SCREENING FOR LEAF CURL VIRUS DISEASE COMPLEX RESISTANCE, GENETIC EVALUATION AND MOLECULAR CHARACTERIZATION OF BIRD CHILLI (*Capsicum frutescens* L.)

NICEY MATHEW

Thesis submitted in partial fulfilment of the requirement for the degree of

Master of Science in Agriculture

Faculty of Agriculture
Kerela Agricultural University, Thrissur

2006

Department of Plant Breeding and genetics
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM - 695 522

DECLARATION

I hereby declare that this thesis entitled **"Screening for leaf curl virus disease complex resistance, genetic evaluation and molecular characterization of bird chilli (*Capsicum frutescens* L.)"** is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar title, of any other university or society.

Vellayani,
07-01 -2006.

NICEY MATHEW
(2003-11-42)

CERTIFICATE

Certified that this thesis entitled **"Screening for leaf curl virus disease complex resistance, genetic evaluation and molecular characterization of bird chilli (*Capsicum frutescens* L.)"** is a record of research work done independently by Ms Nicey Mathew (2003-11-42) 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.

Vellayani,
07-01-2006

Dr. K.M. ABDUL KHADER
(Chairman, Advisory Committee)
Associate Professor,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695 522.

Approved by

Chairperson:

Dr. K.M. ABDUL KHADER
Associate Professor,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

Members :

Dr. P. MANJU
Associate Professor and Head,
Department of Plant Breeding and Genetics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

Dr. K. RAJMOHAN
Associate Professor and Head,
Department of Plant Biotechnology,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

Dr. VIJAYARAGHAVAKUMAR
Associate Professor,
Department of Agricultural Statistics,
College of Agriculture, Vellayani,
Thiruvananthapuram-695522.

External Examiner :

Dedicated to

My Family

ACKNOWLEDGEMENT

I would like to express my heartfelt gratitude to Dr. K.M. Abdul Khader, Associate Professor, Department of Plant Breeding and Genetics, College of Agriculture, Vellayani and Chairman of my Advisory Committee for his kind treatment, constant guidance, timely advice, encouragement, interest in the work, selfless help and moral support which made this research a success.

I would like to extent my sincere thanks to Dr. P. Manju, Professor and Head, Department of Plant Breeding and Genetics and member of my Advisory Committee for her critical suggestions and interest during the course of study.

I express my sincere gratitude to Dr. K. Rajmohan, Associate Professor and Head, Department of Plant Biotechnology and member of my advisory committee for his critical suggestions and valuable advice.

I wish to place on record my sincere thanks to Dr. Vijayaraghavakumar, Associate Professor, Department of Agricultural Statistics for his help during the analysis and interpretation of the experimental data.

I also thank all teaching and non-teaching staff of Department of Plant Breeding and Genetics for their co-operation all throughout the period of study.

I would like to extend my sincere thanks to Dr. D. Chandramony, former Head, Department of Plant Breeding and Genetics for her kind treatment and valuable advice.

I sincerely acknowledge Dr. K.B. Soni, Associate Professor, Department of Plant Biotechnology for her valuable and timely advices.

I would also thank all the members of the Department of Plant Physiology who provided me with the lab facilities.

I express my profound gratitude to Anitha chechi, Pradeep, Prajeesh and Rajeev for their sincere help and support provided during the critical stages of my research work.

Words fail to express my immense thanks to Julie chechi who helped and supported me, with sisterly affection, in each and every part of the thesis work. Without her help, it would not be possible for me to complete the work in time.

I feel happy to acknowledge Avanish C. Pius for his constant support, love and care.

I find special pleasure in placing my wholehearted thanks to my classmates Anandhi and Madhu Kumar and all my senior and junior friends for their kind support and help provided during various stages of my work.

I put forth my immense gratitude to my friends Dhanya Jose, Dhanya K. Prakash, Priya and Sujatha for their loving involvements and care during the entire period of my work.

I express my affection and thanks to my beloved parents and sister for their support and care given to me at all times.

I would like to extent my heartfelt gratitude to Mr. C.E. Ajithkumar, Junior Programmer, Department of Agricultural Statistics for executing the statistical analysis for my study.

My sincere thanks are due to Mr. Biju for his patience and co-operation in neat execution of the manuscript.

I acknowledge Kerala Agricultural University for awarding me the Junior Research Fellowship.

Above all, I thank God for being with me always.

Nicey Mathew

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

Introduction

1. INTRODUCTION

Chilli (*Capsicum* sp.) is an important spice cum vegetable, providing green and dry fruits. They are excellent source of vitamin A and C, iron, phosphorus, calcium etc. India is the largest producer of chillies in the world contributing about ten per cent of the total world production (Berry, 2003). In India, chilli is grown in an area of 9.65 lakh hectare with annual production of 10.75 lakh tonnes (Peter *et al.*, 2004).

Belonging to the family Solanaceae, chilli is indigenous to Central and South America. The genus *Capsicum* includes five domesticated species, 22 wild species and many varieties (Bosland, 1994), making this one of the largest classes in the vegetable kingdom. According to the American Spice Trade Association (ASTA), spice industry uses two species, *Capsicum annuum*, the milder and *Capsicum frutescens*, the hotter one, and denotes the whole hot peppers as chillies.

Bird chilli (*Capsicum frutescens*) or cayenne is a stimulating herb, renowned for its strong heat and smell. It is the Kerala's "kandhari mulaku". Besides its culinary uses, it is believed to possess many medicinal values. Some of the most widely used and reliable ones are to treat toothache, asthma, sore throat, stomachache and flatulence. Medicinally, it is known as a counter-irritant and relieves pain in the muscles and joints. Bird pepper exerts a number of beneficial effects on the cardiovascular system. It reduces the likelihood of developing arteriosclerosis by reducing blood cholesterol and triglyceride levels.

In spite of its wide importance *C. frutescens* is commercially cultivated only in Mizoram (approximately 140 hectare with annual production of 560 tones) and some areas of Manipur (approximately 122 hectare with annual production of 488 tones) whereas in other areas it is widely grown as a homestead crop (Barua and Barua, 2004). One of the

major factors responsible for the low productivity of chilli in India is leaf curl virus disease, especially during the summer months. Most of the *Capsicum annuum* genotypes are very much susceptible to this. However, bird chilli is reported to possess considerable resistance to this virus. It is a DNA virus spread by the vector, white fly (*Bemisia tabaci*). Application of insecticides to control the vector will not be a desirable method to manage the disease, as it makes the cultivation costly and causes many health and environmental problems. This creates an urgent need to develop leaf curl virus resistant varieties for cultivation.

Studies reveal that interspecific cross between *Capsicum annuum* and *Capsicum frutescens* is possible. So if resistant lines of *Capsicum frutescens* are identified, interspecific hybridization or other suitable breeding methods can be adopted to transfer these resistant genes into more economic *Capsicum annuum* cultivars.

Keeping in view the above facts, the present study was undertaken with the following objectives.

1. Collection and evaluation of different genotypes of *Capsicum frutescens* for resistance to chilli leaf curl virus disease and to exploit the variability present in them.
2. Estimation of correlation between fruit yield and yield related characters and path analysis to facilitate selection.
3. Construction of selection index to identify the superior genotypes based on the desirable characters.
4. Clustering of genotypes to facilitate selection of parents for hybridization.
5. Random Amplified Polymorphic DNA (RAPD) analysis to characterize the genotypes at the molecular level.

Review of Literature

2. REVIEW OF LITERATURE

The literature available on various aspects of the present investigation is reviewed here.

2.1 YIELD ANALYSIS

2.1.1 Variability

2.1.1.1 Mean Performance

Variability with respect to different characters is an essential requisite for the selection of superior genotypes from a population. A number of workers studied variability for different characters in chilli (*Capsicum* spp.) and are presented below.

Singh and Singh (1976a) observed high variability among 45 genetic stocks of chilli for plant height, number of branches, days to flowering, days to maturity, fruit length, fruit thickness, number of fruits per plant and yield per plant. Arya and Saini (1977) also observed similar results while studying variability in 30 cultivars.

While comparing the mean performance of 12 varieties of chilli, Ramakumar *et al.* (1981) observed high variability for plant height, plant spread, fruit girth, number of seeds per fruit, number of fruits per plant and yield.

In the study using 30 genotypes of chilli, Nair *et al.* (1984a) observed wide range of variability for number of primary and secondary branches, duration of the crop and number of seeds per fruit. Similar result was obtained by Gopalakrishnan *et al.* (1987) while studying 38 chilli lines.

Fruits per plant, branches per plant and individual fruit weight were found to be the most variable traits in a study involving 16 cultivars of *C. annuum* (Ado *et al.*, 1987).

Bai *et al.* (1987) reported significant variation among varieties for duration of flowering, plant height and fruit length in 12 red pepper varieties. But, Ahmed *et al.* (1990) obtained a low range of variability for days to first fruiting, plant height and plant spread in their study using 64 lines of chilli (*C. annuum*).

Adamu and Ado (1988) obtained high levels of variation for fruits per plant, individual fruit weight and dry fruit yield per plant in *C. frutescens*.

Rajput *et al.* (1991) obtained wide variation in 12 cultivars of chilli (*C. annuum*) for dry chilli yield and fruiting period. .

Acharya *et al.* (1992) reported high variability in cultivars of chilli for fruits per plant, yield per plant, fruit length, circumference of fruit and seeds per fruit. This was similar to earlier works reported by Choudhary *et al.* (1985) and Gopalakrishnan *et al.* (1985).

Singh *et al.* (1994) studied variation for nine yield related traits in 20 chilli genotypes over two seasons and reported greatest variability for fresh red ripe fruits per plant. Kataria *et al.* (1997) reported high variability for fresh fruit weight per plant, number of fruits per plant and plant height among 54 genotypes of *C. annuum*.

Jabeen *et al.* (1998) reported high variability for all the characters studied, especially for fruit yield in 71 genotypes of chilli. Several other workers also obtained similar results (Rani and Singh, 1996 and Singh and Singh, 1998).

While evaluating 119 accessions of chilli, Verma *et al.* (1998) observed wide range of variability in plant height, density of branches, days to 50 per cent flowering, number of fruits per plant, fruit length, fruit width, green fruit weight per ten fruits and dry fruit weight per ten fruits.

Dwivedi and Bhandari (1999) reported high variability for number of seeds per fruit, 1000-seed weight and days to maturity in addition to several other characters in a collection of 160 sweet pepper germplasm.

Munshi and Behera (2000) observed existence of considerable amount of genetic variability for number of fruits per plant, fruit weight, fruit length and yield per plant in a study involving 30 chilli (*C. annuum*) genotypes.

Mishra *et al.* (2001) evaluated nine genotypes of chilli for fruit characters and found considerable variability for fruits per plant and fruit length. Ibrahim *et al.* (2001) in their study using 17 genotypes of chilli reported high variability for fruit length followed by dry fruit weight and number of branches per plant.

In a study using 52 chilli (*Capsicum* spp.) cultivars and lines with regard to yield components, Gogoi and Gautam (2002) observed significant variation for all the characters.

Khurana *et al.* (2003) reported highly significant variation among 46 *C. annuum* genotypes for fruit yield, fruit length, fruit thickness and number of fruits per plant. In a study involving 26 chilli genotypes, Nandadevi and Hosamani (2003b) observed high variability for number of primary branches, fruit length, number of fruits per plant and green fruit yield.

2.1.1.2 Variance

The components of variance give a more clear idea of extent of variability in a population.

Ramalingam and Murugarajendran (1977) obtained high genotypic and phenotypic variances for plant height, weight of dry fruits, number of fruits per plant and number of branches. But, Hiremath and Mathapati (1977) found high phenotypic variance only for yield and number of fruits per plant in 36 cultivars of chilli.

In a study using 30 genotypes of chilli, Elangovan *et al.* (1981) obtained high phenotypic and genotypic variances for plant height, plant spread, number of seeds per fruit and number of fruits per plant.

Bai *et al.* (1987) reported that the genotypic, environmental and phenotypic variances were maximum for fresh fruit yield per plant and minimum for branches per plant and percentage of fruit setting in a set of chilli germplasm.

The genotypic and phenotypic variances were high for number of flowers, plant height and plant spread while it was low for number of primary branches, average fruit weight, fruit length and fruit girth in chilli (Vijayalakshmi *et al.*, 1989).

Shaoo *et al.* (1990) reported that in *C. annuum* seeds per fruit showed the maximum genotypic variance and 100 seed weight the minimum.

In a study using 25 genotypes of chilli, Das and Choudhary (1999a) reported high phenotypic and genotypic variances for fruit length.

2.1.2 Heritability and Genetic Advance

Heritability estimates along with genetic advance is more useful in selecting superior genotypes than using heritability values alone.

Singh and Singh (1977a) noticed high values of heritability and genetic advance for number of fruits per plant, number of branches, plant height, days to maturity and yield per plant in chilli.

Bavaji and Murthy (1982) noticed high heritability coupled with high genetic advance for branches per plant, fruit length, 50 fruit weight and fruits per plant in a study involving 25 varieties of chilli.

Nair *et al.* (1984b) reported high heritability along with low genetic advance for days to flower, plant height, plant spread, number of primary branches and life span.

In a study using 12 varieties of chilli, Shah *et al.* (1986) observed high heritability and expected genetic advance for plant height, number of primary branches, fruit length, fruit width and number of fruits per plant.

Meshram (1987) obtained high heritability and high expected genetic advance for fruit length and days to first flower.

Ghai and Thakur (1987) reported that total yield and number of fruits recorded the lowest value of heritability in narrow sense in a population comprising of parents, F_1s, F_2s and back crosses. The expected genetic advance showed wide range from 8.82 per cent for number of fruits per plant to 73.81 per cent for fruit weight. The highest estimates of heritability and genetic advance were found for yield per plant in a study involving 30 genotypes of chilli (Das *et al.*, 1989). But, Depestre *et al.* (1989a) obtained maximum narrow sense heritability and marked genetic advance for fruit number per plant and yield in a natural population of *C. annuum* var. espanol.

High heritability coupled with high genetic advance was reported by Vijayalakhsmi *et al.* (1989) for number of fruits per plant, fruit weight, fruit length, fruit girth and number of seeds per fruit in a study involving 11 chilli varieties.

High heritability and genetic advance were noticed for yield per plant, number of fruits per plant and weight of ten dry fruits (Sahoo *et al.*, 1989).

Bhagyalakshmi *et al.* (1990) studied 15 F_1 hybrids and their parents in chilli and observed moderate heritability estimates for plant height, branches per plant, fruit weight, number of seeds per fruit and 100 seed weight while it was high for days to fifty per cent flowering, fruit length, fruit girth, number of fruits per plant and ascorbic acid content.

In a study involving nine cultivars of chilli, Nandi (1993) noticed that length and weight of pod and yield per plant had medium to high

heritability and high genetic advance. Kumar *et al.* (1993) evaluated four F_2 progeny for nine fruit characters and observed high heritability and genetic advance for number of fruits per plant, number of seeds per fruit, ascorbic acid content and yield per plant.

Singh *et al.* (1994) obtained high heritability for fruit length, weight of fresh ripe fruits, dry fruit weight, number of fruits per plant and fruit diameter in *C. annuum*.

Pitchaimuthu and Pappiah (1995) found high heritability coupled with high genetic advance for number of fruits per plant, fruit length and fruit girth while evaluating fourteen F_6 families from the cross Acc.1683 x K_2.

Rani and Singh (1996) reported high heritability and genetic advance for fruit length.

Kataria *et al.* (1997) reported high heritability and genetic advance for fruit length, yield and average fruit weight, but according to Devi and Arumurugam (1999) fruit length and yield had moderate heritability. According to them, heritability and genetic advance were high for number of fruits per plant and fruit weight.

Das and Choudhary (1999a) obtained very high heritability (>80 %) for fruit length, fruit number, fruit weight and yield. Similar results were reported by Munshi and Behera (2000).

In chilli, high heritability for plant height (98.12 per cent) was reported by Ibrahim *et al.* (2001).

Number of primary branches had low heritability, while fresh and dry fruit yield per plant and fruit length showed high heritability coupled with high genetic advance in a study involving 52 chilli genotypes (Gogoi and Gautam, 2002).

Sreelathakumari and Rajamony (2002) observed high heritability and genetic advance for fruits per plant, fruit weight, fruit length, fruit girth, yield and leaf area, in both open and shaded condition in a study

involving 70 diverse genotypes of chilli belonging to *C. annuum*, *C. frutescens* and *C. chinense*.

Rathod *et al.* (2002a) in their studies using 13 chilli cultivars observed high heritability for days to fifty per cent flowering, plant height, number of primary branches, fruit number, fruit length, 100 seed weight and fresh fruit yield. Among these, fruit number, fruit yield and plant height had high genetic advance also.

Doshi (2003) observed high heritability for capsaicin (95.2 per cent), fruit weight (82.2 per cent), fruits per plant (76.6 per cent) and plant height (67.10 per cent) while it was low for primary branches per plant (22.10 per cent).

In a genetic diversity study involving 48 *C. annuum* genotypes high heritability was observed for fruit yield, number of fruits per plant, fruit length, fruit diameter and seeds per fruit (Khurana *et al.*, 2003).

2.1.3 Coefficient of Variation

This is a unit free measurement of variation and hence allows the comparison of variability among different characters.

In a study involving seven bell pepper cultivars, Arya and Saini (1976) reported high genotypic and phenotypic coefficients of variation for number of fruits per plant, fruit size and fruit yield per plant while number of seeds per fruit and number of branches gave medium values. But, Hiremath and Mathapati (1977) found high coefficient of variation for number of branches and number of seeds per fruit in 36 cultivars of chilli.

Rao and Chhonkar (1981) observed low to medium phenotypic and genotypic coefficients of variation for several characters in a 10 x 10 diallel cross involving 45 F_1 and F_2 hybrids.

In a study involving 12 parents and their 66 F_1 and F_2 progenies, Gupta and Yadav (1984) found that the genotypic coefficient of variation ranged from 11.1 for plant height to 62.6 for fruit length.

Nair *et al.* (1984a) found high genotypic coefficient of variation among 25 chilli for number of fruits (121.28), weight of fruit (100.65) and total yield (108.93).

Gopalakrishnan *et al.* (1987) obtained high GCV for fruit length, main stem length, fruit weight, fruits per plant and fruit yield per plant in 38 lines of chilli.

Vijayalakshmi *et al.* (1989) observed a greater difference between PCV and GCV for plant height, plant spread, number of flowers, number of pods, total yield and total dry yield indicating greater influence of environment on these characters. Gopalakrishnan *et al.* (1985) also had a similar view with regard to number of branches per plant. But, Pitchaimuthu and Pappiah (1992) reported a close association between the estimates of GCV and PCV for several characters in F_6 generation indicating low environmental influence.

Nandi (1993) in a study using nine cultivars of chilli, observed that length and weight of fruit and yield per plant had the highest GCV.

In a study with 79 genotypes of chillies, Rani (1996) noticed that GCV and PCV were high for fruits per plant, mean fruit weight, yield per plant, fruit length, weight of seeds per fruit and 100 seed weight.

In a study using 71 hot pepper lines, Jabeen *et al.* (1999) noticed that both GCV and PCV were high for fruit yield per plant, fruit number per plant, seed number per fruit and average fruit weight.

Munshi and Behera (2000) obtained a GCV ranging form 5.32 per cent (days to first fruit harvest) to 54.94 per cent (number of fruits per plant) in a study with 30 chilli genotypes.

Rathod *et al.* (2002a) observed high GCV estimate for number of fruits per plant, fresh red chilli yield per plant and plant height.

Nandadevi and Hosamani (2003a) observed high degree of PCV and GCV for number of primary branches, fruit length, pericarp thickness, number of fruits per plant and green fruit yield per plant.

2.1.4 Association of Characters

2.1.4.1 Correlation Coefficient Analysis

A knowledge of correlation between yield and its component characters is essential for choosing the character for selection.

Pandian and Sivasubramanian (1978) found that the total number of fruits harvested per plant in chilli had significant positive association with flowers produced during 66-86 days.

Yield was negatively correlated with days to flowering (Rao *et al.*, 1981). But, Sundaram and Ranganathan (1978) and Veerappa (1982) reported significant positive correlation of yield with days to flowering.

Significant positive association of number of fruits and number of branches with yield was observed by Bavaji and Murthy (1982).

Nair *et al.* (1984a) found positive correlation of fruit yield with fruits per plant, number of secondary branches per plant, fruit weight, fruit circumference and crop duration.

Choudhary *et al.* (1985) observed positive correlation of yield per plant with fruit girth and weight of ten fruits, which also had a significant positive correlation with number of seeds per fruit. But, Gopalakrishnan *et al.* (1985) observed negative correlation of fruit girth with fruit yield per plant while fruit length showed maximum positive correlation with yield.

Ghai and Thakur (1987) found that yield was significantly associated both phenotypically and genotypically with fruit length, number of branches, number of fruits and plant spread.

