (cm)

X5- Fruit length (cm)

X6- Fruit weight (g)

X7- Fruits per cluster

X8- Fruits per plant

X9- Plant height (m)

X10-Number of primary branches

X11- Yield per plant (g)

X12- 100 seed weight (g)

X13- Borer infestation (%)

4.2.4.2 Genotypic correlation studies

Genotypic correlation coefficients were in general higher than phenotypic correlation for the characters under study.

Yield per plant showed significant positive correlation with number of fruits per plant (0.8774), fruits per cluster (0.7090), fruit length (0.4484), fruit weight (0.4385) and number of primary branches (0.4217). It exhibited significant negative correlation with days to first harvest (-0.2462).

Calyx length recorded significant positive correlation with fruit weight (0.4168) and fruit length (0.3397).

Days to first flowering found to be positively correlated with days to first harvest (0.6134), fruit weight (0.3686) and primary branches (0.3013). It was also found to have significant negative correlation with fruits per cluster (-0.3598) and fruits per plant (-0.2906).

Fruits per cluster and fruits per plant recorded significant negative correlation (-0.4511 and -0.3069 respectively) with days to first harvest.

Fruit length showed significant positive correlation with primary branches (0.5783), fruits per cluster (0.4468), fruits per plant (0.4003) and fruit weight (0.3458). Fruit girth recorded significant negative correlation with fruits per cluster (-0.4624), fruit length (-0.4501) and primary branches (-0.2921).

Fruits per cluster had significant positive correlation with fruits per plant (0.8372) and number of primary branches (0.4150). Fruits per plant had a significant positive correlation with number of primary branches (0.3880).

Borer infestation percentage showed positive significant correlation with fruit length (0.6060), primary branches (0.4351) and fruits per cluster (0.3686). It had a significant negative correlation with days to first flower (-0.2470).

4.2.4.3 Environmental correlation studies

Most of the environmental correlation coefficients were very low.

4.2.5 Path coefficient analysis

Genotypic correlation between yield and its component characters were apportioned into different components to find out the direct and indirect contribution of each character on yield. Days to first flowering, days to first harvest, fruit girth, fruit length, fruit weight, fruits per cluster, fruits per plant and number of primary branches were selected for path coefficient analysis.

Direct and indirect effects and correlation of these yield components are presented in Table 15 and Fig 2.

Genotypic correlation of days to first flower with yield was -0.1688. Most of it was contributed by direct effect (-0.1146) and by indirect effect through number of fruits per plant (-0.2420). But it enhanced the yield through indirect effect of fruit weight (0.1911).

Days to first harvest had genotypic correlation of 0.2462 with yield. In this, the direct effect was only 0.0247. Indirect effect of fruits per plant (-0.2554) is the major contributor to the total correlation.

Fruit girth had a genotypic correlation of -0.1755 with yield, of which the direct effect was only 0.0321. This negative correlation was mainly due to its indirect effects through fruits per plant (-0.2261).

The direct effect of fruit length on yield was only -0.0957 but the genotypic correlation with yield was 0.4484. This correlation was mainly contributed by the indirect effect of fruits per plant (0.3334) followed by fruit weight (0.1792) and fruits per cluster (0.0330).

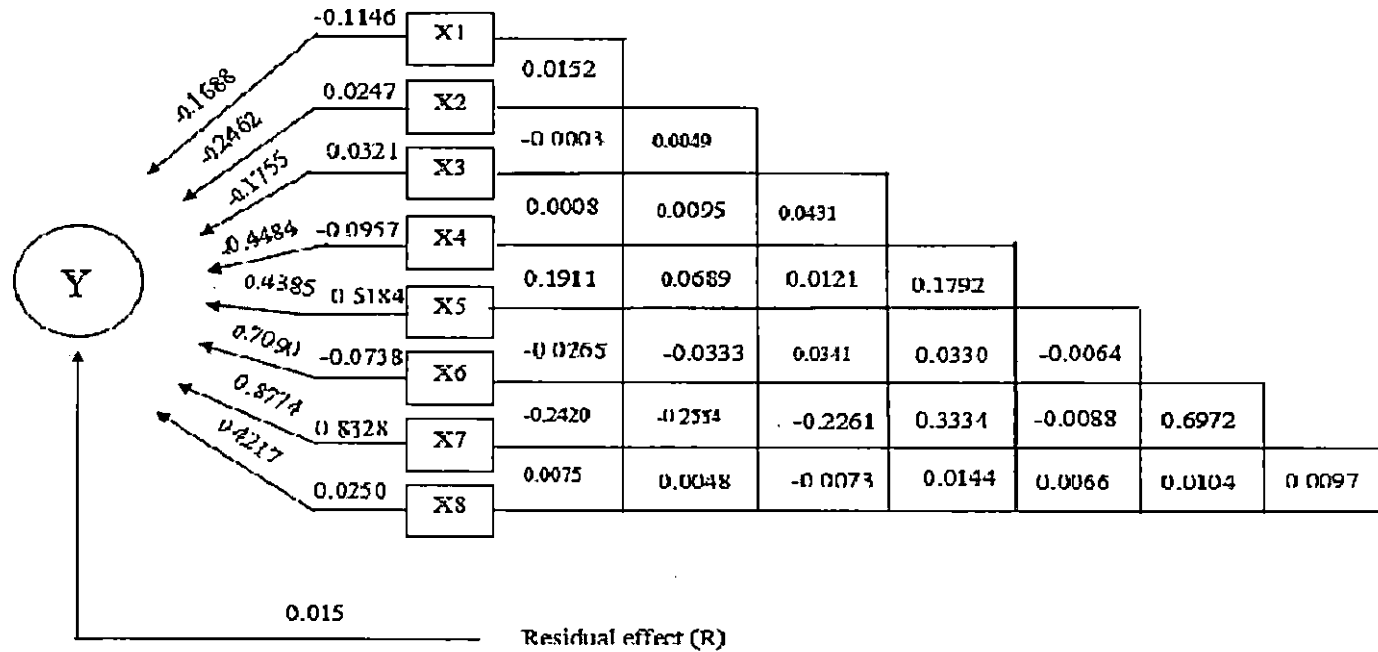
Fruit weight had a genotypic correlation of 0.4385 with yield of which the direct effect alone was 0.5184. This correlation was mainly reduced by the

Table 15. Direct and indirect effects of yield components in brinjal (*Solanum melongena* L.)

