GENETIC ANALYSIS OF RESISTANCE TO POD BORERS AND YIELD IN YARD LONG BEAN (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)

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DECLARATION

I hereby declare that this thesis entitled "**Genetic analysis of resistance to pod borers and yield in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)**" 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 of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

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CERTIFICATE

Certified that this thesis entitled "**Genetic analysis of resistance to pod borers and yield in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)"** is a record of research work done independently by Mr. Jithesh, V.G. (2005-21-111) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to him.

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Ever Loving Memory of My Grand Parents
(P.N. Gowri & K.R. Damodaran)

dedicated
to

my Amma (P.D. Vasundharamma)

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INTRODUCTION

1. INTRODUCTION

Cowpea, a common leguminous vegetable is a rich and inexpensive source of vegetable protein. It is a key dietary staple for the poorest sector of many developing countries. Besides being an important food legume this is an important crop which has the unique ability to fix nitrogen even in poor soils. Because of its quick growth habit it has become an essential component of sustainable agriculture in marginal lands of the tropics.

Verdcourt (1970) identified five subspecies of *Vigna unguiculata*. The two wild forms, *Vigna unguiculata* subsp. *dekindtiana* and *V. unguiculata* subsp. *mensensis* are found in Africa and Ethiopia, while *V. unguiculata* subsp. *unguiculata* is the most common species found in all areas of cultivation. *Vigna unguiculata* subsp. *cylindrica* and *V.unguiculata* subsp. *sesquipedalis* which are common to India and the Far East were introduced from Africa. Africa is considered as the primary centre of origin (Peter, 1998).

The chromosome number of subsp. *unguiculata* was noticed as 2n = 22 and that of subsp. *sesquipedalis* as 2n = 24 and F_1 hybrid, 2n = 23. Length of meiotic and somatic metaphase chromosomes were more in subsp. *sesquipedalis*, lowest in subsp. *unguiculata* and intermediate in their F_1 hybrid.

Yard long bean is considered to be one of the most important vegetable crop in parts of Indonesia, Thailand, Philippine, Taiwan and China. The crop is grown through out India. It is an important tropical Indian pulse and vegetable crop covering an area of about 7.7 million ha. The productivity of this crop is low ($3qha^{-1}$) which needs improvement through systematic breeding programmes (Yadav et al., 2004). The yard long bean is a nutritious vegetable, which supplies protein (3.5 g), calcium (72.0 mg), phosphorus (59 mg), iron (2.5 mg), carotene (564 mg), thiamine (0.07 mg), riboflavin (0.09 mg) and vitamin C (24 mg) per

100 g of edible pods. This crop meets greater demand of the vegetable especially in South India. Among the South Indian states, Kerala has the most extensive cultivation. The traditional vernaculars *viz.*, 'Achingapayar', 'Kuruthola payar', 'Vanpayar', 'Pathinettumanian' etc. used to refer vegetable cowpea / yard long bean indicates that Kerala is the land of vegetable cowpea. Perhaps cowpea is the only vegetable evently distributed and preferred in all the 14 districts of Kerala. This has aggravated pest and disease problems.

The productivity of cowpea is limited by a complexity of biotic and abiotic interactions. Incidence of pests and diseases is considered to be a major limiting factor affecting the production of yard long bean. The growing demand for the vegetable has led to large scale intensive cultivation in the areas of cultivation. This in turn, resulted in enhanced incidence of pests and diseases on cowpea inflicting heavy crop loss.

Pod borers *Maruca vitrata* (Fab.) and *Lampides boeticus* (Linn.), are the most important pest of yard long bean which appears in the post flowering phase. These two borers constitute 99.9 per cent of all known cowpea borers in China (Qinghuai et al., 2003). The pod damage due to *M. vitrata* ranged from 13 to 31 per cent, the seed damage was about 16 per cent and the total yield loss was between 33-53 per cent (Karel, 1985). In high rainfall areas the crop loss due to the pest even goes up to 80 per cent (IITA, 1998).

Genetic resistance in plants is one of the most effective and economic means of controlling pests in an eco-friendly way. Resistant plants are the first line defence against pests. A successful breeding programmes for pest resistance depends upon the sound knowledge of genetics of resistance. Breeding for resistance has been very successful in reducing damage caused by many pests (Maxwell and Jennings, 1980), whereas the use of chemicals can create hazards to human health and produce undesirable side effects on non-target insects, animals and plants. Hence it is desirable to develop genotypes resistant to pod borers in order to enhance production and productivity of vegetable cowpea.

Host plant resistance refers to the heritable qualities of a cultivar to counteract the activities of the pest so as to cause minimum per cent reduction in yield as compared to the other cultivars of the same species under similar conditions (Dhaliwal et al., 1993). Development of crop varieties resistant to infestation by the pest suits better and forms a principal component in Integrated Pest Management (IPM) systems (Dent, 1995).

Farmers usually adopt frequent sprays of chemical insecticides for controlling the population of pod borer in the field. Even crop varieties with moderate levels of resistance or partial resistance to the concerned pest can substantially reduce the use of insecticides for pest control. Such varieties suffer lesser damage than susceptible varieties, since they reduce the viability of the pest and enhance the activity of natural enemies. Low levels of pesticide residues should be ensured in the harvested produce in a crop like cowpea to increase the suitability of consumption and to meet the marketing specification.

In this context, it is high time to evaluate the available land races and cultivars of vegetable cowpea in Kerala. Taking into consideration of all these aspects, the present study was undertaken with the following objectives.

- To study the genetic basis and inheritance pattern of important qualitative and quantitative characters for resistance to pod borers and yield.
- To formulate an appropriate breeding programme for developing high yielding pod borers resistant / tolerant varieties of yard long bean.
- To estimate the additive, dominance and epistatic gene action involved in the inheritance of yield and related characters through generation mean analysis.
- To estimate the heterosis for fifteen hybrids obtained by crossing high yielding lines and low plant resistant index testers in line x tester manner.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

Brief reviews of aspects related to genetic variability, genetic parameters, correlation and path coefficient analysis, genetic diversity, selection index, resistance to pod borers, combing ability, gene action and heterosis are included in this chapter.

2.1 VARIABILITY STUDIES

Wide range of genetic variability is a prerequisite for the identification of superior genotypes from the array of diverse genotypes in the population (Allard, 1960). The breeding procedure and efficiency of selection ultimately depends on the variability available in the germplasm (Zelleke, 2000).

An F_2 population of cowpea exhibited significant range of variation for number of pods per plant, 100 seed weight and seed yield per plant (Gowda et al., 1991). Considerable variation for several yield related characters in cowpea was reported by Kumar and Sangwan (2000).

Rejatha (1992) reported high variability among different genotypes of cowpea for days to flowering, number of pods per cluster, pod length and number of seeds per pod. Significant variability was noticed among different cowpea cultivars for days to flowering, plant height, number of pods per plant, number of seeds per pod, pod length, 100 seed weight and yield per plant (Sudhakumari, 1993).

Wide range of genetic variability was reported for protein content in cowpea by Aghora et al., 1994; De et al., 2001; Kalaiyarasi and Palanisamy, 2001. Sobha (1994) noticed broad spectrum genetic variability for pod length and seed yield per plant in cowpea.

High variation for number of clusters per plant, number of pods per plant and 100 seed weight in cowpea was reported by Backiyarani and Nadarajan (1996). Hazra et al. (1996) observed wide range of genetic variability for plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and yield per plant.

Mehta and Zaveri (1998) noticed high magnitude for genetic variability in segregating generations of cowpea for number of branches, number of clusters, number of pods and seed yield. Resmi (1998) reported high range of variability for all important yield traits among different cultivars of cowpea. Significant variability was noticed for days to 50 per cent flowering, plant height, number of branches per plant, pod length, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant by Sobha and Vahab (1998b).

Harshavardhan and Savithramma (1998b) noted significant variation in 102 accessions of vegetable cowpea genotypes for all characters studied except for dry pod yield.

Wide range of genetic variability for number of pod clusters per plant, number of pods per cluster, peduncle length, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant was observed in cowpea by Dwivedi et al. (1999).

Significant variability among 32 genotypes of cowpea was reported by Backiyarani et al., (2000) for days to 50 per cent flowering, plant height, yield per plant and total chlorophyll content. Panicker (2000) observed high variability for days to flowering, number of inflorescence per plant, number of pods per inflorescence, number of pods per plant, pod length and peduncle length. Wide range of variation for plant height was reported by Anbuselvam et al., (2000); Rangaiah and Mahadevu (2000) and Singh and Verma (2002). Tyagi et al. (2000) reported days to 50 per cent flowering, plant height, pod length, number of pods

per plant, 100 seed weight and seed yield per plant recorded high genetic variability. High variability was noticed among 50 cultivars of cowpea for days to flowering, number of pods per plant, number of inflorescence per plant, number of pods per inflorescence, plant height, pod length, number of branches per plant and number of seeds per pod (Vidya, 2000).

Ajith (2001) reported that the characters, days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod and yield per plant exhibited high range of variability. High range of genetic variability was recorded for days to 50 per cent flowering, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and yield per plant in 50 genotypes of cowpea (Anbuselvam et al., 2001).

Significant variation was observed by Chattopadhyay et al. (2001) for grain yield per plant, number of pods per plant and pod length in cowpea. Jyothi (2001) noticed broad spectrum of variability for number of branches per plant, plant height, number of inflorescence per plant, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant in cowpea. Significant variation in plant height was observed by Purushotham et al. (2001) in cowpea.

Arunachalam et al. (2002) reported high variability for several yield contributing characters in cowpea. Significant genetic variability for days to flowering, number of pods per plant and seed yield per plant in gamma ray induced mutants of Charodi 1 was observed by Henry (2002). Grain yield per plant exhibited wide range of variability in cowpea (Yadava et al., 2002).

In cowpea, Kavita et al. (2003) reported high range of genetic variability for days to 50 per cent flowering. A wide range of variation was observed in almost all the characters studied in a set of 740 germplasm accessions of cowpea including both indigenous and exotic origin when evaluated for 25 descriptors (Mishra et al., 2003).

All the ten yield related characters viz; days to 50 per cent flowering, pods per plant, inflorescence per plant, pods per inflorescence, plant height, primary branches, pod length, seeds per pod, grain yield per plant and 100 seed weight exhibited wide range of variation among the 50 genotypes of cowpea studied by Philip (2004). High genetic variability was observed for pods per cluster, yield per plant, pod weight, pods per plant and clusters per plant in yard long bean by Lovely (2005).

Thirteen parents involving nine lines and four testers of two subspecies of the cultigen cowpea viz; unguiculata and sesquipedalis and their respective hybrids generated through L x T fashion were evaluated for their per se performance for 16 characters. The maximum seed yield and vegetable yield per plant was recorded by crosses L_4 x T_2 (GP 1024/Lola) and L_9 x T_4 (GP 1231/VS 33) respectively. The crosses involving accessions GP 1238, 743 and 1126 with lola, Vaijayanthi and VS 33 showed superior performance for vegetable and seed yield per plant, clusters per plant, earliness, pod length, crude fibre and crude protein content (Valarmathi and Surendran, 2007).

2.2 GENETIC PARAMETERS

Selection acts on genetic differences and the benefits from selection for a given character depends largely on the heritability of the character (Allard, 1960). Genetic component of variation along with heritability would provide a precise insight into the amount of genetic gain expected to achieve through selection (Burton, 1952). Variability available in a population could be partitioned into heritable and non heritable components with the aid of genetic parameters such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability and Genetic Advance (GA), which serves as a basis for selection (Johnson et al., 1955). In crop improvement only the genetic component is transmitted to the next generation. The extent of improvement further depends upon the intensity of selection and genetic advance obtained from the population. High heritability is not always an indication of high genetic advance.

In the case of pod characters, Roquib and Patnaik (1990) reported high heritability and genetic advance for pod length, while Panicker (2000) recorded low genetic advance. Siddique and Gupta (1991) observed high GCV, PCV and heritability for number of pods per plant.

PCV and GCV were high for plant height, seed yield per plant, pods per plant and 100 seed weight in cowpea (Sawant, 1994). High heritability and high genetic advance were observed for plant height, seed yield per plant, pods per plant, 100 seed weight, branches per plant and pod length.

High genetic advance was recorded for number of pods per plant by Damarany (1994); high heritability by Arunachalam et al. (2002); high PCV, GCV and genetic advance by Ranganayaki and Rengasamy, (1992). High heritability, moderate genetic advance and moderate to high PCV and GCV were reported by Malarvizhi (2002). Moderate PCV, GCV, heritability and genetic advance were reported by Venkatesan et al. (2003).

In cowpea, Rewale et al. (1995) reported high estimates of heritability and genetic gain for 100 seed weight, plant height and harvest index. High values of GCV, PCV, heritability and genetic advance were obtained in cowpea for pod length and seeds per pod (Sreekumar et al., 1996) indicating additive gene action. The number of days to flowering and days to harvest had high heritability with low genetic advance indicating non-additive gene action.

Backiyarani and Nadarajan (1996) reported high GCV and PCV for pods per plant, clusters per plant and 100 seed weight in cowpea. Heritability and genetic advance estimates suggested the preponderance of additive gene effects for 100 seed weight, harvest index and single plant yield.

Genotypic coefficient of variation was maximum for pod length in cowpea followed by total seed weight and number of pods per plant and lowest for number of clusters per plant (Rangaiah, 1997). Heritability was high for pod length, total seed weight, plant height, 100 seed weight and pods per plant.

Number of clusters recorded the lowest heritability. High heritability associated with high genetic advance was recorded for pod length and total seed weight.

Ram and Singh (1997) observed high heritability estimates, for pod and peduncle length, green pod yield per plant, days to 50 per cent flowering, days to maturity, plant height, seeds per pod, branches per plant and 100 seed weight in cowpea. High heritability estimates combined with high genetic advance were noticed for pod length and green pod yield per plant. Umaharan et al. (1997) reported high heritability for pod weight.

A wide range of PCV was reported in genetic variability studies conducted in 31 genotypes of vegetable cowpea by Sobha and Vahab (1998b). High GCV was observed for pod weight and pod yield per plant. Heritability and genetic advance were high for pod weight and yield per plant.

Harshavardhan and Savithramma (1998a) recorded high PCV, GCV, heritability and genetic advance for green pod yield, pods per plant and plant height in cowpea. High heritability coupled with high genetic advance was reported by Resmi (1998) for pod yield per plant, pod weight and highest phenotypic coefficient of variation was observed for pod yield per plant.

In cowpea characters such as plant height, pod weight, pod length and pod yield per plant showed high PCV, high GCV, very high heritability and high genetic advance as a percentage of mean (Hazra et al., 1999). Rangaiah and Mahadevu (1999) reported narrow difference between PCV and GCV resulting in high heritability coupled with high genetic advance for number of seeds per plant in cowpea. In cowpea, plant height showed high genetic advance coupled with high heritability and GCV indicating a preponderance of additive gene effects for this trait (Sharma, 1999).

Panicker (2000) reported high heritability and genetic advance in cowpea for pods per plant, yield per plant, pod weight and length of peduncle PCV and

GCV were found to be maximum for pods per plant followed by yield of vegetable pods.

High heritability coupled with high genetic advance was observed for pods per inflorescence, yield per plant, pods per plant, pod weight and main stem length (Vidya, 2000) in cowpea. Yield per plant, pods per plant, pods per inflorescence, main stem length and pod weight recorded high PCV and GCV, it was low for days to first flowering.

In cowpea Ajith (2001) observed high heritability coupled with high genetic advance for main stem length, number of primary branches, pod weight, pod clusters per plant, pod length and seeds per pod. High phenotypic and genotypic coefficients of variation were seen for main stem length, number of primary branches and pod weight. Nehru and Manjunath (2001) obtained high heritability and high genetic advance for pods per plant and moderate for plant height, 100 seed weight and yield per plant in cowpea. The PCV was highest for pods per plant followed by cluster, primary branches and yield per plant. Jyothi (2001) reported high PCV, GCV, heritability and genetic advance for pods per plant, pods per cluster and yield per plant in cowpea.

Tyagi et al. (2000) observed high estimates of GCV, heritability and genetic advance in cowpea for days to 50 per cent flowering, plant height, seed yield per plant and days to maturity. GCV and PCV were moderate for plant height, pod length and seed yield per plant (Kalaiyarasi and Palanisamy, 2000b). Heritability values for all the traits were high. High heritability and genetic gain were observed for plant height, branches per plant, pod length and seed yield per plant.

In cowpea, Rangaiah (2000) observed high phenotypic and genotypic coefficients of variation for number of clusters per plant, number of pods per plant, pod weight and total seed weight. Moderate to high heritability coupled with high genetic advance as a percentage of mean were recorded for plant height, pod length, 100 seed weight, grain yield per plant, number of branches and pods

per plant by Kumar et al. (2000). High genotypic and phenotypic coefficients of variation were observed for plant height, number of pods, seed yield and number of branches per plant in cowpea by Selvam et al. (2000). GCV, heritability and genetic advance were high for plant height and days to 50 per cent flowering indicating the preponderance of additive gene effects.

High coefficient variation was recorded in cowpea for seed yield, plant height, 100 seed weight and pods per peduncle. (Singh and Verma, 2002). Moderate variation was recorded for days to flowering and pod length. High heritability coupled with high genetic advance was observed for fruit yield, pods per plant and weight of pods by Narayankutty et al. (2003). High PCV and GCV were noticed for fruit yield, pods per plant and pod weight.

Pal et al. (2003) observed high heritability and moderate to high genetic advance for plant height, primary branches per plant, peduncles per plant and green pods per plant in cowpea. High heritability with low genetic advance was recorded for days to 50 per cent flowering, pod diameter, seeds per pod and 100 seed weight manifested. Relatively high genotypic and phenotypic coefficients of variation were recorded for plant height, number of primary branches per plant, peduncles, pods and green pod yield.

Twenty genotypes of cowpea were evaluated for variability, heritability and genetic advance for twelve characters. High GCV, PCV and heritability coupled with genetic advance were observed for plant height. Moderate values of GCV, PCV, heritability and genetic advance were recorded for seed yield, 100 seed weight, pods per plant, pod length and clusters per plant by Venkatesan et al. (2003).

High heritability was noticed in cowpea for all the yield characters except days to 50 per cent flowering, which exhibited moderate heritability (Philip, 2004). Grain yield, pods per plant and 100 seed weight recorded high genetic advance. Genetic advance was moderate for days to 50 per cent flowering and plant height, while for numbers of inflorescence per plant it was low. The

phenotypic coefficient of variation was the highest for grain yield per plant followed by 100 seed weight and number of pods per plant. Inflorescence per plant and plant height recorded the minimum phenotypic coefficient of variation. Grain yield per plant had the highest genotypic coefficient of variation followed by 100 seed weight and pods per plant.

Lovely (2005) observed high GCV for pods per cluster, yield per plant, pod weight, pods per plant and clusters per plant. The characters, clusters per plant, pods per cluster, pods per plant, primary branches per plant, pod yield per plant, pod weight, pod length, seeds per pod and main stem length had high heritability coupled with high genetic advance. High heritability and low genetic advance was noted for days to 50 per cent flowering and pod breadth.

High heritability coupled with high genetic advance was observed for yield per plant, pods per plant, pod length and pod weight. Pod weight and yield per plant had the highest PCV and GCV (Manju, 2006).

Analysis of variance revealed significant differences among the genotypes for all the twenty eight characters studied. Genotypic and phenotypic coefficient of variation was high for pod yield per plant, pod clusters per plant, pods per plant and pods per cluster. Pod clusters per plant, pods per plant, pod yield per plant, pods per cluster, pod weight, pod length, 100 seed weight and crude protein content had high heritability coupled with genetic advance by Madhukumar (2006). High estimates of genetic variability coupled with high heritability and genetic advance were observed for plant height at the time of first flowering, plant height at the time of 50 per cent flowering and plant height at the time of 50 per cent maturity indicating their dependability for effecting selection. The characters viz; plant height, days to 50 per cent flowering, 100 seed weight, seed yield per plant showed moderately high GCV, thereby suggesting the scope for improvement of these characters. The relative magnitude of PCV and GCV indicated the presence of environmental influence in the expression of the characters studied (Eswaran et al. 2007).

Biradar et al., (2007) evaluated three crosses viz; KM-1 x Goa local, C152 x Goa local and V-118 x Goa local. The material comprising of all parents, F_1's and F_2's were evaluated. Based on the mean, range and coefficient of variation (both phenotypic and genotypic) for the important components like number of pods, number of clusters and seeds per pod, KM-1 x Goa local may be considered as more potential than the other two. The fact that these two segregating generations, showed higher estimates of GCV, PCV and heritability for these important component traits, indicated the scope for selecting desired productive segregants from these populations. The highest heritability was exhibited by pod length in case of V-118 x Goa local.

Yield attributing traits exhibited higher magnitude of variability parameters in the cross C-152 x Goa local than KM-1 x Goa local (Salimath et al., 2007).

Suganthi and Murugan (2008) reported that thirty genotypes of cowpea (*Vigna unguiculata* L.) exhibited high genotypic coefficient of variation than phenotypic coefficient of variation for all the characters. Maximum phenotypic and genotypic co-efficients of variation were recorded by seed yield per plant followed by pods per plant and clusters per plant. High heritability was recorded by seed yield per plant followed by seeds per pod, pods per plant, pod length and 100 seed weight. Genetic advance as per cent of mean was higher for seed yield per plant followed by pods per plant and clusters per plant. Seed yield had positive and significant association with pod length.

2.3 CORRELATION AND PATH COEFFICIENT ANALYSIS

Selection of desirable genotypes is the principal step of crop improvement. Most of the economically important characters like yield is an extremely complex trait and is the result of many growth functions of the plant. An estimation of inter-relationship of yield with other traits is of immense help in any crop improvement programme. Correlation studies would facilitate effective selection

for simultaneous improvement of one or many yield contributing components. Certain characters contribute indirectly to yield through other components. They may not have significant direct effect on yield. Path coefficient analysis is used to separate the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959).

In cowpea, Patnaik and Roquib (1990) noticed that days to 50 per cent flowering and number of seeds per pod exerted maximum positive direct effect on grain yield per plant. Biradar et al. (1991) reported that plant height and number of inflorescences per plant exerted high positive direct effect on yield per plant and pod length, number of pods per plant and number of seeds per pod showed negative direct effect on yield.

Path coefficient analysis in cowpea showed that pod yield per plant had the highest positive direct effect on seed yield (Golasangi et al., 1992). Oseni et al. (1992) found positive correlations between seed yield and pods per plant and between days to flowering and 100 seed weight, while negative correlations were found between days to flowering and seed yield and between 100 seed weight and seed yield. Days to flowering had the greatest direct effect on seed yield, although this was nullified by the high negative indirect effect via all measured qualitative characters. A similar effect was noted with 100 seed weight, despite its strong direct correlation with seed yield. Seeds per plant had a low direct effect on seed yield but high positive indirect effects via other characters.

In cowpea, strong positive correlation of seed yield per plant with number of pods per plant, number of seeds per pod and number of branches per plant was reported by Altinbas and Sepetoglu (1993). Days to flowering was not associated with seed yield per plant. Number of pods per plant and number of seeds per pod were negatively and significantly correlated with 100 seed weight. Path coefficient analysis indicated that number of pods per plant was the most important yield contributing character affecting seed yield per plant followed by

number of seeds per pod. Sudhakumari (1993) observed strong positive correlation for yield per plant with number of seeds per pod, pod length and 100 seed weight. High positive correlation between days to flowering and maturity was noticed by Perrino et al. (1993). Peduncle length was not correlated with any other character.

Misra et al. (1994) observed that pod weight was positively correlated with green pod yield per plant in cowpea. Path coefficient analysis indicated that pod length had the greatest direct effect on pod yield, followed by pod diameter, while direct but negative effects were observed for average pod weight. Seed yield was significantly and positively correlated with branches per plant, inflorescence per plant, pods per plant, pod length, seeds per pod and 100 seed weight (Sawant, 1994). Path analysis revealed that the pods per plant had the highest positive direct effect on seed yield followed by 100 seed weight, seeds per pod, days to 50 per cent flowering, inflorescences per plant, plant height and pod length.

In cowpea Sobha (1994) reported that yield per plant was significantly and positively correlated with pod weight, pod length, number of seeds per pod and 100 seed weight. Pod weight and 100 seed weight had high direct influence on yield. Sudhakumari and Gopimony (1994) noticed high positive correlation between number of pods per plant and seed yield per plant.

Positive correlation for plant height with days to 50 per cent flowering, number of clusters per plant, pod length and 100 seed weight were observed by Tamilselvam and Das (1994) in cowpea. Number of seeds per pod and 100 seed weight were positively correlated with each other and with pod length. Number of pods per plant was positively correlated with number of clusters per plant and negatively correlated with pod length and 100 seed weight.

Ofori and Djagbletey (1995) reported that seed yield in cowpea depended mainly on seeds per plant, number of fruiting branches and seeds per pod. Pod yield was strongly associated with seeds per pod (Kar et al. 1995). Path analysis

showed that pod length was the main determinants of pod yield. Hussein and Farghali (1995) noted significant correlation of grain yield per plant with days to flowering, pod length and number of seeds per pod. Significant positive correlation was observed by Shakarad et al. (1995) among days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. Sreekumar (1995) noted highly significant negative correlation between 100 seed weight and protein content of seeds.

In cowpea, Sreekumar et al. (1996) observed that the yield of green pods was positively correlated with fruiting points per plant, pods per plant, pod length and seeds per pod. Naidu et al. (1996) noticed significant positive correlation between number of clusters per plant and number of pods per plant.

Chattopadhyay et al. (1997) reported that yield per plant was significantly and positively correlated with pod length, number of seeds per pod and 100 seed weight and negatively correlated with days to flowering. Number of pods per plant was negatively correlated to pod length. Path coefficient analysis revealed that number of pods per plant and number of seeds per plant had high direct effect on yield per plant. Days to flowering had negative direct effect on yield.

Character association studies in cowpea indicated a very high positive association of green pod yield with pods per plant (Harshavardhan and Savithramma, 1998b). Path coefficient analysis for green pod yield indicated that green pods per plant, pod length, pod width and number of primary branches were major traits contributing to yield. Singh et al. (1998) conducted a correlation study which revealed that grain yield per plant was positively and significantly associated with clusters per plant and pods per plant. Based on path coefficient analysis, pods per plant was the most important component character.

High positive correlation was reported for pod weight, pod length, pods per kg and pods per plant with pod yield per plant in cowpea (Resmi, 1998). Path analysis revealed maximum positive direct effect for pods per plant followed by

pod weight on yield per plant. Pods per kilogram exerted negative direct effect on yield. Number of pods per plant had maximum positive direct effect on yield. Mehta and Zaveri (1998) reported that grain yield per plant was significantly and positively correlated with number of branches per plant, number of clusters per plant and number of pods per plant.

In cowpea, Vardhan and Savithramma (1998) observed that yield per plant was significantly and positively correlated with pod length and number of pods per plant. Number of pods per plant, pod length and number of primary branches were the major traits which had positive direct effect with yield per plant. Branches per plant, pods per plant and plant height had positive correlation with seed yield both at genotypic and phenotypic levels (Kalaiyarasi and Palanisamy, 1999). Path analysis showed positive direct effects of branches per plant, plant height, pod length and 100 seed weight on seed yield.

Rangaiah and Mahadevu (1999) noted highly significant and positive association of yield in cowpea with clusters per plant, pods per plant and pod weight. Path analysis indicated a very high direct effect of pod weight. Pods per plant exhibited high indirect effect via pod weight on total seed weight.

In cowpea, Panicker (2000) reported that pod yield per plant was positively correlated with seeds per pod, pods per plant, length of harvest period, pods per inflorescence, pod weight and pod length. Yield per plant in cowpea showed high positive correlation with pods per plant, pods per inflorescence, pod weight, length of harvest period, pod girth, pod length and number of primary branches (Vidya, 2000). Path analysis revealed high direct effect for pods per plant and pod weight and indirect effect through other characters on yield.

Tyagi et al. (2000) reported that highest and lowest positive direct effects on seed yield in cowpea were observed for seed weight per pod and plant height respectively. Days to 50 per cent flowering recorded negative direct effect on seed yield per plant. Path analysis in cowpea revealed that pod weight per plant

had the highest positive and direct effect on total seed weight, followed by 100 seed weight and seeds per plant (Rangaiah 2000).

Kapoor et al. (2000a) reported that the number of seeds per pod and 100 seed weight were the main contributing characters towards the seed yield. Pod length contributed indirectly towards seed yield via seeds per pod and 100 seed weight. Kalaiyarasi and Palanisamy (2000a) reported that pod length, seeds per pod, 100 seed weight and crude protein content had strong positive correlation with seed yield. High positive direct effect on seed yield was observed for pod length (Bastian et al., 2001). The direct effects exhibited by seeds per pod and pod number were negligible. The indirect effects of pod length through other characters on seed yield was either low or negligible.

Ajith (2001) reported high positive genotypic correlation for pods per plant, pod weight, pods per cluster, pod clusters per plant and pod girth with pod yield per plant in cowpea. Pods per plant and pod weight had high direct effect on pod yield. Pods per plant exerted positive indirect effect via pod weight and pod weight exerted positive indirect effect via pods per plant.

In cowpea, plant height, branches per plant, pod yield, number of pods and pod length registered positive direct effect on grain yield while grains per pod had negative direct effect (Neema and Palanisamy, 2001). The highest positive direct effect was recorded by pod yield and the lowest by pod length. The indirect effect was maximum for pod length via pod yield.

Stoilova and Lozanov (2001) reported that high positive correlation were found in cowpea between the weight of plants without pods and pods per plant. Pod weight per plant was also strongly correlated with seeds per plant. Path analysis indicated that seeds per pod, pods per plant and plant height had high positive direct effects on seed yield while pod length 100 seed weight and branches per plant had negative direct effects (Kalaiyarasi and Palanisamy, 2002). Pod length and 100 seed weight had positive indirect effects on seed yield through pods per plant and seeds per pod.

Singh and Verma (2002) observed that seed yield in cowpea was positively correlated with 100 seed weight and pod length. Pod length and plant height were positively correlated with 100 seed weight. A negative correlation between 100 seed weight and number of pods per peduncle, days to 50 per cent flowering and days to 50 per cent maturity was observed.

Grain yield in cowpea showed significant positive association with clusters per plant and pods per plant (Parmar et al., 2003). Other significant positive correlations were found between days to flower with days to maturity and plant height; days to maturity with plant height, pod length with seeds per pod, branches per plant with clusters per plant, clusters per plant with pods per plant and pods per cluster with pods per plant. Pods per plant registered the highest direct effect on seed yield, followed by clusters per plant and seeds per pod. The indirect effect of branches per plant via seeds per pod was also positive and high.

In cowpea, Kutty et al. (2003) observed that pods per plant, pod weight and pod length were positively and significantly correlated with yield per plant. Number of days to first picking showed significant negative correlation with seeds per plant and number of pods per plant. Path analysis indicated that the pods per plant, followed by pod weight had the greatest positive direct effect on yield.

Plant height, pod yield per plant and pod length had significant positive correlation with grain yield in cowpea both at genotypic and phenotypic levels (Neema and Palanisamy, 2003). Yield per plant had significant positive association with number of pods per plant, pod length and number of seeds per pod at the genotypic level and only with pod length at phenotypic level.

Subbiah et al. (2003) studied the cause and effect relationship among the different quantitative traits of cowpea. Number of pods per plant, number of branches per plant, pod length, number of seeds per pod, plant height and 100 seed weight had positive direct effect on yield per plant. Number of pods per plant had positive indirect effect on yield per plant through days to flowering, number of branches per plant, pod length and number of seeds per pod.

In cowpea, Venkatesan et al. (2003) observed that number of branches per plant, number of pods per cluster, number of pods per plant and pod yield had significant positive phenotypic and genotypic correlation with grain yield. Path coefficient analysis revealed positive direct effect of grain yield with number of pods per plant, pod length, number of clusters per plant, number of seeds per pod and 100 seed weight. Number of pods per plant, pod length and number of clusters per plant were the most important yield determinants.

Grain yield per plant in cowpea exhibited highly significant positive correlation with number of pods per plant, inflorescence per plant, seeds per plant and 100 seed weight both at genotypic and phenotypic level (Philip, 2004). Maximum positive direct effect on grain yield was exerted by number of pods per plant followed by 100 seed weight and seeds per pod. Pod length showed insignificant correlation with grain yield, but it contributed to yield through positive indirect effects through other characters considered.

Lovely (2005) reported that yield per plant showed strong positive genotypic correlation with pods per cluster, pods per plant, pod weight, pod length, pod breadth and seeds per pod. A negative correlation was noted for days to 50 per cent flowering, days to first harvest and primary branches per plant. The characters pods per cluster, pods per plant, pod weight, pod length, pod breadth, seeds per pod and main stem length had positive direct effects while length of harvest period had negative direct effect.

Correlation studies revealed that characters like pod length, pod girth, pod weight, pods per plant, seeds per pod, 100 seed weight, number of harvests and pod protein observed high positive correlation with yield, whereas peduncle length were negatively correlated with yield. (Manju, 2006). Path coefficient analysis indicated that pods per plant exerted the highest positive direct effect on yield, while pod weight and vine length had high indirect effects on pod yield.

Madhukumar (2006) noticed that pod yield per plant in cowpea showed significant positive correlation with pods per plant, pod clusters per plant, days to first harvest, pod weight, days to 50 per cent flowering, seeds per pod, pod length, and 100 seed weight at genotypic level. Path analysis revealed that number of pods per plant and pod weight were the primary yield contributing characters due to their high direct effect on pod yield.

Seed yield per plant had high significant positive correlation with harvest index at phenotypic and genotypic levels. The path coefficient analysis indicated that plant height at the time of first flowering, plant height at the time of 50 per cent flowering, plant height at the time of 50 per cent maturity and total dry matter production are important for effecting selection (Eswaran et al., 2007).

The potentiality of a germplasm accession Goa local with exceptionally high seed weight and also diverse from three agronomic backgrounds viz; KM-1, C-152 and V-118 with respect to many other traits was investigated by Biradar et al. (2007). Analysis of covariance indicated that yield is positively and significantly associated with its contributing morphological characters. Highest yield was realized through pod number and indirectly by branch number. Among the three F_2 segregating populations, KM-1 x Goa local can be exploited for simultaneous improvement of pod traits viz; number of pods, seeds per pod and seed weight.

2.4. GENETIC DIVERGENCE ANALYSIS

A knowledge of genetic diversity, its nature and degree is useful in the improvement of any heritable character. Genetic distance is a measure of genetic differences between populations or individuals. A properly maintained world collection of germplasm or genetic stock should be evaluated for the choice of genetically divergent parents for hybridization under transgressive breeding programme. Segregation and recombination produce many new gene combinations in F_2 and later generations, when genotypically different individuals

are crossed. Generally eco-geographic diversity has been considered as an index of genetic variability in crop plants. However this may not be true for every case, as pointed out by many workers, that genetic diversity need not necessarily be related to geographic diversity. Several workers observed that many varieties forming one group were geographically diverse wild varieties obtained from the same region were genetically different.

Renganayaki and Rengaswamy (1991) used Mahalanobis D^2 statistic to cluster six genotypes of cowpea in to four genetically divergent clusters. Pod length, 100 seed weight and grain yield per plant were the characters which contributed maximum to genetic divergence in cowpea. In cowpea, Thiyagarajan and Rajasekharan (1993) grouped diverse genotypes in to 3 distinct groups based on several yield contributing attributes.

Mahalanobis D^2 statistic was used to estimate genetic divergence of ten yield related characters in fifty cowpea genotypes by Santos et al. (1997). Length of the main branch, 100 seed weight and pod length were the most important characters that affect divergence. Sharma and Mishra (1997) measured the genetic divergence in forty two indigenous and exotic strains and grouped them in to six different clusters. Days to 50 per cent flowering, plant height and pods per peduncle contributed the most towards genetic divergence.

Viswanathan et al. (1998) assessed the genetic divergence between cowpea populations consisting of seventy two genotypes and observed high genetic diversity among them. Resmi (1998) used Mahalanobis D^2 analysis to study the genetic divergence of thirty genotypes. Days to flowering, number of branches, pod length, number of pods per inflorescence, number of pods per plant and yield per plant contributed considerable to genetic divergence.

Information on nine characters from twenty four early maturing genotypes of cowpea from different geographical regions were subjected to D^2 analysis by Tyagi

et al. (1999). Genetic diversity was independent of geographical origin. Kapoor et al. (2000b) assessed the genetic divergence of sixty genotypes and grouped them in to fifteen clusters depending upon their genetic distance. Fifteen genotypes were grouped in to thirteen clusters by Ushakumari et al. (2000) based on Mahalanobis D^2 analysis. The highest contributions towards divergence were recorded for plant height, seeds per pod, number of branches, number of pods per cluster and pod length. Thirty two genotypes were evaluated for genetic divergence based on physiological traits by Backyarani et al. (2000). The material was grouped in to six clusters. Geographic diversity was not related to genetic diversity.

Anbuselvam et al. (2001) grouped cowpea genotypes in to four different clusters based on genetic divergence using Mahalanobis D^2 analysis. Cluster I included 45 genotypes. Mahalanobis D^2 analysis was employed to cluster 191 accessions of cowpea in to 10 clusters by Kohli and Agarwal (2001). Clusters I and V had 30 accessions each. The smallest cluster was cluster VIII which had eight accessions.

Mahalanobis D^2 statistic was used to group the fifty genotypes in to ten clusters. Wide range of genetic divergence was noticed among the 50 genotypes. Maximum intercluster distance was noted between clusters I and IV. Cluster VII recorded the maximum mean value for pod length, number of seeds per pod, 100 seed weight and grain yield per plant. Cluster VII had the highest cluster mean value for number of pods per plant and pod length. Cluster I had the least number of pods per plant and number of pods per inflorescence (Philip, 2004).

In yard long bean, Lovely (2005), Mahalanobis D^2 analysis clustered the 50 genotypes in to 4 groups with genotypes from different eco-graphic locations being grouped in the same clusters. The grouping of genotypes by selection indices followed almost the same pattern as their clustering pattern in the D^2 analysis.

Based on Mahalanobis D^2 statistics, the 66 accessions of yard long bean were grouped in to ten clusters. Cluster I was the largest containing 18 accessions, while cluster X was the smallest with two accessions (Manju, 2006). Madhukumar (2006) in yard long bean, clustered the 30 genotypes into eight clusters by Mahalanobis D^2 analysis. Cluster I formed the largest cluster with 10 genotypes while clusters VI, VII and VIII had one genotype each.

Forty four grain cowpea genotypes were evaluated for thirteen characters to quantify the genetic diversity existing among them by Mahalonobis D^2 statistics. The analysis of variance revealed significant differences among the genotypes for each character under study. The genotypes fell into nine clusters. Cluster strength varied from single genotype (Cluster IV to IX) to 31 genotypes (Cluster I). Cluster III had minimum days to first flower opening, days to 50 per cent flowering and stover yield per plant in addition to maximum number of pod per plant and primary branches (Pandey, 2007).

Suganthi et al. (2007) observed genetic divergence analysis among 30 genotypes of cowpea, indicated the existance of considerable diversity. These genotypes were grouped in to XI clusters. The cluster III was largest and consisted of seven genotypes followed by cluster X of 4, cluster II, IV, V and VIII (3 in each). Cluster I and VII (2 in each) and clusters VI, IX and XI consisting of only one genotype each. The diversity among the genotypes measured by inter cluster distance was adequate for improvement of cowpea by hybridization and selection. The genotypes included in those diverse clusters may be used as promising parents for hybridization to obtain better segregants in cowpea.

Genetic divergence assessed in 56 genotypes of cowpea using D^2 statistics for thirteen yield contributing characters showed grouping of genotypes in to nine clusters. Cluster I had the maximum number of genotypes. Character viz; days to maturity, 100 seed weight and days to flowering were the highest contributors to D^2 values. The geographical diversity was not related to genetic diversity (Sulanthi et al., 2007).

Valarmathi et al. (2007a) working with sixty nine cowpea genotypes, which included 60 genotypes from *Vigna unguiculata* subsp. *unguiculata* and eight genotypes from *Vigna unguiculata* subsp. *sesquipedalis* were evaluated for nine quantitative character and replication wise means were subjected to Mahalanobis D^2 analysis. All the accessions were grouped in to twelve clusters in which cluster I was the longest having 47 genotypes from subsp. *unguiculata*. *Unguiculata* were grouped in seven distinct clusters whereas the genotypes of *sesquipedalis* were grouped in to five other distinct clusters. Days to maturity contributed maximum to the genetic divergence followed by 100 seed weight and characters namely number of branches per plant, number of seeds per pod and total exhibited least contribution among the accessions.

2.5. SELECTION INDEX

The economic worth of a plant depends upon several characters so while selecting a desirable plant from a segregating population the plant breeder has to give due consideration to characters of economic importance. Selection index is one such method of selecting plants for crop improvement based on several characters of importance. This method was proposed by Smith (1947) using discriminant function of Fisher (1936). Tikka et al. (1977) proposed on efficient selection index involving the characters viz; plant height, pods per plant and test weight. Jalajakumari (1981) applied discriminant function analysis on 17 varieties of cowpea. Average selection index is more effective than visual pedigree or bulk population methods for developing high yielding lines in cowpea (Yap, 1983).

In yard long bean, Resmi (1998) worked out the selection indices using thirteen characters and found that the genotype VS 6 had the maximum index value followed by VS 11. Superior genotypes were identified by constructing selection indices using the characters namely vine length, primary branches, petiole length, length and breadth of lateral leaflets, days to flowering, pod length, pod girth, pod weight, pods per inflorescence, pods per kilogram, pods per plant and yield.

Philip (2004) worked out selection indices for 50 genotypes of cowpea on the basis of pods per plant, number of inflorescence per plant, pods per inflorescence, pod length, seeds per pod and 100 seed weight. Five superior genotypes were selected for hybridization programme as female parents to develop F_1 hybrids.

Selection index for the genotype was computed based on the nine characters having significant genotypic correlation coefficients namely pods per cluster, pods per plant, pod yield per plant, pod weight, pod length, pod breadth, seeds per pod, length of harvest period and main stem length. The maximum selection index value was obtained for VS 41, while the least value was for VS 7 by Lovely (2005).

Selection index analysis done by Madhukumar (2006) in yard long bean revealed that genotype VS 86 attained the maximum selection index value followed by Tvm-1, Vellavalli payar and the minimum estimates were recorded for Kayamkulam local, Malappuram local-2 and Kollengode local. Manju (2006) observed selection indices involving the characters, peduncle length, pod length, pod girth, pod weight, pods per plant, seeds per pod, 100 seed weight, number of harvests, pod protein and yield per plant. Based on selection index, VS 27 ranked first followed by VS 8 and VS 19.

2.6. EXTENT OF DAMAGE BY POD BORERS

Spotted pod borer *M. vitrata* (Fab.) (Syn. *Maruca testulalis* Geyer) is a major limitation to successful cultivation of cowpea in many countries (Singh and Jackai, 1988). The crop loss caused by the pest in tremendous since the larvae feed on flowers and developing pods (Jackai and Adalla, 1997).

The economic production of cowpea is seriously affected by the infestation by pod borer, *M. vitrata*, a polyphagous pyralid moth which is seen in almost all the areas of cultivation of the crop. It is one of the major pests of cowpea in the

tropics, the population of which is almost above the economic threshold level in all seasons (Taylor and Ezedima, 1964).

Legume pod borer causes tremendous crop loss in cowpea cultivated over wide range of environmental conditions (Taylor, 1978; Singh and Van Emden, 1979; Dabrowski et al., 1983; Ezeuch and Taylor, 1984; Jackai and Daoust, 1986; Ngugi et al., 1985; Suh, 1986). *M. vitrata* is the most abundant species of pod borers feeding on cowpea (Wijayagunasekara and Ranasinghe, 1992; Jaiswal and Patil, 1993).

Infestation by pod borers *M. vitrata* and *L. boeticus* which are the most important post-flowering pests of yard long bean, act as a major limiting factor in vegetable cowpea cultivation in all seasons. Pod borers of these two species constitute 99.9% of all known cowpea borers in China (Qinghuai et al., 2003).

Jackai (1982) assessed levels of legume pod borer infestation on stem, flowers, pods and seeds in cowpea employing different damage parameters. He observed that seed damage was not correlated with flower and pod damage measurements. The pod damage was positively and significantly correlated with flower damage. Karel (1985) observed that the *M. vitrata* larvae are more abundant and injurious to cowpea than any other pest. The pod damage due to the pest range from 13 to 31 per cent, the seed damage is about 16 per cent and the total yield loss average between 33 to 53 per cent. Total yield loss of grains ranging from 30 to 50 per cent was reported by Singh and Allen (1980) and Jackai and Daoust (1986). According to Attachi and Djihou (1994) *V. unguiculata* is one of the most vulnerable species to the attack by pod borer.

Verma and Henry (1988) studied the incidence of insect pests on 24 varieties of mung bean (*V. radiata*). The cultivars P103 and P105 had greatest damage by *L. boeticus*.

Yadava et al. (1988) found that the pest complex infesting early maturity varieties was different from that infesting late maturity ones. *M. testulalis*, was more common on early varieties, where as *H. armigera* and *L. boeticus* were more common on late varieties. Seed damage due to pod borer, was low in the early varieties (13% in H 77-216 and 13.6% in UPAS 120) compared with late varieties (26.7% in Bahar and 34.8% in T7).

In cowpea, Echendu and Akingbohungbe (1989) reported that successful establishment of pod borer larvae occurs at the flower bud stage, and not in the flower primordia or open flowers. An infestation level of two larvae per plant was sufficient to cause noticeable yield reduction.

The infestation by legume pod borer was maximum under high relative humidity and low to moderate temperature, while the reproduction rate and population density were lower in drier weather conditions (Jackai et al., 1990).

Oghiakhe et al. (1991a) reported that percentage of pod damage and larval infestation on flowers were positively correlated with relative humidity and negatively correlated with temperature. Defoliated cultivars suffered less infestation in the field, because relative humidity under the canopy was low, while soil and ambient temperature were high, the conditions negatively influenced the levels of infestation. The amount and distribution of rainfall, relative humidity and temperature were the major environmental factors which influenced the population build up of legume pod borer in different areas of cultivation (Botten berg et al., 1997).

The moth layed eggs on flowers, flower buds or tender pods. The eggs hatch within three days and the first instar larvae started feeding at the oviposition sites. The caterpillars fed on flower buds or on immature seeds in young pods. They bore into the developing pods and fed on the tender seeds. (Anithakumari, 1992).

Oghiakhe et al., (1992b) emphasised the importance of flower and pod damages due to legume pod borer for field screening of resistance. Pod damages caused by legume pod borer resulted in significant reduction of yield in cowpea (Panicker et al., 2002). Pod damage caused by legume pod borer was significantly and positively correlated with seed damage in cowpea. Flower damage caused by the pest, however, was independent of pod damage.

In cowpea plants, Dreyer et al. (1994) noticed attack in more than 80 per cent. Jackai and Adalla (1997) reported legume pod borer as the most important post-flowering pest of legumes inflicting heavy yield loss in all areas of cultivation. The pest which was of minor importance in South East Asia in the past, has recently emerged as one of the most devasting pests of pulses in the region (Tamo et al., 1997).

Legume pod borer is the most devastating pest of cowpea in high rainfall areas, where the production losses due to infestation by the pest may go up to 80 per cent (IITA, 1998).

In pulses, seeds being the economic produce, infestation by legume pod borer assumes serious dimensions. Veeranna et al. (1999) observed that the larvae attacked the terminal shoots of cowpea also, in addition to flower buds, flowers and pods causing damages by binding the plant parts together with silken thread and faecal matter.

Sharma et al. (1999) observed the performance of field bean (*Lablab purpureus*) cultivars Pusa Early, Prolific, Rajni, HDL 53, JDL 79, KDB 403, KDB 405 and Deepaliwal to pod borer (*L. boeticus*, *M. vitrata* and *H. armigera* infestation. The lowest pod damage was observed in Rajni (10.18%) and JDL-53 (10.52%), indicating that these cultivars were least susceptible to pod borers. High pod damage was recorded for KDB 405, KDB 403, JDL 79 and Prolific (13.45 to 14.92%).