Jayasankar *et al.* (1987) reported that fruit length, number of seeds per fruit, fruit girth and number of primary branches could be considered as secondary yield determinants owing to their less association with yield.

Miranda *et al.* (1988) observed positive genotypic correlation of total yield per plant with early yield, average weight per sampled fruit and fruit length.

He *et al.* (1989) reported negative correlation of fruit yield with fruit length.

According to Depestre *et al.* (1989b), fruit number per plant was the most closely correlated character with yield, followed by mean fruit weight, in a study related to yield and seven yield components in chilli.

In an experiment by Kaul and Sharma (1989), information is derived on yield and its correlation with other characters in 14 parents and 24 F_1s. It was found that fruit yield was positively associated with plant height, number of branches per plant, leaf area, number of seeds per fruit and ascorbic acid, dry matter and total soluble solids content of the fruit.

Significant negative correlation of yield with days to 50 per cent flowering and days to fruit set with maturity was reported by Bhagyalakshmi *et al.* (1990). Warade *et al.* (1996) also reported negative correlation of fruit yield with days to 50 per cent flowering and days to maturity.

Ali (1994) reported positive correlation of fruit yield with number of seeds per fruit and number of fruits per plant. Plant height, plant spread, number of primary branches per plant and number of secondary branches per plant showed significant positive correlation with yield (Rani, 1995).

Fruit yield was positively and significantly correlated with number of fruits, number of branches, plant height and fruit length (Pawade *et al.*, 1995).

Ahmed *et al.* (1997) reported that fruit yield was positively associated with number of fruits, fruit weight, plant height and fruit length and negatively associated with days to maturity. Rani (1997) found positive correlation between fruit yield and fruit number, number of primary and secondary branches, plant height and seed weight. Vallejo *et al.* (1997) reported that fruit number and fruit weight were negatively correlated.

Evaluation of 24 varieties of sweet pepper revealed strong positive correlation of yield per plant with fruit weight at genotypic and phenotypic levels. Number of fruits had positive and significant association with fruit weight, plant height and days to flowering (Mishra *et al.*, 1998).

Correlation studies in 25 genotypes revealed positive association of yield with fruit weight, number of fruits and number of primary branches (Das and Choudhary, 1999b). Dimova and Panaystov (1999) observed positive correlation between seed weight and fruit weight. Subashri and Natarajan (1999) obtained positive association of yield with number of branches, number of fruits, fruit weight and fruit length in F_2 population.

According to Aliyu *et al.* (2000) yield per plant was negatively correlated with plant height.

Chaim and Paran (2000) reported the high genetic correlation coefficient of fruit weight with diameter, pericarp thickness and pedicel diameter in chilli. In contrast, fruit weight had a low correlation with fruit length.

Munshi *et al.* (2000) observed positive association of yield with fruit weight and fruit number. Fruit weight had positive correlation with fruit length and negative correlation with fruit number.

Quantitative traits and their correlation in sweet paprika was studied by Wyrzykowska *et al.* (2000) and reported that fruit yield depended significantly on mean fruit weight and fruits per plant.

Studying 17 genotypes of chilli, Ibrahim *et al.* (2001) reported that dry fruit weight per plant exhibited significant positive correlation with number of fruits per plant, number of branches, fruit length, fruit width and plant height. Besides, number of fruits per plant showed highly significant positive correlation with number of branches and plant height but negative correlation with fruit length.

Fruit weight, pericarp thickness, number of seeds per fruit and 1000 seed weight showed positively significant association with fruit yield (Chatterjee *et al.*, 2001).

Acharyya *et al.* (2002) reported positive and significant correlation of total fresh yield per plant with total dry yield per plant

Jose and Khader (2002) reported positive correlation of yield with fruit weight, number of fruits, primary branches per plant, secondary branches per plant, plant height, 100 seed weight, fruit length, fruit girth and crop duration. Correlation was negative with days to flowering.

According to Todovora *et al.* (2003), correlation was unstable and expressed depending on the year of cultivation for some of the morphological characters in *C. annuum* cultivars.

Fruit yield was positively correlated with number of fruits, fruit length, fruit diameter, plant height, capsaicin content and colouring matter but negatively correlated with number of days to flowering (Khurana *et al.*, 2003).

Muthuswamy (2004) reported negative association of days to first flowering with many of the characters studied and positive association with fruit length.

2.1.5 Path Coefficient Analysis

Number of fruits per plant had a positive direct effect on yield, while days to flower had a very strong negative direct effect on early yield (Gill *et al.*, 1977).

In a study using 20 varieties of chilli, Korla and Rastogi (1977) reported that number of fruits per plant had the highest direct effect on fruit yield followed by weight per fruit and plant height.

Path analysis in 50 varieties of chilli revealed that number of fruits and fruit length showed positive direct effect on yield while days to flowering and number of branches exerted small and negative direct effect on yield (Sundaram and Ranganathan, 1978).

Rao *et al.* (1981) reported that days to maturity and flowering, fruit setting ability in summer and fruits per plant were the most important factors, accounting for 55.34 per cent of the variability showed by character correlations in *Capsicum* spp.

Rao and Chhonkar (1981) in their study of a 10 x 10 diallel found that number of fruits, fruit weight and dry yield had a direct effect on ripe fruit yield.

Path coefficient analysis of yield per plant and seven yield related characters in a group of 4 genotypes indicated that the characters fruit number per plant, length and number of primary branches had significant positive direct effect on yield (Joshi and Singh, 1983).

Path analysis in 30 cultivars revealed that number of fruits, secondary branches, fruit weight, fruit circumference and duration had positive direct effect on yield (Nair *et al.*, 1984b).

Solanki *et al.* (1986) reported that number of fruits, plant height, number of primary branches per plant and fruit length had direct positive effect on yield.

In a study using 30 genotypes, Chouvey *et al.* (1986) observed positive direct effect for number of fruits per plant, 10-fruit weight, number of seeds per fruit and fruit circumference on yield.

Path coefficient analysis of 21 varieties showed that mean fruit weight, fruits per plant and fruit width had the greatest direct effect on yield (Depestre *et al*, 1989c).

Path analysis in 14 parents and 24 F_1s revealed that number of fruits per plant, fruit diameter and number of branches per plant were the main contributors to yield (Kaul and Sharma, 1989).

Based on path analysis study in 20 chilli genotypes, Sarma and Roy (1995) reported the importance of fruit diameter, fruit length and days to 50 per cent flowering as selection criteria for improving chilli genotypes.

Das and Choudhary (1999b) observed that fruits per plant and weight of fruits exhibited the highest positive effect on yield.

Legesse *et al.* (1999) found positive direct effect of canopy width, fruit number per plant and pericarp thickness on yield in 18 hot pepper genotypes.

Path analysis in a 6 x 6 diallel excluding reciprocals revealed the strong positive direct effect of total fruit number on total fruit weight (Tavares *et al.*, 1999).

Fruit diameter and number of seeds per plant showed large positive direct effect on yield while plant height had a negative direct contribution to final yield (Aliyu *et al.*, 2000).

Direct positive effect of number of fruits per plant, fruit weight and fruit girth on yield per plant was observed in a study involving 30 chilli genotypes (Munshi *et al.*, 2000).

Mini (2003) found that direct effect of number of fruits per plant and average fruit weight was high and positive, while that of plant height was high and negative.

Ajith (2004) reported positive direct effect of number of fruits per plant on yield while that of number of branches and fruit girth was negative.

2.1.6 Selection Index

Use of selection index will increase the efficiency of selection to improve fruit yield in chilli.

Singh and Singh (1976b) obtained maximum yield advance in F_2 generation and selection indices were based on the seven characters viz., plant height, number of branches, days to flowering, days to maturity, fruit length, fruit thickness and number of fruits per plant. The comparison of different discriminant functions revealed that days to flowering, fruit length and number of fruits per plant were major yield components.

Singh and Singh (1977b) studied 45 strains of chilli and reported that discriminant function using seven characters at a time, plant height, number of branches, days to maturity, fruit length, fruit size and fruits per plant was more efficient than straight selection for yield.

Ramkumar *et al.* (1981) reported that selection based upon discriminant function involving fruit length, number of fruits and plant spread may be more efficient than straight selection for yield.

Rani and Usha (1996) evaluated 73 *C. annuum* genotypes for fruit yield and related characters. Correlation and regression analysis were carried out to determine the selection index.

Vallejo *et al.* (1997) used selection index to evaluate individual genotypes and to select best families from a F_2 generation of 19 hybrids obtained from a 7 x 7 half diallel cross. Mini (2003) constructed selection index based on 14 characters in *C. annuum* genotypes. The genotypes were ranked based on this and observed high selection index values for high yielding types.

Ajith (2004) used selection index to evaluate 76 genotypes of chilli based on yield (fruit weight per plant) and its component characters.

2.1.7 Genetic Divergence

Genetic divergence is a basic requirement for effective selection within the existing population or a population arising out of hybridization.

Singh and Singh (1976a) grouped 45 genotypes of chilli into ten clusters based on the similarities of their D^2 values. The clustering pattern of the strains did not follow the geographic distribution. Considerable diversity within and between the clusters was noted. The characters contributing maximum towards total divergence were number of branches, fruit thickness, number of fruits per plant and yield per plant.

Gill *et al.* (1982) conducted a diversity study in six parents and their 15 hybrids of sweet pepper and the 21 genotypes were grouped into seven clusters.

Varalakshmi and Haribabu (1991) classified 32 geographically diverse chilli genotypes into 11 clusters based on D^2 values. Grouping of genotypes into different clusters was not related to their geographical origin. Considerable differences existed between clusters for all the characters. Fruits per plant, leaf area index, fruit weight and total yield were reported to be the chief contributors towards genetic divergence.

Oliviera *et al.* (1999) used Mahalanobis D^2 values to evaluate the genetic diversity among six sweet pepper lines.

Forty *C. annuum* genotypes of indigenous and exotic origin were subjected to diversity analysis and based on D^2 values the genotypes were grouped into eight clusters. D^2 values ranged between 0.1032 and 8.7702. Fresh fruit weight and fruits per plant had the highest contribution towards divergence (Karad *et al.*, 2002).

Senapati *et al.* (2003) studied genetic divergence using Mahalanobis D^2 values, and the genotypes were clustered into six groups with maximum divergence between clusters II and V. Fresh fruit weight, fruit girth, fruit length and fruits per plant were the chief contributors towards divergence.

2.1.7 Molecular Characterisation

Detection of polymorphism at DNA level is used for estimation of genetic diversity and similarity among the cultivars, their characterization or testing the purity of hybrid seeds. The random amplified polymorphic DNA (RAPD) technique based on the polymerase chain reaction (PCR) has resulted in a potentially useful tool for cultivar discrimination.

As per Williams *et al.* (1990), RAPD markers were generated using the set B of primers. The PCR mixture consisted of dNTP (0.1 mM), Taq DNA polymerase (1.25 U), 1x Taq buffer, $MgCl_2$ (3.5 mM), primer (0.3 mM) and genomic DNA (25 ng) in a total volume of 25 µl. The reaction was programmed as 94°C for 1 minute; 45 cycles (93°C for 1 minute, 40°C for 1 minute, 72°C for 2 minutes) and 72°C for 10 minutes.

Prince *et al.* (1992) performed restriction fragment length polymorphism (RFLP) analysis on 25 accessions of *C. annuum*, *C. chinense* and *C. frutescens* from various regions of Mexico to estimate genetic distance among the accessions.

Prince *et al.* (1995) examined interspecific variation among four *C. annuum* cultivars using restricted fragment length polymorphism (RFLP) and RAPD. They reported the effectiveness of both the methods

for DNA finger printing and discrimination of closely related *C. annuum* genotypes.

. Wang *et al.* (1996) surveyed 14 diverse *Capsicum* sp. by RAPD analysis and obtained high degree of polymorphism from four decamer primers which produced eleven reproducible and effective amplification fragments useful for identification between species. .

Wang *et al.* (1997) evaluated genetic diversity within 44 *Capsicum* germplasm by RAPD markers and the accessions were divided into six groups.

Random amplified DNA analysis was widely used to evaluate genetic distance among accessions within and between different species of *Capsicum* with diverse geographic origin (Kang *et al.*, 1997; Rodriguez *et al.*, 1999; Votava and Bosland, 2001; Fan *et al.*, 2001 and Lanteri *et al.*, 2003).

Paran *et al.* (1998) examined genetic relationship among 34 pepper cultivars using RAPD and AFLP (Amplified Fragment Length Polymorphism). A dendrogram based on RAPD markers separated the large fruited sweet cultivars from the small fruited pungent peppers.

Tae and Hyo (1998) reported that RAPD technique is useful in developing DNA markers although the technique has some drawbacks such as lack of reproducibility. To carry out stable and reproducible RAPD analysis and thereby to develop mappable markers of *C. annuum*, the following conditions were surveyed: DNA template amount, dNTP and $MgCl_2$ concentration, number of PCR cycles, annealing temperature, primer kinds and its concentration. The best RAPD profiles were obtained using 20-50 ng of DNA, 200 μM of dNTP, 200 nM of primer, 3 mM of $MgCl_2$ and one unit of Taq polymerase in the 25 μl reaction mixture.

Wang and Fan (1998) used microsatellite DNA (Inter Simple Sequence Repeats, ISSR) and RAPD markers to compare 90 accessions of

C. annuum from 16 different countries and observed that both ISSR and RAPD markers, in addition to being simple and time efficient, allowed rapid identification of polymorphism within *C. annuum*.

Ballester and Vincento (1998) tested purity of F_1 chilli (*C. annuum* L.) hybrids and their parents using RAPD markers and proved that despite the dominant inheritance, these markers could be an efficient complement in the process of quality testing of hybrid seeds. Chao *et al.* (1998) performed cultivar identification and seed purity test by RAPD. Eleven primers produced 16 polymorhic bands with sizes in the range of 330-1150 base pairs.

Huang *et al.* (2001) established a simple and efficient RAPD assay protocol in *C. annuum* cv. Zhonjiao to screen RAPD markers for genetic purity testing of hybrid cultivars and a total of 12 stable and strong RAPDs were identified to distinguish the hybrids from their parental lines.

Lefebvre *et al.* (2001) evaluated concordance of AFLP and RAPD markers for estimating genetic distance of 47 *C. annuum* inbred lines belonging to five varietal types. Genetic distance and multidimensional scaling results showed a general agreement between AFLP and RAPD markers.

Garcia *et al.* (2002) used RAPD to study the relationship between genetic distance among parental lines of green pepper and the heterosis observed as yield of their F_1 hybrids

Ilbi (2003) evaluated the potential of RAPD markers in varietal identification and genetic purity test of hybrid varieties of *C. annuum*. Five Jalapeno hybrid varieties and their corresponding parents were screened for polymorphic RAPD markers with 12 arbitrary decamer primers and six primers generated useful RAPD markers to determine seed purity of all tested hybrid varieties. Among a total of 177 bands observed

14 bands contributed by nine primers were polymorphic in the five pepper varieties.

. Ma *et al.* (2003) studied the genetic relationship among 46 chilli germplasm accessions by RAPD and genetic polymorphism was observed in 88.68 per cent of the amplified bands from nine primers selected from a total of 160 primers. The accessions were classified into six groups by cluster analysis and the results of RAPD were similar to those obtained using traditional methods of genetic analysis.

Philip (2004) used RAPD technique in chilli (*C. annuum*) to test the hybrid purity.

Adetula (2005) performed RAPD analysis on 40 lines of *C. annuum* and *C. frutescens* to estimate genetic diversity and taxonomic relationship. Cluster analysis using UPGMA separated the lines into four major groups. Based on the morphological and molecular data, remarkable difference was exhibited by the *Capsicum* lines. A high level of polymorphism was detected which will assist in the breeding of Capsicum.

Sitthiwong *et al.* (2005) used RAPD analysis to classify the accessions of chilli.

2.2 SCREENING FOR LEAF CURL VIRUS RESISTANCE

Leaf curl is a major destructive disease of chilli. A yield loss of 80 to 100 per cent has been reported in case of early infection by leaf curl virus (Singh *et al.*, 1979).

Rishi and Dhawan (1988) exposed seedlings of 72 lines of *C. frutescens* to infection by cucumber mosaic virus, potato X virus, potato Y virus, tobacco mosaic virus and chilli leaf curl virus and found that one or other type of disease occurred in all the genotypes.

Munshi and Sharma (1996) reported that the incidence of chilli leaf curl ranged from 11.5 to 96.0 per cent.

Fugro (2000) reported that leaf curl incited by virus is an important disease of chilli.

In spite of its severity, not much work has been done in identifying resistant sources for developing resistant/tolerant varieties. An attempt has been made to review the available literature on leaf curl disease:

2.2.1 Symptomatology

Chilli leaf curl is characterized by stunting of the plants with upward and downward curling of leaves. The newly formed leaves exhibit chlorosis. The old, curled leaves become leathery and brittle. Shortening of internodes leads to dwarfing of the plant (Mishra *et al.*, 1963).

Dhanraj and Seth (1968) reported downward curling, dark green colour and oval to round shape of leaves, pronounced vein-thickening and leafy outgrowths or enations on the under surface of leaves. The diseased plants produced fewer flowers and fruits.

In severe cases, axillary buds were stimulated to produce small cluster of leaves. Flower and fruit formation were also reduced (Nair and Menon, 1983).

Ray and Sarkar (2001) reported that the virus generally found on the upper and lower canopy of the chilli plant caused severe yield loss. Curling of leaves is mainly due to the deformation of the cellular framework. Microtome sections (10 µm) of the virus infected leaves showed cellular destruction in the upper epidermis. Notable changes in cell size and structure were also observed.

2.2.2 Etiology

Chilli leaf curl is a complex disease caused by separate or combined infection of mites, thrips and viruses (Tewari, 1983 and Nawalagatti *et al.*, 1999).

Ayyar *et al.* (1935) observed that *Scirtothrips dorsalis* was involved in the disease while Khodawe and Taley (1978) reported the

involvement of *Hemitarsonemus latus* in the disease. Other workers (Amin, 1979; Mallapur, 2000; Reddy *et al.*, 2000) also reported that *Scirtothrips dorsalis* (thrips) and *Polyphagotarsonemus latus* (mite) caused leaf curl symptoms in chilli.

Sivanathan (1982) suggested that slower spread of the disease during wet weather is rather due to decreased mobility of the vector (*Bemisia tabaci*) than to inadequate inoculum. Slow spread in some cultivars was associated with poor host receptivity to the vector, decreased infection potential, lack of generation of secondary inoculum and longer time taken by the vector for acquisition and inoculation of the disease agent.

2.2.3 The Virus

The virus causing leaf curl in chillies is commonly referred to as chilli leaf curl virus or tobacco leaf curl virus.

Fernando and Peiris (1957) found that the transparent Kroepoek strain of tobacco leaf curl virus was involved in chilli leaf curl complex.

Dhanraj and Seth (1968) reported the presence of two distinct strains of the leaf curl virus and found that one of the strains produced severe enation in chilli and other solanaceous hosts.

Brown *et al.* (1993) found that pepper plants infected by Sinaloa tomato curl virus showed a green mottle on leaves.

Infection by tomato leaf curl virus in *C. annuum* plants resulted in interveinal and marginal chlorosis and upward curling of the leaflet margin (Reina *et al.*, 1999).

Dalmon and Marchoux (2000) reported that the tomato yellow leaf curl virus could also infect paprika (*Capsicum annuum*). But, Gonzalez *et al.* (1993) observed that all the *Capsicum* varieties inoculated with tomato yellow leaf curl bigemini virus showed resistance.

A new virus named as pepper yellow leaf curl virus was found to cause yellow leaf curl disease in *C. annuum* plants in Thailand (Samretwanich *et al.*, 2000).

2.2.4 Breeding for Resistance

Resistant donors identified by screening the varieties under field and/or artificial conditions can be utilized in breeding programmes to develop resistant varieties.

Mishra *et al.* (1963) screened 67 varieties of chilli against leaf curl virus and found that all were susceptible except Puri Red and Puri Orange.

Twenty three mutants of the variety NP 46A along with Puri Red and Puri Orange were screened against the enation strain of leaf curl virus and 100 per cent infection was obtained in all genotypes (Dhanraj *et al.*, 1968).

Singh (1973), on screening 105 chilli genotypes, found that seven of them *viz.*, EC 4020, EC 7277, EC 7338, EC 6589, EC 9293, Puri Red and Puri Orange were free from infection by leaf curl virus.

Tewari (1977) found that four varieties *viz.*, Sel 4, 6, 7 and 15 obtained from advanced generations of the cross NP 46A x Puri Red were superior and tolerant to the disease. Among these, Sel 4 was developed into the high yielding leaf curl virus resistant variety Pusa Jwala. This was confirmed by Tewari and Anand (1977) who obtained higher fruit yield and high degree of resistance for Pusa Jwala as compared to the susceptible variety CP 46 A.

