GENETIC ANALYSIS OF LEGUME POD BORER [*Maruca vitrata* (Fab.)] RESISTANCE AND YIELD IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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DECLARATION

I hereby declare that this thesis entitled "**Genetic Analysis of Legume Pod Borer [*Maruca vitrata* (Fab.)] Resistance and Yield in Cowpea [*Vigna unguiculata* (L.) Walp.]**" 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 award to me of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

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20-03-2004 (2000-21-12)

CERTIFICATE

Certified that this thesis entitled "**Genetic Analysis of Legume Pod Borer [*Maruca vitrata* (Fab.)] Resistance and Yield in Cowpea [*Vigna unguiculata* (L.) Walp.]**" is a record of research work done independently by Mrs. Anu Mary C. Philip (2000-21-12) under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to her.

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CONTENTS

Page No.

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

Introduction

1. INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of the important pulse crops grown over a wide range of environmental conditions throughout the world. It occupies a prominent position in the production systems of the tropics as a rich source of protein and in sustainable agriculture by virtue of the soil bacteria in the nodules enhancing soil fertility. In Kerala, cowpea accounts for about 80 percent of the total area under pulses, grown either as a pure crop or in rice fallows.

The growing demand for the pulse 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. The productivity of cowpea is limited by a complexity of biotic and abiotic interactions.

Infestation by legume pod borer, *Maruca vitrata* (Fab.), which is one of the most important post-flowering pests of cowpea in the tropics, acts as a major limiting factor in cowpea cultivation in all seasons (Taylor and Ezedima, 1964; Jackai and Adalla, 1997). In high rainfall areas, the crop loss due to the pest even goes up to 80 per cent (IITA, 1998).

Farmers usually adopt frequent sprays of chemical insecticides for controlling the population of legume pod borer in the field. Plant protection measures using chemical pesticides cause severe environmental pollution and lead to residual toxicity problems in man and animals, besides increasing the cost of production. According to Bindu (1997), legume pod borer was observed in the field throughout the cropping season, with increased population in the post flowering period, in spite of all the regular insecticidal sprays.

Application of host plant resistance as a major aspect of pest management is currently gaining importance. In this respect, breeding for resistance to the pest assumes utmost importance, both in terms of environmental safety and checking the cost of cultivation. From the farmers' point of view, use of pest resistant varieties is the most simple and economical method of pest control (Kumar, 1984).

Host plant resistance refers to the heritable qualities of a cultivar to counteract the activities of the pest so as to cause minimum percent 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 pests suits better and forms a principal component in Integrated Pest Management (IPM) systems (Dent,1995).

Pest resistance is often found in unimproved or traditional germplasm (Saxena and Khan, 1991). Hence development and standardization of screening techniques for the traditional and local germplasm is a basic requirement in breeding for host plant resistance. The knowledge of the nature and magnitude of gene effects involved in the inheritance of resistance is of great value in deciding the breeding methodology and the breeding strategies to be adopted in developing high yielding pest resistant cultivars.

Identification of morphological and biochemical characteristics of the host plant conferring resistance to pests is important in breeding for pest resistance (Snelling, 1941). The nature of inheritance of these characters must be uncovered for the effective breeding for host plant resistance (Dhaliwal and Dilwari, 1994).

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 specifications.

In the light of these facts, the present study was undertaken with the following objectives.

- To identify the sources of legume pod borer resistance in cowpea through screening of germplasm

- To estimate the magnitude and nature of inheritance of yield and related characters from a collection of cowpea germplasm
- To study the inheritance of biochemical and morphological characteristics related to legume pod borer resistance in cowpea
- To estimate combining ability and gene action by line X tester analysis
- To estimate the additive, dominance and epistatic gene action involved in the inheritance of legume pod borer resistance and yield through generation mean analysis

Review of Literature

2. REVIEW OF LITERATURE

The present study is an attempt to study the genetics of legume pod borer resistance and yield in grain type cowpea. Literature available on different aspects of cowpea relevant to the present study is reviewed in this section.

2.1 ORIGIN AND CYTOGENETICS

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important pulse crop of the tropics. It is widely grown for the seeds or tender pods over a wide range of environmental and climatic conditions throughout the world. The pulse containing about 25 per cent protein in the seed, is a cheap source of protein world wide.

Vigna is a pantropical genus of about 170 species, distributed in Africa, India, South East Asia, America and Australia, the probable primary centre of origin being Africa (Faris, 1965; Rawal, 1975; Dogget, 1979).

Cowpea spread to South East Asia and the Far East and reached Europe from India (Chevalier, 1944). Vavilov (1949) identified India as the primary centre of origin of cowpea and Africa and China as the secondary centres of origin. Several workers considered cowpea originated or was domesticated in Nigeria, where the wild and weedy species co-exist with cultivated types (Harlan, 1971; Rachie and Roberts, 1974).

Dana (1976) reported that out of the 188 species of *Vigna*, 10 are endemic to India and the rest are distributed over Africa. Steele (1976) considered both West Africa and India as modern centres of diversity of cowpea. Once in India, there was accumulation of genetic diversity through the conscious selection for forage and vegetable types, which explained for the two much distantly located centres of diversity (Singh *et al*., 1976; Chandel and Pant, 1982).

The pulse is mainly grown in southern U.S.A., Africa, India, South East Asia, Australia and Central and South America both as main crop or integrated with different cropping systems (Rachie and Roberts, 1974; Singh, *et al*., 1997). Being a

fast growing crop, it curbs erosion by covering the ground and adds to soil fertility by the addition of atmospheric nitrogen.

Rao (1929) and Yarnell (1965) suggested a diploid chromosome number of 2n = 24 for cowpea. Later several workers reported the chromosome number of cowpea as 2n = 2x = 22, the basic chromosome number being 11 (Sen and Bhowal, 1965; Faris, 1964; Leliveld, 1965).

The pachytene chromosome morphology in Vigna unguiculata was analysed by Mukherjee (1968) and the presence of 3 large (41-45 μm), 7 medium (26-36 μm) and 1 small (19 μm) sized chromosomes in the nucleus was reported.

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

Faris (1965) reported interfertility among the five subspecies. Cowpea retained the diploid chromosome number, 2n =22, with little or no chromosome divergence of the cultivars from their putative ancestors (Steele, 1976).

Lush and Evans (1981) reported that the wild species, *Vigna unguiculata* ssp. *dekindtiana* was the progenitor of modern cowpea. The domestication was based on changes associated with pod structure and seed coat. Wild cowpea types were identified in Tanzania, which were similar in chromosome structure to *Vigna unguiculata* ssp. d*ekindtiana* (Singh, 1981).

2.2 LEGUME POD BORER INFESTATION

The economic production of cowpea is seriously affected by the infestation by legume pod borer, *Maruca vitrata* (Fab.) (Syn. *Maruca testulalis*, Geyer) (Lepidoptera : Pyralidae), 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 losses 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). Singh and Jackai (1988) identified legume pod borer as the major limiting factor in the successful cultivation of cowpea in many countries. *Maruca vitrata* is the most abundant species of pod borers feeding on cowpea (Wijayagunasekara and Ranasinghe, 1992; Jaiswal and Patil, 1993).

Karel (1985) observed that the *Maruca vitrata* larvae (Plate 1) are more abundant and injurious to cowpea than any other pest. The pod damage due to the pest ranges from 13 to 31 per cent, the seed damage is about 16 per cent and the total yield loss averages 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). Cowpea, *Vigna unguiculata* (L.) Walp. is one of the most vulnerable species to the attack by legume pod borer (Attachi and Djihou, 1994). Dreyer *et al*. (1994) noticed attack on more than 80 per cent of the cowpea plants in a field. Jackai and Adalla (1997) reported that legume pod borer is 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 devastating 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).

The moth lays eggs on flowers, flower buds or tender pods. The eggs hatch within three days and the first instar larvae start feeding at the oviposition sites. The caterpillars feed on flower buds or on immature seeds in young pods. They bore into the developing pods and feed on the tender seeds (Anithakumari, 1992). In pulses, seeds being the economic produce, infestation by legume pod borer assumes serious

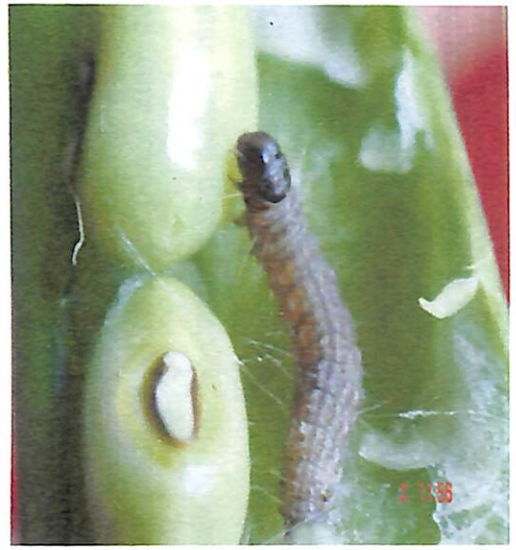


Plate 1. *Maruca vitrata* larva

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 (Plate 2). The larva has five instars, the average total life cycle being 24.92 days.

Echendu and Akingbohungbe (1989) reported that successful establishment of legume pod borer larvae occurs at the flower bud stage, and not in the flower primordia or open flowers. An infestation level of 2 larvae per plant was sufficient to cause noticeable yield reduction in cowpea. Legume pod borer was observed in the field throughout the cropping season, with increased population in the post flowering period, inspite of insecticidal sprays (Bindu, 1997). 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).

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. Oghiakhe *et al*. (1992a) also emphasized the importance of considering the flower and pod damages due to legume pod borer for field screening for resistance. Pod damages caused by legume pod borer results 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 damages caused by the pest, however, was independent of pod damage.

The infestation by legume pod borer is maximum under high relative humidity and low to moderate temperature, while the reproduction rate and population density tends to be lower in drier weather conditions (Jackai *et al*., 1990). Oghiakhe *et.al*. (1991b) reported that percentage of pod damage and larval infestation on flowers were positively correlated with relative humidity and negatively correlated with

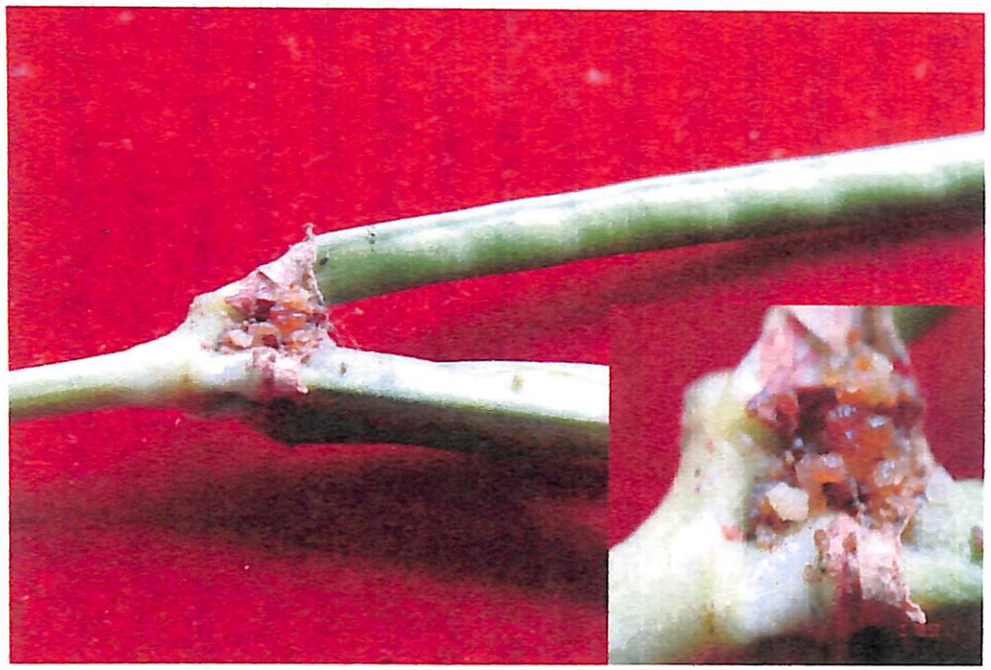


Plate 2. Symptoms of damage

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 are the major environmental factors which influence the population build up of legume pod borer in different areas of cultivation (Bottenberg *et al*., 1997).

Cultural practices like intercropping, weeding, adjusting the time of planting and decreasing the planting density, thereby reducing the relative humidity in the field adversely affected the rate of multiplication and checked the level of infestation of legume pod borer on cowpea (Sharma, 1998). Adipala *et al*. (2000) observed that close spacing promotes infestation of legume pod borer in cowpea under field conditions as a result of increased relative humidity and suggested that intercropping with greengram is effective in controlling the pest population.

2.2.1 Sources of Resistance

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

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

Singh (1978) reported that sources for resistance to legume pod borer can be located within the species itself by screening of cowpea germplasm for pest resistance. 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 (Jackai, 1982).

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; Macfoy *et al*., 1983). Jagginavan *et al*. (1995) noticed that the cowpea lines P120 and C11 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. Singh (1999) opined that the scope of using wild relatives for interspecific 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 IT90K – 277-2, IT93K – 452-1, IT94K – 437-1, IT97K – 569-9, IT95K – 223-3, IT97K – 838 and IT97K – 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.

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

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 *V. pubescens* with *V. unguiculata* and obtained viable hybrids by embryo rescue method.

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

Fatokun (1991) suggested that *V. davyi*, a related wild species of cowpea can be used as a bridge species, while attempting interspecific hybridization with *V. vexillata*. He obtained partially fertile interspecific hybrids of cowpea by this method.

Barone *et al*. (1992) observed that in *V.unguicalata* X *V. vexillata* crosses attempted to transfer legume pod borer resistance to *V. unguicalata*, no viable seeds could be obtained as a result of embryo breakdown in the interspecific 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 resistance to legume pod borer. They screened several accessions of *Vigna 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* ssp. *dekindtiana* var. *pubescens* closely related to *V. vexillata* that can be used as a donor for legume pod borer resistance.

Gomathinayagam *et al*. (1998) used *Vigna 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. The related wild species viz., *Vigna vexillata* and *V. oblongifolia* could be used as donor parents in breeding for legume pod borer resistance, since they were found unsuitable for larval survival, growth and development in screening experiments.

2.2.2 Morphological and Biochemical Basis of Resistance

Different morphological and biochemical characteristics of crop varieties often play a crucial role in providing insect resistance to plants (Norris and Kogan, 1980). The plant architecture deciding the spatial arrangement of the flowers and pods on the plant assumes importance in imparting resistance to legume pod borer in cowpea varieties.

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

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

Cowpea cultivars which held the pods closely within the leaf canopy suffered significantly more damage than the cultivars which held the pods higher than the canopy level (Oghiakhe *et al*., 1991b). Defoliated cultivars sustained significantly less infestation under field conditions, because relative humidity under the canopy was low, while soil and ambient temperature were high, thereby reducing the levels of infestation. They suggested that canopy structure and pod position acting together or independently exerted profound influence on legume pod borer resistance in cowpea.

Oghiakhe *et al*. (1992b) 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*. (1992c) 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. Sharma (1998) observed that the stem and pod wall thickness, the presence or absence of trichomes, podding habit and morphological characters of different cultivars are associated with resistance to legume pod borer. 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. However, Panicker (2000) reported that length of peduncle was

not correlated with resistance to legume pod borer in cowpea. Vidya (2000) reported that there was no significant correlation between pod damage severity and pod wall thickness in cowpea.

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*., 1992d). But the length of non-glandular trichomes on the pod wall (Plate 3) 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. Veeranna and Hussain (1997) reported that the high density of trichomes on the pod surface accounted for the resistance of the variety TVx 7 towards the infestation by legume pod borer. The density of non-glandular trichomes on the pod wall had significant negative correlation with infestation by legume pod borer (Panicker, 2000).

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).

Certain biochemical constituents acts as defensive chemicals in crop varieties playing a crucial role in imparting resistance by influencing the behavioral and physiological responses of the feeding insects (Dent, 1991). Macfoy *et al*. (1983) studied the biochemical mechanism of resistance in cowpea to legume pod borer and observed that the levels of both total sugars and total amino acids were quantitatively lower in resistant than in susceptible cultivars. Okech and Saxena (1990) reported that any type of feeding deterrents or repellants that may inhibit the infestation by legume pod borer is absent in cowpea.

Significant positive correlation was observed between total chlorophyll content and plant resistance index in cowpea (Oghiakhe, 1992). 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

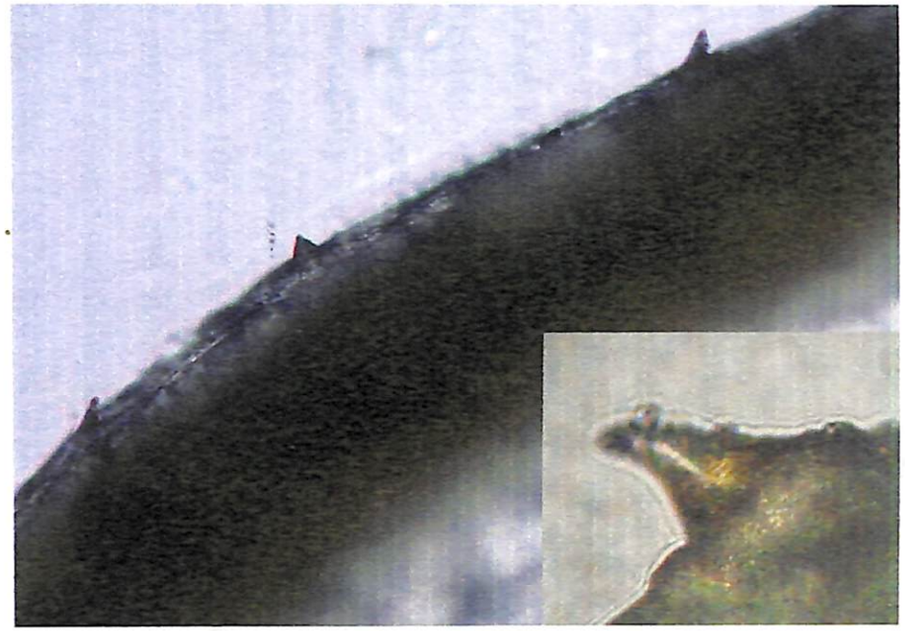


Plate 3. Non-glandular trichomes on pod wall

significant relationship with plant resistance index in relation to legume pod borer (Panicker, 2000).

Levin (1971) opined that phenolics are important group of secondary plant compounds playing a defensive role against insect pests. The relationship between the concentration of phenol in cowpea was studied in variably resistant cultivars by Oghiakhe *et al*. (1993). They did not find any correlation between phenol concentration and field resistance of the cultivars. Legume pod borer resistant accessions of cowpea had higher content of total phenols and tannin compared to susceptible lines (Veerappa, 1998).

Vidya (2000) studied different pod characters in relation to legume pod borer infestation and reported that fibre content of pods was not related to legume pod borer infestation in cowpea varieties.

2.3 VARIABILITY STUDIES

Wide range of genetic variability is a pre-requisite 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).

High variability was observed in cowpea for number of seeds per pod, number of pods per plant and pod yield (Ramachandran *et al*., 1980). Pandita *et al*. (1982) reported high variability for days to flowering, plant height and pod yield in an experiment with 40 genotypes of cowpea.

Pod length and 100 seed weight in cowpea exhibited high range of genetic variability (Dharmalingam and Kadambavanasundaram, 1984). de Mooy (1985) noticed high range of genetic variability for days to flowering and number of pods per plant. Patil and Baviskar (1987) reported high variability for seed yield per plant and number of pods per plant in cowpea.

Significant variability was noticed for days to 50 per cent flowering, number of pods per plant, number of seeds per pod, plant height and yield per plant (Mareena, 1989). Kandasamy *et al*. (1989) reported high variability for days to 50 per cent

flowering, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and seed yield per plant.

Thiyagarajan *et al*. (1989) reported that plant height, clusters per plant, number of pods per plant, number of seeds per plant and seed yield per plant exhibited high variability in a study with 36 Nigerian cowpea types.

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). Rejatha (1992) reported high variability among different genotypes 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 seed per pod, pod length, 100 seed weight and yield per plant (Sudhakumari, 1993).

Wide range of genetic variability existed for the character protein content in cowpea (Aghora *et al*., 1994; De *et al*., 2001; Kalaiyarasi and Palanisamy, 2001).

Sobha (1994) reported broad spectrum genetic variability for pod length and seed yield per plant among different cultivars of 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).

Wide range of genetic variability was observed for plant height, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and yield per plant (Hazra *et al*., 1996). Feng *et al.* (1997) observed high genetic variability for pod length and seed yield per plant in cowpea.

Mehta and Zaveri (1998) noticed high magnitude of genetic variability in segregating generations of cowpea for number of branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant.

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 in cowpea.

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 inflorescences per plant, number of pods per inflorescence, number of pods per plant, pod length and length of peduncle in a study involving 51 cowpea types.

Tyagi *et al.* (2000) reported that the characters 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 among different cultivars. High variability was noticed among 50 cultivars of cowpea for days to flowering, number of pods per plant, number of inflorescences 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).

Grain yield per plant, number of pods per plant and pod length in cowpea exhibited significant variation (Chattopadhyay *et al*., 2001). Jyothi (2001) noticed

broad spectrum of variability for number of branches per plant, plant height, number of inflorescences per plant, number of pods per plant, number of seeds per pod, 100 seed weight and yield per plant in cowpea. Purushotham *et al*. (2001) noticed significant variation in plant height among different cultivars of cowpea.

Arunachalam *et al*. (2002) reported high variability for the yield contributing characters in cowpea. Henry (2002) reported 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. Grain yield per plant exhibited wide range of variability in cowpea (Yadav *et al*., 2002). Kavita *et al.* (2003) reported high range of genetic variability in cowpea for days to 50 per cent flowering.

2.4 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 excepted to achieve through selection (Burton, 1952). The genetic parameters for the different characters in cowpea is presented in Table 1.

2.5 CORRELATION AND PATH COEFFICIENT ANALYSES

Selection for desirable genotypes is the principal step of crop improvement. Yield is a complex character controlled by several component characters. Selection based on yield along with the yield contributing characters would be more efficient than selection based on yield alone (Evans, 1978). Correlation analysis provides a reliable measure of association between the different component traits and helps to differentiate the vital associations useful in breeding from the non- vital ones (Falconer, 1981). 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).

Chauhan and Joshi (1980) observed that number of pods per plant and 100 seed weight in cowpea were negatively correlated with each other.

Table 1. Genetic Parameters in Cowpea

Characters	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability	Genetic advance	References
Days to flowering			High		Ramachandran *et al.*, 1980; Thiyagarajan, 1989; Sreekumar, 1995; Ram and Singh, 1997; Ravindran and Das, 1997
			High	High	Jana *et al.*, 1982; Roquib and Patnaik, 1990
	High	High	High	High	Sreekumar *et al.*, 1996; Sharma, 1999; Ajith, 2001
	High	High	Moderate to high		Anbuselvam *et al.*, 2000
	Moderate to high	Moderate to high	High	High	Tyagi *et al.*, 2000
	Low	Low			Vidya, 2000; Borah and Khan, 2002
	Low	Low	High	Low	Mareena, 1989
Number of pods per plant	High	High			Ramachandran *et al.*, 1980; Patil and Baviskar, 1987; Gowda *et al.*, 1991; Backiyarani and

					Nadarajan, 1996; Rangaiah, 2000
	High	High	High		Siddique and Gupta, 1991
	High	High	High	High	Kandasamy *et al.*, 1989; Sawant, 1994a; Mathur, 1995; Vardhan and Savithramma, 1998; Kalaiyarasi and Palanisamy, 2000; Panicker, 2000; Vidya, 2000; Ajith, 2001; Jyothi, 2001; Nehru and Manjunath, 2001
			High	High	Thiyagarajan *et al.*, 1989;Ram *et al.*, 1994
			High		Thiyagarajan *et al.*, 1990; Damarany, 1994; Arunachalam *et al.*,2002
	High	High		High	Renganayaki and Rengasamy, 1992
				High	Sreekumar, 1995
			Low	High	Ravindran and Das, 1997
	High	High	Moderate to high	Moderate to high	Mareena, 1989; Rangaiah *et al.*, 1999
			Moderate to high	High	Kumar and Sangwan, 2000
	Moderate to high	Moderate to high	High	Moderate	Tyagi *et al.*, 2000; Malarvizhi, 2002

	Moderate	Moderate	Moderate	Moderate	Venkatesan *et al.*, 2003a
Number of clusters per plant	High	High			Radhakrishnan and Jebaraj, 1982; Backiyarani and Nadarajan, 1996; Rangaiah, 2000
			High		Thiyagarajan *et al.*, 1989; Thiyagarajan *et al.*, 1990; Mehta and Zaveri, 1998; Vidya, 2000
			High	High	Sawant, 1994a; Resmi, 1998; Ajith, 2001; Jyothi, 2001
	High	High	High	High	Arunachalam *et al.*, 2002
			High	Moderate	Malarvizhi, 2002
	Moderate	Moderate	Moderate	Moderate	Venkatesan *et al.*, 2003a
Number of pods per cluster	High	High	High	High	Vidya, 2000; Ajith, 2001; Jyothi, 2001
	High	High			Nehru and Manjunath, 2001
			High		Arunachalam *et al.*, 2002
			High	Moderate	Malarvizhi, 2002
Number of branches per plant	High	High			Radhakrishnan and Jebaraj, 1982; Anbuselvam *et al.*, 2000; Nehru and Manjunath, 2001
					Mehta and Zaveri, 1998
			High	High	Vaid and Singh, 1983; Sawant, 1994a;
	High	High	High	High	Kalaiyarasi and Palanisamy, 2000; Borah and

					Khan, 2002
Plant height	High	High			Pandita *et al*., 1982; Sharma *et al*, 1988; Hazra *et al.,* 1999; Anbuselvam *et al*., 2001; Purushotham *et al*., 2001
	High	High	High	High	Siddique and Gupta, 1991; Savithramma, 1992; Sawant, 1994a; Vardhan and Savithramma, 1998; Rangaiah and Mahadevu, 1999; Kalaiyarasi and Palanisamy, 2000; Ajith, 2001; Venkatesan *et al*., 2003a
			High	High	Chikkadyavaiah, 1985; Thiyagarajan *et al*, 1989; Roquib and Patnaik, 1990; Ram *et al*., 1994; Rewale *et al*., 1995; Vidya, 2000; Borah and Khan, 2002
	High	High		High	Renganayaki and Rengasamy, 1992
	High	High	High		Mathur, 1995
			High		Ram and Singh, 1997
	High	High	Moderate to high	High	Mareena, 1989; Anbuselvam *et al*., 2000
			Moderate to	High	Kumar and Sangwan, 2000

			high		
	Moderate to high	Moderate to high	High	High	Tyagi *et al.*, 2000
				Moderate	Nehru and Manjunath, 2001

Pod length			High		Dharmalingam and Kadambavanasundaram, 1984; Patil and Baviskar, 1987; Siddique and Gupta, 1991; Savithramma, 1992; Ram and Singh, 1997; Ravindran and Das, 1997
			High	High	Roquib and Patnaik, 1990; Sobha, 1994
	High	High	High	High	Sawant, 1994a; Sreekumar *et al.*, 1996; Hazra *et al.*, 1999; Kalaiyarasi and Palanisamy, 2000; Ajith, 2001
	High	High	High		Mathur, 1995
			Moderate to high		Anbuselvam *et al.*, 2000
			Moderate to high	High	Kumar and Sangwan, 2000
	Moderate to high	Moderate to high	High	Moderate	Tyagi *et al.*, 2000

	Moderate	Moderate	Moderate	Moderate	Venkatesan *et al.*, 2003a
Number of seeds per pod			High	High	Ramachandran *et al.*, 1980; Apte *et al.*, 1987; Thiyagarajan, 1989; Thiyagarajan *et al.*, 1989; Roquib and Patnaik, 1990; Thiyagarajan *et al.*, 1990; Mehta and Zaveri, 1998
	High	High			Jana *et al.*, 1982
			High		Siddique and Gupta, 1991; Ram and Singh, 1997; Arunachalam *et al.*, 2002
	High	High	High		Mathur, 1995
	High	High	High	High	Sreekumar *et al.*, 1996; Rangaiah and Mahadevu, 1999; Kalaiyarasi and Palanisamy, 2000; Ajith, 2001
	High	High	Moderate to high		Anbuselvam *et al.*, 2000
	Low	Low	Moderate to High	High	Mareena, 1989
100 seed weight			High		Dharmalingam and adambavanasundaram, 1984; Apte *et al.*, 1987; Damarany, 1994; Ram and

					Singh, 1997
	High	High			Gowda *et al*., 1991
	High	High	High		Patil and Baviskar, 1987; Siddique and Gupta, 1991
	High	High	Moderate to high	High	Mareena, 1989
			High	High	Kandasamy *et al*., 1989; Thiyagarajan, 1989; Rewale *et al*., 1995; Sreekumar, 1995; Ram and Singh, 1997
	High	High	High	High	Savithramma, 1992; Sawant, 1994a; Backiyarani and Nadarajan, 1996; Kalaiyarasi and Palanisamy, 2000
	High	High	Moderate to high	Moderate	Anbuselvam *et al*., 2000
			Moderate to high	High	Kumar and Sangwan, 2000
	Moderate to high	Moderate to high	High	Moderate	Tyagi *et al*., 2000
				Moderate	Nehru and Manjunath, 2001

	Moderate	Moderate	Moderate	Moderate	Venkatesan *et al.*, 2003a
Yield per plant	High	High			Ramachandran *et al.*, 1980; Jalajakumari, 1981; Patil and Baviskar, 1987; Gowda *et al.*, 1991; Rangaiah, 2000; Borah and Khan, 2002
	High	High	High	High	Pandita *et al.*, 1982; Vaid and Singh, 1983; Kandasamy *et al.*, 1989; Siddique nd Gupta, 1991; Sawant, 1994a; Mathur, 1995; Resmi, 1998; Vardhan and Savithramma, 1998; Hazra *et al.*, 1999; Rangaiah and Mahadeve, 1999; Kalaiyarasi and Palanisamy, 2000; Panicker, 2000; Vidya, 2000; Ajith, 2000; Jyothi, 2001
			High	High	Thiyagarajan *et al.*, 1989; Roquib and Patnaik, 1990; Thiyagarajan *et al.*, 1990; Ram *et al.*, 1994; Sobha, 1994; Backiyarani and Nadarajan, 1996; Mehta and Zaveri, 1998
			Moderate to high	Moderate to high	Patil and Patil, 1987
	High	High		High	Savithramma, 1992
			High		Damarany, 1994

	High Moderate to high High Moderate	High Moderate to high High Moderate	Moderate Moderate to high High Moderate	Moderate High High Moderate Moderate	Anbuselvam *et al.*, 2000 Kumar and Sangwan, 2000 Tyagi *et al.*, 2000 Nehru and Manjunath, 2001 Venkatesan *et al.*, 2003a
Protien content			Moderate High High High	 High Low	Bliss *et al.*, 1973 Imam, 1979 Sreekumar, 1995 Borah and Khan, 2002
Peduncle length			High		Ram and Singh, 1997

Yield per plant in cowpea had significant positive correlation with number of branches per plant (Jana *et al*., 1982). Number of days to flowering and pod length were positively correlated with yield per plant, but negatively correlated with number of branches per plant. Murthy (1982) identified number of pods per plant, pod length and number of seeds per pod as the major contributors to yield in cowpea.

Jana *et al.* (1983) observed that the character number of pods per plant recorded the maximum direct effect on yield per plant in cowpea.

Path coefficient analysis in cowpea by Obisesan (1985) revealed that number of pods per plant, number of seeds per pod and 100 seed weight were the characters that contributed maximum to yield. Number of inflorescences per plant and peduncle length had indirect positive effect on yield per plant.

Patil and Bhapkar (1987) reported significant negative correlation of number of pods per plant with number of seeds per pod. Ye and Zhang (1987) noted that number of pods per inflorescence was the character which had the greatest direct effect on yield per plant.

Yield per plant in cowpea had significant positive correlation with days to flowering, number of pods per plant, number of seeds per pod and plant height (Sharma *et al*., 1988).

Mareena (1989) reported high positive correlation of yield per plant with number of pods per plant and plant height. Grain yield was significantly and positively correlated with days to 50 per cent flowering, number of pods per plant, number of inflorescences per plant, pod length and 100 grain weight (Patil *et al*., 1989). Number of pods per plant, 100 grain weight and number of seeds per pod had the greatest positive direct effect on seed yield per plant. High positive correlation was observed for yield per plant in cowpea with number of branches per plant, number of pods per cluster, number of inflorescences per plant, 100 seed weight and number of seeds per pod (Tewari and Gautam, 1989).

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. Pod length, number of pods per plant and number of seeds per pod showed negative direct effect on yield 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 in cowpea was noticed by Perrino *et al*. (1993). Peduncle length was not correlated with any other character.

Sawant (1994a) studied the association and path analysis of important yield contributing characters in 10 genotypes and their 45 F_1 hybrids. Seed yield per plant was significantly and positively correlated with number of branches per plant, number of inflorescences per plant, number of pods per plant, pod length, number of seeds per pod and 100 seed weight. Path coefficient analysis indicated that number of pods per plant had the highest positive direct effect on seed yield per plant followed by 100 seed weight, number of seeds per pod, days to 50 per cent flowering, number of inflorescences per plant, plant height and pod length.

Yield per plant in cowpea was significantly and positively correlated to pod weight, pod length, number of seeds per pod and 100 seed weight (Sobha, 1994). 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. Tamilselvam and Das (1994) observed positive correlation for plant height with days to 50 per cent flowering, number of clusters per plant, pod

length and 100 seed weight. 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.

Significant correlation was noted for grain yield per plant with days to flowering, pod length and number of seeds per pod (Hussein and Farghali, 1995). Number of seeds per pod recorded strong positive correlation with yield in cowpea. Path coefficient analysis indicated that pod length had maximum direct effect on yield (Kar *et al*., 1995). Shakarad *et al*. (1995) observed significant positive correlation among days to flowering, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. Highly significant negative correlation was observed between 100 seed weight and protein content of seeds (Sreekumar, 1995).

Naidu *et al.* (1996) noticed significant positive correlation between number of clusters per plant with number of pods per plant. Yield per plant in cowpea was significantly and positively correlated with number of pods per plant, pod length and number of seeds per pod (Sreekumar *et al*., 1996). Days to flowering showed negative correlation with number of pods per plant and significant positive correlation with pod length and number of seeds per pod.

Chattopadhyay *et al*. (1997) reported that yield per plant in cowpea 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.

Significant positive correlation was noted for yield per plant in cowpea with pod length and number of pods per plant by Resmi (1998). 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.

Vardhan and Savithramma (1998) observed that yield per plant in cowpea 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 with yield per plant.

Panicker (2000) reported that number of seeds per pod, number of pods per plant, number of pods per inflorescence and pod length were positively correlated with yield in cowpea. Days to flowering and number of pods per plant exerted the highest positive direct effect on yield while number of inflorescences per plant had negative direct effect. Number of seeds per plant and 100 seed weight exhibited high positive direct effect on grain yield per plant (Rangaiah, 2000). Vidya (2000) observed high positive correlation of yield with number of pods per plant and number of pods per inflorescence. Path coefficient analysis indicated that number of pods per plant was the character contributing the maximum positive direct effect on yield.

Kalaiyarasi and Palanisamy (2001) observed that number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and crude protein content exerted positive direct effect on yield in cowpea. Crude fibre content had strong negative effect on grain yield. Plant height had negative direct effect on yield, but its indirect effect through number of seeds per pod, pod length and crude protein were higher in magnitude resulting in significant positive association with grain yield.

Path analysis in cowpea by Neema and Palanisamy (2001) revealed that plant height, number of branches per plant, pod yield, number of pods per plant, pod length and number of seeds per pod had positive direct effect on grain yield per plant. The highest positive indirect effect on grain yield was for pod length through pod yield.

Kalaiyarasi and Palanisamy (2002) observed that number of seeds per pod, number of pods per plant, crude protein content and plant height had high positive direct effect on grain yield in cowpea. Pod length, 100 seed weight and number of branches per plant had negative direct effect on grain yield. Pod length and 100 seed

weight exhibited positive indirect effect on grain yield through number of pods per plant, number of seeds per pod and crude protein content. Yield per plant was significantly and positively correlated with number of primary branches and plant height (Kohli and Agarwal, 2002).

Ushakumari *et al*. (2002) noticed that grain yield per plant had significant positive association with pod length, plant height and number of pods per plant and negative correlation with number of branches per plant, number of clusters per plant and number of seeds per pod. Number of branches per plant was significantly and positively associated with pod length. Number of clusters per plant and number of pods per plant were positively correlated with each other. Significant positive association was also noticed between number of branches per plant and pod length. Studies on path coefficients denoted that pod length and number of pods per plant were the characters which contributed maximum to grain yield per plant. Maximum positive indirect effect on grain yield was exhibited by number of seeds per plant through pod length. Number of branches per plant had positive indirect effect on grain yield per plant through pod length and number of clusters per plant and negative indirect effect through plant height, number of pods per plant and number of seeds per pod. Number of clusters per plant had positive indirect effect on grain yield per plant through number of pods per plant, pod length and number of branches per plant.

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.

Venkatesan *et al*. (2003b) observed that number of branches per plant, number of clusters 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 in cowpea. 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.

2.6 GENETIC DIVERGENCE

An insight into the genetic divergence among the different genotypes is essential for selecting parents for hybridization aimed at genetic improvement. The more diverse the parents within a reasonable limit, the more would be the chance for improvement of a particular character through crossing (Singh and Gupta, 1968).

Fifty genotypes of cowpea were grouped into 7 clusters with wide genetic diversity by Kumar *et al*. (1982) using Mahalanobis D^2 analysis. Days to 50 percent flowering, pod length and 100 seed weight were the characters which contributed maximum to genetic divergence.

In a study involving 324 diverse genotypes of cowpea, Chikkadyavaiah (1985) grouped 23 stable genotypes into one cluster. Jindal (1985) studied genetic divergence and concluded that genetic divergence in cowpea was independent of their geographical origin. He grouped 52 genotypes of cowpea into 8 clusters using Mahalanobis D^2 analysis. In a Mahalanobis D^2 analysis of 46 varieties of cowpea, Marangappavanar (1986) also reported that genetic divergence was independent of geographical distribution. Patil and Bhapkar (1987) used Mahalanobis D^2 statistic to classify 49 genotypes of cowpea into 16 clusters. Thiyagarajan *et al*. (1988) reported that days to 50 per cent flowering, plant height and 100 seed weight were the characters which contributed maximum to genetic divergence in cowpea.

Parents for hybridization can be selected on the basis of the intercluster mean values and genetic diversity between clusters (Dharmalingam and Kadambavanasundaram, 1989). Wide genetic diversity was noted among the 13 clusters formed from 40 genotypes of cowpea. Days to flowering, plant height and 100 seed weight were the major contributors to genetic divergence in cowpea (Thiyagarajan, 1989).

Thirty genetically diverse genotypes of cowpea were grouped into 4 clusters by Thiyagarajan *et al*. (1989). Seed yield per plant, number of pods per plant and number of seeds per pod were the characters that contributed maximum to genetic divergence. They also reported that there was no relationship between geographic distribution and genetic diversity. Renganayaki and Rengaswamy (1991) used Mahalanobis D^2 statistic to cluster 6 genotypes of cowpea into 4 genetically divergent clusters. Pod length, 100 seed weight and grain yield per plant were the characters which contributed maximum to genetic divergence in cowpea.

Mahalanobis D^2 statistic was used to cluster different genotypes of cowpea to 4 groups based on genetic divergence (Hazra *et al*., 1993a). Genetic divergence did not show any correspondence with geographical distribution of the genotypes. Sudhakumari (1993) grouped 59 varieties of cowpea into eight homogenous clusters using Mahalanobis D^2 statistic. Thiyagarajan and Rajasekharan (1993) grouped diverse genotypes of cowpea into 3 distinct groups based on several yield contributing attributes.

Sobha (1994) grouped 31 genotypes of cowpea into 6 clusters. Strict parallelism was observed between genetic divergence and their geographical distribution. Wide genetic divergence was noted among different accessions of cowpea by Sudhakumari and Gopimony (1994). Fifty nine genotypes of cowpea were grouped into 8 clusters using Mahalanobis D^2 statistic. Genetic divergence was maximum between clusters V and VII which had one and two genotypes respectively.

Forty five genotypes of cowpea were clustered into 4 groups on the basis of genetic divergence using Mahalanobis D^2 analysis by Hazra *et al*. (1996). Clusters I

and IV recorded the maximum intercluster distance. Rewale *et al*. (1996) reported that there was no relationship between genetic divergence and geographical distribution of cowpea genotypes. They estimated the genetic divergence of 70 genotypes using Mahalanobis D^2 statistic and grouped them into 19 clusters. They reported significant contribution of days to 50 per cent flowering, number of inflorescences per plant, number of pods per plant, pod length, 100 seed weight and grain yield per plant to total divergence.

Resmi (1998) used Mahalanobis D^2 analysis to study the genetic divergence of cowpea. Thirty genotypes were grouped into 4 clusters based on genetic distance. Cluster I had 18 genotypes. Maximum intercluster distance was observed between clusters I and III and minimum distance between clusters I and II. Days to flowering, number of branches, pod length, number of pods per inflorescence, number of pods per plant and yield per plant contributed considerably to genetic divergence.