Character	Days to first flower	Days to first harvest	Fruit girth	Fruit length	Fruit weight	Fruits per cluster	Fruits per plant	Number of 1 ⁰ branches	Total correlation with yield
Days to first flower	<u>-0.1146</u>	0.0152	-0.0003	0.0008	0.1911	-0.0265	-0.2420	0.0075	-0.1688
Days to first harvest	-0.0703	<u>0.0247</u>	0.0049	0.0095	0.0689	-0.0333	-0.2554	0.0048	-0.2462
Fruit girth	0.0010	0.0038	<u>0.0321</u>	0.0431	0.0121	-0.0341	-0.2261	-0.0073	-0.1755
Fruit length	0.0010	-0.0025	-0.0144	<u>-0.0957</u>	0.1792	0.0330	0.3334	0.0144	0.4484
Fruit weight	-0.0422	0.0033	0.0007	-0.0331	<u>0.5184</u>	-0.0064	-0.0088	0.0066	0.4385
Fruits per cluster	0.0412	-0.0111	-0.0148	-0.0428	-0.0448	<u>0.0738</u>	0.6972	0.0104	0.7090
Fruits per plant	0.0333	-0.0076	-0.0087	-0.0383	-0.0055	0.0617	<u>0.8328</u>	0.0097	0.8774
Number of 1 ⁰ branches	-0.0345	0.0047	-0.0094	-0.0553	0.1375	0.0306	0.3231	<u>0.0250</u>	0.4217

Residual effect (R) = 0.015

Fig 2. Path diagram showing direct and indirect effects of various characters on yield in brinjal genotypes



Values near arrows indicate genotypic correlations, values near boxes indicate direct effects and others are indirect effects

X1- Days to first flower

X5- Fruit weight

Y- Yield per plant

X2- Days to first harvest

X6- Fruits per cluster

R- Residual effect

X3- Fruit girth

X7- Fruits per plant

X4- Fruit length

X8- Number of primary branches

negative indirect effects of days to first flower (-0.0422) and fruit length (-0.0331).

Fruits per cluster had a genotypic correlation of 0.7090 with yield. Although it had direct effect only of 0.0738 on yield, it contributed to the yield mainly through the indirect effect of fruits per cluster (0.6972).

Fruits per plant had the highest genotypic correlation with yield *i.e.*, 0.8774 and most of it was through direct effect (0.8387).

Number of primary branches had a genetic correlation of 0.4217 with yield of which its direct effect on yield was only -0.0025. This significant positive correlation was mainly through indirect effects of fruits per plant (0.3231) and fruit weight (0.1375)

The residue was only 0.015 indicating that the selected eight characters contributing the remaining ninety eight per cent towards the yield.

4.2.6 Selection index

Discriminate function technique was adopted for the construction of selection index for yield using fruit yield per plant (X11) and the component characters *viz.*, calyx length (X1), days to first flowering (X2), days to first harvest (X3), fruit girth (X4), fruit length (X5), fruit weight (X6), fruits per cluster (X7), fruits per plant (X8), plant height (X9), number of primary branches (X10), 100 seed weight (X12) and percentage of fruit and shoot borer (X13).

The index value for each land race was determined and they were ranked accordingly (Table 16). Ten genotypes *viz.*, SM 11 (8648.269), SM 19 (7796.68), SM 15 (7735.726), SM 1 (6874.852), SM 8 (6637.749), SM 26 (6124.202), SM 24 (5544.573), SM 23(5382.518), SM 13(5028.862) and SM 4 (4972.541) recorded top index values.

Table 16. Ranking of thirty two brinjal genotypes according to selection index

Sl. No.	Accession	Index	Rank
1	SM 1	6874.852	4
2	SM 2	4656.321	12
3	SM 3	4315.076	16
4	SM 4	4972.541	10
5	SM 5	2755.347	32
6	SM 6	2772.887	31
7	SM 7	3906.832	20
8	SM 8	6637.749	5
9	SM 9	2893.604	30
10	SM 10	4142.264	18
11	SM 11	8648.269	1
12	SM 12	2903.371	28
13	SM 13	5028.862	9
14	SM 14	4335.796	15
15	SM 15	7735.726	3
16	SM 16	3462.91	24
17	SM 17	3268.402	27
18	SM 18	4315.873	16
19	SM 19	7796.68	2
20	SM 20	3781.564	22
21	SM 21	4374.668	14
22	SM 22	3305.432	26
23	SM 23	5382.518	8
24	SM 24	5544.573	7
25	SM 25	2894.318	29
26	SM 26	6124.202	6
27	SM 27	4705.992	11
28	SM 28	3394.384	25
29	SM 29	3968.575	19
30	SM 30	3853.919	21
31	SM 31	3693.413	23
32	SM 32	4632.09	13

4.2.7 Divergence analysis

Generally geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be useful for discrimination among the populations occupying ecologically marginal habitats.

The multivariate analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations.

The data collected on yield and its contributing characters *viz.*, calyx length, days to first flowering, days to first harvest, fruit girth, fruit length, individual fruit weight, fruits per cluster, fruits per plant, plant height, primary branches, 100 seed weight and borer infestation percentage for 32 genotypes of brinjal were subjected to multivariate analysis. The quantitative assessment of genetic divergence was made by Mahalanobis' D^2 statistics for yield and its contributing characters.