Konai and Nariani (1980) observed that among 33 indigenous and exotic collections of chilli including five *Capsicum* spp., IC 31339 (*C. frutescens*), Pant C1, Pant C2 and *C. angulosum* were tolerant to leaf curl virus. Peter and Mac Collum (1984) reported "White Kandari" (a *C. frutescens* line) as a source to multiple disease resistance.

Singh and Kaur (1986) found that Punjab Lal selected from Perennial x Long Red was resistant to leaf curl virus.

Selections from the cross Pusa Jwala x Delhi Local *viz.*, 38-2-1, 38-3-19, 42-2-4, 52-1-6, 81-1-1, 96-4-8, 96-4-9, 96-4-3 and 101-2-33 were reported to be tolerant to tobacco leaf curl virus (Tewari and Viswanath, 1986).

Memane *et al.* (1987) on screening 69 varieties against leaf curl complex (caused by thrips and *Bemisia tabaci*, transmitting leaf curl virus) obtained lower disease incidence in Pant C1 (40.22 %). Pant C1, LIC 45 and NI 46 were regarded as moderately resistant to leaf curl virus.

Sangar *et al.* (1988) screened ten varieties of *Capsicum annuum* for resistance to tobacco mosaic virus (TMV) and tobacco leaf curl gemini virus under natural field conditions at Chhindwara. The varieties JCA 248, JCA 218, Pant C1, NP 46A, Pusa Jwala and JCA 196 were resistant to leaf curl virus. JCA 31A, Sel 3, JCA 154 and Pandurna exhibited different degrees of susceptibility. All varieties showed some symptoms of TMV. TCA 248, JCA 218 and Pant C1 were the least affected.

PSP-11 was a new cultivar of *C. frutescens*, which was a virus resistant line developed in India. It was found to be resistant to cucumber mosaic cucumovirus, potato X potex virus and TMV. It produced mild symptoms when infected by tobacco leaf curl gemini virus under green house conditions (Tewari and Viswanath, 1988).

Brar *et al.* (1989) screened 33 genotypes against leaf curl mosaic virus and obtained six lines tolerant to both the disease.

Naitam *et al.* (1990) evaluated seven chilli varieties for resistance against leaf curl and reported that Jwala and Pant C1 showed the least leaf curl incidence (25 %).

The selection PSP 11, named 'Pusa Sadabahar' developed from Pusa Jwala x IC 31339 was found to have high degree of tolerance to leaf curl virus (Tewari, 1991).

Pant C1 and Pant C2 (derived from NP 46A x Kandhari) and Jawahar 218 (derived from Kalipeeth x Pusa Jwala) were found to be tolerant/resistant to leaf curl virus (Singh, 1993).

In a study on genetic control of virus resistance against chilli mosaic and leaf curl viruses (most commonly tomato mosaic virus, cucumber mosaic cucumo virus, potato Y virus and tobacco leaf curl bigemini virus), Bal *et al.* (1995) observed that susceptibility to mosaic as well as leaf curl was controlled by dominant and resistance controlled by monogenic recessive genes. The conventional method of back crossing was suitable for transferring resistant genes to commercial varieties with acceptable fruit size.

Among 35 cultivars of *Capsicum annuum* screened against tomato leaf curl bigemini virus causing leaf curl disease, five were found to be highly resistant (Gandhi *et al.*, 1995).

Arora *et al.* (1996) reported that Hisar Vijay (HC 28) and Hisar Sakti (HC 44) identified from among 11 pure breeding lines were resistant to leaf curl virus.

Munshi and Sharma (1996) screened 66 cultivars for resistance to leaf curl complex and reported that six lines *viz.*, Pusa Sadabahar, RHRC clustering Erect, RHRC clustering Pendula, LGP-8-1, LGP-18-2-4-3 and LGP 18-20-12 were resistant to the disease.

Singh *et al.* (1998) screened seven varieties of chilli against sucking pests and leaf curl virus and observed that no variety was free from infection. But Pusa Sadabahar, JM-218 and Pant C-2 showed only traces of infection.

Among 37 chilli genotypes evaluated for incidence of pepper leaf curl virus, three (Pusa Jwala, Suryamukhi and Japani Loungi) were rated resistant, two moderately resistant, nineteen susceptible and thirteen highly susceptible (Kumar *et al.*, 1999).

Albejo (1999) evaluated 34 pepper cultivars for resistance to pepper leaf curl gemini virus and observed that PCBO 67 was moderately resistant while 26 lines were moderately susceptible.

Resistant sources against virus diseases were reported in different species of chilli; especially *C. frutescens* and these were utilized in improving the cultivated chilli (Bosland, 2000 and Grube *et al.*, 2000).

Jadhav *et al.* (2000) reported that "Phule Sai" (GCH-8) selected from advanced generations of Pant C 1 x Kamandalow was moderately resistant to leaf curl virus under field conditions.

Screening of 33 chilli genotypes against leaf curl caused by thrips and mites showed that Sel 7-11-13-1 exhibited the highest tolerance to leaf curl while the lowest incidence was recorded for Sel 4-1, followed by 7-11, 11-9 and 1-12 (Reddy *et al.*, 2000).

In an experiment involving screening of chilli for leaf curl complex resistance, the experimental material consisted of six parents *viz.*, LCA 301, LCA 312, LCA 304, Pusa Sadabahar, RHRC-clustering Erect and Punjab Lal and six generations *i.e.*, P_1, P_2, F_1, F_2, BC_1 and BC_2. The F_1 progenies and BC_2 generations were resistant to leaf curl complex. However, the BC generations of the cross (Punjab Lal x Pusa Sadabahar) x Punjab Lal was highly resistant with a much reduced coefficient of infection (Acharyya, 2002). He reported that selection on plant basis of such cross combinations in the segregating generation must be done to evolve a leaf curl resistant variety.

In a variability study, Acharyya *et al.* (2002) reported high heritability with enhanced genetic advance for leaf curl incidence

indicating the greater properties of additive genetic variance and consequently a high genetic gain expected from selection. High heritability coupled with high genetic advance for total fresh yield per plant was noticed under both leaf curl infected and non-infected conditions.

Nandadevi and Hosamani (2003b) in a study on 6 x 6 diallel analysis reported that RHRC-Clustering Erect, Pant C1 and PMR-52/88/K had significant gca effects for resistance to leaf curl complex. The magnitude of estimated components of dominant variance was more than additive variance for resistance to leaf curl complex indicating the predominance of non-additive gene effects.

Materials and Methods

3. MATERIALS AND METHODS

The study was undertaken to estimate the genetic variability in a collection of bird chilli (*Capsicum frutescens* L.) genotypes and to understand the reaction of these genotypes to chilli leaf curl virus. Based on the divergence and resistance to leaf curl virus, appropriate types can be chosen and hybridisation programmes can be attempted to combine both high yield and resistance into one genotype. These resistant types can be used in interspecific hybridisation to develop leaf curl resistant *Capsicum annuum* genotypes. The data for the investigation were collected from two field experiments conducted simultaneously. The study was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram during summer 2003-2005. Of the two experiments, experiment-I was for the study of genetic divergence based on yield and related characters and experiment-II for evaluation of the genotypes for leaf curl virus resistance.

3.1 EXPERIMENT-I: STUDY OF GENETIC VARIABILITY

3.1.1 Materials

The materials for the study consisted of 49 genotypes of bird chilli *(Capsicum frutescens* L.) collected from various agro-climatic regions of south India. The list of the genotypes are given in Table 1.

3.1.2 Methods

3.1.2.1 Design and Layout

The experiment was conducted in a Randomised Block Design (RBD) with three replications. Plot size was 5.0 x 0.75 m with spacing of 50 x 75 cm. Ten plants were maintained in each plot.

Table 1. List of genotypes of *Capsicum frutescens*

Accession Number	Name of genotype	Leaf pubescence	Fruit colour at intermediate stage
T_1	Parasuvaikkal local 1	3	Greenish red
T_2	Parasuvaikkal local 2	3	Greenish red
T_3	Kolagappara local	3	Greenish red
T_4	Vadakkupuram local	3	Greenish orange
T_5	Chakkai local 1	3	Greenish orange
T_6	Thavanur local 1	3	Greenish red
T_7	Areekode local	3	Greenish orange
T_8	Ambalavayal local 1	3	Greenish red
T_9	Omallur local	3	Greenish red
T_{10}	Mangalapuram local	3	Dark yellow / orange
T_{11}	Karumukku local	3	Orange
T_{12}	Pattanakkadu local 1	3	Greenish red
T_{13}	Mahe local	3	Greenish red
T_{14}	Thavanur local 2	3	Dark yellow / orange
T_{15}	Thavanur local 3	3	Purple
T_{16}	Ambalavayal local 2	5	Greenish orange
T_{17}	Vamanapuram local	3	Greenish orange
T_{18}	Irumbuzhi local	3	Greenish orange
T_{19}	Meenachil local	7	Greenish orange
T_{20}	Chakkai local 2	3	Greenish orange
T_{21}	Devarupara local	3	Greenish orange
T_{22}	Perumbavur local	3	Orange
T_{23}	Mallassery local	3	Greenish orange
T_{24}	Varkala local	3	Greenish orange
T_{25}	Ambalavayal local 3	3	Yellow / orange
T_{26}	Alappuzha local	5	Greenish orange
T_{27}	Vettoor local	3	Greenish orange
T_{28}	Elavanthitta local	3	Greenish red
T_{29}	Kolanchery local	3	Greenish red
T_{30}	Venjaramoodu local	3	Greenish red
T_{31}	Adoor local	3	Greenish red
T_{32}	Peringamala local	5	Greenish red
T_{33}	Kayamkulam local 4	3	Bluish red
T_{34}	Mariapuram local	3	Greenish red
T_{35}	Kayamkulam local 3	3	Reddish blue
T_{36}	Kayamkulam local 1	3	Greenish red
T_{37}	Mulleria local	3	Dark orange
T_{38}	Edneer local	3	Yellow / orange
T_{39}	Kalanadu local	3	Greenish orange
T_{40}	Puthige local	3	Yellow / orange
T_{41}	Nekraje local	3	Greenish orange
T_{42}	Malla local	5	Dark orange
T_{43}	Paika local	3	Orange
T_{44}	Panchikkal local	3	Greenish orange
T_{45}	Bovikana local 1	3	Greenish red
T_{46}	Sullia local	3	Greenish red
T_{47}	Yethadka local	3	Greenish orange
T_{48}	Bovikana local 2	5	Orange
T_{49}	Paadi local	3	Greenish red

3.1.2.2 Sowing and Cultural Operations

Seeds were sown on raised nursery beds on 2 September, 2004. The seedlings were transplanted on 22 October, 2004, when they were 60 days old; with one seedling per pit.

Cultural operations were carried out as per the package of practices recommendations of the Kerala Agricultural University (KAU, 2003).

3.1.2.3 Biometric Observations

In each genotype, five plants were selected at random excluding the border plants for recording the following biometric observations. The data for statistical analysis were obtained as mean values worked out thereafter.

a. Number of days to first flowering

Number of days taken from sowing to the appearance of first flower was recorded.

b. Plant height

Height was measured in cm from the base of the plant to the tip of the longest branch before the last harvest of fruits.

c. Number of primary branches

The branches originating from the main stem were counted and recorded at the full maturity of the plant.

d. Number of secondary branches

The branches borne on the primary branches were counted and recorded as the secondary branches

e. Plant spread

It is measured as plant canopy width in cm, taken at the widest point of the plant, immediately after the first harvest

f. Number of fruits per plant

The number of fruits at each harvest was recorded from each observational plant to calculate the total number of fruits per plant.

g. Individual fruit weight

The weight (g) of the five fruits taken at random from the observational plants over different harvests was recorded, the average worked out and expressed in grams.

h Fruit yield per plant

The weight (g) of fresh fruits collected from the five observational plants was recorded at each harvest. Total yield per plant was obtained by adding the weight of fruits at each harvest and taking the mean. The value was recorded in grams.

i. Duration of flowering (fruiting span)

It is the number of days from the appearance of first flower to the harvest of the last fruit. Since bird chilli is a perennial crop, it was unable to record the data within the limited period of the experiment

j. Fruit length

Length (cm) of five ripe fruits taken at random from the observational plants was recorded at the second harvest. The average was worked out and expressed in cm. Length was measured from the base of the pedicel (peduncle) to the tip of the fruit.

k. Pedicel: fruit ratio

Fruit length excluding pedicel was measured for those fruits selected for recording the total length of fruits (i^{th} observation, fruit length including the pedicel). This value was subtracted from the total length of fruits and then divided by the fruit length excluding pedicel. The average was calculated and recorded as a unit free observation.

l. Fruit width

The circumference (cm) at the broadest part of the fruits selected for recording length was taken, averaged and expressed in cm.

m. 100-seed weight

Seeds were extracted from a random sample of five ripe fruits and dried uniformly. The weight (g) of 100 fully developed seeds taken at random was recorded and expressed in grams.

n. Number of seeds per fruit

The seeds were extracted from ten ripe fruits taken at random from each observational plant at second harvest, the total number was counted and the average was found out.

o Reaction to leaf curl virus disease

Scoring of leaf curl symptom was done at 4^{th}, 6^{th} and 8^{th} month after planting. The observation on 6^{th} month after planting was used for computation of vulnerability index, during the peak period of fruiting.

p. Leaf pubescence

Leaf pubescence was observed on the youngest mature leaves. It is classified as:

3	Sparse
5	Intermediate
7	Dense

Observations are given in Table 1.

q. Fruit colour at intermediate stage

It was recorded just before ripening stage. The different possible colours were white, yellow, green, orange, purple, deep purple and others. Observations are given in Table 1.

3.1.2.4 Statistical Analysis

3.1.2.4.1 Analysis of variance (ANOVA) and covariance (ANCOVA) for RBD (Panse and Sukhatme, 1967) in respect of the various characters were done.

The mean values for each of the characters for all the accessions were worked out and compared using critical differences.

3.1.2.4.2 Grouping of Genotypes

The genotypes were grouped into poor, average and better categories with respect to each character as follows

Definition	Category
Less than mean –2 SE	Poor
Between mean ± 2 SE	Average
More than mean +2 SE	Better

where mean is the overall mean of 49 accessions for each character and SE is the standard error of mean for each character. The above classification is reversed for days to first flower and vulnerability index, as genotypes with low values are better for these traits.

3.1.2.4.3 Variance and Covariance

The variance and covariance components were calculated as

For the character X_i,

$$\text{Environmental variance, } \sigma^2_{ei} = MSE$$

$$\text{Genotypic variance, } \sigma^2_{gi} = \frac{MST - MSE}{r}$$

$$\text{Phenotypic variance, } \sigma^2_{pi} = \sigma^2_{gi} + \sigma^2_{ei}$$

where MST and MSE are the mean sum of squares for treatment and error respectively from ANOVA, r is the number of replications and X_i is the overall mean of the i^{th} trait calculated from all accessions.

For two characters X_i and X_j, the covariances were worked out from the ANCOVA as

$$\text{Environmental covariance, } \sigma_{eij} = MSPE$$

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

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

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

3.1.2.4.4 Coefficient of Variation

The variability in the genotypes for different characters was expressed using the coefficient of variation which is a unit free measurement. For the i^{th} character,

$$\text{Phenotypic coefficient of variation, PCV} = \frac{\sigma_{pi}}{\overline{X}_i} \times 100$$

$$\text{Genotypic coefficient of variation, GCV} = \frac{\sigma_{gi}}{\overline{X}_i} \times 100$$

$$\text{Environmental coefficient of variation, ECV} = \frac{\sigma_{ei}}{\overline{X}_i} \times 100$$

3.1.2.4.5 Heritability (H^2)

Heritability of a character in broad sense was calculated as a percentage based on the formula given by Jain (1982).

$$H^2 = \frac{\sigma^2_{gi}}{\sigma^2_{pi}} \times 100$$

where σ^2_{gi} and σ^2_{pi} are the genotypic and phenotypic variances of the i^{th} character.

Heritability per cent was categorised as suggested by Robinson *et al.* (1949) viz., low (0-30), moderate (30-60) and high (above 60).

3.1.2.4.6 Genetic Advance under Selection

Genetic advance as a percentage of mean was estimated as per the method suggested by Lush (1940) and Johnson *et al.* (1955a).

$$\text{Genetic advance, GA} = \frac{kH^2\sigma_p}{\overline{X}_i} \times 100$$

where k is the standardised selection differential (k=2.06) at five per cent selection intensity (Miller *et al.*, 1958) and $\overline{X}_i$ is the mean of the i^{th} character over all accessions.

Genetic advance was categorised into low (less than 10 %), moderate (10-20 %) and high (more than 20 %) as suggested by Johnson *et al.* (1955a).

3.1.2.4.7 Correlation Analysis

The correlation coefficients (phenotypic, genotypic and environmental) were worked out as

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

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

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

3.1.2.4.8 Path Coefficient Analysis

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

3.1.2.4.9 Selection Index

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

The selection index is described by the function $I = b_1x_1 + b_2x_2 + \ldots + b_kx_k$ and the merit of a plant is described by the function $H = a_1G_1 + a_2G_2 + \ldots + a_kG_k$ where $x_1, x_1, \ldots x_k$ are the phenotypic values and $G_1, G_2, \ldots, G_k$ are the genotypic values of the plant with respect to the characters $x_1, x_2, \ldots, x_k$ respectively. H is the genetic worth of the plant. It is assumed that the economic weight assigned to each character is equal to unity *i.e.*, $a_1, a_2, \ldots, a_k = 1$.

The regression coefficients (b_i) were determined such that the correlation between H and I was maximum. The procedure was reduced to an equation of the form $b = p^{-1}Ga$, where p is the phenotypic variance – covariance matrix and G is the genotypic variance – covariance matrix.

3.1.2.4.10 Mahalanobis D^2 Analysis

Genetic divergence was estimated using Mahalanobis D^2 statistic as described by Rao (1952). The genotypes were clustered by Tocher's method.

3.2 EXPERIMENT II: EVALUATION OF GENOTYPES FOR LEAF CURL VIRUS RESISTANCE

3.2.1 Materials

Same as in experiment I.

3.2.2 Methods

3.2.2.1 Design and Layout

Same as in experiment I.

3.2.2.2 Sowing and Cultural Operations

Same as in experiment I.

Spraying of insecticides in the field was avoided in order to permit the growth and spread of *Bemisia tabaci*, the vector of leaf curl virus.

3.2.2.3 Methodology

The leaf curl virus was introduced into the field using viruliferous whiteflies.

Mass Culture of *Bemisia tabaci*

Brinjal being a good breeding host for *B. tabaci*, the pure culture of *B. tabaci* was raised and maintained on brinjal plants. Insect proof wooden cages (65 x 65 x 70 cm) were used for this purpose. The potted brinjal plants were placed inside the cages and *B. tabaci* were released into the cages for its multiplication. The old plants inside the cages were replaced from time to time with healthy and fresh ones. Care was taken to keep the cages free of the predators of whiteflies.

Handling of Whiteflies

An aspirator consisting of a glass tube (30 cm length and 0.5 cm diameter) was used for handling whiteflies. By turning the leaves slightly upwards, the whiteflies were gently sucked into the glass tube of the aspirator. Whiteflies, thus

collected, were subsequently used either for acquisition access feeding on infected plants or for inoculation access feeding.

Acquisition and Inoculation Access Feeding

Acquisition and inoculation access feeding were carried out in a single stage in an insect proof cage. Leaf curl virus infected plants and disease free seedlings of *Capsicum annuum* var. Jwalamukhi (one month old) were kept together. The pure culture of white files reared on brinjal plants were released into this cage for transmitting the virus from infected to healthy ones. White flies were released periodically into the cages to maintain a uniform population for transmission.

Acquisition Feeding of White flies for Release into the Field

For acquisition feeding, plastic transmission cages designed by Nene (1972) were used. The top portion of either the main stem or fresh branches showing typical symptoms was introduced into the cage through the rectangular slit on the mouth of the cage. The transmission cage was covered by a black cloth except at the region of the wire netting which was kept facing the light source while releasing the white flies. The cap of the cage was immediately screwed on. The remaining portion of the rectangular slit of the cage was closed with cotton wool. The cages were kept in position by two bamboo slivers and a rubber band. After the desired feeding period (12 hours), the cotton wool was removed and the plant was disturbed by gently tapping it with a needle to disturb the whiteflies. This induced the whiteflies to move to the side of the cage facing the light source. The cages were then taken to the field and viruliferous whiteflies released.

Inoculation of main field

The diseased seedlings of *C. annuum* var. Jwalamukhi were transplanted in the field along the borders. To maintain the vector population and to ensure uniform spread of the virus in the field, viruliferous whiteflies were released at weekly intervals, starting from third month after sowing. This was continued for a period of five months.