Genotypes collected from different geographical area could be clustered together in the same cluster, indicating that geographical diversity was not necessarily related to genetic diversity (Backiyarani *et al*., 2000). Thirty-two genotypes were grouped into six clusters, of which cluster IV was the largest with 18 genotypes. Ushakumari *et al*. (2000) clustered fifty genotypes into thirteen clusters, the cluster I with thirteen genotypes was the largest. Number of seeds per pod, number of branches per plant, number of pods per cluster and pod length contributed maximum to genetic divergence.

Anbuselvam *et al*. (2001) grouped 50 genotypes of cowpea into 4 clusters based on genetic divergence using Mahalanobis D^2 analysis. Cluster I included 45 genotypes. Highest intercluster distance was noted for clusters II and III indicating maximum genetic divergence. Mahalanobis D^2 analysis was employed to cluster 191 accessions of cowpea into 10 clusters by Kohli and Agarwal (2001). Clusters I and V had 30 accessions each. The smallest cluster was cluster VIII which had 8 accessions. Maximum intercluster distance was recorded between clusters III and X.

2.7 HETEROSIS, COMBINING ABILITY AND GENE ACTION

Exploitation of heterosis is one of the most important objectives of the plant breeder. The magnitude of useful heterosis is of utmost importance in its commercial exploitation. Even, the expression of small magnitudes of heterosis for a particular character is also very much desirable in breeding (Hatchcock and Mc Daniel, 1973). According to Singh (2002), high estimates of heterosis is a result of high genetic diversity among parent varieties indicating the possibility of identifying high yielding transgressive segregants from the hybrid populations.

Diallel analysis involving 8 varieties of cowpea by Chauhan and Joshi (1981), revealed the presence of significant general combining ability (GCA) and specific combining ability (SCA) variances for earliness, number of pods per plant pod length, number of seeds per plant, 100 seed weight and seed yield per plant. The magnitude of GCA variances were found to be comparatively higher than the SCA variances indicating the predominance of additive gene action in the expression of these characters.

The significance of both GCA and SCA variances and the preponderance of non-additive genetic variance for number of pods per plant and seed yield per plant were reported by Zaveri *et al*. (1983) in a study on yield and component characters with 6 cowpea types and their 15 non-reciprocal single crosses.

Literature on gene action of resistance to legume pod borer in cowpea is scanty. However, Pathak (1985) suggested additive gene action for resistance to legume pod borer in cowpea.

Patil and Bhapkar (1986) reported the involvement of additive gene action in the expression of days to flowering and 100 seed weight in a study on yield and yield contributing characters through half diallel analysis in cowpea. In all crosses of cowpea with high *sca* effects, either one or both of the parents used were good general combiners for the concerned character (Patil and Shettee, 1986). They suggested both additive and non-additive gene effects in the inheritance of pod length in cowpea.

A line X tester analysis involving 10 lines and 4 testers of cowpea indicated the predominance of both GCA and SCA variances in the inheritance of seed yield per plant (Mishra *et al*., 1987). Combining ability analysis using 6 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-additive 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.

Combining ability analysis with 6 cultivars of cowpea by Rejatha (1992) indicated significant GCA and SCA variances for days to flowering and number of seeds per pod. She suggested the importance of additive gene action in the expression of these characters. High heterosis was obtained over the better parent for yield per plant (118.99%) and number of pods per plant. 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 plant.

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 of cowpea. Number of seeds per pod and 100 seed weight were governed by additive gene effects. Hazra *et al*. (1993b) studied the gene action governing yield characters in 5 parents and 10 hybrids in cowpea. They reported heterosis for the yield traits. The frequency and level of heterosis for yield components were more related to *sca*

effects than to the genetic divergence of parents as estimated by Mahalanobis D^2 statistic.

The predominance of additive gene action for days to flowering and pod length were suggested by Jayarani (1993). She also reported the preponderance of non-additive gene effects for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant in cowpea. Significant line X tester interactions were noticed for number of branches per plant, number of seeds per pod, yield per plant and leaf chlorophyll content.

Thiyagarajan (1992) reported that the GCA and SCA variance indicated the preponderance of non-additive gene action for days to 50 per cent flowering, plant height, pod length, number of seeds per pod, 100 seed weight and yield per plant. Number of branches per plant, number of clusters per plant and number of pods per plant were controlled by additive gene action.

All yield components in cowpea recorded high magnitude of GCA variance compared to SCA variance suggesting the predominant role of additive gene action for these traits. 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 inflorescences 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.

Sangwan and Lodhi (1995) observed heterosis over the better parent for yield (28.8% - 84.0%) in different intervarietal crosses of cowpea. 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%).

Smitha (1995) observed the importance of both *gca* and *sca* effects, the *sca* effects being more prominent 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 that the characters were governed by additive gene action.

Aravindhan and Das (1996) reported that the ratio of GCA and SCA variance for yield traits in cowpea showed a predominance of SCA variance over GCA variance, suggesting the importance of non-additive gene action. They observed heterosis up to 215% for grain yield per plant in the F_1 hybrids. Specific combining ability variance was important in the expression of yield characters in cowpea suggesting non-additive gene action, except days to flowering and pod length which were controlled by additive gene action.

Better parent heterosis was noticed for days to flowering (91.5%), plant height (43.0%) and grain yield per plant (63.8%) in intervarietal crosses of cowpea (Bhor *et al*., 1997). They also observed that the progenies derived from the crosses showing high heterosis exhibited inbreeding depression also.

Significant SCA and GCA variances 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, 1998). The magnitude of GCA variance was higher suggesting the preponderance of additive gene action. 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 in cowpea.

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). Combining ability analysis in cowpea by Rajkumar *et al*. (2000a) 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.

Significant inbreeding depression was noted in intervarietal crosses of cowpea for days to flowering, plant height, number of branches, pod length, number of pods per plant, number of pods per cluster, number of seeds per pod, 100 seed weight, leaf chlorophyll content and length of peduncle (Rajkumar *et al*., 2000b).

Malarvizhi (2002) reported heterosis for protein content in the leaves, pods and seeds in the F_1 and F_2 generation of cowpea crosses. Both additive and dominant gene action were involved in the expression of protein content. Nagaraj *et al*. (2002) noticed that the character days to 50 per cent flowering was governed by additive genes. Epistatic gene action played a major role in the expression of the characters plant height, pod yield per plant and number of branches per plant, whereas dominant gene action was predominant in the inheritance of pod length. According to Pal *et al*. (2002), both GCA and SCA variances were significant for yield traits in cowpea.

Materials and Methods

3. MATERIALS AND METHODS

The present study on genetic analysis of legume pod borer resistance and yield in cowpea was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during the period 2002-2004.

The study utilized the data generated from four field experiments. Evaluation of cowpea germplasm for resistance to legume pod borer and yield was carried out through Experiment I and Experiment II respectively. In Experiment III, the F_1's obtained by hybridization of the parents selected from Experiment I and Experiment II were evaluated along with the parents. Six generations of a selected cross were raised in Experiment IV for collecting data for generation mean analysis.

3.1 MATERIALS

3.1.1 Experiment I and II - Germplasm Evaluation for Legume Pod Borer Resistance and Yield

The material for screening for field legume pod borer resistance and yield comprised of 50 cultivars of cowpea collected from various research stations and areas of cultivation in the state. The test entries are designated by accession numbers T_1 to T_{50}. The identity of the test entries is given in Table 2.

3.1.2 Experiment III - Evaluation of F_1's and Parents

Three accessions (testers) selected from Experiment I, five accessions (lines) selected from Experiment II and the15 F_1 hybrids obtained by crossing them in line X tester manner constituted the material for Experiment III. The variety C-152 which was included in the lines served as the standard variety for estimation of standard heterosis.

3.1.3 Experiment IV - Generation Mean Analysis

The materials for generation mean analysis consisted of 6 populations *viz.*, the F_1 hybrid, the F_2 population, the backcross generations with both the parents and the parents of the most promising cross selected from Experiment III on the basis of yield and resistance to legume pod borer.

Table 2. List of cowpea accessions used for field screening

Treatment Number	Genotypes
T_1	GC 2
T_2	GC 3
T_3	V 16
T_4	V 118
T_5	V 240
T_6	C 152
T_7	Ptb 1 (Kanakamony)
T_8	Ptb 2 (Krishnamony)
T_9	Subhra
T_{10}	Pusa Phalguni
T_{11}	GC 11
T_{12}	GC 12
T_{13}	GC 13
T_{14}	GC- 012
T_{15}	GC- 013
T_{16}	GC- 9040
T_{17}	GC- 9714
T_{18}	GC- 9732
T_{19}	HC 9846
T_{20}	HC 9863
T_{21}	HC 9864
T_{22}	HC 9866
T_{23}	HC 02-39
T_{24}	HC 02-40
T_{25}	HC 270

Treatment Number	Genotypes
T_{26}	CPD 19
T_{27}	CPD 31
T_{28}	CPD 45
T_{29}	CPD 101
T_{30}	DCP 1
T_{31}	DCP 2
T_{32}	DCP 5
T_{33}	DCP 6
T_{34}	DCP 7
T_{35}	DCP 8
T_{36}	DCP 9
T_{37}	V 585
T_{38}	V 625
T_{39}	V 629
T_{40}	CoVu 702
T_{41}	TC 201
T_{42}	TC 99-1
T_{43}	CAZC 21
T_{44}	Culture 9
T_{45}	Palakkad local
T_{46}	Pathanamthitta local
T_{47}	Kottayam local
T_{48}	Changanacherry local
T_{49}	Chengannur local
T_{50}	Alappuzha local

3.2 METHODS

3.2.1 Layout and Conduct of the Experiment

Experiment I and Experiment II were conducted in rabi, 2002 with the 50 accessions of cowpea for evaluation of germplasm for resistance to legume pod borer and yield.

3.2.1.1 Experiment I

The 50 test entries were evaluated in a field experiment in randomized block design with two replications. Plot size was 2.25 m^2 and the spacing was 25 X 15 cm. This particular crop season was selected for the conduct of this experiment so as to coincide with the peak season of natural infestation by the target pest, *Maruca vitrata* (Fab.). One week prior to sowing, a susceptible local cultivar of cowpea was planted along the border of the experimental field. These plants served as multiplication sites for the pest.

Larval release to the experimental field was done to enhance the pest population. Second instar larvae collected from infested plots were released on to experimental plants at the rate of two larvae per plant at the early flowering phase of the crop.

All the crop management practices, except plant protection measures that may reduce the target pest population, as per Package of Practices - Recommendations (KAU, 1996) of Kerala Agricultural University were followed.

3.2.1.2 Experiment II

The 50 test entries were evaluated for yield in a field experiment in randomized block design with two replications. Plot size and spacing were similar to Experiment I. The crop was raised following the Package of Practices - Recommendations (KAU, 1996) of Kerala Agricultural University.

3.2.1.3 Development of F_1 hybrids

The parents used in hybridization were selected based on the results of the previous experiments. From Experiment II, five lines were selected on the basis of selection index. From Experiment I, three testers were selected on the basis of

damage parameters. The five lines and three testers were raised in a crossing block in summer, 2003 and hybridization was done to obtain 15 F_1 hybrids.

The technique of artificial pollination suggested by Krishnaswamy (1970) was followed for the production of hybrids. Flowers which were to bloom the next morning were selected on the lines on the previous evening for emasculation. The bud was held between the thumb and forefinger with the keel petal on the upper side. A needle was used to split the corolla along the ridge where the two edges of standard petal unite. One side of the standard was brought down and held in position with the thumb. Similarly, the wing petal was also brought down and held with the thumb. This exposed the keel petal which was slit on the exposed side. The section of the keel was also lowered and held by the thumb. The immature stamens were exposed and were taken out one by one by seizing the filaments with a forceps. Then the petals were released and the emasculated flower was covered with a folded leaflet from the plant and secured with a pin in order to avoid dessication. Paper covers were used for protecting the emasculated flowers.

The next morning, pollination was done using freshly opened flowers of the selected tester plants. The standard and wing petals of the male flower are removed. The keel petal was gently pressed to expose the stamens covered with pollen grains. This as such was used as a brush to dust the pollen on to the stigma of the emasculated flower. The pollinated flower was then covered and cover was retained for another 2-3 days. Proper tagging was done with all the required data.

3.2.1.4 Experiment III

The fifteen hybrids were evaluated for yield and resistance to legume pod borer along with the 8 parents in a field experiment in randomized block design with three replications during kharif, 2003. The plot size was 2.25 m^2. The seeds were sown at a spacing of 25 X 15 cm. The crop was raised following the Package of Practices - Recommendations (KAU, 1996) of Kerala Agricultural University. However, insecticide application was avoided considering its possible adverse effect on target pest population build up.

3.2.1.5 Building up of generations

The most promising hybrid in terms of yield and legume pod borer resistance was selected based on the results of Experiment III. The F_1 hybrid was backcrossed to the respective parents to obtain the two backcross generations, B_I and B_2. Simultaneously, the F_1 was selfed to produce the corresponding F_2 population.

3.2.1.6 Experiment IV

The materials used for generation mean analysis consisted of 6 generations (P_1, P_2, F_1, F_2, B_1 and B_2) of the selected hybrid combination. The experiment was conducted adopting a randomized block design with three replications in late rabi crop season, 2003- 2004. Plot size was 2.25 m^2 for P_1, P_2 and F_1 generations, whereas, for F_2, B_1 and B_2 generations, a plot size of 4.50 m^2 was used. The spacing was maintained at 25 X 15 cm in all plots. All the crop management practices except plant protection measures which may reduce the target pest population, as per Package of Practices - Recommendations (KAU, 1996) of Kerala Agricultural University were followed.

3.3 Collection of Data

Observations were recorded from ten plants selected at random in each plot, leaving the border rows. In Experiment IV, twenty plants were selected at random in each replication for recording observations of the F_2, B_1 and B_2 generations, while the number of observational plants was kept as ten for other generations. The mean values for each character was used for the statistical analysis.

3.3.1 Yield and its components

Data on yield characters were recorded from the Experiments II, III and IV.

a. Days to 50 per cent flowering

Number of days taken from sowing to 50 per cent of the plants to flower was recorded.

b. Number of pods per plant

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

c. Number of inflorescences per plant

The number of flower clusters on each observational plant was recorded.

d. Number of pods per inflorescence

Number of pods present on the inflorescences on each observational plant was ascertained and mean value worked out.

e. Plant height (cm)

Length of the main stem was measured from the ground level to the tip of the plant at the time of final harvest.

f. Number of primary branches

Number of primary branches were recorded on each observational plant at the time of final harvest.

g. Pod length (cm)

Length of five randomly chosen mature pods from each observational plant was measured in cm. The average value was worked out and recorded.

h. Number of seeds per pod

Number of seeds in five randomly selected mature pods on each observational plant was counted and mean value recorded.

i. Grain yield per plant

The yield of grains from each observational plant was recorded after each harvest. Total weight of grains separated from the harvested pods of each observational plant was calculated and recorded.

j. 100 seed weight

The weight of 100 randomly chosen seeds from each observational plant was recorded.

3.3.2 Damage parameters

Data on different damage parameters related to legume pod borer infestation were recorded from Experiments I, III and IV.

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 legume 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 pod infestation

A sample of 25 pods were randomly collected from each plot at the peak podding phase. Infested pods 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 bore 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 (I_{sd}).

$$I_{sd} = \frac{ds \times 100}{pt}$$

where ds = number of damaged seeds and

pt = number of pods sampled

Plant resistance Index (I_{pr})

A plant resistance index (Jackai, 1982) was computed for each variety using a combination of the following damage parameters,

Number of larvae per 25 flowers

Percentage pod infestation

Seed damage index (I_{sd})

$$I_{pr.} = \frac{W_1S + W_2T + W_3M}{W_1 + W_2 + W_3}$$

where S, T, and M are measurements of damage of seeds, pods and flowers respectively with weights W_1, W_2 and W_3 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.

3.3.3 Morphological and biochemical traits

Data relating to the morphological and biochemical traits were recorded from Experiment II, III and IV.

a. Length of peduncle

Length of five randomly selected fully elongated peduncles from each observational plant was measured and mean values worked out.

b. Density of non-glandular trichomes on pod wall (count / 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. The area of the microscopic field 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.

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

Leaf chlorophyll content was estimated at about 60 days after sowing. Fully expanded leaves collected from the top were used for chlorophyll estimation. Content of total chlorophyll in the leaf tissue was estimated by the method described by Arnon (1949).

d. Protein content

The total soluble protein content of leaves, pods and seeds were estimated in Experiment III and IV. The fully opened functional leaves at flowering initiation

stage *ie*., 30 days after sowing were used for the determination of leaf protein content. Mature pods were used for the determination of protein content in pods. Seed protein was determined from dried grains obtained from each treatment. The procedure described by Bradford (1976) was followed.

e. Crude fibre content

The crude fibre content of pods were estimated in Experiment III and IV. Three mature pods were selected at random from the observational plants for estimation of crude fibre content. The method proposed by Chopra and Kanwar (1976) was used for the determination of crude fibre content.

3.4 Statistical analysis

3.4.1. Analysis of variance (ANOVA)

Analysis of variance (Panse and Sukhatme, 1985) of the data collected from the various experiments was done to test the significance of differences among genotypes with respect to the characters and to estimate the variance components (Table 3).

Table 3. ANOVA for each character

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

Where, r = number of replications,

t = number of treatments,

MSR = Replication mean square,

MST = Treatment mean square and

MSE = Error mean square.

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

Where, t_{α} is the student's t table value at error degrees of freedom and α is the level of significance (0.05).

3.4.2 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 are 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 using the estimates, V_G and V_P and was expressed as percentage (Burton, 1952) for each trait.

i. Phenotypic coefficient of variation (PCV)

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

ii. Genotypic coefficient of variation

$$GCV = \frac{\sqrt{V_G}}{\bar{x}} \times 100$$

Where, $\bar{x}$ is the mean for each character estimated over all the treatments.

c. Heritability

Heritability (broad sense) was calculated for each trait 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%) and high (>60 %) as suggested by Johnson *et al*. (1955).

d. Genetic advance

Genetic advance is calculated using the parameters, phenotypic standard deviation and heritability and a standardized selection differential (Allard, 1960).

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

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

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

Genetic advance was categorized as low (< 10 %), moderate (11 – 20%) and high (>20 %) as suggested by Johnson *et al*. (1955).

3.4.3 Association analyses

a. Correlation analysis

Phenotypic, genotypic and environmental correlation coefficients were estimated using the respective variances and co-variances of the different characters which exhibited significant variation in the ANOVA.

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

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

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

Where, Cov_P (x,y), Cov_G (x,y) and Cov_E (x,y) denote the phenotypic, genotypic and error co-variances between the two traits x and y respectively.

V_P (x), V_G (x) and V_E (x) are the respective phenotypic, genotypic and error variances for the character x and V_P (y), V_G (y) and V_E (y) denotes the phenotypic, genotypic and error variances for the character y respectively.

b. Path coefficient analysis

The direct and indirect effects of the component characters which exhibited high correlation with yield (grain yield per plant) were calculated through path coefficient analysis (Dewey and Lu, 1959).

3.4.4 Selection index

Selection index (Smith, 1936) was computed based on the characters used for path analysis using the discriminant function of Fisher (1936) to discriminate the different genotypes based on the characters under study.

3.4.5 Mahalanobis D^2 analysis

Mahalanobis D^2 analysis was applied to cluster the 50 accessions of cowpea. For i^{th} and j^{th} accessions, D^2 value was computed as,

$$D^2 = \sum_{i=1}^{k} (X_{il} - X_{jl})^2$$ Where,

k = number of characters,

X_{il} = uncorrelated means for the character X_i in the l^{th} genotype and

X_{jl} = uncorrelated means for the character X_j in the l^{th} genotype

Significance of D^2 values were tested by Chi square test with k degrees of freedom. The genotypes were grouped into several clusters based on these D^2 values following Tocher's method of clustering (Rao, 1952).

3.4.6 Line X Tester analysis

3.4.6.1 Combining ability

The general combining ability (GCA) of the parents and the specific combining ability (SCA) of the hybrids were estimated using the L X T method (Kempthorne,

1957). The mean squares due to various sources of variation and their genetic expectations were computed as per Table 4.

Table 4. ANOVA for Line X Tester analysis

Source of variation	Df	Mean square	Expected mean square
Replication	(r-1)		
Treatment	(e-1)		
Line	(l-1)	M_1	MSE + r (Cov F.S. – 2Cov H.S.) + rt (Cov H.S.)
Tester	(t-1)	M_2	MSE + r (Cov F.S. – 2Cov H.S.) + rl (Cov H.S.)
Parents	(l+t)-1		
Crosses	(lt-1)		
Parents Vs crosses	1		
Line X Tester	(l-1) (t-1)	M_3	MSE + r (Cov F.S. – 2Cov H.S.)
Error	(r-1) (e-1)	M_4	MSE
Total	(re-1)		

Where,

r = number of replications,

l = number of lines,

t = number of testers and

e = number of treatments (l+t+lt).

General combining ability (*gca*) effects of parents and specific combining ability (*sca*) effects 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 the i^{th} line,

g_j = *gca* effect of the j^{th} tester,

s_{ij} = *sca* effect of the ij^{th} hybrid and

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

Where,

i = 1,2,….l,

j = 1,2,…..t and

k = 1,2,…..r.

The individual effects were estimated as follows.

$$\text{Mean} = \frac{x\ldots}{rlt}$$

i. *gca* effect of lines

$$g_i = \frac{x_{i..}}{rt} - \frac{x\ldots}{rlt}$$

Where, i = 1,2,….l

ii. *gca* effect of testers

$$g_j = \frac{x_{.j.}}{rl} - \frac{x\ldots}{rlt}$$

Where, j = 1,2,…..t

iii. *sca* effect of the hybrids

$$s_{ij} = \frac{x_{ij.}}{r} - \frac{x_{i..}}{rt} - \frac{x_{.j.}}{rl} + \frac{x\ldots}{rlt}$$

Where,

x… = Sum of all hybrids over ‘r’ replications,

$x_{i..}$ = Sum of all hybrids involving the i^{th} line as one parent over 't' testers and 'r' replications,

$x_{.j.}$ = Sum of all hybrids involving the j^{th} tester as one parent over 'l' lines and 'r' replications and

x_{ij}. = Sum of the hybrids between i^{th} line and j^{th} tester over 'r' replications.

Significance of combining ability effects was tested using 't' test.

i. SE of *gca* (lines) = $\sqrt{MSE / rt}$

ii. SE of *gca* (testers) = $\sqrt{MSE / rl}$

iii. SE of s*ca* (hybrids) = $\sqrt{MSE / r}$

The values for effect / (SE of effect) were computed and compared with the table 't' values at error degrees of freedom for 5 per cent level of significance for testing the significance of these effects.

3.4.6.2 Proportional contribution

The proportional contribution of lines, testers and their interactions to the total variance is calculated.

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

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

$$\text{iii. Contribution of interaction} = \frac{SS\ (l \times t)}{SS\ (hybrids)} \times 100$$

3.4.6.3 Heterosis

The relative heterosis (RH), standard heterosis (SH) and heterobeltiosis (HB) were estimated and expressed as percentage for all the fifteen hybrids to calculate the extent of heterosis. For estimating standard heterosis, C-152 was used as the standard variety.

$$\text{i. Relative heterosis (RH)} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

ii. Standard heterosis (SH) $= \dfrac{\overline{F_1} - \overline{SV}}{\overline{SV}} \times 100$

iii. Heterobeltiosis(HB) $= \dfrac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$

Where,

$\overline{F_1}$ = Mean value of hybrid,

$\overline{MP}$ = Mid parental value,

$\overline{SV}$ = Mean of standard variety,

$\overline{BP}$ = Mean of better parent in the particular cross

The significance of different types of heterosis was tested by the 't' test as follows.

't' for RH $= \dfrac{|F_1 - MP|}{\sqrt{3MSE / 2r}}$

't' for SH $= \dfrac{|F_1 - SV|}{\sqrt{2MSE / r}}$

't' for HB $= \dfrac{|F_1 - BP|}{\sqrt{2MSE / r}}$

Where,

MSE = estimate of error variance and

r = number of replications.

3.4.7 Generation mean analysis

The six parameter model developed by Hayman (1958) was used for generation mean analysis.

i. Development of scales

Additive (D) and dominance (H) components of genetic variance were estimated using the scaling test proposed by Mather (1949) making use of the mean and variance of six generations *viz*.,P_1, P_2, F_1, F_2, B_1 and B_2.

$$A = 2\overline{B_1} - \overline{P_1} - \overline{F_1}$$

$$V_A = 4\,V(\overline{B_1}) + V(\overline{P_1}) + V(\overline{F_1})$$

$$B = 2\overline{B_2} - \overline{P_2} - \overline{F_1}$$

$$V_B = 4\,V(\overline{B_2}) + V(\overline{P_2}) + V(\overline{F_1})$$

$$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_I} - \overline{P_2}$$

$$V_C = 16\,V(\overline{F_2}) + 4\,V(\overline{F_1}) + V(\overline{P_1}) + V(\overline{P_2})$$

$$D = 2\overline{F_2} - \overline{B_1} - \overline{B_2}$$

$$V_D = 4\,V(\overline{F_2}) + V(\overline{B_1}) + V(\overline{B_2})$$

Where, $\overline{P_1}$, $\overline{P_2}$, $\overline{F_1}$, $\overline{F_2}$, $\overline{B_1}$ and $\overline{B_2}$ are the means of respective generations over all replications and $V(P_1)$,$V(P_2)$, $V(F_1)$,$V(F_2)$, $V(B_1)$ and $V(B_2)$ are the respective variances. The standard errors of A, B, C and D were obtained as the square root of V_A, V_B, V_C and V_D.

ii. Testing for epistasis

Significance of any of the four scales indicates the inadequacy of additive - dominance model and the presence of epistasis. The ‘t’ test was used to test the significance of A, B, C and D scales.

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

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

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

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

If the calculated 't' values are found significant (> 1.96), the presence of specific types of epistasis is confirmed.

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

b. The significance of scale C indicates the presence of dominance X dominance type of non-allelic interaction.

c. The significance of scale D denotes additive X additive type of gene interaction.

d. The significance of both C and D scales reveals the presence of additive x additive and dominance X dominance type of gene interaction.

iii. Estimation of genetic components

Jinks and Jones (1958) proposed the following six parameter model to estimate the digenic interactions, when the scales A, B, C and D were significantly different from zero.

$$m = \overline{F_2}$$

$$d = \overline{B_1} - \overline{B_2}$$

$$h = \overline{F_1} - 4\,\overline{F_2} - \tfrac{1}{2}\,\overline{P_1} - \tfrac{1}{2}\,\overline{P_2} + 2\,\overline{B_1} + 2\,\overline{B_2}$$

$$i = 2\overline{B_1} + \overline{2}\,B_2 - \overline{4}\,F_2$$

$$j = (\overline{B_1} - \tfrac{1}{2}\overline{P_1}) - (\overline{B_2} - \tfrac{1}{2}\overline{P_2})$$

$$l = \overline{P_1} + \overline{P_2} + 2\overline{F_1} + 4\overline{F_2} - 4\overline{B_1} - 4\overline{B_2}$$

Where,

m = mean,

d = additive effect,

h = dominance effect,

i = additive X additive interaction,

j = additive X dominance interaction and

l = dominance X dominance interaction.

The variances of these genetic parameters were computed as follows.

$$V(m) = V\overline{F_2} \qquad V(d) = V(\overline{B_1}) + V(\overline{B_2})$$

$$V(h) = V(\overline{F_1}) + 16\,V(\overline{F_2}) + \tfrac{1}{4}V(\overline{P_1}) + \tfrac{1}{4}V(\overline{P_2}) + 4\,V(\overline{B_1}) + 4\,V(\overline{B_2})$$

$$V(i) = 4\,V(\overline{B_1}) + 4\,V(\overline{B_2}) + 16\,V(\overline{F_2})$$

$$V(j) = V(\overline{B_1}) + \tfrac{1}{4}V(\overline{P_1}) + V(\overline{B_2}) + \tfrac{1}{4}V(\overline{P_2})$$

$$V(l) = V(\overline{P_1}) + V(\overline{P_2}) + 4\,V(\overline{F_1}) + 16\,V(\overline{F_2}) + 16\,V(\overline{B_1}) + 16\,V(\overline{B_2})$$

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

Results

4. RESULTS

The results obtained from the various experiments of the present study are furnished below under the following headings.

Experiment I - Evaluation of germplasm for legume pod borer resistance

Experiment II - Evaluation of germplasm for yield

Experiment III – Evaluation of F_1' s and parents

Experiment IV – Generation mean analysis

4.1 Experiment I

4.1.1 ANALYSIS OF VARIANCE

Analysis of variance (ANOVA) for the damage parameters and related traits in cowpea revealed significant differences among the fifty genotypes for all the characters considered (Table 5). The mean values for the different legume pod borer damage measurements and the biochemical and morphological traits of the 50 cowpea genotypes are presented in Table 6 and Table 7 respectively.

4.1.1.1 Damage Parameters

Percentage of infestation of flower buds

The percentage of legume pod borer infestation of flower buds was least for T_{45} and T_{47} (18.00). T_{49} and T_{34} had 20.00% of the flower buds infested by the pest. Flower bud infestation for the genotypes T_8, T_{11}, T_{25}, T_{30}, T_{32}, T_{33}, T_{38}, T_{42}, T_{44} and T_{46} were on par with T_{45} and T_{47}. T_{20} recorded the highest percentage of flower bud infestation (70.00%), followed by T_2, T_4, T_{21} and T_{28}. Nineteen other genotypes were on par with T_{20} for the character.

Number of larvae per 25 flowers

The mean count of legume pod borer larvae per 25 flowers ranged from 7.00 to 25.00. T_{45} recorded the least count, followed by T_{47} and T_{49} (7.50). T_4, T_8, T_9, T_{11}, T_{12}, T_{14}, T_{15}, T_{18}, T_{25},T_{31}, T_{30}, T_{34}, T_{38} and T_{42} had low values and were comparable to T_{45}. Maximum observation for number of larvae per 25 flowers were noticed for T_{20}.

Table 5. ANOVA for the damage measurements, morphological and biochemical traits

Sl. No.	Characters	Mean squares	
		Treatment	Error
		df = 49	df = 49
1	Percentage infestation of flower buds	606.33 **	60.82
2	Number of larvae per 25 flowers	44.99 **	11.81
3	Percentage pod infestation	396.43 **	36.27
4	Number of larval entry / exit holes per pod	0.30 **	0.01
5	Number of damaged seeds in a sample of 25 pods	118.36 **	7.84
6	Seed damage index	1893.76 **	125.57
7	Plant resistance index	233.455**	8.69
8	Length of peduncle	29.09 **	1.43
9	Density of non-glandular trichomes on pod wall	4.37 **	0.29
10	Content of chlorophyll ‘a’ in leaf tissue	0.01 **	0.0001
11	Content of chlorophyll ‘b’	0.01 **	0.0002
12	Total chlorophyll content	0.05 **	0.0009
13	Ratio- chlorophyll ‘a’ / chlorophyll ‘b’	0.10 **	0.006

** Significant at 1 per cent level

* Significant at 5 per cent level

Table 6. Legume pod borer damage measurements and plant resistance indices of 50 cowpea genotypes

Genotype	Infestation on flower buds (%)	Number of larvae per 25 flowers	Pod infestation (%)	Number of larval entry / exit holes per pod	Number of damaged seeds per 25 pods	Seed damage index (I_{sd})	**Plant resistance index**
T_1	66.00	19.50	56.00	0.60	30.00	120.00	**48.42**
T_2	68.00	19.50	64.00	0.58	30.50	122.00	**51.42**
T_3	66.00	14.50	54.00	0.64	29.50	118.00	**44.92**
T_4	68.00	11.00	46.00	0.74	30.00	120.00	**40.84**
T_5	60.00	22.50	56.00	1.80	48.00	192.00	**61.92**
T_6	64.00	18.50	58.00	0.60	26.00	104.00	**45.92**
T_7	56.00	19.50	52.00	0.62	28.00	112.00	**45.75**
T_8	22.00	12.00	58.00	0.36	24.50	98.00	**41.67**
T_9	48.00	11.50	48.00	0.56	26.50	106.00	**39.42**
T_{10}	54.00	20.00	50.00	0.62	23.00	92.00	**42.00**
T_{11}	28.00	10.00	30.00	0.36	20.50	82.00	**28.67**
T_{12}	36.00	10.00	28.00	0.36	22.00	88.00	**29.00**
T_{13}	54.00	18.00	60.00	0.66	22.00	88.00	**43.67**
T_{14}	62.00	12.50	46.00	0.62	29.00	116.00	**40.92**
T_{15}	42.00	8.50	30.00	0.40	23.00	92.00	**29.58**
T_{16}	54.00	21.50	58.00	0.66	22.00	88.00	**44.75**
T_{17}	58.00	15.00	50.00	0.60	26.00	104.00	**41.50**
T_{18}	54.00	13.00	64.00	0.60	21.00	84.00	**41.83**
T_{19}	52.00	15.50	54.00	0.60	25.00	100.00	**42.42**
T_{20}	70.00	23.00	70.00	2.20	47.50	190.00	**66.50**
T_{21}	68.00	15.00	56.00	0.64	24.50	98.00	**42.50**
T_{22}	52.00	18.50	54.00	0.54	24.00	96.00	**43.25**
T_{23}	64.00	21.50	66.00	1.80	41.00	164.00	**60.08**
T_{24}	64.00	16.50	54.00	0.62	26.00	104.00	**43.58**
T_{25}	28.00	8.50	30.00	0.46	20.50	82.00	**27.92**

Table 6 (continued)

Genotype	Infestation on flower buds (%)	Number of larvae per 25 flowers	Pod infestation (%)	Number of larval entry / exit holes per pod	Number of damaged seeds per 25 pods	Seed damage index (I_{sd})	**Plant resistance index**
T_{26}	64.00	15.50	44.00	0.60	22.00	88.00	**37.08**
T_{27}	58.00	19.00	48.00	0.56	23.50	94.00	**41.17**
T_{28}	68.00	20.00	60.00	0.56	23.00	92.00	**45.33**
T_{29}	58.00	18.00	46.00	0.58	22.50	90.00	**39.34**
T_{30}	28.00	9.00	30.00	0.44	21.50	86.00	**28.83**
T_{31}	50.00	13.00	50.00	0.54	23.50	94.00	**38.84**
T_{32}	24.00	15.00	46.00	0.58	23.50	94.00	**38.5**
T_{33}	32.00	20.00	50.00	0.52	24.50	98.00	**43.00**
T_{34}	20.00	9.50	32.00	0.38	21.50	86.00	**29.75**
T_{35}	64.00	20.50	40.00	0.46	25.50	102.00	**40.58**
T_{36}	48.00	20.50	46.00	0.56	22.50	90.00	**40.59**
T_{37}	52.00	19.50	58.00	0.62	24.50	98.00	**45.42**
T_{38}	22.00	10.50	26.00	0.36	21.50	86.00	**28.25**
T_{39}	64.00	20.50	54.00	0.68	21.50	86.00	**42.59**
T_{40}	58.00	21.50	64.00	1.60	46.00	184.00	**62.75**
T_{41}	60.00	22.50	56.00	0.62	36.50	146.00	**54.25**
T_{42}	22.00	9.50	26.00	0.36	20.50	82.00	**27.08**
T_{43}	64.00	16.50	62.00	0.58	22.50	90.00	**43.92**
T_{44}	22.00	15.00	26.00	0.42	19.50	78.00	**29.17**
T_{45}	18.00	7.00	18.00	0.20	11.50	46.00	**17.17**
T_{46}	24.00	15.00	28.00	0.40	18.00	72.00	**28.84**
T_{47}	18.00	7.50	16.00	0.22	10.50	42.00	**16.09**
T_{48}	64.00	10.50	58.00	0.52	24.50	98.00	**40.92**
T_{49}	20.00	7.50	18.00	0.24	10.00	40.00	**16.42**
T_{50}	58.00	16.00	52.00	0.64	22.50	90.00	**40.34**
SE	5.51	2.43	4.26	0.07	1.98	7.92	**2.08**
CD	15.64	6.91	12.11	0.21	5.63	22.52	**5.92**

T_5 and T_{41} also recorded very adjacent mean values for the character. Eighteen other genotypes exhibited comparatively high counts for number of larvae per 25 flowers.

Percentage pod infestation

The percentage of pod infestation due to legume pod borer varied from 16.00 to 70.00% among the fifty genotypes. T_{47} had the minimum percentage of pod infestation followed by T_{45} and T_{49} (18.00%). Genotypes T_{12}, T_{38}, T_{42}, T_{44} and T_{46} were on par with T_{47}. Pod infestation was most severe in T_{20}, followed by T_{23}, T_2, T_{18} and T_{40}.

Number of larval entry / exit holes per pod

The number of larval bore holes per pod was least in T_{45} (0.20). T_{47} (0.22) and T_{49} (0.24) also had low values for the character. The mean values in T_8, T_{11}, T_{12}, T_{15}, T_{34}, T_{38}, T_{42} and T_{46} were comparable with that of T_{45}. The highest number of larval bore holes per pod was noticed in T_{20} (2.20) followed by T_5, T_{23} and T_{40}.

Number of damaged seeds per 25 pods

T_{49} recorded the minimum number of damaged seeds per 25 pods (10.00) followed by T_{47} (10.5) and T_{45} (11.5). T_5 had the highest number of damaged seeds (48.00), followed by T_{20} (47.5), T_{40} (46.00) and T_{23} (41.00).

Seed damage index

Seed damage index was the lowest for T_{49} (40.00) followed by T_{47} (42.00) and T_{45} (46.00). Seed damage index was highest for T_5 (192.00), followed by T_{20} (190.00) and T_{40} (184.00).

Plant resistance index

The highest plant resistance index was recorded for T_{20} (66.50). T_{40} (62.75) and T_5 (61.92) also had high plant resistance index. T_{47} recorded the least plant resistance index (16.09) which was on par with the plant resistance indices of T_{49} (16.42) and T_{45} (17.17).

From the legume pod borer resistant / tolerant genotypes with low plant resistance indices, three genotypes viz. T_{45}, T_{47} and T_{49} were selected as male parents (testers) in hybridization programme to develop F_1 hybrids (Plate 4).

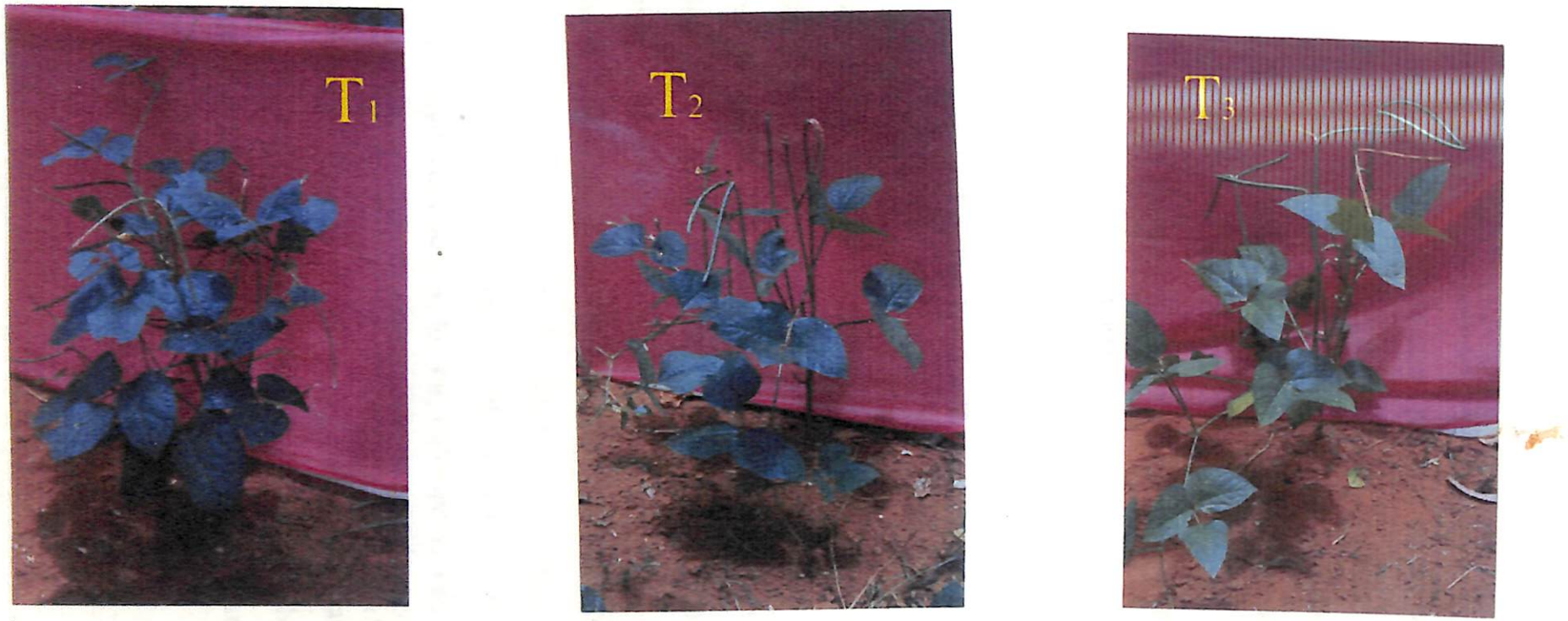


Plate 4. Selected testers

4.1.1.2 Morphological and Biochemical Traits

Length of peduncle

The peduncle length ranged from 21.20cm in T_{23} to 39.30cm in T_{30}. T_{38} and T_{42} were on par with T_{30} and T_5, T_{13} and T_{20} were on par with T_{23} for the character.