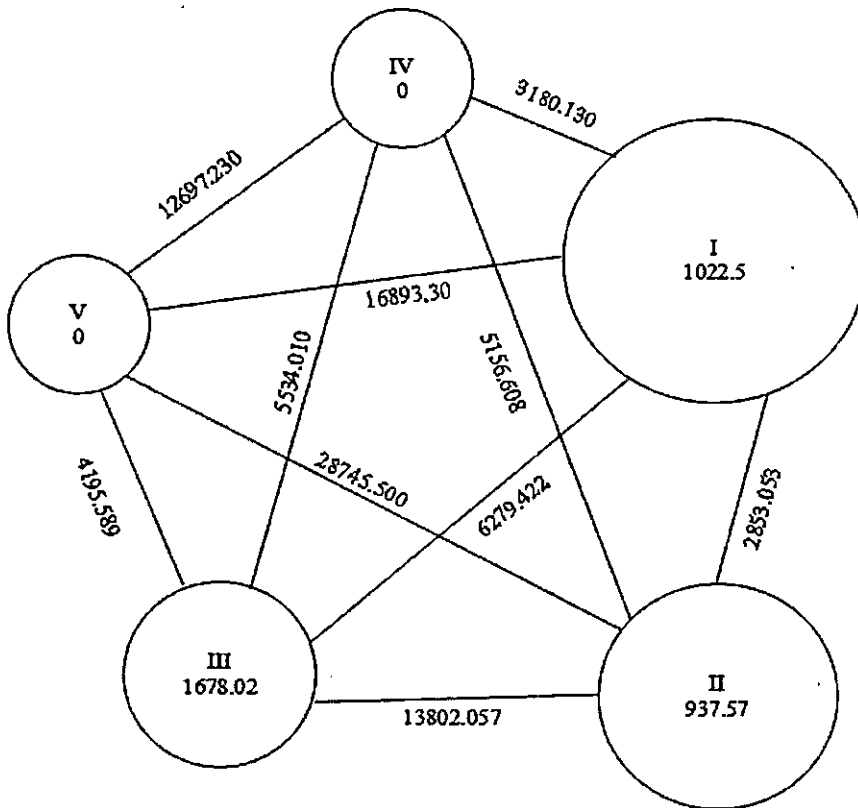
4.2.7.1 Grouping of genotypes into various clusters

Thirty two genotypes were grouped into five clusters based on D^2 values using the Tocher's method (Rao 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 17. Out of the five clusters, cluster I was the largest comprising of fifteen genotypes followed by Cluster II with ten genotypes, cluster III with five genotypes; cluster IV and V were the smallest with one genotype each.

Table 17. Clustering pattern of brinjal (*Solanum melongena* L.) genotypes by Tocher's method

Cluster No	No. of genotypes	Name of the genotypes
I	15	SM 2, SM 3, SM 4, SM 7, SM 10, SM 14, SM 18, SM 20, SM 21, SM 23, SM 24, SM 27, SM 30, SM 31 and SM 32
II	10	SM 5, SM 6, SM 9, SM 12, SM 16, SM 17, SM 22, SM 25, SM 28 and SM 29,
III	5	SM 1, SM 8, SM 15, SM 19 and SM 26
IV	1	SM 13
V	1	SM 11

Fig 3. Cluster diagram showing intra and inter cluster distances and clustering pattern



Yield per plant contributed maximum (73.59%) to the divergence among the genotypes and it was followed by borer infestation percentage (20.77%), fruits per plant (1.61).

The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that there is no parallelism between geographical diversity and genetic diversity.

4.2.7.2 Average intra and inter cluster distances

The average intra and inter cluster D^2 values were presented in Table 18 and Fig. 3. Intra-cluster D^2 values ranged from zero (both cluster IV and V) to 1678.024 (cluster III). Maximum intra cluster distance was observed in cluster III (1678.024), followed by cluster I (1022.500) and Cluster II (937.572).

While the inter-cluster D^2 values ranged from 2853.053 (cluster I and II) to 28745.500 (cluster II and V). The maximum inter cluster distance (28745.500) was observed between II and V clusters followed by clusters I and V (16893.301) and cluster II and III (13802.057). While, the minimum inter cluster distance of 2853.053 was recorded between cluster I and II, it is followed by, cluster I and IV (3180.130) and cluster III and V (4195.589) indicating that genotypes of these clusters had maximum number of gene complexes.

4.2.7.3 Cluster means of the characters

The clusters means for each of thirteen characters are presented in Table 19. From the data it can be seen that considerable differences existed for all the characters under study. Cluster V had high mean value for fruit yield per plant (2509.733), fruits per cluster (3.43), number of fruits per plant (43.80) and primary branches (3.53); cluster IV had high mean value for fruit length (14.180) and borer infestation (82.720) and also it took least days to flower (40.267) and to attain harvest (58.600); cluster III had high mean value for fruit girth (11.873), fruit weight (66.613) and plant height (90.800); cluster I recorded the lowest borer infestation percentage (32.532). The result indicates that selection of genotypes

Table 18. Average intra (bold) and inter cluster distances among five clusters formed by Tocher's method in brinjal (*Solanum melongena* L.) genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	1022.500	2853.053	6279.422	3180.130	16893.301
Cluster II		937.572	13802.057	5156.608	28745.500
Cluster III			1678.024	5534.010	4195.589
Cluster IV				0.000	12697.230
Cluster V					0.000

Table 19. Mean values of five clusters obtained by Tocher's method in brinjal (*Solanum melongena* L.) genotypes