The pod borer moth lays eggs on the flower buds, flowers and young pod and the first instar larvae started feeding at the oviposition sites. It then bores in to the pods and devoured the ripening seed, one after another. The larval burrows were marked by mass of brownish excrement at the entrance of the gallery (Panicker, 2000).

Attachi and Hountondji (2000) reported that the legume pod borer larvae affected the flower buds, flowers and pods of almost all types of cowpea, the flowers being most preferred. Most of the first and second instar larvae were observed on flowers, while majority of fourth and fifth instar larvae were found on pods (Liao and Lin, 2000). Adipala et al. (2000) observed that close spacing promoted infestation of legume pod borer in cowpea under field conditions as a result of increased relative humidity.

The abundance of pod borers in the pigeon pea cultivars UPAS 120 (136 days), C11 (212 days) and Pusa 9 (245 days) was studied by Sahoo and Senapati (2000). *M. testulalis, L. boeticus* on C11 and Pusa 9 were the major pest damaging flowers. *M. testulalis* and *L. boeticus* were the dominant pests in the grain filling stage.

The impact of weather factors on the population incidence of the pod borer *L. boeticus* on pea cv. Rachana. The seasonal activity of the pest was recorded starting from the flowering stage, upto crop harvest. The pod borer damage commenced during the flowering stage with 12.50 and 8.33% in the third and fourth week of January 2000 and 2001, respectively. The infestation continued up to the last picking of pods with 20.20 and 18.52 in the first and third week of March during the two consecutive seasons, respectively. The peak populations of 25.52% and 23.08% were attained in the fourth week of February 2000 and in first week of March 2001, respectively. No rainfall was observed in the period of maximum infestation of the pod in both the cropping seasons (Shantibala and Singh, 2003).

2.6.1. Sources of Resistance

Resistance to legume pod borer is dominant and probably controlled by several genes (Wolley, 1976).

Screening of cowpea germplasm for legume pod borer resistance at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria lead to the isolation of a resistant line which could be used as a resistant parent in breeding programmes. Two resistant cultivars viz; Tvu 946 and Tvu 4557 (VITA 5) were isolated by screening cowpea germplasm for legume pod borer resistance. The cultivar Tvu 946 was completely free from infestation by legume pod borer under green house conditions, hence could be used as a promising resistant donor (Jackai, 1982).

Pathak (1985) studied the nature of inheritance and degree of dominance of legume pod borer resistance in cowpea in relation to percentage pod and seed damage and reported partial dominance of susceptibility over dominance. He suggested polygenic inheritance for legume pod borer resistance.

Vigna pubescens, a legume pod borer resistant relative of cowpea can be used as a source of resistance in interspecific hybridization programmes. Fatokun and Singh (1987) crossed *Vigna pubescens* with *Vigna unguiculata* and obtained viable hybrids by embryo rescue method.

In the field trials 29 cultivars were screened for resistance to *L. boeticus, M. testulalis* and *H. armigera*. ML 337, ML 423 and ML 428 showed the least susceptibility to the pests when compared to the controls, ML5 and ML 131. Preliminary studies on the mechanism of resistance revealed higher percentages of reducing and non-reducing sugars, total phenols and free aminoacid, in the resistant genotypes than in the control and susceptible genotype by Chhabra et al. (1988).

Sources of complete or partial resistance to many insect pests are available in different cultivars within the crop species itself (Van Emden, 1989). He opined that screening of commercial cultivars should be the initial step in the search for resistance.

Genes for legume pod borer resistance had been located in the wild species, *Vigna vexillata*, but the attempts to transfer these resistant genes in to *Vigna unguiculata* types failed due to improper pollen tube development (Barone and Ng, 1990).

Saxena and Khan (1991) reported that sources of resistance should be looked for in traditional varieties or unimproved germplasm of the particular crop.

Fatokun (1991) suggested that *Vigna davyi*, a related wild species of cowpea is a bridge species, while attempting inter specific hybridization with *Vigna vexillata*. He obtained partially fertile inter specific hybrids of cowpea by this method.

While transferring legume pod borer resistance to *V. unguiculata* x *V. vexillata*, Barone et al. (1992) observed that no viable seeds could be obtained as a result of embryo break down in the inter specific hybrid within 5-8 days following pollination.

Fatokun et al. (1993) evaluated several cultivated lines of cowpea and found that none of them possessed desired levels of resistence to legume pod borer. They screened several accessions of *V. vexillata*, *V. davyi*, *V. oblongifolia* and *V. luteola* and reported that *V. vexillata* and *V. oblongifolia* had appreciable levels of resistance to the pest. *V. vexillata* could be effectively used as a source of resistance in breeding for legume pod borer resistance as it is more closer in chromosome morphology to *V. unguiculata*. They also identified a wild cross compatible species of cowpea, *V. unguiculata* subsp. *dekindtiana* var. *pubescens* closely related to *V. vexillata* that can be used as a donor for legume pod borer resistance.

Jagginavan et al. (1995) noticed that the cowpea lines P 120 and C 11 were tolerant to legume pod borer in a screening experiment involving several cultivated cowpea varieties.

Singh et al. (1997) screened several accessions of cowpea and reported that only low levels of resistance was observed for legume pod borer in cultivated cowpea lines.

Gomathinayagam et al. (1998) used *V. vexillata* as donor parent in an interspecific hybridization programme with *V. unguiculata* and obtained successful hybrids by employing embryo culture, but progenies in the segregating generations resembled the wild parent in most morphological characters.

Singh (1999) opined that the scope of using wild relatives for inter specific hybridization for transferring the resistant genes to cultivated types has limited scope because of the retention of wild characters in the segregating generations. He evaluated different improved lines of cowpea for legume pod borer resistance and observed that the lines IT 90 K-277-2, IT 93 K-452-1, IT 94 K-437-1, IT 97 K-569-9, IT 95 K-223-3, IT 97 K-838 and IT 97 K-499-38 suffered lesser damage due to legume pod borer in field conditions. There was no noticeable reduction in yield of these lines even without insecticidal sprays.

In yard long bean, screening for legume pod borer resistance was done by Panicker (2000), who observed a plant susceptibility index ranging from 33.13 to 109.37. Larval count in flowers was not correlated with any of the damage parameters. Significant and positive correlation was found among percentage pod infestation, pod damage severity and seed damage index. No significant correlation was noted between pod fibre content and percentage pod infestation.

Field screening programme for legume pod borer resistance all the 50 yard long bean cultivars were evaluated on the basis of plant resistance index. The cultivars suffering least flower damage were VS 5 and VS 33. Lowest pod damage by VS 34, VS 39 and VS 42. Seed damage index value was the lowest

for cultivar VS 2. VS 34 with the lowest plant resistance index value was identified as the most resistant among all the varieties (Vidya, 2000).

Veeranna et al. (2000) screened 45 genotypes of cowpea for pod borer resistance and reported that the cultivar TVX-7 was completely resistant to infestation by the pest.

In grain cowpea, Philip (2004) observed a seed damage index of 40 to 192 and plant susceptibility index of 16.09 to 66.50. Flower damage was positively correlated with pod damage parameters and negatively with peduncle length. Plant resistance indices were calculated for the 50 cowpea types based on the simultaneous consideration of flower, pod and seed damage parameters. The plant resistance indices were minimum for T45, T47 and T49 which were selected as testers.

Screening of all the 66 accessions for legume pod borer resistance was done by working out plant susceptibility indices based on flower, pod and seed damage parameters. VS 19 was the most tolerant with least damage to flowers, pods and seeds, while VS 42 was the most susceptible. On comparing the accessions for various characters VS 27, VS 8 and VS 19 were found to be promising based on their superiority in yield, quality and tolerance to legume pod borer (Manju, 2006).

Kooner and Cheema (2006) screened eighty nine genotypes of pigeon pea in the field to isolate sources of resistance to pod borers. The pod borer complex comprises of *M. testulalis, L. boeticus* and *H. armigera*. On the basis of per cent pod damage and Pest Susceptibility Rating (PSR), entries AL 1498, AL 1502 and AL 1340 were found promising with mean pod damage of 11.21 to 13.71% (PSR 3-3.50) as compared to 17.67 to 26.25% (PSR 4.00 to 5.50) on the check varieties (AL 15, AL 20 and T21) and 28.21% (PSR 6.00) on the infester. Therefore, genotypes AL 1498, AL 1502 and AL 1340 may be used as resistant donors in the crossing programme to evolve pod borer resistant / tolerant varieties of pigeon pea.

2.6.2. Morphological and biochemical basis of resistance

Cowpea varieties with upright and long peduncles that hold pods away from the canopy as well as from each other suffer less damage by legume pod borer under field conditions (Singh, 1978).

Five *V. radiata* cultivars were chosen from 91 for resistance to *Lampides boeticus, Maruca testulalis, Bemisia tabaci, Empoasca moti, E. terminalis, Heliothis armigera* and yellow mosaic virus. Leaves of all the five cultivars had higher contents of reducing and non-reducing sugars, total phenols and free aminoacids than highly susceptible lines used as infestors in the field by Chhabra et al. (1981).

Different morphological and biochemical characteristics of crop varieties often play a crucial role in providing insect resistance to plants (Norris and Kogan, 1980).

Chhabra et al. (1986) screened cultivars of black gram (*Vigna mungo*) against the major pests. The cultivars LU15, LU 178, LU 190, LU 196, LU 330, LU 397, LU 426 and LU 434 were resistant to *L. boeticus, M. testulalis* and *H. armigera*. The leaves of these cultivars had higher content of reducing and non reducing sugars, total phenols and free amino acids than the others screened. These components may have served as defence mechanisms against the pests.

The plant architecture deciding the spatial arrangement of the flowers and pods on the plant assumes importance in imparting resistance to pod borer in cowpea varieties. Pod size and rate of pod growth are important factors in the susceptibility of cowpea to attack by pod borer (Tayo, 1988).

Jackai and Oghiakhe (1989) reported the presence of glandular and non-glandular trichomes in both cultivated and wild cowpea. Trichomes in the two types of cowpea differ significantly only in their number and non-glandular trichome length. Rather than density, trichome length and angle to pod surface seemed to be more important for resistance. Significantly lower densities of

glandular trichomes was observed in cultivated genotypes of cowpea (*V. unguiculata*) when compared to wild *V.* species (*V. vexillata*) which suffered less damage due to pod bug.

Resistance to pod borers *L. boeticus*, *M. testulalis* were assessed in 60 *Vigna radiata* and 50 *Vigna mungo* cultivars in the field by exposing them to natural infestation. Most of the cultivars tested were resistant or tolerant with high resistance shown by the *V. mungo* cultivar B3-8-8 and the *V. radiata* cultivars PDMS4-146, ML 131 and ML 372 (Sahoo et al. 1989).

Van Emden (1989) attributed resistance in cowpea varieties with long peduncles and those which hold pods widely apart on the peduncle to the reduced accessibility of the larvae of the pest to other pods for further pod infestation.

Oghiakhe et al. (1991a) found that *V. unguiculata* cultivars with pods held within the canopy suffered significantly more damage than cultivars with pods held above the canopy. They opined that larvae penetrate the pods more successfully when pods are in contact with each other or with the foliage.

Anatomical micro-environment of the area close to stem epidermis imposes severe limitations on the movement of pod borer larvae and feeding within the tissue (Oghiakhe et al., 1991b). Stem anatomy is an important factor in stem resistance to pod borer, but was not significant in the case of pod wall resistance in cowpea.

Oghiakhe et al. (1992a) found a negative and significant correlation between pod wall trichome density and pod damage by legume pod borer in cowpea and highlighted the role of trichome density in reducing pod damage. Studies have shown that glandular trichomes contain high concentration of phenol and alkaloids which enhance there biochemical defence against insects.

Oghiakhe et al. (1992c) reported that eventhough the pressure required to penetrate pod wall increases with pod age, the correlation between pod damage

severity and pod wall toughness was not significant. Also noticed a reduced level of pod damage severity due to legume pod borer in cowpea varieties with long peduncles and wide pod angle.

Oghiakhe et al. (1992d) studied the pod wall toughness in cowpea with varying levels of resistance to legume pod borer and reported that there was no relationship between pod damage and pod wall toughness.

A significant negative correlation was noticed between the total trichome density on the pod wall of cowpea and legume pod borer infestation on the pods (Oghiakhe et al., 1992e). But the length of non-glandular trichomes on the pod wall was not related with the intensity of pod infestation by the pest. They emphasized the importance of angle of insertion of the trichomes on the pod surface. Erect trichomes did not cause much obstruction to the movement of larvae on the pods.

Significant positive correlation was observed between total chlorophyll content and plant resistance index in cowpea (Oghiakhe 1992a). He suggested that the content of total chlorophyll can be considered as a criteria for classification of cowpea genotypes for resistance to the pest. Total chlorophyll content did not show any significant relationship with plant resistance index in relation to legume pod borer by Panicker (2000).

Thick and compact collenchyma cells in the stems and fibrous tissues on the petal surface contributed to pod borer resistance in the resistant variety TVNU 72, with trichomes as the principal factors in the resistance (Oghiakhe et al., 1993).

Trichomes in wild and cultivated cowpea adversely affected oviposition, mobility, food consumption and utilization by the pod borer (Oghiakhe, 1995).

Certain biochemical constituents act as defensive chemicals in crop varieties playing a crucial role in imparting resistance by influencing the behavioural and physiological responses of the feeding insects (Dent, 1995).

Veeranna and Hussain (1997) observed a trichome density of 24.41/9 mm^2 in the resistant genotype (TVX-7), while the susceptible genotype DPCL-216 had a low trichome density of 12.82/9 mm^2. High density of trichomes on the pod surface accounted for the resistance of the variety TVX7 towards the infestation by legume pod borer.

Trichomes (pubescence), hair like outgrowths from the aerial plant parts, have been gradually eliminated from cultivars by selection, although they show great promise towards the development of multiple pest-resistant cultivars. The role of trichomes, as evidence to *Maruca vitrata*, *Clavigralla tomentosicollis* and *Callosobruchus maculatus* was described by Oghiakhe (1997).

Legume pod borer is one of the major consistrants in increasing the production and productivity of grain legumes in the tropics. Screening of resistance has been carried out using natural infestation and multi and no-choice tests under green house/laboratory conditions. Information available on genotypic resistance to *M. vitrata* in cowpea, while such information on pigeon pea and other legumes is limited. Stem and pod wall thickness, trichomes and podding habit are associated with resistance to *M. vitrata*. Several natural enemies have been recorded in *M. vitrata* (Sharma, 1998).

Singh (1999) reported that cowpea varieties with pigmented calyx, petioles, pods and pod tips suffered comparatively lesser damage by the infestation of legume pod borer.

In yard long bean Panicker (2000) reported a non-glandular trichomes density range of 1.50 to 7.00 mm^2 area of pod wall surface and length of peduncle was not correlated with pod borer, while Philip (2004) observed a pod trichome count of 1.67 to 6.83/mm^2 in grain cowpea.

Vidya (2000) reported that there was no significant correlation between pod damage severity and pod wall thickness in cowpea. Different pod characters in

relation to legume pod borer infestation and reported that fibre content of pod was not related to legume pod borer infestation. The density of non glandular trichomes on the pod wall had significant negative correlation with infestation by legume pod borer (Panicker, 2000).

Results of the study conducted by Wanjari et al. (2003) showed that Janephal mung bean had more insect infested pods (16%) than Kopergaon (8%) (standard control). Borer *L. boeticus* and *H. armigera* damaged pods had lower number of seeds/pod than un damaged intact pods (82.81%) in Janephal and 89.51% in Kopergaons.

Presence or absence of pubescence and type of cuticle waxes that affect oviposition, locomotion or feeding by insects, tissue toughness that influence feeding and such other characters that impede host feeding and / or utilization by insect pests. Pubescence on plant surface is made up of individual trichomes or hairs. When pubescence is present, the mechanism of reistance may depend upon one or more of the four characteristics of trichomes namely their density, erectness, length and shape (Manju, 2006). Also she reported that non glandular trichome density range of 1.87 to 6.03 mm^2 area of pod surface.

Anantharaju and Muthiah (2008) carried out studies in pigeonpea (*Cajanus cajan* (L.) Millsp.) to identify the resistant sources of *Maruca vitrata* and *Mylabris* spp. The study of *M. vitrata* resistance or tolerance was carried out in open field conditions without spraying any insecticide. The screening was done on seven per cent and twelve F_1's hybrids based on biochemical components. The hybrid LRG 41 x ICPL 87119 registered the highest yield coupled with lowest yield loss. Hence the parent LRG 41 and the cross LRG 41 x ICPL 87119 are potential sources for further breeding programmes. Biochemical basis of resistance may be due to low amount of total free amino acid, crude protein content and high amount of total phenolics in the pigeonpea genotypes against *M. vitrata*.

2.7. COMBINING ABILITY AND GENE ACTION

The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942). Combining ability is the ability of a strain to produce superior progeny on hybridization with other strains. Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value and in the selection of suitable parents for hybridization. Information on the nature of general combining ability and specific combining ability with respect to parents and hybrids will facilitate the breeder to plan the breeding programme effectively.

Knowledge about the gene action is important in any crop improvement programme. Higher magnitude of *gca* variance indicates the predominant role of additive gene action which is fixable and higher *sca* variance indicates dominance deviation and epistatic effect.

Combining ability analysis using six parents in a diallel mating system, Thiyagarajan et al. (1990) revealed that both additive and non-additive gene effects were significant for plant height, number of pods per plant, 100 seed weight and seed yield per plant in cowpea. They reported the preponderance of non-addditive gene action for the expression of these characters.

Emebiri and Obisesan (1991) observed that several yield characters in cowpea were controlled by both additive and non-additive gene effects in a combining ability study through half diallel analysis involving 10 parents. Generation mean analysis in cowpea indicated the preponderance of non-additive gene effects for number of pods per plant and additive gene effects for yield per plant and protein content (Hazra, 1991). Both additive and non-additive gene effects were important in the expression of pod length.

A 6 x 6 diallel analysis done in vegetable cowpea by Rejatha (1992) showed significant difference in most of the characters except number of pods per plant and fruit yield per plant. Variance due to *gca* was significant and higher in magnitude than *sca* for the characters like days to flowering and mean weight of pod.

Thiyagarajan (1992) studied the combining ability for yield related characters in twelve cowpea hybrids and underlined the predominance of additive genetic variance for number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per pod.

In cowpea, Anilkumar (1993) reported the presence of additive and non-additive gene action, the non-additive component being more predominant in the expression of days to flowering and number of pods per plant, in a line x tester analysis. Number of seeds per pod and 100 seed weight were governed by additive gene effects.

Jayarani (1993) observed that sca variance was predominant for all characters in grain cowpea suggesting its importance. Variance due to gca was larger than sca for days to 50 per cent flowering and length of pod. The sca variance was higher than that of gca for days to maturity, branches per plant, seeds per plant and seed yield per plant. High magnitude of sca variance for days to maturity, plant height, branches per plant, pods per plant, seeds per pod, 100 seed weight and seed yield per plant suggested the predominance of additive gene action.

Studies on gene action involving 10 cowpea varieties and their 45 F_1 hybrids (Sawant, 1994b) concluded that the characters seed yield per plant, number of branches per plant, number of inflorescence per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, days to 50 per cent flowering and plant height were controlled by dominant gene action.

Smitha (1995) observed the importance of both *gca* and *sca* effects, the sca effects being more predominant in the expression of the character number of pods per plant. Number of seeds per pod, 100 seed weight and grain yield per plant recorded a preponderance of *sca* effects. Based on this, she suggested that these characters were controlled primarily by non-additive gene action. The *gca* effects were more predominant for days to flowering and number of branches per plant indicating the characters were governed by additive gene action.

Cowpea genotypes Co 4, Guj 2 and C152 were reported as good general combiners for pod yield and seed yield per plant based on a line x tester analysis in cowpea (Madhusuda et al., 1995). The study also indicated the importance of both additive and non-additive genetic variance in the inheritance of seven quantitative traits with a preponderance of non-additive gene effects in most cases. Aravindhan and Das (1996) reported that the ratio of general combining ability (GCA) and specific combining ability (SCA) variance for yield traits in cowpea showed a predominance of SCA variance over GCA variance, suggesting the importance of non-additive gene action.

Nine varieties of cowpea were crossed in a partial diallel design for analysing combining ability by Chaudhari et al. (1998). The parent, GC-940 was good general combiner for grain yield, plant height, branches per plant and pods per plant. Both additive as well as non-additive gene effects were involved in the inheritance for all characters with predominance of non-additive gene action.

The estimated component of variance of general combining ability were higher than specific combining ability for all characters except green pod yield per plant in cowpea indicating the predominance of additive gene action for characters. The cowpea varieties, Sel. 2-2, IHR Sel. 11, Pusa Komal and BC-244002 were good combiners for pod yield per plant (Kumar et al., 1998).

Significant SCA and GCA variance were noted for days to flowering, plant height, number of branches per plant, pod length, number of pods per plant, number of seeds per pod, 100 seed weight and grain yield per plant indicating the role of additive as well as non-additive gene action (Sobha and Vahab, 1998a). The magnitude of GCA variance was higher suggesting the preponderance of additive gene action. Savithramma and Latha (1998) estimated heterosis in 45 hybrids produced by crossing 10 genotypes in diallel fashion without reciprocals. The best crosses for pods per plant were, RC-2 x V-37 and RC-2 x Co-Vu-2.

Sawarkar et al. (1999) evaluated twenty one hybrids of cowpea produced by diallel mating without reciprocals along with seven parents for combining ability

analysis. Preponderance of additive type of gene action was observed for all the characters. The best genotype on the basis of GCA effects and per se performance of pod yield and its contributing characters are Punjab-263 followed by Arka Garima.

Dijee et al. (2000) studied the combining ability for yield and yield component. The variance for general combining ability and specific combining ability showed that gene action was predominantly non-additive for all the characters studied. Anbuselvam et al. (2000) reported that additive gene effects were involved in the expression of the characters, days to 50 per cent flowering and plant height.

Combining ability analysis in cowpea by Rajkumar et al. (2000) also revealed the preponderance of additive gene action for days to 50 per cent flowering through combining ability analysis of a diallel mating system involving 8 parents. Both additive and dominant components of gene effects were significant for maturity in cowpea.

Ten lines and three testers of cowpea were crossed in a line x tester making design by Pal et al. (2002) to investigate the combining ability for green pod yield and yield components of cowpea. Results showed that ADCP-13, Red seeded Kala Zamal and Pusa Komal were good general combines for days to 50 per cent flowering.

Philip (2004) reported significant *gca* effects for grain yield per plant, pods per plant, inflorescence per plant, pod length and seeds per pod in cowpea. Among the lines L_4 and L_1 showed good *gca* effects for important yield characters.

In cowpea, Yadav et al. (2004) studied the genetics of green pod yield and its component characters by combining ability, graphical and numerical approaches of diallel cross analysis. Results on nature of gene action in three sets of genetic analyses showed more or less similar trend for most of the characters with slight over estimation of dominance component of genetic variance in

numerical analysis. All the studied characters were found to be governed by non additive gene action except days to 50 per cent flowering, pod length and seeds per pod. Hence, recurrent selection, diallel selective mating design or by parental mating may be advantageous for improvement of green pod yield in cowpea.

Positive significance of dominance x dominance interactions for pod weight points out that a breeding strategy for improving pod weight should be based on direct selection or hybridization and selection. The negative significance of dominance x dominance interaction for pod yield per plant was reported in yard long bean by Lovely (2005).

Renjana (2006) reported significant differences among treatments for all characters especially pod yield per plant in yard long bean. The magnitude of *sca* variance alone was significant suggesting the importance of the dominance gene action in controlling the quantitative and biochemical characters. VS 86 was found to be good general combiner among lines and Tvm-1 among testers. The cross P-1 x Tvm-1 was found to be promising for main stem length and 100 seed weight and VS-86 x Tvm-1 was superior for pod yield per plant based on *sca* effects.

Influence of environmental variation on combining ability involving eight parents and their 28 cross combinations were evaluated. Eight diverse genotypes of cowpea were crossed in diallel fashion excluding reciprocals. Eight parents and their 28 F_1's were raised. Pooled analysis of variance for combining ability showed significant interaction of *gca* variance and *sca* variance with environmental factors except seeds per pod indicated the role of environment in influencing the gene effects. The *sca* components of variance were higher than *gca* for yield component characters, indicating the predominance of non-additive gene effects. The cross TC-99-1 x TC-2000-4 (high x low gca combiners) showed significant positive sca effect, indicating that this cross will be promising for producing desirable transgressive segregents in subsequent generation (Singh et al., 2006).

Nine genotypes from *V. unguiculata* subsp. *unguiculata* (grain type) as female parents and four genotypes from *V. unguiculata* subsp. *sesquipedalis* (vegetable type) as male parents were recombined through line x tester making design. There was preponderance of *sca* variance over the *gca* variance for all the 12 characters studied, suggesting the predominant role of non-additive gene action. The parent belonging to *V. unguiculata* ssp. *unguiculata* namely GP1024, GP1238 and GP 739 and (Vijayanthi) and VS 33 of *V. unguiculata* ssp. *sesquipedalis* were identified as the best combiners for green pod yield. The hybrid combinations L9 x T4 (GP1231 x VS33), L4 x T3 (GP1024 x Vaijayanthi), L6 x L3 (GP 739 x Vaijayanthi) and L3 x T2 (GP1126 x Lola) were worth pursuing further in view of their best performance and high sca effects for green pod yield. Among the testers red poded varieties were alone identified as good combiners for green pod yield (Valarmathi et al., 2007b).

Pal et al. (2007) reported that the variance due to general and specific combining ability were highly significant denoting importance of additive and non-additive gene action for both the traits in cowpea. Additive genetic variance was predominant for days to 50 per cent flowering whereas non additive genetic variance governs days to first green pod picking. The parents NDCP-13, Kala Zamala, Red seeded, Black seeded, RCV-7, cowpea-263 and Pusa Komal were good general combiners for both the traits. The crosses sel.2-2 x Pusa Komal, cowpea local x Arka Garima and Sel.2-1 x Arka Garima were identified or best specific combiners for days to 50 % flowering whereas crosses sel. 2-2 x Pusa Komal, cowpea local x Arka Garima and Red seeded x Arka Garima were good for days to first green pod pocking.

2.8 HETEROSIS

The superiority of a hybrid in one or more characters over its parents is known as heterosis. The term heterosis was first used by Shull (1914). Existence of significant amount of dominance variance is essential for undertaking heterosis breeding programme. Even, the expression of small magnitudes of heterosis for a

particular character is also very much desirable in breeding. High estimate of heterosis is a result of high genetic diversity among parents indicating the possibility of identifying high yielding transgressive segregants from hybrid population (Singh, 2002).

Maximum heterosis was observed for seed yield per plant and pods per plant by Rejatha (1992) in cowpea. With five parents and ten hybrids, Hazra et al. (1993) found that frequency and level of heterosis was related more to *sca* than to genetic divergence of the parents.

Sawant et al. (1994) observed greatest positive heterosis over mid parent for seed yield per plant followed by inflorescence per plant, pods per plant, branches per plant and plant height in cowpea. A similar trend over better parent was observed except for branches per plant and plant height. Average heterosis over mid parent and better parent was greatest for seed yield per plant followed by pods per plant and inflorescence per plant. In cowpea, Sangwan and Lodhi (1995) observed heterosis over the better parent for yield (28.8 % - 84.0%) in different intervarietal crosses. They also reported heterosis for the yield contributing characters like number of pods per plant (81.6%), pod length (35.6%) and number of seeds per pod (20.4%).

Heterosis over the better parent ranged from 4.33 per cent for plant height to 91.52 per cent for days to maturity in cowpea (Bhor et al., 1997). Hybrids exhibiting high heterosis also showed high inbreeding depression, indicating the importance of non-additive gene action. Viswanatha et al. (1998) studied heterosis and inbreeding depression for yield and yield components in three intervarietal crosses of cowpea. Significant heterosis over mid parent and better parent was observed for most of the characters studied. Crosses showing high heterosis also exhibited high inbreeding depression indicating predominance of non-additive gene action for the traits studied.

Kumar et al. (1999) reported the cowpea genotypes var. 263, Sel. 2-2 and Sel. 2-1 to be promising parents giving high heterosis vigour for most of the

characters in various cross combinations. Estimates of heterosis were made using forty five hybrids produced by crossing ten cowpea genotypes in a diallel fashion without reciprocals by Savithramma and Latha (1999). The best crosses for pods per plant were RC-2 x V-37 and RC-2 x Co-VU-2.

In cowpea, Danam and Chaudhari (2000) crossed nine parents in diallel (excluding reciprocals) and found maximum positive heterosis in seed yield due to the heterosis found in yield component mainly, pods per plant, seeds per pod, clusters per plant and branches per plant.

Shashibushan and Chaudhary (2000) reported maximum positive heterosis for seed yield per plant over mid parent, better parent and standard check. Heterosis over mid parental value was reported for days to 50 per cent flowering (15.9%), number of branches per plant (75.5%), plant height (30.31%), number of pods per plant (11.5%), 100 seed weight (20.0%) and grain yield per plant (Bushana et al., 2000).

Malarvizhi (2002) reported heterosis for protein content in the pods and seeds in the F_1 and F_2 generation. Haibatpure et al. (2003) studied heterosis for quantitative characters in cowpea. Heterosis in yield seemed to be influenced by heterosis in number of pods per plant, seeds per pod, branches per pod and test weight.

In cowpea, Philip (2004) reported desirable negative heterosis for days to flowering. Seven crosses recorded positive and significant estimates of all three types of heterosis for pods per plant. Three crosses had positive and significant estimates of heterosis for inflorescence per plant, pods per inflorescence and grain yield.

Lovely (2005) observed that three crosses showed significant heterosis for maximum number of yield traits in yard long bean. These three crosses also had significant standard heterosis for all the characters studied. Significant negative heterosis for days to 50 per cent flowering indicate earliness. Renjana (2006)

reported six significant negative standard heterosis for days to 50 per cent flowering. Nine crosses exhibited significant positive standard heterosis for pods per plant. The cross P1 x Tvm-1 was found to be superior standard heterosis for main stem length and 100 seed weight.

Line x tester analysis of F_1 generation in cowpea expressed highly significant differences among parents and hybrid for days to 50 per cent flowering and days to first green pod picking. The cross combination black seeded x Pusa Komal showed maximum negative heterosis over better parent and mid parent, whereas Kala Zamala x cowpea – 263 was better over standard parent for days to 50 per cent flowering. The crosses, Ramnagar Kala x Arka Garima, Red seeded x Arka Garima and Red seeded x cowpea-263 showed maximum negative heterosis over better parent, mid parent and standard parent, respectively for days to first green pod picking (Pal et al., 2007).

2.9 GENERATION MEAN ANALYSIS

The concept of generation mean analysis was developed by Hayman (1958) and Jinks and Jones (1958) for the estimation of genetic components of variation. Analysis of this technique is based on six different generations of a cross viz; parents (P_1, P_2), there F_1, F_2 and back crosses (B_1, B_2). The mean values over replications are used for the estimation of gene effects. This technique also provides information about the presence or absence of epistasis besides estimation of additive and dominance variances and effects.

Studies of generation mean analysis in cowpea revealed the preponderance of additive gene action for inheritance of pubescence, but dominant and epistatic gene actions also made significant contributions (Ng et al., 2000).

Predominance of one or multiple epistasis interactions were generally observed for all characters. Additive gene effects were significant for days to 50 per cent flowering, number of pods per inflorescence, number of seeds per pod, 100 seed weight, plant height, and crude fibre content of pods. For all characters

except peduncle length, the direction of dominance effect and dominance x dominance interactions suggest the presence of non-allelic duplicate gene action in their expression. Peduncle length and complimentary gene action plays a major role (Philip, 2004).

Lovely (2005) observed the presence of all three types of digenic interaction for pods per plant in yard long bean. Pod yield per plant also displayed all three types of digenic interactions. The same direction of dominance effect and dominance x dominance interactions for days to flowering, pod length, pods per plant, pod yield per plant suggests non-allelic complimentary gene action in the expression of the character. The negative significance of dominance x dominance interaction for pod yield per plant suggests a limited scope of improvement through heterosis breeding for this traits. The direction of dominance effects and dominance x dominance interactions suggests the presence of non-allelic duplicate gene action for pod weight, pod breadth, pods per cluster, seeds per pod and days to first harvest in their expression.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The study was undertaken at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the period 2006-2008. The study utilized the data generated from four experiments. In experiments I(a) and I(b) were carried out for the evaluation and screening of the yard long bean germplasm for yield and pod borers resistance. In experiment II eight parents selected based on the experiment I(a) and I(b) were hybridized in Line x Tester manner. The F_1's obtained by hybridization were evaluated along with their parents and a standard check variety in Experiment III. In Experiment IV, six generations of selected three crosses were raised and generation mean analysis was conducted.

3.1. MATERIALS

3.1.1. Experiment I(a) and I(b)

The material for screening for field pod borers resistance and yield comprised of 50 cultivars of yard long bean collected from different parts of Kerala. The details of the accessions collected are given in the Table 1.

3.1.2. Experiment II

Five yard long bean genotypes having high yield and three genotypes having high tolerance to pod borers, selected as lines and testers respectively from the Experiment I (a) and (b). 15 F_1's were obtained by crossing them in Line x Tester manner.

Table 1. Particulars of vegetable cowpea genotypes used in the study for yield and resistance to pod borers

Sl. No.	Treatments	Varieties	Sl. No.	Treatments	Varieties
1	G_1	Kayamkulam local	26	G_{26}	VS 86
2	G_2	Kollamcode local	27	G_{27}	Trailing Red poded
3	G_3	Malika	28	G_{28}	TVM-1
4	G_4	Malappuram	29	G_{29}	Palakkad local
5	G_5	Varuvila local-1	30	G_{30}	KMV-1
6	G_6	Ookode-2	31	G_{31}	Vellayani local
7	G_7	Kuttichal	32	G_{32}	Vaikom
8	G_8	TVM-2	33	G_{33}	Moovattupuzha
9	G_9	VS-27	34	G_{34}	Kelakam
10	G_{10}	Ettumanoor local	35	G_{35}	Pathanamthitta
11	G_{11}	Neyyatinkara	36	G_{36}	Thiruvalla
12	G_{12}	Adoor	37	G_{37}	Kozhicode
13	G_{13}	Kottarakkara	38	G_{38}	TVM-3
14	G_{14}	Chingavanam	39	G_{39}	Sarika
15	G_{15}	Kanichar	40	G_{40}	Trailing white poded
16	G_{16}	Ambalapuzha-1	41	G_{41}	Mavelikkara
17	G_{17}	Pallippuram	42	G_{42}	NS 621
18	G_{18}	Palappooru-1	43	G_{43}	Kurappunthara local
19	G_{19}	Piravam	44	G_{44}	Pandalam
20	G_{20}	Cherthala local	45	$G4_5$	Vaijayanthi
21	G_{21}	Edappally	46	G_{46}	Ambayathode
22	G_{22}	Alappuzha	47	G_{47}	Kilimanoor
23	G_{23}	Palappooru-2	48	G_{48}	Ookode-1
24	G_{24}	Trailing Red poded Red seeded	49	G_{49}	Paravur
25	G_{25}	Ambalapuzha-2	50	G_{50}	Varuvila local-2

3.1.3.1. Experiment III(a)

The lines, testers and their 15 hybrids were raised along with a check in randomized block design with three replications during January 2008. The spacing was 1.5 x 0.45 m in plots of size 6.75m^2.

3.1.3.2. Experiment III(b)

Pot culture studies were carried out in Completely Randomised Design with three replications during January 2008.

3.1.4. Experiment IV(a) and (b)

The materials for generation mean analysis consisted of six populations viz; the F_1 hybrid, the F_2 population, the back cross generations with (B_1 and B_2) both the parents and the parents of the most promising cross selected from Experiment III on the basis of yield and resistance to pod borers.

3.2 METHODS

3.2.1. Layout and conduct of the Experiment

3.2.1.1. Experiment I(a) and I(b)

The field experiment using 50 genotypes of yard long bean were laid out in the Randomized Block Design with three replications during February 2007 (Plate 1). The spacing was 1.5 x 0.45 m in plots of size 6.75m^2. The recommended agronomic practices and need based plant protection measures were followed in accordance with the package of practices recommendations of Kerala Agricultural University (KAU, 2002). The observations were recorded on various biometric characters at each harvest from a random sample of five plants (in each replication) each with respect to treatments and the mean values were used for statistical analysis.

In experiment I(b) the genotypes were laid out for screening for resistance to pod borers in February 2007. RBD with two replications at a spacing of 1.5 x 0.45 m (Plate 2). Cultural and manurial practices were followed as per package of practices recommendations of Kerala Agricultural University (KAU, 2002) without adopting any protection measure.

3.2.1.2. Experiment II

The parents used in hybridization were selected based on the results of the previous experiments. From Experiment I(a) five lines were selected on the basis of selection index and with properties high pod yield, pod weight, pod length, seeds per pod and 100-seed weight. From Experiment I(b) three testers were selected on the basis of minimum damage parameters. The five lines and three testers were raised in a crossing block in summer 2007 and hybridization was done to obtain 15 F_1 hybrids. Production of hybrids was done by the technique of artificial pollination as suggested by Krishnaswamy (1970). For crossing the flower, buds due to open on the next day were selected and emasculated on the previous evening. For emasculation, the rest of the flowers and buds in a branch, except for the selected bud is removed. The stamens of selected bud was removed with a pair of fine forceps by gently pushing the keel petals apart. The emasculated floral branch was then bagged. Ripe anthers were collected in the next morning and pollination was done by gently pressing the ripe anthers against the stigma. The flowers were again bagged after pollination. The covers were removed a day after pollination. Pollination was done early in the morning between 6.30 and 8.00 am. The crossed as well as selfed flowers were labelled. The labelled pods were harvested separately on maturity and the seeds of parents and hybrids were collected.

3.2.1.3. Experiment III (a) & (b)

The fifteen hybrids along with their parents and a standard check were evaluated in a field experiment in RBD (Plate 3) with three replications in

Plate 1. Field view – Evaluation of germplasm for yield

Plate 2. Field view – Evaluation of germplasm for resistance to pod borers

Experiment III (a). The crop was raised as per the package of practices recommendations (KAU, 2007) of Kerala Agricultural University.

In Experiment III (b), the fifteen hybrids were evaluated for resistance to pod borers along with the eight parents in a pot culture experiment (Plate 4) in CRD with three replication during January 2008 without application of insecticides.

3.2.1.4. Building up of generations

The most promising hybrids in terms of yield and pod borers resistance was selected based on the results of Experiment III a & b. The F_1 was back crossed to the respective parents to obtain the two back cross generations, B_1 and B_2. Simultaneously, the F_1 was selfed to produce the corresponding F_2 population.

3.2.1.5. Experiment IV (a)

The materials used for generation mean analysis consisted of six generations (P_1, P_2, F_1, F_2, B_1 & B_2) of the selected hybrid combination. The experiment was conducted adopting a randomized block design with three replications with a spacing of 1.5 x 0.45 m for evaluation of yield traits in accordance with the package of practices recommendations of Kerala Agricultural University (KAU, 2007).

3.2.1.6. Experiment IV (b)

Pot culture studies for pod borers resistance analysis consisted of six generations of the selected hybrid combinations using CRD with three replications. Cultural and manurial practices were followed as per package of practices recommendations of Kerala Agricultural University (KAU, 2007) without adopting any plant protection measure.

Plate 3. Field view - Evaluation of F_1's and parents

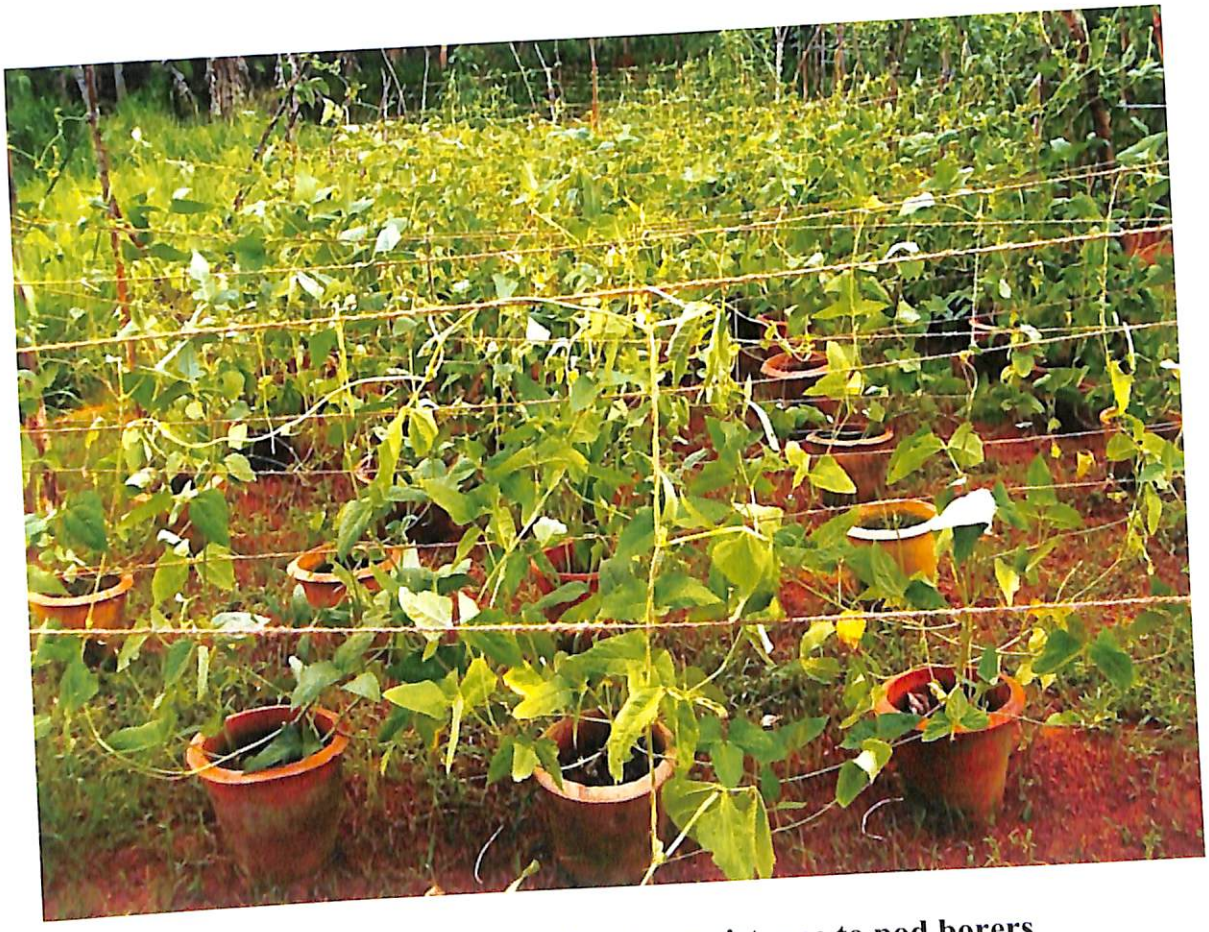


Plate 4. Pot culture studies for resistance to pod borers

3.2.2 Observations

3.2.2.1 Yield traits

a. Days to 50 percent flowering

Number of days taken from sowing to flowering of 50 per cent of the plants were recorded

b. Days to first harvest

Number of days taken from sowing to first harvest was recorded.

c. Length of harvest period (days)

Number of days taken from first harvest to the last harvest were recorded.

d. Crop duration (days)

Number of days taken from sowing to the last harvest was recorded.

e. Primary branches per plant

Number of primary branches was recorded on each observational plant at the time of final harvest (The number of primary branches arising from the main stem in each plant was recorded).

f. Main stem length (cm)

Length of the vine from the base of the plant to the terminal bud was measured and recorded.

g. Pod clusters per plant

Number of pod clusters of the observational plants were counted and recorded.

h. Pods per plant

Pods obtained in each harvest from each of the observational plants were counted and recorded.

i. Pod yield per plant (g)

Weight of pods from observational plants were recorded after each harvest. Total weight of pods of each observational plant was calculated and recorded.

j. Pods per cluster

Number of pods of each cluster of observational plants were recorded and mean worked out.

k. Pod weight (g)

Weight of five randomly selected individual pods (replication wise) were recorded from each observational plant and mean worked out.

l. Pod length (cm)

Length of five randomly selected individual pods (replication wise) were recorded from each observational plant and mean worked out.

m. Pod breadth (cm)

Breadth of 5 randomly selected individual pods were recorded from each observational plant and mean worked out.

n. Seeds per pod

Number of seeds of five randomly selected individual pods were recorded from each observational plant and mean worked out.

o. 100 seed weight (g)

The weight of 100 randomly selected seeds from each observational plants was recorded.

p. Length of peduncle (cm)

The length of five randomly selected fully elongated peduncles from each observational plants was measured at peak podding phase and mean values worked out.

q. Number of trichomes on pod wall (Count per mm^2)

Ten pods were collected at random from each plot. The skin was peeled from the middle portion of the pods and observed under a compound microscope at a magnification of 100X. Non glandular trichomes visible in three different microscopic fields were counted and the mean value was calculated using occular micrometer. The number of trichomes per mm^2 area of pod wall was calculated to represent the density of non – glandular trichomes on pod wall.

r. Leaf chlorophyll content (mg/g of leaf tissue)

Leaf chlorophyll content was estimated at 60 days after sowing. Fully expanded leaves collected from the top were used for chlorophyll estimation. Estimation of chlorophyll content of leaves was done by the Dimethyl Sulfoxide (Dmso) method (Hiscox and Israelstam, 1979).

Reagents

Dimethyl Sulfoxide: 80% acetone (1:1) mixture.

Procedure

A known weight (0.1 g) of the leaf material was taken in a test tube and cut into small bits. Added 10 ml of Dmso – acetone mixture and incubated the test tubes overnight at room temperature. All the pigments were extracted into the solution. Decanted the coloured solution into a measuring cylinder and made up the volume to 25 ml with Dmso – acetone mixture. Recorded the absorbance at

645 and 663 nm using a spectrophotometer. Calculated the chlorophyll content by substituting the absorbance values in the given formula

$$\text{Chlorophyll a} = (12.7\ A_{663} - 2.69\ A_{645}) \times \frac{v}{1000} \times \frac{1}{\text{Fresh weight}}$$

$$\text{Chlorophyll b} = (22.9\ A_{645} - 4.64\ A_{663}) \times \frac{v}{1000} \times \frac{1}{\text{Fresh weight}}$$

$$\text{Total chlorophyll (a + b)} = (8.02\ A_{663} + 20.20\ A_{645}) \times \frac{v}{1000} \times \frac{1}{\text{Fresh weight}}$$

where, A is the absorbance at specific wavelengths and v, the volume of the extract

s. Protein content of pods (%)

Fresh green pod samples were subjected to protein estimation using Lowry's method (Sadasivam and Manickam, 1992).

Reagents

i. 2% sodium carbonate in 0.1N sodium hydroxide (Reagent A)
ii. 0.5% copper sulphate in 1.0% potassium sodium tartrate (Reagent B)
iii. Alkaline copper solution
Mixed 50 ml of A and 1 ml of B prior to use (Reagent C)
iv. Folin – Ciocalteau reagent (Reagent D)

Refluxed gently for 10h a mixture consisting of 100g sodium tungstate, 25g sodium molybdate, 700 ml water, 50 ml of 85% phosphoric acid and 100 ml of concentrated hydrochloric acid in a 1.5 l flask. Added 150 g lithium sulphate, 50 ml water and a few drops of bromine water. Boiled the mixture for 15 minutes without condenser to remove excess bromine, cooled, diluted to 1L and filtered.

v) Protein solution (Stock standard)

Weighed accurately 50mg of bovine serum albumin and dissolved in distilled water and made up to 50ml in a standard flask.

vi) Working standard

Diluted 10ml of the stock solution to 50ml with distilled water in a standard flask. One ml of this solution contains 200mg of protein.