Density of non-glandular trichomes on pod wall (count per mm^2)

The non-glandular trichome count per mm^2 on the pod wall was maximum for T_{49} (6.83). T_{11} (6.67), T_{12} (6.67), T_{47} (6.50) and T_{45} (6.33) also recorded high density of non-glandular trichomes. Other genotypes comparable to T_{49} were T_8, T_{15}, T_{25}, T_{30}, T_{38} and T_{44}. The trichome density was least for T_9 (1.67) followed by T_{48} (2.16).

Content of chlorophyll 'a' in leaf tissue

The content of chlorophyll 'a' varied from 0.70 to 0.97 mg/g of leaf tissue. Content of chlorophyll 'a' was maximum in the genotypes T_{20}, T_{21}, T_{23} and T_{28}. T_2, T_3, T_4 and T_5 were on par with the highest value for the character. T_{45} recorded the minimum content of chlorophyll 'a' followed by T_{47}, T_{49} and T_{12}. The mean values for the character in T_8, T_{15}, T_{25}, T_{34}, T_{38}, T_{42} and T_{44} were comparable with T_{45}.

Content of chlorophyll 'b'

The content of chlorophyll 'b' in the leaf tissues was the highest in T_5 (0.56mg/g) followed by T_3, T_4 and T_{20} (0.55). T_2, T_{21}, T_{23} and T_{28} also exhibited high levels of chlorophyll 'b'. T_{10}, T_{14} and T_{45} (0.31) recorded the least content of chlorophyll b. Comparable low values were noticed in other fifteen genotypes.

Total chlorophyll content

The total chlorophyll content varied from 1.01 to 1.53 mg/g of leaf tissue. The highest observation was recorded for the character in T_{20}, followed by T_3, T_5 and T_{23} (1.51). The mean values in T_2,T_4, T_{21} and T_{28} were on par with T_{20}. The least content of total chlorophyll was observed for T_{45}, followed by T_{47}, T_{12}, T_{34} and T_{49}.

Ratio- chlorophyll 'a' / chlorophyll 'b'

The ratio of chlorophyll 'a' to chlorophyll 'b' was maximum in T_{14} (2.40) followed by T_{30} and T_{50}. T_5 had the least mean value for the character (1.70). Twenty three of the fifty genotypes were on par with T_5 for the character.

Table 7. Mean values for morphological and biochemical traits

Genotype	Length of peduncle (cm)	Density of non-glandular trichomes on pod wall (count /mm^2)	Leaf chlorophyll content (mg / g of leaf tissue)			
			Chl. a	Chl. b	Total chl.	Chl. a / Chl. b
T_1	28.70	2.84	0.85	0.46	1.31	1.85
T_2	29.50	3.50	0.96	0.53	1.50	1.84
T_3	30.30	2.67	0.96	0.55	1.51	1.73
T_4	30.30	2.83	0.95	0.55	1.50	1.73
T_5	22.40	2.67	0.95	0.56	1.51	1.70
T_6	28.70	3.16	0.86	0.47	1.33	1.83
T_7	30.30	3.00	0.87	0.47	1.34	1.85
T_8	34.60	6.16	0.73	0.33	1.06	2.24
T_9	29.90	1.67	0.75	0.34	1.08	2.21
T_{10}	30.40	2.83	0.75	0.31	1.06	2.41
T_{11}	29.60	6.67	0.76	0.34	1.09	2.25
T_{12}	30.00	6.67	0.71	0.33	1.04	2.17
T_{13}	22.80	5.67	0.87	0.47	1.34	1.84
T_{14}	31.20	2.83	0.75	0.31	1.06	2.40
T_{15}	30.50	6.17	0.73	0.34	1.07	2.15
T_{16}	30.10	3.33	0.83	0.48	1.31	1.75
T_{17}	30.20	3.33	0.86	0.49	1.34	1.75
T_{18}	28.70	4.50	0.89	0.46	1.35	1.91
T_{19}	29.80	4.67	0.87	0.45	1.33	1.93
T_{20}	21.60	2.83	0.97	0.55	1.53	1.76
T_{21}	29.90	3.17	0.97	0.53	1.50	1.83
T_{22}	29.60	3.00	0.85	0.48	1.33	1.75
T_{23}	21.20	2.67	0.97	0.53	1.51	1.83
T_{24}	30.00	3.33	0.85	0.47	1.31	1.82
T_{25}	35.40	5.83	0.73	0.34	1.07	2.14

Table 7 continued…

Genotype	Length of peduncle (cm)	Density of non-glandular trichomes on pod wall (count /mm^2)	Leaf chlorophyll content (mg / g of leaf tissue)			
			Chl. a	Chl. b	Total chl.	Chl. a / Chl. b
T_{26}	29.20	3.33	0.84	0.45	1.29	1.87
T_{27}	29.80	3.33	0.83	0.46	1.30	1.80
T_{28}	30.20	3.17	0.97	0.54	1.50	1.79
T_{29}	29.40	3.67	0.85	0.45	1.29	1.90
T_{30}	39.30	6.17	0.75	0.32	1.07	2.36
T_{31}	29.40	3.33	0.86	0.47	1.33	1.82
T_{32}	36.20	5.66	0.82	0.47	1.29	1.73
T_{33}	30.40	5.00	0.83	0.47	1.30	1.79
T_{34}	34.80	5.50	0.72	0.32	1.04	2.27
T_{35}	32.60	3.50	0.84	0.46	1.30	1.83
T_{36}	30.40	2.67	0.87	0.47	1.35	1.84
T_{37}	30.90	2.83	0.87	0.45	1.32	1.93
T_{38}	36.90	6.00	0.73	0.32	1.05	2.29
T_{39}	28.50	3.16	0.84	0.46	1.30	1.83
T_{40}	28.60	2.83	0.85	0.47	1.33	1.82
T_{41}	28.50	3.00	0.85	0.46	1.31	1.84
T_{42}	38.60	5.17	0.74	0.33	1.06	2.27
T_{43}	29.30	3.50	0.87	0.45	1.32	1.93
T_{44}	35.00	6.17	0.72	0.32	1.05	2.25
T_{45}	35.50	6.33	0.70	0.31	1.01	2.29
T_{46}	33.20	4.50	0.75	0.33	1.08	2.27
T_{47}	36.70	6.50	0.71	0.32	1.03	2.23
T_{48}	28.60	2.16	0.77	0.34	1.12	2.26
T_{49}	34.40	6.83	0.71	0.33	1.04	2.19
T_{50}	29.90	2.83	0.87	0.32	1.09	2.32
SE	0.85	0.38	0.01	0.01	0.02	0.06
CD	2.41	1.08	0.04	0.03	0.06	0.16

4.1.2 GENETIC PARAMETERS

Genetic parameters for the different biochemical and morphological traits are presented in Table 8. Density of non-glandular trichomes (37.60) recorded high phenotypic coefficient of variation. Content of chlorophyll ‘a’ in the leaf tissue (10.30), ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (11.70) and length of peduncle (12.75) exhibited low phenotypic coefficient of variation among the characters studied.

The genotypic coefficient of variation was maximum for density of non-glandular trichomes on pod wall (35.21). The characters *viz*., content of chlorophyll ‘a’ in the leaf tissue (9.99), ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (10.95) and length of peduncle (12.14) had low genotypic coefficient of variation also.

All the characters exhibited high heritability. Heritability was maximum for total chlorophyll content (96.67), followed by content of chlorophyll ‘b’ (96.01) and chlorophyll ‘a’ (94.09). The genetic gain was high for all characters except content of chlorophyll ‘a’ in leaf tissue. Maximum genetic gain as percentage of mean was recorded for density of non- glandular trichomes on pod wall (67.98). Genetic gain was least for content of chlorophyll ‘a’ (19.88), followed by ratio of chlorophyll ‘a’ to chlorophyll’b’ (21.20) and total chlorophyll content (26.40).

4.1.3 CORRELATION ANALYSIS

4.1.3.1 Phenotypic Correlation

The phenotypic correlation coefficients for the legume pod borer damage parameters, morphological and biochemical traits are given in Table 9. All the characters exhibited highly significant correlation with each. Percentage of flower bud infestation exhibited maximum positive correlation with plant resistance index (r = 0.7139) followed by percentage pod infestation (0.7061). Positive associations with content of chlorophyll ‘a’, chlorophyll ‘b’ and total chlorophyll were observed, whereas, significant negative correlations were noticed with peduncle length (-0.6761) and density of non-glandular trichomes on pod wall (-0.7934).

Table 8. Genetic parameters for the morphological and biochemical traits

Sl. No.	Characters	PCV	GCV	Heritability (%)	Genetic gain (%)
1	Length of peduncle	12.75	12.14	90.60	23.79
2	Density of non-glandular trichomes on pod wall	37.60	35.21	87.70	67.98
3	Content of chlorophyll ‘a’ in leaf tissue	10.30	9.99	94.09	19.88
4	Content of chlorophyll ‘b’	19.93	19.53	96.01	38.84
5	Total chlorophyll content	13.38	13.16	96.67	26.40
6	Ratio of chlorophyll ‘a’ / chlorophyll ‘b’	11.70	10.95	87.55	21.10

Phenotypic correlation coefficients of number of larvae per 25 flowers with all other damage parameters, plant resistance index (0.7821), content of chlorophyll ‘a’ (0.5972) and chlorophyll ‘b’ (0.6069) and total chlorophyll (0.6106) were also positive and significant. Peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ were negatively correlated with larval count on flowers.

Percentage pod infestation was significantly and positively correlated with plant resistance index (0.8759), content of chlorophyll ‘a’ (0.7210) and chlorophyll ‘b’ (0.6861) and total chlorophyll (0.7135). The character had negatively significant phenotypic associations with peduncle length (-0.7042), density of non-glandular trichomes (-0.6755) and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (-0.5880).

Number of larval entry / exit holes per pod was significantly and positively correlated with plant resistance index (0.7710) and content of leaf chlorophyll (a, b and total). Significant negative phenotypic correlation was noticed for the character with peduncle length (-0.6887). Seed damage index (number of damaged seeds in a sample of 25 pods) was also positively correlated with all the characters except density of non-glandular trichomes on pod wall, ratio of chlorophyll ‘a’ to chlorophyll ‘b’ and peduncle length. Highly significant association with number of damaged seeds per 25 pods and plant resistance index (0.8732) was also evident.

Plant resistance index had highly significant positive phenotypic correlations with all the damage parameters, content of chlorophyll ‘a’ (0.7471), chlorophyll ‘b’ (0.7206) and total chlorophyll content (0.7442). Significant negative correlations were noticed with peduncle length (-0.7408), density of non-glandular trichomes on pod wall (-0.6946) and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (-0.6146).

Negative associations were observed for length of peduncle with all the damage parameters and related characters except ratio of chlorophyll ‘a’ to chlorophyll ‘b’. The phenotypic correlation coefficient of peduncle length with plant resistance index was highly significant (-0.7408). Density of non-glandular trichomes also exhibited negative correlation with all the legume pod borer damage measurements,

Table 9. Phenotypic correlation for damage parameters, biochemical and morphological traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_2	0.5725**										
X_3	0.7061**	0.6201**									
X_4	0.4637**	0.4976**	0.5578**								
X_5	0.5288**	0.5475**	0.5820**	0.8351**							
X_6	0.7078**	0.7821**	0.8759**	0.7710**	0.8732**						
X_7	-0.6761**	-0.5492**	-0.7042**	-0.6887**	-0.6108**	-0.7408**					
X_8	-0.7934**	-0.5743**	-0.6755**	-0.4568**	-0.5289**	-0.6946**	0.5525**				
X_9	0.7139**	0.5972**	0.7210**	0.5837**	0.5841**	0.7471**	-0.6406**	-0.5971**			
X_{10}	0.6704**	0.6069**	0.6861**	0.5462**	0.5566**	0.7206**	-0.6130**	-0.5585**	0.9448**		
X_{11}	0.7020**	0.6106**	0.7135**	0.5729**	0.5784**	0.7442**	-0.6356**	-0.5860**	0.9862**	0.9860**	
X_{12}	-0.5625**	-0.5623**	-0.5880**	-0.4216**	-0.4495**	-0.6146**	0.5253**	0.4575**	-0.7786**	-0.9363**	-0.8694**

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Percentage 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 resistance index
X_7 Length of peduncle
X_8 Density of non-glandular trichomes on pod wall
X_9 Chlorophyll ‘a’ content
X_{10} Chlorophyll ‘b’ content
X_{11} Total chlorophyll content
X_{12} Chlorophyll ‘a’ / chlorophyll ‘b’

morphological and biochemical characters, except ratio of chlorophyll ‘a’ to ‘b’. However, peduncle length and non-glandular trichome density were positively correlated with each other (0.5525).

Content of chlorophyll ‘a’ in the leaf tissues recorded significant positive phenotypic correlation with all the legume pod borer damage measurements and plant resistance index. Density of non-glandular trichomes on pod wall and peduncle length, and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ were negatively correlated with the content of chlorophyll ‘a’ in leaf tissue. The phenotypic correlation of chlorophyll ‘b’ content with plant resistance index was also highly significant. Ratio of chlorophyll ‘a’ to ‘b’, density of non-glandular trichomes on pod wall and peduncle length were negatively correlated with the content of chlorophyll ‘b’. The characters, chlorophyll ‘a’ content and chlorophyll ‘b’ content exhibited very high correlation among each other (0.9448) and with total chlorophyll content (0.9862).

Total chlorophyll content was positively associated with all the damage parameters. The character recorded highly significant positive correlation with percentage pod infestation and plant resistance index. However, the character showed significant negative correlation with peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (-0.8694). The phenotypic correlation coefficients of ratio of chlorophyll ‘a’ to ‘‘b’ was negative with all the damage parameters. Peduncle length and density of non-glandular trichomes on pod wall were positively correlated with ratio of chlorophyll ‘a’ to ‘b’.

4.1.3.2 Genotypic Correlation

The genotypic correlation coefficients for the different damage parameters, morphological and biochemical traits are presented in Table 10.

Percentage of flower bud infestation had highly significant positive genotypic correlations with other damage parameters, plant resistance index (0.8209), content of chlorophyll ‘a’ (0.8292), chlorophyll ‘b’ (0.7784) and total chlorophyll (0.8082). Significant negative correlations were noticed with peduncle length (-0.7933), density of non-glandular trichomes on pod wall (-0.8952) and ratio of chlorophylls (-0.6925).

Table 10. Genotypic correlation for damage parameters, biochemical and morphological traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_2	0.7653**										
X_3	0.9018**	0.9046**									
X_4	0.5303**	0.7260**	0.6268**								
X_5	0.6277**	0.7204**	0.7365**	0.9359**							
X_6	0.8209**	0.9106**	0.9400**	0.8414**	0.9166**						
X_7	-0.7933**	-0.7807**	-0.7594**	-0.7520**	-0.7188**	-0.8064**					
X_8	-0.8952**	-0.7635**	-0.7797**	-0.5142**	-0.6206**	-0.7657**	0.6027**				
X_9	0.8292**	0.7788**	0.8081**	0.6266**	0.6539**	0.7962**	-0.6948**	-0.6477**			
X_{10}	0.7784**	0.8205**	0.7622**	0.5912**	0.6257**	0.7717**	-0.6634**	-0.6067**	0.9779**		
X_{11}	0.8082**	0.8042**	0.7894**	0.6122**	0.6433**	0.7830**	-0.6828**	-0.6306**	0.9944**	0.9945**	
X_{12}	-0.6925**	-0.8246**	-0.6919**	-0.4877**	-0.5232**	-0.6949**	0.6000**	0.5269**	-0.8970**	-0.9683**	-0.9380**

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Percentage 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 resistance index
X_7 Length of peduncle
X_8 Density of non-glandular trichomes on pod wall
X_9 Chlorophyll ‘a’ content
X_{10} Chlorophyll ‘b’ content
X_{11} Total chlorophyll content
X_{12} Chlorophyll ‘a’ / chlorophyll ‘b’

Number of larvae per 25 flowers had highly significant genotypic associations with all other characters studied. Positive correlation coefficients were observed for number of larvae per 25 flowers with percentage flower bud infestation, percentage pod infestation (0.9046), number of larval bore holes per pod (0.7260), seed damage index (0.7204), plant resistance index (0.9106), content of chlorophyll 'a' (0.7788) and chlorophyll 'b' (0.8205) and total chlorophyll content (0.8042). Negative associations were noticed for the character with peduncle length (-0.7807), density of non-glandular trichomes on pod wall (-0.7635) and ratio of chlorophyll 'a' to chlorophyll 'b' (-0.8246).

Percentage pod infestation was also significantly and positively correlated with all the damage parameters. Highly significant positive correlation was also noticed with plant resistance index (0.9400), content of chlorophyll 'a' (0.8081), chlorophyll 'b' (0.7622) and total chlorophyll (0.7894). The character had highly significant negative genotypic associations with peduncle length (-0.7594), density of non-glandular trichomes on pod wall (-0.7797) and ratio of chlorophyll 'a' to chlorophyll 'b' (-0.6919). Number of larval entry / exit holes per pod was also significantly and positively correlated with all the damage parameters, plant resistance index (0.8414), content of chlorophyll 'a' (0.6266), chlorophyll b (0.5912) and total chlorophyll (0.6122). Significant negative genotypic correlation was noticed for the character with peduncle length (-0.7520).

Seed damage index / number of damaged seeds in a sample of 25 pods was also positively correlated with all the characters except peduncle length (-0.7188), density of non-glandular trichomes on pod wall (-0.6206), and ratio of chlorophylls. Highly significant associations were recorded for the character with number of larvae per 25 flowers, percentage pod infestation, number of larval entry / exit holes per pod and plant resistance index (0.9166).

Plant resistance index had highly significant positive genotypic correlations with all the damage parameters, content of chlorophyll 'a' (0.7962), chlorophyll 'b' (0.7717) and total chlorophyll content (0.7830). Significant negative correlations

were noticed with peduncle length (-0.8064), density of non-glandular trichomes on pod wall (-0.7657) and ratio of chlorophyll ‘a’ to chlorophyll ‘b’ (-0.6949).

Highly significant negative genotypic associations were observed for length of peduncle with all the damage parameters. The correlation coefficients with plant resistance index was also highly significant. However, ratio of chlorophyll ‘a’ to chlorophyll ‘b’ had significant positive association with the character (0.6000).

Density of non-glandular trichomes on pod wall exhibited negative correlation with all the legume pod borer damage measurements and biochemical characters, excluding ratio of chlorophylls. Peduncle length was also positively correlated with density of non-glandular trichomes on pod wall. The correlation coefficients were highly significant with percentage flower bud infestation, number of larvae per 25 flowers, percentage pod infestation and plant resistance index.

Content of chlorophyll ‘a’ in the leaf tissues recorded significant positive genotypic correlation with all the legume pod borer damage measurements. Highly significant correlations were recorded for chlorophyll ‘a’ content with percentage of flower bud infestation, number of larvae per 25 flowers, percentage pod infestation and plant resistance index. Density of non-glandular trichomes on pod wall (-0.6477), peduncle length (-0.6948), and ratio of chlorophyll ‘a’ to ‘b’ (-0.8970) were negatively and significantly correlated with chlorophyll ‘a’ in leaf tissue.

The genotypic correlation coefficients of chlorophyll ‘b’ content was highly significant with the different damage parameters and plant resistance index. Ratio of chlorophyll ‘a’ to chlorophyll ‘b’, density of non-glandular trichomes on pod wall and peduncle length were significantly and negatively correlated with the content of chlorophyll ‘b’.

The characters, chlorophyll ‘a’ content and chlorophyll ‘b’ content exhibited very high genotypic correlation among each other (0.9779) and with total chlorophyll content (0.9944). Total chlorophyll content was positively associated with all the damage parameters. The character recorded highly significant positive correlation with percentage flower bud infestation, number of larvae per 25 flowers, percentage

pod infestation and plant resistance index. However, the character showed significant negative correlation with peduncle length (-0.6828), density of non-glandular trichomes on pod wall (-0.6306) and ratio of chlorophylls (-0.9380). The genotypic correlation coefficients of ratio of chlorophyll ‘a’ to chlorophyll ‘b’ was negative with all the damage parameters and related characters except peduncle length and density of non-glandular trichomes on pod wall.

4.1.3.3 Environmental Correlation

The environmental correlation coefficients for the damage parameters of legume pod borer, morphological and biochemical traits are given in Table 11. Number of larvae per 25 flowers was significantly and positively correlated with plant resistance index. Percentage pod infestation exhibited significant positive environmental associations with plant resistance index and negative correlations with number of damaged seeds in 25 pods and peduncle length. Plant resistance index was positively correlated with number of larvae per 25 flowers, percentage pod infestation and number of damaged seeds in a sample of 25 pods.

Chlorophyll ‘a’ content had positive environmental correlations with content of chlorophyll ‘b’ and total chlorophyll and ratio of chlorophyll ‘a’ to chlorophyll ‘b’. Chlorophyll ‘b’ content was positively correlated with content of chlorophyll ‘a’ and total chlorophyll, but negatively correlated with ratio of chlorophyll ‘a’ to ‘b’. Total chlorophyll content was positively correlated with content of chlorophyll ‘a’ and ‘b’.

4.2 Experiment II

4.2.1 ANALYSIS OF VARIANCE

There were significant differences among the genotypes for all the characters studied (Table 12). The mean values for the characters are given in Table 13.

Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 31.00 to 45.00. T_{12} was the earliest to flower. The treatments T_{13}, T_{29} and T_{44} followed T_{12} for days to 50 per cent flowering. Twenty four other genotypes were on par with T_{12} for the character. T_{22} recorded the maximum value followed by T_{30} and T_{34}.

Table 11. Environmental correlation for damage parameters, biochemical and morphological traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}
X_2	0.1585										
X_3	-0.2166	-0.0403									
X_4	0.0045	-0.2301	0.0511								
X_5	-0.0157	0.1421	-0.3421**	-0.1198							
X_6	-0.0651	0.6462**	0.4524**	-0.1754	0.4961**						
X_7	0.0518	0.0951	-0.3566**	0.0351	0.2724	-0.0149					
X_8	-0.2361	-0.1233	-0.0652	0.0929	0.1211	-0.0396	0.1420				
X_9	-0.1287	0.1266	0.0590	-0.0556	-0.1096	0.0447	0.0135	-0.1024			
X_{10}	-0.2267	-0.0583	0.0582	-0.2595	-0.2428	-0.1483	0.0941	-0.0257	0.3143*		
X_{11}	-0.2125	0.0535	0.0724	-0.1813	-0.2083	-0.0514	0.0611	-0.0832	0.8505**	0.7663**	
X_{12}	0.1557	0.1203	0.0180	0.2102	0.0690	0.1263	-0.0836	-0.0339	0.4141**	-0.6887**	-0.0998

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Percentage 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 resistance index
X_7 Length of peduncle
X_8 Density of non-glandular trichomes on pod wall
X_9 Chlorophyll ‘a’ content
X_{10} Chlorophyll ‘b’ content
X_{11} Total chlorophyll content
X_{12} Chlorophyll ‘a’ / chlorophyll ‘b’

Table 12. ANOVA for yield and related traits in cowpea

Sl. No.	Characters	Mean squares	
		Treatment	Error
		df = 49	df = 49
1	Days to 50 per cent flowering	29.60 **	10.86
2	Number of pods per plant	34.27 **	1.91
3	Number of inflorescences per plant	1.65 **	0.77
4	Number of pods per inflorescence	0.28 **	0.04
5	Plant height	47.05 **	9.28
6	Number of primary branches	1.57 **	0.18
7	Pod length	7.50 **	0.20
8	Number of seeds per pod	5.29**	0.27
9	Grain yield per plant	263.34**	12.84
10	100 seed weight	12.24**	0.19

** Significant at 1 per cent level

* Significant at 5 per cent level

Number of pods per plant

Maximum number of pods were produced on T_4 (33.30) followed by T_7 and T_8. T_{45} had the least number of pods per plant (14.15). T_{47} and T_{49} were next to T_{45}.

Number of inflorescences per plant

The highest number of inflorescences per plant was recorded by T_{20} (15.30) followed by T_{23} and T_{16}. Apart from these, T_2, T_3, T_4, T_5 and T_6 were on par with T_{20}. T_{27} had the minimum number of inflorescences (11.60) followed by T_{13} and T_{45}.

Number of pods per inflorescence

The number of pods per inflorescence ranged from 1.75 to 3.55. T_5, T_{23} and T_{16} had the maximum value. T_{45} and T_{47} recorded the least values.

Plant height

T_{17} recorded the highest mean value for plant height (73.60 cm) followed by T_{16} and T_{34}. T_2, T_8, T_{22} and T_{23} were on par with T_{17}. Plant height was least for T_4 (52.25) followed by T_{18} and T_{22}. T_{11}, T_{15}, T_{20}, T_{31}, T_{40} and T_{44} were on par with T_4.

Number of primary branches

The number of primary branches were maximum for T_{34} and T_{43} (6.70). T_{16}, T_{27}, T_{40}, T_{45} and T_{47} had comparable mean values for the character. T_{31} had the least number of primary branches (3.55) followed by T_{24}, T_{32} and T_{25}.

Pod length

Pod length varied from 9.00 to 17.55 cm. Pod length was maximum for T_{42} followed by T_7 and T_{24}. T_2, T_{15}, T_{16}, T_{25}, T_{40} and T_{46} were on par with T_{42}. The least pod length was recorded for T_{26}. T_{21} and T_{12} were the next with low pod length.

Number of seeds per pod

T_1 recorded the highest number of seeds per pod (17.35) followed by T_{42}, T_{40} and T_{25}. Minimum value was noticed for T_{26} (10.55), T_{27} and T_{36} coming next.

Grain yield per plant

Grain yield ranged from 14.20 to 69.09g. T_2 recorded the maximum grain yield per plant followed by T_8, T_6, T_4 and T_7. None of the fifty genotypes except T_8 had comparable grain yield with T_2. T_{22} had least grain yield followed by T_{21}.

Table 13. Mean values for the yield and related traits in 50 cowpea genotypes

Genotype	Days to 50 % flowering	Number of pods per plant	Number of inflorescences per plant	Number of pods per inflorescence	Plant height (cm)	Number of primary branches	Pod length (cm)	Number of seeds per pod	Grain yield per plant (g)	100 seed weight (g)
T_1	32.50	21.00	13.00	2.15	60.10	5.90	16.55	17.35	25.13	8.65
T_2	36.00	28.30	14.45	2.25	68.00	6.30	17.05	16.25	69.09	15.25
T_3	39.50	16.75	14.05	2.25	59.75	5.95	14.65	15.35	18.75	7.65
T_4	32.50	33.30	13.95	2.80	52.25	6.35	14.15	14.95	51.10	10.05
T_5	33.00	21.95	13.75	3.55	58.45	6.50	14.80	11.90	22.94	9.95
T_6	35.00	27.95	14.15	2.45	67.10	6.10	15.65	14.70	53.88	12.80
T_7	40.50	31.60	13.10	2.35	62.00	6.45	17.25	12.65	43.04	9.25
T_8	42.00	31.25	14.05	2.80	67.55	6.30	12.85	14.45	66.18	15.15
T_9	42.00	17.40	12.60	2.00	62.35	5.85	13.90	13.85	21.48	9.95
T_{10}	39.50	17.75	13.00	2.05	62.75	6.20	13.85	12.70	23.04	12.05
T_{11}	33.50	20.85	13.20	1.95	53.75	6.00	12.55	12.65	34.15	13.85
T_{12}	31.00	20.60	12.80	1.95	53.35	6.40	11.15	12.75	30.23	14.15
T_{13}	31.50	19.00	11.70	2.10	64.75	6.20	12.05	12.80	27.95	12.95
T_{14}	33.00	18.30	12.00	2.00	58.45	6.25	12.00	13.35	18.71	8.95
T_{15}	32.50	16.15	13.10	2.00	58.25	6.00	16.75	12.20	26.51	14.95
T_{16}	32.50	20.95	15.10	3.05	72.05	6.55	16.70	14.75	37.86	14.85
T_{17}	37.50	18.20	13.30	2.05	73.60	6.15	13.50	13.65	16.10	6.65
T_{18}	36.00	17.75	12.55	2.25	52.50	6.05	14.20	12.15	22.40	11.75
T_{19}	36.50	17.55	12.35	2.35	61.40	6.40	13.95	12.85	21.48	9.95
T_{20}	34.50	21.75	15.30	2.90	55.20	6.30	11.75	12.45	19.37	7.65
T_{21}	33.50	18.00	12.40	2.55	61.60	6.35	10.90	12.85	14.96	7.75
T_{22}	45.00	19.15	12.70	2.25	67.95	6.00	16.50	15.70	14.20	5.75
T_{23}	40.50	20.90	15.15	3.10	69.35	6.50	14.30	12.85	27.69	12.55
T_{24}	39.00	18.90	12.25	2.25	60.20	3.60	17.15	16.20	38.18	13.95
T_{25}	38.50	17.80	12.15	1.85	63.65	3.70	17.10	16.35	19.66	6.75

Table 13 (continued…)

Genotype	Days to 50 % flowering	Number of pods per plant	Number of inflorescences per plant	Number of pods per inflorescence	Plant height (cm)	Number of primary branches	Pod length (cm)	Number of seeds per pod	Grain yield per plant (g)	100 seed weight (g)
T_{26}	36.00	17.00	12.55	2.25	65.40	6.25	9.00	10.55	21.38	12.65
T_{27}	33.50	19.15	11.60	2.15	60.80	6.55	11.55	10.95	23.79	11.35
T_{28}	35.50	17.45	12.35	2.15	60.40	6.30	13.85	15.85	29.87	12.25
T_{29}	31.50	18.10	12.00	2.35	60.65	6.50	13.55	13.90	30.44	14.45
T_{30}	43.50	19.10	12.90	1.95	60.40	3.80	13.85	13.75	35.75	14.35
T_{31}	40.50	18.30	12.10	2.25	56.50	3.55	13.30	13.35	23.28	10.55
T_{32}	40.50	17.45	12.40	2.15	62.20	3.65	14.95	15.45	24.85	9.75
T_{33}	39.00	19.25	12.20	2.25	65.45	4.00	13.90	13.70	34.63	13.75
T_{34}	42.50	16.95	12.05	1.85	70.75	6.70	14.15	13.85	23.94	10.75
T_{35}	41.00	17.35	12.10	2.20	66.30	5.85	14.45	12.35	28.11	12.85
T_{36}	39.00	17.45	12.10	2.10	59.55	6.10	14.85	11.50	19.05	10.25
T_{37}	34.50	18.70	14.10	2.75	59.40	5.50	13.35	13.50	32.84	13.55
T_{38}	34.00	17.45	12.75	1.85	63.00	4.50	15.25	14.45	28.18	11.55
T_{39}	32.50	17.45	12.40	2.15	63.30	6.10	15.45	14.90	31.36	12.40
T_{40}	39.50	17.95	12.10	2.05	58.30	6.55	17.10	16.95	34.02	11.85
T_{41}	39.50	16.00	12.65	2.50	63.90	5.65	15.35	15.40	33.62	15.15
T_{42}	40.50	17.90	12.35	1.95	63.55	5.85	17.55	17.20	34.54	12.05
T_{43}	32.50	17.30	13.20	2.05	59.85	6.70	16.35	14.95	27.11	11.05
T_{44}	32.00	21.00	13.00	2.75	53.70	6.35	15.20	15.75	30.31	9.15
T_{45}	32.50	14.15	11.95	1.75	65.15	6.60	14.90	14.25	22.1	11.35
T_{46}	33.50	18.00	13.15	2.05	61.55	6.25	16.70	14.15	27.11	10.95
T_{47}	33.00	14.55	12.15	1.80	64.95	6.60	12.25	14.10	15.66	7.95
T_{48}	41.50	18.15	12.35	2.00	62.30	5.75	13.85	13.65	28.44	12.05
T_{49}	40.00	14.60	12.35	1.75	63.75	6.10	12.95	12.35	21.79	12.35
T_{50}	39.50	17.20	12.10	2.05	65.20	5.90	15.60	16.05	24.98	9.25
SE	2.33	0.98	0.62	0.14	2.15	0.30	0.31	0.37	2.53	0.31
CD	6.62	2.78	1.76	0.40	6.12	0.86	0.89	1.04	7.20	0.87

Hundred seed weight

100 seed weight was maximum for T_2 (15.25g).T_8, T_{15}, T_{16}, T_{29} and T_{41} were on par with T_2. T_{22} recorded low value (5.75g), followed byT_{17}, T_3 and T_{20}.

4.2.2 GENETIC PARAMETERS

The genetic parameters for grain yield and related characters are presented in Table 14. The phenotypic coefficient of variation was the highest for grain yield per plant (40.09) followed by 100 seed weight (21.97) and number of pods per plant (21.90). Number of inflorescences per plant (8.54) and plant height (8.55) recorded the minimum phenotypic coefficient of variation. Grain yield per plant (38.56) had highest genotypic coefficient of variation followed by 100 seed weight (21.66) and number of pods per plant (20.71). The least estimate was noticed for number of inflorescences per plant (5.15). Plant height (7.00) and days to 50 per cent flowering (8.34) also recorded low genotypic coefficient of variation. All the yield traits except number of inflorescences per plant (36.29) and days to 50 per cent flowering (46.33) had high heritability. These characters exhibited moderate heritability estimates. Heritability was the highest for 100 seed weight (96.96). Pod length (94.81), grain yield per plant (90.70) and number of seeds per pod (90.29) also had high heritability.

All characters except number of inflorescences per plant showed moderate to high genetic gain. The genetic advance was highest for grain yield per plant (75.67). Hundred seed weight (43.91), number of pods per plant(40.35), number of pods per inflorescence (27.70), pod length (26.37), number of branches (25.91) and number of seeds per pod (22.14) also recorded high genetic advance. Genetic advance was least for number of inflorescences per plant (6.39) followed by days to 50 per cent flowering (11.70) and plant height (11.81).

4.2.3 ASSOCIATION ANALYSIS

4.2.3.1 Correlation Analysis

4.2.3.1.1 Phenotypic Correlation

The phenotypic correlation coefficients for the different yield related characters are given in Table 15.

Table 14. Genetic parameters for yield and related traits

Sl. No.	Characters	PCV	GCV	Heritability (%)	Genetic gain (%)
1	Days to 50 per cent flowering	12.26	8.34	46.33	11.70
2	Number of pods per plant	21.90	20.71	89.42	40.35
3	Number of inflorescences per plant	8.54	5.15	36.29	6.39
4	Number of pods per inflorescence	17.88	15.52	75.32	27.70
5	Plant height (cm)	8.55	7.00	67.04	11.81
6	Number of primary branches	15.91	14.15	79.03	25.91
7	Pod length (cm)	13.49	13.14	94.81	26.37
8	Number of seeds per pod	11.90	11.31	90.29	22.14
9	Grain yield per plant (g)	40.09	38.56	90.70	75.67
10	100 seed weight (g)	21.97	21.66	96.96	43.91

Table 15. Phenotypic correlation for yield and related traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9
X_2	-0.0464								
X_3	-0.0675	0.4223**							
X_4	-0.1058	0.4322**	0.5884**						
X_5	0.2950*	-0.0711	0.0702	-0.0236					
X_6	-0.3014*	0.1269	0.1579	0.1284	0.0533				
X_7	0.1410	0.1194	0.0951	-0.0146	0.1266	-0.1554			
X_8	0.1019	0.0829	0.0091	-0.0999	0.1187	-0.2010	0.6343**		
X_9	-0.0065	0.7622**	0.3271*	0.2340	0.0741	0.0008	0.2634	0.3016*	
X_{10}	-0.0654	0.1042	0.1007	0.0527	0.0440	-0.0315	-0.0005	-0.1054	0.5872**

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Days to 50 per cent flowering

X_2 Number of pods per plant

X_3 Number of inflorescences per plant

X_4 Number of pods per inflorescence

X_5 Plant height (cm)

X_6 Number of primary branches

X_7 Pod length (cm)

X_8 Number of seeds per pod

X_9 Grain yield per plant (g)

X_{10} 100 seed weight (g)

Days to flowering recorded significant negative association with number of primary branches (-0.3014) and positive association with plant height (0.2950). Number of pods per plant showed significant positive associations with number of inflorescences per plant (0.4223), number of pods per inflorescence (0.4322) and grain yield. Number of pods per inflorescence had significant positive association with number of pods per plant and number of inflorescence per plant (0.5884).

Number of seeds per pod was significantly and positively correlated with pod length (0.6343) and grain yield per plant. Significant positive phenotypic correlations were noticed for grain yield per plant with number of pods per plant (0.7622), number of inflorescences per plant (0.3271), number of seeds per pod (0.3016) and 100 seed weight (0.5872).

Negative correlation was noticed for days to 50 per cent flowering with number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, grain yield and 100 seed weight. However, pod length and number of seeds per pod were positively correlated with days to 50 per cent flowering.

Positive correlation was noticed for plant height with all characters except number of pods per plant and number of pods per inflorescence. Pod length was positively correlated with all characters other than number of pods per inflorescence, number of primary branches and 100 seed weight. Grain yield per plant was positively correlated with plant height and pod length also.

4.2.3.1.2 Genotypic Correlation

The genotypic correlation coefficients for the yield component characters of cowpea are given in Table 16.

Days to 50 per cent flowering was positively and significantly correlated with plant height (0.4633) and negatively correlated with number of primary branches (-0.4962).

The genotypic correlation coefficients were significant and positive for number of pods per plant with number of inflorescences per plant (0.7711), number of pods

Table 16. Genotypic correlation for yield and related traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9
X_2	-0.0071								
X_3	-0.1761	0.7711**							
X_4	-0.2078	0.5642**	0.8392**						
X_5	0.4633**	-0.0510	0.0827	-0.0933					
X_6	-0.4962**	0.1624	0.3267*	0.2772	0.0858				
X_7	0.2629	0.1285	0.1710	-0.0392	0.1739	-0.1719			
X_8	0.1637	0.0813	0.0643	-0.1307	0.1292	-0.2393	0.6805**		
X_9	0.0469	0.7754**	0.5610**	0.2971*	0.0997	0.0065	0.2979*	0.2812*	
X_{10}	-0.1095	0.1225	0.1069	0.0642	0.0296	-0.0552	0.0094	-0.1142	0.6144**

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Days to 50 per cent flowering

X_2 Number of pods per plant

X_3 Number of inflorescences per plant

X_4 Number of pods per inflorescence

X_5 Plant height (cm)

X_6 Number of primary branches

X_7 Pod length (cm)

X_8 Number of seeds per pod

X_9 Grain yield per plant (g)

X_{10} 100 seed weight (g)

per inflorescence (0.5642) and grain yield (0.7754). The character recorded positive correlation with all characters except days to 50 per cent flowering and plant height.

Positive associations were noticed for number of inflorescences per plant with all characters except days to flowering. Highly significant positive correlations were noticed for the character with number of pods per inflorescence (0.8392), number of primary branches (0.3267) and grain yield (0.5610).

Number of pods per inflorescence showed significant positive associations with number of pods per plant, number of inflorescences per plant and grain yield (0.2971).

Significant positive correlation was recorded between pod length and number of seeds per pod (0.6805). Pod length was positively correlated with all characters except number of pods per inflorescence and number of branches.

Number of seeds per plant was positively and significantly correlated with pod length (0.6805) and grain yield (0.2812). Plant height was positively correlated with all characters except number of pods per plant and number of pods per inflorescence.

Significant positive genotypic correlation coefficients were noticed for grain yield per plant with number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length (0.2979), number of seeds per pod and 100 seed weight (0.6144).

Hundred seed weight recorded non-significant correlation coefficients with all characters except grain yield per plant (0.6144).

4.2.3.1.3 Environmental Correlation

Environmental correlation coefficients for the different characters are presented in Table 17. Number of pods per plant had significant positive environmental correlation with grain yield per plant and number of seeds per pod.

Positive correlation was noted for number of inflorescences per plant with number of pods per inflorecence. Number of branches per plant was negatively and significantly correlated with number of pods per inflorescence.