Cluster No.	Calyx Length (cm)	Days to First Flowering	Days to First harvest	Fruit Girth (cm)	Fruit Length (cm)	Fruit Weight (g)	Fruits/ Cluster	Fruits/ Plant	Plant Height (cm)	Primary Branches	Yield/ Plant (g)	100 Seed Weight (g)	Borer Infestation %
Cluster I	2.040	45.778	67.484	11.313	7.659	54.436	1.878	20.098	79.840	2.987	1155.787	0.245	32.532
Cluster II	2.228	46.700	70.173	11.665	7.956	54.127	1.547	12.753	89.460	2.927	710.707	0.236	45.281
Cluster III	2.251	44.440	66.680	11.873	9.592	66.613	2.765	27.920	90.800	3.347	1971.453	0.227	48.533
Cluster IV	2.473	40.267	58.600	8.233	14.180	48.000	2.967	26.267	89.133	3.533	1300.733	0.327	82.720
Cluster V	1.807	41.733	59.600	7.960	13.813	56.000	3.433	43.800	79.000	3.533	2509.733	0.330	63.900

having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

Discussion

5. DISCUSSION

The present investigation was conducted at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani to identify suitable genotypes of brinjal resistant to phomopsis blight caused by *Phomopsis vexans* through artificial screening in pot culture and also to study the variability, character association and genetic divergence among the 32 genotypes under field evaluation.

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

1. Screening of brinjal genotypes for yield and phomopsis blight resistance in pot culture.
2. Evaluation of genotypes for genetic variability, yield and tolerance to major pests and diseases under field conditions

The experimental results are discussed under different headings

5.1 Mean performances

In any statistical analysis of data *per se* performance is the true realized mean of the recorded data and this is a direct estimate based on the observation and not on assumption. Selection of superior genotypes based on *per se* performance is more reliable data than any other parameter. The success of crop improvement lies in the selection of suitable parents. While evaluating the genotypes, the high mean value is considered as the acceptable procedure for a long time among the breeders.

In this experiment, there were significant differences among the 32 genotypes of brinjal for all the characters studied.

5.1.1 Growth attributes

The genetic improvement of any crop depends upon the available genetic variability for quantitative traits and its judicious exploitation through efficient breeding methods. Growth characters like plant height, number of primary branches, calyx length, days to first flower and days to first harvest will also contribute to yield indirectly. Therefore these characters are also studied in the present experiment.

There was remarkable difference among the genotypes for days to first flower with a range of 38.73 to 60.33. The number of primary branches also showed a considerable amount of variation among the genotypes ranging between 2.27 and 3.93. Calyx length is another character which shown a considerable variation. It ranged between 1.35 cm and 2.98 cm. Such variances for these characters were in accordance with the earlier reports of Ansari *et al.* (2011), Roychowdhury *et al.* (2011) and Patel *et al.* (2004).

The number of primary branches showed an impressive variation among the genotypes. It ranged between 2.27 to 3.97 cm. Variability for this trait was supported by the earlier reports of Kumar *et al.* (2011), Patel *et al.* (2004) and Ansari *et al.* (2011). Number of days to flower exhibited a wide variation ranging from 38.73 to 60.33 days. Similar variability for number of days to first flower was reported by Ansari *et al.* (2011), Islam and Uddin (2009) and Patel *et al.* (2004).

For the days to first harvest, latest genotype took 79.89 days and earliest genotype took 58.60 days. Difference in days to first harvest was supported by the earlier reports of Shekar *et al.* (2012), Ansari *et al.* (2011) and Roychowdhury *et al.* (2011).

5.1.2 Yield attributes

Notable variation for fruit length and fruit girth was observed among the genotypes. It ranged from 4.93- 15.95 cm and 7.96- 14.81 cm respectively. These

results were in agreement with the findings of Karak *et al.* (2012), Ansari *et al.* (2011), Islam and Uddin (2009) and Patel *et al.* (2004).

Conspicuous variation was noticed for fruit weight. It ranged between 36.5 g to 72.93 g. Shekar *et al.* (2012), Roychowdhury *et al.* (2011), Ansari *et al.* (2011) and Islam and Uddin (2009) also reported wide variation for fruit weight.

Considerable difference was observed among the genotypes for the number of fruits per cluster which ranged between 1.1 to 3.43. Similar difference for number of fruits per cluster was reported by Ansari *et al.* (2011) and Kumar *et al.* (2011). Wide variation was noticed for fruits per cluster and yield per plant in the present investigation *ie.*, 8 to 27 and 821 to 1347 g respectively. Such wide variability for these characters was in corroboration with earlier reports of Shekar *et al.* (2012), Roychowdhury *et al.* (2011) and Islam and Uddin (2009)

5.2 Variability studies

The nature and amount of genetic variability available in the germplasm indicates the scope of improvement of the character by exploiting the genetic variability.

In the present investigation, for all the characters, magnitude of GCV and PCV were closer, suggesting greater contribution of genotype rather than environment. Roychowdhury *et al.* (2011) also reported close values of GCV and PCV which reinforces the present study results. So the selection can be very well based on the phenotypic values.

The PCV was higher than the corresponding GCV for all the traits which might be due to the interaction of the genotypes with the environment to some degree or other denoting environmental factors influencing the expression of these characters.

High PCV and corresponding GCV estimates were recorded for yield per plant, borer infestation percentage, fruits per plant, fruits per cluster, fruit length, seed weight and calyx length indicating the presence of high variability in the

germplasm for selection. Even the differences between PCV and GCV values were minimum, indicating that the traits under study were less influenced by environment. Hence, these characters can be relied upon and simple selection can be practised for further improvement. Similar reports were reported for yield per plant by Kumar *et al.* (2012), Karak *et al.* (2012), Muniappan *et al.* (2010) and Kumar *et al.* (2011); for fruits per plant reported by Kumar *et al.* (2012), Muniappan *et al.* (2010) and Kumar *et al.* (2011); for fruits per cluster by Chourasia and Shree, 2012, Ansari *et al.* (2011) and pate *et al.* (2004); for fruit length by Karak *et al.* (2012), Muniappan *et al.* (2010), Islam and Uddin (2009) and Patel *et al.* (2004).