Procedure

Extraction of protein from sample

Extraction was carried out with Tris – HCl buffer (62.5 mM, pH 6.8). Weighed 200mg of fresh pod at vegetable maturity and grind well with a pestle and mortar in 3.8 ml of the buffer. Centrifuged and the supernatant was taken for protein estimation.

Estimation of protein

Pippetted out 0.2, 0.4, 0.6, 0.8 and 1.0 ml of the working standard into a series of test tubes. 0.1 ml of the sample extract was taken in another test tube. Made up the volume to 1 ml in all the test tubes. A tube with 1 ml of water served as the blank. Added 5ml of reagent to each tube including the blank. Mixed well and incubated at room temperature in the dark for 30 minutes. A blue colour was developed and the optical density was measured at 660nm using a UV spectrophotometer. Standard graph was prepared and calculated the amount of protein in the samples.

t. Crude fibre content of pods (%)

Crude fibre content was percentage of weight of sample taken was estimated as per the procedure given by Maynard (1970). Boiled 2g of dried and grind pod with 200 ml of sulphuric acid for 30 minutes with bumping chips. It was filtered through muslin and washed with boiling water until washings were no longer acidic. Then it was boiled with 200 ml sodium hydroxide solution for 30 minutes

and filtered through muslin cloth, washed with 25 ml boiling 1.25 per cent sulphuric acid, three 50 ml portions of water and 25 ml alcohol. The residue was removed and transferred to ashing dish. The residue was dried for 2 hours at 130 ± 2°C, cooled in a dessicator and weighed. It was ignited for 30 min at 600 ± 15°C, cooled in a dessicator and weighed.

3.2.2.2. Damage parameters

a. Percentage of infestation of flower buds

A sample of 25 fully mature flower buds were randomly collected from each plot at peak flowering stage of the crop and the number of buds with pod borer infestation were counted and expressed as percentage.

b. Number of larvae per 25 flowers

This was determined from a random sample of 25 flowers collected at peak flowering stage from each plot. The flowers were immediately dissected and the larvae were counted.

c. Percentage of pod infestation

A sample of 25 pods were randomly collected from each plot at the peak podding phase. Pods infested by pod borers were counted and expressed as percentage.

d. Number of larval entry / exit holes per pod

Pods used for the assessment of percentage pod infestation were examined for the number of larval entry or exit holes. The count is expressed as number of holes per pod.

e. Number of damaged seeds in a sample of 25 pods

Pods used for the assessment of percentage pod infestation were then used for estimation of seed damage. The pods were split open and the number of

damaged seeds in the 25 pods was ascertained. The observation was made use of in working out the seed damage index; Isd expressed in percentage.

$$Isd = \frac{ds}{pt} \times 100$$

where, ds = number of damaged seeds and
pt = number of pods sampled.

f. Plant resistant index (Ipr)

A plant resistant index was computed for each variety using a combination of the following damage parameters.

1. Number of larvae per 25 flowers
2. Percentage pod infestation
3. Seed damage index

$$Ipr = \frac{W_1S + W_2T + W_3M}{W_1 + W_2 + W_3}$$

where S, T, M are measurement of damaged seeds(S), pods(T) and flowers(M) respectively, with weights W_1, W_2 and W_3 are 3, 2 and 1 respectively. These weighted measurements reflect the relative importance attached to each of the damage parameters with respect to their contribution in reduction of economic yield (Jackai, 1982). Low values of plant resistant index indicate resistance / tolerance. Symptoms of pod borers damage parameters was shown in Plate 5 and 6.

3.3. STATISTICAL ANALYSIS

3.3.1.Analysis of variance (ANOVA)

Analysis of variance of the data (Panse and Sukhatme 1985) collected from the various experiments was done to test the significance of differences among

Plate 5. Symptoms of pod borer damage (*M. vitrata*)

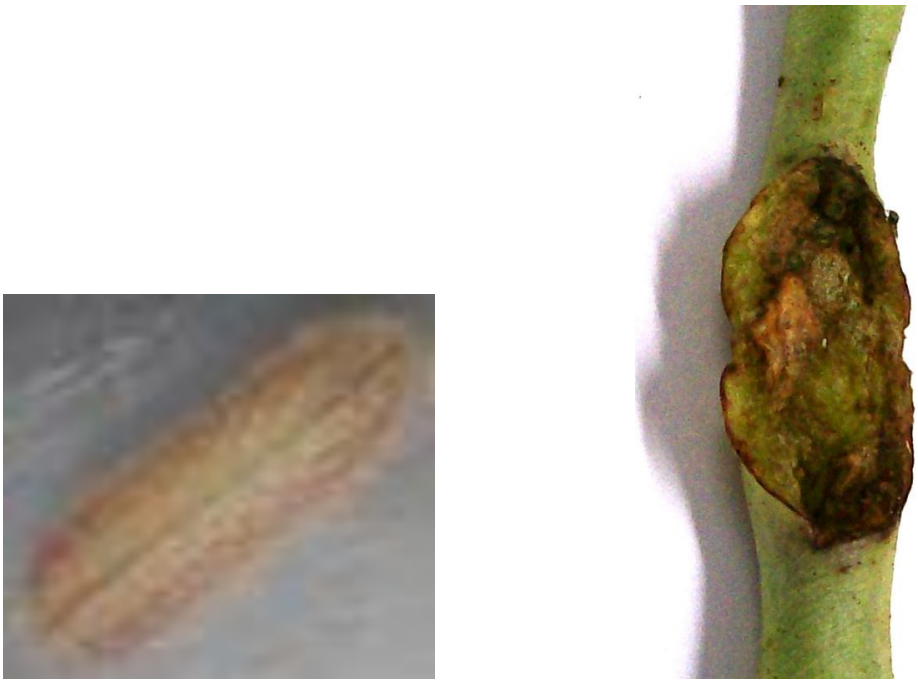


Plate 6. Symptoms of pod borer damage (*L. boeticus*)

genotypes with respect to the character and to estimate the variance components as follows.

Source of variation	Degrees of freedom	Mean square	F
Treatment	(t-1)	MST	MST/MSE
Replication	(r-1)	MSR	MSR/MSE
Error	(t-1) (r-1)	MSE	
Total	(tr-1)		

where, t = number of treatments, r = number of replications, MST = Treatment mean square, MSR = Replication mean square, MSE = Error mean square.

$$\text{Critical difference (CD)} = t_{\alpha} \sqrt{\frac{2MSE}{r}}$$

where, t_{α} is the Student's table value at error degrees of freedom and α is the level of significance (5% level).

3.3.2. Estimation of Genetic parameters

a) Genetic components of variance

For each character, the phenotypic and genotypic components of variance were estimated by equating the expected values of mean squares (MS) to the respective variance components (Jain 1982). Based on this, the following variance components were estimated.

i) Genotypic variance (V_G)

$$V_G = \frac{MST - MSE}{r}$$

ii) Environmental variance (V_E)

$$V_E = MSE$$

iii) Phenotypic variance (V_P)

$$V_P = V_G + V_E$$

b) Coefficients of variation

Genotypic and phenotypic coefficients of variation were worked out for using the estimates of V_G and V_P and expressed in percentage (Burton, 1952).

i) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{V_P}}{(\bar{x})} \times 100$$

ii) Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{V_P}}{(\bar{x})} \times 100$$

where, $\bar{x}$ is the mean of each character over all the treatments.

c) Heritability

For each trait, heritability (broad sense) was calculated as the ratio of genotypic variance to phenotypic variance and expressed as percentage (Jain, 1982).

$$\text{Heritability } (H^2) = \frac{V_G}{V_P} \times 100$$

Heritability was categorized as

Low → <30 %

Moderate → 31 – 60 %

High → >60 %

(Johnson et al., 1955)

d. Genetic advance

Genetic advance, which is the measure of genetic gain under selection, depends upon standardized selection differential, heritability and phenotypic standard deviation (Allard, 1960).

$$\text{Genetic advance (GA)} = k.\ H^2\sqrt{Vp}$$

where, k is the standardized selection differential (2.06 at 5% selection intensity)

$$\text{GA as percentage of mean} = \frac{k.H^2\sqrt{Vp}}{\bar{x}} \times 100$$

Genetic advance was categorized as

Low → <10 %
Moderate → 11 – 20 %
High → >20 %

(Johnson et al., 1955)

3.3.3. Association analysis

a. Correlations

Phenotypic, genotypic and environmental correlation coefficients were calculated using the respective variances and co-variances of the characters.

Phenotypic correlation coefficient (r_{Pxy}) = $\frac{Cov_P(x, y)}{\sqrt{V_P(x) \cdot V_P(y)}}$

Genotypic correlation coefficient (r_{Gxy}) = $\frac{Cov_G(x, y)}{\sqrt{V_G(x) \cdot V_G(y)}}$

Environmental correlation coefficient (r_{Exy}) = $\frac{Cov_E(x, y)}{\sqrt{V_E(x) \cdot V_E(y)}}$

where $Cov_p(x,y)$, $Cov_G(x,y)$ and $Cov_E(x,y)$ denote the phenotypic, genotypic and error covariances between two traits x and y respectively. $V_P(x)$, $V_G(x)$ and $V_E(x)$ respectively are the phenotypic, genotypic and error variances for x, and $V_P(y)$, $V_G(y)$ and $V_E(y)$ respectively indicate the phenotypic, genotypic and error variances for y.

b. Path coefficient analysis

The direct and indirect effects of component characters, on yield were estimated through path analysis technique (Wright, 1954).

3.3.4. Selection Index

To discriminate the genotypes based on characters under study selection index developed by Smith (1936) and discriminant function of Fisher (1936), were employed.

The selection index is described by the function, $I = b_1x_1 + b_2x_2 + \ldots\ldots\ldots + b_kx_k$ and the merit of a plant is described by the function, $H = a_1G_1 + a_2G_2 + \ldots\ldots + a_kG_k$ where, $x_1, x_2, \ldots\ldots x_k$ are the phenotypic values and $G_1, G_2, \ldots\ldots\ldots G_k$ are the genotypic values of the plants with respect to the characters 1 ,2, …… k are economic weightage and H_1 the genetic worth of the plant. It is assumed that economic weight assigned to each character is equal to unity ie: $a_1, a_2, \ldots\ldots, a_k = 1$ and $b_1, b_2, \ldots\ldots, b_k$ are regression coefficients or index values are determined such that correlation between H and I is maximum.

The procedure will reduce to an equation of the form

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

where, P and G are the phenotypic and genotypic variance covariance matrices respectively from which the b values were solved out. The b values are multiplied by the corresponding values of selected characters for each genotype to get the index value of a genotype.

3.3.5 Mahalanobis D^2 analysis

Genetic divergence was studied using Mahalanobis D^2 statistics as described by Rao (1952). The genotypes were clustered by Tochers method.

3.3.6 Line x Tester analysis

3.3.6.1. Combining ability analysis

Combining ability analysis of the Line x Tester was done through ANOVA technique (Dabholkar, 1992) as follows.

Source	Degrees of freedom	Sum of Squares	Mean Sum of Squares	Expected mean square
Replication	r-1	SSR	MSR	
Genotypes	n-1	SSG	MSG	
Parents	(l + t)-1	SSP	MSP	
Parents Vs. Crosses	1	SSO	SMO	
Crosses	l x t -1	SSC	MSC	
a. Lines	l - 1	SSL	ML	$\sigma^2 e + r\sigma^2_{sca} + rt\sigma^2_{gca}$
b. Tester	t – 1	SST	MT	$\sigma^2 e + r\sigma^2_{sca} + rl\sigma^2_{gca}$
c. Line x Tester	(l-1)(t-1)	SSLT	MLT	$\sigma^2 + r\sigma^2_{sca}$
Error	(n-1)(r-1)	SSE	M_e	$\sigma^2 e$
Total	nr-1			

where, n = number of treatment materials = (l + t + l) x t
r = number of replications l = number of lines t = number of testers

3.3.6.1.1. Estimation of General and Specific combining ability effects

General combining ability effect (gca) of parents and specific combining ability effect (sca) of hybrids were estimated using the following model.

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + e_{ijk}$$

where, μ = Population mean

g_i = gca effect of i^{th} line

g_j = gca effect of j^{th} tester

s_{ij} = sca effect of ij^{th} hybrid

e_{ijk} = error associated with ijk^{th} hybrid.

i = 1, 2,….., l

j = 1, 2, ….., t

k = 1, 2, ….., r

The individual effects were estimated as follows

(i) Mean = $\frac{x...}{r_{lt}}$

(ii) gca effect of lines = $\frac{x_{i..}}{r_t} - \frac{x...}{r_{lt}}$

(iii) gca effect of testers = $\frac{x_{j.}}{r_l} - \frac{x...}{r_{lt}}$

(iv) sca effect of hybrids = $\frac{x_{ij.}}{r} - \frac{x_{i..}}{r_t} - \frac{x_{j.}}{r_l} + \frac{x...}{r_{lt}}$

where,

x… = totality of observations on all hybrids over ‘r’ replications

xi.. = totality of observations on i^{th} line over ‘t’ testers and ‘r’ replications.

x.j. = Totality of observations on j^{th} tester over 'l'lines and 'r' replications

$$t = \frac{(\text{Effect})}{SE\ (\text{effect})}$$

where,

$$\text{SE of gca (lines)} = \sqrt{\frac{M_e}{rt}}$$

$$\text{SE of gca (testers)} = \sqrt{\frac{M_e}{rl}}$$

$$\text{SE of sca (hybrids)} = \sqrt{\frac{M_e}{r}}$$

3.3.6.1.2. Combining Ability Analysis

The GCA variance for lines and testers and SCA variance for the hybrids were calculated as follows.

$$\sigma^2_{GCA}\ (\text{lines}) = \frac{ML - MLT}{rt} = \text{cov. H.S. (lines)}$$

$$\sigma^2_{GCA}\ (\text{testers}) = \frac{MT - MLT}{rl} = \text{cov. H.S. (tester)}$$

$$\sigma^2_{SCA}\ (\text{hybrids}) = \frac{MLT - Me}{r}$$

3.3.6.1.3. Proportional contribution

Proportional contribution of lines, testers and their interaction to total variance were calculated. (Singh and Chaudhary, 1985) as follows.

$$\text{Contribution of lines} = \frac{SS(\text{lines})}{SS(\text{hybrids})} \times 100$$

$$\text{Contribution of testers} = \frac{SS(\text{tester})}{SS(\text{hybrids})} \times 100$$

$$\text{Contribution of line x testers} = \frac{SS(\text{line} \times \text{tester})}{SS(\text{hybrids})} \times 100$$

3.3.7. Heterosis

Extent of heterosis was computed for all the fifteen hybrids as relative heterosis (RH), standard heterosis (SH) and heterobeltiosis (HB) using the following formulae and expressed as percentage (Rai, 1979).

3.3.7.1. Relative Heterosis

Relative heterosis was estimated as the percentage deviation of the mean performance of $(\bar{F}_1)$ over the mean performance of the parents $(\overline{\bar{M}\bar{P}})$

$$\text{Relative heterosis (RH)} = \frac{\bar{F}_1 - \overline{\bar{M}\bar{P}}}{\overline{\bar{M}\bar{P}}} \times 100$$

where,

$\overline{\bar{M}\bar{P}}$ = mid parental mean value

$\bar{F}_1$ = average performance of F_1

3.3.7.2 Heterobeltiosis

Heterobeltiosis was estimated in comparison to the better parent as

$$\text{Heterobeltiosis (HB)} = \frac{\bar{F}_1 - \bar{B}\bar{P}}{\bar{B}\bar{P}} \times 100$$

where, $\bar{B}\bar{P}$ = better parental mean of a particular cross.

3.3.7.3. Standard Heterosis

Standard heterosis was estimated in comparison to the standard variety (KMV-1) as

$$\text{Standard heterosis (SH)} = \frac{\bar{F}_1 - \bar{S}\bar{P}}{\bar{S}\bar{P}} \times 100$$

where, $\bar{S}\bar{P}$ = mean of the standard variety

The significance of different types of heterosis was tested by 't' test with (n-1) (r-1) degrees of freedom. The critical difference (CD) for comparison of difference of F_1 is

F_1 with $\bar{M}\bar{P}$ is = $t_\alpha = \sqrt{\frac{3M_e}{2r}}$

F_1 with $\bar{B}\bar{P}$ is = $t_\alpha = \sqrt{\frac{2M_e}{r}}$

F_1 with $\bar{S}\bar{P}$ is = $t_\alpha = \sqrt{\frac{2M_e}{r}}$

where t_α is students 't' table value of five per cent level for (n-1) (r-1) degrees of freedom.

3.3.8. Generation mean analysis

Six parameter model (Hayman, 1958) was used for the analysis, which consisted of the following steps.

i) Development of scales

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

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

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

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

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

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

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

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

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

where, $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$ $\bar{F}_2$, $\bar{B}_1$ $\bar{B}_2$ are the means of respective generations over all replications and V $(\bar{P}_1)$, V $(\bar{P}_2)$, V $(\bar{F}_1)$, V $(\bar{F}_2)$, V $(\bar{B}_1)$, V $(\bar{B}_2)$ are the respective variances. The standard errors of A, B, C and D were obtained as square root of V_A, V_B, V_C and V_D respectively.

ii) Testing for epistasis

Significance of any of the four scales indicates the inadequacy of additive dominance model and presence of epistasis. For testing the significance of A, B, C and D scales, 't' test was employed.

$$t_A = \frac{A}{\sqrt{V_A}}$$

$$t_B = \frac{B}{\sqrt{V_B}}$$

$$t_C = \frac{C}{\sqrt{V_C}}$$

$$t_D = \frac{D}{\sqrt{V_D}}$$

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

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

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

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

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

iii) Estimation of genetic components

When the scales A, B, C and D were significantly different from Zero, a digenic interaction model was assumed and the following six parameters were estimated (Jinks and Jones, 1958).

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

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

$$h = \bar{F}_1 - 4\bar{F}_2 - \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 + 2\bar{B}_1 + 2\bar{B}_2$$

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

$$j = \left(B_1 - \frac{1}{2}P_1\right) - \left(B_2 - \frac{1}{2}P_2\right)$$

$$l = P_1 + P_2 + 2F_1 + 4F_2 - 4B_1 - 4B_2$$

where, m = mean

d = additive effect

h = dominane effect

i = additive x additive interaction

j = additive x dominance interaction

l = dominance x dominance interaction

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

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

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

$$V(h) = V(\bar{F}_1) + 16V(\bar{F}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2) + 4V(\bar{B}_1) + 4V(\bar{B}_2)$$

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

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

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

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

iv. Transgressive segregents (%)

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

v. Inbreeding depression

Inbreeding depression for the various characters were calculated as per the formula given below

$$\text{Inbreeding depression} = \frac{\bar{F}_1 - \bar{F}_2}{\bar{F}_1} \times 100$$

where $\bar{F}_1$ = average performance of F_1

$\bar{F}_2$ = average performance of F_2

RESULTS

4. RESULTS

The results obtained from various experiments of the present investigation are given below.

4.1. EVALUATION OF GERMPLASM FOR YIELD

4.1.1. Mean performance

The results of the analysis of variance for 20 characters that were used to compare the performance of 50 yard long bean genotypes are presented in Table 2. Significant differences were detected among the genotypes with respect to all the characters studied.

The mean value of the 50 genotypes for all the characters namely days to 50 per cent flowering, days to first harvest, length of harvest period, crop duration, primary branches per plant, main stem length, pod clusters per plant, pods per plant, pod yield per plant, pods per cluster, pod weight, pod length, pod breadth, seeds per pod 100 seed weight, length of peduncle, number of trichomes on pod wall, leaf chlorophyll content, pod protein content and crude fibre content of pods are presented in Table 3.

The days to 50 per cent flowering was maximum in genotype G_{11} (53.67) followed by G_{43} (52.67), G_{40} (52.33) and G_6 (51.67). G_{47} was the earliest flowering genotype (38.33) followed by G_{14} (39.00) and G_{13} (39.33).

Days to first harvest ranged from 50.00 to 62.33 in genotypes G_{14}, G_{24}, G_{28} and G_6, G_{20} respectively. Length of harvest period was maximum for G_5 and G_3 (31.00) and minimum for G_{10} (18.67) followed by G_{27} (21.33) (Four genotypes were on par with G_{27} for the character). Crop duration was maximum for G_{34} (87.33) followed by G_5 (86.67) and minimum for the genotype G_1 (72.00) followed by G_2 (72.67) and G_{49} (74.67).

Table 2. Analysis of variance of various characters in 50 yard long bean genotypes

Sl. No.	Characters	Mean squares		
		Treatment	Error	F
I. Yield traits				
1.	Days to 50 per cent flowering	43.73	5.99	7.29**
2.	Days to first harvest	29.22	1.38	21.12**
3.	Length of harvest period	28.68	1.37	20.89**
4.	Crop duration	42.31	6.15	6.88**
5.	Primary branches per plant	0.82	0.10	8.03**
6.	Main stem length	1302.96	71.32	18.26**
7.	Pod clusters per plant	5.06	0.13	38.60**
8.	Pods per plant	8.95	0.20	43.46**
9.	Pod yield per plant	9821.18	828.28	11.86**
10.	Pods per cluster	0.161	0.02	7.35**
11.	Pod weight	54.92	0.29	186.80**
12.	Pod length	265.87	2.60	102.07**
13.	Pod breadth	0.054	0.01	97.74**
14.	Seeds per pod	25.19	0.13	186.30**
15.	100 seed weight	24.19	0.23	105.34**
16.	Length of peduncle	73.76	0.20	370.03**
17.	Number of trichomes on pod wall (count per mm^2)	4.0062	0.1107	36.19**
II. Biochemical traits				
18.	Leaf chlorophyll content (mg/g of leaf tissue)	0.0576	0.0123	4.67**
19.	Protein content of pods	3.1079	0.0396	78.40**
20.	Crude fibre content of pods	0.6404	0.299	2.135**

** Significant at 1 % level

Table 3. Varietal differences with respect to yield and related characters of fifty genotypes of yard long bean

Genotypes	Characters														
	Days to 50% flower-ing	Days to first harvest	Length of harvest period	Crop duration	Primary branches per plant	Main stem length (cm)	Pod cluster per plant	Pods per plant	Pod yield per plant (g)	Pods per cluster	Pod weight (g)	Pod length (cm)	Pod breadth (cm)	Seeds per pod	100 seed weight (g)
G_1	48.00	54.67	30.00	72.00	3.60	475	6.20	7.07	172.17	2.00	8.33	26.01	0.83	10.47	7.47
G_2	46.33	54.33	28.00	72.67	3.60	475.33	5.13	8.13	198.33	2.07	8.20	12.88	0.73	11.53	8.47
G_3	48.00	55.67	31.00	86.33	3.33	495.33	4.40	7.00	196.00	2.20	8.53	20.03	0.91	13.20	9.27
G_4	50.33	57.00	30.00	85.00	4.33	501.33	7.07	6.40	245.00	2.27	15.20	33.53	0.86	13.93	11.47
G_5	45.67	54.00	31.00	86.67	4.87	503.67	8.07	6.40	170.33	2.53	9.53	13.84	0.87	12.13	8.13
G_6	51.67	62.33	29.33	76.67	4.80	455.17	6.07	5.73	222.67	2.07	15.13	26.49	0.63	14.13	7.33
G_7	40.67	52.67	30.67	78.33	3.87	452	7.33	8.47	259.67	2.80	12.33	32.06	0.65	14.46	9.93
G_8	49.00	57.00	24.00	84.33	3.27	469.5	5.73	7.53	221.67	2.20	10.53	18.23	0.95	12.87	12.73
G_9	50.00	59.00	32.00	86.33	3.47	468.5	5.07	6.27	221.67	2.47	8.33	22.12	0.87	12.53	12.73
G_{10}	45.67	51.33	18.67	79.33	5.07	507.83	9.13	11.17	393.50	2.53	20.93	52.72	1.19	21.33	19.47
G_{11}	53.67	60.00	30.00	84.33	3.67	469.5	4.07	8.27	227.00	2.33	10.40	19.55	0.96	15.20	13.53
G_{12}	49.33	53.33	29.33	84.33	4.33	470.83	4.47	7.07	277.33	2.07	15.20	14.28	0.93	16.13	12.53
G_{13}	39.33	52.67	26.00	83.67	3.53	471.67	5.13	7.07	214.00	2.00	10.53	27.03	0.63	15.13	10.07
G_{14}	39.00	50.00	26.67	85.33	3.40	472.83	5.20	5.70	207.00	2.20	10.33	33.82	0.65	16.27	11.07
G_{15}	46.33	54.33	25.33	85.00	3.33	472.17	4.07	7.33	211.00	2.53	8.40	13.64	1.06	18.13	12.33
G_{16}	42.00	56.00	25.67	78.00	3.40	469.33	6.20	7.00	201.00	2.47	8.20	16.45	0.63	19.27	12.27

Table 3. Continued

Genotypes	Characters														
	Days to 50% flower-ing	Days to first harvest	Length of harvest period	Crop duration	Primary branches per plant	Main stem length	Pod cluster per plant	Pods per plant	Pod yield per plant	Pods per cluster	Pod weight	Pod length	Pod breadth	Seeds per pod	100 seed weight
G_{17}	50.33	53.33	25.67	79.67	3.40	469.5	8.07	7.27	216.67	2.40	10.47	26.06	0.76	12.53	13.47
G_{18}	50.67	58.00	25.33	80.00	3.40	514	7.80	6.40	272.33	2.07	14.13	23.97	0.87	15.27	12.67
G_{19}	49.67	56.67	26.00	80.00	3.67	507	6.47	7.27	300.50	2.27	14.13	32.73	0.85	15.20	12.47
G_{20}	50.67	62.33	26.00	82.00	4.13	503.83	6.20	8.40	325.00	2.80	16.40	24.39	0.83	16.13	12.87
G_{21}	47.33	54.67	26.33	77.33	4.13	502.5	4.27	8.67	224.00	2.40	10.53	27.10	0.9	11.07	13.60
G_{22}	43.00	57.33	27.00	83.33	3.93	502.33	4.07	7.00	279.00	2.20	12.73	15.24	0.91	11.87	12.73
G_{23}	40.33	51.33	27.00	81.00	4.13	507.67	6.40	6.33	233.33	2.07	12.40	19.16	0.77	10.80	16.53
G_{24}	44.33	50.00	27.00	84.67	3.40	508.33	4.60	6.20	244.67	2.07	8.47	27.54	0.85	18.20	15.00
G_{25}	44.33	50.67	30.00	81.67	3.40	457.83	4.07	6.80	216.67	2.07	8.27	34.94	0.81	16.13	15.07
G_{26}	43.33	54.33	28.00	77.67	3.33	505.17	6.33	8.13	262.33	2.27	8.40	27.77	0.91	15.67	12.73
G_{27}	49.00	56.67	21.00	80.00	4.80	500.17	7.13	11.73	401.83	2.13	16.07	37.63	1.20	19.20	13.40
G_{28}	44.33	50.00	28.00	79.33	3.53	477.17	7.20	6.13	232.00	2.13	10.47	34.29	0.85	19.20	13.40
G_{29}	45.67	54.33	22.33	78.00	4.40	484.00	6.87	9.60	415.33	2.40	17.87	36.34	1.01	17.37	18.27
G_{30}	48.33	55.67	27.33	81.00	3.33	476.50	5.20	9.07	261.00	2.07	10.07	36.02	0.78	12.47	16.67
G_{31}	43.67	57.00	22.33	80.67	4.73	500.17	6.27	8.33	363.00	2.67	27.73	47.75	1.18	21.40	19.73
G_{32}	46.33	54.67	23.67	84.67	3.73	452.67	4.33	6.27	258.67	2.13	10.20	18.14	0.92	17.47	12.13
G_{33}	42.33	54.00	25.00	76.00	3.27	452.33	6.40	8.93	276.00	2.13	8.40	14.95	0.85	18.33	12.60

Table 3. Continued

Genotypes	Characters														
	Days to 50% flower-ing	Days to first harvest	Length of harvest period	Crop duration	Primary branches per plant	Main stem length (cm)	Pod cluster per plant	Pods per plant	Pod yield per plant (g)	Pods per cluster	Pod weight (g)	Pod length (cm)	Pod breadth (cm)	Seeds per pod	100 seed weight (g)
G_{34}	47.00	54.67	25.00	87.33	3.60	450.00	4.27	6.47	251.00	2.33	8.60	27.88	0.91	15.93	16.47
G_{35}	46.33	53.67	24.30	86.67	3.40	487.17	4.47	11.13	336.33	2.00	15.13	27.79	0.77	14.93	16.53
G_{36}	49.33	53.33	21.00	86.67	3.40	464.50	6.20	7.07	304.83	2.00	15.20	33.73	0.85	16.53	12.27
G_{37}	45.00	54.67	21.00	75.33	3.60	480.17	4.33	7.20	207.17	2.00	9.73	26.79	0.93	15.33	12.54
G_{38}	47.00	54.33	21.00	81.33	3.27	479.50	5.33	14.33	317.00	2.07	9.47	20.82	0.78	15.13	15.07
G_{39}	51.67	58.00	21.33	80.67	3.73	449.17	5.07	8.07	289.00	2.33	10.40	14.33	0.82	19.94	12.67
G_{40}	52.33	52.00	26.67	80.00	4.07	453.50	4.53	7.13	276.33	2.47	10.73	33.87	0.87	19.4	16.73
G_{41}	50.33	59.00	27.33	80.00	4.27	462.17	6.40	6.20	301.33	2.67	12.47	21.92	0.93	16.27	12.93
G_{42}	42.00	51.33	20.00	83.67	5.00	490.00	8.07	8.77	331.50	2.67	27.46	52.26	1.16	22.53	18.53
G_{43}	52.67	61.00	27.00	85.33	4.40	482.00	5.20	6.53	275.50	2.33	12.47	14.87	0.93	19.86	13.53
G_{44}	49.00	52.00	26.00	84.67	4.27	424.83	5.47	7.33	255.33	2.07	12.53	27.52	0.78	12.60	13.73
$G4_5$	50.00	50.67	26.33	82.33	4.00	473.83	4.20	7.13	199.67	2.13	12.07	28.96	0.86	15.60	12.67
G_{46}	41.67	51.33	26.33	82.67	3.27	473.67	6.20	7.20	216.67	2.13	10.53	20.12	0.81	16.20	14.87
G_{47}	38.33	50.67	26.67	82.00	3.40	467.33	6.47	5.27	190.50	2.33	10.53	18.23	0.83	18.13	16.53
G_{48}	47.33	54.67	26.00	80.67	3.53	510.83	4.33	5.53	258.67	2.20	13.33	27.13	0.91	16.27	12.33
G_{49}	47.00	54.67	27.33	74.67	3.40	503.83	5.40	7.47	288.67	2.13	14.27	30.57	0.67	15.13	12.73
G_{50}	48.67	57.67	25.67	78.67	3.53	499.67	7.27	5.07	235.00	2.80	13.67	28.97	0.81	15.33	13.67
Mean	46.68	54.78	26.09	81.36	3.81	480.07	5.76	7.54	259.10	2.27	12.31	26.45	0.86	15.80	13.38
SE	1.999	0.960	0.957	2.025	0.261	6.896	0.296	0.371	23.499	0.121	0.443	1.318	0.019	0.300	0.391
CD	3.967	1.906	1.898	4.019	0.519	13.684	0.587	0.735	46.633	0.240	0.879	2.615	0.038	0.596	0.777

Table 3. Continued

Genotypes	Length of peduncle (cm)	Number of trichomes on pod wall (count per mm^2)	Leaf chlorophyll content (mg/g of leaf tissue)	Protein content of pods (%)	Crude fibre content of pods (%)
G_1	22.25	2.40	1.640	7.420	2.465
G_2	17.35	3.60	1.535	6.615	2.230
G_3	22.50	2.30	1.515	7.980	2.340
G_4	24.10	2.60	1.310	5.985	3.670
G_5	21.30	2.20	1.470	3.745	2.725
G_6	18.10	3.10	1.435	6.135	2.150
G_7	27.30	5.30	1.505	6.475	2.395
G_8	23.65	5.50	1.460	3.530	2.365
G_9	21.00	3.00	1.650	5.870	2.360
G_{10}	26.05	3.20	1.660	8.250	3.740
G_{11}	26.00	1.30	1.620	6.940	2.590
G_{12}	28.80	4.30	1.465	7.225	2.355
G_{13}	31.30	3.90	1.445	7.915	2.295
G_{14}	29.70	2.50	1.405	8.270	2.505
G_{15}	29.20	6.20	1.465	5.565	2.610
G_{16}	20.35	3.10	1.360	6.355	2.885
G_{17}	23.70	2.30	1.260	6.735	2.325
G_{18}	14.70	2.20	1.360	6.335	2.555
G_{19}	15.45	2.40	1.585	6.355	2.365
G_{20}	12.70	3.40	1.365	8.225	2.390
G_{21}	21.35	5.40	1.240	5.230	2.295
G_{22}	11.70	5.10	1.335	6.410	2.680
G_{23}	13.30	5.60	1.425	3.960	2.735
G_{24}	15.20	2.70	1.490	4.995	5.265
G_{25}	20.40	1.50	1.630	5.370	2.740

Table 3. Continued

Genotypes	Length of peduncle (cm)	Number of trichomes on pod wall (count per mm^2)	Leaf chlorophyll content (mg/g of leaf tissue)	Protein content of pods (%)	Crude fibre content of pods (%)
G_{26}	19.40	1.80	1.460	6.940	2.550
G_{27}	22.45	2.20	1.685	8.720	3.615
G_{28}	18.20	1.30	1.350	5.765	3.100
G_{29}	15.20	4.20	1.660	7.995	3.045
G_{30}	17.30	6.45	1.640	6.325	3.360
G_{31}	17.45	2.30	1.865	7.960	3.075
G_{32}	14.40	2.20	1.630	6.160	2.070
G_{33}	15.85	2.70	1.830	6.390	2.355
G_{34}	26.40	3.30	1.835	4.630	3.330
G_{35}	19.50	4.80	1.655	5.570	2.510
G_{36}	29.15	5.00	1.455	5.555	2.460
G_{37}	15.50	4.80	1.570	5.875	2.560
G_{38}	21.95	5.40	1.865	4.090	2.910
G_{39}	17.30	2.30	1.635	4.180	2.180
G_{40}	40.75	6.00	1.560	6.100	1.975
G_{41}	26.25	2.30	1.385	5.855	2.270
G_{42}	16.05	2.50	1.845	6.640	3.280
G_{43}	17.45	5.80	1.470	5.330	2.255
G_{44}	27.80	2.20	1.485	5.340	2.915
G_{45}	18.95	2.30	1.125	8.285	2.355
G_{46}	35.25	3.00	1.305	5.900	2.075
G_{47}	26.05	3.20	1.310	6.310	2.280
G_{48}	24.20	3.70	1.475	5.770	2.720
G_{49}	25.60	4.00	1.560	6.390	2.925
G_{50}	25.70	4.40	1.690	6.390	2.380
Mean	21.831	3.465	1.520	6.257	2.672
SE	0.446	0.333	0.111	0.199	0.548
CD	0.897	0.669	0.223	0.400	1.100

Primary branches per plant was highest for G_{10} (5.07) followed by G_{42} (5.00), G_{31} (4.73), G_{29} (4.40) and G_{27} (4.80) and lowest in four genotypes viz., G_8, G_{33}, G_{38} and G_{46} (3.27). Main stem length was highest on G_{18} (514.00) followed by G_{48} (510.83), G_{24} (508.33), G_{10} (507.83), G_{23} (507.67) and G_{19} (507.00) and lowest in the genotype G_{44} (424.83).

The genotype G_{10} (9.13) recorded the maximum value for pod clusters per plant followed by G_5 (8.07) which was on par with G_{17} and G_{42} and minimum by G_{11}, G_{15}, G_{22} and G_{25} (4.07). Genotype G_{38} had the highest pods per plant (14.33) followed by G_{27} (11.73), G_{10} (11.17) and G_{35} (11.13) and lowest by G_6 (5.73) which was on par with G_{14}. Maximum pod yield per plant was recorded by the genotype G_{29} (415.33) followed by G_{27} (401.83), G_{10} (393.50) and G_{31} (363.00) and minimum by G_5 (170.33) followed by G_1 (172.17). Pods per cluster was highest in G_{20} and G_{50} (2.80) followed by G_{31}, G_{41}, G_{42} (2.67) and lowest in G_{13}, G_{35}, G_{36} and G_{37} (2.00). Maximum pod weight was recorded by G_{31} (27.73) followed by G_{42} (27.46) and G_{10} (20.93) and minimum by G_2 and G_{16} (8.20).

Pod length was highest for genotype G_{10} (52.72) followed by G_{42} (52.26), G_{31} (47.75) and G_{27} (37.63) and lowest for G_2 (12.88) followed by G_{15} (13.64) and G_5 (13.84). Maximum pod breadth was recorded by the genotype G_{27} (1.20) followed by G_{10} (1.19), G_{31} (1.18), G_{42} (1.16) G_{15} (1.06) and G_{29} (1.01) and minimum by G_6 and G_{16} (0.63) which was on par with G_7, G_{13}, G_{14} and G_{49}. Seeds per pod was highest in G_{42} (22.53) followed by G_{31} (21.40) and G_{10} (21.33) and lowest in G_1 (10.47) followed by G_{23} (10.80). Maximum 100 seed weight was noted in G_{31} (19.73) followed by G_{42} (18.53) and G_{40} (16.73) and minimum in G_6 (7.33).

Peduncle length ranged from 11.70 to 40.75. Genotype G_{40} had the more peduncle length measurement (40.75), followed by G_{46} (35.25) and G_{13} (31.30) and less in G_{22} (11.70).

More number of trichomes was observed in the genotype G_{30} (6.45mm^2) which was on par with G_{40} and G_{15} and less in G_{11} and G_{28} (1.3), which was on par with G_{25} and G_{26}.

Maximum chlorophyll content was noted in G_{31} and G_{38} (1.86 mg/g), which was on par with G_{33}, G_{34} and G_{42} and minimum in G_{45} (1.12 mg/g) of leaf tissue.

The pod protein content among the genotypes ranged from 3.74 to 8.72. G_{27} (8.72) recorded the highest protein content while G_5 (3.74) the lowest.

The highest crude fibre content was noted in G_{24} (5.26) and the lowest in G_{40} (1.97).

4.1.2. Genetic parameters

The phenotypic, genotypic and environmental variances for the various characters have been calculated. Estimates of variance showed that for all the characters studied with respect to yield genetic variance makes up the major part of the phenotypic variance with very little contribution by the environment.

4.1.2.1. Coefficient of variation

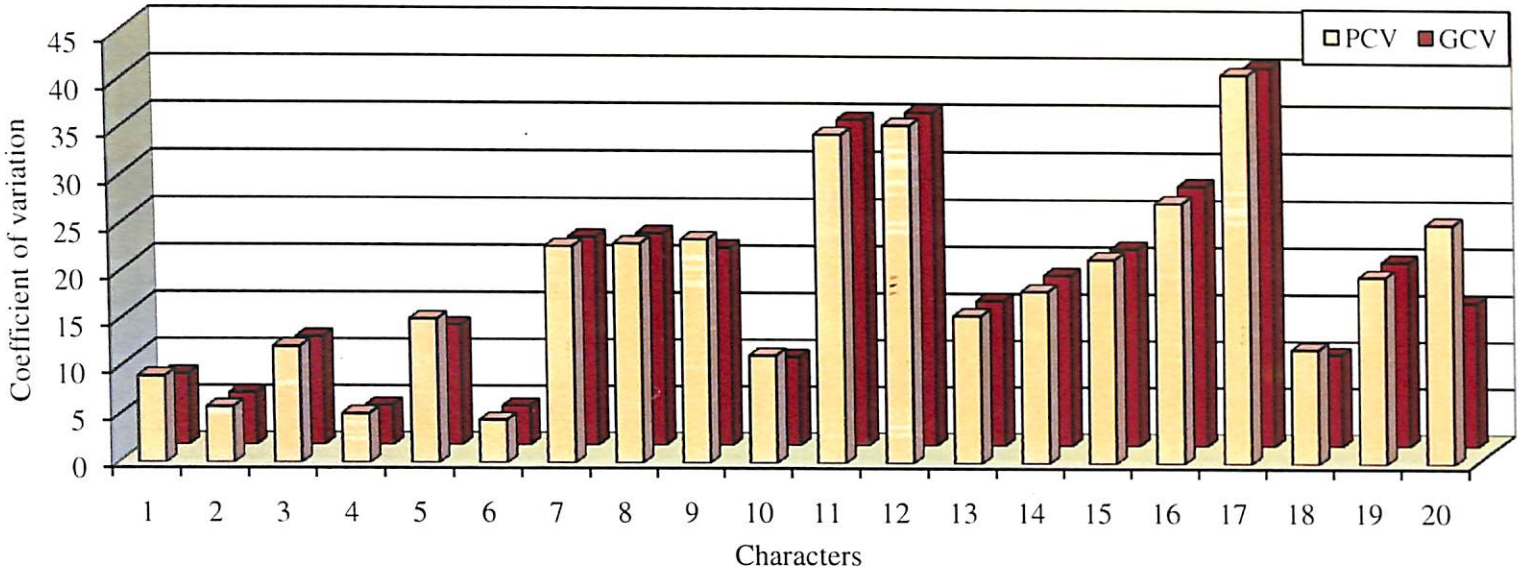
The phenotypic coefficient of variation, genotypic coefficient of variation and environmental coefficient of variation were worked out. The PCV and GCV of the characters are given in the Table 4 and Fig. 1.

4.1.2.1.1. Phenotypic coefficient of variation (PCV)

The PCV was very high for the character pod length (35.94). The pod weight (34.94), pod yield (23.87), pods per plant (23.43), pod clusters per plant (23.10) and 100 seed weight (21.87) also had high PCV indicating a high degree of variation. PCV was very less for main stem length (4.57), crop duration (5.24), days to first harvest (5.96) and days to 50 per cent flowering (9.23). PCV was maximum for number of trichomes on pod wall (41.41) and minimum for leaf chlorophyll content (12.30) followed by protein content of pods (20.05) and crude fibre content of pods (25.66).

Table 4. Estimates of genetic parameters with respect to yield and related characters in yard long bean

Sl. No.	Characters	Coefficient of variation (%)		Heritability (%)	Genetic advance (%)
		PCV	GCV		
I Yield Traits					
1.	Days to 50 per cent flowering	9.23	7.59	67.73	12.88
2.	Days to first harvest	5.96	5.56	87.03	10.68
3.	Length of harvest period	12.40	11.56	86.90	22.20
4.	Crop duration	5.24	4.27	66.21	7.15
5.	Primary branches per plant	15.34	12.85	70.09	22.16
6.	Main stem length	4.57	4.22	85.20	8.02
7.	Pod clusters per plant	23.10	22.23	92.61	44.08
8.	Pods per plant	23.43	22.64	93.40	45.08
9.	Pod yield per plant	23.87	21.13	78.35	38.53
10.	Pods per cluster	11.52	9.49	67.93	16.12
11.	Pod weight	34.94	34.66	98.41	70.84
12.	Pod length	35.94	35.42	97.12	71.89
13.	Pod breadth	15.81	15.57	96.99	31.58
14.	Seeds per pod	18.43	18.29	98.41	37.37
15.	100 seed weight	21.87	21.12	97.21	42.89
16.	Length of peduncle	27.86	27.78	99.46	57.07
17.	Number of trichomes on pod wall (count per mm^2)	41.41	40.28	94.62	80.71
II. Biochemical traits					
18.	Leaf chlorophyll content (mg/g of leaf tissue)	12.30	9.89	64.73	16.41
19.	Protein content of pods	20.05	19.79	97.48	40.26
20.	Crude fibre content of pods	25.66	15.44	36.21	19.15



1. Days to 50 per cent flowering
2. Days to first harvest
3. Length of harvest period
4. Crop duration
5. Primary branches per plant
6. Main stem length
7. Pod cluters per plant
8. Pods per plant
9. Pods yield per plant
10. Pods per cluster
11. Pod weight
12. Pod length
13. Pod breadth
14. Seeds per pod
15. 100-seed weight
16. Length of peduncle
17. Number of trichomes on pod wall (count per mm^2)
18. Leaf chlorophyll content (mg/g of leaf tissue)
19. Protein content of pods
20. Crude fibre content of pods

Fig. 1. Coefficient of variation of yield and biochemical traits in yard long bean

4.1.2.1.2. Genotypic coefficient of variation (GCV)

The highest value for GCV was observed for pod length (35.42) followed by pod weight (34.66), pods per plant (22.64), pod clusters per plant (22.23), pod yield per plant (21.13) and 100 seed weight (21.12). Main stem length, crop duration and days to first harvest has less GCV of 4.22, 4.27 and 5.56 respectively. GCV was maximum for number of trichomes on pod wall (40.28) and minimum for leaf chlorophyll content (9.89).

4.1.2.2. Heritability (broad sense)

The heritability estimate (broad sense) recorded for the characters is given in Table 4 and Fig.2. The highest heritability was observed for peduncle length (99.46) followed by pod weight and seeds per pod (98.41%). High heritability estimate was noticed for 100 seed weight, pod length, pod breadth, pods per plant, pod clusters per plant and pod protein content. The lowest heritability was observed for crop duration (66.21%) followed by days to 50 per cent flowering, pods per cluster and crude fibre content.

4.1.2.3. Genetic Advance (as percentage of mean)

The genetic advance estimated for the various characters as percentage of mean is given in Table 4 and Fig. 2. The highest estimate of genetic advance was observed for trichome number (80.71) followed by pod length (71.89%). High genetic advance was observed for pod weight, 100 seed weight and pod cluster per plant and pods per plant. The lowest genetic advance was observed for crop duration (7.15%), leaf chlorophyll content (16.41) and crude fibre content of pods (19.15).

High heritability coupled with high genetic advance was noticed for the characters pod clusters per plant, pods per plant, pod yield per plant, pod weight, pod length, pod breadth, seeds per pod and 100 seed weight.

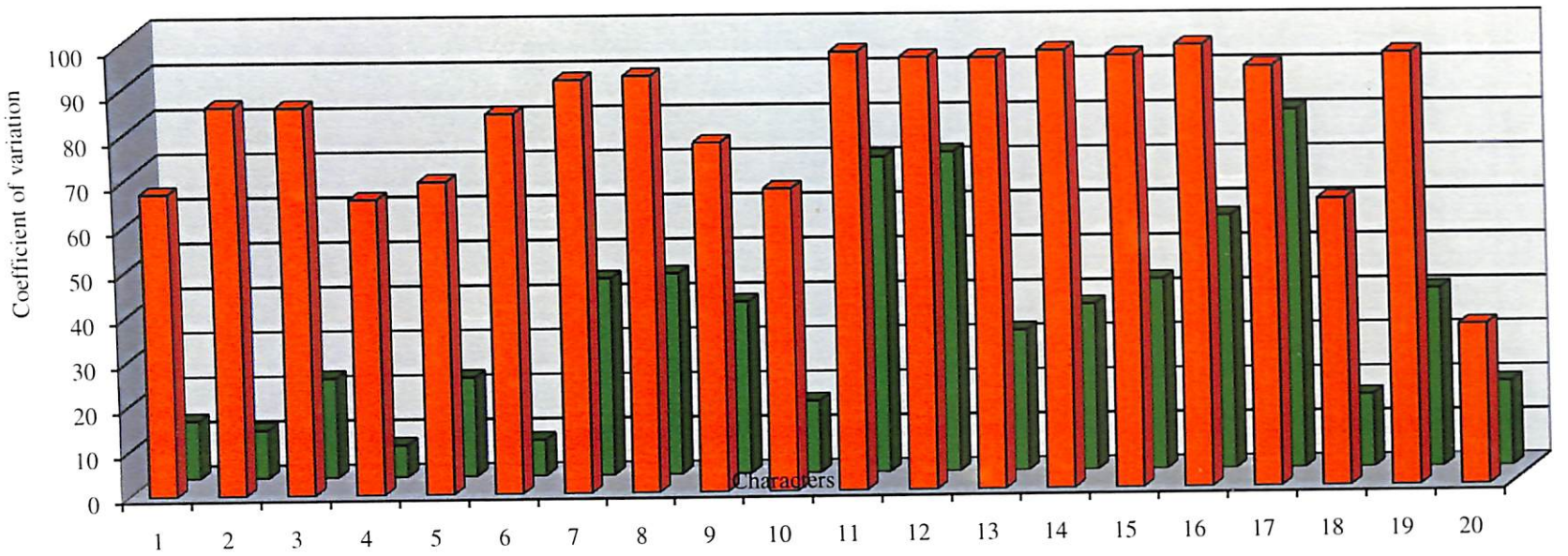


Fig. 2. Heritability and genetic advance estimates as percentage of mean of yield and biochemical traits in yard long bean

4.1.3. Association Analysis

The phenotypic, genotypic and environmental correlations among the various characters were estimated.