3.2.2.4 Biometric Observations

Observations were taken for disease scoring and yield per plant.

a). Disease scoring was done at 4th, 6th and 8th months after sowing (MAS). The observation on 6th MAS was used for computation of vulnerability index, during the peak fruiting period of the crop. The scoring was based on a scale 0 to 4 developed by Rajamony *et al.* (1990) with slight modification. The score, based on the severity of symptom manifestation is as follows

Score	Symptoms
0	No symptoms
1	Slight curling of terminal leaves
2	Curling of terminal and adjacent lower leaves
3	Curling and appearance of blisters on leaves
4	Severe curling and puckering of leaves. Stunted appearance of plants

The individual plant score was utilized to work out the 'severity index' or 'vulnerability index' so as to measure the degree of resistance. The index was calculated using an equation adopted by Silbernagel and Jafri (1974) for measuring the degree of resistance in snap bean (*Phaseolus vulgaris*) to beet curly top virus and modified later by Bos (1982).

$$V.I. = \frac{0n_0+1n_1+2n_2+3n_3+4n_4}{n_t(n_c-1)} \times 100$$

Where V. I. = Vulnerability index

$n_0, n_1, \ldots n_4$ = Number of plants in the category 0, 1,...4 respectively

n_t= Total number of plants

n_c-Total number of categories (5)

The genotypes were classified according to vulnerability index as

V. I.	Category
0.00	Resistant (R)
1.00 – 25.00	Tolerant (T)
25.01 – 50.00	Susceptible (S)
> 50.00	Highly susceptible (HS)

b). Green Fruit Yield per Plant (g)

The yield of the observational plants over different harvests was noted and the average yield per plant was worked out.

3.2.2.5 Statistical Analysis

3.2.2.5.1 Analysis of variance (ANOVA) for yield per plant and vulnerability index.

3.2.2.5.2 Correlation Analysis

The correlation between yield and vulnerability index from experiments I and II were calculated.

3.3 MOLECULAR CHARACTERISATION (RANDOM AMPLIFIED POLYMORPHIC DNA OR RAPD)

3.3.1 Isolation of DNA

Isolation of total DNA was done in all the 49 samples, following the procedure of Rogowsky *et al.* (1991) with required modifications. The procedure is as follows:

Approximately 1.00g of the tender leaf sample was taken in a mortar and crushed by freezing in liquid nitrogen. The powder was transferred to a 2.0ml ependorf tube and 1.0ml of extraction buffer [1.00g SDS (1.00%), 1.576g Tris HCl (100mM), 8.18g sodium chloride (1.4g), 0.75g EDTA (20mm) and the volume is made up to 100ml with distilled water] was added to it along with 2µl of mercaptyl ethanol. The mixture was homogenised well and centrifuged at 10000 rpm for 10 minutes. The aqueous phase was collected and 200µl of phenol: chloroform: isoamyl alcohol (25 : 24 : 1) was added. It was again centrifuged at 10000 rpm for 10 minutes and the aqueous phase was separated to which 200µl of

phenol: chloroform (24: 1) mixture was added. This was centrifuged at 10000.rpm for 10 minutes. To the aqueous phase collected after centrifugation 100µl of sodium acetate (3M) and 600µl of absolute alcohol were added and kept overnight at -20°C for precipitation. It was then centrifuged at 10000 rpm for 10 minutes. The supernatant was poured off without dislodging the pellet. 500µl of 70% ethanol was added to the pellet and centrifuged at 10000 rpm for 10 minutes. The supernatant was discarded and the pellet was air dried. It was resuspended in 0.1x TE buffer.

3.3.2 Quantification of DNA

Quantification of DNA is necessary before it is subjected to amplification. It was carried out with the help of UV Spectrophotometer (Spectronic Genesys 5).

The instrument was calibrated at 260 and 280nm wavelengths using distilled water. Then the optical density (OD) of the DNA samples dissolved in 0.1x TE buffer was recorded at both these wavelengths. The concentration of DNA in the sample was calculated using the formula

$$\text{Amount of DNA } (\mu g/\mu l) = \frac{A_{260} \times 50 \times \text{Dilution Factor}}{1000}$$

where A_{260} is the absorbance at 260nm.

The quality of DNA was judged from the ratio of the OD values at 260 and 280 nm. The ratio (A_{260}/A_{280}) between 1.75 and 1.90 indicated the best quality of DNA, where A_{280} is the absorbance at 280nm.

3.3.3 Agarose Gel Electrophoresis

Agarose gel electrophoresis was carried out in a horizontal gel electrophoresis unit. Required amount of agarose was weighed (0.8 per cent for visualising the genomic DNA and 1.2 per cent for visualising the amplified product) and melted in 1.0x TAE buffer [24.2g Tris buffer, 5.71ml glacial acetic acid and 10ml of 0.5M EDTA (pH 8.0) in 100ml distilled water]. After cooling it to about 50°C ethdium bromide was added at the rate of 13µl per 100ml. The

mixture was poured to a pre-set, sealed gel tray with a comb fixed in position. After polymerisation of agarose into a gel, the comb and the sealing tapes were removed and the gel was submerged in an electrophoresis tank filled with 1.0x TAE buffer. Required volume of DNA sample and loading dye (30 per cent glycerol + bromophenol blue) were mixed and loaded in the wells. Electrophoresis was performed at 60 volts until the loading dye reached $3/4^{th}$ the length of the gel. The gel was visualised with the help of a transilluminator.

3.3.4 Amplification of DNA (Polymerase Chain Reaction, PCR)

The samples for which the ratio (A_{260}/A_{280}) lies between the preferred range and have a clear, single band in electrophoresis were subjected to PCR.

The amplification was done using arbitarily designed decamer primers (Operon Inc.), adopting the procedure of Lim *et al.* (1999) with required modifications.

The reaction was carried out in 25 µl reaction mixture containing 25 ng template DNA, 2.5µl of 10x PCR buffer, 2.5 mM $MgCl_2$, 0.2 M each of dATP, dCTP, dGTP and dTTP, 4 pM primer and 0.6 units of Taq DNA polymerase (Banglore Genei Pvt. Ltd, Bangalore). Amplification was done in a programmable thermocycler (MJ Research Inc.) that was programmed as follows:

An initial denaturation at 94°C for five minutes followed by 43 cycles of dnaturation at 94°C for one minute, annealing at 35°C for one minute 30 seconds and extension at 72°C for two minutes. The synthesis step of the final cycle was extended further by five minutes. Finally the products of amplification were cooled at 4°C. Amplified products were separated by agarose gel electrophoresis as described earlier and photographed using gel documentation system.

3.3.5 Data Analysis

The reproducible bands were scored for their presence (+) or absence (-) for all the genotypes studied. A genetic similarity matrix was constructed using the Jaccard's coefficient method (Jaccard, 1908).

$S_j = a / (a + b + c)$

Where, a = number of bands present in both the genotypes in a pair

b = number of bands present in the first genotype, but not in the other

c = number of bands present in the second genotype, but not in the other

Based on the similarity coefficient a dendrogram was constructed with the help of the software package ' NTSYS ' (Version 2.02). Association between the genotypes was found out from the dendrogram.

Results

4. RESULTS

Forty nine genotypes of bird chilli were evaluated for various characters, *viz.*, morphological, yield and reaction to leaf curl virus and these genotypes were characterized at the molecular level using Random Amplified Polymorphic DNA (RAPD) technique. The field experiment was conducted in two parts. First experiment deals with the analysis of yield and morphological characters and second experiment with the reaction to leaf curl virus. The results of the study are presented in this chapter.

4.1 STUDY OF GENETIC VARIABILITY (EXPERIMENT I)

The performance of 49 genotypes was evaluated for various characters.

4.1.1 Variability

The genotypes showed significant differences for all the traits under study.

4.1.1.1 Mean Performance

Table 2 gives the mean values of the genotypes for yield and other traits.

The genotype T_8 took only 128.5 days to produce the first flower and it was on par with 13 other genotypes *viz.*, T_{33}, T_5, T_{21}, T_{29}, T_{25}, T_{24}, T_{34}, T_{30}, T_4, T_{23}, T_{10}, T_1 and T_{16}. The genotype T_{48} took the longest duration to flower *i.e.*, 170.43 days. It was on par with 19 other genotypes.

Plant height was the highest for T_{35} (85.20 cm) and lowest for T_8 (23.43). T_{35} was on par with T_{11} and T_8 was on par with T_{29}, T_6, T_2 and T_{28}.

Table 2 Varietal difference with respect to various characters

Genotype	Days to first lowering	Plant height (cm)	Number of primary branches	Number of secondary branches	Plant spread (cm)	Number of fruits per plant	Individual fruit weight (g)	Fruit yield per plant (g)
T_1	140.78	38.44	10.22	30.00	78.50	607.33	0.28	100.67
T_2	160.50	32.55	10.44	29.33	41.08	71.00	0.17	11.69
T_3	147.28	58.00	11.00	35.50	62.78	523.67	0.30	114.80
T_4	140.00	43.83	10.43	27.17	52.25	272.67	0.23	51.49
T_5	134.65	55.17	10.50	34.53	60.86	461.72	0.30	157.05
T_6	149.16	32.00	10.50	60.44	92.29	658.55	0.31	210.14
T_7	158.94	60.00	7.33	45.97	75.83	410.67	0.24	155.56
T_8	128.50	23.43	9.20	15.44	31.55	40.67	0.15	5.80
T_9	146.67	40.83	8.67	21.50	35.75	178.33	0.14	25.09
T_{10}	140.64	57.22	10.00	31.17	45.50	234.83	0.56	122.57
T_{11}	148.31	82.11	14.44	55.43	74.17	709.33	0.56	349.10
T_{12}	162.50	46.50	14.50	38.83	41.17	57.00	1.37	75.30
T_{13}	153.78	72.60	14.77	52.00	83.70	592.33	0.18	94.54
T_{14}	155.89	54.28	11.72	43.61	63.99	289.05	0.19	56.40
T_{15}	142.89	69.83	13.83	35.83	75.07	267.67	1.42	282.05
T_{16}	141.33	55.43	8.33	37.47	41.07	216.67	0.32	80.37
T_{17}	162.50	45.03	5.18	16.67	54.00	153.33	0.19	29.47
T_{18}	148.44	42.00	10.10	69.73	80.60	607.83	0.25	181.23
T_{19}	148.17	41.00	14.90	77.17	95.08	724.33	0.37	244.83
T_{20}	169.00	48.00	10.83	30.33	73.72	399.33	0.34	125.05
T_{21}	135.53	57.82	16.49	46.18	45.77	295.78	0.16	47.18
T_{22}	164.03	62.11	10.00	51.72	86.11	447.67	0.23	110.94
T_{23}	140.39	60.07	6.78	45.10	81.77	440.39	0.19	76.70
T_{24}	138.33	41.10	10.30	30.07	36.67	185.33	0.21	37.43
T_{25}	136.00	42.47	7.30	31.10	46.93	56.33	1.43	75.05
T_{26}	153.17	57.17	7.33	26.37	57.75	431.33	0.22	72.32
T_{27}	156.44	46.43	9.50	41.68	63.23	571.67	0.30	144.32
T_{28}	158.11	33.43	15.27	50.35	75.33	669.33	0.28	162.87
T_{29}	135.99	31.43	11.50	66.50	91.50	777.28	0.24	167.17
T_{30}	139.67	54.77	10.63	35.80	56.87	306.00	0.32	66.53
T_{31}	149.37	37.00	5.13	26.56	56.87	229.67	0.36	63.71
T_{32}	148.33	44.97	5.57	15.43	40.57	123.33	0.25	27.13
T_{33}	133.50	58.33	7.89	17.97	74.83	71.17	0.50	35.95
T_{34}	139.57	49.10	12.10	40.10	41.57	47.33	0.22	27.71
T_{35}	157.33	85.20	8.30	15.33	65.67	100.00	0.39	31.33
T_{36}	153.10	40.83	8.30	16.70	42.63	166.33	0.13	26.65
T_{37}	166.50	50.63	8.90	27.70	40.53	37.33	0.12	4.47
T_{38}	163.22	43.00	9.42	18.27	49.92	43.61	0.16	6.27
T_{39}	150.00	43.22	10.28	39.42	57.55	215.44	0.26	36.38
T_{40}	168.33	46.43	8.00	21.57	53.44	113.00	0.35	27.86
T_{41}	163.17	55.17	9.50	20.50	52.58	100.44	0.34	27.23
T_{42}	167.83	54.45	6.40	25.77	62.90	119.67	0.33	30.10
T_{43}	162.17	70.22	8.89	28.10	70.50	487.55	0.39	165.93
T_{44}	162.33	66.05	12.61	42.27	62.33	180.17	0.31	53.89
T_{45}	167.50	47.50	10.30	15.67	34.33	168.78	0.32	39.76
T_{46}	163.89	49.05	13.33	46.39	49.61	267.00	0.11	26.87
T_{47}	159.33	48.50	10.33	26.33	67.92	194.17	0.18	41.25
T_{48}	170.43	42.77	11.77	29.50	35.73	121.67	0.50	55.11
T_{49}	162.88	45.73	8.22	12.23	44.83	62.67	0.18	9.79
Mean	151.97	50.07	10.14	34.79	59.11	298.09	0.34	85.12
F	5.60**	9.10**	6.67**	23.81**	15.97**	11.26**	43.19**	8.88**
SE	4.83	4.17	1.03	3.11	4.34	64.26	0.04	25.50
CD	13.61	11.73	2.91	8.75	12.23	180.84	0.13	71.76

**Significant at 1 per cent level CD – Critical difference at 5 per cent SE – Standard error of mean

Table 2. Continued

Genotype	Fruit length (cm)	Pedicel : fruit ratio	Fruit width (cm)	100 seed weight (g)	Number of seeds per fruit	Vulnerability index
T_1	4.62	1.31	1.95	0.38	10.00	15.00
T_2	3.29	0.75	2.36	0.35	17.55	51.67
T_3	4.10	1.17	2.14	0.37	9.55	36.67
T_4	4.38	1.13	1.94	0.34	9.78	25.00
T_5	3.98	0.94	2.28	0.49	17.66	43.33
T_6	3.83	0.96	2.21	0.43	8.00	28.33
T_7	3.56	0.96	1.79	0.30	10.66	30.00
T_8	3.85	0.10	2.27	0.35	6.89	40.00
T_9	3.83	0.92	1.11	0.34	9.78	38.33
T_{10}	6.42	0.70	2.38	0.55	20.89	3.33
T_{11}	5.49	1.07	2.26	0.54	23.55	6.67
T_{12}	5.88	0.94	3.32	0.44	36.89	23.33
T_{13}	4.01	1.21	2.00	0.36	9.22	16.67
T_{14}	3.75	1.13	1.71	0.40	11.78	20.00
T_{15}	5.38	0.65	3.57	0.57	26.11	0.00
T_{16}	2.71	1.47	2.37	0.29	11.00	51.67
T_{17}	3.71	1.26	1.95	0.26	8.55	43.33
T_{18}	4.03	0.81	2.19	0.45	19.66	38.33
T_{19}	4.34	0.89	2.39	0.46	22.61	26.67
T_{20}	4.70	1.19	2.26	0.28	19.50	35.00
T_{21}	3.65	1.28	1.73	0.29	12.11	40.00
T_{22}	3.82	1.31	2.09	0.42	11.78	23.33
T_{23}	3.16	1.26	2.04	0.44	15.44	50.00
T_{24}	4.03	1.39	1.91	0.48	20.83	30.00
T_{25}	3.43	0.90	4.75	0.23	28.67	16.67
T_{26}	3.29	1.36	1.79	0.28	11.44	35.00
T_{27}	3.94	1.16	2.03	0.28	15.89	46.67
T_{28}	3.67	1.12	1.53	0.36	17.00	33.33
T_{29}	3.13	1.27	1.83	0.36	11.44	21.67
T_{30}	3.48	0.98	1.76	0.38	15.66	23.33
T_{31}	3.75	1.02	2.06	0.27	11.45	35.00
T_{32}	3.05	1.08	1.81	0.41	11.22	20.00
T_{33}	5.20	1.08	2.54	0.44	31.33	0.00
T_{34}	4.32	1.28	1.80	0.20	10.00	21.67
T_{35}	5.50	0.85	2.74	0.46	11.66	5.00
T_{36}	3.96	0.84	1.94	0.32	10.33	43.33
T_{37}	3.80	1.50	1.59	0.35	4.89	31.67
T_{38}	3.13	0.95	1.74	0.34	4.83	20.00
T_{39}	4.17	1.12	1.89	0.39	18.67	28.33
T_{40}	3.71	1.07	1.82	0.32	15.11	30.00
T_{41}	4.26	0.91	1.85	0.35	12.89	33.33
T_{42}	4.07	1.17	2.12	0.36	14.66	35.00
T_{43}	4.27	0.82	2.18	0.29	15.44	20.00
T_{44}	4.03	1.33	1.99	0.31	9.00	23.33
T_{45}	4.31	0.99	1.45	0.39	10.88	23.33
T_{46}	4.12	1.19	2.12	0.25	7.00	26.67
T_{47}	3.86	1.25	1.82	0.29	13.79	25.00
T_{48}	2.83	1.06	1.89	0.29	10.28	25.00
T_{49}	3.46	0.86	2.19	0.29	12.28	8.33
Mean	4.03	1.08	2.11	0.36	14.40	9.17
F	25.50**	6.15**	40.31**	39.19**	7.96**	8.91**
SE	0.15	0.08	0.09	0.13	2.37	4.31
CD	0.42	0.23	0.25	0.30	6.66	12.13