Table 17. Environmental correlation for yield and related traits

Character	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9
X_2	-0.1756								
X_3	0.0081	-0.0654							
X_4	0.0464	-0.1908	0.3774**						
X_5	0.0876	-0.1692	0.0641	0.1496					
X_6	-0.0034	-0.0647	-0.0465	-0.3756**	-0.0349				
X_7	-0.1992	0.0143	-0.0283	0.1630	-0.0925	-0.0636			
X_8	-0.0174	0.0973	-0.1114	0.0510	0.1013	0.0071	0.0672		
X_9	-0.1653	0.6440**	0.0215	-0.0762	-0.0210	-0.0334	-0.1854	0.4964**	
X_{10}	0.0627	-0.1748	0.2679	-0.0252	0.2006	0.2101	-0.2395	0.0260	0.2066

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Days to 50 per cent flowering

X_2 Number of pods per plant

X_3 Number of inflorescences per plant

X_4 Number of pods per inflorescence

X_5 Plant height (cm)

X_6 Number of primary branches

X_7 Pod length (cm)

X_8 Number of seeds per pod

X_9 Grain yield per plant (g)

X_{10} 100 seed weight (g)

Table 18. Direct and indirect effects of six component characters on grain yield

Characters	X_1	X_2	X_3	X_4	X_5	X_6	Total genotypic correlation coefficient
X_1	**0.736**	0.045	-0.096	0.001	0.021	0.068	0.775
X_2	0.568	**0.058**	-0.143	0.002	0.016	0.060	0.561
X_3	0.415	0.048	**-0.169**	-0.001	-0.033	0.037	0.297
X_4	0.094	0.010	0.007	**0.010**	0.172	0.005	0.298
X_5	0.060	0.004	0.021	0.007	**0.253**	-0.064	0.281
X_6	0.090	0.006	-0.011	0.000	-0.029	**0.558**	0.614

R^2 = 0.0305

Values on principal diagonal indicate direct effects

X_1 Number of pods per plant

X_2 Number of inflorescences per plant

X_3 Number of pods per inflorescence

X_4 Pod length (cm)

X_5 Number of seeds per pod

X_6 100 seed weight (g)

Grain yield per plant recorded significant positive environmental correlations with number of pods per plant and number of seeds per pod.

4.2.3.2 Path Analysis

The six characters viz., number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, number of seeds per pod and 100 seed weight were selected for path coefficient analysis. The direct and indirect effects of the selected characters on grain yield are estimated and given in Table 18.

Number of pods per plant exhibited the maximum positive direct effect on grain yield (0.736) followed by 100 grain weight (0.558) and number of seeds per pod (0.253). Pod length (0.010) and number of inflorescences per plant (0.058) had low positive direct effect on grain yield. Negative direct effect was noticed for number of pods per inflorescence (-0.169) on grain yield.

Number of inflorescences per plant had high positive indirect effect on grain yield through number of pods per plant (0.568). Number of pods per inflorescence also exhibited the highest positive indirect effect on grain yield through number of pods per plant (0.415).

Negative indirect effects on grain yield were noticed for number of pods per plant (-0.096), number of inflorescences per plant (-0.143) and hundred seed weight (-0.011) through number of pods per inflorescence.

Pod length had positive indirect effect on grain yield through all the other five characters. Number of seeds per pod exhibited negative indirect effect on yield per plant through 100 seed weight (-0.064). Hundred seed weight also had negative indirect effect on grain yield through number of seeds per pod (-0.029).

4.2.4 SELECTION INDEX

The selection indices for the fifty genotypes are given in Table 19. The selection indices were worked out on the basis of yield and six compenent characters viz., number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, number of seeds per pod and 100 seed weight.

Table 19. Selection indices for the 50 genotypes

Genotypes	Index value	Rank
T_1	229.27	20
T_2	331.14	1
T_3	196.16	44
T_4	294.08	4
T_5	224.43	24
T_6	295.01	3
T_7	278.16	5
T_8	321.44	2
T_9	202.87	38
T_{10}	211.74	32
T_{11}	237.10	13
T_{12}	228.31	21
T_{13}	219.18	29
T_{14}	191.04	47
T_{15}	230.13	19
T_{16}	269.01	6
T_{17}	184.87	48
T_{18}	210.41	33
T_{19}	202.86	39
T_{20}	200.26	41
T_{21}	179.25	49
T_{22}	195.87	45
T_{23}	236.34	14
T_{24}	259.17	7
T_{25}	203.63	36

Genotypes	Index value	Rank
T_{26}	191.13	46
T_{27}	203.12	37
T_{28}	226.84	22
T_{29}	233.58	16
T_{30}	242.01	11
T_{31}	208.03	34
T_{32}	213.59	31
T_{33}	239.81	12
T_{34}	207.46	35
T_{35}	221.28	27
T_{36}	199.33	42
T_{37}	236.03	15
T_{38}	222.26	26
T_{39}	232.23	18
T_{40}	243.60	10
T_{41}	243.79	9
T_{42}	246.44	8
T_{43}	224.16	25
T_{44}	232.96	17
T_{45}	202.00	40
T_{46}	225.20	23
T_{47}	173.99	50
T_{48}	221.06	28
T_{49}	196.94	43
T_{50}	213.74	30

Among the fifty genotypes, T_2 (331.14) ranked first with the highest index value, followed by T_8 (321.44), T_6 (295.01), T_4 (294.08), T_7 (278.16), T_{16} (269.01), T_{24} (259.17), T_{42} (246.44), T_{41} (243.79) and T_{40} (243.60). The genotype with the least index value was T_{47} (173.99), with T_{21} (179.25) and T_{17} (184.87) coming next to T_{47}.

From the superior genotypes with high selection indices, five genotypes viz., T_2, T_4, T_6, T_7 and T_8 were selected for hybridization programme as female parents (lines) to develop F_1 hybrids (Plate 5).

4.2.5 GENETIC DIVERGENCE ANALYSIS

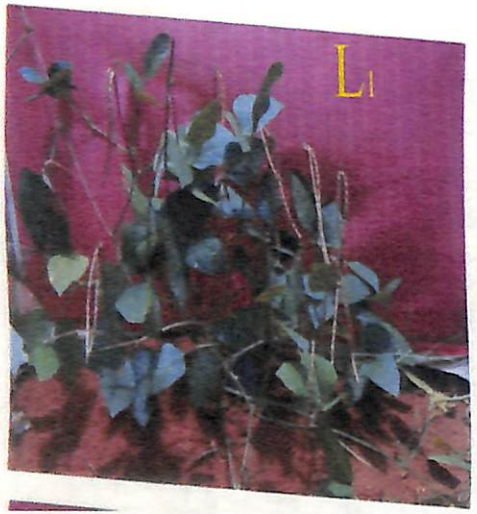
The fifty genotypes of cowpea were subjected to genetic divergence analysis following Mahalanobis D^2 statistic. The clustering was done based on yield and six correlated characters, number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, number of seeds per pod, grain yield per plant and 100 seed weight. The fifty genotypes were grouped into ten clusters based on Mahalanobis D^2 statistic. The clustering pattern of the genotypes is given in Table 20.

Cluster II was the largest one with twenty genotypes, followed by cluster I with sixteen genotypes. Clusters III and IV comprised of three genotypes each and clusters V and VI included two genotypes each. Four clusters, VII, VIII, IX and X were the smallest with only one genotype each.

The intra and intercluster distances among the ten clusters are given in Table 21. The intracluster distance increased with cluster size. Cluster VI recorded the highest intracluster distance (15.48), followed by cluster IV (12.82), clusterIV (12.70) and cluster II (12.57). Cluster III (10.44) had lower intracluster distance.

The intercluster distance was maximum between clusters I and VIII (84.46). High intercluster distance was noticed among clusters V and VIII (80.51), clusters I and IV (71.16), clusters IV and V (64.91), clusters VIII and X (60.75) and clusters I and VII (60.62).

Table 22 shows the cluster mean values for the seven yield traits. Cluster VIII had the highest cluster mean value for number of pods per plant (31.60), followed by



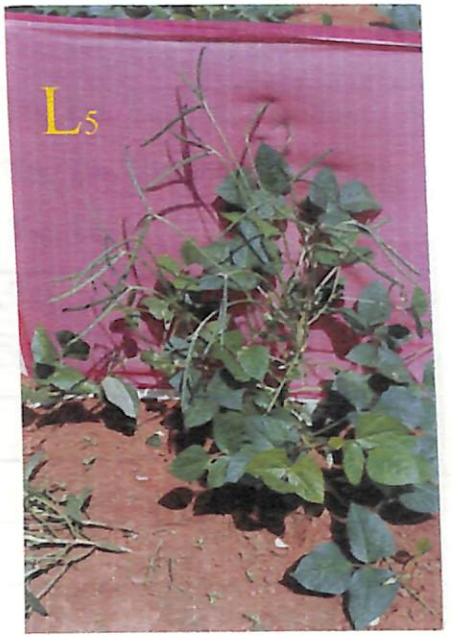


Plate 5. Selected lines

Table 20. Clustering pattern of the fifty genotypes

Cluster number	Number of genotypes	Genotypes
I	16	T_1, T_9, T_{22}, T_{24}, T_{25}, T_{28}, T_{32}, T_{34}, T_{38}, T_{39}, T_{40}, T_{41}, T_{42}, T_{45}, T_{47}, T_{50}
II	20	T_{10}, T_{12}, T_{13}, T_{14}, T_{15}, T_{17}, T_{18}, T_{19}, T_{21}, T_{26}, T_{29}, T_{30}, T_{31}, T_{33}, T_{35}, T_{36}, T_{44}, T_{46}, T_{48}, T_{49}
III	3	T_{16}, T_{20}, T_{23}
IV	3	T_4, T_6, T_8
V	2	T_3, T_{43}
VI	2	T_5, T_{11}
VII	1	T_2
VIII	1	T_7
IX	1	T_{27}
X	1	T_{37}

Table 21. Average inter and intra-cluster D^2 values among the ten clusters (D values in paranthesis)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**131.62 (11.47)**	569.92 (23.87)	3007.76 (54.84)	5064.73 (71.16)	395.59 (19.89)	2178.31 (46.67)	3674.48 (60.62)	7133.71 (84.46)	1374.10 (37.07)	1391.38 (37.30)
II		**158.04 (12.57)**	1590.42 (39.88)	2793.09 (52.85)	537.15 (23.18)	780.70 (27.94)	1960.34 (44.28)	4155.69 (64.46)	408.25 (20.21)	555.96 (23.58)
III			**108.91 (10.44)**	1562.99 (39.53)	1691.90 (41.13)	553.49 (23.53)	945.45 (30.75)	3148.79 (56.11)	1962.66 (44.30)	350.71 (18.73)
IV				**164.27 (12.82)**	4213.87 (64.91)	1000.51 (31.63)	306.94 (17.52)	476.46 (21.83)	1965.45 (44.33)	1976.49 (44.45)
V					**161.19 (12.70)**	1525.82 (39.06)	2812.86 (53.04)	6481.87 (80.51)	1518.23 (38.96)	607.37 (24.64)
VI						**239.52 (15.48)**	668.47 (25.85)	2006.18 (44.79)	623.68 (24.97)	371.97 (19.29)
VII							**0.00**	1291.42 (35.94)	1658.37 (40.72)	1115.55 (33.40)
VIII								**0.00**	2682.72 (51.79)	3690.34 (60.75)
IX									**0.00**	1034.88 (32.17)
X										**0.00**

Figures along the diagonal indicate intracluster values

Table 22. Cluster means for the yield traits

Clusters	Number of pods per plant	Number of inflorescences per plant	Number of pods per inflorescence	Pod length (cm)	Number of seeds per pod	Grain yield per plant (g)	100 seed weight (g)
I	17.42	12.37	2.05	15.48	15.62	26.37	10.38
II	18.08	12.50	2.16	13.50	13.02	25.08	11.63
III	21.20	14.22	3.02	14.25	13.35	28.31	11.68
IV	30.83	14.05	2.68	14.22	14.70	57.05	12.67
V	17.03	13.63	2.15	15.50	15.15	22.93	9.35
VI	21.40	13.48	2.75	13.68	12.28	28.55	11.9
VII	28.30	14.45	2.25	17.05	16.25	69.09	15.25
VIII	31.60	13.10	2.35	17.25	12.65	43.04	9.25
IX	19.50	11.60	2.15	11.55	10.95	23.79	11.35
X	18.70	14.10	2.75	13.35	13.30	32.84	13.55

cluster IV (30.83). Cluster I (17.42), cluster II (18.08), cluster V (17.03), cluster IX (19.15) and cluster X (18.70) had low number of pods per plant.

Number of inflorescences per plant were high in cluster III (14.22), cluster IV (14.05), cluster VII (14.45) and cluster X (14.10). Cluster IX recorded the least number of inflorescences per plant (11.60).

Cluster III exhibited the maximum number of pods per inflorescence (3.02), followed by clusters VI and X (2.75). Cluster I recorded the minimum mean value of 2.05 pods per inflorescence.

Pod length was high in cluster VII (17.05) and VIII (17.25). The least pod length was noticed in cluster IX (11.55). Cluster VII recorded the maximum mean value for number of seeds per pod (16.25), followed by cluster I (15.62) and cluster V (15.15). The minimum mean value for the character was in cluster IX.

Grain yield per plant was the highest in cluster VII (69.09), followed by cluster IV (57.05) and cluster VIII (43.04). Cluster V (22.93) and cluster IX (23.79) recorded low grain yield per plant. Cluster VII also had the highest mean value for 100 seed weight (15.25), followed by cluster X (13.55) and cluster IV (12.67). Cluster VIII had the minimum mean value for 100 seed weight (9.25).

4.3 Experiment III

Results obtained from line X tester analysis of variance revealed significant variation among treatments and parents for almost all the characters (Table 23). Significant differences were noticed among treatments for all characters except number of branches per plant. For crosses also, only number of branches were not significantly different. Parents exhibited significant variation for all the characters. The mean squares of interaction effect of parents and crosses were not significant for number of larval bore holes per pod, number of damaged seeds in 25 pods, non-glandular trichome density, leaf protein content and crude fibre content of pods. Lines X testers interaction mean squares were also significant for all character except number of branches per plant.

Table 23. ANOVA for line X tester analysis in cowpea (Mean squares)

Source	Replication	Treatments	Parents	Crosses	Parent Vs cross	Lines	Testers	Lines X Testers	Error
Df	2	22	7	14	1	4	2	8	44
X_1	2.45	16.79**	21.12**	9.82**	83.99**	5.03	2.07	14.15**	3.06
X_2	4.27	250.30**	233.38**	163.24**	1587.6**	59.86	290.79	183.04**	1.83
X_3	1.47	22.26**	8.27**	24.73**	85.52**	22.60	22.73	26.30**	0.64
X_4	0.02	0.53**	0.68**	0.45**	0.70**	0.34	0.31	0.54**	0.04
X_5	5.11	55.85**	43.11**	60.43**	80.81**	78.19	5.22	65.35**	11.2
X_6	0.13	0.38	0.51*	0.11	3.22**	0.08	0.29*	0.07	0.22
X_7	0.65	5.02**	6.10**	4.52**	4.51**	3.17	0.51	6.20**	0.25
X_8	0.14	6.45**	9.34**	4.29**	16.55**	3.91	0.13	5.52**	0.17
X_9	24.00	1114.5**	1338.28**	595.42**	6815.9**	267.90	887.06	686.28**	10.88
X_{10}	0.23	3.47**	5.46**	1.25**	20.67**	0.48	0.03	1.93**	0.18
X_{11}	30.84	381.53**	457.81**	352.66**	251.83**	356.09	196.62	389.96**	23.8
X_{12}	8.80	119.26**	151.28**	105.23**	91.62**	104.59	93.89	108.39**	8.72
X_{13}	4.58	282.02**	371.81**	251.75**	77.29*	367.56	35.29	247.96**	45.5
X_{14}	0.001	0.021**	0.031**	0.017**	0.002	0.009	0.002	0.023**	0.004
X_{15}	9.44	43.90**	83.47**	26.61**	8.87	20.92	11.02	33.36**	4.84
X_{16}	0.55	86.30**	53.23**	108.24**	10.46*	110.68	97.36	109.75**	2.47
X_{17}	0.03	5.33**	10.39**	3.17**	0.01	1.22	0.45	4.82**	0.11
X_{18}	0.01	0.17**	0.25**	0.14**	0.13**	0.24	0.06	0.11**	0.02
X_{19}	0.12	4.17**	6.11**	3.49**	0.15	4.45	0.41	3.78**	0.05
X_{20}	0.01	2.44**	4.09**	1.74**	0.74**	2.05	0.01	1.98**	0.07
X_{21}	0.01	2.21**	1.88**	2.53**	0.14*	2.73	1.02	2.82**	0.03
X_{22}	0.01	0.19**	0.28**	0.17**	0.00	0.21	0.07	0.17**	0.01

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Days to 50 % flowering
X_2 Number of pods per plant
X_3 Number of inflorescences per plant
X_4 Number of pods per inflorescence
X_5 Plant height (cm)
X_6 Number of branches per plant
X_7 Pod length (cm)
X_8 Number of seeds per pod
X_9 Grain yield per plant (g)
X_{10} 100 seed weight (g)
X_{11} Percentage flower bud infestation
X_{12} Number of larvae per 25 flowers
X_{13} Percentage pod infestation
X_{14} Number of larval bore holes per pod
X_{15} Number of damaged seeds in 25 pods
X_{16} Peduncle length (cm)
X_{17} Density of non- glandular trichomes on od wall
X_{18} Leaf chlorophyll content (mg/g)
X_{19} Leaf protein content (mg/g)
X_{20} Pod protein content (mg/g)
X_{21} Seed protein content (mg/g)
X_{22} Crude fibre content (%)Table 23.

4.3.1 MEAN PERFORMANCE OF PARENTS AND HYBRIDS

The mean values for the different characters of the eight parents and 15 hybrids are given in Tables 24 and 25 respectively.

Days to 50 per cent flowering

Among the lines, L_1, L_2 and L_3 recorded the maximum days to flowering (35.00). L_5 showed the minimum value (31.00). T_3 was the earliest to flower among the testers (37.67), while T_2 was the last to flower (36.00). L_2 X T_1 (39.00) took the maximum days to flower among the crosses, which was on par with L_1 X T_1, L_1 X T_3, L_5 X T_1 and L_5 X T_2. Minimum days to flower was noticed in L_2 X T_2 and L_4 X T_1 (30.00), which was on par with L_1 X T_2 and L_5 XT_3.

Number of pods per plant

Number of pods were maximum for L_2 (38.37) and least for L_4 (26.30) in the lines. T_2 and T_3 recorded 15.30 pods per plant. Among the crosses, L_4 X T_3 (47.23) produced maximum number of pods followed by L_2 X T_2 (46.57).

Number of inflorescences per plant

L_1 exhibited the highest number of inflorescences per plant among the testers (14.67), while L_2 produced only 12.53 inflorescences per plant. The number of inflorescences in testers ranged from 11.47 in T_3 to 10.83 in T_1, while in the crosses, it ranged from 12.40 in L_3 X T_1 to 24.23 in L_2 X T_2.

Number of pods per inflorescence

The number of pods per inflorescence in lines ranged from 2.50 in L_5 to 3.17 in L_2 and in testers, from 1.83 in T_2 to1.93 in T_3. In the crosses, the number of pods per inflorescence (Plate 6) was highest in L_4 X T_3 (3.43) and minimum in L_2 X T_3 (2.17).

Plant height (cm)

Maximum plant height was noticed for L_3 (69.00) in the lines and minimum for L_5 (56.60). The tallest tester was T_1 (60.77). Plant height was maximum in L_3 X T_2 (72.47) among the crosses which was on par with L_5 X T_1 and L_5 X T_2, and minimum in L_2 X T_2 (56.87).

Table 24. Mean performance of parents

Character	L_1	L_2	L_3	L_4	L_5	Mean	SE	CD (0.05)	T_1	T_2	T_3	Mean	SE	CD (0.05)
X_1	35.00	35.00	35.00	33.67	31.00	33.93	0.58	1.52	38.33	39.00	37.67	38.33	0.45	1.18
X_2	28.13	38.37	30.80	26.30	30.93	30.91	0.45	1.18	15.13	15.30	15.30	15.24	0.35	0.92
X_3	14.67	12.53	14.53	14.23	14.33	14.06	0.27	0.70	10.83	11.10	11.47	11.13	0.21	0.54
X_4	2.57	3.17	2.70	2.60	2.50	2.71	0.17	0.45	1.87	1.83	1.93	1.88	0.05	0.23
X_5	63.97	63.77	69.00	65.03	56.60	63.67	1.11	2.92	60.77	59.90	60.60	60.42	0.86	2.26
X_6	6.67	6.50	6.67	6.50	6.50	6.57	0.16	0.41	5.67	5.80	5.90	5.79	0.12	0.32
X_7	16.07	15.97	16.17	16.43	12.73	15.47	0.17	0.44	13.83	14.13	13.73	13.90	0.13	0.34
X_8	16.23	17.13	16.4	15.13	12.93	15.56	0.14	0.36	13.2	13.3	12.93	13.14	0.11	0.28
X_9	59.09	68.23	73.82	54.12	43.85	59.82	1.10	2.88	22.83	24.22	21.48	22.84	0.85	0.33
X_{10}	13.03	11.33	13.67	13.53	10.03	12.32	0.14	0.37	10.83	11.73	11.07	11.21	0.11	0.29
X_{11}	40.00	33.33	41.33	33.33	28.00	35.20	1.63	4.26	12.00	10.67	16.00	12.87	1.26	3.30
X_{12}	21.67	16.67	17.33	16.67	20.67	18.60	0.98	2.58	5.33	5.00	5.67	5.33	0.76	2.00
X_{13}	34.67	36.00	34.67	32.00	24.00	32.27	1.31	3.44	10.67	12.00	13.33	12.00	1.02	2.66
X_{14}	0.32	0.36	0.32	0.36	0.29	0.33	0.02	0.05	0.16	0.15	0.13	0.15	0.02	0.04
X_{15}	21.67	17.00	16.67	20.67	18.33	18.87	0.73	1.92	9.67	7.67	10.67	9.34	0.57	1.49
X_{16}	27.13	30.80	26.43	26.37	28.07	27.76	0.52	1.37	36.1	35.00	35.17	35.42	0.41	1.06
X_{17}	3.22	3.66	3.66	3.11	5.33	3.80	0.11	0.29	7.11	7.00	7.33	7.15	0.09	0.23
X_{18}	1.67	1.58	1.51	1.62	1.56	1.59	0.04	0.11	1.05	1.03	1.04	1.04	0.03	0.09
X_{19}	22.17	21.80	21.67	22.10	21.43	21.85	0.07	0.19	19.17	18.87	19.33	19.12	0.06	0.15
X_{20}	22.33	21.13	21.06	22.10	21.03	21.53	0.09	0.22	19.37	19.93	19.23	19.51	0.07	0.17
X_{21}	22.10	21.87	21.83	22.00	21.77	21.91	0.05	0.14	20.47	20.47	20.27	20.40	0.04	0.11
X_{22}	1.95	1.99	2.00	1.95	2.01	1.98	0.02	0.05	2.58	2.47	2.63	2.56	0.02	0.04

X_1 Days to 50 % flowering
X_2 Number of pods per plant
X_3 Number of inflorescences per plant
X_4 Number of pods per inflorescence
X_5 Plant height (cm)
X_6 Number of branches per plant
X_7 Pod length (cm)
X_8 Number of seeds per pod
X_9 Grain yield per plant (g)
X_{10} 100 seed weight (g)
X_{11} Percentage flower bud infestation
X_{12} Number of larvae per 25 flowers
X_{13} Percentage pod infestation
X_{14} Number of larval bore holes per pod
X_{15} Number of damaged seeds in 25 pods
X_{16} Peduncle length (cm)
X_{17} Density of non- glandular trichomes on pod wall
X_{18} Leaf chlorophyll content (mg/g)
X_{19} Leaf protein content (mg/g)
X_{20} Pod protein content (mg/g)
X_{21} Seed protein content (mg/g)
X_{22} Crude fibre content (%)

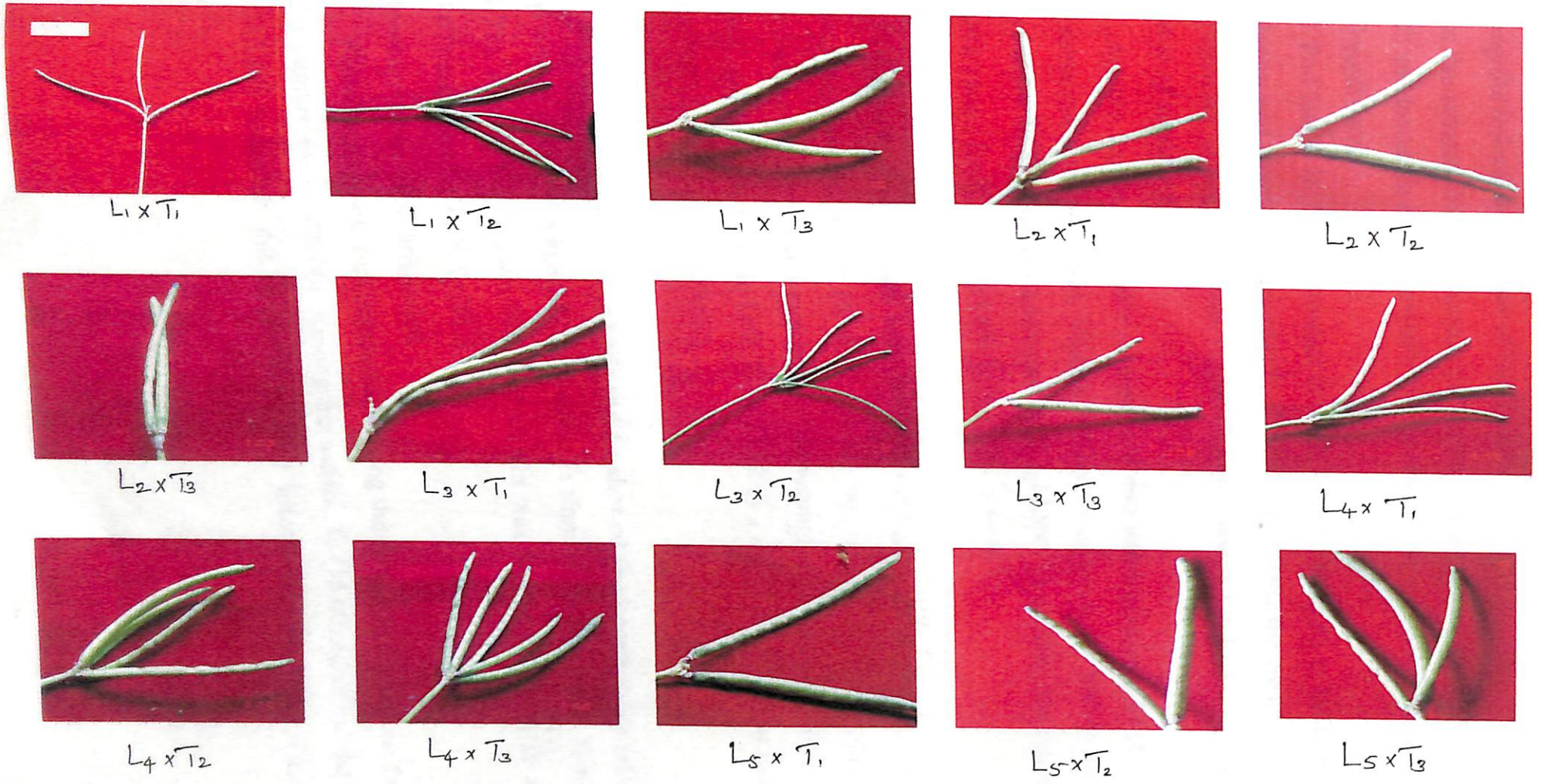


Plate 6. Inflorescence characters of the crosses

Number of branches per plant

L_1 and L_3 recorded 6.67 branches per plant, while for the other lines it was 6.50. Among the testers, the number of branches per plant ranged from 5.67 in T_1 to 5.90 in T_3. In the crosses, highest number of branches was noticed for L_3 X T_1 and L_3 X T_3 (6.97) and lowest in L_1 X T_3 (6.60). All the crosses were on par with each other.

Pod length (cm)

Pod length in the lines varied from 12.73 in L_5 to 16.43 in L_4. In the testers, the maximum pod length was recorded by T_2 (14.13). Among the crosses, pod length was maximum for L_3 X T_2 and L_4 X T_3 (16.43) and minimum in L_5 X T_3 (12.87).

Number of seeds per pod

Among the lines, number of seeds per pod was highest for L_2 (17.13), while it was minimum for L_5 (12.93). Maximum number of seeds per pod in the testers was recorded by T_2 (13.30) and minimum by T_3 (12.93). In crosses, the number of seeds per pod varied from 13.47 in L_5 X T_3 to 17.50 in L_3 X T_1.

Grain yield per plant (g)

Highest grain yield was recorded by L_3 (73.82), followed by L_2 (68.23), while L_5 was the lowest yielder (43.85). Among the testers T_2 (24.22) and T_3 (21.48) recorded the maximum and minimum yield respectively. Grain yield per plant in the crosses ranged from 50.35 in L_3 X T_3 to 97.82 in L_4 X T_3. L_4 X T_3 was followed by L_1 X T_2 (87.15) and L_2 X T_2 (79.01).

Hundred seed weight (g)

L_3 showed the highest (13.67) and L_5 showed the lowest value (10.03) for 100 seed weight among the lines. In the testers, T_1 showed the maximum 100 seed weight (11.73). Among the crosses, 100 seed weight was highest for L_3 X T_2 and L_5 X T_1 (13.67) and least for L_5 X T_3 (11.37).

Percentage flower bud infestation

Percentage flower bud infestation among the lines was maximum for L_3 (41.33) and minimum for L_5 (28.00). Among the testers, T_2 (16.00) recorded the highest and T_2 (10.67) recorded the least flower bud infestation. L_1 X T_3 showed highest

percentage of flower bud infestation (46.67), while the least flower bud infestation was noticed in L_4 X T_3 and L_1 X T_2 (13.33), which were on par with L_2 X T_2.

Number of larvae per 25 flowers

L_1 exhibited the highest values for the character (21.67), while L_2 and L_4 exhibited least number of larvae per 25 flowers (16.67). In the testers, T_3 recorded the highest (5.67) and T_2 (5.00) recorded the least values. Out of the crosses, L_1 X T_3 and L_5 X T_3 (21.33) recorded the maximum value, while L_1 X T_2 (5.33) recorded the minimum value. L_1 X T_2 was on par with the crosses L_2 X T_2 and L_4 X T_3 (5.67).

Percentage pod infestation

Pod infestation percentage was highest for L_2 (36.00) and lowest for L_5 (24.00) in the lines. In the testers, T_3 (13.33) recorded the highest and T_1 (10.67) recorded the minimum percentage pod infestation. Highest percentage of pod infestation in the crosses were noticed in L_3 X T_2 (42.67) and the least in L_2 X T_2 (12.00). L_1 X T_2 and L_4 X T_3 were on par with the least infestation.

Number of larval entry/ exit holes per pod

The number of larval entry/ exit holes per pod was highest in L_2 and L_4 (0.36) and lowest in L_5 (0.29) in the lines. In the testers, mean values for the character varied from 0.16 in T_1 to 0.13 in T_3. Mean value for the character in the crosses ranged from 0.13 in L_4 X T_3 to 0.40 in L_4 X T_2.

Number of damaged seeds in 25 pods

Among the lines, L_1 (21.67) and L_3 (16.67) recorded the maximum and minimum number of damaged seeds in 25 pods. Among the testers, T_3 recorded the highest (10.67) and T_2 (7.67) recorded the least mean values. In the case of crosses, the number of damaged seeds per 25 pods varied from 10.67 in L_1 X T_2 and L_4 X T_3 to 20.67 in L_5 X T_2. L_2 X T_2 was on par with minimum infestation.

Length of peduncle (cm)

Length of peduncle was maximum for L_2 (30.80) and least for L_4 (26.37) in the lines. In the testers peduncle length varied from 36.10 in T_1 to 35.00 in T_2. Among

Table 25. Mean performance of crosses

Character	L_1XT_1	L_1XT_2	L_1XT_3	L_2XT_1	L_2XT_2	L_2XT_3	L_3XT_1	L_3XT_2	L_3XT_3	L_4XT_1	L_4XT_2	L_4XT_3	L_5XT_1	L_5XT_2	L_5XT_3	Mean	SE	CD (0.05)
X_1	34.00	32.00	35.00	36.00	30.00	33.00	32.33	33.67	33.67	30.00	33.67	33.00	35.67	35.00	32.00	33.27	1.01	2.04
X_2	32.77	45.63	32.90	33.50	46.57	24.57	27.40	43.20	25.13	34.30	33.07	47.23	31.93	32.23	36.13	35.10	0.78	1.58
X_3	14.93	14.40	16.07	15.60	24.23	12.83	12.40	13.77	13.10	12.67	15.47	17.57	15.43	15.30	15.73	15.30	0.46	0.93
X_4	2.53	3.33	2.37	2.50	2.50	2.17	2.70	3.13	2.20	2.43	2.57	3.43	2.47	2.33	2.43	2.61	0.11	0.23
X_5	64.80	59.53	64.93	65.83	56.87	66.50	65.90	72.47	65.03	58.40	64.63	62.03	71.87	69.63	62.47	64.73	1.93	3.89
X_6	6.90	6.83	6.60	6.83	6.67	6.53	6.97	6.63	6.97	6.90	6.63	6.67	6.80	6.73	6.27	6.72	NS	0.55
X_7	16.07	16.17	16.20	15.70	13.40	15.77	15.90	16.43	15.53	13.07	16.10	16.43	15.63	16.03	12.87	15.42	0.29	0.59
X_8	15.67	17.40	15.90	15.67	14.03	16.37	17.50	16.03	15.60	13.70	16.27	16.67	15.83	15.20	13.47	15.69	0.24	0.49
X_9	63.54	87.15	60.84	67.17	79.01	55.34	58.58	85.81	50.35	55.24	65.37	97.82	62.04	60.70	53.38	66.82	1.90	3.85
X_{10}	13.23	12.93	13.63	13.40	12.40	13.47	12.80	13.67	13.33	12.13	13.33	13.27	13.67	13.17	11.37	13.05	0.24	0.49
X_{11}	25.33	13.33	46.67	25.33	14.67	29.33	41.33	38.67	33.33	40.00	30.67	13.33	41.33	40.00	29.34	30.84	2.82	5.69
X_{12}	20.00	5.33	21.33	17.33	5.67	11.33	17.33	20.00	20.00	19.67	18.00	5.67	18.67	19.00	21.33	16.04	1.71	3.44
X_{13}	29.33	14.67	40.00	26.00	12.00	21.33	30.67	42.67	37.33	26.67	30.67	13.33	29.33	26.67	22.67	26.89	2.27	4.59
X_{14}	0.27	0.19	0.29	0.29	0.15	0.35	0.33	0.32	0.33	0.27	0.40	0.13	0.27	0.25	0.25	0. 27	0.04	0.07
X_{15}	18.00	10.67	16.33	15.67	11.66	18.00	16.00	14.67	18.67	17.00	17.67	10.67	16.67	20.67	18.33	16.05	1.27	2.57
X_{16}	27.30	42.93	26.77	29.10	34.67	28.20	26.73	26.73	25.90	26.43	30.93	43.87	26.07	25.70	25.90	29.82	0.91	1.83
X_{17}	4.44	5.66	4.11	4.44	7.33	4.22	5.11	4.44	4.22	6.11	4.11	6.22	4.33	4.33	6.11	5.03	0.19	0.39
X_{18}	1.23	1.06	1.59	1.32	1.05	1.24	1.31	1.67	1.74	1.28	1.19	1.04	1.21	1.24	1.21	1.29	0.08	0.15
X_{19}	20.43	19.23	22.20	20.40	19.03	19.67	20.60	22.00	22.37	20.70	21.70	19.60	20.57	21.77	20.50	20.72	0.12	0.25
X_{20}	20.67	19.57	21.40	20.67	19.00	19.90	20.63	21.27	21.47	20.67	21.17	19.43	20.60	21.30	20.63	20.56	0.15	0.30
X_{21}	21.07	20.37	22.80	21.30	20.30	20.53	21.23	22.63	22.87	21.10	22.30	20.47	21.00	22.43	21.20	21.44	0.09	0.19
X_{22}	2.13	2.57	1.94	2.09	2.65	2.41	2.13	1.97	1.92	2.16	2.18	2.54	2.14	1.99	2.12	2.20	0.04	0.07

X_1 Days to 50 % flowering
X_2 Number of pods per plant
X_3 Number of inflorescences per plant
X_4 Number of pods per inflorescence
X_5 Plant height (cm)
X_6 Number of branches per plant
X_7 Pod length (cm)
X_8 Number of seeds per pod
X_9 Grain yield per plant (g)
X_{10} 100 seed weight (g)
X_{11} Percentage flower bud infestation
X_{12} Number of larvae per 25 flowers
X_{13} Percentage pod infestation
X_{14} Number of larval bore holes per pod
X_{15} Number of damaged seeds in 25 pods
X_{16} Peduncle length (cm)
X_{17} Density of non- glandular trichomes on pod wall
X_{18} Leaf chlorophyll content (mg/g)
X_{19} Leaf protein content (mg/g)
X_{20} Pod protein content (mg/g)
X_{21} Seed protein content (mg/g)
X_{22} Crude fibre content (%)

the crosses, L_4 X T_3 (43.87) exhibited the maximum peduncle length, followed by L_1 X T_2 (42.93). The lowest peduncle length was noticed in L_5 X T_2 (25.70).

Density of non-glandular trichomes on pod wall (count/mm^2)

Among the lines, L_5 (5.33) and L_4 (3.11) exhibited the highest and lowest density of non-glandular trichomes. T_3 (7.33) and T_2 (7.00) recorded the highest and lowest mean values among the testers. The density of non-glandular trichomes ranged from 7.33 in L_2 X T_2 to 4.11 in L_1 X T_3 and L_4 X T_2 among the crosses.

Leaf chlorophyll content (mg/g)

Among the lines, L_1 (1.67) and L_3 (1.51) recorded the maximum and minimum leaf chlorophyll content. The mean values for the character ranged from 1.05 in T_1 to 1.03 in T_2. Among the crosses, the highest chlorophyll content was noticed in L_3 X T_2 (1.74) and the lowest in L_4 X T_3 (1.04). L_2 X T_2 was on par with L_4 X T_3.

Leaf protein content (mg/g)

Leaf protein content varied 21.43 in L_5 to 22.17 in L_1 in the lines. Among the testers, T_3 (19.33) recorded the maximum and T_2 (18.87), the minimum leaf protein content. L_3 X T_3 (22.37) recorded the highest leaf protein among the crosses, whereas L_1 X T_2 (19.23) had the least content of leaf protein.

Pod protein content (mg/g)

The range of pod protein content in the lines was 21.03 in L_5 to 22.33 in L_1. In the testers, T_2 (19.93) showed highest pod protein content. Among the crosses, pod protein varied from 19.00 in L_2 X T_2 to 21.47 in L_3 X T_3.

Seed protein content (mg/g)

Among the lines, L_1 (22.10) and L_5 (21.77) showed the maximum and minimum content of pod protein. T_1 and T_2 (20.47) among the testers showed high seed protein content. Seed protein content was maximum in L_3 X T_3 (22.87) in the crosses and least in L_2 X T_2 (20.30). L_1 X T_3 was on par with L_3 X T_3.

Crude fibre content of pods (%)

Maximum fibre content among the lines was noticed for L_5 (2.01) and minimum in L_1 and L_4 (1.95).Among the testers, T_3 (2.63) and T_2 (2.47) recorded the

maximum and minimum values for the character. The crude fibre content of pods ranged from 2.65 in L_2 X T_2 to 1.92 in L_3 X T_3.

4.3.2 HETEROSIS

Tables 26 to 47 shows the relative heterosis, heterobeltiosis and standard heterosis for the 15 crosses with respect to the 22 characters. C- 152 was used as the check variety for estimation of standard heterosis.

Days to 50 per cent flowering

Ten of the 15 crosses exhibited desirable significant negative relative heterosis for days to flowering, whereas, only three crosses exhibited significant negative heterobeltiosis (Table 26). Two crosses showed highly significant positive heterobeltiosis also. Significant negative standard heterosis was exhibited by four crosses. In all three cases, the maximum heterosis was shown by L_2 X T_2 (-18.92%, -14.29% and –14.29% respectively).

Number of pods per plant

Highly significant positive relative heterosis was exhibited for number of pods per plant by 14 crosses (Table 27). L_4 X T_3 (127.08%) recorded the highest relative heterosis followed by L_1 X T_2 (110.13%). Nine crosses showed significant positive heterobeltiosis, whereas, eight crosses exhibited positive significant standard heterosis. In all the cases, L_4 X T_3 recorded the maximum desirable heterosis. L_2 X T_3 recorded highly significant negative heterosis in all the three cases.

Number of inflorescences per plant

For number of inflorescences per plant, high positive significance of relative heterosis was shown by 11 crosses, heterobeltiosis by five and standard heterosis by three crosses (Table 28). The maximum heterosis was shown by L_2XT_2 (105.08%, 93.35% and 66.76% respectively). L_3 X T_1recorded negative values for all three estimates of heterosis.