4.1.3.1. Phenotypic correlation coefficient

The phenotypic correlation coefficients of the various characters are given in the Table 5. Days to 50 per cent flowering had high positive correlation with days to first harvest. Length of harvest period showed significant negative correlation with pod yield per plant, pod weight, pod breadth, seeds per pod and 100 seed weight. Primary branches per plant recorded positive correlation with pod breadth. Pod clusters per plant had high positive correlation with pod weight. Pods per plant showed high positive correlation with pod yield per plant and 100 seed weight. Pod yield per plant recorded high positive correlation with pod weight, pod length, pod breadth, seeds per pod and 100 seed weight. Pod weight had high positive correlation with pod length, pod breadth, seeds per pod and 100 seed weight. Pod length and pod breadth showed high positive correlation with 100 seed weight. Seeds per pod had high positive correlation with 100 seed weight.

4.1.3.2. Genotypic correlation coefficient

The genotypic correlation among the various characters was studied and the coefficients are given in the Table 6. Days to 50 per cent flowering showed high positive correlation with days to first harvest. Days to first harvest exhibited positive correlation with pods per cluster and negative correlation with pod length.

Length of harvest period recorded high negative correlation with pods per plant, pod yield, pod weight, pod length, pod breadth, seeds per pod and 100 seed weight.

Table 5. Estimates of phenotypic correlation coefficients among the yield components in yard long bean

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}`	X_{15}
X_1	1.000														
X_2	0.526**	1.000													
X_3	0.074	0.115	1.000												
X_4	0.047	-0.064	0.038	1.000											
X_5	0.158	0.112	-0.152	0.014	1.000										
X_6	-0.053	0.095	-0.071	-0.057	0.115	1.000									
X_7	-0.110	-0.024	-0.198	-0.189	0.331*	0.242	1.000								
X_8	0.016	-0.024	-0.471**	-0.114	0.135	0.081	0.125	1.000							
X_9	0.147	0.129	-0.534**	-0.014	0.365**	0.201	0.258	0.556**	1.000						
X_{10}	-0.007	0.239**	-0.021	0.025	0.261	0.095	0.333*	-0.020	0.181	1.000					
X_{11}	0.014	0.092	-0.455**	0.018	0.600**	0.311**	0.425**	0.239**	0.640**	0.309**	1.000				
X_{12}	-0.078	-0..258	-0.350*	-0.075	0.341*	0.208	0.376**	0.253	0.488**	0.165	0.659**	1.000			
X_{13}	0.126	0.049	-0.433**	0.146	0.419**	0.285*	0.151	0.290*	0.486**	0.242	0.508**	0.358*	1.000		
X_{14}	-0.090	-0.105	-0.516**	0.076	0.221	-0.033	0.179	0.145	0.466**	0.267	0.448**	0.378**	0.460**	1.000	
X_{15}	-0.120	-0.229	-0.528**	0.129	0.187	0.137	0.125	0.385**	0.584**	0.178	0.495**	0.523**	0.532**	0.510**	1.000

* Significant at 5 per cent level

** Significant at 1 per cent level

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

Table 6. Estimates of genotypic correlation coefficients among the yield components in yard long bean

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
X_1	1														
X_2	0.670**	1													
X_3	0.086	0.122	1												
X_4	0.077	-0.032	0.055	1											
X_5	0.159	0.200	-0.185	0.011	1										
X_6	-0.077	0.106	-0.061	-0.105	0.195	1									
X_7	-0.137	-0.040	-0.201	-0.265	0.422**	0.272	1								
X_8	0.036	-0.018	-0.523**	-0.141	0.161	0.108	0.116	1							
X_9	0.120	0.155	-0.676**	-0.015	0.507**	0.254	0.309*	0.651**	1						
X_{10}	0.065	0.278*	-0.023	0.029	0.435**	0.103	0.407**	-0.036	0.227	1					
X_{11}	0.011	0.100	-0.484**	0.030	0.725**	0.341*	0.443**	0.251	0.731**	0.375**	1				
X_{12}	-0.115	-0.272*	-0.390**	-0.098	0.424**	0.227	0.398**	0.262	0.544**	0.216	0.676**	1			
X_{13}	0.171	0.065	-0.463**	0.174	0.517**	0.309*	0.150	0.291*	0.557**	0.300	0.521**	0.366**	1		
X_{14}	-0.123	-0.118	-0.557**	0.088	0.277*	-0.037	0.183	0.151	0.523**	0.330*	0.454**	0.382**	0.468**	1	
X_{15}	-0.140	-0.257	-0.590**	0.162	0.245	0.150	0.136	0.399**	0.662**	0.217	0.505**	0.536**	0.549**	0.523**	1

* Significant at 5 per cent level

** Significant at 1 per cent level

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

Primary branches per plant had high positive correlation with pod clusters per plant, pod yield, pods per cluster, pod weight, pod length, pod breadth and seeds per pod. Main stem length recorded positive correlation with pod weight and pod breadth. Pod clusters per plant exhibited high positive correlation with pod yield per plant, pods per cluster, pod weight and pod length. Pods per plant had positive correlation with pod yield per plant, pod breadth and 100 seed weight.

Pod yield per plant exhibited high positive correlation with pod weight, pod length, pod breadth, seeds per pod and 100 seed weight. Pods per cluster had positive correlation with pod weight and seeds per pod. Pod weight showed high positive correlation with pod length, pod breadth, seeds per pod and 100 seed weight. Pod length recorded positive correlation with pod breadth, seeds per pod and 100 seed weight. Pod breadth had high positive correlation with seeds per pod and 100 seed weight. Seeds per pod showed high positive correlation with 100 seed weight.

4.1.3.3. Environmental Correlation Coefficient

The environmental correlation coefficient among the yield components are shown in Table 7. Pod breadth had significant positive environmental correlation with pods per plant. All other environmental correlation values were not significant.

4.1.4. Path analysis

The character pod yield per plant was taken as the dependent character and path analysis was done. The component characters selected for the analysis were pod clusters per plant, pods per plant, pods per cluster, pod weight, seeds per pod and 100-seed weight. The direct and indirect effect of various characters on yield are presented in Table 8.

Table 7. Estimates of environmental correlation coefficients among the yield components in yard long bean

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
X_1	1.000														
X_2	0.057	1.000													
X_3	0.042	0.071	1.000												
X_4	-0.012	-0.192	-0.021	1.000											
X_5	0.154	-0.227	-0.035	0.022	1.000										
X_6	0.023	0.027	-0.136	0.097	-0.168	1.000									
X_7	-0.012	0.118	-0.172	0.117	-0.060	0.001	1.000								
X_8	-0.087	-0.076	0.007	-0.021	0.033	-0.148	0.256	1.000							
X_9	0.226	0.004	0.144	-0.012	-0.041	-0.038	-0.037	-0.004	1.000						
X_{10}	-0.160	0.123	-0.017	0.016	-0.127	0.075	0.066	0.039	0.058	1.000					
X_{11}	0.074	-0.016	-0.153	-0.081	-0.028	-0.038	0.039	-0.076	-0.041	0.035	1.000				
X_{12}	0.158	-0.126	0.145	0.032	-0.098	0.023	-0.037	0.089	0.171	-0.112	-0.071	1.000			
X_{13}	-0.125	-0.170	-0.131	0.067	-0.077	0.068	0.196	0.275*	0.007	-0.017	-0.036	0.096	1.000		
X_{14}	0.147	0.088	-0.027	0.064	-0.132	0.011	0.117	-0.012	0.118	-0.042	0.018	0.222	0.115	1.000	
X_{15}	-0.060	0.118	0.230	-0.009	-0.168	0.019	-0.084	0.120	0.083	0.009	0.048	0.071	-0.042	-0.068	1.000

* Significant at 5 per cent level

** Significant at 1 per cent level

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

Table 8. Direct and indirect effects of component characters on yield in yard long bean

Characters	X_1	X_2	X_3	X_4	X_5	X_6	Genotypic correlation with yield
Pod clusters per plant – X_1	**0.0083**	0.0508	-0.0105	0.207	0.0297	0.0231	0.3085
Pods per plant – X_2	0.0009	**0.4393**	0.0009	0.1174	0.0246	0.0678	0.6510
Pods per cluster – X_3	0.0034	-0.0159	**-0.0258**	0.1749	0.0537	0.0368	0.2273
Pod weight – X4	0.0037	0.1105	-0.0097	**0.4669**	0.0739	0.0858	0.7312
Seeds per pod – X_5	0.0015	0.0665	-0.0085	0.2122	**0.1626**	0.0889	0.5233
100 – Seed weight – X_6	0.0011	0.1752	-0.0056	0.2358	0.0851	**0.1699**	0.6616

Residue - 0.42228

Direct effects - Diagonal elements

Indirect effects - Off diagonal elements

The residual value was 0.4223 indicating that 57.77 per cent of the variation in yield was contributed by the characters selected for analysis.

The highest direct effect was observed for pod weight (0.4669) followed by pods per plant (0.4393), 100-seed weight (0.1699), seeds per pod (0.1625) and pod clusters per plant (0.0083). Pods per cluster has a negative direct effect (-0.0257) on pod yield per plant.

The character pod weight has a high indirect effect via 100-seed weight (0.2358) to yield per plant. Pod weight has indirect effect on seeds per pod (0.2122) and pod clusters per plant (0.2070). Pods per plant had indirect effect on 100-seed weight (0.1752). Pod weight had indirect effect on pods per cluster (0.1749).

4.1.5. Genetic divergence analysis

The fifty genotypes of yard long bean were subjected to genetic divergence analysis following Mahalanobis D^2 statistics. The clustering was done based on yield and correlated characters, namely pod clusters per plant, pods per plant, pods per cluster, pod weight, seeds per pod, 100-seed weight and pod yield per plant.

The genotypes were grouped in to nine clusters using Tocher's method of clustering. The clustering pattern is presented in the Table 9. The cluster II had the highest number of genotypes ie., sixteen; cluster III had fifteen genotypes while cluster I, IV, V and VI had genotypes 7, 4, 3 and 2 respectively. Three clusters (VII, VIII and IX) had 1 genotype each.

The average inter and intra cluster distance were estimated based on the D^2 values. The inter and intra cluster distances (D^2) of the various clusters were worked out and presented in Table 10. The intra cluster distances varied from 0 (cluster VII, VIII and IX) to 143.38 (Cluster I). The inter cluster distance varied from 216.28 (between cluster VI and VII) to 2190.15 (between cluster I and VI).

Table 9. Clustering pattern of the fifty genotypes

Sl. No.	Cluster number	Number of genotypes	Genotypes
1	I	7	1, 2, 3, 4, 5, 8, 9
2	II	16	11, 14, 15, 16, 24, 25, 28, 32, 33, 34, 37, 39, 40, 43, 47, 48
3	III	15	7, 12, 13, 17, 18, 19, 20, 26, 36, 41, 44, 45, 46, 49, 50
4	IV	4	21, 22, 23, 30
5	V	3	27, 29, 35
6	VI	2	31. 42
7	VII	1	10
8	VIII	1	38
9	IX	1	6

Table 10. Average inter and intra cluster D^2 values among the nine clusters

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	143.38	413.48	239.01	219.46	725.45	2190.15	1581.53	511.21	941.96
II		115.507	209.811	399.785	402.08	1407.97	881.93	402.26	358.54
III			114.39	221.534	330.04	1325.88	860.06	382.24	498.39
IV				108.103	479.98	1821.66	1265.93	374.24	429.47
V					136.67	700.816	329.07	320.92	305.47
VI						36.442	216.28	1689.68	560.79
VII							0	927.35	1315.80
VIII								0	697.35
IX									0

Diagonal elements - Intra cluster distance

Off diagonal elements - Inter cluster distance

The maximum 'inter cluster' distance of cluster I was from cluster VI followed by cluster VII, IX, V, VIII, II, III and IV. The cluster II was at the greatest distance from cluster VI followed by cluster VII, I, V, IV, IX and III. The maximum distance of cluster III was from cluster VI followed by VII, IX, VIII, V, I, IV and II. The cluster IV was at the maximum distance from VI, followed by VII, V, IX, II, VIII, III and I. Cluster V was at maximum distance from cluster I followed by VI, IV, II, III, VII, VIII and IX. The cluster VI was at maximum distance from cluster I, followed by IV, VII, II, III, V, IX and VII. The maximum distance of cluster VII was from cluster I followed by IX, IV, VIII, II, III, V and VI. Cluster VIII was at maximum distance from cluster VI followed by VII, IX, I, II, III, IV and V. The maximum distance of cluster IX was from cluster VII followed by cluster I, VIII, VI, III, IV, II and V. The cluster means for each character is represented in the Table 11. Among the seven characters considered pod yield per plant contributed maximum towards divergence, comparatively lesser variation was observed for the characters pods per cluster, pod clusters per plant and pods per plant. The selected genotypes for line x tester analysis were coming under the clusters V, VI and VIII. The cluster VII contributing the maximum mean values for pod yield (393.5), 100-seed weight (19.5) and pod clusters per plant (9.1). Cluster VI had highest mean values for pod per plant (11.9), pods per cluster (2.7), pod weight, seeds per pod (22.0). So these three clusters were used for further hybridization programme.

4.1.6. Selection index

Selection index for the genotype was computed based on the nine characters having significant genotypic correlation coefficients, namely harvest period, primary branches per plant, pods per plant, pod weight, pod length, pod breadth, seeds per pod, 100 seed weight and pod yield per plant. The selection index worked out was as follows.

$I = -0.6234\ X_1 + 4.2653\ X_2 + 7.8676\ X_3 + 4.3952\ X_4 + 0.7294\ X_5 + 3.7963\ X_6 + 2.1289\ X_7 + 2.8787\ X_8 + 0.4046\ X_9$.

Table 11. Cluster means of the various characters in yard long bean

Clusters	Pod clusters per plant	Pods per plant	Pods per cluster	Pod weight	Seeds per pod	100-seed weight	Pod yield
I	6.0	7.0	2.2	9.8	12.4	10.0	190.3
II	5.0	6.8	2.3	9.9	17.7	13.6	258.5
III	6.2	7.2	2.3	12.8	15.2	12.6	250.6
IV	5.0	7.8	2.2	11.4	11.6	14.9	234.8
V	6.2	10.8	2.2	16.4	17.1	17.1	372.5
VI	7.2	11.9	2.7	27.6	22.0	19.1	347.3
VII	9.1	11.2	2.5	20.9	21.3	19.5	393.5
VIII	5.3	14.3	2.1	9.5	15.1	15.1	252.5
IX	6.1	5.7	2.1	15.1	14.1	7.3	180.7
Mean	6.2	9.2	2.3	14.8	14.8	14.4	275.6

Accordingly to selection index scores were worked out for all 50 genotypes and presented in the Table 12 in the descending order. The maximum selection index value was obtained for G_{10} (493.50), while the least value was for G_1 (224.44). From the superior genotypes with high selection indices and cluster analysis five genotypes viz; G_{10}, G_{31}, G_{42}, G_{27} and G_{29} were selected for hybridization programme as female parents (lines) to develop F_1 hybrids.

4.2. EVALUATION OF GERMPLASM FOR POD BORERS RESISTANCE

4.2.1. Damage parameters – *M. vitrata*

The mean value of the 50 genotypes for all the damage parameters were shown in the Table 13.

a. Percentage infestation of flower buds

Percentage of infestation of flower buds ranged from 16 to 72. A minimum percentage attack of flower buds was noticed in G_{15} (16%) followed by G_{30} and G_{43} (20% each) and maximum in G_{11} (72%).

b. Number of larvae per 25 flowers

Number of larvae was less in the genotype G_{15} (8) followed by G_{30} (10) and G_{43} (11). More number of larvae per 25 flowers were seen in G_{11} (23) followed by G_{31}, G_{35}, G_{45}, G_{46} (20 each).

c. Percentage pod infestation

Pod infestation ranged from 12% to 68%. Minimum percentage pod infestation was recorded by the genotype G_{43} (12%) followed by G_{30} (16%) and G_{15} (18%) and maximum by G_{11} (68%).

Table 12. Selection indices of 50 genotypes arranged in descending order

Sl. No.	Genotypes	Selection index value	Sl. No.	Genotypes	Selection index value
1.	G_{10}	493.51	26.	G_{34}	295.14
2.	G_{31}	482.28	27.	G_{28}	293.46
3.	G_{42}	476.54	28.	G_{21}	292.24
4.	G_{27}	453.18	29.	G_{50}	290.28
5.	G_{29}	446.66	30.	G_{32}	288.81
6.	G_{35}	392.34	31.	G_{11}	288.77
7.	G_{38}	377.23	32.	G_{24}	287.92
8.	G_{20}	363.42	33.	G_{23}	287.04
9.	G_{36}	345.52	34.	G_{45}	284.66
10.	G_{19}	335.66	35.	G_{46}	283.16
11.	G_{40}	333.33	36.	G_{25}	279.58
12.	G_{49}	329.45	37.	G_{37}	277.32
13.	G_{30}	322.12	38.	G_{6}	276.82
14.	G_{39}	321.21	39	G_{17}	276.69
15.	G_{12}	319.18	40.	G_{8}	275.20
16.	G_{41}	318.03	41.	G_{13}	270.67
17.	G_{43}	315.23	42.	G_{15}	266.50
18.	G_{18}	311.15	43.	G_{14}	265.54
19.	G_{7}	308.50	44.	G_{47}	265.33
20.	G_{44}	307.49	45.	G_{16}	261.66
21.	G_{33}	306.68	46.	G_{9}	253.23
22.	G_{4}	306.48	47.	G_{3}	239.62
23.	G_{22}	300.38	48	G_{2}	239.27
24.	G_{48}	299.06	49.	G_{5}	225.24
25.	G_{26}	297.56	50.	G_{1}	224.44

Table 13. *Maruca vitrata* damage parameters and plant resistant indices of 50 yard long bean genotypes

Genotypes	Damage parameters						
	Percentage infestation of flower buds	Number of larvae per 25 flowers	Percentage pod infestation	Number of larval entry / exit holes per pod	Number of damaged seeds in a sample of 25 pods	Seed damage index	Plant resistant index (Ipr)
G_1	42.00	11.50	34.00	0.26	13.50	54.00	26.08
G_2	48.00	14.00	48.00	0.34	13.50	54.00	32.00
G_3	30.00	10.50	28.00	0.26	18.00	72.00	26.58
G_4	38.00	11.00	34.00	0.30	18.50	74.00	29.17
G_5	68.00	21.00	62.00	0.60	21.00	84.00	45.17
G_6	60.00	17.00	54.00	0.36	13.00	52.00	35.17
G_7	34.00	11.00	34.00	0.34	13.50	54.00	25.83
G_8	34.00	16.00	28.00	0.28	20.50	82.00	31.00
G_9	30.00	11.00	32.00	0.28	17.00	68.00	27.50
G_{10}	28.00	12.00	28.00	0.32	18.00	72.00	27.33
G_{11}	72.00	23.00	68.00	0.66	17.50	70.00	46.00
G_{12}	44.00	15.00	40.00	0.58	20.50	82.00	34.50
G_{13}	34.00	15.00	34.00	0.36	20.50	82.00	32.50
G_{14}	34.00	12.50	28.00	0.28	20.50	82.00	29.25
G_{15}	16.00	8.00	18.00	0.20	10.00	40.00	16.67
G_{16}	40.00	11.50	28.00	0.32	20.50	82.00	28.75
G_{17}	42.00	11.50	30.00	0.30	23.00	92.00	31.08
G_{18}	46.00	16.00	58.00	0.72	29.50	118.00	47.00
G_{19}	48.00	12.00	42.00	0.52	27.00	108.00	38.00
G_{20}	52.00	14.00	42.00	0.40	23.50	94.00	36.67
G_{21}	54.00	15.50	38.00	0.42	24.00	96.00	36.42
G_{22}	46.00	16.50	36.00	0.38	19.50	78.00	33.25
G_{23}	30.00	17.00	26.00	0.36	20.50	82.00	30.83
G_{24}	30.00	17.00	20.00	0.32	20.50	82.00	28.83
G_{25}	36.00	13.00	32.00	0.30	23.00	92.00	32.50
G_{26}	38.00	17.00	28.00	0.32	29.50	118.00	37.50

Table 13. Continued

Genotypes	Damage parameters						
	Percentage infestation of flower buds	Number of larvae per 25 flowers	Percentage pod infestation	Number of larval entry / exit holes per pod	Number of damaged seeds in a sample of 25 pods	Seed damage index	Plant resistant index (Ipr)
G_{27}	40.00	18.00	24.00	0.26	21.50	86.00	31.33
G_{28}	30.00	18.00	20.00	0.26	13.50	54.00	24.67
G_{29}	38.00	14.00	22.00	0.34	17.00	68.00	25.67
G_{30}	20.00	10.00	16.00	0.20	12.00	48.00	18.33
G_{31}	68.00	20.00	60.00	0.42	46.00	184.00	60.67
G_{32}	62.00	18.00	44.00	0.78	28.50	114.00	42.67
G_{33}	30.00	13.00	26.00	0.52	23.50	94.00	30.83
G_{34}	46.00	19.50	40.00	0.50	19.50	78.00	36.08
G_{35}	62.00	20.00	54.00	0.64	45.00	180.00	58.00
G_{36}	60.00	19.50	42.00	0.42	38.50	154.00	49.42
G_{37}	48.00	16.50	38.00	0.52	21.50	86.00	35.25
G_{38}	44.00	15.00	40.00	0.32	18.50	74.00	33.17
G_{39}	38.00	12.50	24.00	0.30	18.50	74.00	26.58
G_{40}	40.00	13.00	22.00	0.32	14.00	56.00	23.17
G_{41}	48.00	18.50	38.00	0.50	38.00	152.00	47.25
G_{42}	58.00	19.00	64.00	0.76	40.00	160.00	57.50
G_{43}	20.00	11.00	12.00	0.24	10.00	40.00	16.17
G_{44}	68.00	19.00	62.00	0.86	46.00	184.00	60.83
G_{45}	64.00	20.00	38.00	0.88	43.00	172.00	51.33
G_{46}	54.00	20.00	48.00	0.80	41.00	164.00	53.33
G_{47}	42.00	21.50	28.00	0.28	31.00	124.00	40.75
G_{48}	34.00	16.00	26.00	0.34	28.00	112.00	35.33
G_{49}	38.00	14.50	28.00	0.38	20.50	82.00	30.25
G_{50}	30.00	13.50	36.00	0.46	31.00	124.00	39.42
SE	4.39	1.00	2.86	0.08	1.82	7.28	1.73
CD	8.82	2.00	5.75	0.16	3.66	14.63	3.47

d. Number of larval entry / exit holes per pod

A minimum number of larval entry / exit holes per pod was observed in G_{15} and G_{30} (0.20), followed by G_{43} (0.24), G_1, G_3, G_{27}, G_{28} (0.26). Maximum number of larval entry was on G_{45} (0.88) followed by G_{44} (0.86) and G46 (0.80).

e. Number of damaged seeds in a sample of 25 pods

Number of damaged seeds per 25 pods ranged from 10.0 to 46.0. Less number of damaged seeds was shown by G_{15} and G_{43} (10 each), followed by G_{30} (12) and more by G_{31} and G_{44} (46).

f. Seed damage index

Seed damage index was minimum for G_{15} and G_{43} (40 each) followed by G_{30} (48) and maximum for G_{31} and G_{44} (184 each).

g. Plant resistant index (Ipr)

Plant resistant index ranged from 16.167 to 60.833. A minimum plant resistant index was for G_{43} (16.167) followed by G_{15} (16.667) and G_{30} (18.333) and maximum for the genotype G_{44} (60.833) followed by G_{31} (60.667).

4.2.2. Damage parameters – *L. boeticus*

The mean value of the 50 genotypes for all the damage parameters are presented in the Table 14.

a. Percentage infestation of flower buds

Flower bud infestation ranged from 12 to 56. The lowest infestation of flower buds was noticed in the genotype G_{43} (12%) followed by G_{30} (16%) and G_{15} (20%) and the highest by G_{44} (56%).

Table 14. *Lampides boeticus* damage measurements and plant resistant indices of 50 yard long bean genotypes

Genotypes	Damage parameters						
	Percentage infestation of flower buds	Number of larvae per 25 flowers	Percentage pod infestation	Number of larval entry / exit holes per pod	Number of damaged seeds in a sample of 25 pods	Seed damage index	Plant resistant index (Ipr)
G_1	22	7.0	18	0.20	10.0	40	16.17
G_2	26	8.5	22	0.22	11.5	46	19.25
G_3	22	7.5	18	0.24	11.5	46	17.42
G_4	22	7.0	18	0.26	17.0	68	20.83
G_5	40	10.0	30	0.28	21.0	84	29.00
G_6	38	12.5	24	0.22	10.0	40	20.92
G_7	24	8.0	20	0.26	11.5	46	18.33
G_8	30	13.5	32	0.30	15.0	60	27.42
G_9	24	9.5	26	0.32	17.0	68	24.75
G_{10}	24	11.0	20	0.28	11.0	44	19.50
G_{11}	48	23.0	40	0.60	21.0	84	38.83
G_{12}	38	18.0	32	0.56	18.0	72	31.67
G_{13}	24	9.5	28	0.28	15.0	60	24.08
G_{14}	26	8.0	28	0.28	17.0	68	24.67
G_{15}	20	6.0	12	0.16	8.0	32	12.33
G_{16}	30	12.0	20	0.20	14.5	58	22.33
G_{17}	32	12.5	24	0.22	17.0	68	25.58
G_{18}	28	12.0	26	0.24	21.5	86	29.00
G_{19}	42	19.0	34	0.26	21.0	84	34.83
G_{20}	38	19.5	34	0.26	20.5	82	34.75
G_{21}	38	20.5	30	0.32	21.0	84	34.25
G_{22}	36	17.0	26	0.32	21.0	84	31.17
G_{23}	28	10.0	20	0.20	16.0	64	22.33
G_{24}	28	10.0	24	0.28	10.0	40	19.67
G_{25}	24	11.0	20	0.22	12.5	50	20.50
G_{26}	32	11.0	16	0.22	21.5	86	25.17

Table 14. Continued

Genotypes	Damage parameters						
	Percentage infestation of flower buds	Number of larvae per 25 flowers	Percentage pod infestation	Number of larval entry / exit holes per pod	Number of damaged seeds in a sample of 25 pods	Seed damage index	Plant resistant index (Ipr)
G_{27}	32	10.0	18	0.20	10.0	40	17.67
G_{28}	30	8.5	18	0.16	9.0	36	16.25
G_{29}	24	9.5	26	0.28	9.5	38	19.75
G_{30}	16	5.0	16	0.16	8.0	32	13.17
G_{31}	42	20.0	40	0.38	31.0	124	44.00
G_{32}	44	21.5	36	0.34	27.0	108	40.75
G_{33}	28	16.0	32	0.28	20.5	82	32.33
G_{34}	46	20.0	28	0.24	15.0	60	29.33
G_{35}	48	22.0	28	0.28	33.0	132	42.33
G_{36}	46	21.0	34	0.26	30.0	120	41.83
G_{37}	30	20.0	30	0.26	20.0	80	33.33
G_{38}	30	18.0	28	0.26	18.0	72	30.33
G_{39}	26	17.0	16	0.16	14.0	56	23.17
G_{40}	26	10.5	24	0.28	10.0	40	19.92
G_{41}	34	19.0	20	0.20	28.5	114	35.17
G_{42}	32	14.0	18	0.20	28.0	112	31.67
G_{43}	12	5.0	12	0.12	6.0	24	10.50
G_{44}	56	7.0	20	0.20	14.0	56	19.50
G_{45}	46	7.0	40	0.26	9.5	38	23.17
G_{46}	43	8.0	34	0.56	21.0	84	29.33
G_{47}	32	10.0	24	0.20	10.5	42	20.00
G_{48}	28	14.0	20	0.24	12.5	50	22.00
G_{49}	28	15.0	22	0.28	10.0	40	21.50
G_{50}	26	19.0	18	0.32	13.0	52	24.17
Mean	26	19.0	18	0.32	13.0	65.52	24.17
SE	4	0.5	1.62	0.02	0.9	3.446	0.69
CD	7	1.1	3.256	0.04	1.7	6.924	1.39

b. Number of larvae per 25 flowers

Number of larvae was minimum in G_{30} and G_{43} (5 in each), followed by G_{15} (6) and maximum in G_{11} (23.0) followed by G_{35} (22.0) and G_{32} (21.5). Four genotypes showed less number of larvae per 25 flowers (7) viz; G_1, G_4, G_{44} and G_{45}.

c. Percentage of pod infestation

Pod infestation was lowest in genotypes, G_{15} and G_{43} (12 in each), followed by 3 genotypes G_{26}, G_{30} and G_{39} (16 in each) and highest in G_{11}, G_{31} and G_{45} (40).

d. Number of larval entry / exit holes per pod

Number of larval entry / exit holes per pod ranged from 0.12 to 0.60. A minimum number of larval entry / exit holes was recorded by G_{43} (0.12) followed by G_{15}, G_{28}, G_{30} and G_{39} (0.16) and maximum by G_{11} (0.60).

e. Number of damaged seeds in a sample of 25 pods

Number of damaged seeds per 25 pods ranged from 6 to 33. A minimum number of damaged seeds was recorded by the the genotype G_{43} (6) followed by G_{15} and G_{30} (8 in each) and G_{28} (9), which was on par with G_{29} and G_{45} and maximum by G_{35} (33) followed by G_{31} (31) and G_{36} (30).

f. Seed damage index

Seed damage index was lowest in G_{43} (24) followed by G_{15} and G_{30} (32 in each) and highest in G_{35} (132).

g. Plant resistant index (Ipr)

Plant resistant index ranged from 10.5 to 44.00. Plant resistant index was lowest for G_{43} (10.50) followed by G_{15} (12.33) and G_{30} (13.17) and highest for G_{31} (44.00) followed by G_{35} (42.33), G_{36} (41.83) and G_{32} (40.75). Among the pod borers *M. vitrata* had severe yield loss as compared to *L. boeticus*.

Three genotypes viz., G_{43}, G_{15} and G_{30} which are resistant or tolerant to pod borers (*M. vitrata* and *L. boeticus*) with low plant resistant indices were selected as male parents (testers) in hybridization programme to develop F_1 hybrids.

4.2.3 Correlation coefficients among the pod borer damage parameters and biochemical traits and selected yield traits

Number of trichomes on pod wall had negatively significant correlation with all the damage parameters of *M. vitrata* and negative correlation with *L. boeticus*. Crude fibre content also showed negative correlation with all the damage parameters of both the pests. Length of harvest period showing negative correlation with all the damage parameters. Pod clusters per plant showed negative correlation with number of larvae per 25 flowers and percentage infestation of flower buds for both borers. Pod yield had negative correlation with percentage pod infestation of borers (Table 15).

4.3 LINE x TESTER ANALYSIS

Based on selection indices and cluster analysis genotypes with high yield were selected as lines and genotypes with least plant resistant index value were chosen as testers for line x tester analysis. High yielding lines selected were G_{10}, G_{31}, G_{42}, G_{27} and G_{29} having selection index values 493.51, 482.28, 476.54, 453.18 and 446.66 respectively. Testers with least plant resistant index values selected were G_{43} (16.17), G_{15} (16.67) and G_{30} (18.33) for *M. vitrata* and *L. boeticus* with 10.50, 12.33, 13.17 respectively.

The 5 selected lines and 3 testers were crossed in the L x T fashion to produce 15 hybrids.

4.4 LINE x TESTER ANALYSIS FOR EVALUATION OF F_1's AND PARENTS

The F_1 seeds obtained along with the parents were raised in RBD with 3 replications and observations on various characters were recorded.

Characters

X1	Percentage of infestation of flower buds	*Maruca vitrata*
X2	Number of larvae per 25 flowers	
X3	Percentage pod infestation	
X4	Plant resistant index	
X5	Percentage of infestation of flower buds	*Lampides boeticus*
X6	Number of larvae per 25 flowers	
X7	Percentage pod infestation	
X8	Plant resistant index	
X9	Peduncle length	Yield and biochemical traits
X10	Number of trichomes on pod wall	
X11	Leaf chlorophyll content	
X12	Protein content of pods	
X13	Crude fibre content	
X14	Days to 50 per cent flowering	
X15	Length of harvest period	
X16	Crop duration	
X17	Pods per plant	
X18	Pod clusters per plant	
X19	Pod weight	
X20	Pod yield	

Table 15. Estimates of correlation coefficients among the pod borer damage parameters and biochemical traits and selected yield trait components in yard long bean

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}	X_{16}	X_{17}	X_{18}	X_{19}	X_{20}
X_1	1.000																			
X_2	0.730**	1.000																		
X_3	0.867**	0.596**	1.000																	
X_4	0.835**	0.756**	0.828**	1.000																
X_5	0.860**	0.753**	0.702**	0.806**	1.000															
X_6	0.489**	0.395**	0.421**	0.414**	0.543**	1.000														
X_7	0.647**	0.507**	0.510**	0.544**	0.660**	0.543**	1.000													
X_8	0.665**	0.502**	0.603**	0.620**	0.642**	0.838**	0.743**	1.000												
X_9	-0.049	-0.012	-0.046	-0.019	0.040	-0.157	-0.026	-0.096	1.000											
X_{10}	-0.349*	-0.300*	-0.343*	-0.343*	-0.296*	-0.009	-0.136	-0.102	0.114	1.000										
X_{11}	0.005	-0.012	0.142	0.053	-0.053	0.304*	0.012	0.209	-0.120	0.040	1.000									
X_{12}	0.029	-0.109	-0.018	0.025	-0.057	-0.116	0.128	-0.028	0.058	-0.292*	-0.031	1.000								
X_{13}	-0.137	-0.008	-0.056	-0.036	-0.111	-0.145	-0.290*	-0.246	-0.114	-0.091	0.287*	0.117	1.000							
X_{14}	0.160	-0.110	0.102	-0.067	0.102	0.182	0.028	0.067	0.015	-0.012	-0.062	-0.041	-0.115	1.000						
X_{15}	-0.096	-0.165	-0.010	-0.231	-0.134	-0.356*	-0.114	-0.258	0.116	-0.159	-0.366*	-0.061	-0.302*	0.081	1.000					
X_{16}	0.108	0.221	0.137	0.224	0.265	0.029	0.117	0.172	0.188	0.015	-0.072	-0.209	0.045	0.064	0.048	1.000				
X_{17}	0.162	0.056	0.186	0.189	0.064	0.191	0.080	0.227	-0.144	0.116	0.554**	0.162	0.438**	-0.048	-0.568**	-0.099	1.000			
X_{18}	-0.024	-0.145	0.053	-0.023	-0.088	0.115	-0.093	0.119	0.089	0.013	0.074	0.098	0.063	0.035	-0.022	0.027	0.092	1.000		
X_{19}	0.303*	0.223	0.357*	0.435**	0.177	0.225	0.129	0.291*	-0.141	-0.044	0.253	0.348*	0.394**	0.012	-0.474**	0.026	0.473**	0.348*	1.000	
X_{20}	-0.065	0.100	-0.144	0.012	0.021	0.305*	-0.055	0.216	-0.219	-0.109	0.411**	0.273*	0.370**	0.037	-0.534**	0.007	0.421**	0.202	0.497**	1.000

4.4.1 Evaluation of F_1's and parents

4.4.1.1 Mean performance of parents

Among the lines the first flowering line was L_2 and in testers T_2 (Table 16) Days to first harvest is less for all the lines except L_5 and in testers T_2. Among lines L_2 and L_3 recorded the maximum yield traits followed by L_5 and L_1. In testers T_1 showed good performance followed by T_2 and T_3.

4.4.1.2 Mean performance of hybrids

The mean performances of the hybrids were estimated which revealed a wide variation among the crosses. The mean values of the various characters for the crosses are presented in the Table 17. The cross L_1 x T_2 took only 42.67 days to flower, which was the earliest. The last to achieve 50 per cent flowering was the cross L_4 x T_3. Length of harvest period, pod weight and pod breadth was maximum for the cross L_5 x T_1, 26.33, 23.4 g and 1.063 respectively. L_1 x T_3 had the maximum pod clusters per plant (5.53), which was on par with L_1 x T_1 and L_3 x T_2 (5.4). Days to first harvest was highest value for the cross L_1 x T_3 (56.67) and lowest for L_3 x T_1 (52.33) which was on par with L_3 x T_2 and L_2 x T_1 (52.33). Maximum crop duration and seeds per pod for the cross L_1 x T_2 was 86.33 and 18.13 respectively. The cross L_1 x T_1 showed the highest value for pods per plant (15.80) and 100 seed weight (20.53). Maximum pod yield was observed in L_3 x T_1 (323.17) and minimum in L_1 x T_3 (191.67). Pod length was maximum for L_4 x T_2 (47.47). Maximum pods per cluster was shown by crosses L_2 x T_2, L_2 x T_3 and L_3 x T_2 (2.6 each). Length of peduncle (29.07) and crude fibre content of pods (3.72) were maximum for the cross L_3 x T_1. The cross L_5 x T_1 showed the maximum number of trichomes on pod wall (5.6) followed by L_3 x T_1 (5.40) and L_1xT_1 (5.20). Three crosses showed the maximum leaf chlorophyll content (1.84 for L_2 x T_1, L_3 x T_1 and L_4 x T_1. The cross L_1 x T_1 (8.75) showing maximum pod protein content.

Table 16. Mean values of 20 yield characters used for line x tester analysis

	Plants	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
L_1	Trailing Red Poded (G_{27})	42.33	51.00	21.00	80.33	3.4	503.33	5.67	9.27	266.50	2.4	17.20	38.30	1.12	14.27	18.33
L_2	NS 621 (G_{42})	42.00	51.33	19.67	84.00	3.4	535.33	9.60	12.40	247.17	2.2	17.47	29.00	0.85	12.33	19.27
L_3	Ettumanoor local (G_{10})	45.00	51.00	20.67	78.33	3.4	448.00	7.47	8.40	416.50	2.2	25.00	47.27	0.93	20.40	16.53
L_4	Vellayani local (G_{31})	45.00	51.00	21.33	81.00	3.4	446.33	4.60	10.60	270.83	2.6	14.00	44.67	0.74	13.60	19.27
L_5	Palakkad local (G_{29})	42.67	55.00	23.67	81.67	3.6	491.67	5.47	10.20	272.83	2.6	14.20	35.27	0.96	14.00	15.67
T_1	Kurappunthara local (G_{43})	47.33	53.67	24.67	81.33	3.6	476.00	6.33	13.13	308.50	2.2	24.00	25.43	0.97	11.40	19.80
T_2	Kanichar local (G_{15})	46.67	52.67	23.67	87.33	3.4	468.17	4.44	10.40	173.00	2.2	16.47	31.50	0.93	15.60	16.67
T_3	KMV-1 (G_{30})	51.67	57.33	24.67	84.67	3.4	522.67	5.00	11.53	156.00	2.0	16.40	45.60	0.76	11.40	15.20

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant (g)
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

Table 16. Continued

	Plants	X_{16}	X_{17}	X_{18}	X_{19}	X_{20}
L_1	Trailing Red Poded (G_{27})	24.73	3.4	1.67	8.74	3.64
L_2	NS 621 (G_{42})	18.20	2.6	1.85	8.26	3.31
L_3	Ettumanoor local (G_{10})	18.20	3.4	1.65	8.25	3.73
L_4	Vellayani local (G_{31})	22.33	2.6	1.85	8.74	3.06
L_5	Palakkad local (G_{29})	18.17	4.2	1.65	7.90	3.09
T_1	Kurappunthara local (G_{43})	26.67	5.6	1.59	6.34	3.36
T_2	Kanichar local (G_{15})	18.55	6.2	1.48	5.59	2.66
T_3	KMV-1 (G_{30})	17.8	6.0	1.46	5.31	2.22

X_{16} Peduncle length
X_{17} Number of trichomes on pod wall
X_{18} Leaf chlorophyll content
X_{19} Pod protein content
X_{20} Crude fibre content of pods

Table 17. Mean performance of crosses (yield and biochemical traits)

Crosses	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
L_1xT_1	43.67	52.33	24.33	79.00	3.40	514.83	5.40	15.80	250.67	2.20	15.33	32.97	0.71	11.80	20.53
L_1xT_2	42.67	53.00	23.67	86.33	3.40	488.83	4.40	10.40	199.00	2.20	15.73	37.67	0.74	18.13	17.00
L_1xT_3	47.00	56.67	23.33	80.33	3.40	502.00	5.53	12.20	191.67	1.67	21.13	35.17	0.95	17.60	19.27
L_2xT_1	45.33	52.33	23.00	80.00	3.40	518.17	5.33	9.20	275.83	1.73	16.47	37.63	0.83	10.60	15.20
L_2xT_2	45.00	53.67	23.33	80.33	3.53	490.50	4.60	14.00	199.33	2.60	14.27	37.60	0.96	17.00	15.47
L_2xT_3	48.33	55.33	20.00	82.33	3.40	500.83	5.00	12.20	204.00	2.60	16.53	35.47	0.66	15.20	15.13
L_3xT_1	45.67	52.33	21.67	81.00	3.60	462.50	4.27	11.20	323.17	2.00	18.20	38.3	0.64	15.80	18.47
L_3xT_2	44.33	52.33	24.00	84.00	3.53	463.67	5.40	11.20	222.50	1.87	14.40	30.97	0.86	13.67	19.47
L_3xT_2	45.00	56.33	24.33	78.33	3.40	483.33	4.67	11.40	212.67	2.60	13.20	25.47	1.05	11.47	16.47
L_4xT_1	45.00	54.33	23.67	80.33	3.40	448.83	2.50	10.47	299.17	1.60	16.47	34.30	0.76	11.53	20.33
L_4xT_2	45.00	53.67	21.67	84.67	3.27	452.83	2.60	4.47	200.50	1.40	16.80	47.47	0.65	17.47	16.40
L_4xT_3	49.67	54.67	24.33	85.00	3.53	489.33	2.20	6.33	279.17	1.60	21.67	40.63	0.73	13.47	15.47
L_5xT_1	44.00	55.00	26.33	78.33	3.40	503.83	4.20	8.07	282.33	1.53	23.40	41.70	1.06	13.27	13.07
L_5xT_2	44.00	54.00	25.00	83.67	3.40	514.83	3.20	7.20	214.50	1.80	16.60	35.47	0.82	13.73	19.27
L_5xT_3	47.33	56.00	23.33	85.67	3.60	497.00	3.40	7.27	205.33	1.60	12.73	33.03	0.66	13.73	14.40
CD	2.35	2.670	4.07	2.92	0.28	20.73	0.38	0.61	4.36	0.31	0.76	1.13	0.03	0.74	0.46

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant (g)
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

Table 17. Continued

Crosses	Length of peduncle (cm)	No. of trichomes on pod wall (mm^2)	Leaf chlorophyll content (mg/g)	Protein content of pods (%)	Crude fibre content of pods (%)
L_1xT_1	23.27	5.20	1.63	8.75	3.64
L_1xT_2	24.83	3.20	1.57	5.49	1.96
L_1xT_3	19.40	4.40	1.64	6.18	2.66
L_2xT_1	19.67	4.73	1.84	8.26	2.97
L_2xT_2	20.50	4.27	1.79	8.74	3.64
L_2xT_3	28.00	4.40	1.44	7.22	2.52
L_3xT_1	29.07	5.40	1.84	8.24	3.72
L_3xT_2	19.80	4.60	1.42	7.88	2.32
L_3xT_2	21.27	4.67	1.45	6.09	2.27
L_4xT_1	28.83	5.47	1.84	8.72	3.03
L_4xT_2	21.43	4.6	1.35	4.61	2.62
L_4xT_3	19.53	3.87	1.34	5.31	2.64
L_5xT_1	16.60	5.6	1.44	5.25	2.53
L_5xT_2	19.27	4.00	1.37	5.55	2.08
L_5xT_3	21.57	5.20	1.48	5.31	2.33
CD	2.42	0.35	0.07	0.55	0.25

4.4.1.3 General combining ability

The general combining ability (gca) for the various parents are presented in the Table 18 and Fig. 3. Among lines L_4 (1.09) and among testers T_3 (2.00) recorded the significant gca effects for days to 50 per cent flowering, while T_2 (-1.27) showed negative gca effect.

None of the lines showed any significant values for days to first harvest, but the tester T_3 (1.67) showed significant gca effects and T_1 showed negative effect. Length of harvest period did not show any significant gca effects among the lines and testers. L_4 (1.38) and T_2 (1.84) showed highest significant gca effects for crop duration.

Highest gca effects of main stem length was for line L_5 (16.47) and tester T_2 (-6.62) showed negative significant gca effects. Three lines showed positive gca effects for the character pod clusters per plant namely L_1 (0.93), L_2 (0.79), L_3 (0.59) and L_4 (-1.75) and L_5 (-0.58) showed negative significant gca effects. Among the testers, T_1 (0.16) showed positive gca value while T_2 (-0.14) showed negative values.

L_1 (2.71) showed the highest significant gca effects for pods per plant followed by L_2 (1.71) and L_3 (1.17). But L_4 (-3.00) and L_5 (-2.58) showed negative significant gca effect. Among the testers T_1 (0.85) showed positive gca and T_2 (-0.64) showed negative.

Regarding the pod yield per plant L_4 (22.29) showed highest gca effects followed by L_3 (15.45). Three lines showed negative gca effects (L_1, L_2 and L_5). Among testers T_1 (48.91) showed positive gca effects, while T_2 (-30.15) and T_3 (-18.75) were negative values. L_2 (0.38) showed highest positive gca effects for pods per cluster followed by L_3 (0.22) and L_1 (0.09). Lines L_4 (-0.40), L_5 (-0.29) and tester T_1 (-0.12) showed negative gca effects.