**Significant at 1 per cent level CD – Critical difference at 5 per cent SE – Standard error of mean

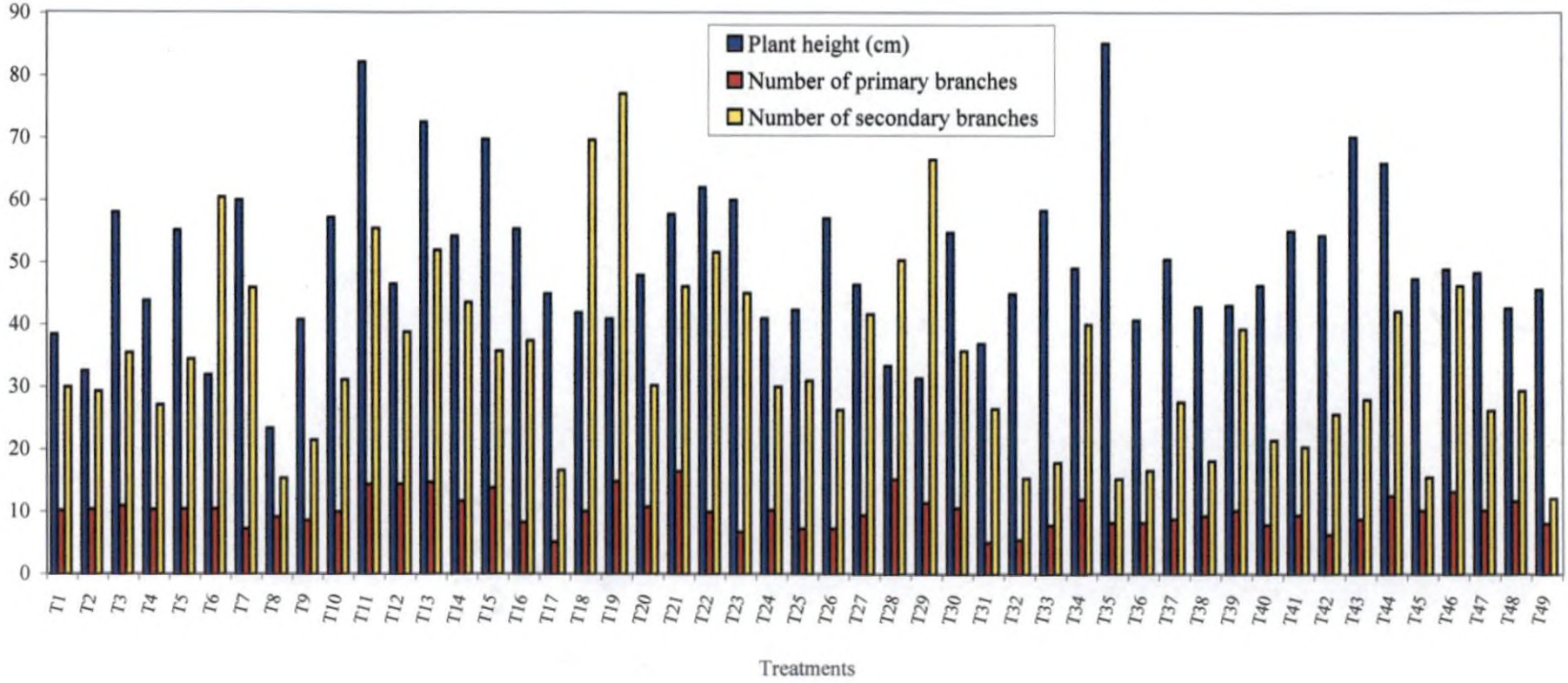


Fig. 1. Variability of mean values of selected characters

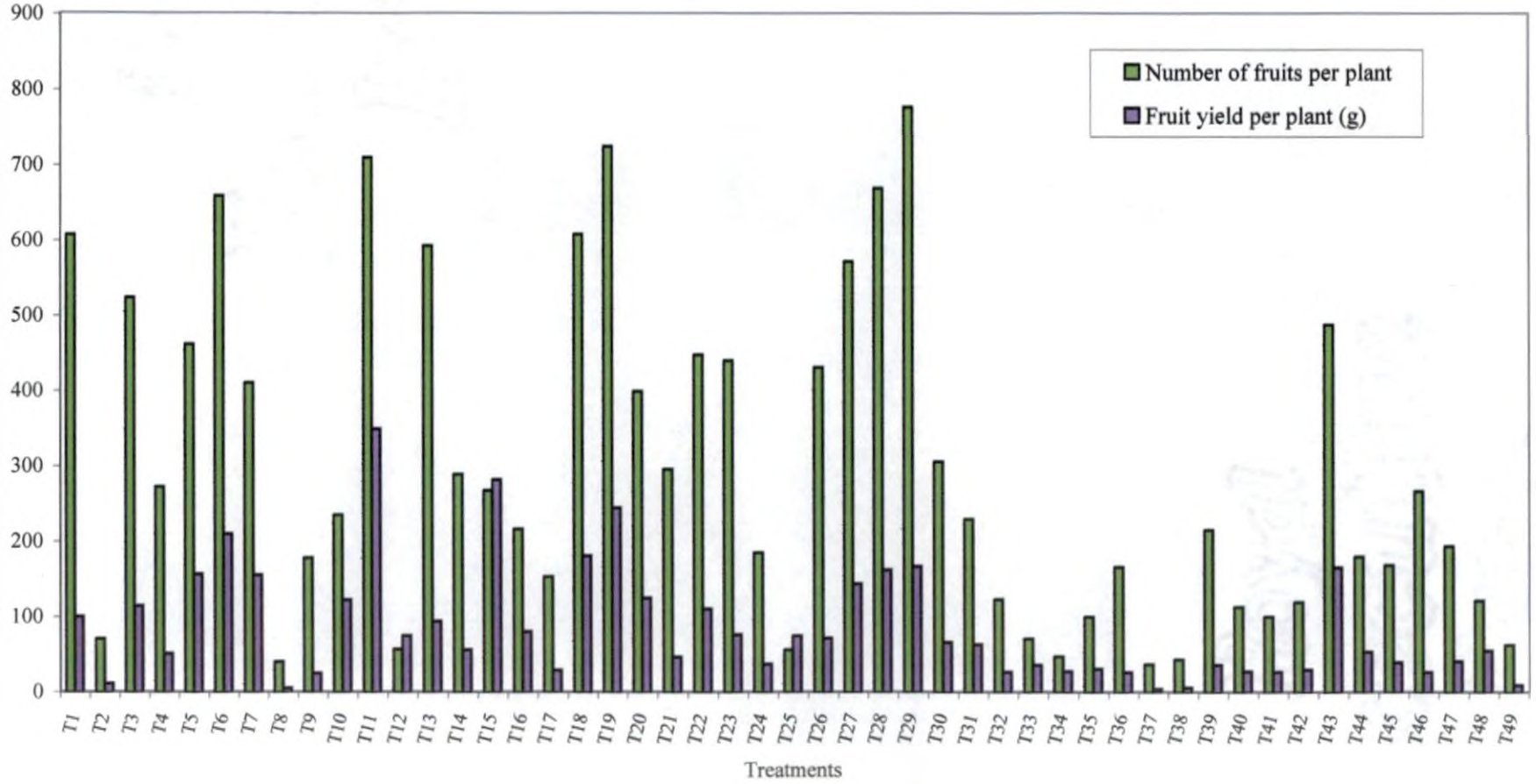


Fig. 2. Variability of mean values of selected characters

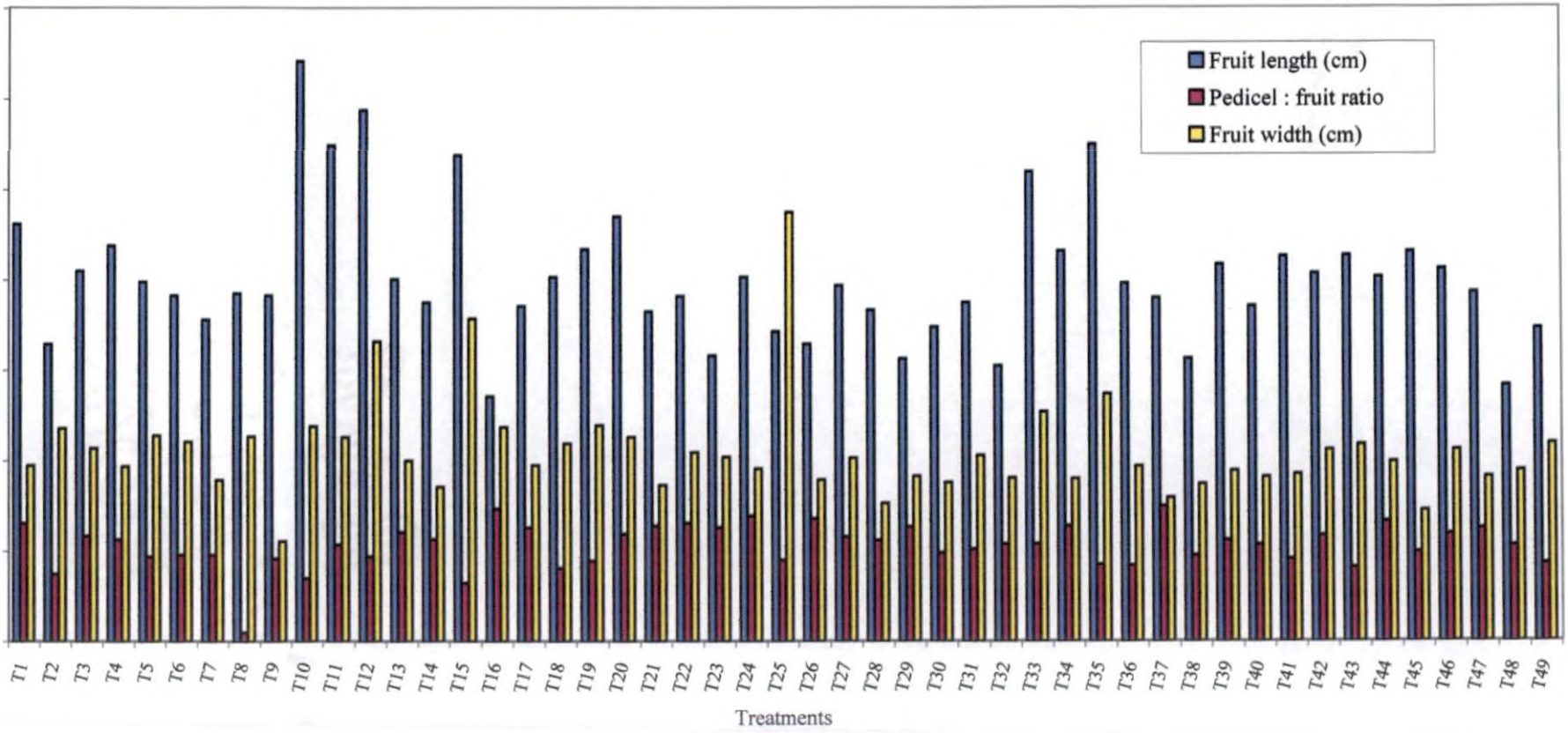


Fig. 3. Variability of mean values of selected characters

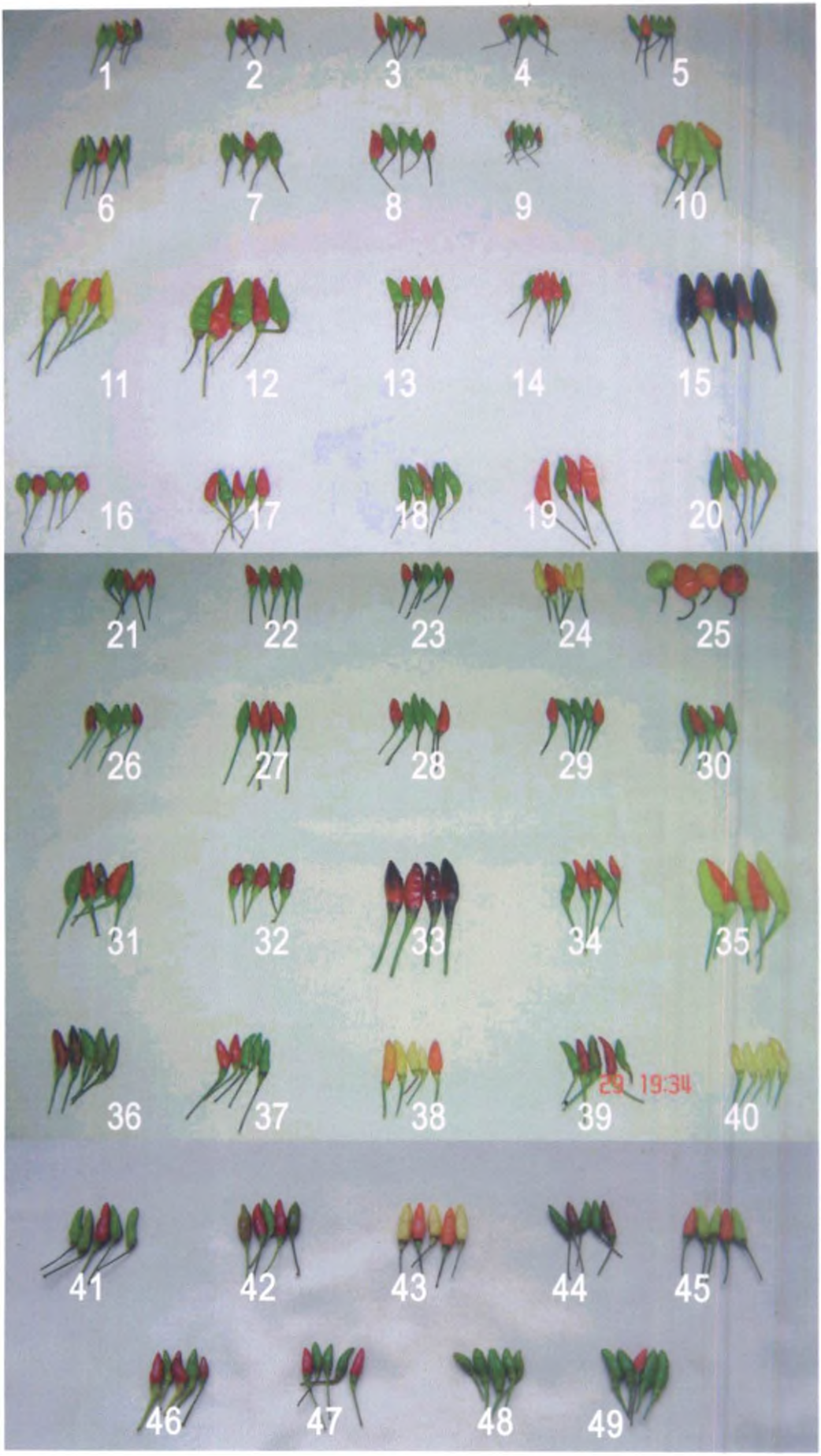


Plate 1. Variability in fruit characters of bird chilli

Karumukku local (T_{11})

Thavanur local 3 (T_{15})

Irumbuzhi local (T_{18})

Plate 2. High yielding genotypes of bird chilli

Number of primary branches varied from 5.13 (T_{31}) to 16.49 (T_{21}). The genotype T_{31} was on par with T_{17}, T_{32}, T_{42}, T_{23}, T_{25}, T_{26}, T_7, T_{33} and T_{40}. T_{21} was on par with T_{28}, T_{19}, T_{13}, T_{12}, T_{11} and T_{15}.

The genotype T_{19} had the highest number of secondary branches per plant (77.17) and was on par with T_{18}. T_{49} had the lowest number (12.23) and was on par with T_{35}, T32, T_8, F_{45}, T_{17}, T_{36}, T_{33}, T_{38} and T_{41}.

Maximum plant spread was observed in the genotype T_{19} (95.08 cm) and the minimum was in T_8 (31.55 cm). The genotype T_{19} was on par with four other genotypes T_6, T_{29}, T_{22} and T_{13}. T_8 was on par with T_{45}, T_{48}, T_9, T_{24}, T_{37}, T_{31}, T16, T_2, T_{12}, T_{23} and T_{35}.

The genotype T_{29} produced the largest number of fruits per plant (777.28) and was on par with T_{19}, T_{11}, T_{28}, T_6, T_{18} and T_1, whereas T_{37} produced the least number (37.33) and was on par with twenty three other genotypes.

Individual fruit weight ranged from 0.11 g (T_{46}) to 1.43 g (T_{25}). T_{46} was on par with the genotypes T_{37}, T_{36}, T_9, T_8, T_{21}, T_{38}, T_2, T_{13}, T_{49}, T_{47}, T_{17}, T_{23}, T_{14}, T_{24}, T_{34}, T_{26}, T_4, T_{22} and T_7. T_{25} was on par with T_{15} and T_{12}.

Fruit yield per plant was the highest for T_{11} (349.10 g) and lowest for T_{37} (4.47 g). T_{11} was on par with T_{15} (Plate 2) and T_{37} was on par with twenty nine other genotypes.

The longest fruit was produced by T_{10} (6.42 cm) and was statistically superior to all other genotypes. The shortest one was produced by T_{16} (2.71 cm) and was on par with T_{48} and T_{32} (Plate 1).

Maximum pedicel : fruit ratio was obtained for the genotype T_{37} (1.5) and the ratio was minimum for T_{15} (0.65). T_{37} was on par with T_{16}, T_{24}, T_{26}, T_{44}, T_{22}, T_1, T_{21} and T_{34}. T_{15} was on par with T_{10}, T_2, T_{18}, T_{43}, T_{36}, T_{35} and T_{49}.

The genotype T_{25} showed the highest fruit width (4.75 cm) and it was superior to all other genotypes. Fruit width was the lowest for T_9 (1.11 cm) (Plate 1).

The genotypes T_{15} (0.569 g), T_{10} (0.5487 g) and T_{11} (0.5363 g) had the highest 100 seed weight and were on par with each other while it was the least for T_{34}. It was on par with T_{25}.

Number of seeds per fruit ranged from 36.89 (T_{12}) to 4.83 (T_{38}). T_{12} was on par with T_{33} and T_{38} was on par with T_{21} other genotypes.

The vulnerability index, calculated on the basis of virus scoring, showed a range of 0 (T_{15}) to 51.67 (T_2 and T_{16}). T_{15} was on par with T_{33}, T_{10}, T_{35}, T_{11} and T_{49}. T_2 and T_{16} were on par with seven other genotypes *viz.*, T_{23}, T_{27}, T_5, T_{17}, T_{36}, T_8 and T_{21}.

4.1.1.2 Classification of Genotypes

The 49 genotypes were classified as poor, average and better with respect to each trait (Table 3).

Fifteen genotypes took less than 142.3 days to produce the first flower and were grouped under the better class while 13 genotypes took more than 161.64 days (poor). The remaining 21 genotypes were grouped in the average category (142.3 – 161.64).

For plant height, 12 genotypes were grouped under poor (<41.73 cm), 28 under average (41.73 – 58.41 cm) and nine under the better category (>58.41 cm).

The average category had the largest number (30) of genotypes lying in the range 8.07 – 12.21 for number of primary branches. Nine genotypes were classified as better (>12.21) and ten as poor (<8.07).

Fifteen genotypes each were included in the better (>41.01) and average (28.57 – 41.01) categories for number of secondary branches

Table 3 Classification of genotypes

Character	Poor	Average	Better
Days to first flowering	>161.64	142.32 – 161.64	< 142.3
	T_{12}, T_{17}, T_{20}, T_{22}, T_{37}, T_{38}, T_{40}, T_{41}, T_{42}, T_{45}, T_{46}, T_{48}, T_{49}	T_2, T_3, T_6, T_7, T_9, T_{11}, T_{13}, T_{14}, T_{18}, T_{19}, T_{26}, T_{27}, T_{28}, T_{31}, T_{32}, T_{35}, T_{36}, T_{39}, T_{43}, T_{44}, T_{47}	T_1, T_4, T_5, T_8, T_{10}, T_{15}, T_{16}, T_{21}, T_{23}, T_{24}, T_{25}, T_{29}, T_{30}, T_{33}, T_{34},
Plant height (cm)	<41.73	41.73 – 58.41	> 58.41
	T_1, T_2, T_6, T_8, T_9, T_{19}, T_{24}, T_{25}, T_{28}, T_{29}, T_{31}, T_{36}	T_3, T_4, T_5, T_{10}, T_{12}, T_{14}, T_{16}, T_{17}, T_{18}, T_{20}, T_{21}, T_{26}, T_{27}, T_{30}, T_{32}, T_{33}, T_{34}, T_{37}, T_{38}, T_{39}, T_{40}, T_{41}, T_{42}, T_{45}, T_{46}, T_{47}, T_{48}, T_{49}	T_7 T_{11}, T_{13}, T_{15}, T_{22}, T_{23}, T_{35}, T_{43}, T_{44}
Number of primary branches	<8.07	8.07 – 12.21	>12.21
	T_7, T_{17}, T_{23}, T_{25}, T_{26}, T_{31}, T_{32}, T_{33}, T_{40}, T_{42}	T_1, T_2, T_3, T_4, T_5, T_6, T_8, T_9, T_{10}, T_{14}, T_{16}, T_{18}, T_{20}, T_{22}, T_{24}, T_{27}, T_{29}, T_{30}, T_{34}, T_{35}, T_{36}, T_{37}, T_{38}, T_{41}, T_{43}, T_{45}, T_{47}, T_{48}, T_{49}	T_{11}, T_{12}, T_{13}, T_{15}, T_{19}, T_{21}, T_{28}, T_{44}, T_{46}
Number of secondary branches	<28.57	28.57 – 41.01	>41.01
	T_4, T_8, T_9, T_{17}, T_{26}, T_{31}, T_{32}, T_{33}, T_{35}, T_{36}, T_{37}, T_{38}, T_{40}, T_{41}, T_{42}, T_{43}, T_{45}, T_{47}, T_{49}	T_1, T_2, T_3, T_5, T_{10}, T_{12}, T_{15}, T_{16}, T_{20}, T_{24}, T_{25}, T_{30}, T_{34}, T_{39}, T_{48}	T_6, T_7, T_{11}, T_{13}, T_{14}, T_{18}, T_{19}, T_{21}, T_{22}, T_{23}, T_{27}, T_{28}, T_{29}, T_{44}, T_{46}
Plant spread (cm)	<50.42	50.42 – 67.79	>67.79
	T_2, T_8, T_9, T_{10}, T_{12}, T_{16}, T_{21}, T_{24}, T_{25}, T_{31}, T_{33}, T_{35}, T_{36}, T_{37}, T_{38}, T_{45}, T_{46}, T_{48}, T_{49}	T_3, T_4, T_5, T_{17}, T_{26}, T_{27}, T_{30}, T_{34}, T_{39}, T_{40}, T_{41}, T_{42}, T_{44}	T_1, T_6, T_7, T_{11}, T_{13}, T_{14}, T_{15}, T_{18}, T_{19}, T_{20}, T_{22}, T_{23}, T_{28}, T_{29}, T_{32}, T_{43}, T_{47}
Number of fruits per plant	<173.57	173.57 – 426.61	>426.61
	T_2, T_8, T_{12}, T_{17}, T_{25}, T_{32}, T_{33}, T_{34}, T_{35}, T_{36}, T_{37}, T_{38}, T_{40}, T_{41}, T_{42}, T_{45}, T_{48}, T_{49}	T_4, T_7, T_9, T_{10}, T_{14}, T_{15}, T_{16}, T_{20}, T_{21}, T_{24}, T_{30}, T_{31}, T_{39}, T_{44}, T_{46}, T_{47}	T_1, T_3, T_5, T_6, T_{11}, T_{13}, T_{18}, T_{19}, T_{22}, T_{23}, T_{26}, T_{27}, T_{28}, T_{29}, T_{43}
Individual fruit weight (g)	<0.25	0.25 – 0.43	<0.43
	T_2, T_4, T_7, T_8, T_9, T_{13}, T_{14}, T_{17}, T_{18}, T_{21}, T_{22}, T_{23}, T_{24}, T_{26}, T_{29}, T_{32}, T_{34}, T_{36}, T_{37}, T_{38}, T_{46} T_{47}, T_{49}	T_1, T_3, T_5, T_6, T_{16}, T_{19}, T_{20}, T_{27}, T_{28}, T_{30}, T_{31}, T_{35}, T_{39}, T_{40}, T_{41}, T_{42}, T_{43}, T_{44}, T_{45}	T_{10}, T_{11}, T_{12}, T_{15}, T_{25}, T_{33}, T_{48}