Moderate PCV and GCV values were registered for plant height, fruit weight, fruit girth, number of primary branches, days to first flowering and days to first harvest. These findings were in accordance with the reports of Karak *et al.* (2012) and Kumar *et al.* (2011) for plant height; Danquah and Orfori (2012) for fruit weight; Kumar *et al.* (2012) and Danquah and Orfori (2012) for fruit girth; Patel *et al.* (2004) and Karak *et al.* (2012) for primary branches; Ansari *et al.* (2011), Kumar *et al.* (2011) and Islam and Uddin (2009) for days to first flower and days to first harvest.

5.3 Heritability and genetic advance

Heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

. With the help of GCV alone, it is not possible to determine the amount of variation that is heritable. The GCV together with heritability estimates would give reliable indication of the expected progress in a selection programme.

In the present investigation, high heritability estimates were obtained for all the thirteen characters studied. High heritability values were also reported for days to first flower, fruit girth, fruit length and fruit weight by Ansari *et al.*

(2011), Kumar *et al.* (2011), Karak *et al.* (2012) and Patel *et al.* (2004). Patel *et al.* (2004) reported high heritability for fruits per cluster but Kumar *et al.* (2011) reported moderate heritability.

However, in contradiction to the present results Islam and Uddin (2009) reported low heritability for days to first flower.

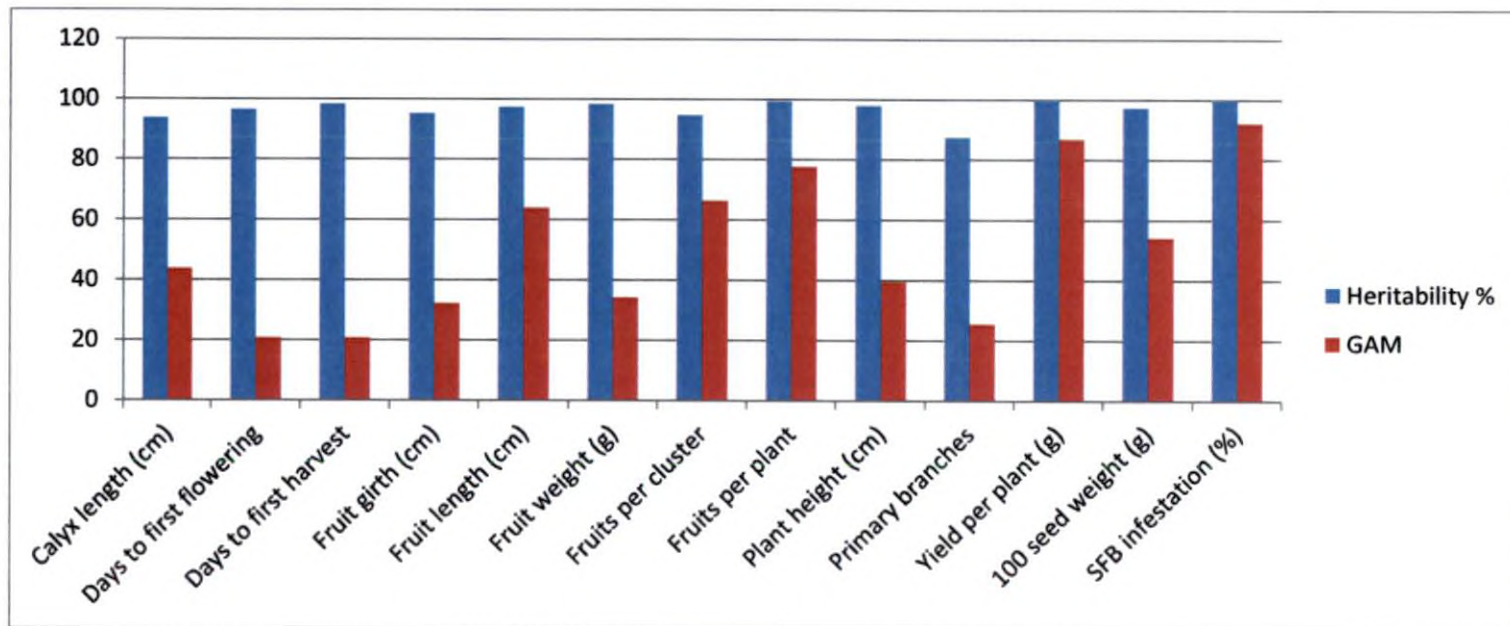
High heritability estimates for fruits per plant, plant height and primary branches in the present investigation were in confirmatory with the earlier reports of Karak *et al.* (2012), Kumar *et al.* (2011), Islam and Uddin (2009), Mohanty (1999) and Ansari *et al.* (2011).

High heritability value for yield per plant by Patel *et al.* (2004), Negi *et al.* (2000) and Karak *et al.* (2012) are in accordance with the present results. However, Ansari *et al.* (2011) and Kumar *et al.* (2011) found low heritable estimates for yield per plant and primary branches respectively which are contrary to the present investigation results. The high estimates of heritability for the aforesaid characters suggested that selection based on phenotypic performance would be more effective.

However, heritability values alone may not provide clear predictability of the breeding value. Heritability in conjugation with genetic advance over mean (GAM) is more effective and reliable in predicting the effectiveness of selection.