Table 18. General combining ability effects of lines and testers

Character/ Treatments	Days to 50 per cent flowering	Days to first harvest	Length of harvest period	Crop duration	Primary branches per plant	Main stem length	Pod clusters per plant	Pods per plant	Pod yield per plant	Pods per cluster	Pod weight	Pod length	Pod breadth	Seeds per pod	100-Seed weight
Lines															
L_1	-1.02	-0.13	0.31	-0.07	-0.04	13.13**	0.93**	2.71**	-23.54**	0.09**	0.54**	-0.99**	-0.01	1.55**	1.87**
L_2	0.75	-0.35	-1.35	-1.07	0.00	14.41**	0.79**	1.71**	-10.93**	0.38**	-1.11**	0.64**	0.01	-0.03	-1.79**
L_3	-0.47	-0.47	-0.13	-0.84	0.07	-18.92**	0.59**	1.17**	15.45**	0.22**	-1.59**	-4.68**	0.05**	-0.65**	1.07**
L_4	1.09*	0.09	-0.24	1.38*	-0.04	-25.09**	-1.75**	-3.00**	22.29**	-0.40**	1.45**	4.54**	-0.09**	-0.14	0.34**
L_5	-0.35	0.87	1.42	0.60	0.02	16.47**	-0.58**	-2.58**	-3.27**	-0.29**	0.71**	0.48	0.04**	-0.72**	-1.48**
SE	0.47	0.54	0.82	0.59	0.06	4.19	0.08	0.12	0.88	0.06	0.15	0.228	0.01	0.15	0.09
CD	1.36	1.54	2.35	1.69	0.16	11.96	0.22	0.35	2.52	0.18	0.44	0.65	0.02	0.45	0.27
Testers T_1	-0.73	-0.87*	0.33	-2.22**	-0.004	0.88	0.16**	0.85**	48.91**	-0.12*	1.11**	0.72**	-0.01	-1.69**	0.46**
T_2	-1.27**	-0.80	0.07	1.84**	-0.02	-6.62*	-0.14**	-0.64**	-30.15**	0.04	-1.30**	1.58**	0.00	1.70**	0.46**
T_3	2.00**	1.67**	-0.40	0.38	0.02	5.74	-0.02	-0.21*	-18.75**	0.08	0.19	-2.30**	0.01	-0.004	-0.91**
SE	0.37	0.42	0.64	0.46	0.04	3.24	0.06	0.09	0.68	0.05	0.12	0.176	0.004	0.12	0.07
CD	1.05	1.19	1.82	1.31	0.13	9.27	0.17	0.27	1.95	0.14	0.34	0.50	0.012	0.33	0.21

* Significant at 5 per cent level ** Significant at 1 per cent level

Table 18. Continued

Character/ Treatments	Length of peduncle	No. of trichomes on pod wall	Leaf chlorophyll content	Protein content of pods	Crude fibre content of pods
Lines L_1	0.29	-0.37**	0.05**	0.03	0.02
L_2	0.52	-0.17*	0.13**	1.29**	0.31**
L_3	1.17*	0.25**	0.006	0.63**	0.04
L_4	1.06*	0.004	-0.05**	-0.56**	0.03
L_5	-3.06**	0.29**	-0.13**	-1.40**	-0.41**
SE	0.49	0.07	0.01	0.11	0.05
CD	1.39	0.20	0.04	0.32	0.15
Testers T_1	1.28**	0.64**	0.16**	1.07**	0.45**
T_2	-1.03**	-0.51**	-0.06**	-0.32**	-0.21**
T_3	-0.25	-0.13*	-0.09**	-0.75**	-0.24**
SE	0.38	0.05	0.01	0.09	0.04
CD	1.08	0.15	0.03	0.25	0.11

* Significant at 5 per cent level ** Significant at 1 per cent level

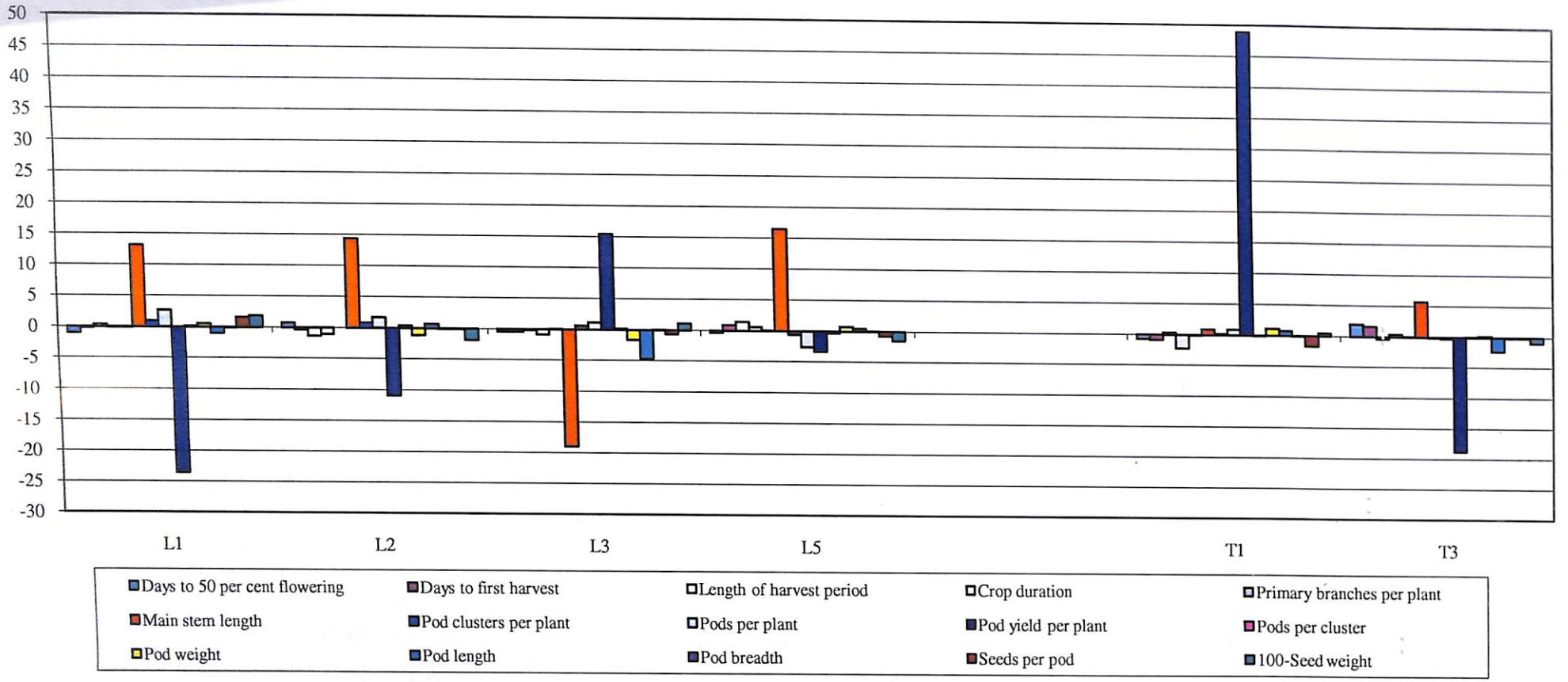


Fig. 3. General combining ability effects of selected parents for yield and related characters in yard long bean

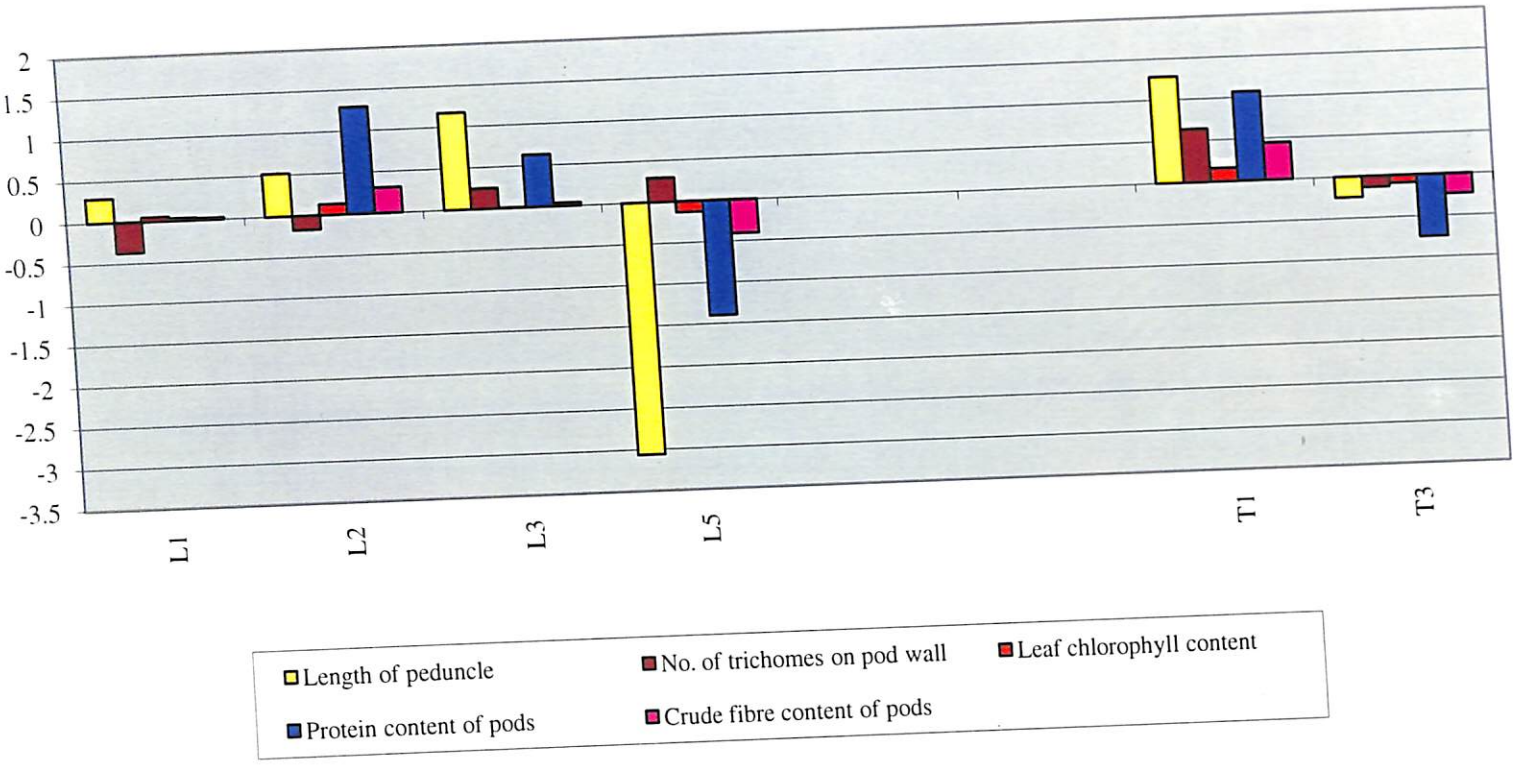


Fig. 3. Continued

Highest gca effect was recorded for pod weight by L_4 (1.45) among lines and T_1 (1.11) among testers. Lines L_4 (1.45), L_5 (0.71), L_2 (-1.11), L_3 (-1.59) and tester T_2 (-1.30) showed significant values for this character. For pod length L_4 (4.54) and T_2 (1.58) showed highest gca effects. Pod breadth showed significant positive gca effects for L_3 (0.05), L_5 (0.04) and L_4 (-0.09) showed negative.

Seeds per pod showed significant gca effects for L_1 (1.55) and T_2 (1.70). The line L_1 (1.87) and testers T_1 and T_2 (0.46) showed significant gca effects for 100-seed weight.

Among lines L_3 and L_4 and among testers T_1 showed significant positive gca effects for peduncle length. L_5 and T_1 showed negative significant gca effect for peduncle length. L_3 and L_5 and T_1 had significant positive gca effects for trichome number. L_1, L_2 and T_1 had significant positive gca effects for leaf chlorophyll content. L_2, L_3 and T_1 had significant positive gca effects for protein content of pods. L_2 and T_1 showed significant positive gca effects for crude fibre content. Parents L_4, L_5, T_2 and T_3 had negative significant gca effects for leaf chlorophyll content.

4.4.1.4 Specific combining ability

The specific combining ability (sca) of the various crosses were estimated and presented in the Table 19 and Fig. 4. Negative significant sca effect for days to 50 per cent flowering was shown by the cross $L_3 \times T_3$ (-2.00). Crop duration showed positive significant sca effects for crosses $L_1 \times T_2$ (2.60) and $L_3 \times T_1$ (2.11) while $L_3 \times T_3$ (-3.15) and $L_2 \times T_2$ (-2.40) showed negative significant sca effects.

Significant positive sca effect for main stem length was shown by the crosses $L_4 \times T_3$ (19.92) and $L_5 \times T_2$ (16.23). The significant sca effects for pod clusters per plant was shown by the crosses $L_3 \times T_2$ (0.76), $L_1 \times T_3$ (0.44), $L_5 \times T_1$ (0.44), $L_4 \times T_2$ (0.31), $L_1 \times T_2$ (-0.57) and $L_3 \times T_1$ (-0.67). Ten crosses showed significant sca effects for pods per plant. The cross $L_2 \times T_2$ (2.84) showed highest significant value followed by $L_4 \times T_1$ (2.52) and $L_1 \times T_1$ (2.15).

Table 19. Specific combining ability effects of hybrids

Characters/ Treatments	Days to 50 per cent flowering	Days to first harvest	Length of harvest period	Crop duration	Primary branches per plant	Main stem length	Pod cluster per plant	Pods per plant	Pod yield per plant	Pods per cluster	Pod weight	Pod length	Pod breadth	Seeds per pod	100-Seed weight
L_1xT_1	-0.04	-0.80	0.22	-0.67	0.004	12.07	0.12	2.15**	-12.02**	0.29*	-3.18**	-3.02**	-0.08**	-2.35**	1.14**
L_1xT_2	-0.51	-0.20	-0.18	2.60*	0.017	-6.43	-0.57**	-1.76**	15.38**	0.14	-0.36	0.82*	-0.06**	0.59*	-2.39**
L_1xT_3	0.55	1.00	-0.04	-1.93	-0.022	-5.63	0.44**	-0.39	-3.35*	-0.435**	3.54**	2.20**	0.14**	1.76**	1.25**
L_2xT_1	-0.15	-0.58	0.55	1.33	-0.040	14.12	0.19	-3.45	0.53	-0.46**	-0.40	0.01	0.02*	-1.97**	-0.52**
L_2xT_2	0.04	0.68	1.15	-2.40*	0.106	-6.04	-0.23	2.84**	3.10*	0.25*	-0.18	-0.88*	0.14**	1.03**	-0.26
L_2xT_3	0.11	-0.11	-1.71	1.06	-0.066	-8.08	0.04	0.61**	-3.63*	0.21	0.59*	0.87*	-0.16**	0.94*	0.78**
L_3xT_1	1.40	-0.47	-2.00	2.11*	0.093	-8.21	-0.67**	-0.92**	21.48**	-0.03	1.82**	5.99**	-0.21**	3.85**	-0.12
L_3xT_2	0.60	-0.53	0.60	1.04	0.040	0.46	0.76**	0.57*	-0.12	-0.33**	0.43	-2.19**	0.01	-1.68**	0.88**
L_3xT_3	-2.00*	1.00	1.40	-3.15**	-0.130	7.26	-0.09	0.35	-21.35**	0.36**	-2.26**	-3.81**	0.20**	-2.17**	-0.75**
L_4xT_1	-0.82	0.98	0.11	-0.78	0.0014	-15.71	-0.09	2.52**	-9.35**	0.19	-2.95**	-7.22**	0.05**	-0.92**	2.48**
L_4xT_2	-0.28	0.24	-1.62	-0.51	-0.115	-4.21	0.31**	-1.98**	-28.95**	-0.17	-0.21	5.09**	-0.06	1.61**	-1.46**
L_4xT_3	1.11	-1.22	1.51	1.29	0.111	19.92**	-0.21	-0.54*	38.31**	-0.01	3.16**	2.13**	0.01	-0.68*	-1.02**
L_5xT_1	-0.38	0.87	1.11	-2.00	-0.062	-2.27	0.44**	-0.29	-0.63	0.01	4.71**	4.24**	0.22**	1.39**	-2.97**
L_5xT_2	0.15	-0.20	0.04	-0.73	-0.048	16.23*	-0.26	0.33	10.60**	0.12	0.32	-2.84**	-0.03**	-1.55**	3.23**
L_5xT_3	0.22	-0.67	-1.15	2.73	0.111	-13.97	-0.18	-0.03	-9.97**	-0.12	-5.03**	-1.39**	-0.19**	0.16	-0.26
SE±	0.82	0.93	1.42	1.02	0.09	7.26	0.13	0.21	1.52	0.11	0.27	0.39	0.01	0.26	0.16
CD	2.35	2.67	4.07	2.92	0.28	20.73	0.38	0.61	4.36	0.31	0.76	1.13	0.03	0.74	0.46

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 19. Continued

Characters/ Treatments	Peduncle length	Number of trichomes on pod walls	Leaf chlorophyll content	Crude protein content	Crude fibre content of pods
L_1xT_1	-0.52	0.29*	-0.14**	0.87**	0.438**
L_1xT_2	3.37**	-0.56**	0.02	-0.99**	0.59**
L_1xT_3	-2.85**	0.27*	0.11**	0.12	0.15
L_2xT_1	-4.34**	-0.37**	-0.005	-0.88**	-0.52**
L_2xT_2	-1.19	0.31*	0.16**	0.98**	0.80**
L_2xT_3	5.33**	0.07	-0.15**	-0.10	-0.28**
L_3xT_1	4.40**	-0.13	0.11**	-0.23	0.50**
L_3xT_2	-2.54**	0.22	-0.09**	0.79**	-0.25**
L_3xT_3	-1.86*	-0.09	-0.03	-0.56**	-0.25**
L_4xT_1	4.28**	0.18	0.17**	1.43*	-0.19*
L_4xT_2	-0.79	0.46**	-0.09**	-1.28**	0.06
L_4xT_3	-3.48**	-0.64**	-0.08**	-0.15	0.12
L_5xT_1	-3.83**	-0.03	-0.15**	-1.19**	-0.23*
L_5xT_2	1.16	-0.43**	0.001	0.50**	-0.03
L_5xT_3	2.67**	0.40**	0.14**	0.69**	0.26**
SE±	0.85	0.12	0.02	0.19	0.09
CD	2.42	0.35	0.07	0.55	0.25

* Significant at 5 per cent level

** Significant at 1 per cent level

Six crosses showed significant sca effects for pods per cluster. The cross L_3 x T_3 showed the highest sca value (0.36). Nine crosses showed significant sca effect for pod weight, among them L_5 x T_1 showed highest value (4.71). Among the fifteen crosses, 14 had significant sca effect for pod length. The cross L_3 x T_1 (5.99) showed the highest value followed by L_4 x T_2 (5.09) and L_5 x T_1 (4.24).

Significant sca effects for pod breadth was shown by 12 crosses. Among them L_5 x T_1 (0.22), L_3 x T_3 (0.20), L_1 x T_3 (0.14) and L_2 x T_2 (0.141) showed positive sca effects. Fourteen crosses showed significant sca effects for seeds per pod and twelve crosses for 100-seed weight. The cross L_3 x T_1 (3.85) showed highest value for seeds per pod and L_5 x T_2 (3.23) for 100-seed weight.

Significant positive sca effects for peduncle length was shown by the crosses L_1 x T_2 (3.37), L_2 x T_3 (5.53), L_3 x T_1 (4.40), L_4 x T_1 (4.28) and L_5 x T_3 (2.67) and negative by crosses L_1 x T_3 (-2.85), L_2 x T_1 (-4.34), L_3 x T_2 (-2.54), L_3 x T_3 (-1.86), L_4 x T_3 (-3.48), L_5 x T_1 (-3.83).

The crosses L_1 x T_1 (0.29), L_1 x T_3 (0.27), L_2 x T_2 (0.31), L_4 x T_2 (0.46) and L_5 x T_3 (0.40) showed significant positive sca effects for number of trichomes on pod wall and negative by crosses L_1 x T_2 (-0.56), L_2 x T_1 (-0.37), L_4 x T_3 (-0.64) and L_5 x T_2 (-0.43).

Leaf chlorophyll content showed significant positive sca effects for the crosses L_1 x T_3 (0.11), L_2 x T_2 (0.16), L_3 x T_1 (0.11), L_4 x T_1 (0.17) and L_5 x T_3 (0.14) and negative for crosses L_1 x T_1 (-0.14), L_2 x T_3 (-0.15), L_3 x T_2 (-0.09), L_4 x T_2 (-0.09), L_4 x T_3 (-0.08) and L_5 x T_1 (-0.15).

The crosses L_1 x T_1 (0.87), L_2 x T_2 (0.98), L_3 x T_2 (0.79), L_4 x T_1 (1.43), L_5 x T_2 (0.50) and L_5 x T_3 (0.69) showed significant positive sca effects for pod protein content, while L_1 x T_2 (-0.99), L_2xT_1 (-0.88), L_3xT_3 (-0.56), L_4 x T_2 (-1.28) and L_5 x T_1 (-1.19) crosses showed negative.

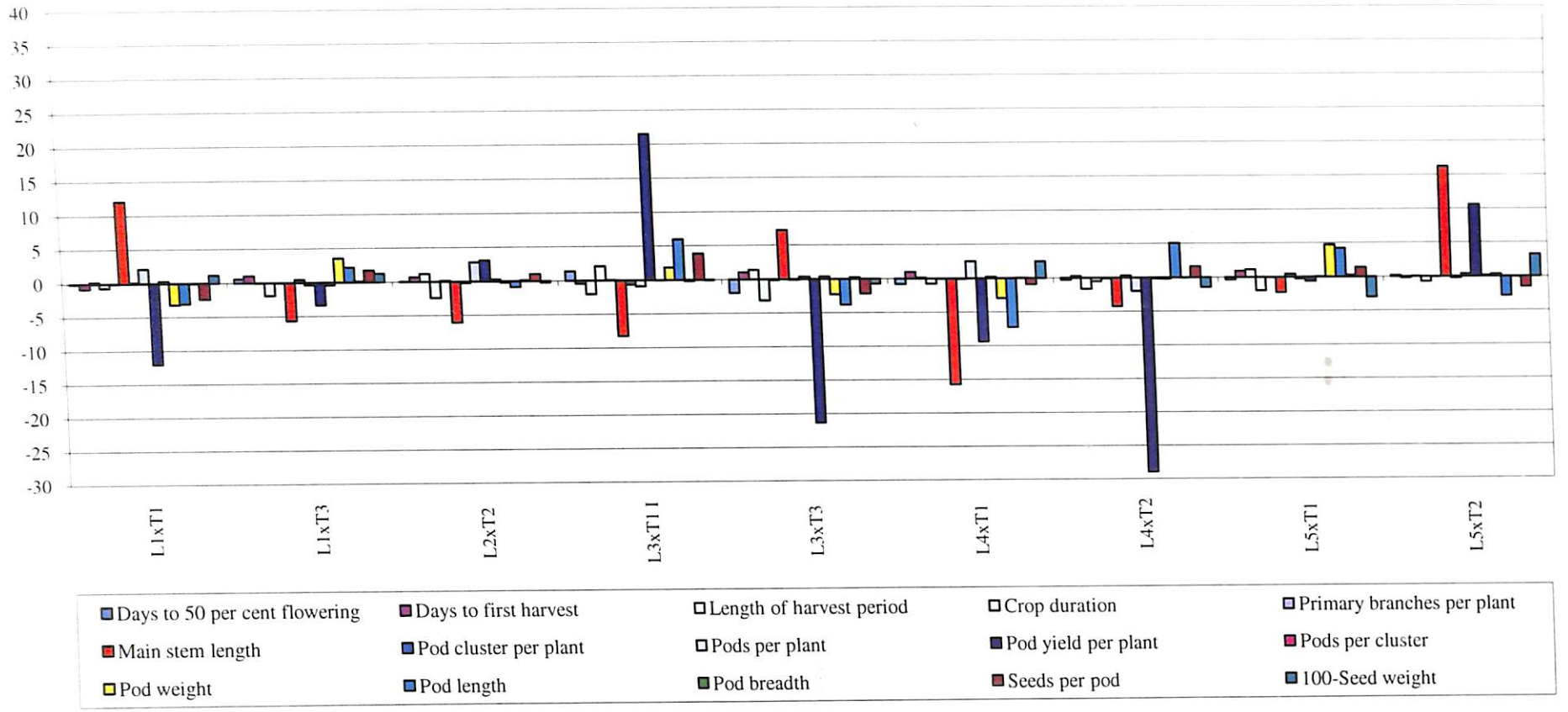


Fig. 4. Specific combining ability effects of selected crosses for yield and related characters in yard long bean

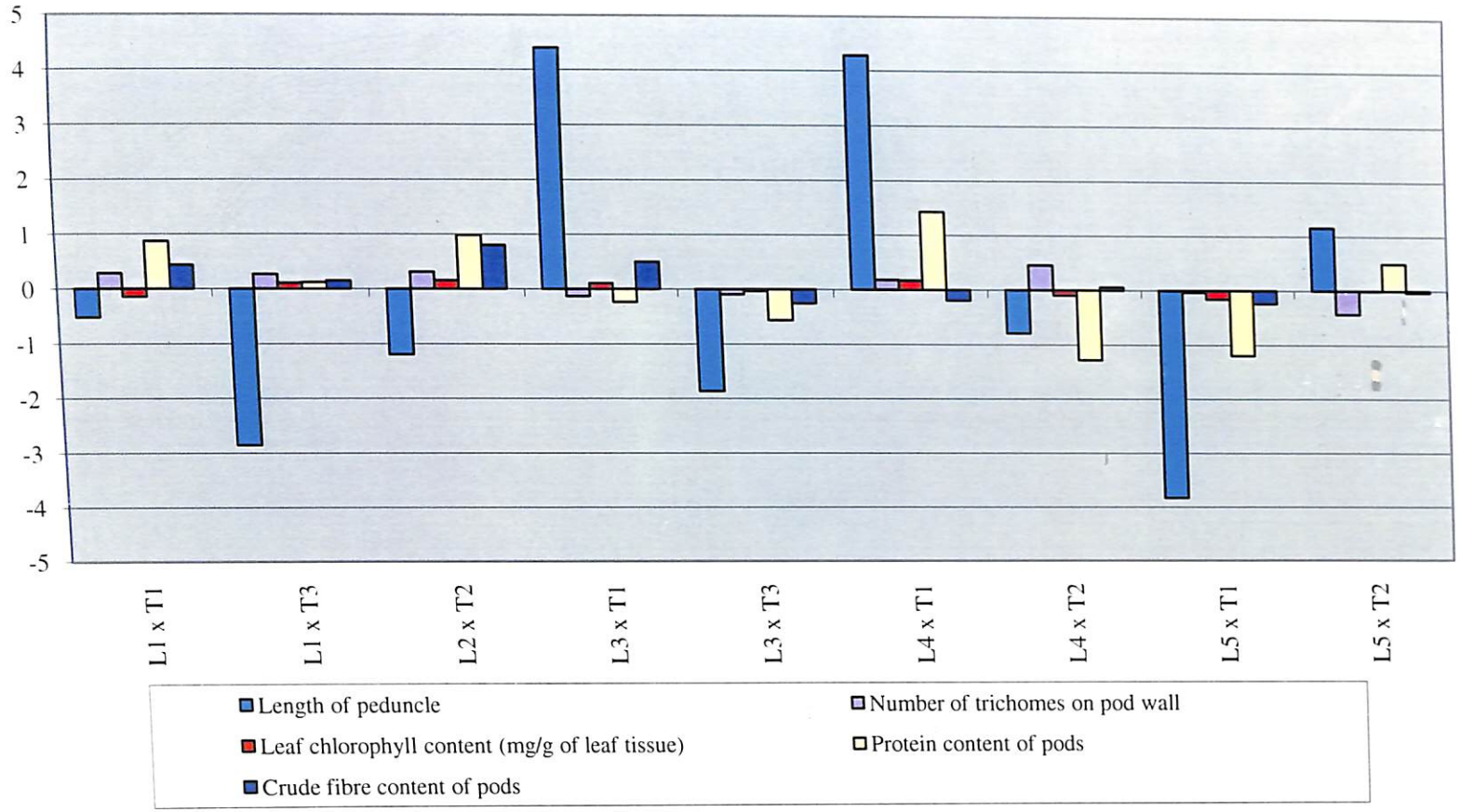


Fig. 4. Continued

The crosses L_1 x T_1, L_1 x T_2, L_2 x T_2, L_3 x T_1 and L_5 x T_3 showed significant positive sca effects for crude fibre content of pods and crosses L_2 x T_1, L_2 x T_3, L_3 x T_2, L_3 x T_3, L_4 x T_1, and L_5 x T_1 showed negative sca effects.

4.4.1.5 Proportional contribution

The proportional contribution of lines, testers and crosses to total variance of the characters under study are presented in Table 20 and Fig. 5.

The values ranged from 10.52 for days to first harvest to 87.04 for pod clusters per plant among lines. Among testers, the values ranged from 0.06 for pod breadth to 69.02 for pod yield per plant. In the case of crosses the values ranged from 11.70 for pod clusters per plant to 86.96 for pod breadth.

The crosses had contributed maximum to the total variance for all characters except days to 50 per cent flowering, days to first harvest, main stem length, pod clusters per plant, pods per plant, pod yield per plant and pods per cluster. The testers had the least contribution to the total variance with respect to crosses and lines.

The values ranged from 15.46 for number of trichomes of pod wall to 40.26 for protein content of pods among lines. Among testers, the values ranged from 6.80 for length of peduncle to 55.54 for number of trichomes on pod wall. In the case of hybrids, the values ranged from 28.99 for number of trichomes on pod wall to 75.26 for peduncle length.

4.4.1.6 Heterosis

The relative heterosis, heterobeltiosis and standard heterosis for the 15 crosses with respect to the 20 characters are presented in the Table 21 and Fig. 6.

Table 20. Proportional contribution of lines, testers and hybrids to total variance

Sl. No.	Characters	Lines (%)	Testers (%)	L x T (%)
I Yield Traits				
1	Days to 50 per cent flowering	19.15	62.31	18.54
2	Days to first harvest	10.52	65.23	24.25
3	Length of harvest period	37.88	4.31	57.81
4	Crop duration	11.82	40.62	47.56
5	Primary branches per plant	21.95	3.42	74.62
6	Main stem length	69.47	5.48	25.05
7	Pod cluster per plant	87.04	1.26	11.70
8	Pods per plant	63.93	4.62	31.45
9	Pod yield per plant	16.09	69.02	14.88
10	Pods per cluster	55.64	4.68	39.68
11	Pod weight	15.02	11.13	73.84
12	Pod length	37.19	11.67	51.14
13	Pod breadth	12.98	0.06	86.96
14	Seeds per pod	11.94	34.24	53.81
15	100-Seed weight	40.04	8.23	51.73
16.	Length of peduncle	17.91	6.80	75.28
17.	Number of trichomes on pod wall	15.46	55.54	28.99
II Biochemical traits				
18.	Leaf chlorophyll content	23.49	37.48	39.03
19.	Protein content of pods	40.26	27.73	32.01
20.	Crude fibre content of pods	18.46	34.26	47.28

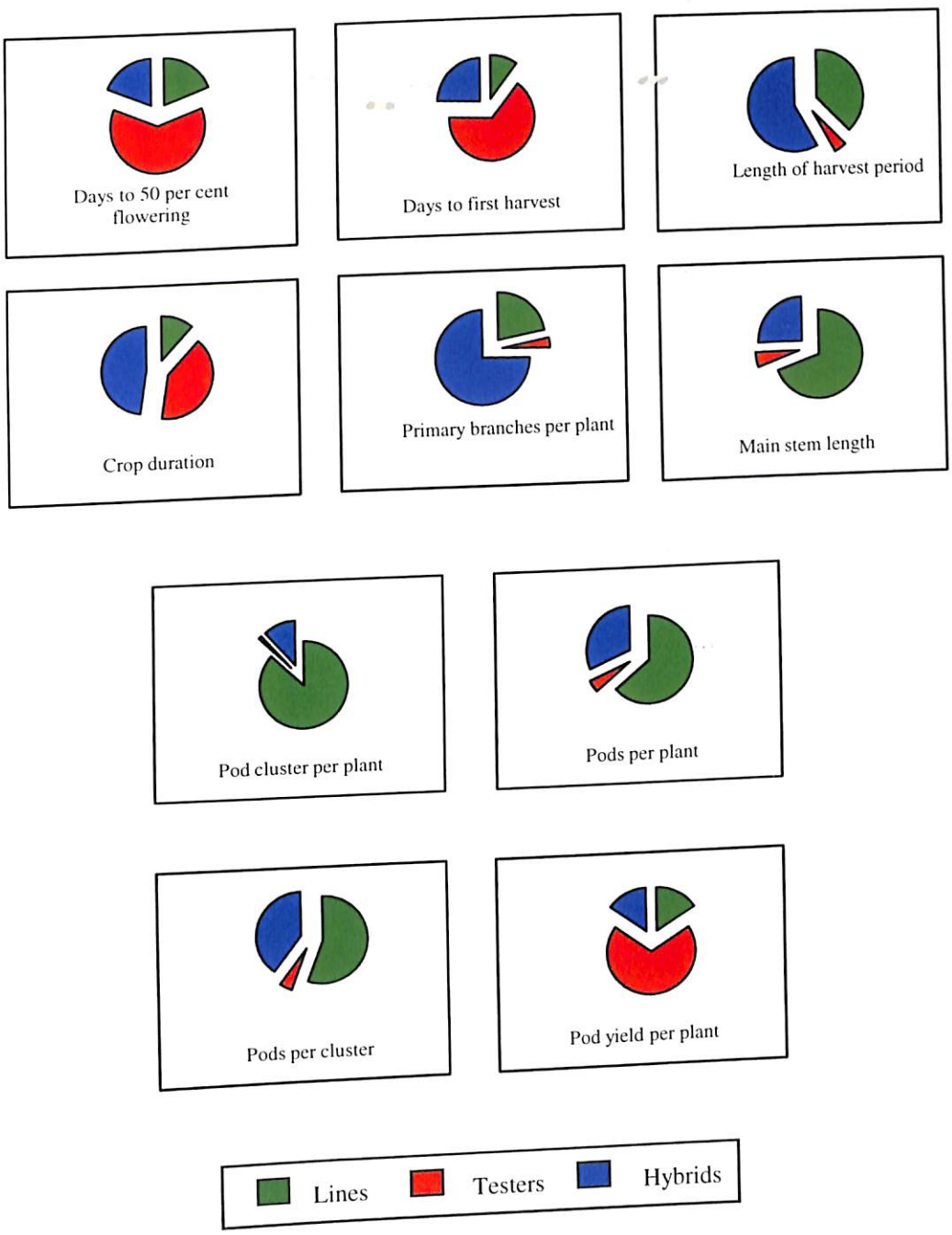


Fig. 5. Proportional contribution of lines, testers and hybrids of yield and biochemical traits in yard long bean

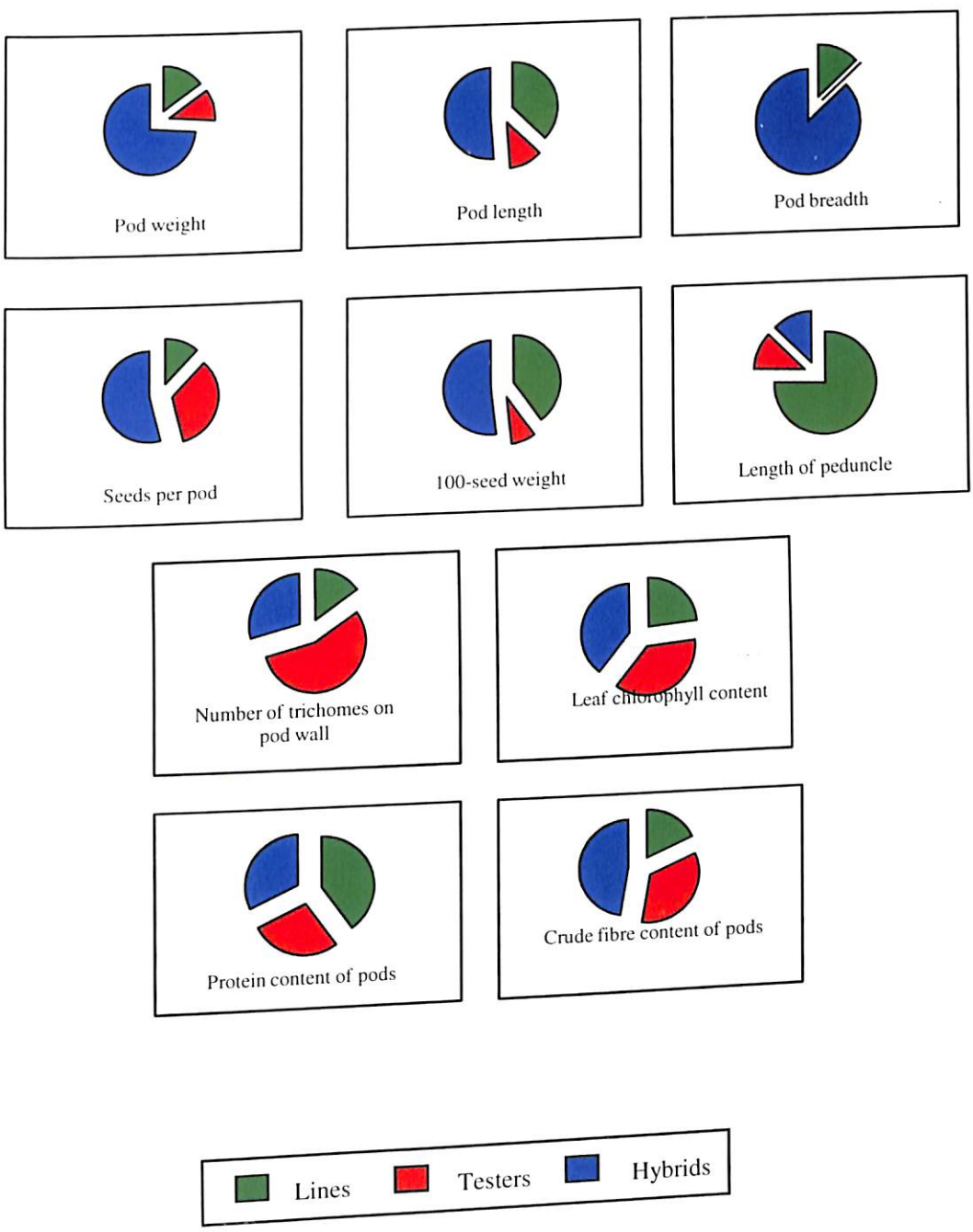


Fig. 5. Continued

Table 21 Heterosis per cent for yield parameters in yard long bean

Hybrids	Days to 50% flowering			Days to first harvest			Length of Harvest period			Crop duration			Primary branches per plant			Main stem length		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
$L_1 \times T_1$	-2.60	-7.75	-15.48**	-0.00	-2.48	-8.72**	6.57	-1.35	-1.35	-2.27	-2.87*	-9.54**	-2.86	-5.56	-5.56	5.14**	2.28	-1.49**
$L_1 \times T_2$	-4.12**	-8.57	-17.42**	2.25	0.63	-7.56**	5.97	0.00	-4.05	2.98*	-1.14	-1.14	0.00	0.00	-5.56	0.63	-2.88	-6.47*
$L_1 \times T_3$	0.00	-9.03**	-9.03**	4.61	-1.16**	-1.16	2.19	-5.40	-5.40	-2.63	-5.12**	-8.01**	0.00	0.00	-5.56	-2.14	-3.95*	-3.95
$L_2 \times T_1$	1.49	-4.22**	-12.26**	-0.32	-2.48	-8.72**	3.76	-6.76	-6.76	-3.23*	-4.76**	-8.39**	-2.86	-5.56	-5.56	2.47	-3.21*	-0.86**
$L_2 \times T_2$	1.50	-3.57*	-12.90**	3.20	1.89	-6.39**	7.69	-1.41	-5.40	-6.23**	-8.01**	-8.01**	3.92	3.92	-1.85	-2.24	-8.37**	-6.15**
$L_2 \times T_3$	3.20	-6.45**	-6.45**	1.84	-3.49**	-3.49	-9.77	-18.92**	-18.92**	-2.37	-2.76*	-5.72**	-0.00	-0.00	-5.56	-5.32**	-6.44**	-4.18**
$L_3 \times T_1$	-1.08	-3.52	-11.61**	-0.00	-2.48	-8.72**	-4.41	-12.16	-12.16	1.46	-0.41	-7.25**	2.86	0.00	0.00	0.11	-2.84	-11.51**
$L_3 \times T_2$	-3.27	-5.00	-14.19**	0.96	0.63	-8.72**	8.27	1.40	-2.70	1.41	-3.82**	-3.82**	3.92	3.92	-1.85	1.22	-0.96	-11.28**
$L_3 \times T_3$	-6.89**	-12.90	-12.90**	4.00	-1.74	-1.74	7.35	-1.35	-1.35	-3.89*	-7.48**	-10.30**	0.00	0.00	-5.56	-0.41	-7.53**	-7.53**
$L_4 \times T_1$	-2.53	-4.93	-12.90**	3.82	1.24	-5.23**	2.89	-4.05	-4.05	-1.03	-1.23	-8.01**	-2.86	-5.56	-5.56	-2.67	-5.71**	-14.13**
$L_4 \times T_2$	-1.82	-3.57	-12.90**	3.54	1.89	-6.39**	-3.70	-8.45	-12.16	0.59	-3.05*	-3.05*	-3.92	-3.92	-9.26**	-0.97	-3.27	-13.36**
$L_4 \times T_3$	2.76	-3.87**	-3.87**	0.92**	-4.65**	-4.65*	5.79	-1.35	-1.35	2.62	0.39	-2.67*	3.92	3.92	-1.85	0.99	-6.38**	-6.38**
$L_5 \times T_1$	-2.22	-7.04	-14.84**	1.23	0.00	-4.07**	8.97	6.76	6.76	-3.89**	-4.08**	-10.30**	-5.56	-5.56	-5.56	4.13*	2.47	-3.60**
$L_5 \times T_2$	-1.49**	-5.71	-14.84**	0.31	-1.82	-5.81**	5.63	5.63	1.35	-0.99	-4.19**	-4.19**	-2.86	-5.56	-5.56	7.28**	4.71**	-1.49
$L_5 \times T_3$	0.35	-8.39**	-8.39**	-0.29	-2.33	-2.33	-3.45	-5.40	-5.40	3.00*	1.18	-1.91	2.86	0.00	0.00	-2.00	-4.91**	-4.91**
CD (0.05)	2.03	2.35	2.35	2.31	2.66	2.66	3.52	4.07	4.07	2.53	2.92	2.92	0.24	0.28	0.28	17.95	20.73	20.73

* Significant at 5 per cent level ** Significant at 1 per cent level

Table 21. Continued

Hybrids	Pod cluster per plant			Pods per plant			Pod yield per plant			Pods per clusters			Pod weight		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
L_1 x T_1	-10.00**	-14.74**	-14.74**	41.07**	20.30**	20.30**	-12.81**	-18.75**	-18.75**	-4.35	-8.33	0.01	-26.28**	-37.16**	-37.16**
L_1 x T_2	-12.58**	-22.35**	-30.53**	5.76*	-0.00	-20.81**	-9.44**	-25.33**	-35.49**	-4.35	-8.33	0.00	-6.53**	-8.53**	-35.52**
L_1 x T_3	3.75	-2.35	-12.63**	17.31**	5.78**	-7.11**	-9.27**	-28.08**	-37.87**	-24.24**	-30.56**	-24.24**	25.79**	22.87**	-13.39**
L_2 x T_1	-33.05**	-44.44**	-15.79**	-27.94**	-29.95**	-29.95**	-0.72	-10.59**	-10.59**	-21.21**	-21.21**	-21.21**	-21.34**	-32.51**	-32.51**
L_2 x T_2	-34.29**	-52.08**	-27.37**	22.81**	12.90**	6.59**	-5.12**	-19.35**	-35.39**	18.18**	18.18**	18.18**	-15.91**	-18.32**	-41.53**
L_2 x T_3	-31.51**	-47.92**	-21.05**	1.95	-1.61	-7.11**	1.19	-17.46**	-33.87**	23.81**	18.18	18.18**	-2.36	-5.34**	-32.24**
L_3 x T_1	-38.16**	-42.86**	-32.63**	4.02	-14.72**	-14.72**	-10.85**	-22.41**	4.75**	-9.09	-9.09**	-9.09	-26.32**	-27.2**	-25.41**
L_3 x T_2	-8.99**	-27.68**	-14.74**	19.15**	7.69**	-14.72**	-24.51**	-46.58**	-27.88**	-15.15**	-15.15**	-15.15**	-30.55**	-42.4**	-40.98**
L_3 x T_3	-25.13**	-37.5**	-26.32**	14.38**	-1.16	-13.19**	-25.71**	-48.94**	-31.06**	23.81**	18.18**	18.18**	-36.23**	-47.2**	-45.90**
L_4 x T_1	-54.27**	-60.53**	-60.53**	-11.79**	-20.30**	-20.30**	3.28**	-3.02**	-3.02**	-33.33**	-38.46**	-27.27**	-14.24**	-32.51**	-32.51**
L_4 x T_2	-42.22**	-43.48**	-58.95**	-57.46**	-57.86**	-65.99**	-9.65**	-25.97**	-35.01**	-41.67**	-46.15**	-36.36**	10.28**	2.02	-31.15**
L_4 x T_3	-54.17**	-56.00**	-65.26**	-42.77**	-45.09**	-51.78**	30.81**	3.08**	-9.51**	-30.43**	-38.46**	-27.27**	42.54**	32.11**	-11.20**
L_5 x T_1	-26.81**	-33.68**	-33.68**	-30.86**	-38.58**	-38.58**	-2.87**	-8.48**	-8.48**	-36.11**	-41.03**	-30.30**	21.24**	-4.09**	-4.09**
L_5 x T_2	-35.13**	-41.46**	-49.47**	-30.09**	-30.77**	-45.18**	-3.78**	-21.38**	-30.47**	-25.00**	-30.77**	-18.18**	8.26**	0.81	-31.97**
L_5 x T_3	-35.03**	-37.80**	-46.32**	-33.13**	-36.99**	-44.67**	-4.24**	-24.74**	-33.44**	-30.435**	-38.46**	-27.27**	-16.78**	-22.36**	-47.81**
CD (0.05)	0.33	0.38	0.38	0.53	0.61	0.61	3.77	4.36	4.36	0.27	0.31	0.31	0.60	0.76	0.76

* Significant at 5 per cent level ** Significant at 1 per cent level

Table 21. Continued

Hybrids	Pod length			Pod breadth			Seeds per pod			100-Seed weight		
	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
L_1xT_1	3.45*	-13.92**	-27.70**	-32.17**	-36.61**	-27.05**	-8.05**	-17.29**	-24.36**	7.69**	3.70**	3.70**
L_1xT_2	7.93**	-1.65	-17.39**	-27.69**	-33.93**	-23.97**	21.43**	16.24**	16.24**	-2.86**	-7.27**	-14.14**
L_1xT_3	-16.17**	-22.88**	-22.88**	0.71	-15.48**	-2.74*	37.14**	23.36**	12.82**	14.91**	5.09**	-2.69**
L_2xT_1	38.27**	29.77**	-17.47**	-8.42**	-14.38**	-14.38**	-10.67**	-14.05**	-32.05**	-22.18**	-23.23**	-23.23**
L_2xT_2	24.29**	19.36**	-17.54**	8.27**	3.59**	-1.37	21.72**	8.97**	8.97**	-13.91**	-19.72**	-21.89**
L_2xT_3	-4.91**	-22.22**	-22.22**	-17.84**	-22.05**	-32.19**	28.09**	23.24**	-2.56	-12.19**	-21.45**	-23.57**
L_3xT_1	5.36**	-18.97**	-16.01**	-32.63**	-34.25**	-34.25**	-0.63	-22.55**	1.28	1.65	-6.73**	-6.73**
L_3xT_2	-21.37**	-34.48**	-32.09**	-7.19**	-7.19**	-11.64**	-24.07**	-33.01**	-12.39**	17.27**	16.8**	-1.68
L_3xT_3	-45.15**	-46.12**	-44.15**	24.90**	13.67**	8.22**	-27.88**	-43.79**	-26.49**	3.78**	-0.40	-16.83**
L_4xT_1	-2.14	-23.21	-24.78**	-11.28**	-21.92**	-21.92**	-7.73**	-15.19**	-26.07**	4.09**	2.69**	2.69**
L_4xT_2	24.64**	6.27**	4.09**	-21.6**	-29.49**	-32.88**	19.63**	11.97**	11.97**	-8.72**	-14.88**	-17.17**
L_4xT_3	-9.97**	-10.89**	-10.89**	-3.11*	-4.39**	-25.34**	7.73**	-0.98	13.67**	-10.25**	-19.72**	-21.89**
L_5xT_1	37.39**	18.24**	-8.55**	9.62**	9.25**	9.25**	4.46*	-5.24*	-14.96**	-26.32**	-34.01**	-34.01**
L_5xT_2	6.24**	0.57	-22.22**	-13.38**	-15.17**	-15.75**	-7.21**	-11.97**	-11.97**	19.17**	15.6**	-2.69**
L_5xT_3	-18.30**	-27.56**	-27.56**	-23.55**	-31.72**	-32.19**	8.14**	-1.90	-11.97**	-6.69**	-8.08**	-27.27**
CD (0.05)	0.98	1.13	1.13	0.02	0.03	0.03	0.65	0.75	0.75	0.40	0.47	0.47

* Significant at 5 per cent level ** Significant at 1 per cent level

Table 21 Continued

Sl.No		Peduncle length			No. of trichomes on pod wall			Leaf chlorophyll content			Protein content of pods			Crude fibre content in pods		
	Hybrids	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH	RH	HB	SH
1.	$L_1 \times T_1$	-9.47*	-12.75**	30.71**	15.98**	-6.59*	-13.33**	0.10	-2.19	11.87**	16.02**	0.11	64.89**	4.05	0.09	63.87**
2.	$L_1 \times T_2$	14.75**	0.40	39.51**	-33.33**	-48.39**	-46.67**	-0.10	-5.79**	7.76**	-23.38**	-37.18**	3.45	-37.78**	-46.15**	-11.84
3.	$L_1 \times T_3$	-8.78	-21.56**	8.99	-6.38	-26.67**	-26.67**	4.58*	-1.99	12.10**	-11.96**	-29.25**	16.52**	-9.27*	-26.92**	19.64**
4.	$L_2 \times T_1$	-12.33*	-26.25**	10.49	15.92**	-14.97**	-21.11**	6.98**	-0.36	26.03**	13.08**	-0.04	55.59**	-10.93**	-11.59**	33.73**
5.	$L_2 \times T_2$	11.56*	10.51	15.17*	-3.03	-31.18**	-28.89**	7.41**	-3.25	22.37**	26.16**	5.77	64.64**	21.76*	9.76*	63.57**
6.	$L_2 \times T_3$	55.56**	53.85**	57.30**	2.33	-26.67**	-26.67**	-12.90**	-22.02**	-1.37	6.44	-12.59**	36.05**	-9.09**	-24.04**	13.19*
7.	$L_3 \times T_1$	29.57**	9.00	63.29**	20.45**	-2.99	-10.00**	13.58**	11.74**	26.03**	12.90**	-0.16	55.28**	4.93	-0.27	67.47**
8.	$L_3 \times T_2$	7.75	6.74	11.24	-4.17	-25.81**	-23.33**	-9.38**	-13.97**	-2.97	13.84**	-4.52	48.49**	-27.53**	-37.95**	4.19
9.	$L_3 \times T_3$	18.15**	16.85*	19.48**	-0.71	-22.22**	-22.22**	-6.87**	-12.15**	-0.91	-10.08**	-26.13**	14.89**	-23.78**	-39.19**	2.09
10.	$L_4 \times T_1$	17.69**	8.12	61.98**	33.88**	-1.79	-8.89**	6.97**	-0.36	26.03**	15.60**	-0.23	64.26**	-5.66	-9.91*	36.28**
11.	$L_4 \times T_2$	4.85	-4.03	20.41**	4.54	-25.81**	-23.33**	-18.84**	-26.89**	-7.53**	-35.59**	-47.19**	-13.06*	-8.27*	-14.27**	17.99**
12.	$L_4 \times T_3$	-2.66	-12.54*	9.74	-10.08**	-35.56**	-35.56*	-19.15**	-27.62**	-8.45**	-24.33**	-39.18**	0.13	0.06	-13.62**	18.89**
13	$L_5 \times T_1$	-25.95**	-37.75**	-6.74	14.68**	0.59	-6.67**	-11.29**	-12.90**	-1.37	-26.33**	-33.59**	-1.13	-21.55**	-24.78**	13.79**
14.	$L_5 \times T_2$	4.95	3.86	8.24	-23.08**	-35.48**	-33.33**	-12.55**	-17.14**	-6.16**	-17.67**	-29.70**	4.65	-27.73**	-32.72**	-6.59
15.	$L_5 \times T_3$	19.93**	18.72**	21.16**	1.96	-13.33**	-13.33**	-4.71**	-10.28**	1.59	-19.54**	-32.74**	0.13	-12.12**	-24.41**	4.95
	CD (0.05)	2.09	2.42	2.42	0.30	0.35	0.35	0.06	0.07	0.07	0.48	0.55	0.55	0.22	0.25	0.25

* Significant at 5 per cent level ** Significant at 1 per cent level

a. Days to 50 per cent flowering

Significant negative relative heterosis, indicating earliness was observed for days to 50 per cent flowering for the crosses L_3 x T_3 (-6.89), L_1 x T_2 (-4.12) and L_5 x T_2 (-1.49). None of the crosses recorded significant positive relative heterosis. The cross L_3 x T_1 (-3.52) recorded highest heterobeltiosis. Earliness indicated by significant negative standard heterosis for the character days to 50 per cent flowering was observed for all the 15 crosses.

b. Days to first harvest

The cross L_4 x T_3 (0.92) showed significant positive relative heterosis. None of the crosses rendered significant negative relative heterosis. The cross L_4 x T_1 (1.24) and L_4 x T_2 (1.89) recorded a significant positive heterobeltiosis, while L_2 x T_3 (-3.49) and L_4 x T_3 (-4.65) showed negative significant heterobeltiosis. Eleven crosses showed significant negative standard heterosis for this character.

c. Length of harvest period

The value of heterosis ranged from -9.77 (L_2 x T_3) to 8.97 (L_5 x T_1) for relative heterosis -18.92 (L_2 x T_3) to 6.76 (L_5 x T_1) for heterobeltiosis and standard heterosis. The crosses L_2 x T_3 showed negative significant heterobeltiosis and standard heterosis for length of harvest period.

d. Crop duration

The crosses L_1 x T_2 (2.98) and L_5 x T_3 (3.00) exhibited significant positive relative heterosis for crop duration. Significant negative Heterobeltiosis was observed for L_1 x T_1, L_1 x T_3, L_2 x T_1, L_2 x T_2, L_2 x T_3, L_3 x T_2, L_3 x T_3, L_4 x T_2, L_5 x T_1, and L_5 x T_2. All the crosses showed significant negative standard heterosis except the crosses L_1 x T_2 and L_5 x T_3.

e. Primary branches per plant

The cross L_4 x T_2 (-9.26) showed significant negative standard heterosis for primary branches per plant. None of the crosses showed significant positive standard heterosis, heterobeltiosis and standard heterosis.