Table 3 Continued

Character	Poor	Average	Better
Fruit yield per plant (g)	<34.12	34.12 – 136.12	>136.12
	T_2, T_8, T_9, T_{17}, T_{32}, T_{34}, T_{35}, T_{36}, T_{37}, T_{38}, T_{40}, T_{41}, T_{42}, T_{46}, T_{49}	T_1, T_3, T_4, T_{10}, T_{12}, T_{13}, T_{14}, T_{16}, T_{20}, T_{21}, T_{22}, T_{23}, T_{24}, T_{25}, T_{26}, T_{30}, T_{31}, T_{33}, T_{39}, T_{44}, T_{45}, T_{47}, T_{48}	T_5, T_6, T_7, T_{11}, T_{15}, T_{18}, T_{19}, T_{27}, T_{28}, T_{29}, T_{43}
Fruit length (cm)	<3.73	3.73 – 4.33	>4.33
	T_2, T_7, T_{16}, T_{17}, T_{21}, T_{23}, T_{25}, T_{26}, T_{28}, T_{29}, T_{30}, T_{32}, T_{38}, T_{40}, T_{48}, T_{49}	T_3, T_5, T_6, T_8, T_9, T_{13}, T_{14}, T_{18}, T_{22}, T_{24}, T_{27}, T_{31}, T_{34}, T_{36}, T_{37}, T_{39}, T_{41}, T_{42}, T_{43}, T_{44}, T_{45}, T_{46}, T_{47}	T_1, T_4, T_{10}, T_{11}, T_{12}, T_{15}, T_{19}, T_{20}, T_{33}, T_{35}
Pedicel : fruit ratio	>1.24	0.92 – 1.24	<0.92
	T_1, T_{16}, T_{17}, T_{21}, T_{22}, T_{23}, T_{24}, T_{26}, T_{29}, T_{34}, T_{37}, T_{44}, T_{47}	T_3, T_4, T_5, T_6, T_7, T_8, T_9, T_{11}, T_{12}, T_{13}, T_{14}, T_{20}, T_{27}, T_{28}, T_{30}, T_{31}, T_{32}, T_{33}, T_{38}, T_{39}, T_{40}, T_{42}, T_{45}, T_{46}, T_{48},	T_2, T_{10}, T_{15}, T_{18}, T_{19}, T_{25}, T_{35}, T_{36}, T_{41}, T_{43}, T_{49}
Fruit width (cm)	<1.93	1.93 – 2.29	>2.29
	T_7, T_9, T_{14}, T_{21}, T_{24}, T_{26}, T_{28}, T_{29}, T_{30}, T_{32}, T_{34}, T_{37}, T_{38}, T_{39}, T_{40}, T_{41}, T_{45}, T_{47}, T_{48}	T_1, T_3, T_4, T_5, T_6, T_8, T_{11}, T_{13}, T_{17}, T_{18}, T_{20}, T_{22}, T_{23}, T_{27}, T_{31}, T_{36}, T_{42}, T_{43}, T_{44}, T_{46}, T_{49}	T_2, T_{10}, T_{12}, T_{15}, T_{16}, T_{19}, T_{25}, T_{33}, T_{34}
100-seed weight (g)	<0.33	0.33 – 0.39	>0.39
	T_7, T_{16}, T_{17}, T_{20}, T_{21}, T_{25}, T_{26}, T_{27}, T_{31}, T_{34}, T_{36}, T_{40}, T_{43}, T_{44}, T_{46}, T_{47}, T_{48}, T_{49}	T_1, T_2, T_3, T_4, T_8, T_9, T_{13}, T_{28}, T_{29}, T_{30}, T_{37}, T_{38}, T_{41}, T_{42}, T_{45}	T_5, T_6, T_{10}, T_{11}, T_{12}, T_{14}, T_{15}, T_{18}, T_{19}, T_{22}, T_{23}, T_{24}, T_{32}, T_{33}, T_{35}, T_{39}
Number of seeds per fruit	<9.66	9.66 – 19.14	>19.14
	T_3, T_6, T_8, T_{13}, T_{17}, T_{37}, T_{38}, T_{44}, T_{46}	T_1, T_2, T_4, T_5, T_7, T_9, T_{14}, T_{16}, T_{21}, T_{22}, T_{23}, T_{26}, T_{27}, T_{28}, T_{29}, T_{30}, T_{31}, T_{32}, T_{34}, T_{35}, T_{36}, T_{39}, T_{40}, T_{41}, T_{42}, T_{43}, T_{45}, T_{47}, T_{48}, T_{49}	T_{10}, T_{11}, T_{12}, T_{15}, T_{18}, T_{19}, T_{20}, T_{24}, T_{25}, T_{33}
Vulnerability index	>17.8	0.54 – 17.8	<0.54
	T_2, T_3, T_4, T_5, T_6, T_7, T_8, T_9, T_{12}, T_{14}, T_{16}, T_{17}, T_{18}, T_{19}, T_{20}, T_{21}, T_{22}, T_{23}, T_{24}, T_{26}, T_{27}, T_{28}, T_{29}, T_{30}, T_{31}, T_{32}, T_{34}, T_{36}, T_{37}, T_{38}, T_{39}, T_{40}, T_{41}, T_{42}, T_{43}, T_{44}, T_{45}, T_{46}, T_{47}, T_{48}	T_1, T_{10}, T_{11}, T_{13}, T_{25}, T_{35}, T_{49}	T_{15}, T_{33}

whereas the remaining 19 genotypes were included in the poor class (<28.57).

Nineteen genotypes had poor plant spread (<50.42 cm) while 17 genotypes were included in the better category (>67.79 cm). Remaining 13 genotypes belonged to the average class (50.42 – 67.79 cm).

Fifteen genotypes produced more than 426.61 fruits per plant and were classified as better. The average (173.57 – 426.61) and poor (<173.57) classes comprised of 16 and 18 genotypes respectively.

The individual fruit weight was less than 0.25 g for 23 genotypes (poor) while it was more than 0.43 g for seven genotypes (better). Nineteen genotypes had an average fruit weight ranging from 0.25 – 0.43 g.

Fifteen genotypes were low yielders (poor) producing less than 34.12 g per plant while 11 genotypes producing more than 136.12 g per plant were included under the better class. The average class consisted of 23 genotypes, producing between 34.12 g and 316.12 g per plant.

Fruit length in 23 genotypes ranged from 3.73 – 4.33 cm (average) whereas 16 genotypes had fruits shorter than 3.73 cm (poor) and ten genotypes had fruits longer than 4.73 cm (better).

For pedicel: fruit ratio, 11 genotypes were included under the better class (<0.92) and 13 genotypes were in the poor class (> 1.24). Remaining 25 genotypes came in the average class (0.92-1.24)

Nineteen genotypes had fruit width less than 1.93 cm (poor) while nine genotypes had more than 2.29 cm (better). The average class comprised of 21 genotypes lying within the range 1.93 – 2.29 cm of fruit width.

Hundred seed weight was less than 0.33 g (poor) for 18 genotypes whereas it was more than 0.39 g (better) for 16 genotypes. Fifteen genotypes fell in the average class (0.33 – 0.39 g).

Nine genotypes had less than 9.66 seeds per fruit (poor) while 30 genotypes had seeds in the rage of 9.66 – 19.14 (average). Ten genotypes had more than 19.14 seeds per fruit (better).

In case of vulnerability index, only two genotypes (T_{15} and T_{33}) fell in the better class (<0.54). A maximum of 40 genotypes were included under the poor class (>17.80) and seven genotypes in the average class (0.54-17.80).

4.1.1.3 Components of Variability

The details of components of variance *viz.*, phenotypic, genotypic and environmental variances are given in Table 4.

The values of genotypic variance were close to the phenotypic variance in almost all the characters, suggesting the predominance of genetic component over environmental effect on its phenotype.

4.1.2 Coefficient of Variation

The phenotypic, genotypic and environmental coefficients of variation were worked out and are furnished in Table 4.

4.1.2.1 Phenotypic Coefficient of Variation

The phenotypic coefficient of variation (PCV) was the highest for fruit yield per plant (98.79) and the lowest for days to first flowering (8.77). Other traits showing high PCV were individual fruit weight (87.92), number of fruit per plant (78.51), number of seeds per fruit (51.92), vulnerability index (51.76) and number of secondary branches (45.38) (Fig. 4).

4.1.2.2 Genotypic Coefficient of Variation

Genotypic coefficient of variation (GCV) ranged from 6.83 for days to first flowering to 84.95 for individual fruit weight (Fig. 4). High values of GCV were also obtained for fruit yield per plant (84.07), number of

Table 4 Genetic parameters

Genetic parameters / Characters	Variance			Coefficient of variation			Heritability (%)	Genetic advance (as % of mean)
	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV		
Days to first flowering	177.76	107.63	70.13	8.77	6.83	1.95	60.55	10.94
Plant height (cm)	193.03	140.88	52.14	27.75	23.71	4.04	72.98	41.72
Number of primary branches	9.26	6.06	3.21	29.99	24.25	5.74	65.39	40.42
Number of secondary branches	249.32	220.34	28.98	45.38	42.66	2.72	88.38	82.63
Plant spread (cm)	339.25	282.62	56.63	31.16	28.44	2.72	83.31	53.48
Number of fruits per plant	54769.14	42382.00	12387.14	78.51	69.06	9.45	77.38	125.15
Individual fruit weight (g)	0.09	0.09	0.01	87.92	84.95	2.97	93.36	170.64
Fruit yield per plant (g)	7072.39	5121.50	1950.90	98.79	84.07	14.72	72.42	151.46
Fruit length (cm)	0.62	0.55	0.07	19.57	18.47	1.10	89.09	35.86
Pedicel : fruit ratio	0.05	0.03	0.02	21.46	17.06	4.40	63.18	26.95
Fruit width (cm)	0.33	0.31	0.02	27.26	26.27	0.98	92.91	52.11
100-seed weight (g)	0.01	0.01	0.001	23.65	22.77	0.88	92.72	44.39
Number of seeds per fruit	55.91	39.06	16.85	51.92	43.40	8.52	69.87	74.74
Vulnerability index	202.83	147.04	55.79	51.76	44.07	7.69	72.49	77.29

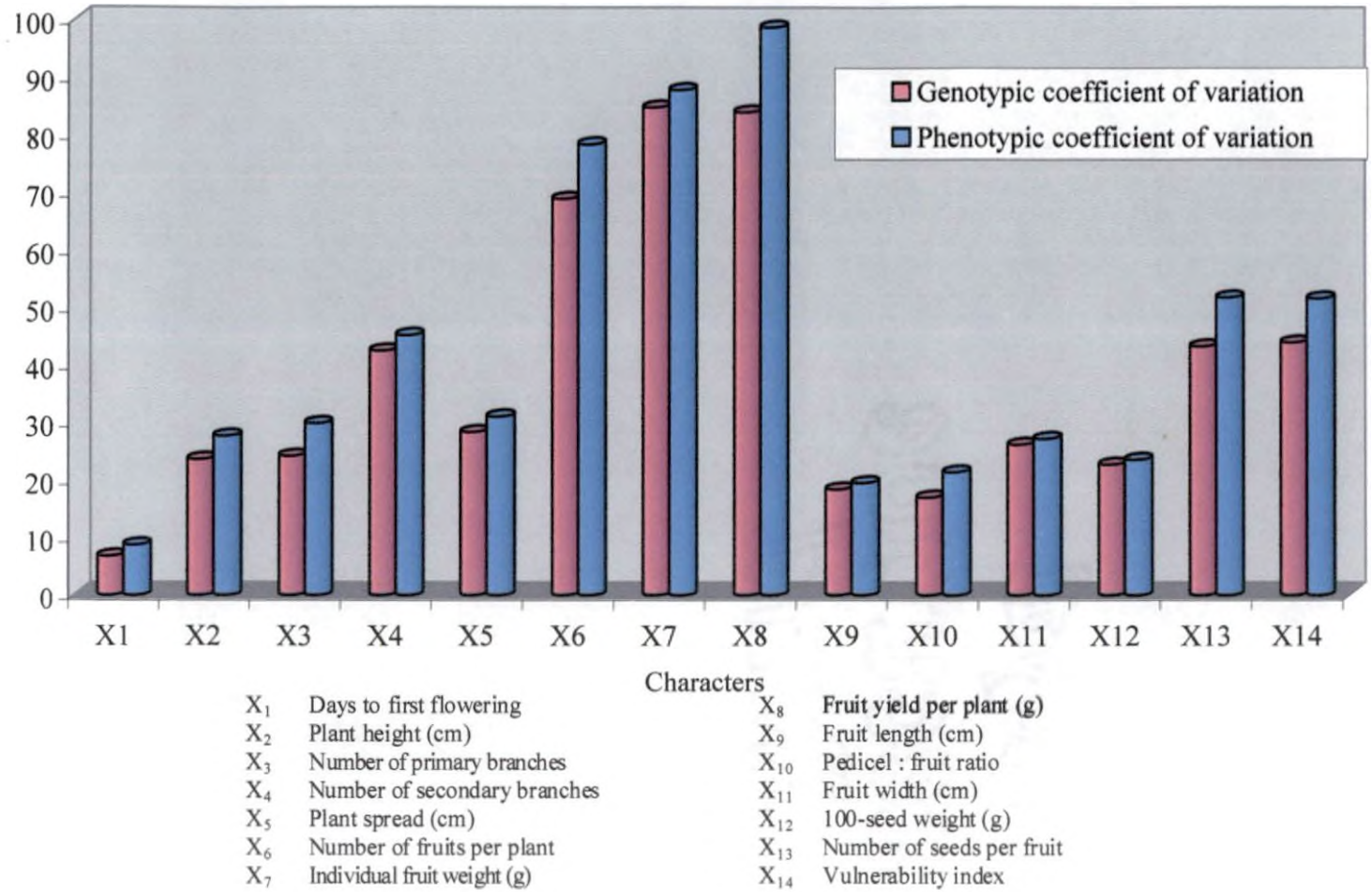
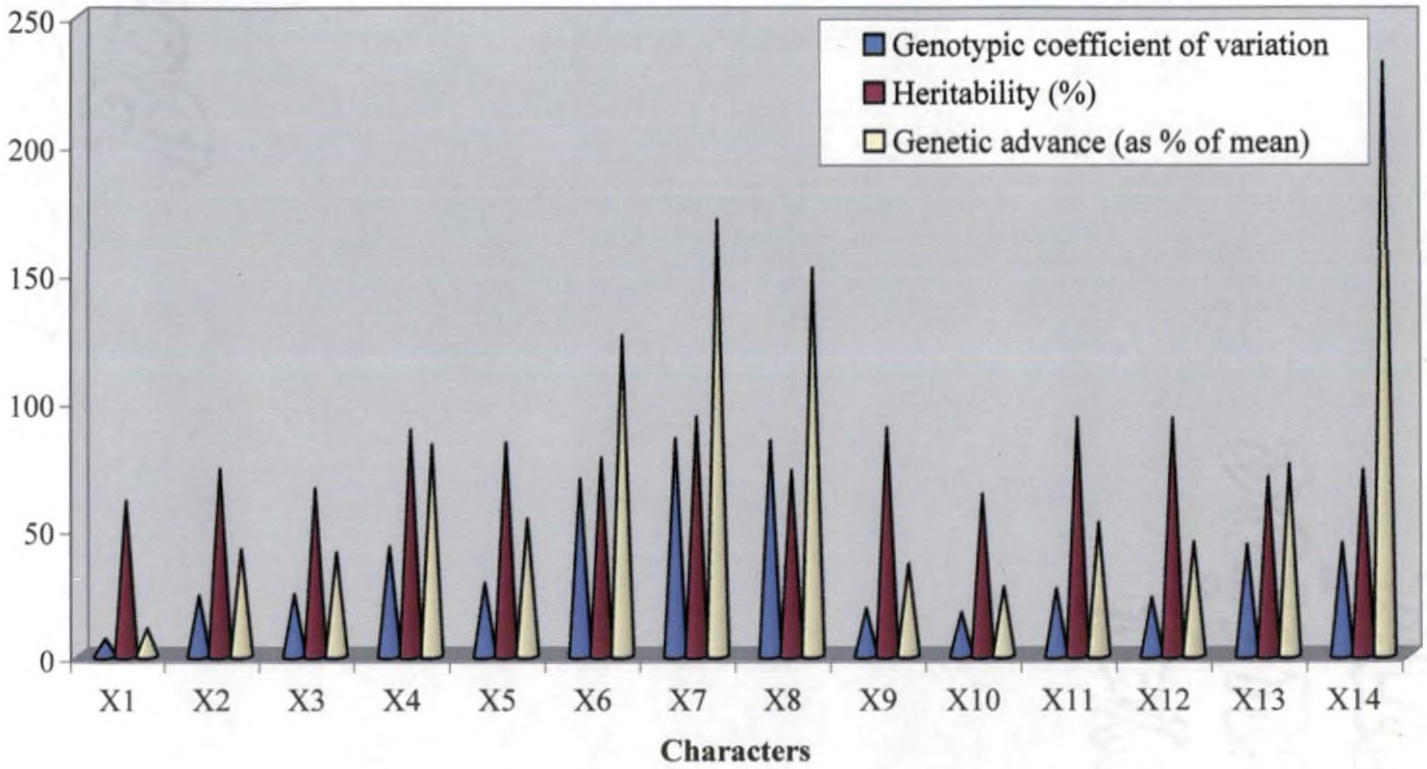


Fig. 4. Genotypic coefficient of variation and phenotypic coefficient of variation for 14 characters



X_1	Days to first flowering	X_8	Fruit yield per plant (g)
X_2	Plant height (cm)	X_9	Fruit length (cm)
X_3	Number of primary branches	X_{10}	Pedicel : fruit ratio
X_4	Number of secondary branches	X_{11}	Fruit width (cm)
X_5	Plant spread (cm)	X_{12}	100-seed weight (g)
X_6	Number of fruits per plant	X_{13}	Number of seeds per fruit
X_7	Individual fruit weight (g)	X_{14}	Vulnerability index

Fig. 5. Genotypic coefficient of variation, heritability and genetic advance for 14 characters

fruits per plant (69.06), vulnerability index (44.07), number of seeds per fruit (43.40) and number of secondary branches (42.66).

4.1.2.3 Environmental Coefficient of Variation (ECV)

In general, the environmental coefficient of variation (ECV) was low for most of the characters. However, fruit yield per plant (14.72), fruit number per plant (9.45), number of seeds per fruit (8.52), vulnerability index (7.69), number of primary branches (5.74), pedicel : fruit ratio (4.40) and plant height (4.04) showed comparatively higher ECV indicating the influence of environment on these characters.

4.1.3 Heritability (in broad sense)

High heritability estimate was recorded for all the characters under study (Table 4). The highest heritability was obtained for individual fruit weight (93.36 %) followed by fruit width (92.91 %) and 100 seed weight (92.72 %). The lowest value of heritability was recorded for days to first flowering (60.55 %) followed by pedicel: fruit ratio (63.18), number of primary branches (65.39 %) and number of seeds per fruit (69.87 %).

4.1.4 Genetic Advance (as percentage of mean)

All the characters except days to first flowering exhibited high genetic advance (Table 4). The highest estimate of genetic advance obtained was 170.64 per cent (individual fruit weight) followed by 151.46 (fruit yield per plant) and 125.15 (number of fruits per plant). Days to first flowering showed moderate genetic advance (10.94 per cent).

4.1.5 Correlation Analysis

The correlation between different traits was computed as phenotypic, genotypic and environmental correlation coefficients.

4.1.5.1 Phenotypic Correlation Coefficient

The phenotypic correlation coefficients are presented in Table 5.