In the present experiment, all the characters studied had registered high heritability coupled with high genetic advance as percentage of mean (Fig. 4). Revelation of high heritability and high genetic advance together may be ascribed to the conditioning of the characters by additive effect of the polygenes which could be improved upon by adopting selection without progeny testing. High genetic advance is also reported by Ansari *et al.* (2011), Kafyullah *et al.* (2011), Mishra *et al.* (2008), Kamani and Monpara (2007), Singh and Kumar (2005) and Kumar *et al.* (2011) for fruit girth, fruit length, fruit weight, yield per plant and fruits per cluster. Kumar *et al.* (2011) and (Muniappan *et al.*, 2010) reported low genetic advance for fruit girth and fruit length in contrary to the present results.

Fig 4. Heritability and Genetic advance as percentage of mean (GAM) for 13 characters in brinjal genotypes



Karak *et al.* (2012) reported high genetic advance for plant height and number of primary branches in support to the present results. Conversely, Islam and Uddin (2009) reported low genetic advance for plant height.

Antagonistic to the present results, Kumar *et al.* (2012) and Islam and Uddin (2009) reported low genetic advance for yield per plant and days to first flowering.

5.4 Correlation studies

Yield is a complex character; its direct improvement is difficult. Knowledge of correlation studies help plant breeder to ascertain the real components of yield and provide an effective basis for selection. The characters contributing significantly to yield can be identified and could be used as an alternate selection criterion in yield improvement programme. Ahmed *et al.* (2013) opined that a crop breeding programme, aimed at increasing the plant productivity requires consideration of not only yield but also of its components that have a direct or indirect bearing on yield. The genotypic correlation between characters provides a reliable measure of genotypic association between characters and helps to differentiate the vital associations useful in breeding from non-vital ones (Falconer, 1981).

The findings in this experiment clearly indicated that genotypic correlations were of higher magnitude to the corresponding phenotypic ones, thereby establishing strong inherent relationship among the characters studied. It is in confirmatory with the findings of Ahmed *et al.* (2013).

In the present investigation, yield per plant exhibited significant positive correlation with number of fruits per plant, fruits per cluster, fruit length, fruit weight and number of primary branches both at phenotypic and genotypic levels. It exhibited significant negative correlation with days to first harvest only at genotypic level.

The positive genotypic association of yield per plant with number of fruits per plant is in accordance with the results reported by Praneetha *et al.* (2011), Dahatonde *et al.* (2010), Muniappan *et al.* (2010), Nalini *et al.* (2009), Bansal and Mehta (2008) and Mohanty (1999).

Kafytullah *et al.* (2011), Nalini *et al.* (2009) and Lohakare *et al.* (2008) also reported positive association of yield per plant with fruits per plant which supports the present investigation's results.

In support to the positive genotypic correlation of fruit length with yield per plant, Danquah and Orofi (2012), Kafytullah *et al.* (2011) and Sinha (1983) reported similar association.

In corroboration with the present investigation's positive genotypic correlation of yield per plant with fruit weight, Praneetha *et al.* (2011), Dahatonde *et al.* (2010), Muniappan *et al.* (2010), Nalini *et al.* (2009), Islam and Uddin (2009) and Naliyadhara *et al.* (2007) reported similar findings.

The positive association of yield per plant with number of primary branches was reinforced by the earlier reports of Praneetha *et al.* (2011), Muniappan *et al.* (2010), Nalini *et al.* (2009) and Bansal and Mehta (2008).

Days to first harvest has negative association with yield per plant which was supported by the earlier findings of Thangamni and Jansirani (2012). Nalini *et al.* (2009) also obtained weak negative association of days to first flowering with fruits per plant; it is in line with the present findings.

5.5 Path analysis

The correlation coefficient indicates the degree of relationship between characters but it alone does not give clear picture of measure of association between yield and its components. It is most important to know the direct and indirect influences of yield components for selecting suitable genotypes for improving the yield. Selection for yield is more effective when it is based on component characters which are highly heritable and positively correlated. When

more number of variables are considered in correlation the association becomes more complex and less obvious. The path analysis is useful under such circumstances. This gives a clear picture of the direct and indirect effects of various traits on yield. Therefore, present investigation, path analysis was carried out to generate such information of direct and indirect effects on yield by its components.

In the present study, fruit girth, fruit weight, fruits per cluster and fruits per plant exhibited positive direct effects on yield per plant. Days to first flower and fruit length showed negative effects but not significant.

High direct effect of fruits per plant on yield per plant was recorded which was supported by the earlier reports of Muniappan *et al.* (2010), Dahatonde *et al.* (2010), Bansal and Mehta (2008) and Mohanty (2009).

Fruit weight revealed high direct effect on yield. This was in accordance with the findings of Muniappan *et al.* (2010), Dahatonde *et al.* (2010), Bansal and Mehta (2008), Naliyadhara *et al.* (2007) and Lokahare *et al.* (2008).

Even though fruits per cluster found to have negligible positive direct effects on yield, it has appreciable indirect effect through fruits per plant. Similar indirect effect by fruits per cluster was also reported by Nalini *et al.* (2009).

Negative direct effect of days to first flowering was reinforced by the earlier findings of Nalini *et al.* (2009).

Studies of Shekar *et al.* (2013) are in corroboration with the negligible direct effects of calyx length, 100 seed weight, fruit girth as in the present findings.

Therefore, fruits per plant, fruit weight, fruits per cluster and fruit girth can be identified as major characters contributing towards yield directly and indirectly and selection based on these characters are effective in developing high yielding brinjal varieties.

5.6 Selection index

Discriminant function analysis developed by Fisher (1936) gives information on the proportionate weightage to be given to a yield component. Thus, selection index was formulated to increase the efficiency of selection by taking into account the important characters contributing to yield.

Plant height, number of primary branches, days to first flower, days to first harvest, fruit length, fruit girth, fruit weight, fruits per plant, fruits per cluster, calyx length, fruit and shoot borer infestation percentage, 100 seed weight and together with yield per plant used for constructing selection index.