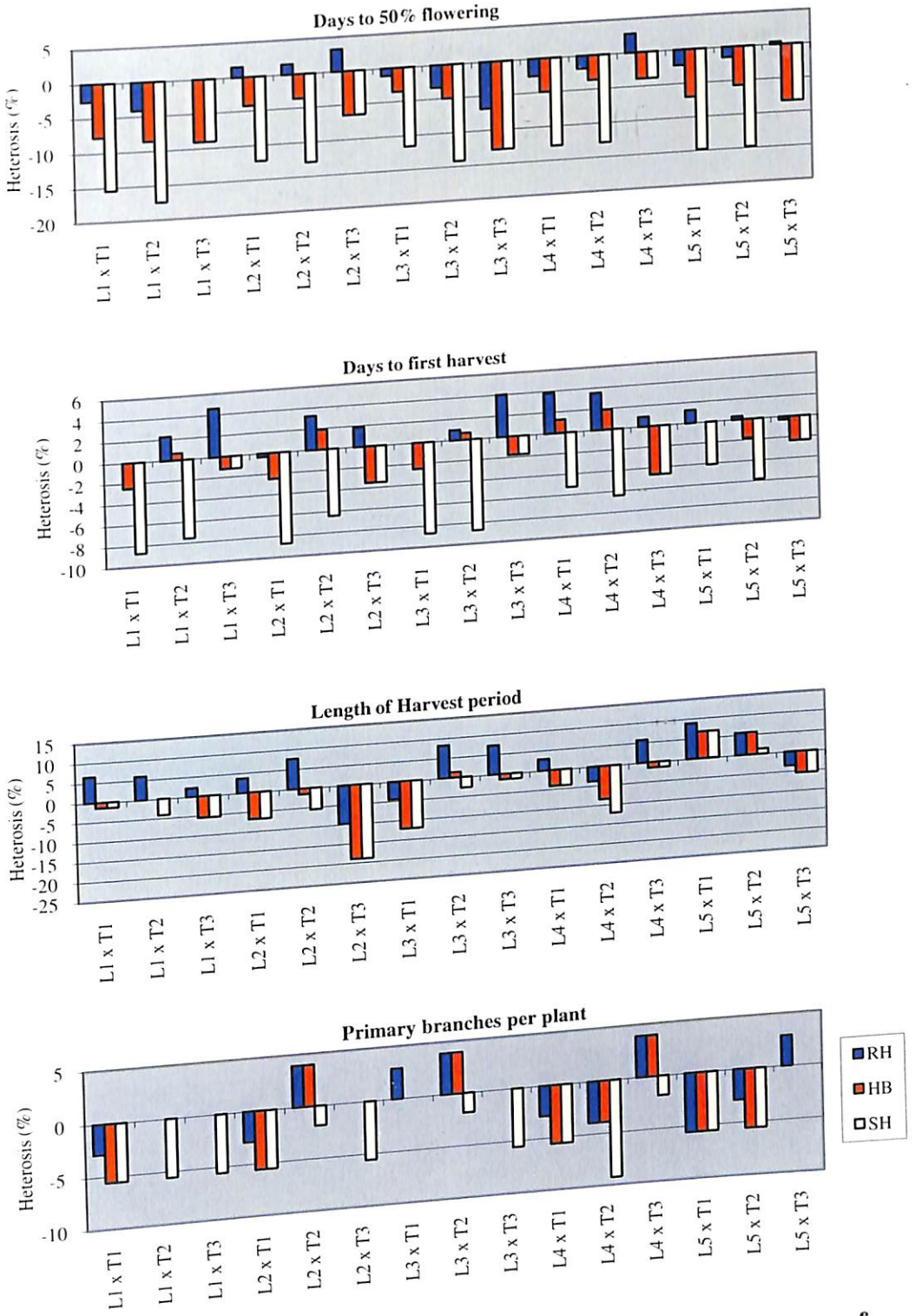


Fig. 6. Heterosis for various selected yield and related characters of 15 crosses in yard long bean

f. Main stem length

Significant positive relative heterosis was observed for L_1 x T_1 (5.14), L_5 x T_1 (4.13) and L_5 x T_2 (7.28); but the cross L_2 x T_3 (-5.32) showed negative significant relative heterosis. Heterobeltiosis value ranged from -8.37 (L_2 x T_2) to 4.71 (L_5 x T_2). All the crosses showed significant negative standard heterosis except L_1 x T_3 and L_5 x T_2.

g. Pod clusters per plant

The value of heterosis ranged from -65.26 (L_4 x T_3) to -12.63 (L_1 x T_3) for standard heterosis, -60.53 (L_4 x T_1) to -2.35 (L_1 x T_3) for heterobeltiosis and -54.27 (L_4 x T_1) to 3.75 (L_1 x T_3) for relative heterosis. All the crosses showed significant negative standard heterosis for pod clusters per plant. All crosses showed negative significant relative heterosis and heterobeltiosis except for the cross L_1 x T_3.

h. Pods per plant

Significant positive standard heterosis was shown by crosses, L_1 x T_1 (20.30) and L_2 x T_2 (6.59). All other crosses recorded negative significant standard heterosis. The crosses L_1 x T_1 (41.07), L_1 x T_2 (5.76), L_1 x T_3 (17.31), L_2 x T_2 (22.81), L_3 x T_2 (19.15) and L_3 x T_3 (14.38) showed positive significant relative heterosis for pods per plant. L_1 x T_1 (20.30), L_1 x T_3 (5.78) L_2 x T_2 (12.90) and L_3 x T_2 (7.69) showed significant positive heterobeltiosis for this character.

i. Pod yield per plant

The cross L_3 x T_1 (4.75) showed significant positive standard heterosis for pod yield per plant. The crosses L_4 x T_3 (30.81) and L_4 x T_1 (3.28) showed significant positive relative heterosis and L_4 x T_3 (3.08) showed significant positive heterobeltiosis.

j. Pods per cluster

Significant relative heterosis was recorded for pods per cluster by the crosses L_2 x T_3 and L_3 x T_3 (23.81) and L_2 x T_2 (18.18). Two crosses showed significant positive heterobeltiosis and 10 crosses showed negative standard heterosis ranged from -36.36 (L_4 x T_2) to 18.18 (L_2 x T_2, L_2 x T_3 and L_3 x T_3) for pods per cluster.

k. Pod weight

All the crosses showed significant negative standard heterosis for pod weight. It ranged from -47.81 (L_5 x T_3) to -4.09 (L_5 x T_1). The crosses L_1 x T_3 (25.79), L_4 x T_2 (10.28), L_4 x T_3 (42.54) and L_5 x T_2 (8.26) showed significant positive relative heterosis for pod weight. Heterobeltiosis value ranged from -47.2 (L_3 x T_3) to 32.11 (L_4 x T_3) for this character.

l. Pod length

The cross L_2 x T_1 (38.27) recorded highest relative heterosis followed by L_5 x T_1 (37.39) and L_4 x T_2 (24.64). Significant negative relative heterosis was observed for crosses L_1 x T_3, L_2 x T_3, L_3 x T_2, L_3 x T_3, L_4 x T_3 and L_5 x T_3. The cross L_4 x T_2 (4.09) showed significant positive standard heterosis, while all other crosses showed significant negative standard heterosis. Heterobeltiosis ranged from -46.12 (L_3 x T_3) to 29.77 (L_2 x T_1) for pod length.

m. Pod breadth

The values of heterosis ranged from -32.63 (L_3 x T_1) to 24.90 (L_3 x T_3) for relative heterosis, -36.61 (L_1 x T_1) to 13.67 (L_3 x T_3) for heterobeltiosis and -34.25 (L_3 x T_1) to 9.25 (L_5 x T_1) for standard heterosis. Significant positive standard heterosis was shown by crosses L_5xT_1 (9.25) and L_3 x T_3 (8.22). Significant positive heterobeltiosis was shown by crosses L_2 x T_2, L_3 x T_3 and L_5 x T_1. Three

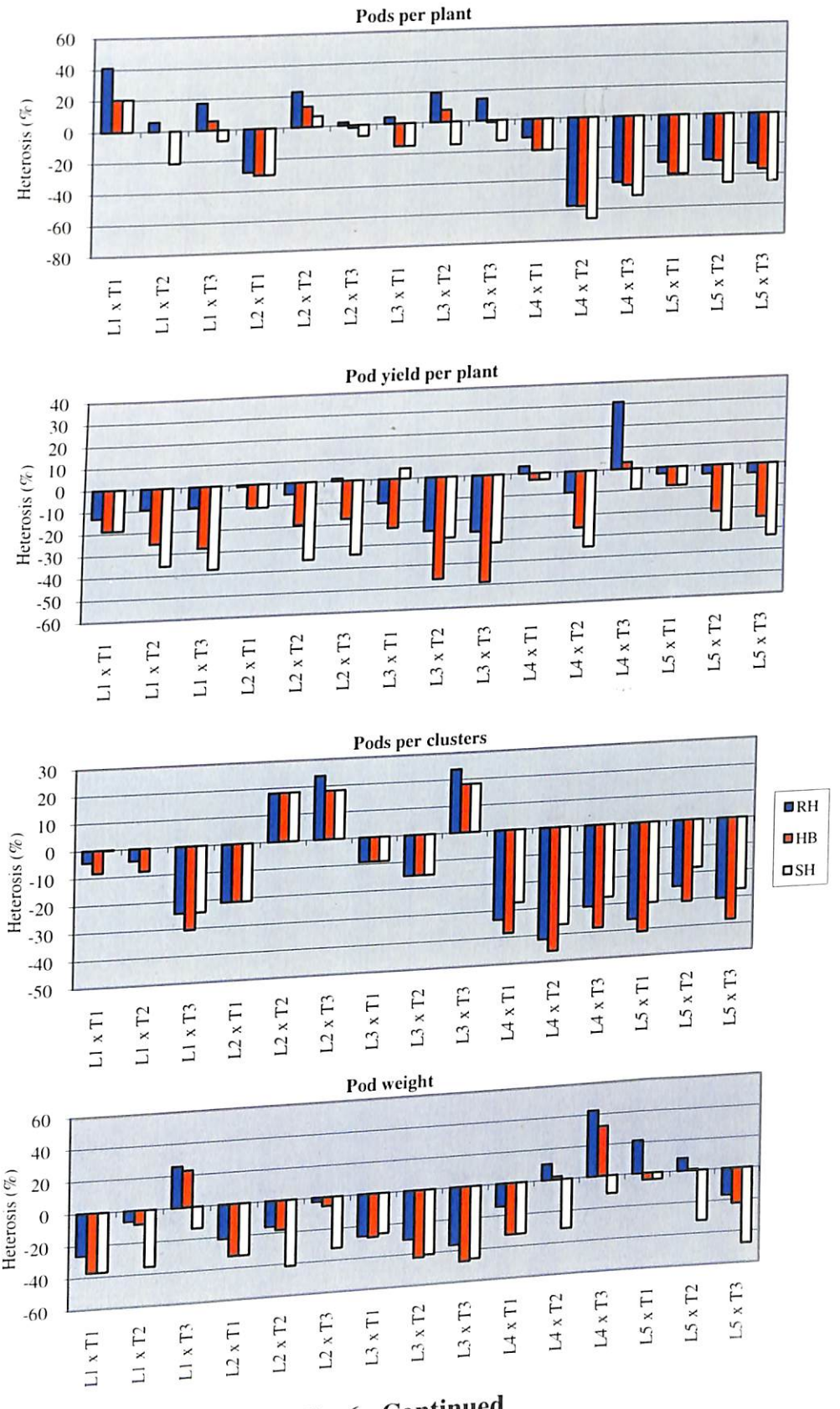


Fig. 6. Continued

crosses, L_3 x T_3, L_2 x T_2 and L_5 x T_1 showed significant positive relative heterosis for pod breadth.

n. Seeds per pod

Significant positive standard heterosis was shown by crosses, L_1 x T_2 (16.24), L_1 x T_3 (12.82), L_4 x T_2 (11.97) and L_2 x T_2 (8.97). The crosses L_1 x T_2, L_1 x T_3, L_2 x T_2, L_2 x T_3, L_4 x T_2, L_4 x T_3, L_5 x T_1 and L_5 x T_3 exhibited positive relative heterosis for seeds per pod. Others showed significant negative relative heterosis. Heterobeltiosis ranged from -43.79 (L_3xT_3) to 23.36 (L_1xT_3).

o. 100-Seed weight

The heterosis value ranged from -26.32 (L_5 x T_1) to 19.17 (L_5 x T_2) for relative heterosis, -34.01 (L_5 x T_1) to 16.8 (L_3xT_2) for heterobeltiosis and -34.01 (L_5 x T_1) to 3.70 (L_1 x T_1) for standard heterosis. All the hybrid showing significant negative standard heterosis except L_1 x T_1 and L_4 x T_1. Six hybrids showed significant positive relative heterosis and five hybrids showed significant positive heterobeltiosis. The crosses L_1 x T_2, L_2 x T_1, L_2 x T_2, L_2 x T_3, L_4 x T_2, L_4 x T_3, L_5 x T_1 and L_5 x T_3 showed negatively significant relative heterosis for 100-seed weight.

p. Length of penduncle

Significant positive relative heterosis in crosses (L_1 x T_2, L_2 x T_2, L_2 x T_3, L_3 x T_1, L_3 x T_3, L_4 x T_1 and L_5 x T_3), heterobeltiosis in crosses (L_2 x T_3, L_3 x T_3 and L_5 x T_3) and standard heterosis in crosses (L_1 x T_1, L_1 x T_2, L_2 x T_2, L_2 x T_3, L_3 x T_1, L_3 x T_3, L_4 x T_1, L_4 x T_2 and L_5 x T_3) were noticed for length of peduncle. None of the crosses had significant negative standard heterosis for peduncle length.

q. Number of trichomes on pod wall

Five crosses had significant positive relative heterosis for number of trichomes on pod wall. None of the crosses had significant positive heterobeltiosis and standard heterosis. All the 15 hybrids showed significant

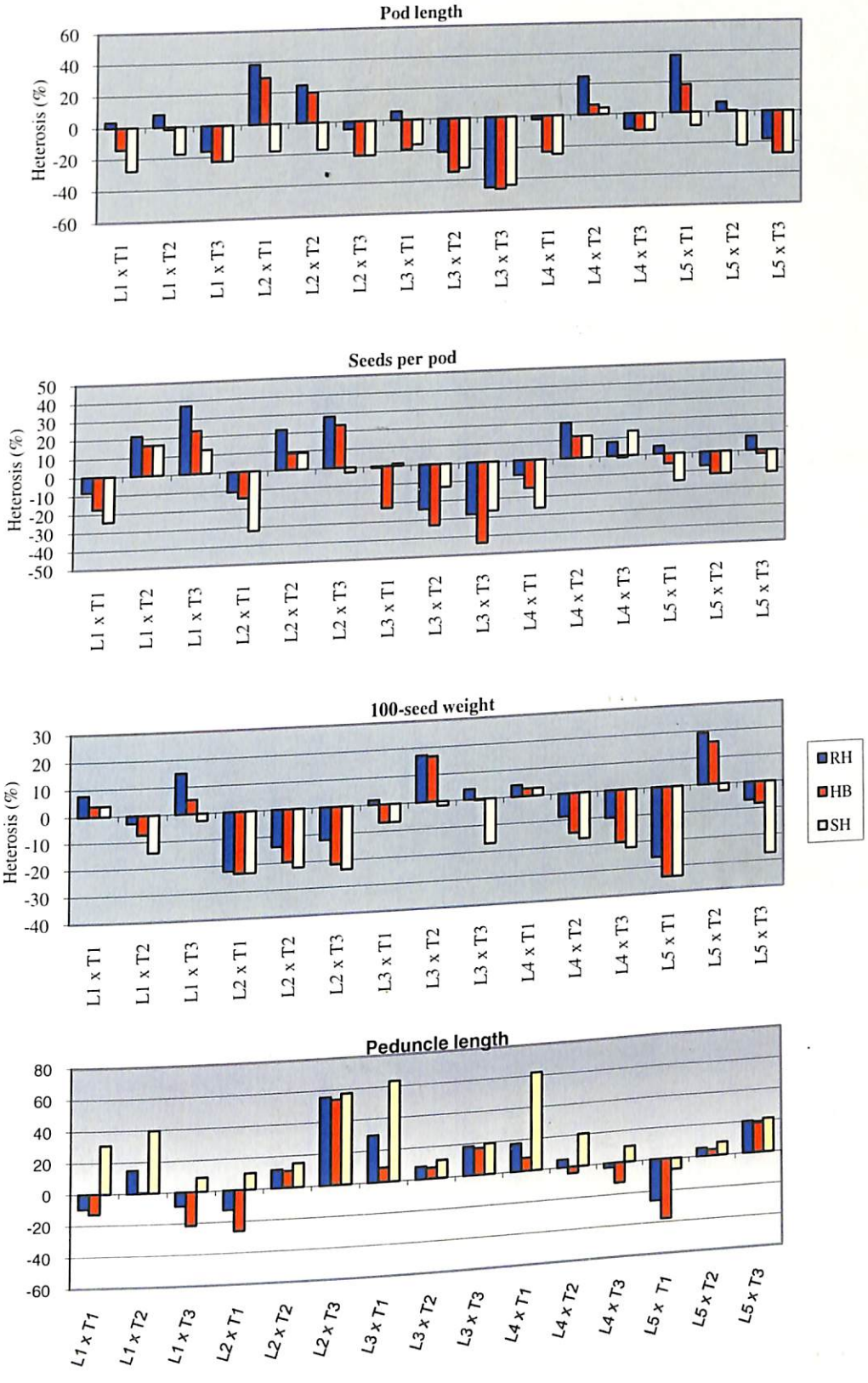


Fig. 6. Continued

negative standard heterosis and twelve hybrids showed significant negative heterobeltiosis.

r. Leaf chlorophyll content

The crosses, L_1 x T_3, L_2 x T_1, L_2 x T_2, L_3 x T_1 and L_4 x T_1 had significant positive relative heterosis for leaf chlorophyll content. The hybrid L_3 x T_1 (11.74%), showed significant positive heterobeltiosis. Seven hybrids had significant positive and three had significant negative standard heterosis.

s. Protein content of pods

Pod protein content in six crosses were significant and positive for relative heterosis. Maximum relative heterosis was noticed in L_2 x T_2 (26.16). Eight hybrids had significant negative relative heterosis and none of them had significant positive heterobeltiosis. Nine crosses had significant positive standard heterosis and the maximum value was for the cross L_1 x T_1 (64.89). The cross L_4 x T_2 (-13.06) had significant negative standard heterosis.

t. Crude fibre content of pods

The cross L_2 x T_2 had significant positive relative heterosis (21.76) and heterobeltiosis (9.76) for crude fibre content of pods. Ten hybrids showed significant positive standard heterosis and the maximum was for the cross L_3 x T_1 (67.47). No hybrids had significant negative standard heterosis for crude fibre content of pods.

4.5 LINE x TESTER ANALYSIS – POT CULTURE STUDIES FOR RESISTANCE TO POD BORERS

4.5.1 Evaluation of F_1's and parents

4.5.1.1 Mean performance of parents

Among the lines L_1 showing the minimum damage parameters for both the pod borer attack for all the damage parameters except for percentage of infestation of flower buds and number of larvae per 25 flowers (Table 22).

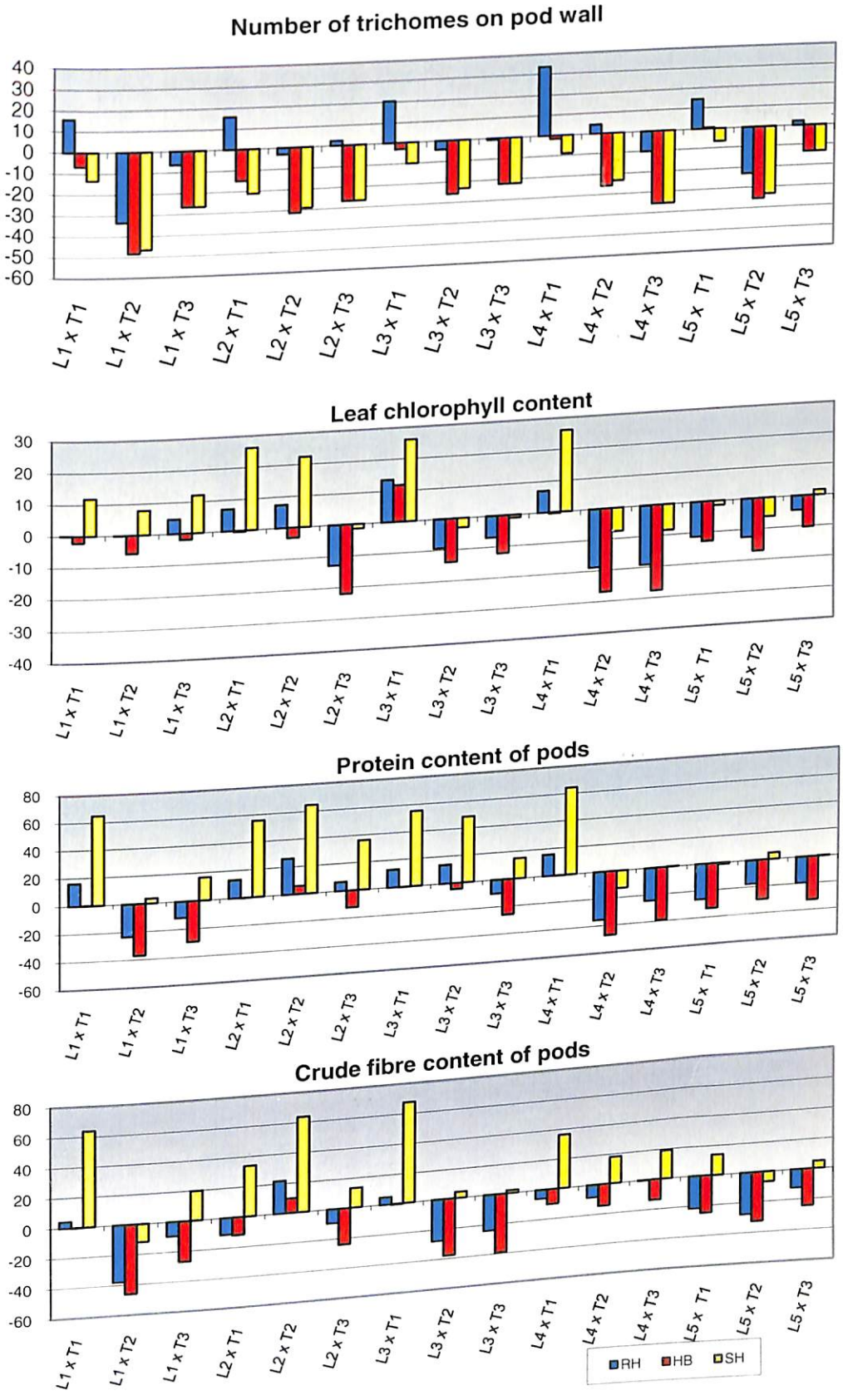


Fig. 6. Continued

Table 22. Mean values of damage parameters of pod borers and morphological and biochemical traits in yard long bean

Sl. No.	Treatments	*Maruca vitrata*						*Lampides boeticus*					
		X_1	X_2	X_3	X_4	X_5	X_6	X_1	X_2	X_3	X_4	X_5	X_6
L_1	Trailing Red poded	48.00	20.33	28.00	0.31	17.33	31.05	30.67	13.33	18.67	0.19	13.67	21.99
L_2	NS 621	60.00	20.67	65.33	0.84	43.00	60.78	28.00	14.00	18.67	0.21	32.00	34.55
L_3	Ettumanoor local	36.00	16.33	32.00	0.36	24.00	35.05	29.33	14.00	20.00	0.25	18.67	26.11
L_4	Vellayani local	66.67	23.67	62.67	0.41	53.00	68.05	41.33	20.33	33.33	0.36	35.67	45.06
L_5	Palakkad local	44.00	18.00	28.00	0.31	20.33	31.89	22.67	9.67	29.33	0.27	16.33	25.50
T_1	Kurappunthara local	20.00	10.67	17.33	0.21	13.00	19.78	17.33	5.33	18.67	0.16	8.33	14.44
T_2	Kanichar local	16.00	8.33	21.33	0.23	13.00	19.94	21.33	7.00	13.33	0.17	10.67	15.06
T_3	KMV-1	21.33	11.00	13.33	0.25	11.67	17.72	14.67	7.00	20.00	0.15	9.33	16.39

Characters

X_1 Percentage of infestation of flower buds
X_2 Number of larvae per 25 flowers
X_3 Percentage pod infestation
X_4 Number of larval entry / exit holes per pod
X_5 Number of damaged seeds in a sample of 25 pods
X_6 Plant resistant index (Ipr)

Palakkad local (L_5) showing the least percentage of infestation of flower buds and number of larvae per 25 flowers for *M. vitrata* and L_3 for *L. boeticus*. L_1 recorded the highest peduncle length and pod protein content, whereas L_4 showed the maximum chlorophyll content and pod protein content. Number of trichomes were more in L_5 and crude fibre content in L_3.

In the case of testers T_3 recorded the least attack for *M. vitrata* for all the damage parameters except percentage flower bud infestation, number of larvae per 25 flowers and larval entry per pod. T_1 showed the minimum percentage pod infestation. But T_2 recorded the minimum percentage flower bud infestation and larval number in 25 flowers.

Tester T_1 showed the minimum value for plant resistant index, damaged seeds and number of larvae per 25 flowers for *Lampides boeticus*. T_2 recorded the least percentage pod infestation and T_3 least larval entry. Related to morphological and biochemical traits T_1 showed the maximum mean values for peduncle length, leaf chlorophyll content, pod protein content and crude fibre content. But T_2 recorded maximum number of trichomes on pod wall.

4.5.1.2 Mean performance of hybrids based on damage parameters and morphological and biochemical traits

The mean values of the various characters for the crosses are presented in the Table 23.

4.5.1.2.1 *M. vitrata*

Percentage of infestation of flower buds (13.33), number of larvae per 25 flowers (7.67) and percentage of pod infestation (13.33) were least recorded for the cross L_3 x T_1. The crosses L_1 x T_1 and L_5 x T_1 showed least percentage of infestation of flower buds (14.67) and less pod infestation. The cross L_1 x T_1 showed least values for number of larval entry / exit holes per pod (0.147) and number of damaged seeds (9.33). Plant resistant index was less for the cross L_1 x T_1 (15.00) followed by L_3 x T_1 (15.39) and L_5 x T_1 (17.11).

Table 23. Mean performance of hybrids based on damage parameters

Crosses	*Maruca vitrata*						*Lampides boeticus*					
	% of infestation of flower buds	No. of larvae per 25 flowers	% of pod infestation	Number of larval entry / exit holes per pod	No. of damaged seeds in a sample of 25 pods	Plant resistant index	% of infestation of flower buds	Number of larvae per 25 flowers	% of pod infestation	No. of larval entry / exit holes per pod	No. of damaged seeds in a sample of 25 pods	Plant resistant index
$L_1 \times T_1$	14.67	8.67	13.33	0.15	9.33	15.00	9.33	4.67	16.00	0.13	4.67	10.78
$L_1 \times T_2$	36.00	17.33	28.00	0.24	15.33	28.22	32.00	13.67	28.00	0.25	15.67	26.61
$L_1 \times T_3$	40.00	16.67	24.00	0.32	20.00	29.67	40.00	16.33	32.00	0.28	20.00	32.17
$L_2 \times T_1$	52.00	20.00	60.00	0.76	46.00	60.67	48.00	15.67	24.00	0.28	32.67	37.61
$L_2 \times T_2$	64.00	21.67	56.00	0.76	50.33	63.06	52.00	20.33	32.00	0.36	36.33	45.05
$L_2 \times T_3$	60.00	17.33	52.00	0.68	53.33	61.56	56.00	13.00	28.00	0.39	28.00	34.50
$L_3 \times T_1$	13.33	7.67	13.33	0.19	10.67	15.39	13.33	6.00	9.33	0.09	6.33	10.33
$L_3 \times T_2$	28.00	15.00	28.00	0.36	18.33	29.05	29.33	12.00	24.00	0.28	15.67	24.44
$L_3 \times T_3$	32.00	15.33	32.00	0.32	23.67	34.11	40.00	14.00	40.00	0.24	17.33	31.89
$L_4 \times T_1$	66.00	17.00	64.00	0.40	50.67	63.61	48.00	18.00	44.00	0.48	39.00	49.67
$L_4 \times T_2$	60.00	18.67	56.00	0.44	53.67	63.78	56.00	18.00	52.00	0.48	46.00	57.00
$L_4 \times T_3$	52.00	21.67	52.00	0.47	51.33	62.39	56.00	19.67	52.00	0.56	49.00	59.83
$L_5 \times T_1$	14.67	9.33	13.33	0.19	12.00	17.11	20.00	7.33	20.00	0.21	7.67	15.44
$L_5 \times T_2$	36.00	15.00	25.33	0.36	27.00	33.94	28.00	11.33	36.00	0.36	10.67	24.78
$L_5 \times T_3$	40.00	18.00	30.67	0.36	26.33	36.78	44.00	15.33	44.00	0.40	14.00	31.67
CD	5.98	3.84	6.50	0.07	6.19	6.83	6.92	3.58	6.64	0.06	5.53	5.71

4.5.1.2.2 *L. boeticus*

The cross L_1 x T_1 showed the least damage parameters for percentage of infestation of flower buds (9.33), number of larvae per 25 flowers (4.67) and number of damaged seeds in a sample of 25 pods (4.67). The cross L_3 x T_1 showed less pod infestation (9.33) and number of larval entry / exit holes per pod (0.093). Plant resistant index was least for the cross L_3 x T_1 (10.33), followed by L_1 x T_1 (10.78) and L_5 x T_1 (15.44).

4.5.1.3 Proportional contribution

The proportional contribution of lines, testers and crosses to total variance of the characters under study are presented in Table 24 and Fig. 7.

M. vitrata

The values ranged from 46.11 for number of larvae per 25 flowers to 92.55 for number of damaged seeds in a sample of 25 pods among lines. Among testers, the values ranged from 2.27 for percentage pod infestation to 33.03 for number of larvae per 25 flowers. In the case of hybrids, the values ranged from 1.97 for number of damaged seeds in a sample of 25 pods to 20.85 for number of larvae per 25 flowers.

The crosses had contributed minimum values to the total variance for the characters number of larvae per 25 flowers, number of larval entry per exit holes per pod, number of damaged seeds in a sample of 25 pods and plant resistant index.

L. boeticus

Damage parameters values ranged from 46.71 for number of larvae per 25 flowers to 89.86 for number of damaged seeds in a sample of 25 pods among lines. Among testers, the values ranged from 5.84 for number of damaged seeds in a sample of 25 pods to 32.27 for percentage pod infestation. In the case of hybrids, the values ranged from 4.30 for number of damaged seeds to 26.66 for number of larvae per 25 flowers.

Table 24. Proportional contribution of pod borer damage parameters

Sl. No.	Characters	Lines (%)	Testers (%)	LxT (%)
I	***Maruca vitrata***			
1.	Percentage of infestation of flower buds	75.74	11.7	12.55
2.	Number of larvae per 25 flowers	46.11	33.03	20.85
3.	Percentage pod infestation	87.66	2.27	10.07
4.	Number of larval entry per exit holes per pod	89.28	5.51	5.19
5.	Number of damaged seeds in a sample of 25 pods	92.55	5.48	1.97
6.	Plant resistant index	89.52	6.32	4.15
II.	***Lampides boeticus***			
1.	Percentage of infestation of flower buds	63.29	28.45	8.26
2.	Number of larvae per 25 flowers	46.71	26.62	26.66
3.	Percentage pod infestation	56.17	32.27	11.56
4.	Number of larval entry per exit holes per pod	74.05	21.08	4.87
5.	Number of damaged seeds in a sample of 25 pods	89.86	5.84	4.30
6.	Plant resistant index	77.41	15.32	7.26

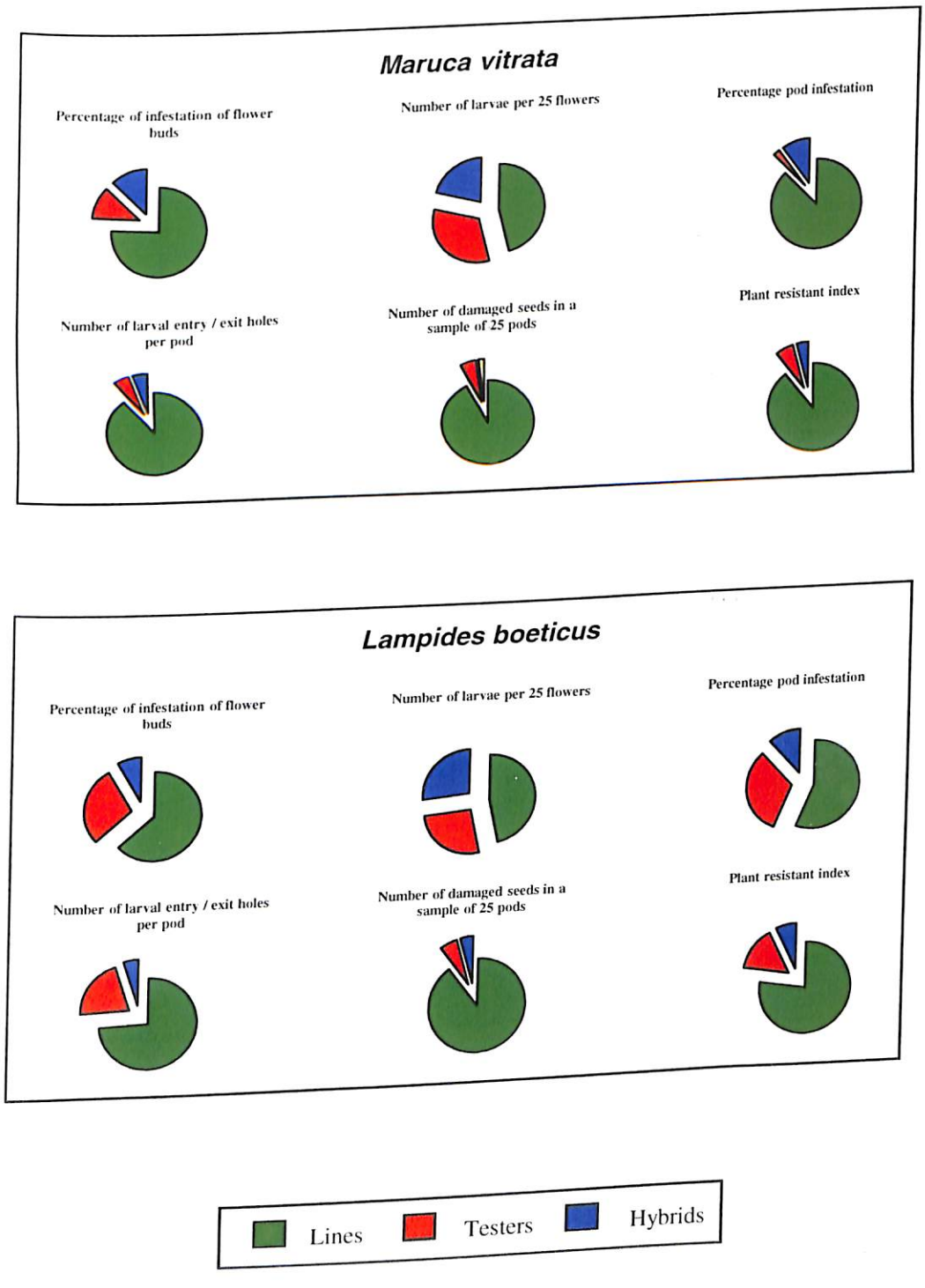


Fig. 7. Proportional contribution of pod borers damage parameters

Hybrids contributed minimum values for all the damage parameters except number of larvae per 25 flowers.

Based on the mean performance, specific combining ability and standard heterosis, three crosses (L_1 x T_1, L_3 x T_1 and L_5 x T_1) were selected for further breeding programme.

4.6 GENERATION MEAN ANALYSIS

Generation mean analysis was done for the three selected crosses L_1 x T_1 (Trailing Red poded x Kurappunthara local), L_3 x T_1 (Ettumanoor local x Kurappunthara local) and L_5 x T_1 (Palakkad local x Kurappunthara local), with respect to 15 yield characters and their pod borers damage measurements (both *M. vitrata* and *L. boeticus*) and morphological and biochemical traits. The results of generation mean values for three selected crosses and scale values and estimates of genetic components are presented in Table 25 and 26.

a. Days to 50 per cent flowering

Among the generations, the lowest and the highest means were recorded by B_1 and P_2 in cross L_1 x T_1; B_2 and P_1 in cross L_3 x T_1 and B_2 and P_2 in cross L_5 x T_1. The mean values of F_1 were less than those of F_2 in crosses L_1 x T_1 and L_5 x T_1.

Scale A was non significant in the crosses L_3 x T_1 and L_5 x T_1, while scale B was significant in crosses L_1 x T_1 and L_5 x T_1 indicating the presence of non-allelic interactions. Significance was observed in scale C for cross L_5 x T_1 and scale D for L_1 x T_1 and L_5 x T_1.

Among the genetic component, ‘m’ was significant and greater than all other effects in both the crosses. Negative significant additive effect (d) for the cross L_5 x T_1 and dominance effect (h) was observed for L_1 x T_1 and L_5 x T_1.