Number of pods per inflorescence

Relative heterosis for number of pods per inflorescence was positively significant for seven crosses (Table 29). Relative heterosis, heterobeltiosis and

Table 26. Heterosis (%) for days to 50% flowering in cowpea

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-7.27*	-2.86	-2.86
L_1XT_2	-13.51**	-8.57*	-8.57*
L_1XT_3	-3.67	0.00	0.00
L_2XT_1	-1.82	2.86	2.86
L_2XT_2	-18.92**	-14.29**	-14.29**
L_2XT_3	-9.17*	-5.71	-5.71
L_3XT_1	-11.82**	-7.63	-7.63
L_3XT_2	-9.01*	-3.80	-3.80
L_3XT_3	-7.34*	-3.80	-3.80
L_4XT_1	-16.67**	-10.90*	-14.29**
L_4XT_2	-7.34*	0.00	-3.80
L_4XT_3	-7.48*	-1.99	-5.71
L_5XT_1	-2.88	15.07**	1.91
L_5XT_2	0.00	12.90**	0.00
L_5XT_3	-6.80	3.23	-8.57*

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

Table 27. Heterosis (%) for number of pods per plant

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	51.36**	16.47**	6.40
L_1XT_2	110.13**	62.20**	48.15**
L_1XT_3	51.50**	16.94**	6.82
L_2XT_1	25.23**	-12.68**	8.77*
L_2XT_2	73.54**	21.37**	51.20**
L_2XT_3	-8.48**	-35.97**	-20.23**
L_3XT_1	19.30**	-11.04**	-11.04**
L_3XT_2	87.42**	40.26**	40.26**
L_3XT_3	9.04**	-18.40**	-18.40**
L_4XT_1	65.57**	30.42**	11.36**
L_4XT_2	58.97**	25.73**	7.37*
L_4XT_3	127.08**	79.59**	53.34**
L_5XT_1	38.64**	3.23	3.67
L_5XT_2	39.44**	4.20	4.64
L_5XT_3	56.31**	16.81**	17.31**

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

Table 28. Heterosis (%) for number of inflorescences per plant

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	17.12**	1.82	2.75
L_1XT_2	11.77**	-1.82	-0.89
L_1XT_3	22.96**	9.55*	10.60*
L_2XT_1	33.52**	24.47**	7.36
L_2XT_2	105.08**	93.35**	66.76**
L_2XT_3	6.94**	2.39	-11.70*
L_3XT_1	-2.23	-14.67**	-14.67**
L_3XT_2	7.41	-5.27	-5.27
L_3XT_3	0.77	-9.86*	-9.86*
L_4XT_1	1.06	-11.01**	-12.87**
L_4XT_2	22.11**	8.67	6.47
L_4XT_3	36.71**	23.42**	20.92**
L_5XT_1	22.65**	7.67	6.19
L_5XT_2	20.31**	6.74	5.30
L_5XT_3	21.96**	9.77*	8.26

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

Table 29. Heterosis (%) for number of pods per inflorescence

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	14.29*	-1.30	-6.30
L_1XT_2	51.52**	29.87**	23.33**
L_1XT_3	5.19	-7.79	-12.22*
L_2XT_1	-0.66	-21.05**	-7.41
L_2XT_2	0.00	-21.05**	-7.41
L_2XT_3	-15.03**	-31.58**	-19.63**
L_3XT_1	18.25**	0.00	0.00
L_3XT_2	38.24**	16.00*	16.00*
L_3XT_3	-5.04	-18.52**	-18.52**
L_4XT_1	8.96	-6.41	-10.00
L_4XT_2	15.79*	-1.28	-4.81
L_4XT_3	51.47**	32.05**	27.04**
L_5XT_1	12.98*	-1.33	-8.52
L_5XT_2	7.69	-6.66	-13.70*
L_5XT_3	9.77	-2.66	-10.00

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

standard heterosis were positive and significant in three crosses, L_1 X T_2, L_3 X T_2 and L_4 X T_3. Eleven of the 15 crosses showed negative heterobeltiosis and standard heterosis for the character.

Plant height (cm)

Three crosses exhibited positive significant relative heterosis for plant height, while for one cross it was negatively significant (Table 30). For heterobeltiosis, two crosses each exhibited significance in both directions. Standard heterosis was negatively significant for five crosses, but none of the crosses showed significant standard heterosis in positive direction.

Number of branches per plant

Six crosses recorded significant positive relative heterosis (Table 31). Significant heterobeltiosis and standard heterosis was not seen in any of the crosses.

Pod length (cm)

Twelve hybrids showed highly significant positive relative heterosis for pod length, while three crosses exhibited negative significant relative heterosis (Table 32). The crosses, L_5 X T_1 (17.69%) and L_5 X T_2 (19.35%) recorded high positive values for relative heterosis. For heterobeltiosis, two crosses each exhibited significance in either direction. Three crosses were negative and significant for standard heterosis, but none of the crosses showed significant standard heterosis in positive direction.

Number of seeds per pod

For number of seeds per pod, 11 crosses were positive and significant for relative heterosis (Table 33), with the highest magnitude of heterosis being 21.17% in L_5XT_1. Significant positive heterobeltiosis was noticed in seven crosses. For standard heterosis, two crosses were positive and significant and seven crosses were negative and significant. L_1 X T_2 and L_3 X T_1 exhibited positive significance for all the three estimates of heterosis, while for L_2 X T_2, they were negative.

Grain yield per plant (g)

Highly significant positive relative heterosis was noticed for 14 crosses (Table 34). Maximum relative heterosis was recorded for L_4 X T_3 (158.82%), followed by L_1

Table 30. Heterosis (%) for plant height

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	3.90	1.30	-6.09
L_1XT_2	-3.87	-6.93	-13.72**
L_1XT_3	4.25	1.51	-5.90
L_2XT_1	5.73	3.24	-4.59
L_2XT_2	-8.03*	-10.82*	-17.58**
L_2XT_3	6.94	4.29	-3.62
L_3XT_1	1.57	-4.49	-4.49
L_3XT_2	12.44**	5.02	5.02
L_3XT_3	0.36	-5.75	-5.75
L_4XT_1	-7.15	-10.20*	-15.36**
L_4XT_2	3.47	-0.62	-6.33
L_4XT_3	-1.25	-4.61	-10.10*
L_5XT_1	22.47**	18.27**	4.14
L_5XT_2	19.54**	16.25**	0.91
L_5XT_3	6.60	3.08	-9.46*

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

Table 31. Heterosis (%) for number of branches per plant

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	11.89*	3.50	3.45
L_1XT_2	9.63	2.50	2.40
L_1XT_3	5.04	-1.00	-1.00
L_2XT_1	12.33*	5.13	2.40
L_2XT_2	8.40	2.56	0.00
L_2XT_3	5.38	0.51	-2.10
L_3XT_1	12.97*	4.50	4.50
L_3XT_2	6.42	-0.50	-0.60
L_3XT_3	10.88*	4.50	4.50
L_4XT_1	13.42*	6.15	3.45
L_4XT_2	7.86	2.05	-0.60
L_4XT_3	7.53	2.56	0.00
L_5XT_1	11.78*	4.62	1.95
L_5XT_2	9.49	3.59	0.90
L_5XT_3	1.08	-3.59	-6.00

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

Table 32. Heterosis (%) for pod length

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	7.47**	0.00	-0.62
L_1XT_2	7.06**	0.62	0.00
L_1XT_3	8.72**	0.83	0.19
L_2XT_1	5.37**	-1.67	-2.91
L_2XT_2	-10.96**	-16.07**	-17.13**
L_2XT_3	6.17**	-1.25	-2.47
L_3XT_1	6.00**	-1.66	-1.66
L_3XT_2	8.47**	1.63	1.63
L_3XT_3	3.90**	-3.92	-3.96
L_4XT_1	-13.66**	-20.49**	-19.17**
L_4XT_2	5.34**	-2.03	-0.43
L_4XT_3	8.95**	0.00	1.61
L_5XT_1	17.69**	13.01**	-3.34
L_5XT_2	19.35**	13.44**	-0.87
L_5XT_3	-2.77**	-6.31	-20.41**

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

Table 33. Heterosis (%) for number of seeds per pod

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	6.46**	-3.49	-4.45*
L_1XT_2	17.83**	7.19**	6.10**
L_1XT_3	9.03**	-2.05	-3.05
L_2XT_1	3.30	-8.56**	-4.45*
L_2XT_2	-7.78**	-18.09**	-14.45**
L_2XT_3	8.87**	-4.47*	-0.18
L_3XT_1	18.24**	6.71**	6.71**
L_3XT_2	7.96**	-2.25	-2.25
L_3XT_3	6.36**	-4.88*	-4.88**
L_4XT_1	-3.29	-9.47**	-16.46**
L_4XT_2	14.42**	7.49**	-0.79
L_4XT_3	18.76**	10.13**	1.65
L_5XT_1	21.17**	19.95**	-3.48
L_5XT_2	15.88**	14.29**	-7.31**
L_5XT_3	4.12	4.12*	-17.87**

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

Table 34. Heterosis (%) for grain yield per plant

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	55.11**	7.53	-13.93**
L_1XT_2	109.22**	47.48**	18.06**
L_1XT_3	51.03**	2.96	-17.58**
L_2XT_1	47.51**	-1.56	-9.01**
L_2XT_2	70.93**	15.80**	7.03
L_2XT_3	23.34**	-18.92**	-25.05**
L_3XT_1	21.22**	-20.64**	-20.64**
L_3XT_2	75.05**	16.24**	16.24**
L_3XT_3	5.67	-31.79**	-31.79**
L_4XT_1	43.57**	2.07	-25.16**
L_4XT_2	66.90**	20.80**	-11.45**
L_4XT_3	158.82**	80.77**	32.51**
L_5XT_1	86.08**	41.49**	-15.96**
L_5XT_2	78.36**	38.44**	-17.77**
L_5XT_3	63.44**	21.75**	-27.69**

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

Table 35. Heterosis (%) for 100 seed weight

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	10.89**	1.53	-3.22
L_1XT_2	4.44	-0.77	-5.41*
L_1XT_3	13.14**	4.60	-0.29
L_2XT_1	20.90**	18.24**	-1.98
L_2XT_2	7.51**	5.68	-9.29**
L_2XT_3	20.24**	18.82**	-1.46
L_3XT_1	4.49	-6.34*	-6.36*
L_3XT_2	7.61**	0.00	0.00
L_3XT_3	7.82**	-2.43	-2.49
L_4XT_1	-0.41	-10.34**	-11.27**
L_4XT_2	5.54*	-1.48	-2.49
L_4XT_3	7.86**	-1.97	-2.93
L_5XT_1	30.99**	26.15**	0.00
L_5XT_2	20.98**	12.22**	-3.66
L_5XT_3	7.74**	2.71	-16.83**

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

X T_2 (109.22%). Eight crosses had significant positive heterobeltiosis also. Three crosses, L_1 X T_2 (18.06%), L_3 X T_2 (16.24%) and L_4 X T_3 (32.51%) exhibited significant positive standard heterosis and 11 crosses showed significant negative standard heterosis.

Hundred seed weight (g)

Twelve crosses exhibited significant positive relative heterosis for the character (Table 35). Maximum positive relative heterosis was recorded for L_5 X T_1 (30.99%). Four crosses showed significant positive heterobeltiosis, but none of the crosses showed significant standard heterosis in positive direction.

Percentage flower bud infestation

Desirable negative relative heterosis was significant for three crosses for percentage flower bud infestation (Table 36). The highest negative heterosis was noticed for L_1 X T_2 (-47.37%) followed by L_4 X T_3 (-45.95%) and L_2 X T_2 (-33.33%). Only one cross, L_4 X T_3 (-16.69%) exhibited negative heterobeltiosis. Eight of the crossed recorded significant negative standard heterosis also.

Number of larvae per 25 flowers

Three crosses, L_1 X T_2 (-60.00%), L_2 X T_2 (-47.69%) and L_4 X T_3 (-49.25%) had significant negative relative heterosis for number of larvae per 25 flowers (Table 37). No crosses had negatively significant heterobeltiosis, but four crosses including L_1 X T_2, L_2 X T_2 and L_4 X T_3 had significant negative standard heterosis.

Percentage pod infestation

L_1 X T_2 (-37.14%), L_2 X T_2 (-50.00%) and L_4 X T_3 (-41.18%) exhibited significant negative relative heterosis and standard heterosis for percentage pod infestation also (Table 38). No cross had significant negative heterobeltiosis.

Number of larval entry/ exit holes per pod

Three crosses, L_1 X T_2 (-20.00%), L_2 X T_2 (-42.10%) and L_4 X T_3 (-45.95%) had significant and desirable negative relative heterosis for number of larval bore holes per pod (Table 39). No cross had significant negative heterobeltiosis. L_1 X T_2, L_2 X T_2 and L_4 X T_3 showed significant negative standard heterosis.

Table 36. Heterosis (%) for percentage flower bud infestation

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-2.56	111.08**	-38.71**
L_1XT_2	-47.37**	24.93	-67.75**
L_1XT_3	66.67**	191.69**	12.92
L_2XT_1	11.76	111.08**	-38.71**
L_2XT_2	-33.33**	37.48	-64.51**
L_2XT_3	18.92	83.31**	-29.03**
L_3XT_1	55.00**	244.42**	0.00
L_3XT_2	48.72**	262.42**	-6.44
L_3XT_3	16.28	108.31**	-19.36
L_4XT_1	76.47**	233.32**	-3.22
L_4XT_2	39.39*	187.44**	-25.79*
L_4XT_3	-45.95**	-16.69	-67.75**
L_5XT_1	106.67**	244.42**	0.00
L_5XT_2	106.90**	274.88**	-3.22
L_5XT_3	33.33*	83.31**	-29.03**

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

Table 37. Heterosis (%) for number of larvae per 25 flowers

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	48.15**	275.23**	15.41
L_1XT_2	-60.00**	6.60	-69.24**
L_1XT_3	56.10**	276.19**	23.08
L_2XT_1	57.58**	225.14**	0.00
L_2XT_2	-47.69*	13.40	-67.28**
L_2XT_3	1.49	99.82*	-34.62*
L_3XT_1	52.94**	225.14**	0.00
L_3XT_2	79.10**	300.00**	15.41
L_3XT_3	73.91**	252.73**	15.41
L_4XT_1	78.79**	269.04**	13.50
L_4XT_2	66.15**	260.00**	3.87
L_4XT_3	-49.25**	0.00	-67.28**
L_5XT_1	43.59**	250.28**	7.73
L_5XT_2	48.05**	280.00**	9.64
L_5XT_3	62.03**	276.19**	23.08

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

Table 38. Heterosis (%) for percentage pod infestation

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	29.41*	174.88**	-15.40
L_1XT_2	-37.14**	22.25	-57.69**
L_1XT_3	66.67**	200.08**	15.37
L_2XT_1	11.43	143.67**	-25.01**
L_2XT_2	-50.00**	0.00	-65.39**
L_2XT_3	-13.51	60.02*	-38.48**
L_3XT_1	35.29**	187.48**	-11.54
L_3XT_2	82.86**	255.58**	23.04*
L_3XT_3	55.56**	180.05**	7.67
L_4XT_1	25.00**	149.95**	-23.07*
L_4XT_2	39.39**	155.58**	11.54
L_4XT_3	-41.18**	0.00	-61.55**
L_5XT_1	69.23**	174.88**	-15.40
L_5XT_2	48.15**	122.25**	-23.07*
L_5XT_3	21.43	70.09**	-34.61**

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

Table 39. Heterosis (%) for number of larval entry / exit holes per pod

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	11.11	68.75*	-15.63
L_1XT_2	-20.00	26.67	-40.63*
L_1XT_3	29.41	123.07**	-9.38
L_2XT_1	12.82	81.25*	-9.38
L_2XT_2	-42.10*	0.00	-53.13**
L_2XT_3	40.54*	169.23**	9.38
L_3XT_1	38.89*	106.25**	3.13
L_3XT_2	37.14*	113.33**	0.00
L_3XT_3	47.06*	153.84**	3.13
L_4XT_1	2.56	68.75*	-15.63
L_4XT_2	57.89**	166.75**	25.00
L_4XT_3	-45.95**	0.00	-59.38**
L_5XT_1	17.65	68.75*	-15.63
L_5XT_2	15.15	66.67	-21.88
L_5XT_3	18.75	92.31*	-21.88

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

Table 40. Heterosis (%) for damaged seeds per 25 pods

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	14.89	86.14**	7.98
L_1XT_2	-27.27*	39.13	-35.99**
L_1XT_3	1.03	53.05**	-2.04
L_2XT_1	17.50	62.05**	-6.00
L_2XT_2	-5.41	52.02*	-29.99**
L_2XT_3	30.12*	68.70**	7.98
L_3XT_1	21.52	65.46**	-4.02
L_3XT_2	20.55	91.26**	-12.00
L_3XT_3	36.59**	74.98**	12.00
L_4XT_1	12.09	75.80**	1.98
L_4XT_2	24.71*	130.38**	6.00
L_4XT_3	-31.91**	0.00	-35.99**
L_5XT_1	19.05	72.38**	0.00
L_5XT_2	58.97**	169.49**	24.00*
L_5XT_3	26.44*	71.79**	9.96

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

Table 41. Heterosis (%) for peduncle length

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-13.65**	-24.38**	3.29
L_1XT_2	38.20**	22.67**	62.43*
L_1XT_3	-14.07**	-23.89**	1.29
L_2XT_1	-13.00**	-19.39**	10.10*
L_2XT_2	5.37	-0.95	31.18**
L_2XT_3	-14.50**	-19.81**	6.70
L_3XT_1	-14.50**	-25.95**	1.14
L_3XT_2	-12.97**	-23.62**	1.14
L_3XT_3	-15.91**	-26.35**	-2.01
L_4XT_1	-15.37**	-26.78**	0.00
L_4XT_2	0.81	-11.62**	17.03**
L_4XT_3	42.58**	24.74**	65.99**
L_5XT_1	-18.75**	-27.79**	-1.36
L_5XT_2	-18.50**	-26.57**	-2.76
L_5XT_3	-18.08**	-26.35**	-2.01

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

Number of damaged seeds in 25 pods

For number of damaged seeds per 25 pods, two crosses, L_1 X T_2 (-27.27%) and L_4 X T_3 (-31.91%) had significant negative relative heterosis (Table 40). No crosses had negative and significant heterobeltiosis, but three crosses, L_1 X T_2, L_2 X T_2 and L_4 X T_3 had significant negative standard heterosis.

Length of peduncle (cm)

Significant positive relative heterosis and heterobeltiosis were noticed in two crosses, L_1 X T_2 (38.20% and 22.67% respectively) and L_4 X T_3 (42.58% and 24.74% respectively) for peduncle length (Table 41). However, five crosses including L_1 X T_2 and L_4 X T_3 were found to possess significant positive standard heterosis.

Density of non-glandular trichomes on pod wall (count/mm^2)

Significant positive relative heterosis was noticed for non-glandular trichome density in four crosses (Table 42), L_1 X T_2 (15.17%), L_2 X T_2 (37.52%),L_4 X T_1 (19.54%) and L_4 X T_3 (19.16%) None of the crosses had significant positive heterobeltiosis for the character, but 11 crosses showed positive and significant standard heterosis.

Leaf chlorophyll content (mg/g)

The different estimates of heterosis for leaf chlorophyll content are given in Table 43. Three crosses each showed highly significant relative heterosis for the character in both directions. Eleven crosses had significant negative heterobeltiosis, while 12 crosses had significant negative standard heterosis. Only L_3 X T_3 had positive significant estimates for both (15.54% and 15.23% respectively).

Leaf protein content (mg/g)

Five crosses recorded positive significant relative heterosis for leaf protein content, while in four crosses, it was negative and significant (Table 44). Eleven crosses showed positive negative heterobeltiosis, while only one cross had significant positive heterobeltiosis. Standard heterosis was positive and significant for three crosses, but for nine, it was negative and significant. For L_3 X T_3, all estimates of heterosis were positive and highly significant.

Table 42. Heterosis (%) for density of non-glandular trichomes on pod wall

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-14.01**	-37.52**	21.31**
L_1XT_2	15.17**	-15.91**	60.66**
L_1XT_3	-22.09**	-43.93**	12.30
L_2XT_1	-17.55**	-37.52**	21.31**
L_2XT_2	37.52**	4.76	100.27**
L_2XT_3	-23.23**	-42.43**	15.30
L_3XT_1	-5.11	-28.10**	39.62**
L_3XT_2	-16.70**	-36.54**	21.31**
L_3XT_3	-23.23**	-42.43**	15.30
L_4XT_1	19.54**	-14.07**	66.94**
L_4XT_2	-18.67**	-41.26**	12.30
L_4XT_3	19.16**	-15.14**	69.95**
L_5XT_1	-30.37**	-39.07**	18.31*
L_5XT_2	-29.75**	-38.11**	18.31*
L_5XT_3	-3.48	-16.64**	66.94**

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

Table 43. Heterosis (%) for leaf chlorophyll content

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-9.29	-26.33**	-18.54**
L_1XT_2	-21.94**	-36.99**	-29.80**
L_1XT_3	17.51*	-4.80	5.30
L_2XT_1	0.80	-16.28*	-12.58
L_2XT_2	-19.57**	-33.61**	-30.46**
L_2XT_3	-5.37	-21.59**	-17.88*
L_3XT_1	2.49	-13.24	-13.24
L_3XT_2	31.46**	10.58	10.58
L_3XT_3	36.83**	15.54*	15.23*
L_4XT_1	-3.83	-20.98**	-15.23*
L_4XT_2	-10.10	-26.58**	-21.19**
L_4XT_3	-22.10**	-36.15**	-31.13**
L_5XT_1	-7.16	-22.51**	-19.87**
L_5XT_2	-4.18	-20.52**	-17.88**
L_5XT_3	-7.09	-22.64**	-19.87**

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

Table 44. Heterosis (%) for leaf protein content

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-1.13	-7.82**	-5.72**
L_1XT_2	-6.26**	-13.23**	-11.26**
L_1XT_3	6.99**	0.15	2.45**
L_2XT_1	-0.41	-6.42**	-5.86**
L_2XT_2	-6.39**	-12.69**	-12.18**
L_2XT_3	-4.38**	-9.76**	-9.23**
L_3XT_1	0.90	-4.93**	-4.93**
L_3XT_2	8.55**	1.53	1.53
L_3XT_3	9.11**	3.23**	3.23**
L_4XT_1	0.32	-6.33**	-4.48**
L_4XT_2	5.64**	-1.81*	0.14
L_4XT_3	-5.39**	-11.31**	-9.55**
L_5XT_1	1.31	-4.04**	-5.08**
L_5XT_2	8.02**	1.56	0.46
L_5XT_3	0.57	-4.35**	5.40**

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

Table 45. Heterosis (%) for pod protein content

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-0.88	-7.46**	-1.90
L_1XT_2	-7.41**	-12.39**	-7.12**
L_1XT_3	2.97**	-4.18**	1.57
L_2XT_1	2.06*	-2.21*	-1.95
L_2XT_2	-7.47**	-10.09**	-9.82**
L_2XT_3	-1.40	-5.81**	5.55*
L_3XT_1	2.06*	-2.07*	-2.07*
L_3XT_2	3.74**	0.95	0.95
L_3XT_3	6.53**	1.90	1.90
L_4XT_1	-0.32	-6.49**	-1.90
L_4XT_2	0.71	-4.22**	0.47
L_4XT_3	-5.97**	-12.07**	-7.78**
L_5XT_1	1.98*	-2.06*	-2.23*
L_5XT_2	3.99**	1.27	1.09
L_5XT_3	2.48**	-1.90	-2.09*

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

Table 46. Heterosis (%) for seed protein content

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-1.02	-4.68**	-3.48**
L_1XT_2	-4.31**	-7.84**	-6.69**
L_1XT_3	7.63**	3.17**	4.44**
L_2XT_1	0.63	-2.59**	-2.43**
L_2XT_2	-4.09**	-7.16**	-7.01**
L_2XT_3	-2.53**	-6.10**	-5.96**
L_3XT_1	0.39	-2.75**	-2.75**
L_3XT_2	7.01**	3.66**	3.66**
L_3XT_3	8.63**	4.74**	4.74**
L_4XT_1	-0.63	-4.09**	-3.34**
L_4XT_2	5.02**	1.36*	2.15**
L_4XT_3	-3.15**	-6.97**	-6.23**
L_5XT_1	-0.55	-3.52**	-3.80**
L_5XT_2	6.24**	3.06**	2.75**
L_5XT_3	0.87	-2.60**	-2.89**

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

Table 47. Heterosis (%) for crude fibre content of pods

Cross	Relative heterosis	Heterobeltiosis	Standard heterosis
L_1XT_1	-5.88**	-17.42**	6.50*
L_1XT_2	16.23**	4.05	28.50**
L_1XT_3	-15.14**	-26.11**	-3.00
L_2XT_1	-8.68**	-19.23**	4.50
L_2XT_2	18.86**	7.30**	32.50**
L_2XT_3	4.55*	-8.24**	20.50**
L_3XT_1	-6.99**	-17.55**	6.50*
L_3XT_2	-11.87**	-20.27**	-1.50
L_3XT_3	-17.15**	-27.12**	-4.00
L_4XT_1	-4.63*	-16.26**	8.00**
L_4XT_2	-1.36	-11.62**	9.00**
L_4XT_3	10.84**	-3.42	27.00**
L_5XT_1	-6.89**	-17.16**	7.00**
L_5XT_2	-11.01**	-19.19**	-0.50
L_5XT_3	-8.68**	-19.39**	6.00*

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

Pod protein content (mg/g)

Pod protein content in eight crosses were significant and positive for relative heterosis (Table 45). Maximum relative heterosis was noticed in L_3 X T_3 (6.53%). No cross had positive significant heterobeltiosis for the character, but L_2 X T_3 (5.55%) showed significant positive standard heterosis.

Seed protein content (mg/g)

Pod protein content in five crosses were significant and positive for relative heterosis, heterobeltiosis and standard heterosis (Table 46). Maximum estimates of all cases of heterosis were noticed in L_3 X T_3 (8.63%, 4.74% and 4.74% respectively).

Crude fibre content of pods (%)

Relative heterosis was positive and significant for four crosses for crude fibre content of pods, while 10 crosses were negatively significant (Table 47). Only one cross had significant positive heterobeltiosis, whereas, nine crosses had significant positive standard heterosis. All estimates of heterosis were positive and maximum in magnitude for L_2 X T_2 (18.86%, 7.30% and 32.50% respectively).

4.3.3 COMBINING ABILITY

The general combining ability (*gca*) effects of the five lines and three testers for the 22 characters are presented in Table 48. Table 49 gives the specific combining ability (*sca*) effects of the 15 crosses with respect to each character.

Days to 50 per cent flowering

The *gca* effect of L_4 (-1.04) for days to flowering was negative and significant. All other lines and testers showed non-significant *gca* effects for the character.

Among the crosses, significant positive *sca* effects was noticed for days to flowering in L_1 X T_2 (2.67). The *sca* effects were negatively significant in L_2 X T_1 (-2.56), L_3 X T_1 (-2.60) and L_5 X T_3 (-2.30).

Number of pods per plant

Two lines, L_1 (2.00) and L_4 (3.10) showed positively significant *gca* effects for number of pods, while L_3 (-3.19) and L_5 (-1.68) showed negatively significant *gca*

Table 48. General combining ability effects of parents

Character	L_1	L_2	L_3	L_4	L_5	SE (lines)	T_1	T_2	T_3	SE (testers)
1. Days to 50 % flowering	0.40	-0.27	-0.04	-1.04**	0.95	0.58	0.33	-0.40	0.07	0.45
2. Number of pods per plant	2.00**	-0.23	-3.19**	3.10**	-1.68**	0.45	-3.12**	5.03**	-1.91**	0.35
3. Number of inflorescences per plant	-0.17	2.26**	-2.21**	-0.07	0.19	0.27	-1.09**	1.33**	-0.24	0.21
4. Number of pods per inflorescence	0.14	-0.21**	0.07	0.20**	-0.20**	0.07	-0.08	0.17**	-0.09	0.05
5. Plant height (cm)	-1.64	-1.66	3.07**	-3.04**	3.27**	1.11	0.63	-0.10	-0.53	0.86
6. Number of branches per plant	0.05	-0.05	0.13	0.00	-0.13	0.16	0.15	-0.03	-0.12	0.12
7. Pod length (cm)	0.72**	-0.46**	0.54**	-0.22	-0.58**	0.17	-0.15	0.21	-0.06	0.13
8. Number of seeds per pod	0.64**	-0.33*	0.69**	-0.15	-0.85**	0.14	-0.01	0.10	-0.09	0.11
9. Grain yield per plant (g)	3.69**	0.35	-1.91	5.98**	-8.11**	1.10	-5.51**	8.79**	-3.28**	0.85
10. Hundred seed weight (g)	0.21	0.04	0.21	-0.14	-0.32*	0.14	-0.01	0.05	-0.04	0.11
11. Percentage flower bud infestation	-2.40	-7.73**	6.93**	-2.84	6.04**	1.63	3.82**	-3.38**	-0.44	1.26
12. Number of larvae per 25 flowers	-0.49	-4.60**	3.07**	-1.60	3.62**	0.98	2.55**	-2.44**	-0.11	0.76
13. Percentage pod infestation	1.11	-7.11**	10.00**	-3.33*	-0.67	1.31	1.51	-1.55	0.04	1.02
14. Number of larval bore holes per pod	-0.02	-0.01	0.06**	-0.01	-0.02	0.02	0.01	-0.01	0.00	0.02
15. Number of damaged seeds in 25 pods	-1.04	-0.93	0.40	-0.93	2.50**	0.73	0.62	-0.98	0.36	0.57
16. Peduncle length (cm)	2.52**	0.84	-3.36**	3.93**	-3.93**	0.52	-2.69**	2.38**	0.31	0.41
17. Density of non- glandular trichomes on pod wall	-0.22	0.30**	-0.43**	0.45**	-0.10	0.11	-0.14	0.19	-0.05	0.09
18. Leaf chlorophyll content (mg/g)	0.00	-0.09*	0.28**	-0.12**	-0.07	0.04	-0.02	-0.05	0.07*	0.03
19. Leaf protein content (mg/g)	-0.10	-1.02**	0.94**	-0.05	0.23**	0.07	-0.18**	0.03	0.15*	0.06
20. Pod protein content (mg/g)	-0.01	-0.70**	0.56**	-0.14	0.29**	0.09	0.09	-0.10	0.01	0.07
21. Seed protein content (mg/g)	-0.03	-0.73**	0.80**	-0.15**	0.11*	0.05	-0.30**	0.17**	0.13**	0.04
22. Crude fibre content (%)	0.02	0.19**	-0.19**	0.09**	-0.11**	0.02	-0.07**	0.07**	0.00	0.02

** Significant at 1 per cent level

* Significant at 5 per cent level

effects. T_2 (5.03) had positive and significant *gca* effects and for T_1 (-3.12) and T_3 (-1.91), it was negative and significant. Seven crosses exhibited positive and significant *sca* effects for number of pods per plant. L_5 X T_2 (10.94) had the maximum *sca* effect followed by L_3 X T_1 (6.65) and L_3 X T_2 (6.25). Negative *sca* effects were exhibited by five crosses.

Number of inflorescences per plant

L_2 (2.26) exhibited positive and L_3 (-2.21) exhibited negative *gca* effects. Among the testers, T_2 (1.33) exhibited positive and T_1 (-1.09) exhibited negative *gca* effects. L_3 X T_1 (5.34) followed by L_5 X T_2 (2.57) displayed the highest significant positive *sca* effects. Significant negative *sca* effects were exhibited by five crosses.

Number of pods per inflorescence

Significant positive *gca* effect was noticed for number of pods per inflorescence in L_4 (0.20). For L_2 (-0.21) and L_5 (-0.20) the effects were negative and significant. Among the testers, T_2 (0.17) showed significant positive *gca* effect. L_5 X T_2 (0.71), L_3 X T_2 (0.42) and L_2 X T_3 (0.29) exhibited positive and significant *sca* effects. Significant negative *sca* effects were exhibited by five crosses.

Plant height (cm)

For plant height, two lines, L_3 (3.07) and L_5 (3.27) showed significant positive *gca* effects, while L_4 (-3.04) showed negatively significant *gca* effect. No testers had any significant *gca* effects. Positive and significant *sca* effects were noticed for plant height in L_3 X T_2 (4.77) and L_4 X T_3 (3.97). L_3 X T_1 (-6.10), L_5 X T_3 (-4.99) and L_2 X T_1 (-3.92) showed negative *sca* effects.

Number of branches per plant

The *gca* effects of lines and testers were not significant for number of branches per plant. None of the crosses also displayed any significant *sca* effect.

Pod length (cm)

Two lines, L_1 (0.72) and L_3 (0.54) showed significant positive *gca* effects for pod length, while L_2 (-0.46) and L_5 (-0.58) showed significant negative *gca* effects. The *gca* effects of testers were not significant for the character. Six crosses showed

Table 49. *Specific combining ability effects of crosses*

Character	L1XT1	L1XT2	L1XT3	L2XT1	L2XT2	L2XT3	L3XT1	L3XT2	L3XT3	L4XT1	L4XT2	L4XT3	L5XT1	L5XT2	L5XT3	SE
X_1	0.00	2.67*	-1.22	-2.56*	1.11	-1.27	-2.60*	0.84	1.84	1.18	1.27	-0.07	0.38	0.71	-2.3*	1.01
X_2	-1.21	1.75*	-1.39	-0.78	1.62*	3.50**	6.65**	6.25**	-10.2**	-6.2**	-2.3**	-8.4**	-4.9**	10.94**	4.61**	0.78
X_3	0.89	-0.86	0.40	-1.47**	1.04*	-2.07**	5.34**	-0.66	-1.10*	-1.5**	1.17*	-4.5**	0.25	2.57**	0.48	0.46
X_4	-0.13	0.19	0.10	-0.30**	0.14	0.42**	-0.06	0.29*	-0.41**	-0.24*	-0.29*	-0.14	-0.4**	0.71**	0.11	0.11
X_5	1.08	2.13	-2.53	-3.92*	3.24	-3.46	-6.10**	4.77*	3.04	1.74	2.38	3.97*	-2.23	0.88	-4.99*	1.93
X_6	-0.03	0.01	-0.04	0.02	0.05	0.08	0.02	-0.19	-0.07	0.16	-0.06	-0.02	0.23	0.06	-0.21	0.27
X_7	0.07	0.89**	0.09	-1.99**	0.94**	-0.18	-1.76**	0.27	0.69*	0.98**	0.12	0.87**	-0.36	1.29**	-1.9**	0.29
X_8	-0.64*	0.32	1.14**	-1.83**	1.01**	0.98**	-1.42**	-0.44	0.62*	0.27	-0.34	1.10**	-0.7**	1.21**	-1.3**	0.24
X_9	-1.46	5.51**	-0.82	-12.1**	8.84**	7.85**	3.06	12.11**	-16.2**	-6.8**	-6.4**	-8.6**	-11.3**	28.29**	-2.05	1.90
X_{10}	-0.03	0.32	-0.46	-0.77**	0.94**	-0.38	-0.74	0.35	0.38	0.39	0.41	0.42	0.11	0.40	-1.3**	0.24
X_{11}	-6.93*	-1.60	-0.27	8.18**	0.62	-11.3**	-5.07	4.27	6.04*	6.49*	18.7**	6.67*	-4.00	-14.2**	-7.11*	2.82
X_{12}	1.89	3.33	-4.33*	2.67	3.56*	-7.78**	-3.33	3.33	6.00**	1.78	5.89**	0.00	1.00	-8.67**	1.78	1.71
X_{13}	-0.18	4.71*	-7.73**	1.60	1.60	-11.8**	-6.22*	7.33**	8.67**	2.00	11.9**	1.51	0.40	-10.3**	-3.60	2.27
X_{14}	0.01	0.02	-0.01	-0.01	-0.01	-0.05	-0.10*	0.00	0.14**	0.01	0.05	0.09*	0.01	-0.13**	-0.01	0.04
X_{15}	2.38	-0.07	-1.07	1.27	-2.51	-3.36*	-2.47	-0.80	3.53**	3.09*	0.98	2.53	1.87	-4.80**	-0.58	1.27
X_{16}	-2.34*	1.13	2.97**	-4.62**	2.87**	8.22**	1.63	-2.10*	-5.19**	-2.6**	-5.9**	-2.8**	-0.87	9.81**	0.30	0.91
X_{17}	-0.23	-0.8**	0.66**	0.77**	-0.45*	0.88**	1.81**	-0.34	-1.56**	-0.8**	-0.7**	-1.1**	-0.32	0.79**	1.24**	0.19
X_{18}	-0.04	0.14	-0.24**	0.13	0.01	-0.19*	-0.10	0.15	0.07	0.07	0.23**	-0.04	0.10	-0.21*	-0.08	0.08
X_{19}	-0.01	0.88**	-0.88**	0.21	-0.20	-1.42**	-0.70**	0.32*	1.00**	0.79**	1.43**	-0.18	0.56**	-1.22**	-0.6**	0.12
X_{20}	0.03	0.72**	-0.58**	0.16	-0.33*	-0.88**	-0.76**	0.24	0.84**	0.55**	0.85**	0.04	0.34*	-1.0**	-0.22	0.15
X_{21}	-0.04	0.89**	-0.71**	0.11	-0.24*	-1.21**	-0.58**	0.22*	0.84**	0.72**	1.26**	-0.3**	0.49**	-0.96**	-0.5**	0.09
X_{22}	-0.02	-0.2**	0.19**	-0.07	0.12**	0.28**	0.19**	-0.11**	-0.19**	-0.2**	-0.3**	0.04	-0.08	0.25**	0.04	0.04

** Significant at 1 per cent level

* Significant at 5 per cent level

X_1 Days to 50 % flowering
X_2 Number of pods per plant
X_3 Number of inflorescences per plant
X_4 Number of pods per inflorescence
X_5 Plant height (cm)
X_6 Number of branches per plant
X_7 Pod length (cm)
X_8 Number of seeds per pod
X_9 Grain yield per plant (g)
X_{10} 100 seed weight (g)
X_{11} Percentage flower bud infestation
X_{12} Number of larvae per 25 flowers
X_{13} Percentage pod infestation
X_{14} Number of larval bore holes per pod
X_{15} Number of damaged seeds in 25 pods
X_{16} Peduncle length (cm)
X_{17} Density of non- glandular trichomes on pod wall
X_{18} Leaf chlorophyll content (mg/g)
X_{19} Leaf protein content (mg/g)
X_{20} Pod protein content (mg/g)
X_{21} Seed protein content (mg/g)
X_{22} Crude fibre content (%)

positive significant *sca* effects and three crosses showed negative significant *sca* effects. Out of the positive effects, L_5 X T_2 (1.29), L_4 X T_1 (0.98) and L_2 X T_2 (0.94) were the crosses with high *sca* effects.

Number of seeds per pod

L_1 (0.64) and L_3 (0.69) showed significant positive *gca* effects for pod length, while L_2 (-0.33) and L_5 (-0.85) showed significant negative *gca* effects. The *gca* effects of the testers were not significant for the character. Six crosses exhibited positive and significant *sca* effects for number of seeds per pod. L_5 X T_2 (1.21) had the maximum *sca* effect followed by L_1 X T_3 (1.14) and L_4 X T_3 (1.10). Significant negative *sca* effects were exhibited by five crosses.

Grain yield per plant (g)

For grain yield per plant, two lines, L_1 (3.69) and L_4 (5.98) showed positive and significant *gca* effects, while L_5 (-8.11) showed significant negative *gca* effect. All the testers had highly significant *gca* effects for grain yield, T_2 (8.79) had positive significant *gca* effects, while for T_1 (-5.51) and T_3 (-3.28) negative significance was observed. Five crosses exhibited positive and significant *sca* effects for grain yield per plant, the maximum being L_5 X T_2 (28.29) followed by L_3 X T_2 (12.11) and L_2 X T_2 (8.84). Negative *sca* effects were exhibited by six crosses. The highest negative *sca* effect was noticed for L_3 X T_3 (-16.20).

Hundred seed weight (g)

The *gca* effect of L_5 (-0.32) for 100 seed weight was negative and significant. All other lines and testers showed non-significant *gca* effects for the character. Among the crosses, L_5 X T_2 (0.94) showed positive and significant *sca* effects for 100 seed weight, whereas, L_5 X T_3 (-1.30) and L_2 X T_1 (-0.77) showed significant negative *sca* effects.

Percentage flower bud infestation

For percentage flower bud infestation, two lines, L_3 (6.93) and L_5 (6.04) showed significant positive *gca* effects, while L_2 (-7.73) showed significant negative *gca* effect. Among the testers, T_1 (3.82) exhibited positive and T_2 (-3.38) exhibited

negative *gca* effects. Five crosses exhibited positive and significant *sca* effects for percentage flower bud infestation, the maximum being L_4 X T_2 (18.70) followed by L_2 X T_1 (8.18). Negative *sca* effects were exhibited by four crosses. The highest negative *sca* effect was noticed for L_5 X T_2 (-14.20) followed by L_2 X T_3 (-11.30).

Number of larvae per 25 flowers

L_3 (3.07) and L_5 (3.62) showed significant positive *gca* effects, while L_2 (-4.60) showed significant negative *gca* effect. Among the testers, T_1 (2.55) exhibited positive and T_2 (-2.44) exhibited negative *gca* effects. L_3 X T_3 (6.00), L_4 X T_2 (5.89) and L_2 X T_2 (3.56) showed positively significant *sca* effects, while L_5 X T_2 (-8.67), L_2 X T_3 (-7.78) and L_1 X T_3 (-4.33) showed significant negative *sca* effects.

Percentage pod infestation

Significant positive *gca* effect was noticed for percentage pod infestation in L_3 (10.00). For L_2 (-7.11) and L_4 (-3.33) the effects were negative and significant. The *gca* effects of testers were not significant for the character. Among hybrids, four crosses recorded positive and significant and four crosses recorded negative and significant *sca* effects. The maximum positive and negative effects were observed for L_4 X T_2 (11.90) and L_2 X T_3 (-11.80) respectively.

Number of larval entry/ exit holes per pod

The *gca* effect of L_3 (0.06) was positive and significant. All testers showed non-significant *gca* effects. Among hybrids, two crosses recorded positive and two crosses recorded negative, but significant *sca* effects. The maximum positive and negative effects were observed for L_3 X T_3 (0.14) and L_5 X T_2 (-0.13) respectively.