Table 5 Phenotypic correlation coefficients

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	1.0000													
X_2	0.0980	1.0000												
X_3	-0.0412	0.1349	1.0000											
X_4	-0.1647	0.0477	0.5126**	1.0000										
X_5	-0.0220	0.1511	0.2381	0.6818**	1.0000									
X_6	-0.1596	0.0863	0.3481**	0.7452**	0.7477**	1.0000								
X_7	-0.0984	0.1438	0.1303	0.0289	-0.0467	-0.1300	1.0000							
X_8	-0.1273	0.2606	0.3573**	0.6453**	0.6077**	0.7678**	0.2855*	1.0000						
X_9	-0.0536	0.3050*	0.2615	0.0065	-0.0273	0.0106	0.4139**	0.2636	1.0000					
X_{10}	-0.0271	0.0087	-0.0077	0.0840	0.0819	0.0886	-0.3413**	-0.1782	-0.2907*	1.0000				
X_{11}	-0.1883	0.1272	0.0376	0.0474**	-0.0220	-0.1206	0.8058**	0.2272	0.3225**	-0.3152*	1.0000			
X_{12}	-0.2499	0.2279	0.2155	0.2446	0.2114	0.2263	0.2608	0.4461**	0.5219**	-0.3024*	0.1765	1.0000		
X_{13}	-0.1435	0.1252	0.1766	0.1484	0.0159	0.0035	0.6415**	0.2799*	0.4848**	-0.3093*	0.5593**	0.4075**	1.0000	
X_{14}	0.0467	-0.3443**	-0.1423	0.0350	-0.0800	0.0446	-0.3769**	-0.1605	-0.4792**	0.2394	-0.2771*	-0.3438**	-0.2605	1.0000

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

X_1 Days to first flowering
X_2 Plant height (cm)
X_3 Number of primary branches
X_4 Number of secondary branches
X_5 Plant spread (cm)
X_6 Number of fruits per plant
X_7 Individual fruit weight (g)
X_8 Fruit yield per plant (g)
X_9 Fruit length (cm)
X_{10} Pedicel : fruit ratio
X_{11} Fruit width (cm)
X_{12} 100-seed weight (g)
X_{13} Number of seeds per fruit
X_{14} Vulnerability index

High positive correlation was recorded for fruit yield per plant with number of fruits per plant (0.7678), number of secondary branches (0.6453), plant spread (0.6077) and 100 seed weight (0.4461). The association was negative with pedicel : fruit ratio (-0.1782), vulnerability index (-0.1605) and days to first flowering (-0.1273).

Fruit length had the maximum positive phenotypic correlation with 100 seed weight (0.5219) and maximum negative correlation with vulnerability index (-0.4792). Fruit length showed negative correlation with pedicel: fruit ratio (-0.2907), days to first flowering (-0.0536) and plant spread (-0.0273) and positive correlation with the rest of the characters

Pedicel : fruit ratio had negative phenotypic correlation with all the characters except vulnerability index (0.2394), number of fruits per plant (0.0886), number of secondary branches (0.0840), plant spread (0.0819) and plant height (0.0087).

Fruit width had strong positive correlation with individual fruit weight (0.8058), number of seeds per fruit (0.5595) and fruit length (0.3225). The correlation was strong and negative with pedicel : fruit ratio (-0.3152).

Strong positive correlation of 100 seed weight was obtained with fruit length (0.5219), fruit yield per plant (0.4461) and number of seeds per fruit (0.4075). The value was strong and negative with vulnerable index (-0.3438)

The interrelationship of number of seeds per fruit was high and positive with individual fruit weight (0.6415), fruit width (0.5593), fruit length (0.4848) and 100 seed weight (0.4075). It was negative with pedicel : fruit ratio (-0.03093), vulnerability index (-0.2605) and days to first flowering (-0.1435).

Vulnerability index had negative phenotypic correlation with most of the characters. The phenotypic correlation was significantly positive with pedicel : fruit ratio (0.2394).

4.1.5.2 Genotypic Correlation Coefficient

The genotypic correlation coefficients are presented in Table 6.

Days to first flowering showed negative genotypic correlation with all the characters except plant height (0.1530) and vulnerability index (0.0515).

Plant height had positive correlation with all the characters. However, its correlation values with vulnerability index (0.3906) and fruit length (0.3692) were substantial.

The interrelationship of number of primary branches was negative with vulnerability index (-0.2450) and days to first flowering (-0.0725) while it was positive for rest of the characters. It showed high positive genotypic correlation with number of secondary branches (0.6211), fruit yield per plant (0.4556), number of fruits per plant (0.4137) and fruit length (0.3208).

Number of secondary branches had positive correlation with all the characters except days to first flowering (-0.1916). Its positive genotypic correlation was substantial with the characters number of fruits per plant (0.7795), plant spread (0.7026), fruit yield per plant (0.6928) and number of primary branches (0.6211).

The genotypic correlation of plant spread was high and positive with number of fruits per plant (0.8130), number of secondary branches (0.7026) and fruit yield per plant (0.6829).

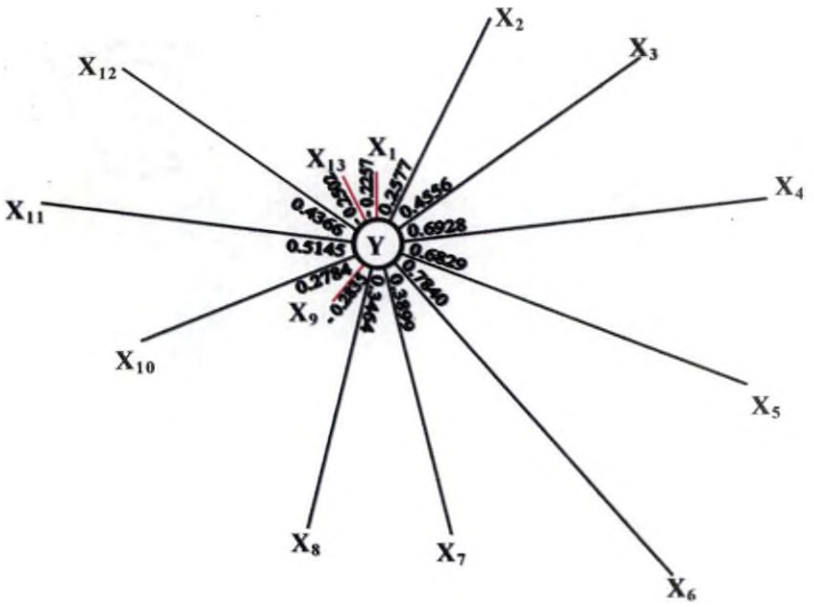
Number of fruits per plant had positive correlation with most of the characters except days to first flowering (-0.2114), fruit width (-0.1400) and individual fruit weight (-0.1265). Its positive correlation was high

Table 6 Genotypic correlation coefficients

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	1.0000													
X_2	0.1530	1.0000												
X_3	-0.0725	0.1260	1.0000											
X_4	-0.1916	0.2222	0.6211**	1.0000										
X_5	-0.0450	0.1570	0.2502	0.7026**	1.0000									
X_6	-0.2114	0.0804	0.4137**	0.7795**	0.8130**	1.0000								
X_7	-0.1228	0.1770	0.1873	0.0439	-0.0452	-0.1265	1.0000							
X_8	-0.2257	0.2577	0.4556**	0.6928**	0.6829**	0.7840**	0.3899**	1.0000						
X_9	-0.0827	0.3692**	0.3208**	0.0345	-0.0265	0.0260	0.4548**	0.3464**	1.0000					
X_{10}	-0.0232	0.0596	0.007	0.0949	0.0832	0.1052	-0.4309**	-0.2835*	-0.3847**	1.0000				
X_{11}	-0.2521	0.1511	0.019	0.0492	-0.0322	-0.1400	0.8655**	0.2784*	0.3360**	-0.4084**	1.0000			
X_{12}	-0.3050*	0.2611	0.2504	0.2570	0.2285	0.2499	0.2841*	0.5145**	0.5568**	-0.3795**	0.1823	1.0000		
X_{13}	-0.2615	0.1013	0.2334	0.1903	0.0236	0.0314	0.7946**	0.4366**	0.5476**	-0.3888**	0.7031**	0.4762**	1.0000	
X_{14}	0.0515	0.3906**	-0.2450	0.0395	-0.1185	0.0456	-0.4478**	-0.2502	-0.5965**	0.2961*	-0.3290**	-0.3825**	-0.3136*	1.0000

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

X_1 Days to first flowering
X_2 Plant height (cm)
X_3 Number of primary branches
X_4 Number of secondary branches
X_5 Plant spread (cm)
X_6 Number of fruits per plant
X_7 Individual fruit weight (g)
X_8 Fruit yield per plant (g)
X_9 Fruit length (cm)
X_{10} Pedicel : fruit ratio
X_{11} Fruit width (cm)
X_{12} 100-seed weight (g)
X_{13} Number of seeds per fruit
X_{14} Vulnerability index



X_1	Days to first flowering	Positive correlation
X_2	Plant height (cm)	
X_3	Number of primary branches	Negative correlation
X_4	Number of secondary branches	
X_5	Plant spread (cm)	
X_6	Number of fruits per plant	
X_7	Individual fruit weight (g)	
X_8	Fruit length (cm)	
X_9	Pedicel : fruit ratio	
X_{10}	Fruit width (cm)	
X_{11}	100-seed weight (g)	
X_{12}	Number of seeds per fruit	
X_{13}	Vulnerability index	
Y	Fruit yield per plant (g)	

Fig. 6. Genotypic correlation of yield with other characters

with plant spread (0.8130), fruit yield per plant (0.7840), number of secondary branches (0.7795) and number of primary branches (0.4137).

The genotypic correlation of individual fruit weight was positive with most of the characters except vulnerability index (-0.4478), pedicel : fruit ratio (-0.4309), number of fruits per plant (-0.1265), days to first flowering (-0.1228) and plant spread (0.0452). Individual fruit weight had high positive correlation with fruit width (0.8655), number of seeds per fruit (0.7946), fruit length (0.4548) and fruit yield per plant (0.3899).

Fruit yield per plant had positive correlation with all the characters except pedicel : fruit ratio (-0.2835), vulnerability index (-0.2502) and days to first flowering (-0.2257). It had high positive genotypic correlation with number of fruits per plant (0.7840), number of secondary branches (0.6928), plant spread (0.6829), 100 seed weight (0.5145), number of primary branches (0.4556), number of seeds per fruit (0.4366), individual fruit weight (0.3899) and fruit length (0.3464).

Fruit length showed high positive genotypic correlation with 100 seed weight (0.5568), number of seeds per fruit (0.5476), individual fruit weight (0.4548), plant height (0.3692), fruit yield per plant (0.3464), fruit width (0.3360) and number of primary branches (0.3208).

Pedicel : fruit ratio had negative genotypic correlation with fruit width, individual fruit weight, fruit length , number of seeds per fruit, 100 seed weight, fruit yield per plant and days to first flowering and positive genotypic correlation with rest of the characters. Its negative correlation was strong with individual fruit weight (-0.4309), fruit width (-0.4085), number of seeds per fruit (-0.3888), fruit length (-0.3847) and 100 seed weight (-0.3795).

Fruit width had strong positive association with individual fruit weight (0.8655), number of seeds per fruit (0.7031) and length of fruit (0.3360). The association was negative with pedicel : fruit ratio (-0.4085),

vulnerability index (-0.3290), days to first flowering (-0.2521), number of fruits per plant (-0.1400) and plant spread (-0.0322).

The genotypic correlation of 100 seed weight was positive with most of the characters except vulnerability index (-0.3290), pedicel : fruit ratio (-0.3795) and days to first flowering (-0.3050). Strong positive correlation of 100 seed weight was recorded with fruit length (0.5568), fruit yield per plant (0.5145) and number of seeds per fruit (0.4762).

Number of seeds per fruit also showed the same pattern of genotypic correlation as in the case of 100 seed weight, *i.e.*, the association was negative with pedicel : fruit ratio, vulnerability index and days to first flowering and positive with rest of the characters. Strong positive correlation was shown with individual fruit weight (0.7946), fruit width (0.7031), fruit length (0.5476) and 100 seed weight (0.4762).

Vulnerability index showed negative correlation with many of the characters. Negative association was strong with length of fruit length (-0.5965), individual fruit weight (-0.4478), 100 seed weight (-0.3825), fruit width (-0.3290) and number of seeds per fruit (-0.3136).

4.1.5.3 Environmental Correlation Coefficient

The environmental correlation coefficients are presented in Table 7. Most of the characters showed a low value for environmental correlation.

However, high positive correlation was observed for number of secondary branches with fruit number per plant (0.6204) and plant spread (0.5666). Number of fruits per plant showed a high positive correlation with plant spread (0.4888) and fruit yield per plant (0.7243).

4.1.6 Path Coefficient Analysis

The direct and indirect effects of the component characters on yield were estimated using path coefficient analysis (Table 8). The characters with high genotypic correlation with yield were selected and they included number of primary branches, number of secondary branches, plant spread,

Table 7 Environmental correlation coefficients

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}
X_1	1.0000													
X_2	-0.0112	1.0000												
X_3	0.0121	0.1567	1.0000											
X_4	-0.1144	0.1686	0.2015	1.0000										
X_5	0.0389	0.1351	0.2226	0.5666**	1.0000									
X_6	-0.0497	0.0450	0.1924	0.6204**	0.4888**	1.0000								
X_7	-0.0371	-0.0173	-0.1057	-0.1243	-0.0656	-0.1840	1.0000							
X_8	0.0670	0.2681	0.1416	0.5085**	0.3602**	0.7243**	-0.2591	1.0000						
X_9	0.0341	0.0425	0.0854	-0.2146	-0.0333	-0.0703	-0.0108	-0.0842	1.0000					
X_{10}	-0.1088	-0.1009	-0.0342	0.0634	0.0867	0.0522	-0.0660	0.0427	-0.0103	1.0000				
X_{11}	0.0043	0.0202	0.1456	0.0307	0.0492	-0.0152	-0.0048	-0.0088	0.1900	-0.0135	1.0000			
X_{12}	-0.1261	0.0933	0.1293	0.1299	0.0962	0.1136	-0.0514	0.1730	0.1782	-0.0729	0.1019	1.0000		
X_{13}	0.0771	0.1850	0.0580	-0.0059	-0.0091	-0.0753	-0.0016	-0.1064	0.2909*	-0.1531	-0.0494	0.1631	1.0000	
X_{14}	0.0384	-0.2209	0.0856	0.0191	0.0564	0.0420	-0.0632	0.0754	0.0007	0.1226	-0.0512	-0.2136	-0.1294	1.0000

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

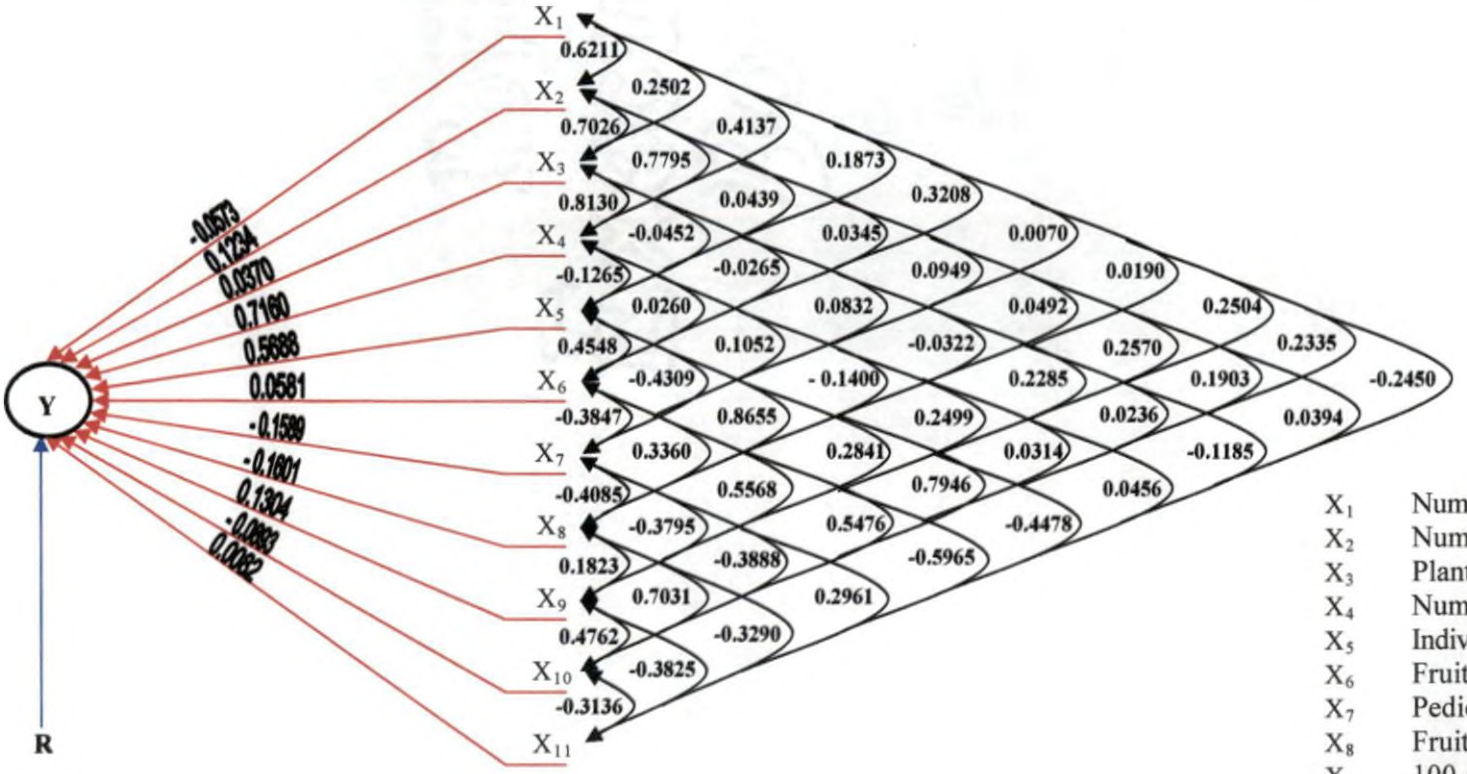
X_1 Days to first flowering
X_2 Plant height (cm)
X_3 Number of primary branches
X_4 Number of secondary branches
X_5 Plant spread (cm)
X_6 Number of fruits per plant
X_7 Individual fruit weight (g)
X_8 Fruit yield per plant (g)
X_9 Fruit length (cm)
X_{10} Pedicel : fruit ratio
X_{11} Fruit width (cm)
X_{12} 100-seed weight (g)
X_{13} Number of seeds per fruit
X_{14} Vulnerability index

Table 8. Path coefficient analysis

		X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	Genotypic correlation coefficients
X_1	Number of primary branches	**-0.0573**	0.0767	0.0093	0.2962	0.1065	0.0188	-0.0011	-0.0030	0.0326	-0.0209	-0.0020	0.4556
X_2	Number of secondary branches	-0.0356	**0.1234**	0.0260	0.5581	0.0250	0.0020	-0.0151	-0.0079	0.0335	-0.0170	0.0003	0.6928
X_3	Plant spread (cm)	-0.0143	0.0867	**0.0370**	0.5821	-0.0257	-0.0015	-0.0132	0.0052	0.0298	-0.0021	-0.0010	0.6829
X_4	Number of fruits per plant	-0.2370	0.0962	0.0301	**0.7160**	-0.0719	0.0015	-0.0167	0.0224	0.0326	-0.0028	0.0004	0.7840
X_5	Individual fruit weight (g)	-0.0107	0.0054	-0.0017	-0.0906	**0.5688**	0.0264	0.0685	-0.1386	0.0370	-0.0710	-0.0037	0.3899
X_6	Fruit length (cm)	-0.1840	0.0043	-0.0010	0.0186	0.2587	**0.0581**	0.0611	-0.0538	0.0726	-0.0489	-0.0049	0.3464
X_7	Pedicel : fruit ratio	-0.0004	0.0117	0.0031	0.1530	-0.2451	-0.0224	**-0.1589**	0.0654	-0.0495	0.0347	0.0024	-0.2835
X_8	Fruit width (cm)	-0.0011	0.0061	-0.0012	-0.1002	0.4923	0.0195	0.0649	**-0.1601**	0.0238	-0.6280	-0.0027	0.2784
X_9	100-seed weight (g)	-0.0144	0.0317	0.0085	0.1789	0.1616	0.0324	0.0603	-0.2920	**0.1304**	-0.4250	-0.0031	0.5145
X_{10}	Number of seeds per fruit	-0.0134	0.0235	0.0009	0.0225	0.4519	0.0318	0.0618	-0.1126	0.0621	**-0.0893**	-0.0026	0.4366
X_{11}	Vulnerability index	0.0140	0.0049	-0.0044	0.0326	-0.2547	-0.0347	-0.0470	0.0527	-0.0499	0.0280	**0.0082**	-0.2502

R = 0.2926

Figures in bold are the direct effects



X_1	Number of primary branches
X_2	Number of secondary branches
X_3	Plant spread (cm)
X_4	Number of fruits per plant
X_5	Individual fruit weight (g)
X_6	Fruit length (cm)
X_7	Pedicel : fruit ratio
X_8	Fruit width (cm)
X_9	100-seed weight (g)
X_{10}	Number of seeds per fruit
X_{11}	Vulnerability index
Y	Fruit yield per plant (g)
R	Residual effect

Direct effect shown in red arrows
Intercorrelations shown in curved arrows

Fig. 7. Path diagram showing direct effects and intercorrelations

number of fruits per plant, individual fruit weight, length of fruit, pedicel : fruit ratio, fruit width, 100 seed weight, number of seeds per fruit and vulnerability index.