Table 25. Mean values for yield and related characters of the selected crosses and generation mean analysis

Crosses	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
Cross I P_1 (L_1)	47.67	55.00	23.33	78.67	4.00	501.17	6.00	10.40	351.17	2.40	16.73	37.30	1.15	16.2	17.27
P_2 (T_1)	49.67	52.33	23.67	79.67	3.93	477.67	5.60	10.07	293.17	2.27	18.47	19.87	0.94	15.8	16.00
F_1 (L_1 x T_1)	45.00	54.33	22.67	79.67	3.40	504.00	5.20	10.67	357.33	1.53	20.40	33.90	1.81	17.27	19.40
F_2	47.33	55.33	23.67	78.00	3.40	499.27	5.40	11.73	479.00	2.73	16.47	42.50	1.40	18.93	19.07
B_1 (L_1 x T_1) x L_1	43.00	55.00	24.33	79.67	3.47	485.60	6.07	14.33	471.00	2.60	19.60	40.33	2.19	18.47	17.60
B_2 (L_1 x T_1) x T_1	45.33	55.67	23.67	79.00	3.33	479.40	7.00	11.00	488.50	2.20	20.80	46.10	1.31	19.67	17.20
Cross II P_1 (L_3)	45.33	51.00	23.33	79.67	4.07	471.60	7.467	10.07	404.17	2.53	23.60	49.17	0.89	16.13	17.07
P_2 (T_1)	45.00	59.67	24.00	79.67	4.60	486.57	5.20	6.53	266.00	2.40	13.00	20.27	0.94	16.13	12.40
F_1 (L_3 x T_1)	45.00	54.67	24.00	80.67	3.67	467.00	4.20	11.13	330.33	2.07	18.27	36.50	1.08	13.47	13.60
F_2	44.33	50.67	25.33	83.33	3.87	459.10	5.20	11.87	462.67	2.73	15.00	47.00	1.79	18.60	18.53
B_1 (L_3 x T_1) x L_3	45.00	52.33	21.67	78.33	3.40	480.50	6.20	15.33	471.17	2.60	20.40	47.67	2.08	17.80	18.80
B_2 (L_3 x T_1) x T_1	42.33	53.00	20.67	81.67	3.47	479.33	6.00	12.93	373.83	2.53	14.60	42.33	2.17	18.73	17.53
Cross III P_1 (L_5)	42.33	54.67	22.33	79.67	3.93	486.83	6.00	9.67	418.17	2.53	16.33	35.50	0.89	16.13	17.07
P_2 (T_1)	50.00	52.67	25.00	80.33	4.33	471.17	5.00	6.13	269.17	2.47	12.47	20.03	0.94	16.13	12.40
F_1 (L_5 x T_1)	44.00	54.33	25.00	78.67	3.40	501.60	4.27	8.07	279.33	1.73	23.87	40.00	1.08	13.47	13.60
F_2	47.00	55.33	21.67	81.00	3.40	500.67	5.40	9.73	485.00	2.60	20.20	51.33	1.79	18.00	18.53
B_1 (L_5 x T_1) x L_5	41.67	52.00	25.00	76.67	3.47	501.33	6.60	12.67	472.50	2.27	20.53	49.17	2.08	17.80	18.80
B_2 (L_5 x T_1) x T_1	40.67	53.67	21.33	79.33	3.40	495.10	6.20	12.47	400.33	2.73	16.47	50.33	2.17	18.73	17.53

Characters

X_1 Days to 50 per cent flowering
X_2 Days to first harvest
X_3 Length of harvest period (days)
X_4 Crop duration (days)
X_5 Primary branches per plant
X_6 Main stem length (cm)
X_7 Pod clusters per plant
X_8 Pods per plant
X_9 Pod yield per plant
X_{10} Pods per cluster
X_{11} Pod weight (g)
X_{12} Pod length (cm)
X_{13} Pod breadth (cm)
X_{14} Seeds per pod
X_{15} 100 seed weight (g)

P_1, P_2 – Parents
F_1, F_2 – Filial generations
B_1, B_2 – Back crosses

Table 25. Continued

Crosses	X_{16}	X_{17}	X_{18}	X_{19}	X_{20}
Cross I P_1 (L_1)	21.48	2.13	1.67	8.71	3.65
P_2 (T_1)	17.82	5.60	1.44	5.44	2.33
F_1 (L_1 x T_1)	23.59	5.20	1.58	8.75	3.64
F_2	25.67	5.60	.1.28	8.26	3.61
B_1 (L_1 x T_1) x L_1	28.17	3.20	1.67	7.22	2.66
B_2 (L_1 x T_1) x T_1	24.17	5.47	1.09	8.26	3.64
Cross II P_1 (L_3)	26.35	3.13	1.64	8.25	3.73
P_2 (T_1)	17.65	5.73	1.44	5.33	2.34
F_1 (L_3 x T_1)	29.36	5.33	1.79	8.25	3.73
F_2	27.67	6.47	1.86	8.24	3.73
B_1 (L_3 x T_1) x L_3	31.00	5.67	1.86	8.74	3.33
B_2 (L_3 x T_1) x T_1	27.00	6.13	1.63	7.88	3.64
Cross III P_1 (L_5)	15.40	4.20	1.63	7.91	3.03
P_2 (T_1)	18.48	5.73	1.44	5.32	2.29
F_1 (L_5 x T_1)	16.00	5.53	1.39	5.24	2.39
F_2	16.00	5.20	1.44	4.67	2.94
B_1 (L_5 x T_1) x L_5	17.17	5.67	1.48	5.21	3.27
B_2 (L_5 x T_1) x T_1	19.67	6.07	1.67	5.24	2.67

X_{16} Length of peduncle
X_{17} Number of trichomes on pod wall
X_{18} Leaf chlorophyll content
X_{19} Protein content of pods
X_{20} Crude fibre content of pods

Table 26. Scale values and estimates of yield related genetic components in three selected crosses of yard long bean

	Days to 50 per cent flowering			Days to first harvest			Length of harvest period			Crop duration		
	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T1$	$L_5 \times T1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$
A	-6.67*	-0.33	-3.00	0.67	-1.00	-5.00	2.67	-4.00	2.67	1.00	-3.67	-5.00**
B	-4.00*	-5.33	-12.67**	4.67*	-8.33**	0.33	1.00	-6.67*	-7.33**	-1.33	3.00	-0.33
C	2.00	-3.00	7.67*	5.33	-17.33**	5.33	2.33	-6.00	-10.67	-5.67	12.67**	6.67*
D	6.33**	1.33	11.67**	-0.00	-4.00*	5.00*	-0.67	8.33**	-3.00	-2.67	6.67**	6.00**
m	61.33**	47.83**	69.50**	53.67**	47.33**	63.67**	22.17**	40.33**	17.67**	73.83**	93.00**	92.00**
d	-1.00	0.17	-3.83**	1.33*	-4.33**	1.00	-0.17	-0.33	-1.33*	-0.50	0.00	-0.33
h	-39.67**	-11.17	-64.50**	6.00	6.00	-24.00*	5.50	-43.67**	8.67	10.83	-26.33*	-30.67**
i	-12.67**	-2.67	-23.33**	0.00	8.00*	-10.00*	1.33	-16.67**	6.00	5.33	-13.33**	-12.00**
j	-1.33	2.50	4.83**	-2.00*	3.67*	-2.67	0.83	1.33	5.00**	1.17	-3.33*	-2.33*
l	23.33**	8.33	39.00**	-5.33	1.33	14.67*	-5.00	27.33**	-1.33	-5.00	14.00*	17.33**

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 26. Continued

	Primary branches per plant			Main stem length			Pod clusters per plant			Pods per plant		
	L_1 x T_1	L_3 x T_1	L_5 x T_1	L_1 x T_1	L_3 x T1	L_5 x T1	L_1 x T_1	L_3 x T_1	L_5 x T_1	L_1 x T_1	L_3 x T_1	L_5 x T_1
A	-0.47	-0.93	-0.40	-33.97**	22.4	14.23**	0.93	0.73	2.93**	7.60**	9.47**	7.60**
B	-0.67*	-1.33**	-0.93**	-22.87**	5.10	17.43**	3.20**	2.60**	3.13**	1.27	8.20**	10.73**
C	-1.13	-0.53	-1.47*	10.23	-55.77*	41.47**	-0.40	-0.27	2.07**	5.13	8.60**	7.00**
D	0.00	0.87**	-0.07	33.53**	-41.63**	4.90	-2.27**	-1.80**	-2.00**	-1.87	-4.53**	-5.67**
m	3.97**	6.07**	4.00**	556.48**	395.82**	488.80**	1.27*	2.73**	1.50*	6.50	-0.77	-3.43**
d	0.03	-0.27	-0.20	11.75**	-7.48	7.83**	0.20	1.13**	0.50*	0.17	1.77**	1.77**
h	-1.70	-6.40**	-1.80	-176.38**	181.95**	34.67	12.60**	8.40**	12.83**	16.77	38.63**	41.17**
i	-0.00	-1.73**	0.13	-67.07**	83.27**	-9.80	4.53**	3.60**	4.00**	3.73	9.07**	11.33**
j	0.10	0.20	0.27	-5.55	8.65	-1.60	-1.13**	-0.93*	-0.10	3.17**	0.63	-1.57**
l	1.13	4.00**	1.20	123.90**	-110.77**	-21.87	-8.67**	-6.93**	-10.07**	-12.60*	-26.73**	-29.67**

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 26. Continued

	Pod yield per plant			Pods per cluster			Pod weight			Pod length		
	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$
A	233.50**	207.83**	247.50**	1.27**	0.60*	0.27	2.07**	-1.07	0.87	9.47**	9.67**	22.83**
B	326.50**	151.33**	252.17**	0.60*	0.60**	1.27**	2.73	-2.07**	-3.40**	38.43**	27.90**	40.63**
C	557.00**	519.83**	694.00**	3.20**	1.87**	1.93**	-10.13**	-13.13**	4.27**	45.03**	45.57**	69.80**
D	-1.50	80.33**	97.17**	0.67**	0.33	0.20	-7.47**	-5.00**	3.40**	-1.43	4.00	3.17*
m	319.17**	495.75**	538.00**	3.67**	3.13**	2.90**	2.67	8.30**	21.20**	25.72**	42.72**	34.10**
d	29.00	69.08**	74.50**	0.07	0.07	0.03	-0.67	5.30**	1.93**	8.72**	14.45**	7.73**
h	601.17**	33.08	46.67	-1.60	-0.53	-0.03	37.47**	16.83**	-6.67**	58.95**	23.35	63.03**
i	3.00	-160.67**	-194.33**	-1.33**	-0.67	-0.40	14.93**	10.00**	-6.80**	2.87	-8.00	-6.33**
j	-46.50*	28.25**	-2.33	0.33	-0.00	-0.50**	-0.33	0.50	2.13**	-14.48**	-9.12**	-8.90**
l	-563.00**	-198.50**	-305.33**	-0.53	-0.53	-1.13	-19.73**	-6.87**	9.33**	-50.77**	-29.57**	-57.13**

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 26. Continued

	Pod breadth			Seeds per pod			100-Seed weight		
	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$
A	1.44**	2.19**	2.19**	3.47*	6.00**	6.00**	-1.47	6.93**	6.93**
B	-0.13	2.31**	2.31**	6.27*	7.87**	7.87**	-1.00	9.07**	9.07**
C	-0.10	3.18*	3.18*	9.20**	15.20**	12.80**	4.20*	17.47**	17.47**
D	-0.70	-0.66	-0.66	-0.27	0.67	-0.53	3.33**	0.73	0.73
m	-0.36	-0.41	-0.41	15.47**	17.47**	15.07**	23.30**	16.20**	16.20**
d	0.10**	-0.02	-0.02	0.20	0.00	0.00	0.63	2.33**	2.33**
h	4.88	7.32*	7.32*	12.07*	8.53**	13.33*	-13.03**	11.93**	11.93**
i	1.41	1.33	1.33	0.53	-1.33	1.07	-6.67**	-1.47	-1.47
j	0.79**	-0.06	-0.06	-1.40	-0.93	-0.93	-0.23	-1.07	-1.07
l	-2.71	-5.83**	-5.83**	-10.27**	-12.53**	-14.93**	9.13**	-14.53**	-14.53**

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 26. Continued

	Length of peduncle			Number of trichomes on pod wall			Leaf chlorophyll content			Pod protein content			Crude fibre content of pods		
	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$	$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$
A	11.26**	6.29**	2.93**	-0.93**	2.87**	1.60**	0.077	0.290**	-0.053	-3.02**	0.98**	2.73**	-1.96**	-0.797**	1.11**
B	6.93**	6.99**	4.85**	0.13	1.20**	0.87**	-0.833**	0.037	0.513**	2.32**	2.18**	-0.09	1.31**	1.20**	0.65**
C	16.19**	7.95**	-1.88	4.27**	6.33**	-0.20	-1.177**	0.773**	-0.093	1.38**	2.88**	-5.03**	1.19**	1.397**	1.65**
D	-1.00	-2.67*	-4.83**	2.53**	1.13**	-1.33**	-0.210**	0.223**	-0.277**	1.04**	-0.14	-1.11**	0.92**	0.497**	-0.05
m	17.65**	16.67**	7.27**	8.93**	6.70**	2.30**	1.138**	1.987**	0.983**	9.15**	6.51**	4.40**	4.83**	4.028**	2.56**
d	1.83**	4.35**	-1.54**	-1.73**	-1.30**	-0.77**	0.115**	0.097**	0.093**	1.63**	1.46**	1.29**	0.66**	0.695**	0.36**
h	26.13**	31.31**	26.17**	-9.60**	0.43	8.37**	0.108	-0.320	1.420**	-3.17**	5.17**	0.23	-3.69**	-0.885	1.71**
i	2.00	5.33	9.67**	-5.07**	-2.27**	2.67**	0.420**	-0.447**	0.553**	-2.07**	0.28	2.21**	-1.85**	-0.993**	0.11
j	2.17**	-0.35	-0.96	-0.53**	0.83**	0.37**	0.455**	0.127**	-0.283**	-2.67**	-0.60**	-1.32**	-1.63**	-0.998**	0.23**
l	-20.19**	-18.62**	-17.45**	5.87**	-1.80**	-5.13**	0.337**	0.120	-1.013**	2.77**	-3.43**	0.60*	2.50**	0.39	-1.87**

* Significant at 5 per cent level

** Significant at 1 per cent level

Among the interaction effects additive x additive (i) was negatively significant for L_1 x T_1 and L_5 x T_1 and dominance x dominance (l) interactions were positively significant. Opposite signs of 'h' and 'l' indicating the duplicate nature of epistasis is noticed in both the crosses.

b. Days to First harvest

Among the generations, the lowest and highest means were recorded by P_2 and B_2 in cross I; F_2 and P_2 in cross II and B_1 and F_2 in cross III.

Scale A was non significant in all the three crosses while scale B was significant in cross I and II indicating the presence of non-allelic interactions. In cross II scale C had negative significance and scale D had positive significance in cross III and negative in cross II.

Among the genetic component 'm' was significant and greater than all other effect. Positive significant additive effect (d) was noticed for cross I and II. Negative significant dominance effect (h) was noted for the cross L_5 x T_1.

Among the interactions, crosses L_3 x T_1 and L_5 x T_1 had positive significance for additive x additive (i) interactions. While L_1 x T_1 had additive x dominance (j) negative interactions and L_5 x T_1 had dominance x dominance (l) significant interaction.

c. Length of harvest period

Length of harvest period was maximum for B_1 in L_1 x T_1; F_2 in L_3 x T_1 and B_1, F_1 and P_2 for the cross L_5 x T_1. It was minimum in B_2 in cross L_3 x T_1.

Significance was noticed for scales B and D in cross L_3 x T_1 and L_5 x T_1.

Significance was observed for 'm' in three crosses. Negative significant additive effect (d) was noticed in the cross L_5 x T_1, same dominance effect (h) in L_3 x T_1.

Among the interactions additive x additive (i) was negative and significant in the cross L_3 x T_1 indicating that epistasis was duplicate in the cross. Significant positive values was recorded for additive x dominance (j) in cross L_5 x T_1 and dominance x dominance (l) in cross L_3 x T_1.

d. Crop duration

Crop duration was minimum for F_2 and maximum for P_2, F_1 and B_1 in cross L_1 x T_1, B_1 and F_2 in cross L_3 x T_1 and B_1 and F_2 in cross L_5 x T_1.

Scale A had significant negative values for the cross L_5 x T_1 and no significant values in scale B. Scale C and D had significant positive values for the crosses L_3 x T_1 and L_5 x T_1.

Among the genetic component `m' was significant and greater than all other effects in all the crosses. Dominance effect was negatively significant for the cross L_3 x T_1 and L_5 x T_1.

Additive x additive and additive x dominance interactions were negatively significant in the crosses L_3 x T_1 and L_5 x T_1, while dominance x dominance interaction was positively significant and duplicate epistasis was also evident.

e. Number of primary branches per plant

Primary branches were highest for P_1 and lowest for B_2 in cross L_1 x T_1; P_2 and B_1 in L_3 x T_1 and P_2 and F_1, F_2 and B_2 L_5 x T_1.

No significance was noticed in scale A but scale B had negative significance in all the 3 crosses indicating the presence of non allelic interactions. Scale C had negative significance on L_5 x T_1 and scale D had positive significance on L_3 x T_1.

Among the genetic component 'm' was significant and highest in all the 3 crosses. No crosses had significance in additive effect. Dominance effect was negatively significant in cross L_3 x T_1.

Additive x additive interactions were negatively significant, while dominance x dominance was positively significant in cross L_3 x T_1.

f. Main Stem Length

Generation F_1 had maximum main stem length for the cross L_1 x T_1 and P_2 for L_3 x T_1 and minimum in P_2 and F_2. Generation F_1 had the maximum and P_2 the minimum mean values for L_5 x T_1.

Scale A and B were significant in crosses L_1 x T_1 and L_5 x T_1. Scale C was significant in cross L_5 x T_1 and scale D was significant in crosses L_1 x T_1 and L_3 x T_1.

Among the genetic component 'm' was significant and highest in all the three crosses. The cross L_5 x T_1 had positive significant additive effects (d). Dominance effect and additive x additive interactions were negative for the cross L_1 x T_1 and positive for L_3 x T_1. Dominance x dominance interaction was positive on L_1 x T_1 and negative on L_3 x T_1 and duplicate epistasis was also evident.

g. Pod clusters per plant

Among the generations, the highest and the lowest means were recorded by B_2 and F_1 in cross L_1 x T_1; P_1 and F_1 in L_3 x T_1 and B_1 and F_1 in L_5 x T_1.

The cross L_5 x T_1 had significance in scale A and C. Scale B and D were significant in all the three crosses.

Significance was observed in 'm', 'd' effects and additive x additive and dominance x dominance interactions. Additive effect was positively significant in L_3 x T_1 and L_5 x T_1, while significant negative interactions additive x dominance were noted in crosses L_1 x T_1 and L_3 x T_1. Additive x dominance interaction was negative indicating that epistasis was duplicate in the crosses.

h. Pods per plant

Among the generations, the maximum pods per plant and minimum were recorded by B_1 and P_2 in all the three crosses.

Scale A was significant for all the crosses. Scales B, C and D were significant for the crosses L_3 x T_1 and L_5 x T_1.

Effect of 'm' is negatively significant in cross L_5 x T_1. Additive effects, dominance effects and additive x additive interactions were positively significant in crosses L_3 x T_1 and L_5 x T_1. Additive x dominance interactions were positively significant in cross L_1 x T_1 and negatively significant for the cross L_5 x T_1. So epistasis was duplicate in the crosses. All the crosses were negatively significant for dominance x dominance interactions.

i. Pod yield per plant

Among the generations, the highest and lowest pod yield means were recorded by B_2 and P_2 in L_1 x T_1; B_1 and P_2 in L_3 x T_1 and F_2 and P_2 in L_5 x T_1.

Scale values of A, B and C were significant in all the crosses while scale D had significance only for the crosses L_3 x T_1 and L_5 x T_1.

Among the genetic component `m' was significant and greater than all other effects in all the crosses. Additive effect was positively significant for the crosses L_3 x T_1 and L_5 x T_1. The cross L_1 x T_1 had significant positive dominance effects.

Additive x additive interactions had negatively significance for the crosses L_3 x T_1 and L_5 x T_1. Additive x dominance interactions was positively significant for L_3 x T_1 and negative for L_1 x T_1. All the crosses showed significant negative values for dominance x dominance interactions (l).

j) Pods per cluster

Pods per cluster was maximum for B_1 generation in the cross L_1 x T_1, F_2 in L_3 x T_1 and B_2 in L_5 x T_1. Minimum in F_1 in all the crosses.

Scale values of B and C were significant for all the crosses, while scale A was significant for the crosses L_1 x T_1 and L_3 x T_1 and scale D for the cross L_1 x T_1.

Among the genetic component `m' was significant and highest in all the crosses. No crosses had any effect on dominance (h) and additive values. Epistasis was complementary in these crosses.

Additive x additive interactions had negative significance for L_1 x T_1, but the cross L_5 x T_1 had negative significance for additive x dominance interaction because of epistasis was duplicate in this cross. No crosses had any interaction on dominance x dominance.

k) Pod weight

Pod weight was maximum for B_2 and minimum for F_2 in cross L_1 x T_1; P_1 and P_2 in L_3 x T_1 and F_1 and P_2 in L_5 x T_1.

Scales C and D was significant for all the crosses, while scale A and B was significant for the crosses L_3 x T_1 and L_5 x T_1.

Among the genetic component 'm' and 'd' was significant for L_3 x T_1 and L_5 x T_1. Dominance effect and additive x additive interactions were positive for L_1 x T_1 and L_5 x T_1, but it was negative for L_5 x T_1. Dominance x dominance interactions was positive for L_5 x T_1 is due to duplicate epistasis. A negative significance for L_1 x T_1 and L_3 x T_1 is due to dominance x dominance interaction. Additive x dominance has positive significance in the cross L_5 x T_1.

l) Pod length

Among generations, pod length was maximum for F_2 and minimum for P_2 in cross L_1 x T_1, P_1 and P_2 in L_3 x T_1 and F_2 and P_2 in L_5 x T_1.

Scales A, B and C were significant in all the three crosses, while in the scale D cross L_5 x T_1 was significant.

Among the genetic component, 'm' and 'd' had significant positive effect for all the crosses. Dominance effect was positively significant for the crosses L_1 x T_1 and L_5 x T_1.

Among the interactions negative significance was noticed for all the crosses in additive x dominance and dominance x dominance. This is due to epistasis which was duplicate in these crosses. But the cross L_5 x T_1 had negative significance in additive x additive interaction.

m) Pod breadth

Maximum pod breadth was recorded by B_1 generation and minimum in P_2 in the cross L_1 x T_1 and B_2 and P_1 in the crosses L_3 x T_1 and L_5 x T_1.

Scale A had significance for all the crosses and scales B and C had significance for the crosses L_3 x T_1 and L_5 x T_1.

No crosses had significance for `m' and additive x additive interactions. Additive effect and additive x dominance interactions were positively significant for the cross L_1 x T_1, because of complementary epistasis. Dominance x dominance interactions was negatively significant for the crosses L_3 x T_1 and L_5 x T_1.

n) Seeds per pod

Seeds per pod was maximum for B_2 in cross L_1 x T_1 and B_1 in the crosses L_3 x T_1 and L_5 x T_1 and minimum for P_2.

Scales A, B and C was significant for all the crosses. Among the genetic component `m' was significant and greater than all other effects in all the crosses. Dominance effect has positive significance in all the three crosses indicating complementary epistasis. Dominance x dominance interaction was negatively significant in all the crosses.

o) 100-Seed weight

Among the generations, the highest mean value for 100-seed weight was recorded by F_1 for L_1 x T_1 and B_1 for L_3 x T_1 and L_5 x T_1 and lowest by P_2 in all crosses.

Scale C had significance for all the crosses, while scale D only for the cross L_1 x T_1. Scale A and B had significance in the crosses L_3 x T_1 and L_5 x T_1.

Among the genetic component 'm' was significant and greater than all other effects in all the crosses. Additive effect was positively significant for L_3 x T_1 and L_5 x T_1. Dominance effect was negatively significant for L_1 x T_1 and positive for L_3 x T_1 and L_5 x T_1.

Dominance x dominance was negative for L_3 x T_1 and L_5 x T_1 and positive for L_1 x T_1. This is because of duplicate epistasis. Additive x additive had negative significance for L_1 x T_1.

p) Length of peduncle

Peduncle length was maximum for the generation B_1 and minimum for P_2 generation for the crosses L_1 x T_1 and L_3 x T_1. In the cross L_5 x T_1, the peduncle length was maximum for B_2 and minimum for P_1.

Scale A and B had significance in all the three crosses. Scale C had significant value in the crosses L_1 x T_1 and L_3 x T_1. Scale D had negative significance in the crosses L_3 x T_1 and L_5 x T_1.

The effect of 'm' was significant and greater than all other effect. Additive effect was positively significant in the first two crosses and negatively significant in the other one. Dominance effect was positive significant in all the three crosses while negative significant in dominance x dominance interaction. Additive x additive interactions were significant in the crosses L_3 x T_1 and L_5 x T_1. The cross L_1 x T_1 had positive significance in additive x dominance interaction.

q) Number of trichomes on pod wall

P_2 and F_2 generations exhibited the maximum values for trichome number in the cross L_1 x T_1 and minimum for P_1 generation. F_2 had maximum and minimum for P_1 in L_3 x T_1. B_2 had maximum and P_1 had minimum trichome number in the cross L_5 x T_1.

Scale A was positively significant in the crosses L_3 x T_1 and L_5 x T_1 while L_1 x T_1 was negatively significant. Scale B had positive significance in L_3 x T_1 and L_5 x T_1. Scale C had significance in the first two crosses. Scale D had significance in first two crosses but negative significance in the other one.

The effect of 'm' was significant and greater than all other effect. Additive effect (d) had negative significance in all the three crosses. The cross L_5 x T_1 had positive significance in dominance effect, while the cross L_1 x T_1 had negative significance effect. Additive x additive interactions were positively significant in the first crosses but negative in the other one. The cross L_3 x T_1 and L_5 x T_1 had positive significance in additive x dominance interaction, while L_1 x T_1 had negative interaction. Dominance x dominance interaction had negative significance in L_3 x T_1 and L_5 x T_1 but positive in L_1 x T_1.

r) Leaf chlorophyll content

The content of chlorophyll in the leaf tissues were highest in P_1 and B_1 generations and lowest in B_2 for the cross L_1 x T_1. F_2 and B_1 had maximum

chlorophyll content and P_2 the minimum for the cross L_3 x T_1. The cross L_5 x T_1 had the highest value in B_2 and lowest in F_1.

The scale A had positive significance in the cross L_3 x T_1. Scale B, positive significance in L_5 x T_1, but negative significance in L_1 x T_1. Scale C had positive significance in L_3 x T_1, while L_1 x T_1 had negative significance. Scale D had negative significance in the crosses L_1 x T_1 and L_5 x T_1 but positive significance in the cross L_3 x T_1.

The effect of 'm' and 'd' had significance in all the three crosses. Dominance effect (h) had positive significance in the cross L_5 x T_1.

Additive x additive interaction was positively significant in the crosses L_1 x T_1 and L_5 x T_1, but negative effect in the cross L_3 x T_1. Additive x dominance interactions was positive for the first two crosses while negative for the other one. Dominance x dominance effect was positively significant in L_1 x T_1 is due to duplicate epitasis and negatively significant in L_5 x T_1.

s) Pod protein content

Pod protein content was maximum in P_1 generation for the crosses L_1 x T_1 and L_5 x T_1, but minimum in P_2 and F_2 respectively. In the cross L_3 x T_1, the maximum was in B_1 and minimum in P_2 generation.

The scale A had positive significance in L_3 x T_1 while negative significance in other two crosses. The crosses L_1 x T_1 and L_3 x T_1 had positive significance for scale B values and scale C values, but the cross L_5 x T_1 had negative scale C value. Scale D had positive significance in L_1 x T_1 and negative significance for L_5 x T_1.

The effect of 'm' was significant and greater than all other effect. Additive effect was significant for all the three crosses. Dominance effect had positive effect in L_3 x T_1, while negative effect in L_1 x T_1. Additive x additive

interaction was positive for L_5 x T_1 but negative for L_1 x T_1. All the 3 crosses had negative significance in additive x dominance interaction. Dominance x dominance had positive interaction for L_1 x T_1 and L_5 x T_1 was due to duplicate epistasis but negative for L_3 x T_1.

t) Crdue fibre content

Crude fibre content was maximum in P_1 for the cross L_1 x T_1 and minimum in P_2. The generation P_1, F_1 and F_2 had high values and B_1 had low values for the cross L_3 x T_1. For L_5 x T_1, the maximum value in B_1 and minimum in P_2 generation.

Scale A had positive significance in L_5 x T_1 but negative in other two crosses. Scales B and C had positive significance in all the three crosses. Scale D had positive significance in the crosses L_1 x T_1 and L_3 x T_1.

The effect of 'm' was significant and greater than all other effect. Additive (d) effect was positively significant for all the three crosses. Dominance effect was positive for L_5 x T_1 but negative for L_1 x T_1. Additive x additive (i) had negative significant interaction in first two crosses. Additive x dominance interaction was negative in first two crosses and positive for other one. Dominance x dominance was positive due to duplicate epistasis in the cross L_1 x T_1 but negative in the cross L_5 x T_1.

4.6.1 Damage parameters – *M. vitrata*

The results of (damage parameters of *M. vitrata*) generation mean values for three selected crosses are presented in Table 27.

a) Percentage infestation of flower buds

The highest percentage of flower bud infestation was observed in P_1 and least in three generations ie., F_1, F_2 and B_2 in the cross L_1 x T_1.

Table 27. Mean values for pod borers damage parameters of the selected three crosses in yard long bean and generation mean analysis

Crosses	*Maruca vitrata*						*Lampides boeticus*					
	X1	X2	X3	X4	X5	X6	X1	X2	X3	X4	X5	X6
P_1 (L_1)	40.00	20.00	26.67	0.29	15.00	28.89	36.00	12.00	24.00	0.21	13.33	22.89
P_2 (T_1)	20.00	11.00	13.33	0.23	9.67	16.39	12.00	6.00	13.33	0.15	7.00	12.11
F_1 (L_1 x T_1)	13.33	8.67	16.00	0.15	9.67	16.11	9.33	4.67	14.67	0.13	4.33	10.11
F_2	13.33	7.33	14.67	0.13	9.67	15.00	10.67	5.33	13.33	0.13	4.33	10.00
B_1 (L_1 x T_1) x L_1	20.00	6.33	26.67	0.23	12.00	20.05	10.67	3.00	14.67	0.15	3.00	8.39
B_2 (L_1 x T_1) x T_1	13.33	8.33	16.00	0.15	8.00	14.83	9.33	5.33	21.33	0.11	6.33	14.00
P_1 (L_3)	26.67	10.33	32.00	0.33	19.67	28.94	24.00	12.00	21.33	0.32	14.33	22.67
P_2 (T_1)	17.33	10.33	10.67	0.24	11.67	16.50	13.33	5.33	10.67	0.13	7.00	10.89
F_1 (L_3 x T_1)	13.33	4.33	13.33	0.13	9.00	12.61	16.00	6.33	6.67	0.09	5.67	9.17
F_2	5.33	5.67	6.67	0.07	12.00	13.06	13.33	5.67	5.33	0.08	5.33	8.17
B_1 (L_3 x T_1)xL_3	5.33	7.67	9.33	0.05	8.00	12.28	14.67	7.67	10.67	0.07	6.00	11.39
B_2 (L_3 x T_1)xT_1	8.00	6.00	10.67	0.09	12.33	14.78	10.67	5.33	6.67	0.09	6.67	9.33
P_1 (L_5)	38.67	15.33	28.00	0.37	19.00	29.67	24.00	8.67	28.67	0.29	10.00	20.56
P_2 (T_1)	18.67	10.00	16.00	0.24	14.67	20.11	13.33	5.33	12.00	0.12	8.00	12.00
F_1 (L_5 x T_1)	17.33	8.67	13.33	0.19	18.00	20.78	24.00	6.33	18.67	0.21	6.67	13.83
F_2	22.67	7.33	14.67	0.16	14.67	18.33	18.67	4.67	14.67	0.19	7.67	12.33
B_1 (L_5 x T_1)xL_5	18.67	7.33	24.00	0.21	16.00	22.33	21.33	8.00	18.67	0.21	9.00	16.22
B_2 (L_5 x T_1) x T_1	13.33	11.00	18.67	0.15	10.00	18.39	17.33	11.00	21.33	0.23	9.00	18.61

Characters

X_1 Percentage of infestation of flower buds
X_2 Number of larvae / 25 flowers
X_3 Percentage pod infestation X_6 Plant resistant index (Ipr)
X_4 Number of larval entry /exit holes per pod
X_5 Number of damaged seeds in a sample of 25 pods

b) Number of larvae per 25 flowers

The mean value for number of larvae per 25 flowers was maximum in P_1 for all the crosses and minimum for the generations B_1 in L_1 x T_1, F_1 in L_3 x T_1 and F_2 and B_1 in the cross L_5 x T_1.

c) Percentage pod infestation

Maximum percentage of pod infestation was noticed in P_1 generation for all the three crosses and the minimum percentage for P_2 generation for the cross L_1 x T_1; F_2 in L_3 x T_1 and F_1 in L_5 x T_1.

d) Number of larval entry / exit holes per pod

The highest number of larval entry was noted for P_1 generation for all the crosses and lowest number in F_2 for L_1 x T_1; B_1 for L_3 x T_1 and B_2 for L_5 x T_1.

e) Number of damaged seeds in a sample of 25 pods

The mean value for the number of damaged seeds in a sample of 25 pods was maximum in P_1 generation for all the three crosses and minimum for B_1 in L_3 x T_1 and B_2 in L_1 x T_1 and L_5 x T_1.

f) Plant resistant index

Generation P_1 had the highest plant resistant index value for all the crosses and lowest for B_2 in L_1 x T_1, B_1 in L_3 x T_1 and F_2 in the cross L_5 x T_1.

4.6.2 Damage parameters – *L. boeticus*

a) Percentage infestation of flower buds

The highest percentage of flower bud infestation was observed in P_1 generation for all the crosses and lowest for B_1 and F_1 in cross L_1 x T_1; B_2 in cross L_3 x T_1 and P_2 in cross L_5 x T_1.

b) Number of larvae per 25 flowers

The mean value for number of larvae per 25 flowers was maximum for P_1 and minimum for B_1 in the cross L_1 x T_1. P_1 and P_2 generations showed the maximum and minimum values for the crosses L_3 x T_1 and L_5 x T_1.

c) Percentage pod infestation

Maximum percentage of pod infestation was for P_1 in all the three crosses and the minimum in P_2 and F_2 generations for L_1 x T_1, P_2 and B_2 for L_3 x T_1 and F_2 for L_5 x T_1.

d) Number of larval entry / exit holes per pod.

The highest number of larval bore holes per pod was observed for P_1 in all the three crosses and minimum in B_2 in L_1 x T_1, F_2 in L_3 x T_1 and P_2 in L_5 x T_1.

e) Number of damaged seeds in a sample of 25 pods

The mean value for number of damaged seeds in a sample of 25 pods was maximum for P_1 in all the three crosses and the minimum for B_1 in the cross L_1 x T_1 and F_1 generation in the other two crosses.

f) Plant resistant index

The plant resistant index was maximum for P_1 generation in all the three crosses and minimum for B_1 in L_1 x T_1, F_2 in L_3 x T_1 and P_2 in L_5 x T_1.

4.7 TRANGRESSIVE SEGREGANTS AND INBREEDING DEPRESSION

The transgression and inbreeding depression of the various characters were estimated as percentage and presented in the Table 28 and 29. Pod yield per plant had high transgression ie., 76.67% for L_1 x T_1, 83.33% for L_3 x T_1 and 73.33% for L_5 x T_1. Pods per plant, 100-seed weight, pod length, pods per cluster, main stem length, crop duration and days to first harvest had high estimates of transgression.

Table 28. Transgressive segregants in three crosses of yard long bean

Sl. No.	Characters	Transgressive segregants (%)		
		L_1 x T_1	L_3 x T_1	L_5 x T_1
1	Days to 50 per cent flowering	Nil	Nil	3.33
2	Days to first harvest	53.33	56.67	50.00
3	Length of harvest period (days)	13.33	16.67	13.33
4	Crop duration (days)	63.33	66.67	56.67
5	Primary branches per plant	6.67	10.00	3.33
6	Main stem length (cm)	40.00	43.33	50.00
7	Pod clusters per plant	16.67	16.67	20.00
8	Pods per plant	66.67	66.67	70.00
9	Pod yield per plant	76.67	83.33	73.33
10	Pods per cluster	46.67	50.00	46.67
11	Pod weight (g)	16.67	20.00	13.33
12	Pod length (cm)	43.33	46.67	43.33
13	Pod breadth (cm)	26.67	30.00	23.33
14	Seeds per pod	Nil	Nil	Nil
15	100-Seed weight (g)	66.67	66.67	70
16	Length of peduncle	30	36.67	23.33
17	Number of trichomes on pod wall	16.60	23.33	13.33
18	Leaf chlorophyll content	6.67	9.00	Nil
19	Pod protein content	16.67	10.00	10.00
20	Crude fibre content of pods	26.67	23.33	13.33

Table 29. Inbreeding depression of yield characters and damage parameters and morphological and biochemical traits in three crosses of yard long bean

Character		Inbreeding Depression (%)		
		$L_1 \times T_1$	$L_3 \times T_1$	$L_5 \times T_1$
I Yield Traits				
1.	Days to 50 per cent flowering	-5.18	1.48	-6.82
2	Days to fist harvest	-1.84	7.32	-1.84
3	Length of harvest period (days)	-4.41	-5.55	13.33
4	Crop duration (days)	2.09	-3.30	-2.96
5	Primary branches per plant	0.00	-5.45	0
6	Main stem length (cm)	0.94	1.69	0.19
7	Pod clusters per plant	-3.85	-23.81	-26.55
8	Pods per plant	-9.99	-6.59	-20.65
9	Pod yield per plant	-34.05	-40.06	-73.63
10	Pods per cluster	-78.28	-32.22	-50.03
11	Pod weight (g)	19.28	17.88	15.36
12	Pod length (cm)	-25.37	-28.76	-28.33
13	Pod breadth (cm)	22.52	-66.01	-66.02
14	Seeds per pod	-9.65	-30.11	-33.66
15	100-Seed weight	1.72	-36.27	-36.27
16	Length of peduncle	-8.82	5.76	0
17	Number of trichomes on pod wall	-7.69	-21.26	6.0
II Biochemical traits				
18	Leaf chlorophyll content	19.33	-3.92	-3.59
19	Pod protein content	5.63	0.12	10.88
20	Crude fibre content of pods	0.82	0	-22.78

A minimum values of transgressive segregants were observed for primary branches per plant in L_1 x T_1 (6.67%), L_3 x T_1 (10.00%) and L_5 x T_1 (3.33%). This was followed by length of harvest period, pod clusters per plant and pod weight.

The inbreeding depression estimates were negative for all the yield parameters except for main stem length and pod weight.

DISCUSSION

5. DISCUSSION

The primary aim of plant breeding programmes is to evolve superior genotypes with high yield, quality and resistance to pests and diseases. The success of crop improvement programme aimed at production of superior varieties, depends solely on selection of suitable genotypes to be used as parents in hybridization programme. The results of the experiment conducted on "Genetic analysis of resistance to pod borers and yield in yard long bean (*Vigna unguiculata* subsp. sesquipedalis (L.) Verdcourt)" are discussed under different headings.

5.1 GERMPLASM EVALUATION

5.1.1 Mean performance

Variability refers to the presence of differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they are grown. Selection is also effective when there is genetic variability among the individuals in a population. A wide variation was noticed for all the characters studied in the 50 genotypes of vegetable cowpea.

Variation in varietal mean for days to 50 per cent flowering observed in the present study was supported by the findings of Rejatha (1992), Sudhakumari (1993), Backiyarani et al. (2000), Tyagi et al. (2000), Ajith (2001), Anbuselvam et al. (2001), Henry (2002), Kavita et al. (2003) and Philip (2004) in cowpea and Sobha and Vahab (1998b), Panicker (2000), Vidya (2000), Madhukumar (2006) and Valarmathi and Surendran (2007a) in yard long bean.

Main stem length showed high variability, which was in accordance with the reports of Sudhakumari (1993), Hazra (1996), Backiyarani et al. (2000), Anbuselvam (2000), Rangaiah and Mahadevu (2000), Tyagi et al. (2000), Ajith (2001), Anbuselvam et al. (2001), Jyothi (2001), Purushotham et al. (2001), Singh and Verma (2002), Philip (2004) and Manju (2006) in cowpea and Sobha and Vahab (1998b) and Vidya (2000) and Madhukumar (2006) in yard long bean.

Characters like, pod clusters per plant and pods per plant showed notable varietal variation. The same was supported by Backiyarani and Nadarajan (1996), Mehta and Zaveri (1998) and Dwivedi et al. (1999) in cowpea and Lovely (2005) and Valarmathi and Surendran (2007a) in yard long bean.

In the present study high variability was noticed for pod yield per plant. Similar results were obtained in cowpea by Sudhakumari (1993), Hazra (1996), Resmi (1998), Backiyarani et al. (2000), Ajith (2001), Philip (2004) and in yard long bean by Sobha and Vahab (1998b), Jyothi (2001), Lovely (2005) and Madhukumar (2006).

A wide range of variation in pod length noticed in the study was supported by Rejatha (1992), Sudha kumari (1993), Sobha (1994), Hazra (1996), Tyagi et al. (2000), Ajith (2001), Anbuselvam et al. (2001) and Philip (2004) in cowpea and Sobha and Vahab (1998b), Panicker (2000), Vidya (2000), Lovely (2005), Madhukumar (2006) and Valarmathi and Surendran (2007a) in yard long bean. Wide variations of pod weight observed in the study was reported earlier in yard long bean by Lovely (2005).

The results purpose that there is ample scope for selection based on plant types with high yield, more number of pods with longer pods for developing high yielding varieties. The wide variation noticed for the various characters may be due to the presence of variability among the genotypes evaluated.

Peduncle length and number of trichomes on pod wall exhibited high range of variability. This results in agreement with findings of Panicker (2000) in yard long bean.

High variability in peduncle length was reported by Dwivedi et al. (1999). Among the biochemical traits high variability was expressed in pod protein content, leaf chlorophyll content and crude fibre content of pods. High variability in pod protein content was earlier reported by Aghora et al. (1994), De et al. (2001), Kalaiyarasi and Palanisamy (2001) and Valarmathi and Surendran (2007a). Backiyarani et al. (2000) observed high variability for leaf chlorophyll content in cowpea. High variability in crude fibre content of pods was earlier reported by Valarmathi and Surendran (2007a) in yard long bean.

5.1.2 Genetic parameters

5.1.2.1 Coefficient of variation

Coefficient of variation, phenotypic and genotypic are better indices for comparison of characters with different units of measurements. The GCV provides a valid basis for comparing and assessing the range of genetic diversity for quantitative characters and PCV measures the extent of total variation.

In the current study, a high PCV was recorded for pod length, pod weight, pod yield, pods per plant, pod clusters per plant and 100-seed weight. High GCV was observed for pod length, pod weight, pods per plant, pod clusters per plant, pod yield per plant and 100-seed weight, which indicate that there exists high genetic variability and better scope for improvements of these characters through selection.

Comparatively low GCV was observed for main stem length, crop duration and days to first harvest indicating the presence of low variability and thus limiting the scope for further improvement through selection.

High PCV for pod yield per plant observed in this study was supported by similar findings of Resmi (1998) in cowpea. In the present study pod yield had maximum GCV values, same was reported by Sobha and Vahab (1998b) and Lovely (2005) in yard long bean. High GCV and PCV was observed in pod yield per plant. Similar results were obtained in cowpea by Sobha and Vahab (1998b), Harshavardhan and Savithramma (1998b), Resmi (1998), Hazra et al. (1999), Vidya (2000), Jyothi (2001), Madhukumar (2006) and Manju (2006).

In the present study pods per plant had very high estimates of GCV and PCV. Similar results were reported in cowpea by Siddique and Gupta (1991), Ranganayaki and Rengasamy (1992), Sawant (1994), Backiyarani and Nadarajan (1996), Harshavardhan and Savithramma (1998b), Jyothi (2001), Rangaiah (2000), Selvam et al. (2000), Narayankutty et al. (2003), Madhukumar (2006). Moderate GCV and PCV was reported by Malarvizhi (2002) and Venkatesan et al. (2003a).

GCV for pod length was high in the present study, which was supported by the findings of Sreekumar et al. (1996), Hazra et al. (1999) and Kalaiyarasi and Palanisamy (2000b) in cowpea and Lovely (2005) in yard long bean. The study also revealed high estimates of GCV for pod weight which was earlier reported by Sobha and Vahab (1998b), Hazra et al. (1999), Rangaiah (2000), Ajith (2001), Narayankutty et al. (2003) and Manju (2006) in cowpea and Vidya (2000) and Lovely (2005) in yard long bean.

In the present study pod clusters per plant showed high GCV and PCV was supported by Backiyarani and Nadarajan (1996), Rangaiah (2000) in cowpea and Madhukumar (2006) in yard long bean. Pods per cluster showed high coefficient of variation both at genotypic and phenotypic level was observed earlier by Jyothi (2001), Lovely (2005) and Madhukumar (2006) in yard long bean.

High coefficient of variation was recorded for 100-seed weight in the present study was supported by Sawant (1994) and Backiyarani and Nadarajan

(1996) and Philip (2004) in cowpea. High coefficient of both genotypic and phenotypic variation were noticed for number of trichomes on pod wall.

High GCV and PCV were observed for pod yield per plant, pod clusters per plant and pods per plant. This suggests the scope for improvement of these characters through selection. Comparatively low GCV for days to first harvest and crop duration observed in the study. indicates the presence of low variability and limiting the scope for further improvement through selection.

5.1.2.2 Heritability and Genetic advance

Heritability and genetic advance are the important selection parameters. Heritability estimates are influenced by type of genetic material, sample size, method of sampling, conduct of experiment, method of calculation and effect of linkage. Genetic advance refers to the improvement in the mean genotypic value of selected individuals over the parental population. It is influenced by the genetic variability, heritability and selection intensity.

High heritability estimates were recorded for all the characters except days to 50 per cent flowering, pods per cluster and crop duration, which had moderate heritability. Heritability was maximum for pod weight and seeds per pod, this was followed by 100-seed weight, pod length, pod breadth, pods per plant and pod clusters per plant.

High genetic advance was noted for pod length and pod weight followed by pod clusters per plant, pods per plant, pod yield per plant, pods per cluster, and 100-seed weight. However days to first harvest, pod breadth, length of harvest period and crop duration recorded low genetic advance indicating.

High heritability and high genetic advance of characters is indicative of additive gene action suggesting the possibility of genetic improvement of those characters through selection. The characters pod clusters per plant, pods per plant, pod yield per plant, pod weight, pod length, seeds per pod and 100-seed weight

had high heritability coupled with high genetic advance, which indicates that there is possibility of genetic improvement of these characters through selection.

Heritability was high for primary branches per plant in the present study is in agreement with the findings of Sawant (1994), Ram and Singh (1997), Ajith (2001), Kalaiyarasi and Palanisamy (2000b) and Philip (2004) in cowpea.

Main stem length showed high heritability in the present study was supported by Sawant (1994), Rewale et al. (1995), Rangaiah (1997), Ram and Singh (1997), Harshavardhan and Savithramma (1998b), Sharma (1999), Vidya (2000), Tyagi et al. (2000), Kalaiyarasi and Palanisamy (2000b), Ajith (2001), Nehru and Manjunath (2001), and Venkatesan et al. (2003). High heritability for pod clusters per plant observed in the present investigation is in accordance with the reports of Sawant (1994) and Ajith (2001) in cowpea and Resmi (1999), Vidya (2000) and Madhukumar (2006) in yard long bean.

In the present study pods per plant recorded high heritability coupled with high genetic advance indicating the presence of additive gene action. Similar results were reported by Sawant (1994), Malarvizhi (2002), Venkatesan et al. (2003a), Harshavardhan and Savithramma (1998b), Panicker (2000), Nehru and Majunath (2001), Jyothi (2001), Narayankutty et al. (2003), Lovely (2005), Manju (2006) and Suganthi and Murugan (2008).

The high genetic advance of pod clusters per plant noted in this study was in agreement with the findings of Ajith (2001) and Suganthi and Murugan (2008) in cowpea and Madhukumar (2006) in yard long bean.

High heritability coupled with high genetic advance was recorded for pod yield per plant suggesting the possibility of improvement through selection. It was supported by the reports of Ram and Singh (1997), Harshavardhan and Savithramma (1998b), Manju (2006) in cowpea and Resmi (1998), Vidya (2000), Jyothi (2001) and Lovely (2005) in yard long bean.

High heritability coupled with high genetic advance was recorded for pod length in the present study was earlier observed in cowpea by Roquib and Patnaik (1990), Sawant (1994), Sreekumar et al. (1996), Rangaiah (1997), Ram and Singh (1997), Ajith (2001), Kalaiyarasi and Palanisamy (2000b), Manju (2006), Madhukumar (2006) and Suganthi and Murugan (2008).

High heritability and low genetic advance of characters is indicative of dominant gene action suggesting the possibility of genetic improvement through hybridization. In the present study high heritability and low genetic advance was noted for pod breadth and seeds per pod.

The present study reveal the preponderance of additive gene effects for important yield traits viz., pod clusters per plant, pods per plant, pod yield per plant, pods per cluster, pod weight, pod length and 100 seed weight in yard long bean which indicate that there is possibility of genetic improvement of these yield traits through selection.

High heritability coupled with high genetic advance was recorded for 100 seed weight in this study was supported by Sawant (1994), Rewale et al. (1995) and Backiyarani and Nadarajan (1998) in cowpea and Madhukumar (2006) in yard long bean.

Crude fibre content recorded moderate heritability. High genetic advance was noticed for peduncle length, number of trichomes on pod wall and protein content of pods where as leaf chlorophyll content and crude fibre content of pods had low genetic advance.

High heritability in peduncle length was noticed early by Ram and Singh (1997) in cowpea. Pod protein content showed high heritability in yard long bean by Madhukumar (2006). Analysis of variance revealed significant differences among the accessions for all the morphological and biochemical traits, except chlorophyll content by Manju (2006) in cowpea.

5.1.3 Correlation studies

Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two or more variables. Thus correlation measures the mutual relationship between two or more variables. In plant breeding, correlation analysis provides information about yield components and thus helps in the selection of superior genotypes from diverse genetic populations.

5.1.3.1 Correlation among the yield components

In the present study pod yield per plant showed strong positive genotypic and phenotypic correlation with pod weight, pod length, pod breadth, seeds per pod and 100 seed weight.

A positive correlation of pods per plant with pod yield per plant, pod breadth and 100-seed weight were noticed in the present study. Similar results were reported by Oseni et al. (1992), Swant (1994), Sreekumar et al. (1996), Harshavardhan and Savithramma (1998b), Resmi (1998), Kalaiyarasi and Palanisamy (1999), Rangaiah and Mahadevu (1999), Ajith (2001), Parmer et al. (2003), Kutty et al. (2003), Philip (2004) and Manju (2006) in cowpea and Panicker (2000), Vidya (2000), Lovely (2005) and Madhukumar (2006) in yard long bean.

A positive correlation of pod clusters per plant with pod yield per plant, pods per cluster, pod weight and pod length were noticed in the present study. Similar results were reported by Sawant (1994), Tamilselvam and Das (1994), Singh et al. (1998), Ajith (2001), Parmar et al. (2003) and Philip (2004) in cowpea and Madhukumar (2006) in yard long bean.

Pod length showed positive correlation with 100-seed weight in the present study was earlier reported by Singh and Verma (2002) in cowpea, which was supported by the findings of Sudha Kumari (1995), Sobha (1994), Kar et al.

(1995), Sreekumar et al. (1996), Resmi (1996), Rangaiah and Mahadevu (1999), Kalaiyarasi and Palanisamy (2000a), Bastian et al. (2001), Kalaiyarasi and Palanisamy (2002), Singh and Verma (2002) and Kutty et al. (2003) in cowpea.

The positive genotypic association of yield per plant with pod breadth observed in this study was supported by Sobha (1994), Harshavardhan and Savithramma (1998b) and Ajith (2001) in cowpea.

Significant positive phenotypic and genotypic correlation of yield per plant with pods per plant, pod clusters per plant, days to first harvest, pod weight and seeds per pod imply that selection of these characters would lead to simultaneous improvement of pod yield per plant in yard long bean.

In this study pod length had high positive genotypic correlation with seeds per pod. This was in agreement with the reports by Chattopadhyay et al. (1997), Parmar et al. (2003) and Philip (2004) in cowpea and Sreekumar et al. (1996) in yard long bean.