Number of damaged seeds in 25 pods

Among the lines and testers only the *gca* effect of L_5 (2.50) was positive and significant for number of larval bore holes per pod. Among hybrids, the maximum positive and negative effects were observed for L_3 X T_3 (3.53) and L_5 X T_2 (-4.80) respectively. Two crosses each recorded positive and negative, significant *sca* effects.

Length of peduncle (cm)

L_1 (2.52) and L_4 (3.93) had significant positive *gca* effects, while L_3 (-3.36) and L_5 (-3.93) had significant negative *gca* effects. Among the testers, T_2 (2.38) exhibited positive and T_1 (-2.69) exhibited negative *gca* effects. Four crosses exhibited positive significant *sca* effects. L_5 X T_2 (9.81) had the maximum *sca* effect followed by L_2 X T_3 (8.22) and L_1 X T_3 (2.97). Negative *sca* effects were exhibited by seven crosses.

Density of non-glandular trichomes on pod wall (count/mm^2)

L_2 (0.30) and L_4 (0.45) showed positive and significant *gca* effects for non-glandular trichomes on pod wall, while L_3 (-0.43) showed significant negative *gca* effect. The *gca* effects of the testers were not significant for the character. Among hybrids, six crosses each recorded significant *sca* effects in both directions. The highest positive *sca* effect was noticed for L_3 X T_1 (1.81) followed by L_5 X T_3 (1.24)..

Leaf chlorophyll content (mg/g)

Significant positive *gca* effect was noticed for leaf chlorophyll content in L_3 (0.28). For L_2 (-0.09) and L_4 (-0.12) the effects were negative and significant. Among the testers, T_3 (0.07) showed significant positive *gca* effect. One cross L_4 X T_2 (0.23) recorded positive and three crosses recorded negative, but significant *sca* effects.

Leaf protein content (mg/g)

For leaf protein content, two lines, L_3 (0.94) and L_5 (0.23) showed significant positive *gca* effects, while L_2 (-1.02) showed significant negative *gca* effect. Among the testers, T_3 (0.15) exhibited positive and T_1 (-0.18) exhibited negative *gca* effects. Six crosses exhibited positive and significant *sca* effects for leaf protein content. L_4 X T_2 (1.43) had the maximum *sca* effect followed by L_3 X T_3 (1.00) and L_1 X T_2 (0.88). Negative *sca* effects were exhibited by five crosses.

Pod protein content (mg/g)

For pod protein content also, L_3 (0.56) and L_5 (0.29) showed significant positive *gca* effects, while L_2 (-0.70) showed significant negative *gca* effect. The *gca* effects of the testers were not significant for the character. Among hybrids, five crosses each recorded significant *sca* effects in both directions. The maximum

positive effect was observed for L_4 X T_2 (0.85) followed by L_3 X T_3 (0.84) and L_1 X T_2 (0.72).

Seed protein content (mg/g)

L_3 (0.80) and L_5 (0.11) showed significant positive *gca* effects for seed protein content, while L_2 (-0.73) and L_4 (-0.15) showed significant negative *gca* effects. All the testers had highly significant *gca* effects for seed protein content. T_2 (0.17) and T_3 (0.13) had positive *gca* effects, while for T_1 (-0.30), it was negative. Six crosses exhibited positive and significant *sca* effects for seed protein content. L_4 X T_2 (1.26) had the maximum *sca* effect followed by L_1 X T_2 (0.89) and L_3 X T_3 (0.84). Negative *sca* effects were exhibited by seven crosses.

Crude fibre content of pods (%)

L_2 (0.19) and L_4 (0.09) showed significant positive *gca* effects for crude fibre content of pods, while L_3 (-0.19) and L_5 (-0.11) showed negatively significant *gca* effects. Among the testers, T_2 (0.07) exhibited positive and T_1 (-0.07) exhibited negative *gca* effects. Five crosses each recorded positive and negative, but significant *sca* effects for crude fibre content of pods. The maximum positive and negative effects were observed for L_2 X T_3 (0.28) and L_4 X T_2 (0.30) respectively.

4.3.4 PROPORTIONAL CONTRIBUTION OF LINES, TESTERS AND CROSSES

The relative contribution of lines, testers and hybrids towards the total variation is presented in Table 50.

For days to flowering, the relative contribution of crosses (82.34) was the highest towards total diversity followed by lines (14.65). Crosses (64.07) and testers (25.45) were the major contributors for number of pods per plant. For number of inflorescences per plant and number of pods per inflorescence proportional contribution of crosses and lines were higher than testers.

For plant height and pod length, the relative contribution of testers (1.23 and 1.61 respectively) towards the total variability was much less. In the case of number of seeds per pod and 100 seed weight, the proportional contribution of testers were less than one per cent.

Table 50. Proportional contribution of lines, testers and crosses

Character	Lines	Testers	Crosses
1. Days to 50 % flowering	14.65	3.01	82.34
2. Number of pods per plant	10.48	25.45	64.07
3. Number of inflorescences per plant	26.11	13.13	60.76
4. Number of pods per inflorescence	21.66	9.94	68.40
5. Plant height (cm)	36.97	1.23	61.80
6. Number of branches per plant	22.93	39.18	37.89
7. Pod length (cm)	20.01	1.61	78.38
8. Number of seeds per pod	26.06	0.44	73.50
9. Grain yield per plant (g)	12.86	21.28	65.86
10. Hundred seed weight (g)	11.07	0.34	88.59
11. Percentage flower bud infestation	28.85	7.96	63.19
12. Number of larvae per 25 flowers	28.40	12.75	58.85
13. Percentage pod infestation	41.72	2.00	56.28
14. Number of larval bore holes per pod	16.22	1.91	81.87
15. Number of damaged seeds in 25 pods	22.46	5.92	71.62
16. Peduncle length (cm)	29.21	12.85	59.94
17. Density of non- glandular trichomes on pod wall	11.04	2.01	86.95
18. Leaf chlorophyll content (mg/g)	49.22	6.33	44.45
19. Leaf protein content (mg/g)	36.44	1.68	61.88
20. Pod protein content (mg/g)	33.73	1.08	65.19
21. Seed protein content (mg/g)	30.78	5.74	63.48
22. Crude fibre content (%)	36.47	6.43	57.10

Lines (39.18) contributed maximum to total variability followed by crosses (37.89) for number of branches per plant. For grain yield per plant, contribution of crosses (65.86) towards total variation was maximum followed by that of testers (21.28).

For percentage flower bud infestation and number of larvae per 25 flowers, the relative contribution of lines were almost equal (28.85 and 28.40 respectively). The relative contribution of crosses were maximum towards the total variability for percentage flower bud infestation, number of larvae per 25 flowers, percentage pod infestation, number of larval bore holes per pod and number of damaged seeds in 25 pods (63.19, 58.85, 56.28, 81.87 and 71.62 respectively). In all the cases, proportional contribution of testers were the least.

The relative contribution of crosses were the highest for peduncle length and non-glandular trichome density (59.94 and 86.95 respectively) followed by that of lines (29.21 and 11.04 respectively).

For leaf chlorophyll content, the proportional contribution of lines was the highest (49.22) followed by crosses (44.45). Crosses contributed maximum towards total variability for leaf protein content, pod protein content, seed protein content and crude fibre content of pods (61.88, 65.19, 63.48 and 57.10) followed by lines (36.44, 33.73, 30.78 and 36.47 respectively).

4.4 Experiment IV

Generation mean analysis was done for the best cross, L_4 X T_3 (Plate 7) selected from Experiment III with respect to the 22 characters. The means of the six populations, *viz*., P_1, P_2, F_1, F_2, B_1 and B_2 with respect to the different characters are provided in Table 51. The scale values and estimates of genetic components are given in Table 52.

Days to 50 per cent flowering

P_2 recorded the maximum mean values for days to flowering (38.03) among the six generations, while the minimum days to flowering was noticed in the F_1 generation (32.47). Days to flowering in the F_1 and F_2 generation were lower than

Table 51. Generation mean values (± SE) for the selected cross

Character	Generations					
Character	P_1	P_2	F_1	F_2	B_1	B_2
Days to 50 % flowering	33.33 ± 0.23	38.03 ± 0.24	32.47 ± 0.20	33.08 ± 0.36	34.53 ± 0.27	37.18 ± 0.29
Number of pods per plant	25.33 ± 0.47	17.33 ± 0.54	40.10 ± 1.22	40.48 ± 1.12	33.65 ± 0.40	28.23 ± 0.48
Number of inflorescences per plant	13.83 ± 0.30	9.80 ± 0.21	13.67 ± 0.36	15.28 ± 0.47	13.55 ± 0.34	12.02 ± 0.36
Number of pods per inflorescence	2.77 ± 0.15	2.06 ± 0.09	3.29 ± 0.11	3.14 ± 0.10	2.85 ± 0.06	2.05 ± 0.07
Plant height (cm)	63.44 ± 0.57	57.48 ± 0.82	58.73 ± 0.53	57.98 ± 0.86	58.73 ± 0.78	55.25 ± 1.10
Number of branches per plant	6.33 ± 0.19	4.23 ± 0.15	7.20 ± 0.12	6.77 ± 0.21	6.00 ± 0.20	4.80 ± 0.16
Pod length (cm)	16.17 ± 1.03	12.54 ± 0.14	15.79 ± 0.15	15.25 ± 0.27	15.09 ± 0.09	12.78 ± 0.12
Number of seeds per pod	14.90 ± 0.22	11.97 ± 0.22	15.70 ± 0.21	15.37 ± 0.24	15.97 ± 1.67	12.40 ± 0.23
Grain yield per plant (g)	61.21 ± 0.85	28.72 ± 0.51	80.84 ± 1.24	76.59 ± 1.75	61.59 ± 0.80	37.74 ± 0.59
Hundred seed weight (g)	13.21 ± 0.15	10.47 ± 0.16	13.58 ± 0.10	14.44 ± 0.26	12.41 ± 0.09	11.25 ± 0.12
Percentage flower bud infestation	32.13 ± 0.65	14.13 ± 0.42	15.20 ± 0.45	16.60 ± 0.97	22.14 ± 0.90	16.67 ± 0.41
Number of larvae per 25 flowers	16.47 ± 0.33	5.20 ± 0.23	6.20 ± 0.18	7.32 ± 0.52	8.67 ± 0.33	5.87 ± 0.25
Percentage pod infestation	29.20 ± 0.82	12.40 ± 0.62	14.00 ± 0.46	14.13 ± 0.86	26.00 ± 0.72	10.27 ± 0.37
Number of larval bore holes per pod	0.27 ± 0.01	0.13 ± 0.01	0.14 ± 0.01	0.16 ± 0.01	0.24 ± 0.01	0.17 ± 0.01
Number of damaged seeds in 25 pods	17.83 ± 0.39	8.60 ± 0.20	9.33 ± 0.21	9.50 ± 0.59	11.97 ± 0.41	9.72 ± 0.24
Peduncle length (cm)	28.49 ± 0.35	36.53 ± 0.44	35.33 ± 0.40	34.00 ± 0.59	39.47 ± 0.36	27.55 ± 0.37
Density of non- glandular trichomes	3.67 ± 0.06	6.98 ± 0.09	6.52 ± 0.08	6.79 ± 0.11	3.03 ± 0.05	7.45 ± 0.07
Leaf chlorophyll content (mg/g)	1.62 ± 0.02	1.19 ± 0.01	1.20 ± 0.02	1.27 ± 0.02	1.68 ± 0.01	1.10 ± 0.01
Leaf protein content (mg/g)	21.71 ± 0.18	17.83 ± 0.13	19.10 ± 0.15	19.29 ± 0.21	20.86 ± 0.07	19.45 ± 0.08
Pod protein content (mg/g)	23.01 ± 0.14	18.67 ± 0.22	20.35 ± 0.20	19.79 ± 0.21	22.02 ± 0.10	18.47 ± 0.08
Seed protein content (mg/g)	23.25 ± 0.37	19.27 ± 0.17	19.83 ± 0.13	20.09 ± 0.27	21.90 ± 0.10	19.60 ± 0.16
Crude fibre content (%)	1.96 ± 0.02	2.49 ± 0.02	2.28 ± 0.01	2.20 ± 0.03	1.85 ± 0.01	2.52 ± 0.01

Table 52. Scale values (± SE) and estimates of genetic components (± SE)

Character	Scale values				Genetic components					
	A	B	C	D	m	d	h	i	j	l
Days to 50% flowering	3.27**± 0.63	3.87** ± 0.66	-3.97* ± 1.54	-5.55** ± 0.83	33.08** ± 0.36	-2.65** ± 0.40	7.88** ± 1.68	11.10** ± 1.66	-0.30 ± 0.43	-18.23** ± 2.22
Pods per plant	1.86 ± 1.54	-0.97 ± 1.64	39.07** ± 5.14	19.08** ± 2.32	40.48** ± 1.12	5.42** ± 0.62	-19.40** ± 4.81	-38.17** ± 4.64	1.42 ± 0.72	37.27** ± 5.71
Inflorescence per plant	-0.40 ± 0.82	0.57 ± 0.84	10.17** ± 2.06	5.00** ± 1.06	15.28** ± 0.47	1.53** ± 0.50	-8.15** ± 2.17	-10.00** ± 2.13	-0.48 ± 0.53	9.83** ± 2.86
Pods per inflorescence	-0.36 ± 0.22	-1.24** ± 0.20	1.15* ± 0.47	1.37** ± 0.21	3.14** ± 0.10	0.80** ± 0.10	-1.88** ± 0.44	-2.75** ± 0.42	0.44** ± 0.12	4.35** ± 0.59
Plant height (cm)	-4.70** ± 1.74	-5.70* ± 2.41	-6.47 ± 3.70	1.96 ± 2.17	57.98** ± 0.85	3.48* ± 1.35	-5.66 ± 4.41	-3.93 ± 4.35	0.50 ± 1.44	14.33* ± 6.54
Branches per plant	-1.53** ± 0.46	-1.87** ± 0.37	2.07* ± 0.92	2.73** ± 0.50	6.77** ± 0.21	1.20** ± 0.26	-3.57** ± 1.01	-5.47** ± 1.00	0.17 ± 0.28	8.87** ± 1.38
Pod length (cm)	-1.77 ± 1.06	-2.77** ± 0.32	0.69 ± 1.52	2.62** ± 0.56	15.25** ± 0.27	2.31** ± 0.15	-3.80** ± 1.24	-5.23** ± 1.11	0.50 ± 0.54	9.77** ± 1.64
Seeds per pod	1.27 ± 3.35	-2.95** ± 0.55	3.06** ± 1.10	2.37 ± 1.75	15.37** ± 0.24	3.58* ± 1.69	-2.41 ± 3.52	-4.74 ± 3.51	2.11 ± 1.69	6.42 ± 6.83
Grain yield per plant (g)	-18.87** ± 2.20	-34.09** ± 1.79	54.74** ± 7.51	53.86** ± 3.65	76.59** ± 1.75	23.85** ± 0.99	-71.84** ± 7.41	-107.7** ± 7.29	7.61** ± 1.11	160.68** ± 8.49
Hundred seed weight	-1.96** ± 0.25	-1.55** ± 0.30	6.91** ± 1.09	5.21** ± 0.54	14.44** ± 0.26	1.16** ± 0.15	-8.68** ± 1.10	-10.42** ± 1.09	-0.21 ± 0.18	13.93 ± 1.24
% flower bud infestation	-3.06 ± 1.96	4.00** ± 1.01	-10.27* ± 4.05	-5.60* ± 2.17	16.60** ± 0.97	5.47** ± 0.98	3.28 ± 4.39	11.21* ± 4.35	-3.53** ± 1.06	-12.15* ± 5.65
Larvae per 25 flowers	-5.33** ± 0.76	0.33 ± 0.59	-4.80* ± 2.14	0.10 ± 1.12	7.32** ± 0.52	2.80** ± 0.42	-4.83* ± 2.25	-0.20 ± 2.23	-2.83** ± 0.46	5.20 ± 2.71
% pod infestation)	8.80** ± 1.72	-5.87** ± 1.07	-13.07** ± 3.70	-8.00** ± 1.90	14.13** ± 0.86	15.73** ± 0.81	9.20* ± 3.86	16.00** ± 3.80	7.33** ± 0.96	-18.93** ± 4.92
Larval bore holes per pod	0.06** ± 0.07	0.07** ± 0.01	-0.06 ± 0.04	-0.09** ± 0.02	0.16** ± 0.01	0.07** ± 0.01	0.13** ± 0.03	0.19** ± 0.03	0.00 ± 0.01	-0.32** ± 0.04
Damaged seeds/25 pods	-3.23** ± 0.93	1.50** ± 0.56	-7.10** ± 2.43	-2.68* ± 1.27	9.50** ± 0.59	2.25** ± 0.47	1.48 ± 2.56	5.37* ± 2.54	-2.37** ± 0.52	-3.63 ± 3.09
Peduncle length (cm)	15.12** ± 0.90	-16.77** ± 0.95	0.32 ± 2.54	0.99 ± 1.28	34.00** ± 0.59	11.93** ± 0.52	0.85 ± 2.61	-1.97 ± 2.56	15.9** ± 0.59	3.62 ± 3.28
Trichome density	-4.13** ± 0.15	1.40** ± 0.19	3.48** ± 0.50	3.11** ± 0.25	6.79** ± 0.11	-4.43** ± 0.09	-5.03** ± 0.50	-6.22** ± 0.49	-2.77** ± 0.10	8.95** ± 0.60
Leaf chlorophyll	0.54** ± 0.04	-0.12** ± 0.03	-0.07 ± 0.10	-0.24** ± 0.05	1.27** ± 0.02	0.59** ± 0.02	0.32** ± 0.10	0.49** ± 0.10	0.33** ± 0.02	-0.90** ± 0.12
Leaf protein (mg/g)	0.92** ± 0.27	1.96** ± 0.25	-0.59 ± 0.92	-1.73** ± 0.44	19.29** ± 0.21	1.42** ± 0.11	2.80** ± 0.89	3.47** ± 0.87	-0.52** ± 0.15	-6.34** ± 1.02
Pod protein (mg/g)	0.69* ± 0.31	-2.09** ± 0.34	-3.22** ± 0.98	-0.92* ± 0.45	19.79** ± 0.21	3.56** ± 0.13	1.34 ± 0.92	1.83* ± 0.90	1.39** ± 0.18	-0.43 ± 1.11
Seed protein (mg/g)	0.72 ± 0.44	0.09 ± 0.38	-1.83 ± 1.17	-1.32* ± 0.56	20.09** ± 0.27	2.30** ± 0.19	1.22 ± 1.15	2.64* ± 1.13	0.32 ± 0.28	-3.45* ± 1.39
Crude fibre (%)	-0.54** ± 0.04	0.26** ± 0.04	-0.20 ± 0.13	0.04 ± 0.06	2.20** ± 0.03	-0.67** ± 0.02	-0.02 ± 0.13	- 0.08 ±0.13	-0.40** ± 0.02	0.35* ± 0.15

** Significant at 1 per cent level

* Significant at 5 per cent level

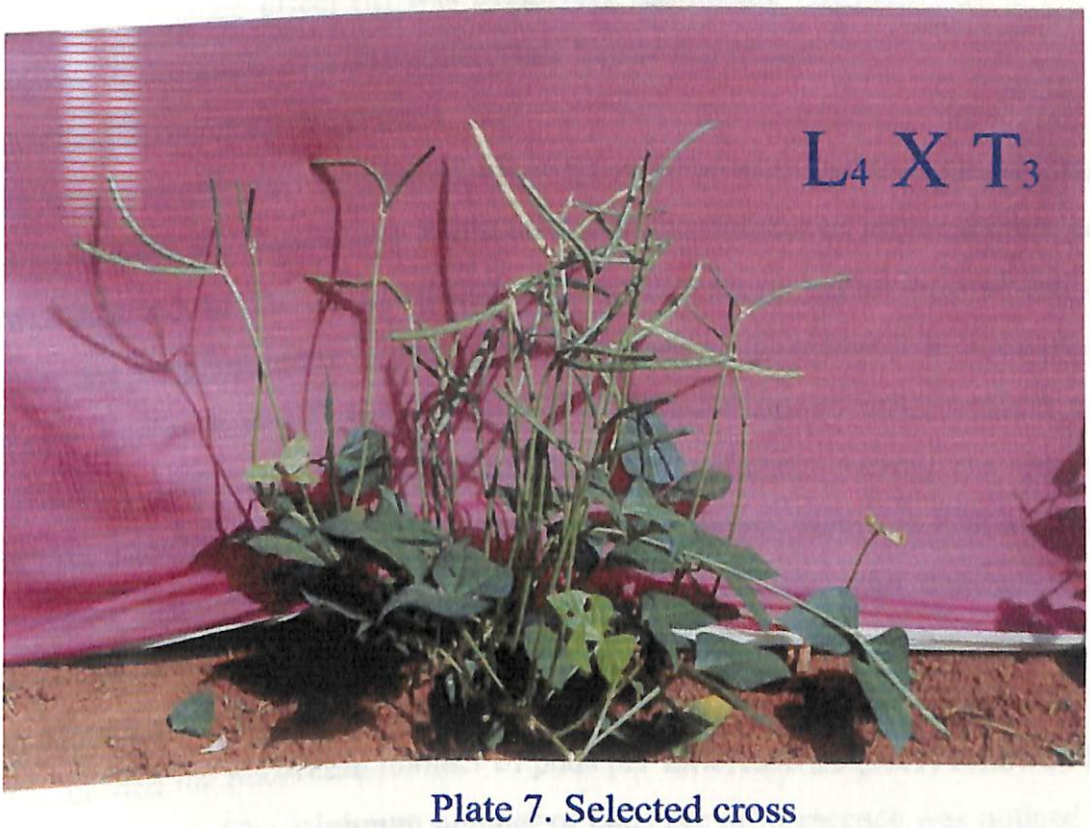


Plate 7. Selected cross

that in the other generations. Scales A and B were positive and highly significant. Additive gene effect (d) was significant. All gene effects other than additive X dominance (j) interaction were highly significant.

Number of pods per plant

The number of pods per plant was high in F_1 (40.10) and F_2 (40.48) generations. The least number of pods per plant was recorded in P_2 (17.33). The number of pods in the B_1 and B_2 generations were higher than the parental generations. Scales A and B were not significant, while C and D were highly significant. Dominance effect (h) was negatively significant. All gene effects other than additive X dominance (j) interaction were highly significant.

Number of inflorescences per plant

F_2 recorded the maximum mean value for number of inflorescences per plant (15.28) among the six generations, while the minimum number of inflorescences per plant was noticed in the P_2 generation (9.80). The mean value for number of inflorescences per plant in the F_1 and F_2 generation were higher than that in the other generations. Scales A and B were not significant for number of inflorescences per plant, while C and D were positive and highly significant. Among the genetic components, dominance effect (h) was negatively significant. Additive X dominance (j) interaction was not significant, while additive X additive and dominance X dominance interaction were highly significant.

Number of pods per inflorescence

F_1 recorded the maximum number of pods per inflorescence (3.29) followed by F_2 generation (3.14). The minimum number of pods per inflorescence was noticed in B_2 generation (2.05). Scales B and D were highly significant for the character. All gene effects and gene interactions were also highly significant. The magnitude of dominance x dominance (l) interaction was higher than all other gene interactions.

Plant height

The highest mean value for plant height (cm) was noticed in P_1 (63.44), while B_2 recorded the least plant height (55.25). Scale A value was negative and

significant, while scale C and D were not significant. Additive (d) genetic effect and dominance x dominance (l) gene interaction were significant.

Number of primary branches

F_1 recorded the maximum number of primary branches per plant (7.20) followed by F_2 generation (6.77). The least value was noticed in P_2 generation (4.23). Scales A and B were negative and highly significant, while scale C and D was positively significant. Dominance X dominance (l) was higher in magnitude than other effects. Dominance effect (h) was highly significant and negative. All gene effects except additive X dominance (j) interaction were highly significant.

Pod length

Pod length (cm) was maximum in P_1 (16.17) and minimum in P_2 (12.54). Mean values for the character in the B_1 and B_2 generations were intermediate to the parental generations. Significance of scale B indicate the presence of non-allelic interactions in the expression of the character. All gene effects other than additive X dominance (j) interaction were highly significant. Dominance effect (h) was negatively significant.

Number of seeds per pod

B_1 recorded the highest mean value (15.97) followed by F_1. The least number of seeds per pod was noticed in P_2 (11.97). Scale B was significantly negative, while scale D was significantly positive. Additive (d) genetic effect was significant.

Grain yield per plant

F_1 recorded the maximum grain yield per plant (80.84) followed by F_2 generation (76.59). The least mean value for grain yield was noticed in P_2 generation (28.72). All the scales were highly significant indicating the presence of epistasis in the expression of the character. All the genetic components were also found highly significant. Dominance (h) gene effect was negative.

Hundred seed weight

F_2 recorded the maximum mean value (14.44) among the six generations, while the minimum value was noticed in P_2 (10.47). The mean values in the B_1 and B_2

generations were in between the parental means. All the scales were highly significant indicating gene interactions. Additive and dominant gene effects were highly significant, but only additive X additive (i) interaction was significant.

Percentage infestation of flower buds

The highest percentage of flower bud infestation was observed in P_1 (32.13) and the least in P_2 generation (14.13). Scale B was highly significant underlining the presence of epistatic gene action for the character. Scale C and D were negative and significant. Positive and highly significant additive gene effects were noticed. Additive x dominance (j) and dominance X dominance (l) gene interaction were significant and dominance X dominance interaction was in the negative direction.

Number of larvae per 25 flowers

The mean value for number of larvae per 25 flowers was maximum in P_1 (16.47) and the minimum in P_2 (5.20). All generations recorded much lower mean values for the character compared to the P_1 generation. High significance of scale A was noticed indicating gene interactions in the expression of the character. Scale C was also significant. d was highly significant underlining additive gene effects. Additive x dominance (j) gene interaction was also significant.

Percentage pod infestation

Maximum percentage of flower bud infestation was observed in P_1 (29.20) and the least in B_2 generation (10.27). All generations except P_1 and B_1 recorded low mean values. All the four scales were significant. Dominance X dominance (l) gene interaction had the highest magnitude of gene interaction in the negative direction.

Number of larval entry / exit holes per pod

The highest number of larval bore holes per pod was observed in P_1 (0.27) and the least in P_2 generation (0.13). Scale A, B and D were highly significant. All gene effects except additive X dominance (j) interaction were also highly significant.

Number of damaged seeds in a sample of 25 pods

The mean value for number of damaged seeds per 25 pods was maximum in P_1 (17.83) and the minimum in P_2 (8.60). All generations recorded low number of

damaged seeds for the character compared to the P_1 generation. All the four scales were significant. d was highly significant indicating additive gene effects. Additive X additive and additive X dominance interaction were significant.

Length of peduncle

Peduncle length was maximum in the B_1 generation (39.47) and minimum in the B_2 generation (27.55). Scales A and B were highly significant indicating non-allelic interactions. d and j highly significant suggesting additive gene effects and additive X dominance gene interactions.

Density of non-glandular trichomes on pod wall

B_2 generation exhibited the maximum mean value for density of non-glandular trichomes on pod wall (7.45). The least density of non-glandular trichomes was noticed in the B_1 generation (3.03). All the four scales were significant, scale A being negative and having the highest magnitude. All the genetic components were also highly significant for the character.

Leaf chlorophyll content

The content of chlorophyll (mg/g)in the leaf tissues was highest in B_1 (1.68) and the lowest in B_2 generation (1.10). Scales A, B and D were highly significant. All the genetic components were also highly significant for leaf chlorophyll content.

Leaf protein content

The highest mean value for leaf protein content (mg/g) was observed in P_1 (21.71) and the least in P_2 generation (17.83). Scales A, B and D were highly significant pointing out to the presence of gene interactions. All the different genetic components were also highly significant for the character.

Pod protein content

Pod protein content (mg/g) was maximum in the in P_1 (23.01), while the least mean value was observed in B_2 (18.47). Scales B and C were negative and highly significant. d was significant among the gene effects. Additive X dominance (j) gene interaction was also highly significant.

Seed protein content

The highest mean value for seed protein content (mg/g) was recorded in P_1 generation (23.25) and the least in P_2 (19.27). The scale values except D were not significant indicating additive X additive gene interaction. d and i were significant, while l was negatively significant.

Crude fibre content of pods

Crude fibre content of pods (%) was highest in B_2 generation (2.52) and the least in B_1 (1.85). The mean value for crude fibre content of pods in the F_1 and F_2 generation were intermediate to both the parental and backcross generations. Significance of scales A and B indicate epistatic gene interactions. Additive effect, additive X additive and domimance X dominance interactions were significant. Dominance X dominance interactions were positive. A predominance of additive gene effects were noticed in the expression of crude fibre content of pods.

Discussion

5. DISCUSSION

The results obtained from the various field experiments conducted for the present study are discussed herewith under different headings.

5.1 VARIABILITY

The breeding methodology, effectiveness of selection and ultimate improvement depends on the variability present in the germplasm (Zelleke, 2000). Fifty genotypes of cowpea obtained from various sources were evaluated for resistance to legume pod borer and yield. The analysis of variance and estimation of genetic variability indicated the presence of a broad spectrum of variability in the population.

5.1.1 Pod Borer Damage and Plant Resistance Indices

All the damage measurements exhibited remarkable variability with respect to different genotypes. Percentage flower bud infestation and intensity of flower infestation reflect the ultimate severity of yield loss due to legume pod borer, since the damages to flower buds and flowers results in cent percent yield loss. For both characters, 14 genotypes recorded low levels of infestation compared to others.

Eight genotypes out of the 50 genotypes exhibited low levels of pod damage and 11 genotypes recorded low number of larval bore holes per pod. Three genotypes had low number of damaged seeds per 25 pods also. For all the damage measurements, the selected testers *viz*., T_{45}, T_{47}, and T_{49} exhibited values falling within low levels of infestation, in spite of the high variability noticed for these characters. Panicker (2000) and Vidya (2000) have earlier reported significant variability for the legume pod borer damage measurements.

High coefficients of both phenotypic and genotypic variation were noticed for all the damage parameters. These results indicate the presence of large amount of useful variability for these characters and suggest the suitability of obtaining pest resistant types by direct selection based on visual assessment.

Seed damage indices and plant resistance 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 views of Panicker (2000) and Vidya (2000). High PCV and GCV were noticed for both the indices also.

Plant resistance index served as the selection criterion for identifying the testers. The plant resistance indices were minimum for T_{45}, T_{47} and T_{49} which were statistically on par with each other, and significantly different from other genotypes.

5.1.2 Morphological and Biochemical Characters

Significant variability was present for the different morphological and biochemical characters among the 50 genotypes. The two morphological attributes, peduncle length and non-glandular trichome density exhibited high range of variability. This result is in agreement with findings of Panicker (2000). Dwivedi *et al.* (1999) also observed high variation for peduncle length. Density of non-glandular trichomes on pod wall had high PCV and GCV, but for peduncle length, coefficients of variation were moderate. The content of chlorophyll 'a' in the leaf tissues were generally higher than that of chlorophyll 'b'. Eight genotypes recorded high values for total chlorophyll content compared to others. The ratio of chlorophyll 'a' to 'b' exhibited low mean values for 24 out of the fifty genotypes. High range of variability for total chlorophyll was reported by Backiyarani *et al*. (2000) and Panicker (2000). The characters possessed low to moderate coefficients of variation, limiting the scope of improvement through direct selection.

5.1.3 Yield Characters

Broad spectrum of genetic variability is a pre-requisite for the identification of superior genotypes from the array of diverse genotypes in the population (Allard, 1960). The magnitude of variability is of utmost importance as it provides the scope for effective selection.

All the ten yield characters exhibited wide range of variation among the 50 genotypes screened for yield. Some of the similar reports highlighting the extent of variability in cowpea with respect to the different characters are listed herewith.

Days to flowering (Sobha *et al*., 1998; Backiyarani *et al*., 2000; Tyagi *et al*., 2000; Ajith, 2001; Anbuselvam *et al*., 2001and Kavita *et al*., 2003).

Number of pods per plant (Gowda *et al*., 1991; Mehta and Zaveri, 1998; Resmi, 1998; Sobha *et al*., 1998; Dwivedi *et al*., 1999; Chattopadhyay *et al*., 2001and Henry, 2002).

Number of inflorescences per plant and number of pods per inflorescence (Rejatha, 1992; Mehta and Zaveri, 1998; Tyagi *et al*., 2000; Vidya, 2000 and Arunachalam *et al*., 2002).

Plant height and number of branches per plant (Sudhakumari, 1993; Sobha *et al*., 1998; Backiyarani *et al*., 2000; Ajith, 2001; Anbuselvam *et al*., 2001; Jyothi, 2001and Purushotham *et al*., 2001).

Pod length and number of seeds per pod (Rejatha, 1992; Sudhakumari, 1993; Ajith, 2001; Anbuselvam *et al*., 2001and Chattopadhyay *et al*., 2001).

Yield per plant and 100 seed weight (Gowda *et al*., 1991; Sudhakumari, 1993; Dwivedi *et al*., 1999; Tyagi *et al*., 2000; Henry, 2002 and Yadav *et al*., 2002).

Coefficients of variation gives a unit free comparison of characters measured in different units. Further, the magnitude of the coefficients of variation dictates the appropriate breeding strategy suitable for improving each character.

Number of pods per plant, grain yield and 100 seed weight showed high PCV and GCV, while number of inflorescences per plant and plant height had low coefficients of variation. The other characters exhibited moderate PCV and GCV. Ajith (2001) and Nehru and Manjunath (2001) reported high PCV and GCV for yield per plant and number of pods per plant, while contradictory results were reported by Venkatesan *et al*. (2003a). Ajith (2001) and Anbuselvam *et. al*. (2001) also pointed out high PCV and GCV for number of inflorescences per plant and plant height which is contrary to the present results.

The results suggests that there is ample scope for direct selection based on plant types with high yield, more number of pods with larger grains in the process of developing high yielding varieties. However, selection of tall plant types with more number of clusters is of limited application in yield improvement.

5.2 HERITABILITY AND GENETIC ADVANCE

5.2.1 Damage and Related Characters

Heritability and genetic advance provides a clear insight into the extent of heritable variability present in a population. The observed variability in a population is the sum of variability due to genotypic and environmental effects. Hence, knowledge on the nature and magnitude of genetic variation resulting in genetic gain under selection is essential for effective selection (Allard, 1960).

All the characters showed high heritability estimates (Fig 1). High genetic advance was also observed for all the characters except content of chlorophyll 'a', which recorded moderate genetic advance. Ram and Singh (1997) reported high heritability for peduncle length.

High heritability coupled with high genetic advance noticed for most characters is a desirable phenomenon from the breeder's point of view. This feature is an indication of the underlying additive gene action which suggests that immense improvement is possible for the characters through selection.

5.2.2 Yield and Related Characters

The phenotypic expression is an unreliable indicator of the genotype for quantitative characters, hence it is desirable to evaluate the genetic value of the genotypes prior to selection. Selection based on characters with high heritability combined with high genetic advance provides a better tool for indicating the response to selection (Johnson *et al*., 1955).

High heritability was noticed for all the yield characters except days to 50 per cent flowering and number of inflorescences per plant, which exhibited moderate heritability (Fig 2). Malarvizhi (2002) reported moderate heritability for number of inflorescences per plant. On the contrary, high heritability for days to flowering and

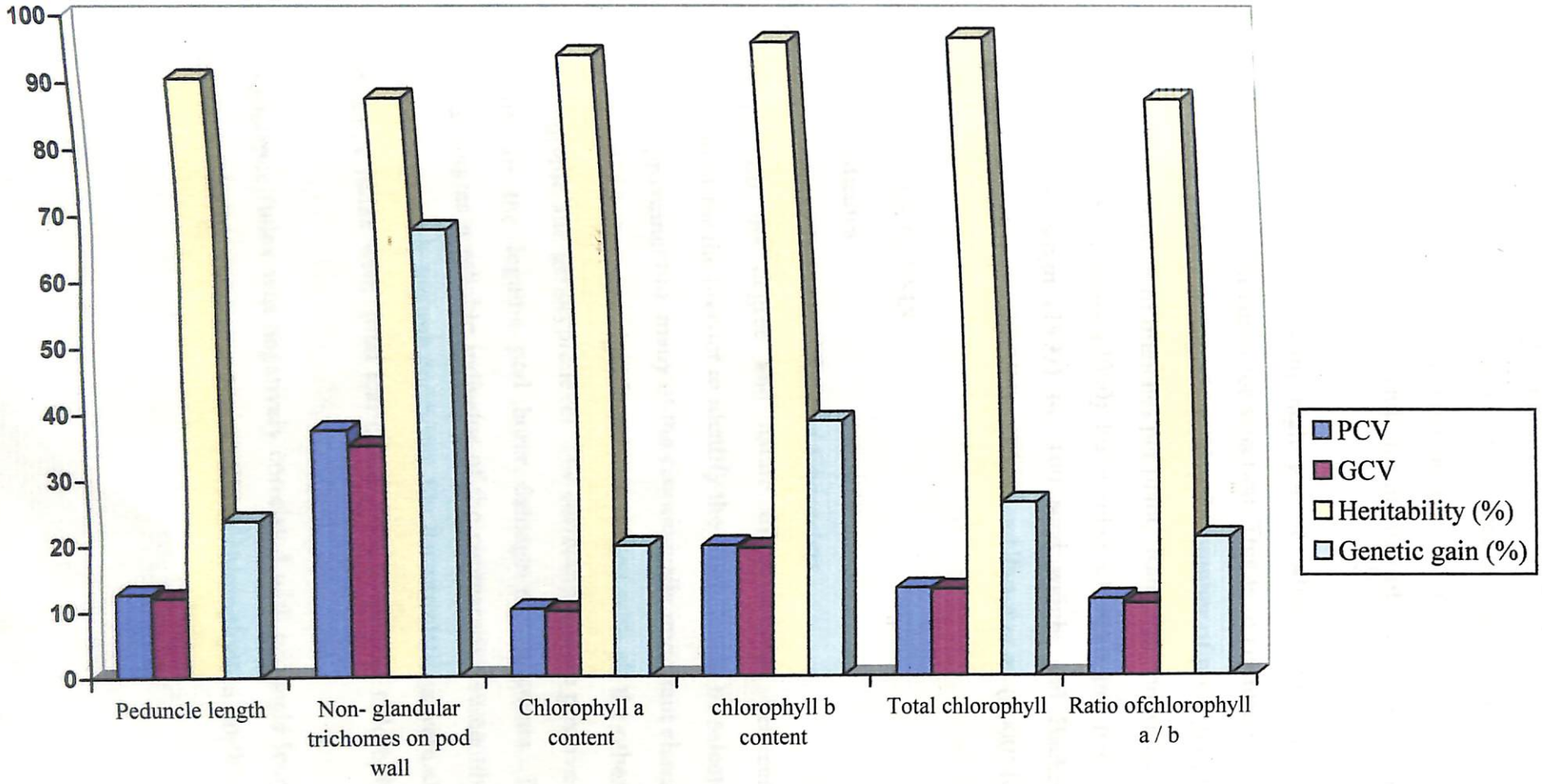


Fig 1. Genetic parameters for the biochemical and morphological traits

number of inflorescences per plant were projected by Ajith (2001). Ravindran and Das (1997) observed low heritability for number of pods per plant.

Seven characters including grain yield, number of 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 number of inflorescences per plant it was low.

High heritability coupled with high genetic advance for the major yield characters offers congenial situation for selection. This is in conformity with reports of Thiyagarajan *et al*. (1989) and Jyothi (2001) for number of pods per plant, Mehta and Zaveri (1998) for number of branches per plant, Rangaiah and Mahadevu (1999) and Kalaiyarasi and Palanisamy (2000) for number of seeds per pod, Sreekumar (1995) and Ram and Singh (1997) for 100 seed weight and Backiyarani and Nadarajan (1996), Panicker (2000), Vidya (2000) and Tyagi *et al*. (2000) for yield per plant.

5.3 ASSOCIATION ANALYSIS

5.3.1 Correlation Studies

5.3.1.1 Plant Resistance Index and Related Characters

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

Plant resistance index was significantly correlated with all the other characters both at the phenotypic and genotypic level. The correlations were positive and highly significant with all the legume pod borer damage measurements. Thus, plant resistance index acts as a reliable indicator of the comparative susceptibility of the different genotypes towards legume pod borer. Similar correlations were also noticed for plant resistance index with total leaf chlorophyll, content of chlorophyll ‘a’ and chlorophyll ‘b’.

Plant resistance index was negatively correlated with peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll ‘a’ to ‘b’. This result

agrees with the reports of Oghiakhe *et.al*. (1992d), Veeranna and Hussain (1997) and Panicker (2000) for non-glandular trichome density on pod wall, but is in disagreement to the reports of Panicker (2000) for peduncle length.

All the damage parameters were significantly and positively correlated among themselves both at phenotypic and genotypic level, which is in agreement with the findings of Panicker (2000) and Vidya (2000) that percentage pod infestation was positively correlated with other damage parameters. But, the same authors have also placed a contradictory view by emphasizing that flower damage was not correlated with pod or seed damage. Further, Jackai (1982) and Panicker *et al*. (2002) also published similar results.