Based on the selection index values, top ranking accessions namely *SM* 11 (8648.269), *SM* 19 (7796.68), *SM* 15 (7735.726), *SM* 1 (6874.852), *SM* 8 (6637.749), *SM* 26 (6124.202), *SM* 24 (5544.573), *SM* 23(5382.518), *SM* 13(5028.862) and *SM* 4 (4972.541) were identified as superior ones in terms of yield.

5.7 Divergence analysis

The multivariate analysis using Mahalanobis D^2 statistics is a valuable tool for obtaining quantitative estimates of divergence between biological populations. For an effective breeding program, information concerning the extent and nature of genetic diversity within a crop species is essential. It is particularly useful for characterizing individual accessions and cultivars and as a general guide in the selection of the parents for hybridization. Selection of parents based on individual attributes may not be as advantageous as the one based on a number of important traits collectively. In any breeding programme inclusion of such genetically diverse parents is essential to generate new variability and desirable recombinants. Therefore, in the present study information on genetic diversity present in the thirty two genotypes of brinjal was generated.

Thirty two genotypes were grouped into five clusters. Out of the five clusters, cluster I was the largest one comprising of fifteen genotypes followed by Cluster II with ten genotypes, cluster III with five genotypes, cluster IV and V with one genotype each, indicating high degree of heterogeneity among the genotypes. The grouping pattern of genotypes was observed to be random indicating that geographical diversity and genetic divergence were unrelated as reported by Golani *et al.* (2007) and Roosevelt and Shanthi (2009). Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographical diversity.

Maximum contribution towards genetic divergence was noticed for fruit yield per plant. This finding is reinforced by earlier reports of Kumar *et al.* (2007), Bansal and Mehta (2007) and Roosevelt and Shanthi (2009). These result suggested that crossing of the genotypes having high mean yield and high inter cluster distance may lead to greater heterotic expression and broad spectrum of favourable genetic variability in segregating generations for improvement of fruit yield in brinjal.

Maximum intra cluster distance was observed in cluster III followed by cluster I indicating that some divergence still existed among the genotypes. The maximum inter cluster distance was observed between II and V clusters suggesting that the crosses involving varieties from these clusters would give desirable recombination as reported by Kumar *et al.* (2007). Minimum inter cluster distance was recorded between clusters I and II indicating close relationship among the genotypes included in these clusters. Similar findings were reported by Golani *et al.* (2007).

Cluster V had high mean value for fruit yield per plant, fruits per cluster, number of fruits per plant and primary branches; cluster IV had high mean value for fruit length and also it took least days to flower and to attain harvest; cluster III had high mean value for fruit girth, fruit weight and plant height; cluster I recorded the lowest borer infestation. The results indicated that selection of

genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character (Bansal and Mehta, 2007).

5.8 Germplasm evaluation for phomopsis blight resistance

Eggplant suffers from many diseases caused by fungi, bacteria, virus, nematode and mycoplasma. Of them Phomopsis fruit rot of eggplant caused by the fungus *Phomopsis vexans* (Sacc. and Syd) Harter is a serious disease which attacks all above ground parts of the plant (Islam *et al.*, 2010). Therefore, the present experiment has been conducted to artificially screen brinjal genotypes resistant to fruit rot caused by the pathogen.

In the present study, out of thirty two genotypes screened against phomopsis blight based on the percentage disease index, no genotype was categorised to be resistant to the disease. Similar findings were reported by Patil *et al.* (2002). Disease severity among the genotypes ranged from moderately resistant to highly susceptible as reported by Akhtar (2006). *SM 9*, *SM 23* and *SM 25* were moderately resistant to the disease. Of which *SM 9* and *SM 25* were poor yielders, but *SM 23* was relatively good yielder, therefore it can be used in hybridization programme with suitable parents to develop cultivars with high yield and resistance to the disease.

5.9 Germplasm evaluation for fruit and shoot borer resistance

Several biotic and abiotic factors contribute to losses in the production of brinjal. Among the biotic stress factors that hamper the production of brinjal, the shoot and fruit borer (*Leucinodes orbonalis* Guen.) is the most serious one, which occurs throughout the year at all the stages of crop growth.

Screening experiments by various workers have indicated highly differential response of brinjal germplasm to the attack of this pest (Darekar *et al.*, 1991; Gangopadhyay *et al.*, 1996; Singh and Kalda, 1997; Doshi *et al.*, 2002; Hossain *et al.*, 2002 and Jat *et al.*, 2003). In the present investigation also, the

accessions showed significant variation for the incidence of fruit and shoot borer. It ranged from 12.87 to 82.72 per cent and 15.50 to 80.81 per cent for plant and fruit infestation respectively. Accessions *SM 25*, *SM 27*, *SM 26*, *SM 30*, *SM 31* and *SM 32* showed moderate resistance to fruit borer. These accessions could be very well utilized in the intervarietal crossing programme in brinjal for combining high yield and borer resistance.

Summary

6. SUMMARY

The present study entitled “Genetic evaluation for yield and resistance to phomopsis blight in brinjal (*Solanum melongena* L.)” was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during the period 2012-13. Thirty two brinjal genotypes were collected from different sources across the country. The study was carried out in two experiments i.e., pot culture experiment and field experiment.

The pot culture experiment was aimed at artificial screening of accessions for resistance to phomopsis blight caused by *Phomopsis vexans*. Observations on biometric characters like days to first flowering, days to first harvest, fruit length, fruit girth, fruit weight, calyx length, fruits per cluster, fruits per plant, plant height, and yield per plant were also collected.

Analysis of variance revealed significant difference among the accessions for all the characters studied. *SM* 15 (2095.50 g) recorded the highest yield per plant and *SM* 11 (33) recorded the highest fruits per plant. Fruit weight was highest in *SM* 19 (76.20 g) whereas it was recorded lowest in *SM* 31 (39.67 g).