5.1.4 Path analysis

The path analysis reveals whether the association of the component characters with yield is due to their direct effect on yield or is a consequence of their indirect effect via some other trait(s). Thus path coefficient analysis helps in partitioning the genotypic correlation coefficient into direct and indirect effects of the component characters on the yield, on the basis of which improvement programme can be decided effectively. If the correlation between yield and any of its components is due to the direct effect, it reflects a true relationship between them and selection can be practiced for such a character in order to improve yield. But if correlation is mainly due to indirect effect of the character through another component trait, the breeder has to select the later trait through which the indirect effect is exerted.

In the present investigation, the highest positive and direct effect on yield was exhibited by pod weight, followed by pods per plant, 100-seed weight, seeds per pod and pod clusters per plant.

High direct effect of pods per plant is in accordance with earlier findings of Sawant (1994), Chattopadhyay et al. (1997), Singh et al. (1998), Harshavardhan and Savithramma (1998b), Ushakumari et al. (2001), Ajith (2001), Kalayarasi and Palanisamy (2002), Kutty et al. (2003), Parmar et al. (2003), Subbaiah et al. (2003), Venkatesan et al. (2003 a), Philip (2004) in cowpea and Resmi (1998), Pournami (2000) and Vidya (2000), Lovely (2005) and Madhukumar (2006) in yard long bean.

The positive direct effect of pod weight on yield was observed in the study was supported by Sobha (1994), Chattopadhyay et al. (1997), Ajith (2001), Kutty et al. (2003), and Subbiah et al. (2003) in cowpea and Resmi (1998) and Vidya (2000) in yard long bean.

In the present investigation, seeds per pod showed a positive direct effect on yield. Similar results were obtained by Sawant (1994), Chattopadhyay et al. (1997), Ram and Singh (1997), Kapoor et al. (2000b), Bastian et al. (2001), Kalayarasi and Palanisamy (2002), Parmar et al. (2003), Subbiah et al. (2003), Venketesan et al. (2003) and Philip (2004) in cowpea.

Pod cluster per plant showed a positive direct effect on yield in the present investigation was in agreement with findings of Sawant (1994), Singh and Singh (1997), Parmar et al. (2003) and Venketesan et al. (2003a) in cowpea.

From the study it is evident that selection of genotypes based on pods per plant and pod weight is effective for improving yield of the crop.

5.1.5 Genetic divergence

D^2 statistics measures the forces of differentiation at intra and inter cluster levels and determines the relative contribution of each component trait to the total

divergence. The cluster which are separated by the largest statistical distance show the maximum divergence. This is a powerful tool in the hands of plant breeders to assess the degree of relationship among the genotypes and to group them based on their phenotypic expression.

Following Mahalanobis D^2 statistics, the fifty genotypes were grouped into nine clusters. The maximum number of genotypes (16) was included in cluster II, followed by cluster III (15), Cluster I (7), Cluster IV (4), Cluster V (3) and Cluster VI (2). The clusters VII, VIII and IX had only one genotype in them. The maximum divergence was shown between the cluster I and Cluster VI, while the minimum divergence was between cluster II and Cluster III.

Grouping of genotypes into different cluster did not reflect the geographical origins of the varieties. Similar results were reported by Tyagi et al. (1999), Backiyarani et al. (2000) in cowpea. Among the nine clusters considered pod yield per plant contributed maximum towards divergence. So this technique helps in the selection of genetically divergent parents for their exploitation in hybridization programmes.

5.1.6 Selection index

Discriminant function technique involves, development of selection criterion on a combination of various characters and aids the breeder in indirect selection for genetic improvement in yield. In plant breeding, selection index refers to a linear combination of characters associated with yield. Selection of genotypes based on a suitable index is highly efficient in any breeding programme. An estimates of discriminant function on reliable and effective characters is a valuable tool for the practical plant breeder. Superior genotypes can be selected from a collection of germplasm using a selection index employing the discriminent function for characters with favourable association.

In the present study, the selection index for the genotype was computed on the basis of nine characters namely harvest period, primary branches per plant, pods per plant, pod weight, pod length, pod breadth, seeds per pod, 100-seed weight and pod yield per plant.

The maximum selection index value was obtained for T_{10} and minimum for T_1. The grouping of genotypes by selection indices followed almost the same pattern as their clustering in the D^2 analysis.

5.2 SCREENING FOR RESISTANCE TO STUDY DAMAGE PARAMETERS AND PLANT RESISTANT INDICES

Pod borer causes severe loss to both flower buds and young pods. The number of webbing in flowers and young pods is a criterion to assess the relative resistance of a genotype. The assessment of damage to the flower buds and young pods has been the most reliable method to determine the pod borers resistance.

All the damage measurements exhibited remarkable variability with respect to different genotypes. Percentage of infestation of flower buds and percentage pod infestation reflect the ultimate severity of yield loss due to pod borers ie., *M. vitrata* and *L. boeticus*; since these two damage parameters showed 100 per cent yield loss. Sixteen genotypes recorded low levels of percentage pod infestation of both the pests.

Wide variability in the plant resistant indices was observed in the 50 genotypes of yard long bean screened under unprotected field condition. A totally tolerant genotypic cannot be identified but three genotypes (Kurappunthara local, Kanichar local and KMV-1) withy low plant resistant indices were identified. From all the damage parameters these three genotypes were selected as male parents (testers) in hybridization programme to develop F_1 hybrids. These three genotypes showing low levels of infestation for both Maruca and Lampides borers. But high variability was noticed for these characters. Panicker (2000),

Vidya (2000), Philip (2004) and Manju (2006) in cowpea have earlier reported significant variability for the *Maruca vitrata* damage measurements.

Seed damage indices and plant resistant indices were worked out (Jackai, 1982) for all the genotypes using a combination of different damage parameters. Both the indices exhibited significant differences among genotypes, as supported by the findings of Panicker (2000) and Vidya (2000) in yard long bean and Philip (2004) and Manju (2006) in cowpea. Plant resistant index served as the selection criteria for identifying the testers. The plant resistant indices were minimum for G_{43}, G_{15} and G_{30} which were significantly different from other genotypes.

5.2.1 Correlation studies for plant resistant index and related characters

Information on the degree and nature of association between different characters is essential for the breeders to identify the characters to be selected, so as to get a profound improvement in many of the economically important characters.

Plant resistant index was significantly correlated with all other characters except peduncle length and leaf chlorophyll content both at genotypic and phenotypic level. The correlation was positive and highly significant with all the pod borers damage measurements. Thus plant resistant index acts as a reliable indicator of the comparative susceptibility of the different genotypes towards the pod borers.

Plant resistant index had negative phenotypic correlation with number of trichomes on pod wall for *M. vitrata*. This results agree with the reports of Oghiakhe et al. (1992e) and Veeranna and Hussain (1997) in cowpea and Panicker (2000) in yard long bean. Plant resistant index was positively correlated with length of peduncle for *L. boeticus*. But it is in disagreement to the reports of Panicker (2000) for peduncle length in *M. vitrata*.

5.3 LINE x TESTER ANALYSIS

In the present study, the parents selected for the screening trials were crossed in a line x tester pattern and the crosses were evaluated in a field experiment along with the parents. The mean performance of parents, estimates of heterosis, general combining ability of parents and specific combining ability of the crosses were evaluated through L x T analysis.

5.3.1 Mean performance of parents and crosses

In general, the lines excelled in yield and biochemical characters, while testers displayed noticeable low values of pod borers damage measurements. Peduncle length and number of trichomes on pod wall had high magnitude in testers, whereas leaf chlorophyll content, pod protein content and crude fibre content in lines. The trend of variability for morphological and biochemical traits suggest that plant types with long peduncles, more trichome numbers and high content of crude fibre offer tolerant to attack by pod borers. The larvae prefer feeding on varieties with more chlorophyll content and protein content of pods. The result supports the findings of Oghiakhe (1992) in cowpea that the content of chlorophyll in leaf tissue could be considered as a criterion for classification of vegetable cowpea genotypes for resistance to the pest. Oghiakhe et al. (1992e) and Veeranna and Hussain (1997) has reported in cowpea the role of trichomes in relation to legume pod borer resistance as observed in the present study of yard long bean. Panicker (2000) has placed a confirmatory view with respect to trichome number and contradictory view with respect to peduncle length and leaf chlorophyll content in yard long bean.

Among lines L_2 and L_3 recorded the maximum yield traits followed by L_5 and L_1. L_1 recorded the highest peduncle length and pod protein content. Number of trichomes on pod wall was more in L_5 and crude fibre content in L_3.

Tester T_1 showing the least attack of pod borers damage parameters. Also showing the maximum mean values for peduncle length, leaf chlorophyll content, pod protein content and crude fibre content, but T_2 recorded maximum trichome number on pod wall.

Among the crosses L_1 x T_1, L_3 x T_1 and L_5 x T_1 had high mean values with respect to the yield characters and low mean values for damage parameters. Length of peduncle and crude fibre content of pods were maximum for the cross L_3 x T_1. The cross L_5 x T_1 showed the maximum number of trichomes. Three crosses (L_1 x T_1, L_3 x T_1 and L_5 x T_1) showing the maximum leaf chlorophyll content but the cross L_1 x T_1 had high pod protein content.

The significance of line x tester interaction indicates the involvement of different gene effects for most of the characters. Anilkumar (1993) and Smitha (1995) reported the significance of line x tester interaction for most yield traits in cowpea. Jayarani (1993) reported significant line x tester interaction for number of seeds per pod, yield per plant and leaf chlorophyll content in cowpea.

5.3.2 Combining ability

Estimation of combining ability effect is done to assess the relative ability of a genotype to transmit its desirable performance to its hybrids. Combining ability analysis provide information about the components of genetic variance involved in the expression of various polygenic characters and thus help in the selection of desirable parents for hybridization and also in deciding the breeding procedure for the genetic improvement of such characters.

5.3.2.1 General combining ability effects of parents

General combining ability is the average performance of a strain in a series of hybrid combinations. It's significance in a parent reflect the preponderance of additive gene effects.

The parents, L_4 and T_3 had significant gca effects for days to 50 per cent flowering. Significant gca effects for days to 50 per cent flowering was reported by Rejatha (1992), Jayarani (1993), Pal et al. (2002), Philip (2004) in cowpea and Lovely (2005) in yard long bean.

Two parents, L_4 and T_2 had significant gca for crop duration. Highest gca effect for main stem length was for L_5 and negative significant gca effect for T_2. Anbuselvam et al. (2000) also reported that strong gca effect were involved in the expression of plant height in cowpea. Three lines showing positive gca effects for pod clusters per plant and T_1 among the testers.

L_1 showing the highest significant gca effect among lines and T_1 among the testers for pods per cluster. No lines and testers had significant gca effects for primary branches per plant and length of harvest periods. However, Thiyagarajan et al. (1992) in cowpea, Sobha and Vahab (1998a) in yard long bean noticed significant gca effects for number of branches per plant.

The parents L_4 and L_3 had significant positive gca effects for yield while L_1, L_2 and L_5 had significant negative gca effects. Among the testers T_1 showing the positive significant gca effect. Excellent gca effects for yield per plant was described by Madhusuda et al. (1995), Kumar et al. (1998), Sawarkar et al. (1999) and Philip (2004) in cowpea and Lovely (2005) in yard long bean.

The parents L_4, L_5, T_1 had significant positive gca effects and L_2, L_3 and T_2 had significant negative gca effects for pod weight. Rejatha (1992) stressed the importance of gca effect for pod weight in cowpea. L_1, T_1, T_2 had positive significant gca effect for pod length and L_5 had significant positive gca effect for pod breadth. Rejatha (1992), Jayarani (1993) and Philip (2004) recorded significant gca effects for pod length.

The parents L_1, L_2, L_3 and T_1 had positive significant gca effect for pods per plant. L_1 and L_2 had positive significant gca effect for seeds per pod. Hundred seed weight had significant positive gca values for L_1, L_3, L_4, T_1 and T_2. The

significant gca effect for pods per plant was noticed by Chaudhari et al. (1998) and Philip (2004) in cowpea and Lovely (2005) in yard long bean.

The parents L_3, L_4 and T_1 recorded the significant positive gca effects for peduncle length. L_3, L_5 and T_1 had significant positive gca effect for number of trichomes on pod wall. L_1, L_2 and T_1 were significant gca effect for leaf chlorophyll content. The parents L_2, L_3 and T_1 had significant positive gca effect for pod protein content and L_2 and T_1 for crude fibre content.

High significance of gca effects is an indication of the underlying additive gene effects for the particular character. In view of the gca effects exhibited by different characters, it can rightly be assumed that additive gene effects play an important role in the expression of the yield traits like pod clusters per plant, pods per plant, pod yield per plant, pods per cluster and 100-seed weight. Similarly for damage parameters also, the appreciable levels of gca effects points out the importance of additive gene effects.

5.1.2.2 Specific combining ability effects of hybrids

The performance of a parent in a specific cross is known as specific combining ability. Thus sca refers to the deviation of a particular cross from the general combining ability. The sca variance is higher than (gca) variance, this indicates that dominance and epistatic interactions are predominant for the character.

Significant negative sca effects for days to 50 per cent flowering was reported by the cross L_3 x T_3 in the study was earlier reported in yard long bean by Sobha and Vahab (1998a). Two crosses, L_1 x T_2 and L_3 x T_1 had significant positive sca effects for crop duration. None of the hybrids showed any significant sca effects for days to first harvest, length of harvest period and primary branches per plant. But Jayarani (1993) reported that sca was high for primary branches per plant in cowpea.

The crosses L_4 x T_3 and L_5 x T_2 had significant sca effect for main stem length. Significant sca effects for pod clusters per plant shown by the crosses L_3 x T_2, L_1 x T_3, L_5 x T_1, L_4 x T_2, L_1 x T_2 and L_3 x T_1. Ten crosses had significant sca effect for pods per plant, six for pods per cluster, nine for pod weight, forteen for pod length, twelve for pod breadth, forteen for seeds per pod and twelve crosses for 100-seed weight. Five crosses, L_1 x T_2, L_2 x T_2, L_3 x T_1, L_4 x T_3 and L_5 x T_2 had significant positive sca effect for pod yield per plant. Significant sca effects were earlier reported in yard long bean by Sobha and Vahab (1998a) for plant height, primary branches per plant, pod length, pods per plant, seeds per pod and 100 seed weight.

Sca effects was more predominant in the expression of pods per plant was reported by Smitha (1995) in cowpea. Higher magnitude of sca variance for plant height and pods per plant noted in this study was supported by Jayarani (1993) in cowpea.

Significant positive sca effects for most of the biochemical characters was noticed in large number of crosses.

So the combining ability analysis provide, information about the gene action involved in the expression of various quantitative characters and thus helps in deciding the breeding procedure for genetic improvement of such traits.

5.3.3 Heterosis

Heterosis refers to increase of F_1 in fitness and vigour over the parental values. Exploitation of heterosis is one of the most important objectives of the plant breeder. High estimate of heterosis is a result of high genetic diversity among parents indicating the possibility of identifying high yielding transgressive segregants from the hybrid populations (Singh, 2002).

Negative heterosis indicating earliness was observed for days to 50 per cent flowering for 3 crosses, L_3 x T_3, L_1 x T_2 and L_5 x T_2. All the hybrids had

significant negative standard heterosis for this character. Significant negative heterosis for days to 50 per cent flowering was reported in cowpea by Bhushana et al. (2000) and Philip (2004).

None of the crosses recorded significant negative relative heterosis for days to first harvest. Eleven crosses had significant negative standard heterosis. Two crosses had significant positive relative heterosis, for length of harvest period. Two crosses, L_1 x T_2 and L_5 x T_3 had significant positive standard heterosis for crop duration.

None of the hybrids exhibited significant heterosis value for relative heterosis, heterobeltiosis and standard heterosis for primary branches per plant. L_4 x T_2, had significant negative standard heterosis. Heterosis for primary branches per plant was reported by Bhushana et al. (2000); Danam and Chaudhari (2000) and Haibatpure et al. (2003) in cowpea. But positive relative heterosis was reported in cowpea by Sawant et al. (1994).

Three crosses had significant positive standard heterosis for main stem length in this study. Three crosses had significant positive relative heterosis for main stem length. Similar findings were reported by Sawant et al. (1994), Bhor et al. (1997), Danam and Chaudhari (2000), Tyagi and Srivastava (2001) and Singh and Dikshit (2003) in cowpea.

All the crosses showed negative significant relative heterosis and heterobeltiosis except, L_1 x T_3 for pod cluster per plant. Two crosses had significant positive standard heterosis for pods per plant. Heterosis in pod clusters per plant was reported by Danam and Chaudhari (2000) and Singh and Dikshit (2003) in cowpea. Rejatha (1992), Sawant et al. (1994), Haibatpure et al. (2003) and Philip (2004) detected positive heterosis in cowpea for pods per plant.

Yield per plant showed significant positive standard heterosis for the cross L_3 x T_1, while 2 crosses had significant positive relative heterosis. Positive

heterosis for yield was also reported by Haibatpure et al. (2003), Rejatha (1992), Sawant et al. (1994) and Shashibushan and Chaudari (2000) in cowpea.

Significant relative heterosis was noticed for pods per cluster in 2 crosses. Majority of the crosses had significant positive heterobeltiosis. Three hybrids had significant positive standard heterosis. Positive heterosis for pods per cluster was recorded by Philip (2004) in cowpea.

Significant positive standard heterosis for two crosses in related to pod breadth. Majority of the hybrids had significant negative standard heterosis for pod weight. Five crosses had significant positive relative heterosis for pod weight. One cross had significant positive standard heterosis, while others showed significant negative standard heterosis for pod length. Similar findings were earlier reported in cowpea by Bhushana et al. (2000), and Philip (2004) for pod length.

Significant positive standard heterosis was shown by 4 crosses for seeds per pod. Eight crosses had positive relative heterosis, while others showing significant negative relative heterosis. This was accordance with the findings of Danan and Chaudhari (2000) and Haibatpure et al. (2003) in cowpea. Six hybrids had significant positive relative heterosis and five showed heterobeltiosis for 100 seed weight. One hybrid had significant positive standard heterosis for 100-seed weight. This was earlier reported by Bhushana (2000), in cowpea.

Significant positive relative heterosis, heterobeltiosis and standard heterosis for peduncle length was noticed for most of the crosses. Five crosses had significant positive relative heterosis for number of trichomes on pod wall. None of the crosses had significant positive heterobeltiosis and standard heterosis for this character.

Five crosses had significant positive relative heterosis for leaf chlorophyll content. One hybrid showed significant positive heterobeltiosis and seven had standard heterosis for leaf chlorophyll content. Nine of the crosses had significant

positive standard heterosis for pod protein content. This result agree with the reports of Malarvizhi (2002) of protein content in pods in the F_1 generation of cowpea crosses. For crude fibre content ten hybrids had significant positive standard heterosis and one had positive relative heterosis and heterobeltiosis.

The crosses L_1 x T_1, L_3 x T_1 and L_5 x T_1 exhibited significant positive estimates with high magnitude of yield attributes and biochemical traits indicating considerable heterosis with respect to the important yield characters.

This results leads to the conclusion that low relative preference of pod borers larvae to these crosses may be due to its trichome numbers or fibre content coupled with mechanical barriers which restrict their assess to pod surface, compared to other genotypes. Several screening techniques are available for a number of insect pests but more knowledge on other aspects of host plant resistance viz., genetics of resistance, basis and mechanisms of resistance is required to be understood in a better way, to develop durable insect resistant varieties of yard long bean. Breeding for resistance is a powerful tool in crop improvement and once it is achieved, it will not only reduce the cost of production but also substantially prevents the environmental pollution.

5.5.5 Proportional contribution of parents and hybrids

In the present study, the proportional contribution of hybrids were the maximum for the total variability for all the characters except main stem length, pod clusters per plant, pods per plant, pods per cluster, days to first harvest and pod yield. The proportional contribution of lines exceeded that of testers for all characters except pod yield per plant.

In biochemical traits, protein content of pods showed high contribution in lines. Hybrids contributing high peduncle length and leaf chlorophyll content but testers contributing more number of trichomes and crude fibre content.

For all the damage parameters, proportional contribution of crosses were less for all the damage measurements except for percentage infestation of flower buds and pods for *M. vitrata*. For *L. boeticus* all the damage parameters were less for the crosses except number of larvae per 25 flowers. The tester showed less number of larvae per 25 flowers.

5.4 GENERATION MEAN ANALYSIS

5.4.1 Yield and yield components

Generation mean analysis is a statistical technique for estimating the components of variance that provide information about the predominant type of gene action for important traits of a crop species. This helps in deciding a suitable breeding procedure for the improvement of various quantitative traits of the species.

Generation mean analysis was done for the selected crosses, Trailing red poded x Kurappunthara local, Ettumanoor local x Kurappunthara local and Palakkad local x Kurappunthara local.

Almost all the yield characters and damage parameters and morphological and biochemical traits exhibited highly significant `m' values indicating the high degree of variation among the different generations. Significance of scale A and B for most of the characters suggested that the simple additive dominance model was inadequate for defining the inheritance of these characters.

Presence of non-allelic interactions was noticed for days to 50 per cent flowering. Additive gene effects and dominance gene effects were negatively significant for the crosses. Dominance x dominance interaction acted in a favourable direction in all the hybrids. Hybridization and selection can be resorted to for improving the character earliness in this crop. Different gene actions for the character was earlier reported by Jayarani (1993), Smitha (1995)

Anbuselvam et al. (2000) and Lovely (2005) as additive, Philip (2004) as non-additive and Sawant (1994) as dominance in cowpea.

Non allelic interactions was noticed for days to first harvest. Additive x additive and dominance x dominance interactions had favourable direction in all crosses, but additive x dominance had negative direction.

Negative significant additive and dominance effects were noticed in some crosses for length of harvest period. Additive x additive interactions was negatively significant indicating that epistasis was duplicate in the crosses. Additive x dominance and dominance x dominance have favourable direction.

Dominance gene effects were negatively significant and additive x additive and additive x dominance interactions were acted in a favourable negative direction in two crosses for crop duration. Dominance x dominance had favourable sign indicating duplicate epistasis which was evident for the crosses.

Presence of non allelic interaction was noticed for primary branches per plant. Dominance effect was negatively significant but additive effect was non significant. Significance of both additive and non-additive gene action for primary branches per plant was reported by Sobha and Vahab (1998a) in yard long bean. Additive x additive interaction had favourable negative direction, but dominance x dominance had positive direction. Nagaraj et al. (2002) noticed that epistatic gene action played a major role in the expression of primary branches.

Dominance x dominance interaction had favourable direction in first cross but negative direction in another cross is due to duplicate epistasis which was evident for the crosses. Nagaraj et al. (2002) noted that epistatic gene action played a major role in the expression of main stem length which was governed by non-additive gene action.

Additive gene effects were highly significant and additive x additive and dominance x dominance interactions was noticed for pod clusters per plant.

Additive x dominance interaction acted in a favourable negative direction in two crosses indicating that epistasis was duplicate in action.

Presence of all three types of digenic interaction was observed for pods per plant. The additive x dominance interaction was found to be significantly positive in one cross and negative in another one. Additive x additive interaction acted in a positive direction. Predominance of non-additive gene action for pods per plant was reported by Jayarani (1993), Smitha (1995) in cowpea and Lovely (2005) in yard long bean.

For pod yield per plant all the hybrids showed dominance x dominance interaction in favourable negative direction. Pod yield per plant displayed all three types of digenic interactions. Predominance of non-additive gene action for pod per plant was suggested by Jayarani (1993) in cowpea and Lovely (2005) in yard long bean.

No crosses had dominance and additive effect for pods per cluster because of epistasis which was complementary in these hybrids. No crosses had any dominance x dominance interaction.

Dominance effect was highly significant for all crosses and additive x additive interaction was also noticed in pod weight. The positive significance of dominance x dominance interactions for pod weight points out that a breeding strategy for improving pod weight should be based on selection or hybridization and selection.

Significance of scale A, B and C for pod length noted in the study suggests the presence of dominance x dominance and additive x additive gene action in negative direction. Dominance x dominance interaction for pod length was reported by Philip (2004). Significance of both additive and non-additive types of gene action was observed for pod length by Rejatha (1992) in cowpea. Predominant gene action in the inheritance of pod length was reported by Nagaraj et al. (2002).

Additive x dominance interactions and additive effect were significantly positive for first cross is due to complementary epistasis in pod breadth, but dominance x dominance interaction was in favourable positive direction due to duplicate epistasis.

Dominance effect was significant for seeds per pod in yard long bean. However dominance x dominance interaction was in favourable negative direction. In 100-seed weight additive gene action was significant for all the hybrids. Dominance x dominance had negative significance for two crosses but positive in other cross due to duplicate epistasis. Several workers reported different types of gene action for seeds per pod, 100 seed weight viz, additive (Thiyagarajan, 1992 and Anilkumar, 1993), non additive (Jayarani, 1993; Thiyagarajan et al, 1993 and Smitha, 1995), dominant (Sawant, 1994b) and epistasis (Nagaraj et al; 2002) in cowpea. Significant role of additive as well as non-additive gene action for these characters were observed by Sobha and Vahab (1998) in yard long bean.

Two types of gene action were reported for the various characters in cowpea by many workers. Predominance of non-additive gene action was suggested by Jayarani (1993), Smitha (1995), Madhusuda et al. (1995) and Chaudhari et al. (1998) and non additive gene action by Kumar et al. (1998), Sawakar et al. (1999) and Philip (2004) for most of the characters in cowpea.

Among the crosses L_3 x T_1 was best with low percentage infestation of flower buds and pods which indicate that genetic improvement for developing genotypes with tolerance to *M. vitrata*.

In general, the magnitude and direction of the gene effects underlying the pest damage parameters offers a favourable back ground for the breeder to develop legume pod borer resistant cowpea types, through recombination breeding and selection based on the damage parameters. Wolley (1976) attributed dominance gene action for inheritance of pod borer resistance whereas, Pathak

(1985) observed partial dominance of susceptibility for percentage pod and seed damage due to pod borer in cowpea.

Among the crosses L_1 x T_1 was best with low percentage infestation of flower buds and pods which indicating the possibility of genetic improvement for developing genotypes with tolerance to *L. boeticus*.

Additive gene effects, dominance effect and additive x additive interactions were significant for peduncle length. The same direction of dominance gene effect and dominance x dominance interactions is an indication of non-allelic complementary gene action for the expression of the character. Hybridization and direct selection of genotypes with long peduncles could be effectively used to improve peduncle length.

Dominance x dominance epistatic interaction was negatively significant for number of trichomes on pod wall but positively significant in L_1 x T_1. Additive x dominance was significant in two hybrids. Ng et al. (2000) reported significant dominant and epistatic gene action on the contrary, he also noted a predominance of additive gene action in the inheritance of trichome number.

For leaf chlorophyll content, additive gene action was significant for all the hybrids. Maximum crosses had significant interaction in all the direction because they are highly significant. This indicates that several breeding approaches like direct and recurrent selection, hybridization and selection and heterosis breeding can be employed for improving leaf chlorophyll content.

Predominance of additive gene action in the positive direction was observed for pod protein content. All the crosses showed significant additive x dominance interaction in the negative direction. Dominance x dominance interaction had positive effect in one cross and negative effect in the other cross. However, the negative significant interactions limits the scope of heterosis breeding for this trait. For simultaneous improvement of these characters hybridization and selection can be successfully used. Malarvizhi (2002) reported both additive and dominant gene action in the inheritance of pod protein content in cowpea.

Additive gene effects had significance for crude fibre content of pods. The positive significance of dominance x dominance interactions points out that a breeding strategy for reducing the fibre content should be based on direct selection or hybridization and selection for low fibre types. This is due to duplicate epistasis.

5.5 TRASGRESSION AND INBREEDING DEPRESSION

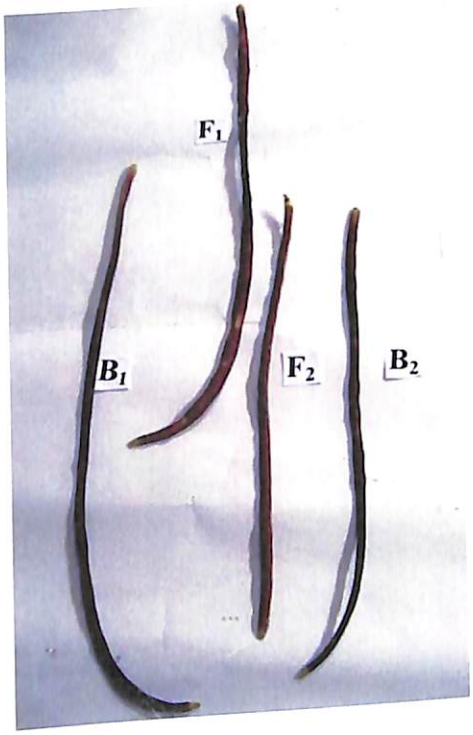
Pod yield per plant had high transgression followed by pods per plant, 100-seed weight, pod length, pods per cluster, main stem length, crop duration and days to first harvest. Inbreeding depression estimates were negative for all the yield parameters except for main stem length and pod weight.

Among the three crosses, L_3 x T_1 was best with high peduncle length, trichome number, chlorophyll content, protein content and crude fibre content and tolerant to *M. vitrata* which indicates genetic improvement is possible in yard long bean. Also the cross L_1 x T_1 had tolerant to *L. boeticus* and best in pods per plant, seeds per pod and 100-seed weight (Plate 7).

Critical assessment of the results, suggests ample scope of improvement of yield through selection based on the characters pod weight and pod length as they have high heritability coupled with genetic advance. These characters also have a high positive direct effect on yield. The genetic analysis for pod yield per plant also suggested selection as the best strategy for improvement. Three superior crosses could be identified which were high yielding as well as with reduced pod borer incidence.

The work can be continued with these three crosses. The three F_2 genotypes identified can be proceeded upto F_7 generation. In each generation selection can be done for pod borer resistance and yield. The selected accessions can be undertaken for the general procedures adopted for variety release after confirmation of the results obtained in the study through further trials.

Trailing Red Poded x Kurappunthara local (L_1 x T_1)



Ettumanoor local x Kurappunthara local (L_3 x T_1)

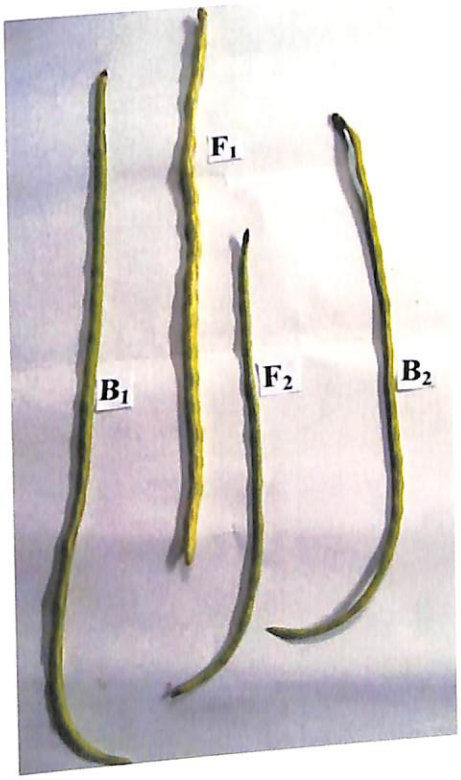


Plate 7. Pod characters of the selected crosses

SUMMARY

6. SUMMARY

Yard long bean is an inexpensive source of vegetable protein and a handy crop well adapted to relatively dry environments. It has equivalent nutritional composition and is an excellent replacement for other types of beans, which are very expensive for the poorer community. Incidence of pests and diseases is considered to be a major limiting factor affecting the production of yard long bean. This study is envisaged to evolve high yielding varieties resistant to pod borers and to study the sources and the inheritance of resistance.

The present investigation was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2006-2008 with the objective to study the genetic basis and inheritance pattern of important quantitative and qualitative characters for resistance to pod borers, *Maruca vitrata* (Fab.) and *Lampides boeticus* (Linn.) and yield and to formulate a suitable breeding programme for developing varieties resistant to pod borers and with high yield in yard long bean. Fifty genotypes collected from different parts of Kerala were evaluated in the study.

The genotypes were evaluated for various characters using randomized block design with three replications. Analysis of variance revealed significant differences for almost all the characters. High GCV was observed for pod length, pod weight, pods per plant, pod clusters per plant, pod yield per plant and 100-seed weight, which indicated high genetic variability and better scope for improvement of these characters through selection. High PCV was recorded for pod length, pod weight, pod yield, pods per plant, pod clusters per plant and 100-seed weight.

The characters pod clusters per plant, pods per plant, pod yield per plant, pod weight, pod length, seeds per pod and 100-seed weight had high heritability coupled with high genetic advance suggesting the possibility of genetic improvement of those characters through selection. In the present study high heritability and low genetic advance was noted for pod breadth and seeds per pod suggesting the possibility of genetic improvement through hybridization.

Significant variability was present for different morphological and biochemical characters among the 50 genotypes. Peduncle length and trichome number exhibited high variability among the morphological characters. Among the biochemical traits high variability was observed in pod protein content, leaf chlorophyll content and crude fibre content of pods. High coefficient of variation was noticed for number of trichomes on pod wall. High genetic advance was observed for peduncle length, trichome number and protein content of pods. High heritability estimates were noticed for all the characters except for crude fibre content of pods.

Yield per plant showed strong positive correlation with pod weight, pod length, pod breadth, seeds per pod and 100-seed weight. The characters pod weight, pods per plant, 100-seed weight, seeds per pod and pod clusters per plant had positive direct effects. For selection of genotypes those characters with positive direct effects are useful. From the present study it was evident that selection of genotypes based on pods per plant and pod weight is effective for improving yield of the crop.

Mahalanobis D^2 analysis clustered 50 genotypes into nine groups. Maximum divergence was shown between the clusters I and VI. Among the seven characters considered pod yield per plant contributed maximum towards divergence, which indicated the selection of genetically divergent parents based on the trait for their exploitation in hybridization programmes.

Selection indices were computed based on yield and eight component traits for 50 genotypes of yard long bean. Five genotypes viz; Trailing Red poded (L_1), NS 621 (L_2), Ettumanoor local (L_3), Vellayani local (L_4) and Palakkad local (L_5) with high yield were selected as female parents (line) in the line x tester analysis.

The same fifty genotypes were screened for various damage parameters of pod borers by using randomized block design with two replications. All the damage parameters exhibited remarkable variability with respect to different genotypes. Percentage infestation of flower buds and percentage pod infestation reflect the ultimate severity of yield loss due to *Maruca vitrata* and *Lampides boeticus*. Based on the study of damage parameters three genotypes namely Kurappunthara local (T_1), Kanichar local (T_2) and KMV-1 (T_3) were selected as male parents (tester) showing low levels of infestation.

Hybridization was done between five selected genotype of yard long bean with high yield (lines) and three genotypes with low plant resistant index (testers) in line x tester mating design. The 15 hybrids along with their parents were evaluated in RBD with three replications for mean performance, combining ability, heterosis and gene action based on 20 characters namely, days to 50 per cent flowering, days to first harvest, length of harvest period, crop duration, primary branches per plant, main stem length, pod clusters per plant, pods per plant, pod yield per plant, pods per cluster, pod weight, pod length, pod breadth, seeds per pod,100-seed weight, peduncle length, trichome number, leaf chlorophyll content, pod protein content and crude fibre content.

Studies on combining ability showed higher magnitude of sca variance for all characters indicating the predominance of dominance gene action. Based on the mean performance, the line Ettumanoor local (L_3) was found to be superior for most of the yield traits followed by Trailing Red Poded (L_1) and Palakkad local (L_5). The tester Kurappunthara local showed superior performance for pod yield per plant and maximum yield related characters.

Based on general combining ability, L_1 showed maximum gca for pods per plant, seeds per pod, pods per cluster, 100 seed weight, pod length and L_4 showing maximum gca effect for pod weight, pod yield and crop duration. Among testers T_1 showed maximum gca effect for yield and related characters. The line L_5 showed significant gca effects for main stem length, pod weight and pod breadth while L_3 showed significant gca effect for pods per plant, 100 seed weight and pod yield per plant. In view of the gca effects exhibited by different characters it can rightly be assumed that additive gene effects play an important role in the expression of yield traits.

The parents L_3 and T_1 recorded significant positive gca effects for peduncle length and L_3, L_5 and T_1 had same effect for number of trichomes on pod wall. L_1, L_2 and T_1 had significant gca effect for leaf chlorophyll content. The parents L_2, L_3 and T_1 had significant gca for pod protein content and L_2 and T_1 for crude fibre content of pods. Here also, high significance of gene effects is an indication of the underlying additive gene effects for that particular character.

Based on specific combining ability, the crosses $L_1 \times T_1$, $L_3 \times T_1$ and $L_5 \times T_1$ showed maximum sca for yield attributes. Maximum crosses showed significant positive sca effects for most of the biochemical traits.

Negative standard heterosis indicating earliness was observed for days to 50 per cent flowering for all the crosses and significant positive for pods per plant in two crosses. The cross $L_3 \times T_1$ had significant positive standard heterosis. Five crosses had significant positive relative heterosis and four crosses had significant positive standard heterosis for pod weight and one cross had significant positive standard heterosis for 100-seed weight.

Most of the crosses recorded significant positive relative heterosis, heterobeltiosis and standard heterosis for peduncle length. Five crosses had significant positive relative heterosis for number of trichomes on pod wall and leaf chlorophyll content. Significant positive standard heterosis was noticed for

nine hybrids for pod protein content and in 10 hybrids for crude fibre content of pods and one hybrid showed significant positive relative heterosis and heterobeltiosis.

The crosses L_1 x T_1, L_3 x T_1 and L_5 x T_1 exhibited significant positive estimates with high magnitude of yield attributes and biochemical traits indicating considerable heterosis with respect to the important yield characters. In these crosses the relative and standard heterosis exhibited significance in the negative direction for all damage parameters. This results leads to the conclusion that less attack of pod borers larvae to these crosses may be due to high values for any of the two characters namely trichome number or fibre content coupled with mechanical barriers with restricts their assess to pod surface compared to other crosses.

The proportional contribution of hybrids were the maximum towards the total variability for all the characters except main stem length, pod clusters per plant, pods per plant, pods per cluster, days to first harvest and pod yield. The proportional contribution of lines exceeded that of testers for all characters except pod yield per plant. The testers showed less number of larvae per 25 flowers. Hybrids contributes high peduncle length and chlorophyll content, Lines contributes high protein content and testers contributes more number of trichomes and crude fibre content of pods. For all the damage parameters, proportional contribution of crosses were less, except percentage infestation of flower buds and percentage pod infestation for *Maruca vitrata* and in the case of *L. boeticus* all the damage parameters were less for the crosses except number of larvae per 25 flowers.

The three superior crosses were identified from line x tester analysis viz; cross I (Trailing Red Poded x Kurappunthara local), cross II (Ettumanoor local x Kurappunthara local) and cross III (Palakkad local x Kurappanthara local) were utilized for generation mean analysis, ie., L_1 x T_1, L_3 x T_1 and L_5 x T_1. Six generations P_1, P_2, F_1, F_2, B_1 and B_2 were developed from three selected crosses.

The generation mean analysis was done to detect the gene action with respect to 20 characters, their biochemical traits and pod borers damage parameters.

Significance of scale A and B for most of the characters suggested that the simple additive x dominance model was inadequate for defining the inheritance of these characters. Presence of non-allelic interactions was noticed for days to 50 per cent flowering, primary branches per plant and days to first harvest. Dominance x dominance interaction acted in a favourable negative direction in all the crosses. Hybridization and selection can be resorted to for improving the character of earliness in this crop.

The positive significance of dominance x dominance interactions for pod weight points out that a breeding strategy for improving pod weight should be based on direct selection or hybridization and selection for high pod weight. Significance of scale A, B and C for pod length suggests the presence of dominance x dominance and additive x additive types of gene action.

Presence of all three types of digenic interaction was observed for pods per plant and pod yield per plant. The dominance x dominance interaction had favourable negative direction. The negative significance of dominance x dominance interaction for pod yield per plant suggests a limited scope for improvement of yard long bean through heterosis breeding. The direction of dominance effect and dominance x dominance interactions suggests the presence of non-allelic duplicate gene action for crop duration, main stem length, pod clusters per plant, pod weight and pod breadth in their expression.

Additive x dominance gene action was significant for peduncle length. The same direction of dominance gene effect and dominance x dominance interaction is an indication of non-allelic complementary gene action in the expression of the character. Hybridization and direct selection of types with long peduncles could be effectively used to improve peduncle length.

Dominance x dominance epistatic interactions were negatively significant for number of trichomes on pod wall but positively significant in the cross L_1xT_1. Additive x dominance was significant in two hybrids.

In leaf chlorophyll content additive gene action was significant for all the hybrids. Maximum crosses had significant interaction for all the characters which are highly significant. This indicates that several breeding approaches like direct and recurrent selection, hybridization and selection and heterosis breeding could be employed for improving the leaf chlorophyll content.

Predominance of additive gene action in a positive direction was observed for pod protein content. All the crosses showed significant additive x dominance interaction in the negative direction. Dominance x dominance interaction had positive effect on one cross and negative in another one. However the negative significant interactions limits the scope of heterosis breeding for this trait.

Additive gene effects showed significant effects for crude fibre content of pods. The positive significance of dominance x dominance interactions points out that a breeding strategy for fibre content should be based on direct selection or hybridization.

Among the crosses L_3 x T_1 was the best with high pod length, pod clusters per plant, primary branches, pods per cluster, pod length and pod breadth and with low percentage infestation for developing genotypes with tolerance to *M. vitrata*. Also, the cross L_1 x T_1 had more number of pods per plant, seeds per pod and 100-seed weight with tolerance to *L. boeticus*. So these two crosses could be identified which were high yielding as well as with reduced pod borer incidence.

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GENETIC ANALYSIS OF RESISTANCE TO POD BORERS AND YIELD IN YARD LONG BEAN (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)

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ABSTRACT

Yard long bean [*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt] known as asparagus bean or vegetable cowpea is one of the important vegetable crops grown in Kerala. The long tender pods are highly nutritious containing carbohydrate, minerals, fibre, calcium, phosphorus, iron and many vitamins. Infestation by pod borers *Maruca vitrata* (Fab.) and *Lampides boeticus* (Linn.) which are the most important post-flowering pests of yard long bean. This research programme was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2006-2008 with the objective to study the genetic basis and inheritance pattern of important quantitative and qualitative characters for resistance to pod borers and yield and to formulate a suitable breeding programme for developing varieties resistant to pod borers and with high yield in yard long bean.

Fifty genotypes of yard long bean collected from different parts of Kerala were evaluated adopting randomized block design with three replications. Analysis of variance revealed significant differences for almost all the characters. High GCV was observed for pod length, pod weight, pods per plant, pod clusters per plant, pod yield per plant and 100-seed weight, which indicate that there exists high genetic variability and better scope for improvement of these characters through selection. The characters pod clusters per plant, pods per plant, pod yield per plant, pod weight, pod length, seeds per pod and 100-seed weight had high heritability coupled with high genetic advance. In the present study high heritability and low genetic advance was noted for pod breadth and seeds per pod.

Yield per plant showed strong positive correlation with pod weight, pod length, pod breadth, seeds per pod and 100-seed weight. The characters pod weight, pods per plant, 100-seed weight, seeds per pod and pod clusters per plant had positive direct effect.

Mahalanobis D^2 analysis clustered the 50 genotypes in to nine groups. Maximum divergence was shown between the clusters I and VI. Among the seven characters considered pod yield per plant contributed maximum towards divergence. Selection indices were computed based on yield and yield related traits, five genotypes viz; Trailing Red Poded (L_1), NS 621 (L_2), Ettumanoor local (L_3), Vellayanai local (L_4) and Palakkad local (L_5) with high yield were selected as female parents in the line x tester analysis.

The same fifty genotypes were screened for various damage parameters of pod borers by using randomized block design with two replications. All the damage parameters exhibited remarkable variability with respect to different genotypes. Based on all the damage parameters three genotypes with low plant resistant indices namely Kurappunthara local (T_1), Kanichar local (T_2) and KMV-1 (T_3) were selected as testers in the line x tester analysis.

Significant variability was present for different morphological and biochemical characters among the 50 genotypes. High coefficient of variation was noticed for number of trichomes on pod wall. High heritability was noticed for all the characters except crude fibre content. The characters peduncle length, trichome number and protein content of pods showing high genetic advance.

In line x tester analysis L_1 showed high values of gca effect for pods per plant, seeds per pod, pods per cluster, 100-seed weight and pod length. Among the testers T_1 showed significant negative gca effects for all the damage parameters for pod borers. In morphological and biochemical traits line L_3 showed positive gca effect for peduncle length, trichome number and protein content of pods but L_1 for leaf chlorophyll content. Tester T_1 showing positive gca effect for all the morphological and biochemical traits.

Based on specific combining ability, the crosses $L_1 \times T_1$, $L_3 \times T_1$ and $L_5 \times T_1$, showed maximum sca for yield attributes and minimum for damage parameters.

Many of the crosses showed significant positive sca effects for most of the morphological and biochemical traits.

The crosses L_1 x T_1, L_3 x T_1 and L_5 x T_1 exhibited significant positive estimates with high magnitude of yield attributes and morphological and biochemical traits indicating considerable heterosis with respect to the important yield characters. Further the relative and standard heterosis exhibited significance in the negative direction for all damage parameters. This results leads to the conclusion that low relative performance of pod borers larvae in these crosses may be due to its trichome number, protein content of pods, leaf chlorophyll content or fibre content which can offer resistance to pod borers in yard long bean and can form the basis for selection of yard long bean genotypes for pod borer resistance or tolerance.

The three superior crosses viz., L_1 x T_1 (Traling Red poded x Kurappunthara local), L_3xT_1 (Ettumanoor local x Kurappunthara local) and L_5 x T_1 (Palakkad local x Kurappunthara local) were utilized for generation mean analysis inorder to detect the gene action with regard to the various traits. Presence of epistasis was tested and subsequently interaction effects viz; additive x additive, additive x dominance and dominance x dominance effects were computed.

Significance of scale A and B for most of the characters suggested that the simple additive x dominance model was inadequate for defining the inheritance of these characters. Presence of non-allelic interactions was noticed for days to 50 per cent flowering, primary branches per plant and days to first harvest. Hybridization and selection can be resorted to for improving the character of earliness in this crop.

The positive significance of dominance x dominance interactions for pod weight points out that a breeding strategy for improving pod weight should be based on direct selection or hybridization and selection for high pod weight. Presence of all three types of digenic interactions was observed for pods per plant and pod yield per plant. The direction of dominance effect and dominance x

dominance interactions suggests the presence of non-allelic duplicate gene action for crop duration, main stem length, pod clusters per plant, pod weight and pod breadth in their expression.

For damage measurements additive gene action was significant for all the damage parameters. Additive x dominance gene action was significant for peduncle length. The same direction of dominance gene effect and dominance x dominance interactions is an indication of non-allelic complementary gene action in the expression of this character. For leaf chlorophyll content additive gene action was significant for all the hybrids. The L_1 x T_1 had positive significance in dominance x dominance epistatic interaction for number of trichomes on pod wall. Predominance of additive gene action in a positive direction was observed for protein content but significant additive x dominance interaction in a negative direction. Additive gene effect was significant for crude fibre content of pods. The positive significance of dominance x dominance interactions points out that a breeding strategy for reducing the fibre content should be based on direct selection or hybridization.

The result suggest ample scope of improvement of yield through selection based on the characters pod weight and pod length. The genetic analysis for yield and resistance to pod borers brought to light genotypes which could be used as source of resistance. Two superior crosses in which high yield potential and tolerant to pod borers were identified. Less attack of pod borers larvae to these crosses may be due to high values for any of the two characters namely trichome number or crude fibre content coupled with mechanical barriers with restricts their access to pod surface compared to other crosses. The magnitude and direction of the gene effects underlying the pest damage parameters offers a favourable background for the breeder to develop pod borer resistant/tolerant yard long bean genotypes. Presence of additive, dominance and epistatic interactions for all the characters identified indicated that recurrent selection or recombination breeding can be followed for future breeding programme.