All the damage parameters in general showed highly significant positive correlations with content of chlorophyll 'a', chlorophyll 'b' and total chlorophyll, whereas, highly significant negative correlations were noticed for these characters with peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll 'a' to chlorophyll 'b'.

Non-glandular trichome density and peduncle length were negatively correlated with the damage measurements and plant resistance index indicating that cowpea types with long peduncles and more trichomes on pod wall suffered less attack by legume pod borer.

Singh (1978), van Emden (1989) and Oghiakhe *et.al*. (1991b) has published confirmatory reports that cowpea varieties with upright and long peduncles that hold flowers and pods away from the canopy as well as from each other suffered less damage by legume pod borer under field conditions. However Panicker (2000) noticed a contradictory result that peduncle length was not correlated with legume pod borer infestation. According to Perrino *et al*. (1993), peduncle length in cowpea was not correlated with any other character.

The different legume pod borer damage parameters and plant resistance index were positively correlated with content of chlorophyll 'a', chlorophyll 'b' and total chlorophyll in the leaf tissue. This result is supported by the findings of Oghiakhe

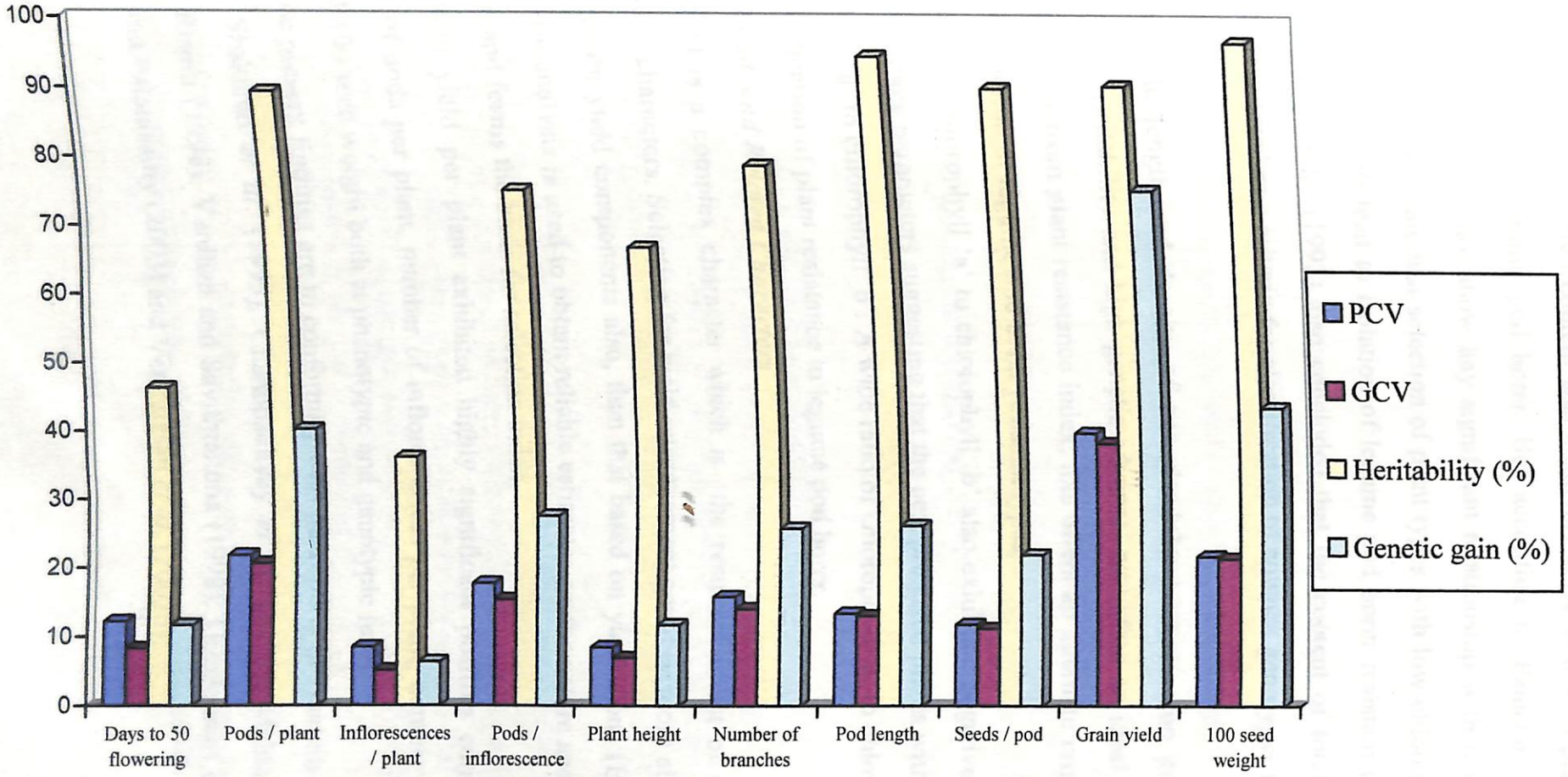


Fig 2. Genetic parameters for the yield traits in cowpea

(1992) that total chlorophyll content was positively correlated with plant resistance index in relation to legume pod borer. But according to Panicker (2000), total chlorophyll content did not show any significant relationship with plant resistance index. The results indicate that selection of plant types with low chlorophyll content in the leaf tissue will lead to isolation of legume pod borer resistant types in later generations. Oghiakhe (1992) also concluded that the content of total chlorophyll could be considered as a criteria for classification of cowpea genotypes for resistance to the pest.

Peduncle length and density of non-glandular trichomes on pod wall also possess high heritability and high genetic advance, providing an ideal situation for selection. Apart from plant resistance index, this offers an alternate criterion for the effective selection of legume pod borer resistant types.

Ratio of chlorophyll 'a' to chlorophyll 'b' also exhibited negative correlations with the damage parameters suggesting that the pest preferred plants with low ratio of chlorophyll 'a' to chlorophyll 'b'. A wide ratio of chlorophyll 'a' to chlorophyll 'b' is thus an indication of plant resistance to legume pod borer.

5.3.1.2 Yield and Related Characters

Yield is a complex character which is the resultant effect of a number of component characters. Selection for yield improvement could be more effective when it is based on yield components also, than that based on yield alone (Evans, 1978). Correlation analysis is used to obtain reliable estimates on the nature and direction of selection and forms the basis for selection index.

Grain yield per plant exhibited highly significant positive correlation with number of pods per plant, number of inflorescences per plant, number of seeds per pod and 100 seed weight both at phenotypic and genotypic level.

The present findings are in conformity with the reports of Hussein and Farghali (1995), Shakarad *et al*. (1995), Chattopadhyay *et al*. (1997), Mehta and Zaveri (1998), Resmi (1998), Vardhan and Savithramma (1998), Ushakumari *et al*. (2002), Neema and Palanisamy (2003) and Venkatesan *et al*. (2003b).

Number of pods per plant showed positive correlation coefficients with number of branches per plant, pod length, number of seeds per pod, and 100 seed weight and negative correlations with days to flowering and plant height. Sudhakumari (1993), Sobha (1994), Sudhakumari and Gopimony (1994) and Rangaiah (2000) observed similar trend of associations in cowpea. However, Chauhan and Joshi (1980) and Tamilselvam and Das (1994) observed that number of pods per plant and 100 seed weight in cowpea were negatively correlated with each other.

Number of inflorescences per plant showed highly significant positive correlations with number of pods per plant and number of pods per inflorescence. Naidu *et al.* (1996) has published a similar view with respect to number of inflorescences per plant.

Significant positive association was noticed for pod length with number of seeds per pod both at phenotypic and genotypic level. Chattopadhyay *et al*. (1997), Panicker (2000) and Neema and Palanisamy (2001) has earlier noticed a similar nature of correlation in cowpea.

Days to flowering had negative phenotypic associations with all characters except plant height, pod length and number of seeds per pod. This agrees with the reports of Sreekumar *et al*. (1996) and Chattopadhyay *et al*. (1997). Selection should be practiced for early flowering and dwarf plants in order to get an appreciable level of yield improvement.

The nature and magnitude of association between yield and related traits imply that selection for plant types based on more than one character will ultimately lead to high improvement in yield. Plant types with more number of pods and pod clusters per plant, more number of seeds per pod and larger seeds provide an ideal base material for effective selection for yield enhancement.

5.3.2 Path Analysis

Some characters exhibit statistically non- significant correlation with yield, but exert significant indirect influence on yield through other component characters. Path

coefficient analysis is used to separate the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959).

Maximum positive direct effect on grain yield was exerted by number of pods per plant followed by 100 seed weight and number of seeds per pod. The high correlation coefficients of number of pods per plant with grain yield could be attributable to its high positive direct effect. The results are also supported by the findings of Kalaiyarasi and Palanisamy (2001), Neema and Palanisamy (2001), Ushakumari *et al*. (2002) and Subbiah *et al*. (2003) with respect to different characters.

Murthy (1982) identified number of pods per plant and number of seeds per pod as the major contributors to yield in cowpea. Patnaik and Roquib (1990) and Sawant (1994a) also opined that number of seeds per pod was the major contributor towards grain yield in cowpea. Kalaiyarasi and Palanisamy (2002) observed positive direct effect of number of seeds per pod and negative direct effect of 100 seed weight on grain yield.

The correlation of number of inflorescences per plant and number of pods per inflorescence with grain yield were significant, these characters also exerted high positive indirect effect on grain yield through number of pods per plant. Ushakumari *et al*. (2002) also published similar reports. But Panicker (2000) reported negative direct effect of number of inflorescences per plant on grain yield.

Similarly, pod length showed insignificant correlation with grain yield, but it contributed to yield through positive indirect effects through all other characters. Sobha (1994) and Vardhan and Savithramma (1998), on the contrary, reported high positive direct effect of pod length on grain yield.

5.4 SELECTION INDEX

The use of a selection index offers ample scope for the breeder for effective selection based on component characters rather than direct selection based on yield alone. Superior genotypes can be selected from a collection of germplasm using a

selection index employing the discriminant function for characters with favourable association.

The selection indices were worked out for the fifty genotypes on the basis of yield and six compenent characters *viz*., number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, number of seeds per pod and 100 seed weight. The genotypes T_2, T_4, T_6, T_7 and T_8 were selected as parents, on the basis of index scores.

5.5 GENETIC DIVERGENCE ANALYSIS

The effective utilization of heterosis depends on the genetic divergence between the parents for the particular character. If the parents selected for hybridization are more genetically diverse within a reasonable range, the chance of improving the character in question is more (Singh and Gupta, 1968).

Mahalanobis D^2 statistic was used to group the fifty genotypes into ten clusters. Wide range of genetic divergence was noticed among the 50 genotypes. Sudhakumari and Gopimony (1994) also reported the presence of high genetic divergence among different accessions of cowpea.

Cluster II was the largest one with twenty genotypes, followed by cluster I with sixteen genotypes. Clusters III and IV comprised of three genotypes each and clusters V and VI included two genotypes each. Four clusters, VII, VIII, IX and X had only one genotype each.

The intracluster distance exhibited an increasing trend with increase in cluster size. Cluster VI and V had lower intracluster distances while, Cluster II, I, IV and III showed high intracluster distance.

Maximum intercluster distance was noted between clusters I and IV suggesting that hybridization between diverse genotypes selected from these clusters may display the maximum heterosis. Genotypes belonging to the same cluster may be more closely related with each other than that of diverse clusters.

Cluster VII recorded the maximum mean value for pod length, number of seeds per pod, 100 seed weight and grain yield per plant. Cluster VIII 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.

Dharmalingam and Kadambavanasundaram (1989) opined that, in cowpea parents for hybridization can be effectively selected on the basis of the intercluster mean values and genetic diversity between clusters. Hazra *et al*. (1993a), Rewale *et al*. (1996) and Backiyarani *et al*. (2000) reported that there was no relationship between genetic divergence and geographical distribution of cowpea genotypes. According to Resmi (1998), days to flowering, number of branches, pod length, number of pods per inflorescence, number of pods per plant and yield per plant contributed considerably to genetic divergence. Ushakumari *et al*. (2000) reported that number of seeds per pod, number of branches per plant, number of pods per cluster and pod length contributed maximum to genetic divergence in cowpea.

5.6 LINE X TESTER ANALYSIS

In the present study, the parents selected from 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 line X tester analysis.

5.6.1 Performance of Parents and Crosses

Selection for superior types based on phenotypic evaluation alone may not bring about the expected improvement through hybridization. The parental attributes dictate the performance of crosses developed through hybridization. Hence the mean performance and general combining ability effects of the individuals need to be evaluated to highlight the performance of their crosses.

Significant variability was noticed for most of the characters among the lines, testers and crosses. The significance of line X tester interaction indicates the involvement of different gene effects for most 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 interactions for

number of branches per plant, number of seeds per pod, yield per plant and leaf chlorophyll content in cowpea.

Among the lines, L_2 and L_3 exhibited the high mean values for the several yield characters. The highest estimates of grain yield, 100 seed weight, plant height and number of branches per plant was noticed in L_3. L_3 also recorded the minimum number of damaged seeds per 25 pods among the lines. L_2 exhibited maximum mean values for number of pods per plant, number of pods per inflorescence, number of seeds per pod and peduncle length.

Among the testers, T_2 exhibited the least mean values for percentage flower bud infestation, number of larvae per 25 flowers and number of damaged seeds per 25 pods. T_2 also showed the highest mean values for number of pods per plant, pod length, number of seeds per pod, grain yield, 100 seed weight, pod protein content and seed protein content among the testers.

In general, the lines excelled in yield and biochemical characters, while the testers displayed noticeably low values of legume pod borer damage measurements. Peduncle length, non-glandular trichome density and crude fibre content of pods were noticed in high magnitude in testers, whereas, leaf chlorophyll content, leaf protein content, pod protein content and seed protien content were high in lines.

The trend of variability for morphological and biochemical traits suggest that plant types with long peduncles, high density of non-glandular trichomes and high content of crude fibre offer resistance to attack by legume pod borer. The larvae prefer feeding on varieties with more chlorophyll and protien in leaf tissue, high pod protein and seed protein. The result supports the findings of Oghiakhe (1992) that the content of total chlorophyll in leaf tissue could be considered as a criterion for classification of cowpea genotypes for resistance to the pest. Oghiakhe *et.al*. (1992d) and Veeranna and Hussain (1997) has reported the role of trichomes in relation to legume pod borer resistance as observed in the present study. Panicker (2000) has placed a confirmatory view with respect to trichome density and a contradictory view with respect to peduncle length and leaf chlorophyll content.

Among the crosses, L_4 X T_3 stood outstanding from other crosses by virtue of its high mean values with respect to the yield characters and low mean values for damage parameters. The cross exhibited the best performance for nine characters *viz*., number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, grain yield per plant, percentage pod infestation, number of larval bore holes per pod, number of damaged seeds in 25 pods and peduncle length.

L_1 X T_2 followed L_4 X T_3 with maximum mean values for three characters and second highest mean value for six characters including grain yield per plant. L_3 X T_2 exhibited maximum values combined with low scores for damage measurements.

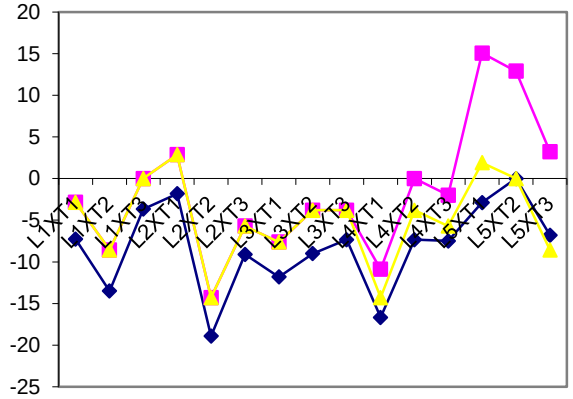
Several crosses with high yield and appreciable levels of legume pod borer resistance, recorded low contents of leaf chlorophyll, leaf protein, pod protein and seed protein compared to other crosses.

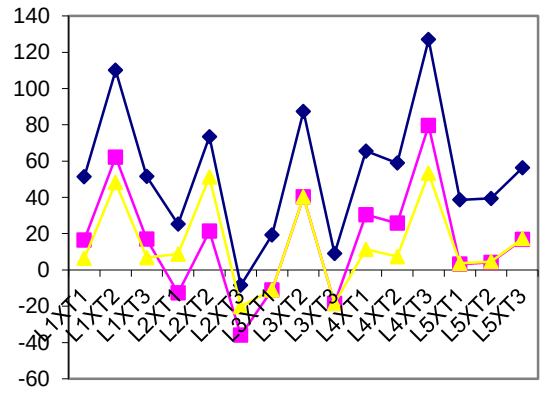
5.6.2 Heterosis

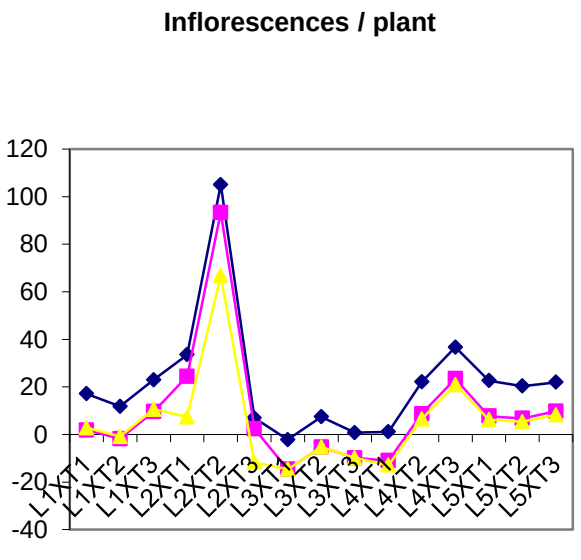
Heterosis breeding makes use of the hybrid vigour in the crosses for attaining noticeable increase in production and productivity of crop plants. If the contribution of additive gene effects is higher in the expression of the character, there is greater chance of recovery of genotypes with higher expression in the segregating generations. The magnitude of heterosis for the yield and related characters is of utmost importance for exploitation of heterosis. According to Hatchcock and Mc Daniel (1973), even small degrees of heterosis for component characters is a desirable attribute in heterosis breeding. Singh (2002) opined that high estimates of heterosis is a result of high genetic diversity among parent varieties indicating the possibility of identifying high yielding transgressive segregants from the hybrid populations.

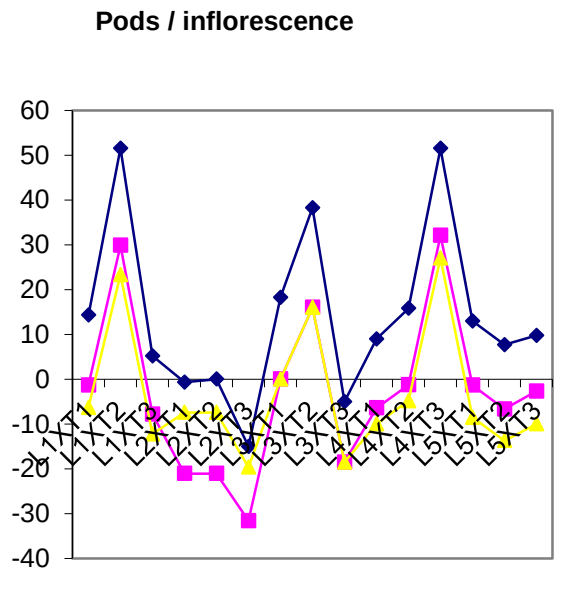
In the present study, the relative heterosis, heterobeltiosis and standard heterosis were estimated for the 15 crosses with respect to the different characters (Fig 3). Desirable negative estimates for all three cases of heterosis was noticed for days to flowering. Similar reports were earlier published by Bhor *et al*. (1997) and

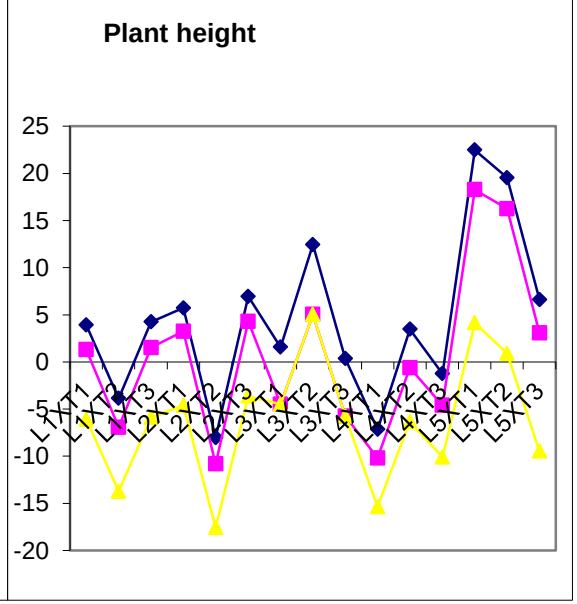
Fig 3. Heterosis for the different characters



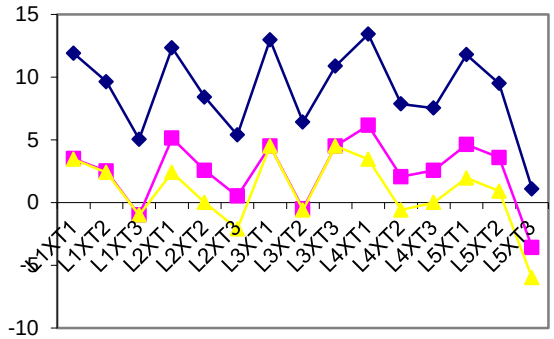




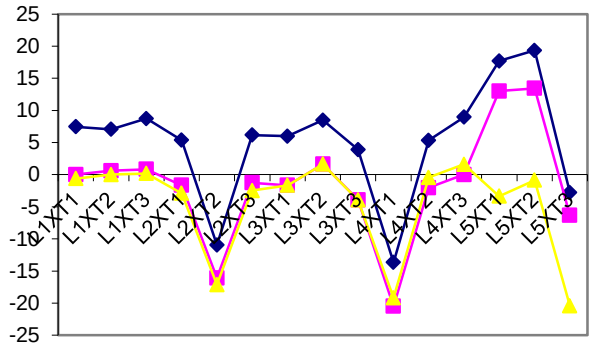




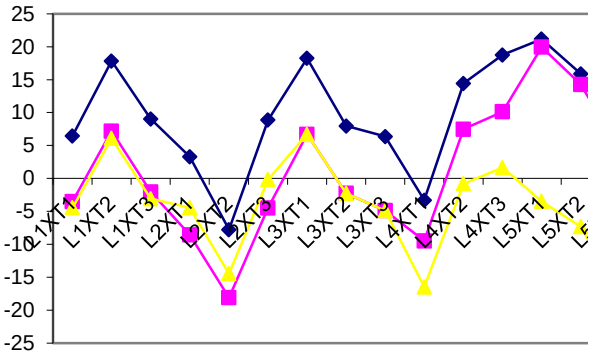
Number of branches / plant



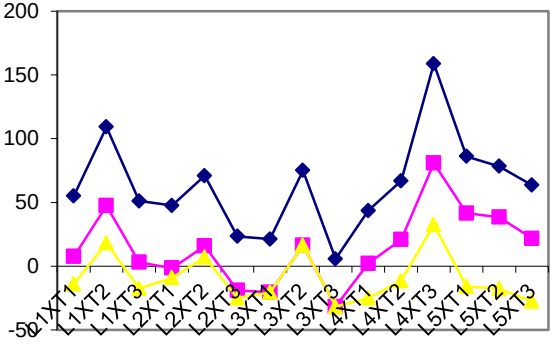
Pod length



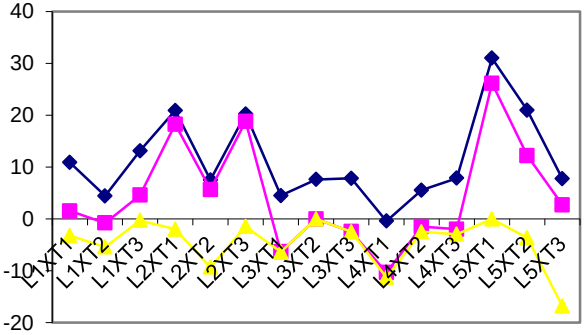
Number of seeds per pod



Grain yield per plant



100 seed weight



% flower bud infestation

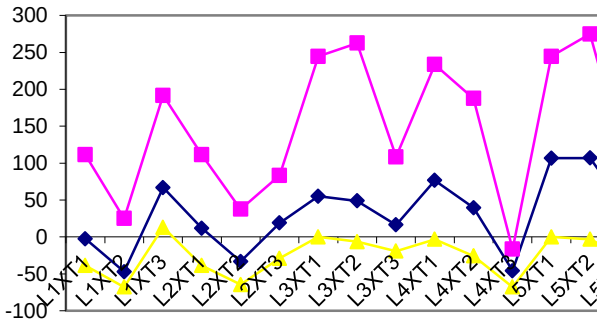


Fig 3 (contd).

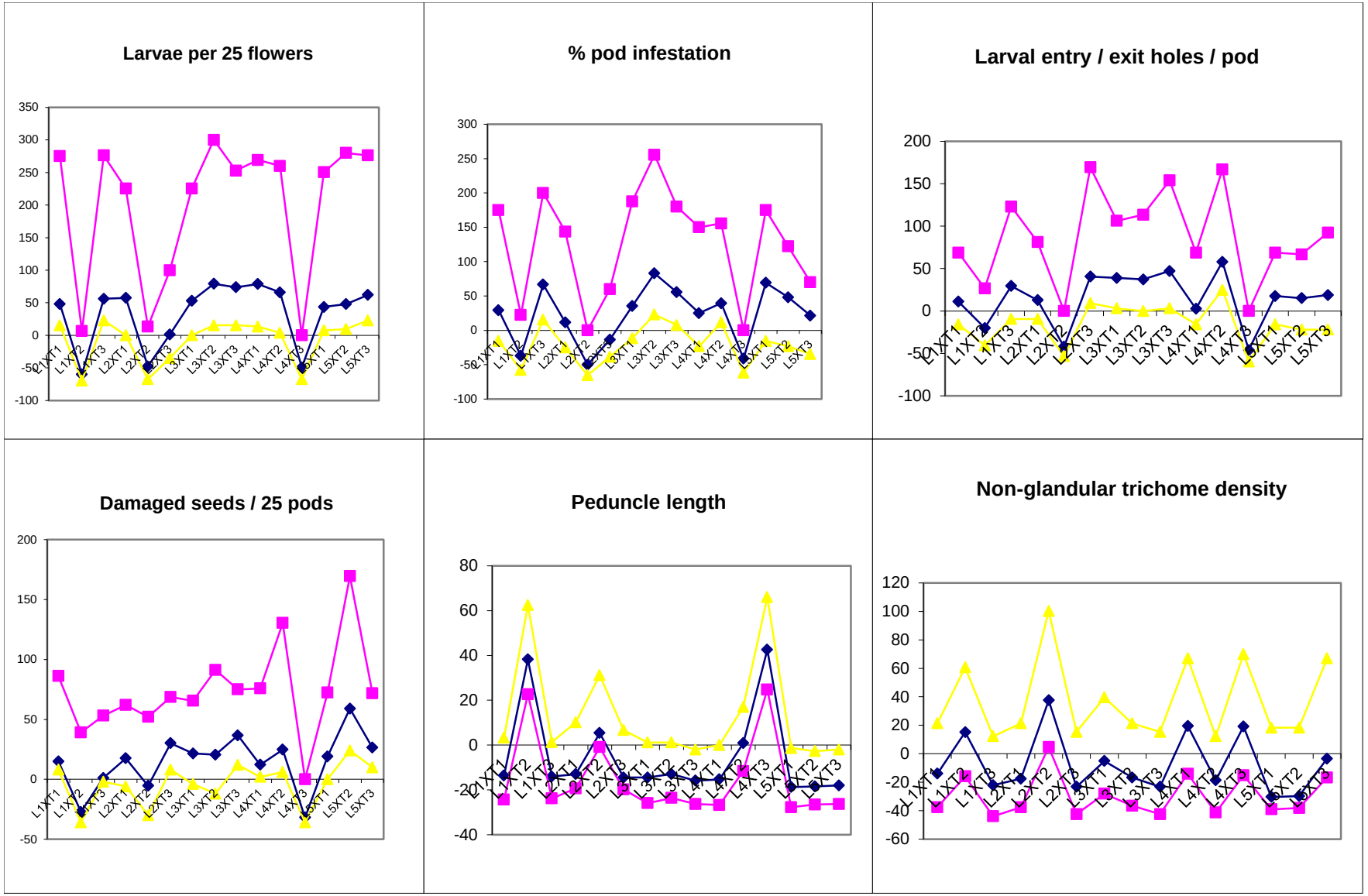
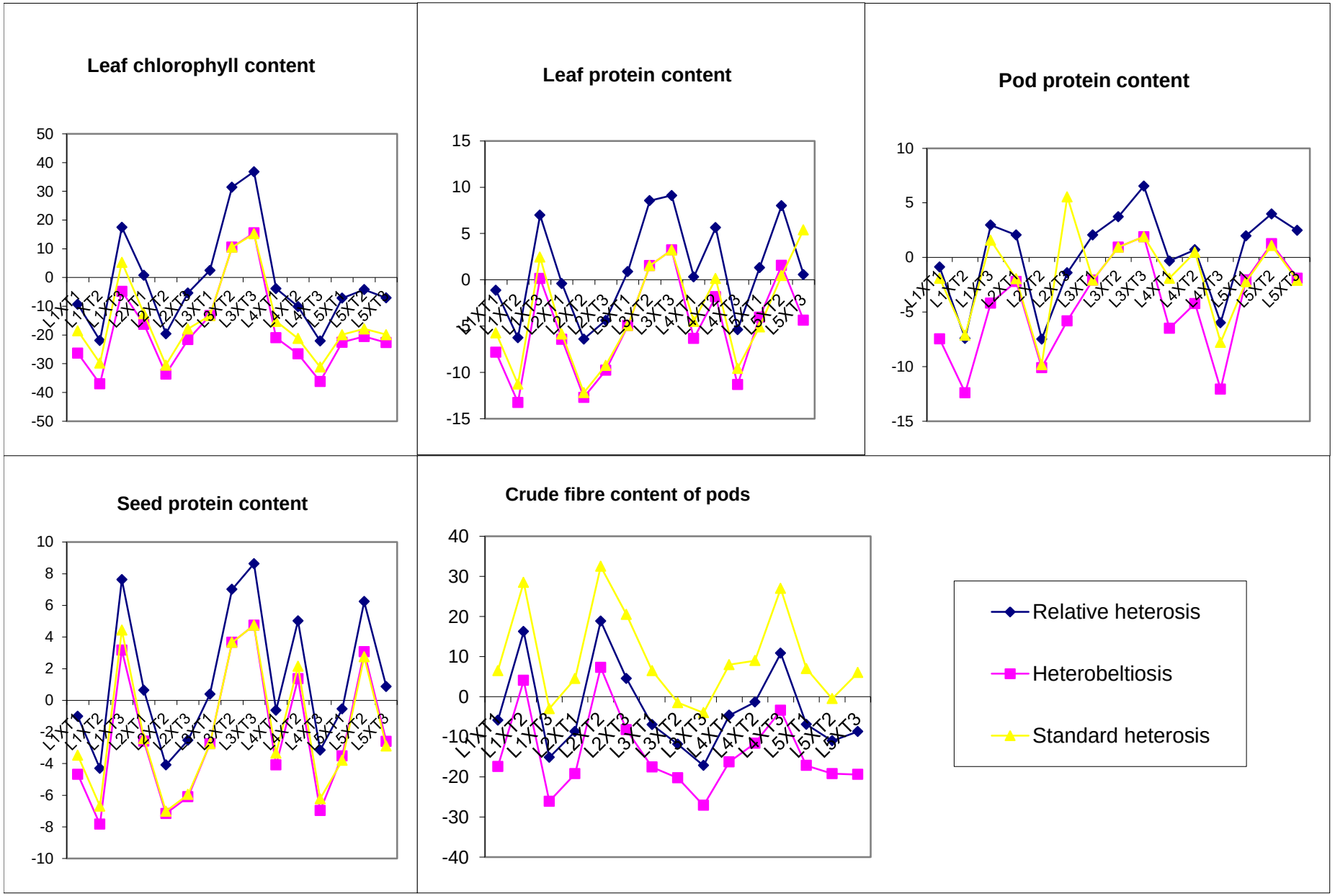

Larvae per 25 flowers
% pod infestation
Larval entry / exit holes / pod
Damaged seeds / 25 pods
Peduncle length
Non-glandular trichome density

Fig 3 (contd).


Leaf chlorophyll content
Leaf protein content
Pod protein content
Seed protein content
Crude fibre content of pods
Relative heterosis
Heterobeltiosis
Standard heterosis

Bushana *et al*. (2000), whereas, Rajkumar *et al*. (2000b) noticed results in contrary to the present obsevation.

Seven crosses recorded positive and significant estimates of all three types of heterosis for number of pods per plant and three crosses each for number of inflorescences per plant, number of pods per inflorescence and grain yield. The results are in conformity with that of Rejatha (1992), Sangwan and Lodhi (1995) and Bushana *et al*. (2000), who reported heterosis for grain yield and number of pods per plant. Aravindhan and Das (1996) and Bhor *et al*. (1997) reported heterosis for yield in cowpea. Rajkumar *et al*. (2000b) published contradictory results with respect to number of pods per plant and number of pods per inflorescence.

Three crosses had significant positive relative heterosis for plant height, while majority of estimates of standard heterosis were in the negative direction. Six crosses had significant positive relative heterosis for number of branches per plant also. No crosses showed heterobeltiosis or standard heterosis for this character. Bhor *et al*. (1997) has published reports in conformity to the present results with respect to plant height. Bushana *et al*. (2000) observed heterosis for plant height and number of branches, while Rajkumar *et al*. (2000b) observed a depression in both these characters. For pod length, 12 crosses had positive significance for relative heterosis. Positive significance of all types of heterosis was observed in two crosses with respect to number of seeds per pod. For 100 seed weight, 11 crosses recorded highly significant positive relative heterosis and heterobeltiosis. Sangwan and Lodhi (1995) also observed significant heterosis for pod length and number of seeds per pod in cowpea. Bushana *et al.* (2000) published confirmatory reports with respect to 100 seed weight. However, Rajkumar *et al*. (2000b) observed inbreeding depression for pod length, number of seeds per pod and 100 seed weight in intervarietal crosses.

Three crosses each exhibited negative and significant relative heterosis for percentage flower bud infestation and percentage pod infestation while for number of damaged seeds per 25 pods, two crosses showed negative and significant relative heterosis. None of the crosses expressed significant negative heterobeltiosis for any

of the damage parameter. Standard heterosis of eight crosses each were negatively significant for percentage flower bud infestation and percentage pod infestation while for number of damaged seeds per 25 pods, three crosses showed significance in the negative direction.

Peduncle length in two crosses were positive and significant for all three types of heterosis. No cross exhibited positive and significant estimates for all types of heterosis for non-glandular trichome density, but four crosses exhibited positive significance for relative and standard heterosis. However, Rajkumar *et al*. (2000b) observed a reduction in peduncle length following intervarietal hybridization in cowpea.

Leaf chlorophyll content in the crosses showed a predominance of negative heterosis. Three crosses had all the three estimates of heterosis in the negative direction, while only one cross showed a positive trend. This result is supported by the findings of Rajkumar *et al*. (2000b).

Five crosses showed positive and significant estimates of all three types of heterosis for seed protein content, while it was so for one cross with respect to leaf protein content. No cross had significant positive estimates for all types of heterosis for pod protein content. For crude fibre of pods, one cross exhibited positive significance for all estimates of heterosis. The results agree with the reports of Malarvizhi (2002) for protein content in the leaves, pods and seeds in the F_1 generation of cowpea crosses.

The cross L_4 X T_3 exhibited significant positive estimates with high magnitude for number of pods per plant, number of inflorescences per plant, number of pods per inflorescence and grain yield indicating considerable heterosis with respect to the important yield characters. Further, the relative and standard heterosis exhibited significance in a desirable negative direction for all damage measurements. The cross also possessed significant positive heterosis with respect to peduncle length and non-glandular trichome density. However, for leaf protein, pod protein and seed protein

content the cross exhibited negative significance and for crude fibre content of pods the cross showed positive estimates of heterosis.

This result leads to the conclusion that the low relative preference of legume pod borer larvae to this cross may be due to its low protein content, coupled with mechanical barriers which restrict their access to pod surface, compared to other types in a multiple choice field situation.

5.6.3 Combining Ability

Estimation of combining ability effects is done to assess the relative ability of a genotype to transmit its desirable performance to its crosses. A combined evaluation of the combining ability effects and mean performance of the parents and hybrids is more useful in the identification of superior types.

A general assessment of *gca* effects revealed that grain yield per plant exhibited *gca* effects with high magnitude followed by percentage flower bud infestation and pod infestation. Similar reports have earlier been published for grain yield per plant by Mishra *et al*. (1987).

High *sca* effect was also observed for grain yield per plant, percentage flower bud infestation, percentage pod infestation and number of pods per plant. Zaveri *et al*. (1983) and Thiyagarajan *et al*. (1990) noticed *sca* effects of high magnitude for grain yield and number of pods per plant. For grain yield similar reports have been published by Thiyagarajan *et al*. (1993) and Mishra *et al*. (1987).

5.6.3.1 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 reflects the preponderance of additive gene effects.

L_4 exhibited remarkable general combining ability effects with respect to important yield characters, grain yield per plant, number of pods per plant, number of pods per inflorescence, percentage pod infestation, peduncle length, non-glandular trichome density, leaf chlorophyll content and crude fibre content (Fig 4). Sobha *et al*. (1998) has discussed high *gca* effects for yield per plant The high *gca* effects of

Fig 4. General combining ability effects of parents

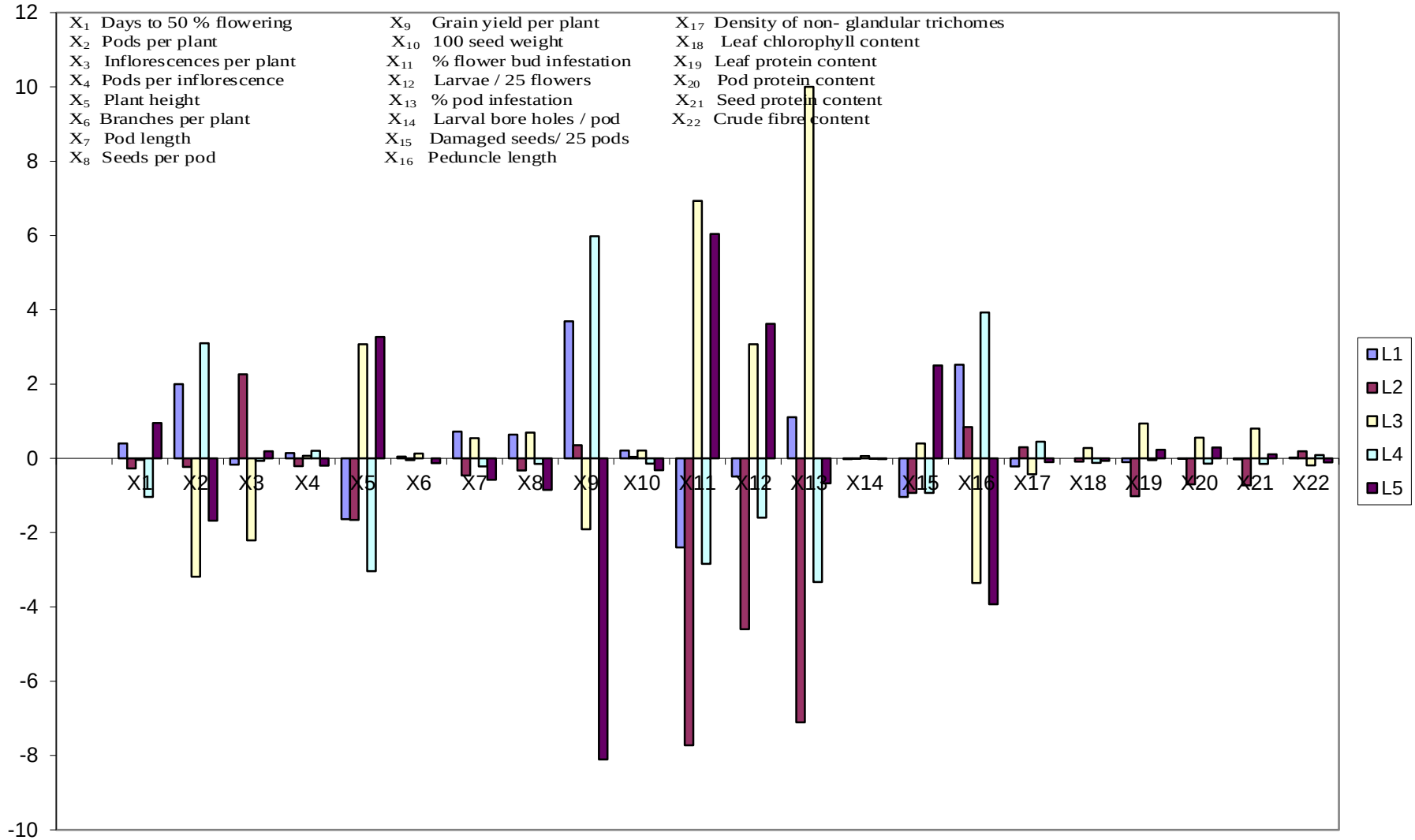
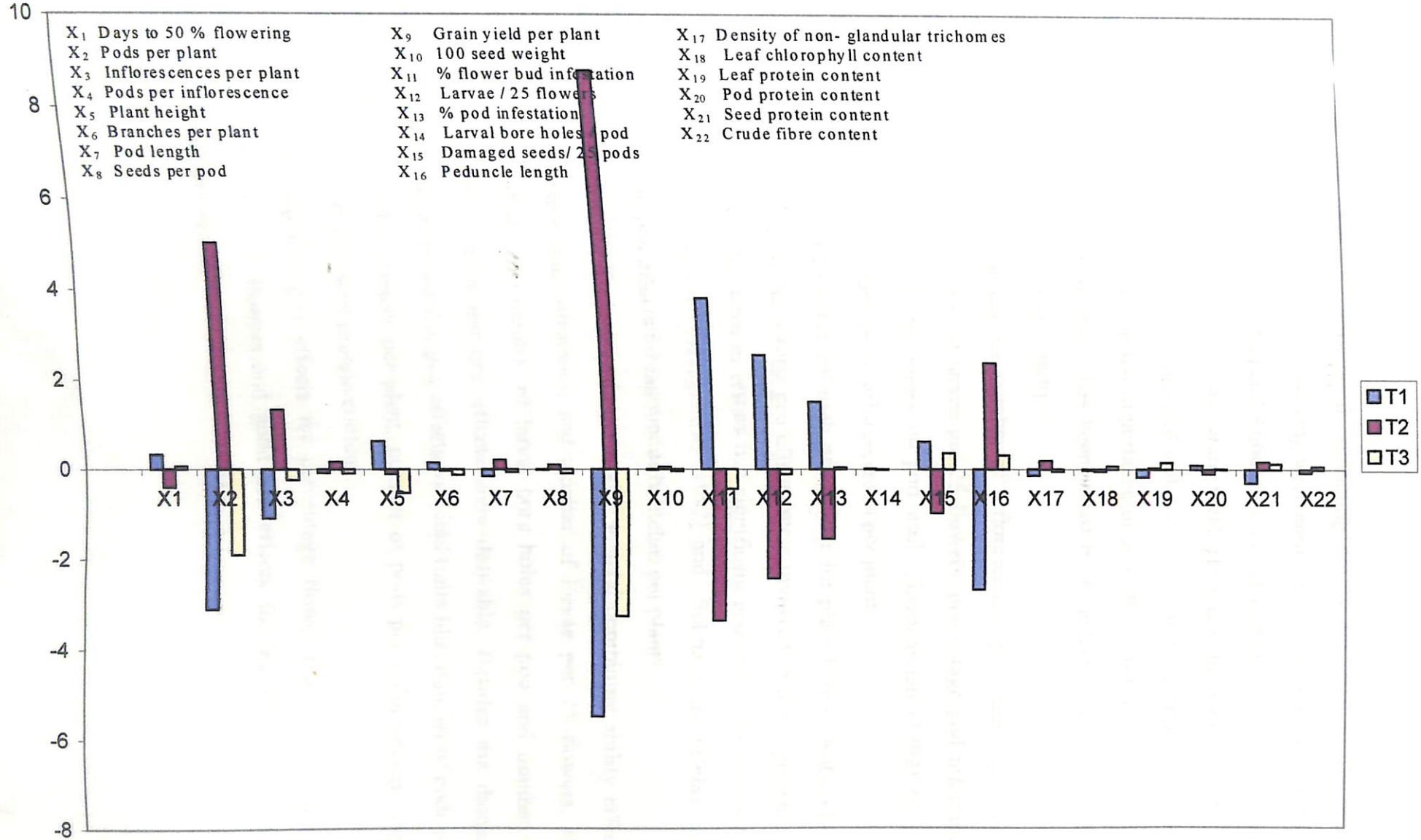


Fig 4 (contd). General combining ability effects of parents



number of pods per plant is supported by the reports of Rejatha (1992), Thiyagarajan (1992) and Sobha *et al*. (1998).