Screening for phomopsis blight disease through artificial inoculation revealed that remarkable variation existed in the germplasm for the disease damage percentage. Out of 32 genotypes screened against phomopsis blight based on the percentage disease index, none was found to be resistant to the disease. *SM* 9 (12.22), *SM* 23 (16.67) and *SM* 25 (12.22) were moderately resistant to the disease.

In field experiment, the brinjal accessions were subjected to detailed evaluation for genetic variability, yield and tolerance to shoot and fruit borer under field conditions.

The analysis of variance revealed that significant variation among all the characters studied. *SM* 11 recorded highest yield per plant (2509.73 g) while *SM* 9

recorded the lowest yield (599.13 g). *SM 11* (43.8) recorded highest fruits per plant while *SM 25* was the lowest (9.47). The highest fruit weight was recorded in *SM 26* (72.93 g) and the lowest was recorded in *SM 6* (35.6 g). The longest fruits were produced by *SM 19* (14.95 cm) whereas *SM 30* (4.93 cm) had the smallest fruits.

The fruit infestation percentage by shoot and fruit borer ranged from 15.50 to 80.81. Accessions *SM 25*, *SM 27*, *SM 26*, *SM 30*, *SM 31* and *SM 32* showed moderate resistance and no genotype was completely resistant to the pest.

High PCV and their corresponding GCV estimates were recorded for yield per plant, borer infestation percentage, fruits per plant, fruits per cluster, fruit length, seed weight and calyx length. Moderate PCV and GCV values were registered for plant height, fruit weight, fruit girth, number of primary branches, days to first flowering and days to first harvest.

In the present experiment, all the characters studied had registered high heritability coupled with high genetic advance as percent of mean.

Correlation studies shown that yield per plant exhibited significant positive correlation with number of fruits per plant, fruits per cluster, fruit length, fruit weight and number of primary branches both at phenotypic and genotypic levels. It exhibited significant negative correlation with days to first harvest only at genotypic level.

Path analysis revealed that fruit girth, fruit weight, fruits per cluster and fruits per plant exhibited positive direct effects on yield per plant while, days to first flower and fruit length showed negative effects but not significant.

Based on the selection indices worked out for the thirty two genotypes, the top five are *SM 11*, *SM 19*, *SM 15*, *SM 1* and *SM 8* in order.

Genetic divergence analysis was carried out using Mahalanobis' D^2 statistic and the 32 accessions were grouped into five clusters. Out of the five clusters, cluster I was the largest one comprising of fifteen genotypes. Maximum

contribution towards genetic divergence was noticed for fruit yield per plant. Maximum intra cluster distance was observed in cluster III followed by cluster I. The maximum inter cluster distance was witnessed between II and V clusters and minimum inter cluster distance was recorded between clusters I and II. Cluster V had high mean value for fruit yield per plant, fruits per cluster, number of fruits per plant and primary branches.

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**GENETIC EVALUATION FOR YIELD AND RESISTANCE TO PHOMOPSIS
BLIGHT IN BRINJAL (*Solanum melongena* L.)**

By
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ABSTRACT

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ABSTRACT

The present study entitled "Genetic evaluation for yield and resistance to phomopsis blight in brinjal (*Solanum melongena* L.)" was conducted at College of Agriculture, Vellayani with 32 brinjal genotypes collected from various parts of India to identify suitable genotypes of brinjal resistant to phomopsis blight caused by *Phomopsis vexans* through pot culture screening and yield evaluation in field.

Out of 32 genotypes artificially screened against phomopsis blight, based on the percentage disease index, none was found to be resistant to the disease. *SM* 9 (12.22), *SM* 23 (16.67) and *SM* 25 (12.22) were moderately resistant to the disease. But in field conditions, both *SM* 9 (599.13g) and *SM* 25 (607.93g) were poor yielders, while *SM* 23 (1416.20g) was relatively mediocre.

The field experiment was conducted in RBD and the genotypes differed significantly for all the characters studied. *SM* 11(2509.73g) was the highest yielder and also it recorded maximum number of fruits per plant (43.8). Longest fruits were produced by *SM* 19 (14.95 cm) while the heaviest fruits by *SM* 26 (72.93 g) which was on par with *SM* 19 (71.13 g). *SM* 25, *SM* 27 and *SM* 30 were moderately resistant to borer infestation. No incidence of phomopsis blight was noticed in the field.

High estimates of heritability coupled with high genetic advance as percentage of mean was observed for all the characters studied.

Yield per plant showed significant positive correlation with number of fruits per plant, fruits per cluster, fruit length, fruit weight and primary branches both at phenotypic and genotypic levels. Path analysis revealed that fruits per plant and fruit weight are the major contributors to the yield. It also indicated that both fruit length and fruits per cluster had appreciable indirect effects through fruits per plant on yield.

Mahalanobis' D^2 statistics was employed to study genetic divergence among 32 genotypes and were grouped into five clusters on the basis of relative magnitude of D^2 values using Tocher's method. Cluster I accommodated maximum number of

genotypes and in sequence clusters were having 15, 10, 5, 1 and 1 genotypes respectively. The maximum inter-cluster distance was observed between II and V. It has been observed that there was no close correspondence between geographical distribution and genetic divergence.

SM 26 ranked 6th based on selection index with considerable yield and also was tolerant to borer infestation in the field and only moderately susceptible to phomopsis blight in the pot culture.

SM 11 was the highest yielder in field, but it was susceptible to phomopsis blight in pots. On the other hand, *SM 25* was moderately resistant to phomopsis blight in pot but was a poor yielder in field. Therefore, *SM 11* and *SM 25* along with *SM 26* can be used in hybridization programme to obtain better cultivars with high yield, tolerance to phomopsis blight and borer infestation.