L_4 was the only line with good combining ability for days to flowering. Significant *gca* effects for days to flowering were earlier reported by Rejatha (1992), Jayarani (1993); Sobha *et al*. (1998) and Anbuselvam *et.al*. (2000).

L_1 displayed good *gca* effects for grain yield per plant, number of pods per plant, pod length, number of seeds per pod and peduncle length. Rejatha (1992) and Sobha *et al*. (1998) have stressed the importance of *gca* effects for number of seeds per pod, while that for pod length has been stated by Chauhan and Joshi (1981); Jayarani (1993) and Sobha *et al*. (1998).

L_2 was a good combiner for number of inflorescences per plant, percentage flower bud infestation, number of larvae per 25 flowers, percentage pod infestation and density of non-glandular trichomes on pod wall. Thiyagarajan (1992) noticed significant *gca* effects for number of inflorescences per plant.

Two lines, L_3 and L_5 exhibited high *gca* effects for plant height. Anbuselvam *et.al*. (2000) also reported that strong *gca* effects were involved in the expression of plant height in cowpea. No lines or testers had significant *gca* effects for number of branches per plant. However, Thiyagarajan (1992) and Sobha *et al*. (1998) have described significant *gca* effects for number of branches per plant.

Among the testers, T_2 displayed appreciable general combining ability effects for percentage flower bud infestation and number of larvae per 25 flowers. For percentage pod infestation, number of larval bore holes per pod and number of damaged seeds in 25 pods the *gca* effects were desirable. Besides the damage measurements, T_2 had remarkable *gca* effects for yield traits like, number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, grain yield, peduncle length and seed protein content.

T_3 showed negative *gca* effects for percentage flower bud infestation and number of larvae per 25 flowers and good *gca* effects for leaf chlorophyll, leaf protein and seed protein 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 number of pods per plant, number of inflorescences per plant, pod length, number of seeds per pod and grain yield. Chauhan and Joshi (1981) also noticed a preponderance of additive gene action for the important yield traits, whereas, Zaveri *et al*. (1983) put forth a contradictory view. Patil and Bhapkar (1986) observed additive gene effects for days to flowering and 100 seed weight. Patil and Shettee (1986) and Hazra (1991) suggested both additive and non-additive gene action for pod length. . Nagaraj *et al*. (2002) observed that days to 50 per cent flowering was governed by additive genes.

Similarly, for the damage parameters also, the appreciable levels of *gca* effects points out the importance of additive gene effects. Additive gene action was suggested for legume pod borer damage parameters in cowpea by Pathak (1985), which is in conformity with the present results. Hazra (1991) and Malarvizhi (2002) reported additive gene effects for seed protein content in cowpea as noticed in the present study.

L_2 exhibited high mean values for some important yield traits coupled with desirable *gca* effects for yield and pest resistance in the present study suggesting the suitability of this line as parent in hybridization programmes.

5.6.3.2 Specific Combining Ability Effects of Crosses

Specific combining ability indicates those situations in which certain crosses do relatively better or worse than would be expected on the basis of average performance of their respective parents. It is an indication of non-additive gene action. For an evaluation of the superiority of crosses, a combination of the mean performance, heterosis and specific combining ability should give a more reliable criteria than considering any one at a time.

L_5 X T_2 and L_2 X T_3 displayed appreciable levels of *sca* effects with respect to the damage parameters (Fig 5). Apart from the damage parameters, these crosses

Fig 5.Specific combining ability effects of crosses

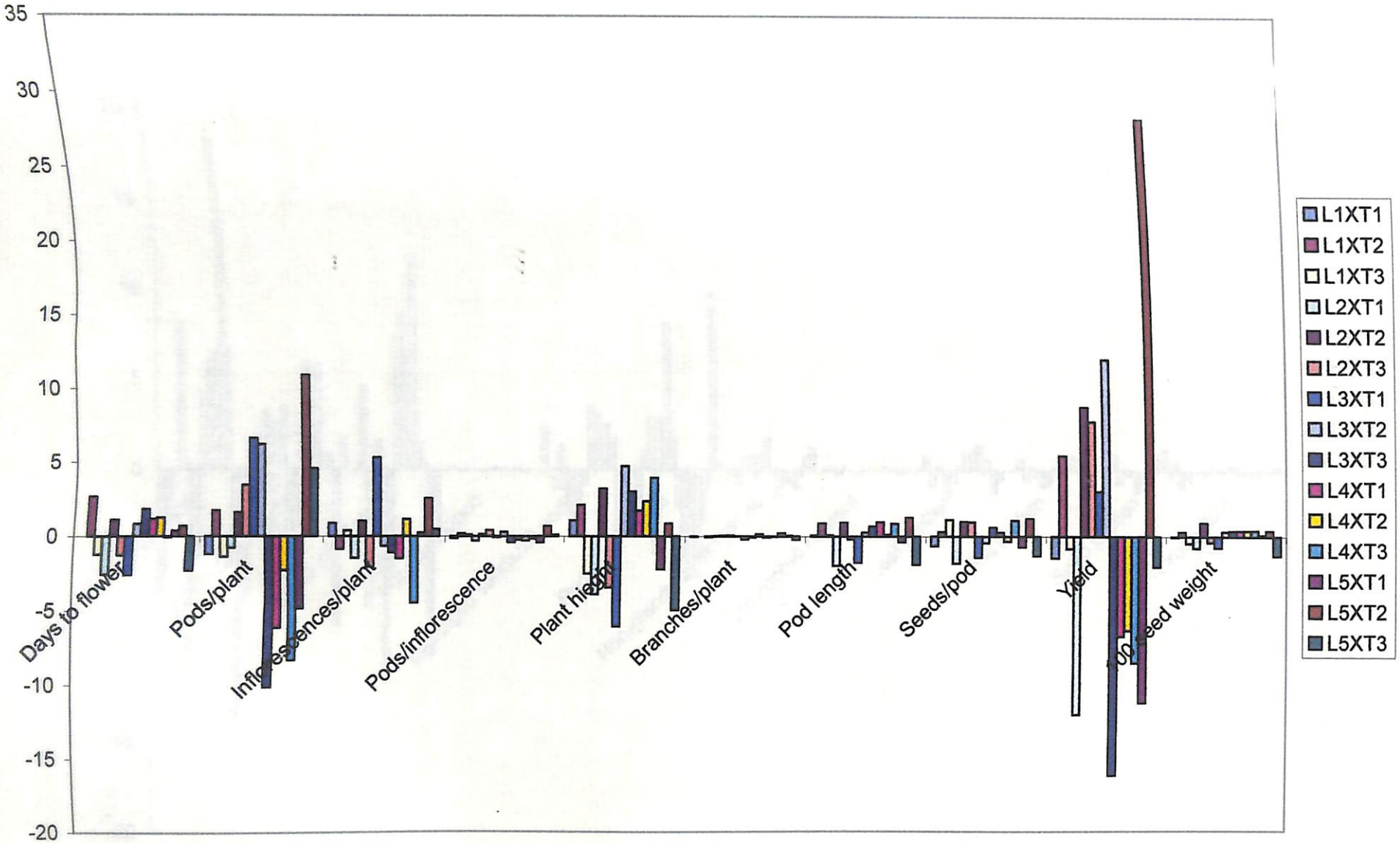
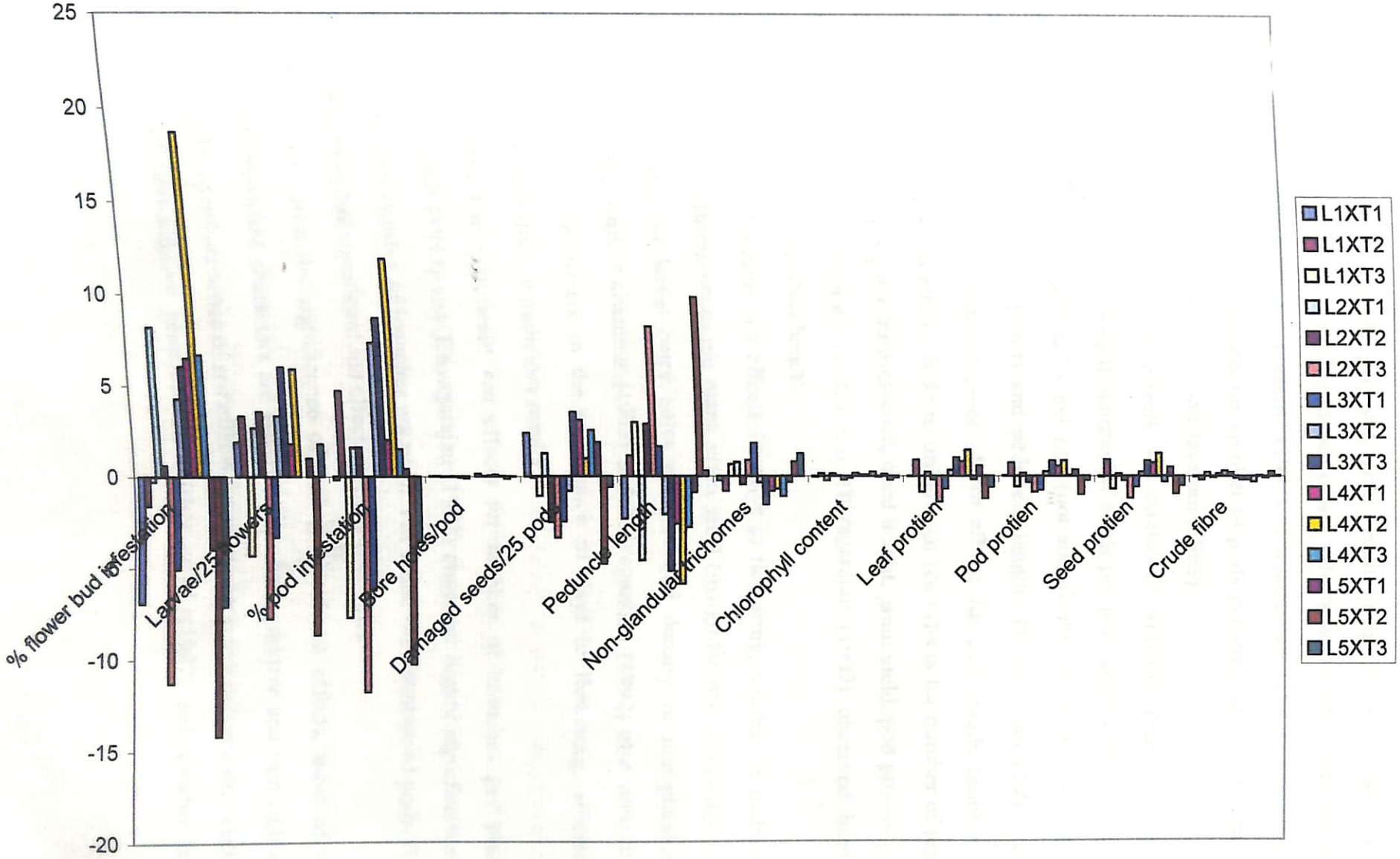


Fig 5 (contd). Specific combining ability effects of crosses



showed remarkable *sca* effects for number of pods per plant, number of pods per inflorescence, number of seeds per pod, grain yield, peduncle length and non-glandular trichome density. A predominance of sca effects were earlier reported for yield per plant in cowpea by Jayarani (1993), Thiyagarajan (1992) and Smitha (1995). The significance *sca* effects for number of pods per plant are in conformity with the reports of Anilkumar (1993) and Jayarani (1993).

L_2 X T_2 exhibited good *sca* effects for number of pods per plant, number of inflorescences per plant, pod length, number of seeds per pod, grain yield, 100 seed weight, number of larval bore holes per pod (not significant), number of damaged seeds in 25 pods (not significant) and peduncle length. Thiyagarajan (1992) and Smitha (1995) reported a preponderance of *sca* effects for pod length, number of seeds per pod and pod length. L_3 X T_3 recorded high *sca* effects for number of pods per plant, number of pods per inflorescence, plant height, grain yield, pod protein and seed protein content. Jayarani (1993) and Thiyagarajan (1992) observed highly significant *sca* effects for plant height.

L_3 X T_1 had desirable *sca* effects for days to flowering, number of pods per plant, number of inflorescences per plant, grain yield (insignificant), percentage pod infestation, number of larval entry holes per pod and density of non-glandular trichomes on pod wall. Anilkumar (1993) and Thiyagarajan (1992) also noticed a preponderance of *sca* effects in the inheritance of days to flowering, whereas, Jayarani (1993) reported contradictory results.

No crosses had significant *sca* effects for number of branches per plant. However, Jayarani (1993) and Thiyagarajan (1992) observed highly significant *sca* effects underlying number of branches per plant. For crude fibre content of pods, five crosses each recorded significant *sca* effects in both directions.

As evident from the significance of both *gca* and *sca* effects, most of the economically important characters are governed by both additive and non-additive gene effects. The predominance of *sca* effects for most characters indicate the relative importance of non-additive gene effects. Mishra *et al*. (1987) and Emebiri and

Obisesan (1991) reported both additive and non-additive gene action for grain yield. Thiyagarajan *et al*. (1990) also observed similar results for plant height, number of pods per plant, 100 seed weight and seed yield per plant in cowpea.

Superior crosses should be isolated on the basis of mean performance, heterosis and specific combining ability effects of the crosses, which offers a more accurate background for selection. There are cases where the mean performance and heterosis may not rightly reflect the specific combining ability effects of the crosses. In such cases, selection should be practiced by giving more consideration to the first two aspects as it provides an indication of the real performance in the field. L_4 X T_3 recorded high mean values for yield related characters and low mean values for legume pod borer damage measurements. The cross also showed desirable magnitude and direction of all three estimates of heterosis with respect to the important characters. Hence the cross could be rightly selected as the superior one irrespective of the estimates of *sca* effects.

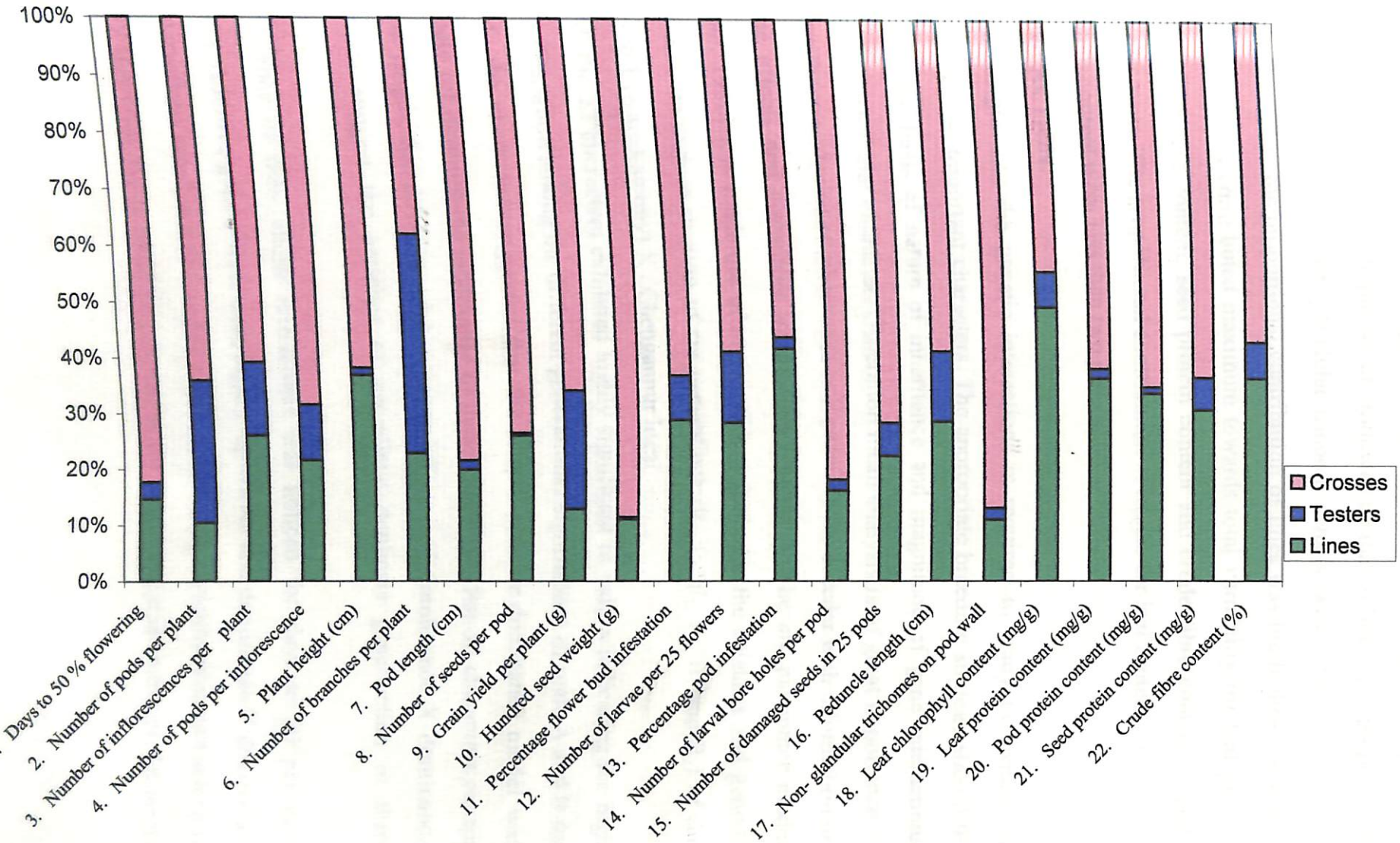
Cowpea is a self pollinated crop in which pedigree breeding method is found appropriate. Based on the combining ability studies, the cross L_4 X T_3 is found suitable in terms of crop improvement followed by L_5 XT_2 and L_2 X T_3.

5.6.4 Proportional Contribution of Lines, Testers and Crosses

In general, the hybrids contributed maximum towards the total variability for all characters except number of branches per plant and leaf chlorophyll content (Fig 6). The proportional contribution of lines exceeded that of testers for all characters except number of pods per plant, number of branches per plant and grain yield per plant. The proportional contribution of hybrids were greater than 80 per cent of the total variance for days to 50 per cent flowering, 100 seed weight, number of larval bore holes per pod and density of non-glandular trichomes on pod wall.

For all the damage measurements, proportional contribution of crosses were high followed by that of lines. Testers contributed the least towards the total variance for these characters. For percentage flower bud infestation and number of larvae per 25 flowers, the relative contribution of lines were almost same. The relative

Fig 6. Proportional contribution of lines, testers and crosses



contribution of crosses were the highest for the morphological characters, peduncle length and non-glandular trichome density followed by that of lines. The proportional contribution of testers for non glandular trihome density was very low. For leaf chlorophyll content, the proportional contribution of lines was the highest followed by crosses. Crosses contributed maximum towards total variability for leaf protein content, pod protein content, seed protein content and crude fibre content of pods followed by lines. The proportional contribution of testers for leaf protein content and pod protein content were less than two percent.

5.7 GENE ACTION

An insight into the genetic interactions is required to study the nature of inheritance of the important characters. The appropriate breeding strategy should be devised on the basis of nature of inheritance and magnitude of gene interactions underlying a particular character. Generation mean analysis is of great importance in unveiling the complexity of inheritance as it provides the breeder with information on the gene effects and non-allelic interactions (epistasis). The six parameter model (Hayman, 1958) was made use of in the present study for the epistasis and genetic components through evaluation of six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of the cross, Ptb 1 (Kanakamony) X Chengannur local.

All the 22 characters 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. For all characters except peduncle length, the direction of dominance effects and domimance X dominance interactions suggest the presence of non-allelic duplicate gene action in their expression.

Presence of non- allelic interactions was noticed for days to 50 per cent flowering. Additive gene effects were highly significant and dominance X dominance gene interactions acted in a favourable negative direction. Hybridization and selection for early flowering types could be resorted to for improving this character. Different

gene actions were reported for the character by earlier workers like, additive (Jayarani, 1993; Anbuselvam *et al*., 2000; Nagaraj *et al*., 2002), non-additive (Anilkumar, 1993 and dominance (Sawant, 1994b).

For number of pods per plant, dominance X dominance interactions acted in a favourable positive direction. Significance of scales C and D suggests the predominance of additive X additive and dominance X dominance effects for number inflorescences per plant. However, dominance X dominance interactions were positive and significant. Significance of additive effects suggests the scope for improvement throughg recombination breeding. Thiyagarajan *et al*. (1990) reported that number of inflorescences per plant and number of pods per plant were controlled by additive gene action, while Sawant (1994b) attributed dominance gene action for these characters.

Number of pods per inflorescence and plant height also displayed dominance X dominance interactions in a favourable positive direction. Additive gene action was highly significant and dominance X dominance interactions were positive for number of branches per plant and pod length. Hybridization and selection could be effectively employed for improving these characters. Thiyagarajan *et al*. (1990) reported that plant height and pod length were governed by non-additive gene action. Sawant (1994b) opined that number of branches per plant, pod length and plant height were controlled by dominance gene action. Significance of both additive and non-additive gene action for plant height, number of branches per plant and pod length was reported by Sobha *et al*. (1998). Nagaraj *et al*. (2002) noticed that epistatic gene action played a major role in the expression of plant height and number of branches per plant, whereas dominance gene action was predominant in the inheritance of pod length.

Additive gene action alone was significant for number of seeds per pod and 100 seed weight, outlining the importance of recombination breeding for improving these traits. However, the significance of additive gene effects, additive X dominance and positive direction of dominance X dominance epistatic interactions underlines the

suitability of exploiting heterosis and selection in an efficient manner. Several workers different types of gene action for number of seeds per pod, 100 seed weight and seed yield per plant *viz*., additive (Thiyagarajan, 1992 and Anilkumar, 1993), non-additive (Jayarani, 1993; Thiyagarajan *et al*., 1990 and Smitha, 1995), dominant (Sawant, 1994b) and epistatic (Nagaraj *et al*., 2002). Significant role of additive as well as non-additive gene action for these characters were observed by Sobha and Vahab (1998).

Percentage flower bud infestation was influenced by dominance X dominance epistatic interactions in a negative direction. Dominance gene action was negative and additive X dominant interactions were significant for the number of larvae per 25 flowers also. Dominance X dominance epistatic interactions were highly significant and negative for percentage pod infestation and number of larval bore holes per pod. Number of damaged seeds per 25 pods were influenced by additive X dominance epistasis in the negative direction.

In general, the magnitude and direction of the gene effects underlying the pest damage parameters offers a favourable background for the breeder to develop legume pod borer resistant cowpea types, through recombination breeding and selection based on the damage characters. Woolley (1976) attributed dominance gene action for inheritance of legume pod borer resistance whereas, Pathak (1985) observed partial dominance of susceptibility for percentage pod and seed damage due to legume pod borer in cowpea.

Additive gene effects and additive X dominance gene interactions were significant for peduncle length. The same direction of dominance gene effect and dominance X dominance interactions is an indication of non-allelic complimentary 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 positive and highly significant for density of non-glandular trichomes on pod wall, whereas all other gene effects and interactions were negatively significant. On the contrary, Ng *et al*. (2000)

reported a preponderance of additive gene action in the inheritance of trichome density. However, he also stated that dominant and epistatic gene actions also made significant contributions.

For leaf chlorophyll content, all the gene interactions except dominance X dominance epistatic interactions were highly significant. This indicates that several breeding approaches like direct and recurrent selection, hybridization and selection and heterosis breeding could be employed for improving leaf chlorophyll content.

Predominance of dominant gene action in a positive direction was observed for leaf protein content. Additive gene action and additive X additive interactions were also significant. Additive gene effects and additive X additive gene effects were significant and dominance X dominance interactions acted in a favourable positive direction for pod protein content. Additive gene effects and additive X additive epistatic interactions were significant for seed protein content also. However, the negative significance of dominance X dominance interactions limits the scope of heterosis breeding for this trait. For simultaneous improvement of these characters hybridization and selection could successfully be made use of. Malarvizhi (2002) reported both additive and dominant gene action in the inheritance of protein content in the leaves, pods and seeds of cowpea.

Additive gene effects and additive X dominance gene interactions were 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 and selection for low fibre types.

Summary

6. SUMMARY

Cowpea is an important pulse crop and a major source of protein worldwide. However, the production and productivity of cowpea is limited by the incidence of several major pests, legume pod borer being the most devastating one in all areas of cultivation. Hence, evolution of legume pod borer resistant varieties becomes essential, both in terms of environmental safety and reducing the cost of cultivation.

The present investigation was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2002 to 2004, with the objective of studying the genetic basis and mode of inheritance of yield and legume pod borer resistance in cowpea.

Cowpea germplasm consisting of 50 varieties was evaluated for resistance to legume pod borer and yield. Flower, pod and seed damage measurements formed the basis of legume pod borer resistance evaluation. Significant variability was noticed for all the damage measurements, the related biochemical and morphological traits and yield related characters. The phenotypic and genotypic coefficients of variation, heritability and genetic gain were worked out for each character. Coefficients of both phenotypic and genotypic variation were high for all the damage parameters. Number of pods per plant, grain yield and 100 seed weight also showed high coefficients of variation. All the damage related biochemical and morphological traits except content of chlorophyll a in the leaf tissues exhibited high heritability and high genetic gain.

Plant resistance indices were calculated for the 50 cowpea types based on the simultaneous consideration of flower, pod and seed damage parameters, which served as the selection criteria for identifying the testers for L X T analysis. The plant resistance indices were minimum for T_{45}, T_{47}, and T_{49} which were selected as testers. Important yield contributing characters also showed high heritability coupled with

high genetic gain. These offers a congenial situation for the breeder for direct selection based on these characters.

All the damage parameters were positively and significantly correlated with each other, but negatively and significantly correlated with non-glandular trichome density, peduncle length and ratio of chlorophyll ‘a’ to ‘b’, indicating that cowpea types with high trichome density, long peduncles and wide chlorophyll ‘a’ / ‘b’ ratio offer resistance to infestation by legume pod borer. Plant resistance index was positively correlated with all damage parameters and negatively correlated with peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll ‘a’ to ‘b’.

Grain yield per plant exhibited highly significant positive correlation with number of pods per plant, number of inflorescences per plant, number of seeds per pod and 100 seed weight. Path coefficient analysis revealed that number of pods per plant followed by 100 seed weight and number of seeds per pod exerted the maximum positive direct effect on grain yield. Pod length contributed to yield through positive indirect effects through all other characters.

Selection indices were worked out for the fifty genotypes on the basis of yield and six compenent characters *viz*., number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, pod length, number of seeds per pod and 100 seed weight. The genotypes T_2, T_4, T_6, T_7 and T_8 were selected as lines in the L X T analysis, on the basis of index scores. Mahalanobis D^2 statistic was used to group the fifty genotypes into ten clusters. Wide range of genetic divergence was noticed among the 50 genotypes.

The five lines and three testers were crossed in a line X tester fashion to obtain 15 crosses. The mean performance of parents, estimates of heterosis, general combining ability of parents and specific combining ability of the crosses were evaluated through line X tester analysis. Significant variability was noticed for most

of the characters among the lines, testers and crosses. The significance of line X tester interaction suggested the involvement of different gene effects for most characters.

Among the lines, L_2 and L_3 showed high mean values for yield and related characters. The highest values of grain yield and least estimate for number of damaged seeds per 25 pods were noticed in L_3. L_2 exhibited maximum mean values for number of pods per plant, number of pods per inflorescence, number of seeds per pod and peduncle length. Among the testers, T_2 exhibited the least estimates of percentage flower bud infestation, number of larvae per 25 flowers and number of damaged seeds per 25 pods and highest mean values for number of pods per plant and grain yield. L_4 X T_3 showed high mean values for yield characters and low mean values for damage parameters among the crosses. L_1 X T_2 followed L_4 X T_3 with high mean values for several yield characters including grain yield per plant. L_3 X T_2 also exhibited high mean values for yield traits combined with low scores for damage measurements.

Desirable negative heterosis was noticed for days to flowering in all the crosses. Seven crosses recorded positive and significant estimates of all three types of heterosis for number of pods per plant. Three crosses had positive and significant estimates of heterosis for number of inflorescences per plant, number of pods per inflorescence and grain yield. Positive and significant heterosis was observed in two crosses with respect to number of seeds per pod. For 100 seed weight, 11 crosses recorded highly significant positive relative heterosis and heterobeltiosis.

Three crosses each exhibited negative and significant relative heterosis for percentage flower bud infestation and percentage pod infestation while for number of damaged seeds per 25 pods, two crosses showed negative and significant relative heterosis. None of the crosses expressed significant negative heterobeltiosis for any of the damage parameter. Peduncle length in two crosses were significant and positive for all three types of heterosis. Four crosses exhibited positive significance for relative and standard heterosis for non-glandular trichome density. Leaf

chlorophyll content in the crosses showed a predominance of negative heterosis. Five crosses showed positive and significant estimates of all three types of heterosis for seed protien content, while for leaf protein content one cross was positive and significant. For crude fibre of pods, one cross exhibited positive and significant estimates for all types of heterosis.

General and specific combining ability effects of the parents and crosses were estimated. Among the lines, L_4 showed good *gca* effects for characters like grain yield per plant, number of pods per plant, number of pods per inflorescence, days to flowering, percentage pod infestation, peduncle length, non-glandular trichome density, leaf chlorophyll content and crude fibre content. L_1 was a good combiner for grain yield per plant, number of pods per plant, pod length, number of seeds per pod and peduncle length. L_2 displayed favourable *gca* effects for number of inflorescences per plant, percentage flower bud infestation, number of larvae per 25 flowers, percentage pod infestation and density of non-glandular trichomes on pod wall. Among the testers, T_2 displayed desirable *gca* effects for percentage flower bud infestation, percentage pod infestation, number of larval bore holes per pod, number of larvae per 25 flowers and number of damaged seeds in 25 pods. Besides the damage measurements, T_2 had remarkable *gca* effects for yield traits like number of pods per plant, number of inflorescences per plant, number of pods per inflorescence, grain yield, peduncle length and seed protein content.

L_5 X T_2 and L_2 X T_3 exhibited good *sca* effects for damage parameters, number of pods per plant, number of pods per inflorescence, number of seeds per pod, grain yield, peduncle length and non-glandular trichome density. L_2 X T_2 displayed desirable *sca* effects for number of pods per plant, number of inflorescences per plant, pod length, number of seeds per pod, grain yield, 100 seed weight, number of larval bore holes per pod, number of damaged seeds in 25 pods and peduncle length. L_3 X T_3 recorded high *sca* effects for number of pods per plant, number of pods per inflorescence, plant height, grain yield, pod protein and seed protein content. L_3 X T_1

had desirable *sca* effects for days to flowering, number of pods per plant, number of inflorescences per plant, grain yield, percentage pod infestation, number of larval entry holes per pod and density of non-glandular trichomes on pod wall.

The proportional contribution of hybrids were the maximum towards the total variability for all characters except number of branches per plant and leaf chlorophyll content. The proportional contribution of lines exceeded that of testers for all characters except number of pods per plant, number of branches per plant and grain yield per plant. For all the damage measurements, proportional contribution of crosses were high followed by that of lines. For leaf chlorophyll content, the proportional contribution of lines was the highest followed by crosses.

Analysis of the various gene effects and interactions underlying the different characters were made through generation mean analysis. Involvement of one or multiple epistatic interactions was generally observed in the expression of all characters.

Additive gene effects were highly significant for days to 50 per cent flowering, number of pods per inflorescence, number of seeds per pod, 100 seed weight, plant height, peduncle length and crude fibre content of pods. The direction of dominance X dominance gene interactions were favourable for all the damage parameters and yield traits like days to flowering, number of pods per plant, number inflorescences per plant, number of pods per inflorescence. The significance of additive gene effects and desirable direction of dominance X dominance epistatic interactions underlines the suitability of exploiting heterosis and selection in an efficient manner.

The magnitude and direction of the gene effects underlying the pest damage parameters offers a favourable background for the breeder to develop legume pod borer resistant cowpea types, through recombination breeding and selection.

Additive X dominance gene interactions were significant for peduncle length. The same direction of dominance gene effect and dominance X dominance interactions is an indication of non-allelic complimentary gene action underlying the

expression of the character. Hybridization and direct or repeated selection of types with long peduncles in segregationg generations could be effectively used to improve peduncle length. Dominance X dominance epistatic interactions were positive and highly significant for density of non-glandular trichomes on pod wall, whereas all other gene effects and interactions were negatively significant.

For leaf chlorophyll content, all the gene interactions except dominance X dominance epistatic interactions were highly significant. This indicates that several breeding approaches like direct selection and hybridization and selection could be employed for improving leaf chlorophyll content. Predominance of dominant gene action was observed for leaf protein content. Additive X additive interactions were also significant for leaf protein content, pod protein content and seed protein content.

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7. REFERENCES

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- Originals not seen

GENETIC ANALYSIS OF LEGUME POD BORER [*Maruca vitrata* (Fab.)] RESISTANCE AND YIELD IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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Abstract of the
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ABSTRACT

Legume pod borer is one of the most important post-flowering pests of cowpea in the tropics, which acts as a major limiting factor in cowpea cultivation in all seasons. The present investigation was conducted in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2002 to 2004, with the objective of studying the nature of inheritance and magnitude gene effects of yield and legume pod borer resistance in cowpea.

Fifty varieties of cowpea were evaluated for resistance to legume pod borer and yield. ANOVA revealed significant variability for all the damage measurements of legume pod borer, the related biochemical and morphological traits and yield characters. Major yield contributing characters like number of pods per plant, grain yield and 100 seed weight showed high coefficients of variation. All the damage related biochemical and morphological traits except content of chlorophyll 'a' in the leaf tissues exhibited high heritability and high genetic gain. Important yield contributing characters also showed high heritability coupled with high genetic gain. This results indicate that the underlying additive gene action provides immense scope for improvement through selection.

Plant resistance indices served as the selection criteria for identifying the testers for L XT crossing programme. The plant resistance indices were minimum for T_{45}, T_{47}, and T_{49} which were selected as testers.

Significant positive correlation was noticed between the damage parameters, but significant negative correlation was noticed with non-glandular trichome density, peduncle length and ratio of chlorophyll 'a' to 'b'. Plant resistance index was positively correlated with all damage parameters and negatively correlated with peduncle length, density of non-glandular trichomes on pod wall and ratio of chlorophyll 'a' to 'b'. Grain yield per plant exhibited highly significant positive correlation with number of pods per plant, number of inflorescences per plant, number of seeds per pod and 100 seed weight. Path coefficient analysis revealed that

number of pods per plant followed by 100 seed weight and number of seeds per pod exerted the maximum positive direct effect on grain yield. Pod length contributed to yield through positive indirect effects through all other characters.

Selection indices were worked out for the fifty genotypes for selection of lines for L XT analysis. The genotypes T_2, T_4, T_6, T_7 and T_8 were selected on the basis of index scores. Mahalanobis D^2 statistic was used to group the fifty genotypes into ten clusters. Wide range of genetic divergence was noticed among the 50 genotypes.

The mean performance of parents, estimates of heterosis, general combining ability of parents and specific combining ability of the crosses were evaluated through line X tester analysis. The significance of line X tester interaction suggested the involvement of different gene effects for most characters.

L_2 and L_3 showed high mean values for major yield characters among the lines. Among the testers, T_2 exhibited the least estimates for damage measurements and highest mean values for number of pods per plant and grain yield. L_4 X T_3 showed high mean values for yield characters and low mean values for damage parameters among the crosses. L_1 X T_2 followed L_4 X T_3 with high mean values for important characters like grain yield. L_3 X T_2 also exhibited high mean values for yield traits combined with low scores for damage measurements.

Desirable negative heterosis was noticed for days to flowering in all the crosses. Positive and significant estimates of all three types of heterosis for number of pods per plant was noticed in seven crosses. Three crosses had positive and significant estimates of heterosis for number of inflorescences per plant, number of pods per inflorescence and grain yield. Negative and significant relative heterosis for percentage flower bud infestation and percentage pod infestation was noticed in three crosses, while for number of damaged seeds per 25 pods, two crosses showed negative and significant relative heterosis. None of the crosses expressed significant negative heterobeltiosis for any of the damage parameter.

Grain yield per plant, number of pods per plant, number of inflorescences per plant, pod length and number of seeds per pod exhibited significant *gca* effects.

Among the lines, L_4 and L_1 showed good *gca* effects for important yield characters. Among the testers, T_2 displayed desirable *gca* effects for damage parameters and yield traits.

High *sca* effect were observed for grain yield per plant, percentage flower bud infestation, percentage pod infestation and number of pods per plant. L_5 X T_2 and L_2 X T_3 exhibited good *sca* effects for damage parameters, yield traits and morphological characters. L_2 X T_2 and L_3 X T_3 displayed desirable *sca* effects for several yield characters.

Crosses contributed maximum towards the total variability for all characters except number of branches per plant and leaf chlorophyll content. For number of branches and leaf chlorophyll content, the proportional contribution of lines was the highest followed by crosses. For all the damage measurements, proportional contribution of crosses were followed by that of lines.

Predominance of one or multiple epistatic interactions was 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 effects and domimance X dominance interactions suggest the presence of non-allelic duplicate gene action in their expression. For peduncle length, complimentary gene action plays a major role.

The significance of additive gene effects and desirable direction of dominance X dominance epistatic interactions underlines the suitability of exploiting heterosis and selection in an efficient manner. The magnitude and direction of the gene effects underlying the pest damage parameters offers a favourable background for the breeder to develop legume pod borer resistant cowpea types, through recombination breeding and / or selection.