Number of primary branches, pedicel : fruit ratio, fruit width and number of seeds per fruit had negative direct effect on yield, while the other character *viz*., number of secondary branches, plant spread, number of fruits per plant, individual fruit weight, fruit length and 100 seed weight had positive direct effect. Direct effect of number of fruits per plant and individual fruit weight on yield were high.

Number of primary branches had negative direct effect (-0.0573) on yield. Its direct effect was less, but it exerted greater positive indirect effect on yield via number of fruits per plant. It had a high positive genotypic correlation with yield (0.4556).

The direct effect of number of secondary branches on yield was positive (0.1234). It had a high positive indirect effect on yield via number of fruits per plant (0.5581) and high positive genotypic correlation with yield (0.6928).

Plant spread had a positive direct effect (0.0370) on yield and its indirect effect on yield via number of fruits per plant was positive and high (0.5821). Its genotypic correlation with yield was high and positive (0.6829).

Number of fruits per plant showed a very high positive direct effect on yield (0.7160). Its indirect effects on yield via other characters were negative except for number of secondary branches, plant spread, fruit length, fruit width, 100 seed weight and vulnerability index. It had a high positive genotypic correlation with yield (0.7840).

The direct effect of individual fruit weight on yield was high and positive (0.5688). Its indirect effects on yield via other characters were low and included both positive and negative effects. Its genotypic correlation with yield was 0.3899.

Days to first flowering showed negative phenotypic correlation with all the characters except plant height and vulnerability index with which the correlations were 0.0980 and 0.0467 respectively.

Plant height had positive phenotypic correlation with all the characters except vulnerability index (-0.3443). The positive phenotypic correlation of plant height was significant only with fruit length (0.3050).

Number of primary branches showed strong positive phenotypic correlation with number of secondary branches (0.5126), fruit yield per plant (0.3573) and number of fruits per plant (0.3481). There was a negative correlation of the character with vulnerability index (-0.1423) days to first flowering (-0.0412) and pedicel : fruit ratio (-0.0077) but the values were negligible.

A strong positive association was observed for number of secondary branches with number of fruits per plant (0.7452), plant spread (0.6818) fruit yield per plant (0.6453) and number of primary branches (0.5126). Number of secondary branches had negative correlation with only one character *viz.*, days to first flowering (-0.1647).

Plant spread had high and positive correlation with number of fruits per plant (0.7477), number of secondary branches (0.6818) and fruit yield per plant (0.6077). The negative correlations were very low to be mentioned.

The phenotypic association of number of fruits per plant was strong and positive with fruit yield per plant (0.7678), plant spread (0.7477), number of secondary branches (0.7452) and number of primary branches (0.3481).

Individual fruit weight had strong positive phenotypic correlation with fruit width (0.8058), number of seeds per fruit (0.6415) and fruit length (0.4139). But, it had strong negative association with vulnerability index (-0.3769).

Fruit length had meager positive direct effect on yield (0.0581). Its indirect effects on yield were positive except that via number of primary branches, plant spread, fruit width, number of seeds per fruit and vulnerability index. It had positive genotypic correlation with yield (0.3464). Fruit length contributed to the correlation through the indirect effect via individual fruit weight (0.2587).

Pedicel : fruit ratio showed negative direct effect on yield (-0.1589). It had negative indirect effect on yield via number of primary branches, individual fruit weight, fruit length and 100 seed weight and its genotypic correlation with fruit yield was negative (-0.2835).

Fruit width had negative direct effect on yield (-0.1601). It had high positive indirect effect on yield via individual fruit weight (0.4923). Its genotypic correlation with yield was positive (0.2784).

The direct effect of 100 seed weight on fruit yield was positive (0.1304). Its genotypic correlation with yield was also positive and high (0.5145). Its indirect effect via other characters was low and included both positive and negative values.

Number of seeds per fruit had negative direct effect on yield (-0.0893). Its indirect effect on yield via individual fruit weight (0.4519) and its genotypic correlation with yield (0.4366) were high and positive.

The direct effect of vulnerability index on yield was positive but very low and its genotypic correlation with yield was negative (0.0082 and –0.3507 respectively). It had positive indirect effect on yield via number of primary branches, number of secondary branches, number of fruits per plant, fruit width and number of seeds per fruit. Its indirect effect on yield via individual fruit weight was negative and high and contributed to its negative correlation with yield.

The residual effect obtained was of 0.2926.

4.1.7 Selection Index

Selection index was computed based on the eleven characters selected for path coefficient analysis and the result is provided in Table 9. The selection indices were closer for genotypes with characters of similar nature.

The selection index value was the highest for genotype T_{19} (3546.88) followed by T_{29} (3316.08), T_{11} (3209.81), T_6 (3122.31) and T_{18} (3102.95) (Plate 3). It was the lowest for the genotype T_8 (646.73).

4.1.8 Genetic Divergence Analysis

The 49 genotypes were subjected to Mahalanobis D^2 analysis based on 12 characters selected for computing selection index. The genotypes were grouped into five clusters based on Tocher's method (Table 10 and Fig. 8).

Cluster I was the largest with 29 genotypes followed by cluster II with 11 genotypes. Cluster III contained seven genotypes while clusters IV and V had one genotype each.

The cluster means for 12 characters are furnished in Table 11.

Cluster I had the maximum cluster means for number of fruits per plant (576.69). Cluster II showed the maximum mean values for pedicel: fruit ratio (1.71) and vulnerability index (29.24). With respect to number of primary branches (11.11) and plant spread (66.27 cm), Cluster III excelled the other clusters. Mean value for number of secondary branches (37.17), fruit yield per plant (122.57 g), fruit length (6.42) and 100 seed weight (0.55) were found to be the maximum for cluster IV. This cluster had the minimum mean values for vulnerability index (3.33) and pedicel : fruit ratio (0.70). Individual fruit weight (1.43 g), fruit width (4.75 cm) and number of seeds per fruit were having the highest mean values in Cluster V.

Meenachil local (T_{19})

Kolanchery local 1 (T_{29})

Plate 3. Genotypes of bird chilli with high selection index value

Table 9 Selection index

Genotype	Selection index	Rank
T_1	2457.08	8
T_2	1022.01	42
T_3	2242.80	13
T_4	1492.44	26
T_5	2218.93	14
T_6	3122.31	4
T_7	2272.20	12
T_8	646.73	49
T_9	1214.39	35
T_{10}	1770.80	21
T_{11}	3209.81	3
T_{12}	1484.50	27
T_{13}	2640.93	7
T_{14}	1873.49	18
T_{15}	2209.67	15
T_{16}	1327.94	32
T_{17}	1121.67	38
T_{18}	3102.95	5
T_{19}	3546.88	1
T_{20}	2051.77	17
T_{21}	1650.38	22
T_{22}	2444.39	10
T_{23}	2394.46	11
T_{24}	1282.37	33
T_{25}	1017.40	43
T_{26}	1827.50	19
T_{27}	2454.05	9
T_{28}	2897.12	6
T_{29}	3316.08	2
T_{30}	1775.56	20
T_{31}	1334.34	30
T_{32}	1271.83	34
T_{33}	982.23	44
T_{34}	1420.69	29
T_{35}	949.79	45
T_{36}	1119.24	39
T_{37}	864.23	46
T_{38}	824.53	47
T_{39}	1646.97	23
T_{40}	1177.55	37
T_{41}	1181.21	36
T_{42}	1331.42	31
T_{43}	2186.99	16
T_{44}	1521.51	25
T_{45}	1113.91	40
T_{46}	1522.88	24
T_{47}	1422.58	28
T_{48}	1053.65	41
T_{49}	684.76	48

Table 10. Clustering pattern of genotypes

Cluster	Number of genotypes	Genotypes
I	29	T_1, T_2, T_3, T_4, T_5, T_6, T_7, T_8, T_9, T_{11}, T_{13}, T_{17}, T_{18}, T_{19}, T_{21}, T_{24}, T_{26}, T_{33}, T_{34}, T_{40}, T_{41}, T_{42}, T_{43}, T_{44}, T_{45}, T_{46}, T_{47}, T_{48}, T_{49}
II	11	T_{12}, T_{14}, T_{16}, T_{23}, T_{29}, T_{30}, T_{31}, T_{32}, T_{35}, T_{36}, T_{39}
III	7	T_{15}, T_{20}, T_{22}, T_{27}, T_{28}, T_{37}, T_{38}
IV	1	T_{10}
V	1	T_{25}

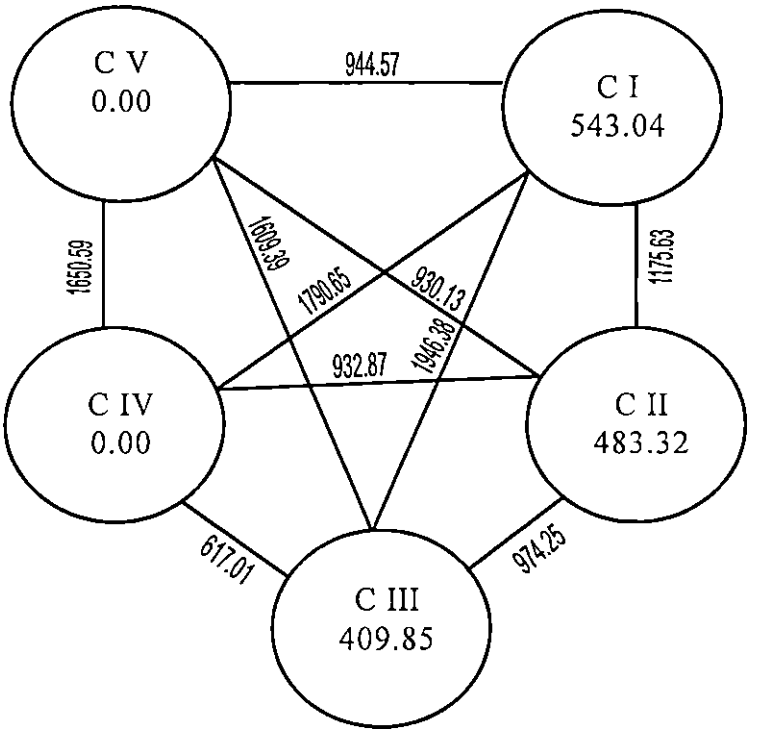
Table 11. Cluster means

Characters	Clusters					Mean
	I	II	III	IV	V	
Number of primary branches	10.38	9.18	11.11	10.00	7.30	9.59
Number of secondary branches	33.74	34.62	36.56	37.17	31.10	34.64
Plant spread (cm)	58.62	58.22	66.27	45.50	46.93	55.11
Number of fruits per plant	576.69	265.56	348.09	234.83	56.33	296.30
Individual fruit weight (g)	0.27	0.37	0.41	0.56	1.43	0.61
Fruit yield per plant (g)	83.79	64.33	119.42	122.57	75.05	93.03
Fruit length (cm)	3.88	3.87	4.06	6.42	3.43	4.33
Pedicel : fruit ratio	1.08	1.71	1.13	0.70	0.90	1.10
Fruit width (cm)	2.00	3.35	2.12	2.38	4.75	2.92
100-seed weight (g)	0.33	0.38	0.37	0.55	0.23	0.37
Number of seeds per fruit	12.69	15.05	14.28	20.89	28.67	18.32
Vulnerability index	28.16	29.24	27.14	3.33	16.67	20.91

Table 12. Average inter and intracluster D^2 values

	I	II	III	IV	V
I	294894.94 (543.04)	1382103.24 (1175.63)	3788409.50 (1946.38)	3206430.55 (1790.65)	892220.77 (944.57)
II		233596.49 (483.32)	949165.58 (974.25)	870241.58 (932.87)	865149.76 (930.13)
III			167979.81 (409.85)	380702.89 (617.01)	2590144.71 (1609.39)
IV				0 (0)	2724458.00 (1650.59)
V					0 (0)

D values given in parenthesis



Values in circles indicate intracluster distances and others indicate intercluster distances

Fig. 8. Cluster diagram showing intra and intercluster distances

The minimum value for individual fruit weight (0.27 g), fruit width (2.00 cm) and number of seeds per fruit (12.69) were shown by Cluster I. Cluster II had the minimum value for fruit yield per plant (64.33 g). The minimum values for plant spread (45.5 cm), pedicel : fruit ratio (0.70) and vulnerability index (3.33) were obtained for cluster IV. Cluster V had the minimum value for the remaining characters *viz.*, number of primary branches (7.30), number of secondary branches (31.10), number of fruits per plant (56.33), fruit length (3.43) and 100-seed weight (0.23).

Average inter and intracluster D^2 values and D values were calculated based on the D^2 values and are presented in Table 12. The intra cluster distances (D values) ranged from 409.85 (Cluster III) to 543.04 (Cluster I). Cluster IV and V had only one genotype each. The distance between Cluster I and III was the highest (1946.38) while it was the least between Clusters III and IV (617.01). In general, the intercluster distances were much higher than the intracluster distances.

4.2 EVALUATION OF GENOTYPES FOR LEAF CURL VIRUS RESISTANCE (EXPERIMENT II)

The 49 genotypes were screened against leaf curl virus under field conditions.

4.2.1 Vulnerability Index

Vulnerability index varied from 5.00 (T_{35}) to 85.00 (T_{16}). T_{35} was on par with T_{33}, T_{11}, T_{15}, T_{10} and T_{49} whereas T_{16} was on par with T_{23}, T_1, T_{17}, T_8, T_9, T_{36}, T_{28}, T_{14}, T_2, T_{31}, T_{27}, T_{20} and T_4 (Table 13).

The cultivars were classified according to their reaction to leaf curl virus, estimated as vulnerability index, and is furnished in Table 13. It was observed that none of the varieties showed an absolute resistance to the virus, *i.e.*, no variety had a vulnerability index of zero and score of zero. Six accessions, *viz.*, T_{35}, T_{11}, T_{15}, T_{33}, T_{10} and T_{49} having vulnerability index between 1.00 to 25.00 and showing slight curling of

Table 13 Reaction to leaf curl virus

Genotype	Vulnerability index (%)	Range of score	Reaction
T_1	78.33 (8.90)	3-4	HS
T_2	71.67 (8.52)	2-3	HS
T_3	61.67 (7.91)	2-3	HS
T_4	63.33 (8.02)	3	HS
T_5	61.67 (7.86)	2-4	HS
T_6	58.33 (7.68)	2-3	HS
T_7	31.67 (5.66)	1-4	HS
T_8	76.67 (8.81)	4	HS
T_9	76.67 (8.81)	3-4	HS
T_{10}	8.33 (3.03)	1	T
T_{11}	6.67 (2.74)	1	T
T_{12}	51.67 (7.24)	2-3	HS
T_{13}	55.00 (7.48)	3	HS
T_{14}	73.33 (8.61)	3-4	HS
T_{15}	6.67 (2.74)	1	T
T_{16}	85.00 (9.27)	4	HS
T_{17}	78.33 (8.87)	3-4	HS
T_{18}	46.67(6.84)	2-3	S
T_{19}	36.67 (6.04)	1-3	S
T_{20}	65.00 (8.11)	3	HS
T_{21}	41.67 (6.32)	1-3	S
T_{22}	45.00 (6.78)	2-3	S
T_{23}	83.33 (9.18)	3-4	HS
T_{24}	61.67 (7.91)	3	HS
T_{25}	38.33 (6.26)	2	S
T_{26}	60.00 (7.72)	3-4	S
T_{27}	66.67 (8.21)	3-4	HS
T_{28}	75.00 (8.72)	3	HS
T_{29}	53.33 (7.23)	2-4	HS
T_{30}	51.67 (7.23)	2-3	HS
T_{31}	71.67 (8.52)	3-4	HS
T_{32}	50.00 (7.14)	2-3	S
T_{33}	6.67 (2.74)	1	T
T_{34}	61.67 (7.89)	3-4	HS
T_{35}	5.00 (2.26)	1	T
T_{36}	76.67 (8.80)	3-4	HS
T_{37}	46.67 (6.73)	1-3	S
T_{38}	41.67 (6.39)	2-3	S
T_{39}	35.00 (5.75)	1-2	S
T_{40}	60.00 (7.81)	3	HS
T_{41}	60.00 (7.78)	3-4	HS
T_{42}	53.33 (6.9)	3	HS
T_{43}	36.67 (6.09)	1-2	S
T_{44}	38.33 (6.25)	2	S
T_{45}	46.67 (6.84)	2-3	S
T_{46}	51.67 (7.24)	2-3	HS
T_{47}	46.67 (6.69)	1-3	S
T_{48}	56.67 (7.51)	2-4	HS
T_{49}	16.69 (4.14)	1	T

Value in parenthesis shows the transformed means

Table 14 Vulnerability index and fruit yield per plant in Experiments I and II

Genotype	Experiment I with control measures		Experiment II without control measures	
	Vulnerability index (%)	Fruit yield per plant (g)	Vulnerability index (%)	Fruit yield per plant (g)
T_1	05.00 (3.91)	100.67	78.33 (8.90)	47.83
T_2	51.67 (7.23)	11.69	71.67 (8.52)	10.57
T_3	36.67 (6.12)	114.80	61.67 (7.91)	64.35
T_4	25.00 (5.08)	51.49	63.33 (8.02)	35.03
T_5	43.33 (6.66)	157.05	61.67 (7.86)	101.10
T_6	28.33 (5.40)	210.14	58.33 (7.68)	130.47
T_7	30.00 (5.53)	155.56	31.67 (5.66)	118.18
T_8	40.00 (6.40)	5.80	76.67 (8.81)	6.07
T_9	38.33 (6.26)	25.09	76.67 (8.81)	21.33
T_{10}	3.33 (1.97)	122.57	8.33 (3.03)	115.46
T_{11}	6.67 (2.74)	349.10	6.67 (2.74)	272.01
T_{12}	23.33 (4.91)	75.30	51.67 (7.24)	49.40
T_{13}	16.67 (4.19)	94.54	55.00 (7.48)	69.43
T_{14}	20.00 (4.58)	56.40	73.33 (8.61)	53.62
T_{15}	0.00 (1.00)	282.05	6.67 (2.74)	356.18
T_{16}	51.67 (7.26)	80.37	85.00 (9.27)	60.92
T_{17}	43.33 (6.65)	29.47	78.33 (8.87)	19.00
T_{18}	38.33 (6.27)	181.23	46.67 (6.84)	177.79
T_{19}	26.67 (5.19)	244.83	36.67 (6.04)	193.88
T_{20}	35.00 (5.99)	125.05	65.00 (8.11)	98.20
T_{21}	40.00 (6.40)	47.18	41.67 (6.32)	38.26
T_{22}	23.33 (4.91)	110.94	45.00 (6.78)	89.40
T_{23}	50.00 (7.14)	76.70	83.33 (9.18)	56.91
T_{24}	30.00 (5.52)	37.43	61.67 (7.91)	26.12
T_{25}	16.67 (4.19)	75.05	38.33 (6.26)	63.83
T_{26}	35.00 (5.83)	72.32	60.00 (7.72)	53.03
T_{27}	46.67 (6.86)	144.32	66.67 (8.21)	98.90
T_{28}	33.33 (5.83)	162.87	75.00 (8.72)	97.97
T_{29}	21.67 (4.72)	167.17	53.33 (7.23)	142.30
T_{30}	23.33 (4.89)	66.53	51.67 (7.23)	45.94
T_{31}	35.00 (5.99)	63.71	71.67 (8.52)	43.37
T_{32}	20.00 (4.58)	27.13	50.00 (7.14)	22.50
T_{33}	0.00 (1.00)	35.95	6.67 (2.74)	42.40
T_{34}	21.67 (4.75)	27.71	61.67 (7.89)	19.80
T_{35}	5.00 (2.45)	31.33	5.00 (2.26)	35.53
T_{36}	43.33 (6.66)	26.65	76.67 (8.80)	19.91
T_{37}	31.67 (5.59)	4.47	46.67 (6.73)	2.90
T_{38}	20.00 (4.56)	6.27	41.67 (6.39)	5.10
T_{39}	28.33 (5.29)	36.38	35.00 (5.75)	21.11
T_{40}	30.00 (5.57)	27.86	60.00 (7.81)	20.60
T_{41}	33.33 (5.86)	27.23	60.00 (7.78)	15.68
T_{42}	35.00 (5.88)	30.10	53.33 (6.98)	19.58
T_{43}	20.00 (4.56)	165.93	36.67 (6.09)	112.84
T_{44}	23.33 (4.93)	53.89	38.33 (6.25)	36.53
T_{45}	23.33 (4.93)	39.76	46.67 (6.84)	29.60
T_{46}	26.67 (5.26)	26.87	51.67 (7.24)	23.85
T_{47}	25.00 (4.99)	41.25	46.67 (6.69)	38.57
T_{48}	25.00 (5.08)	55.11	56.67 (7.51)	45.30
T_{49}	8.33 (2.97)	9.79	16.67 (4.14)	8.57
Mean	27.52	85.12	51.66	66.88
F	8.91**	8.88**	7.06**	13.89**
CD	12.34	71.76	22.50	51.85

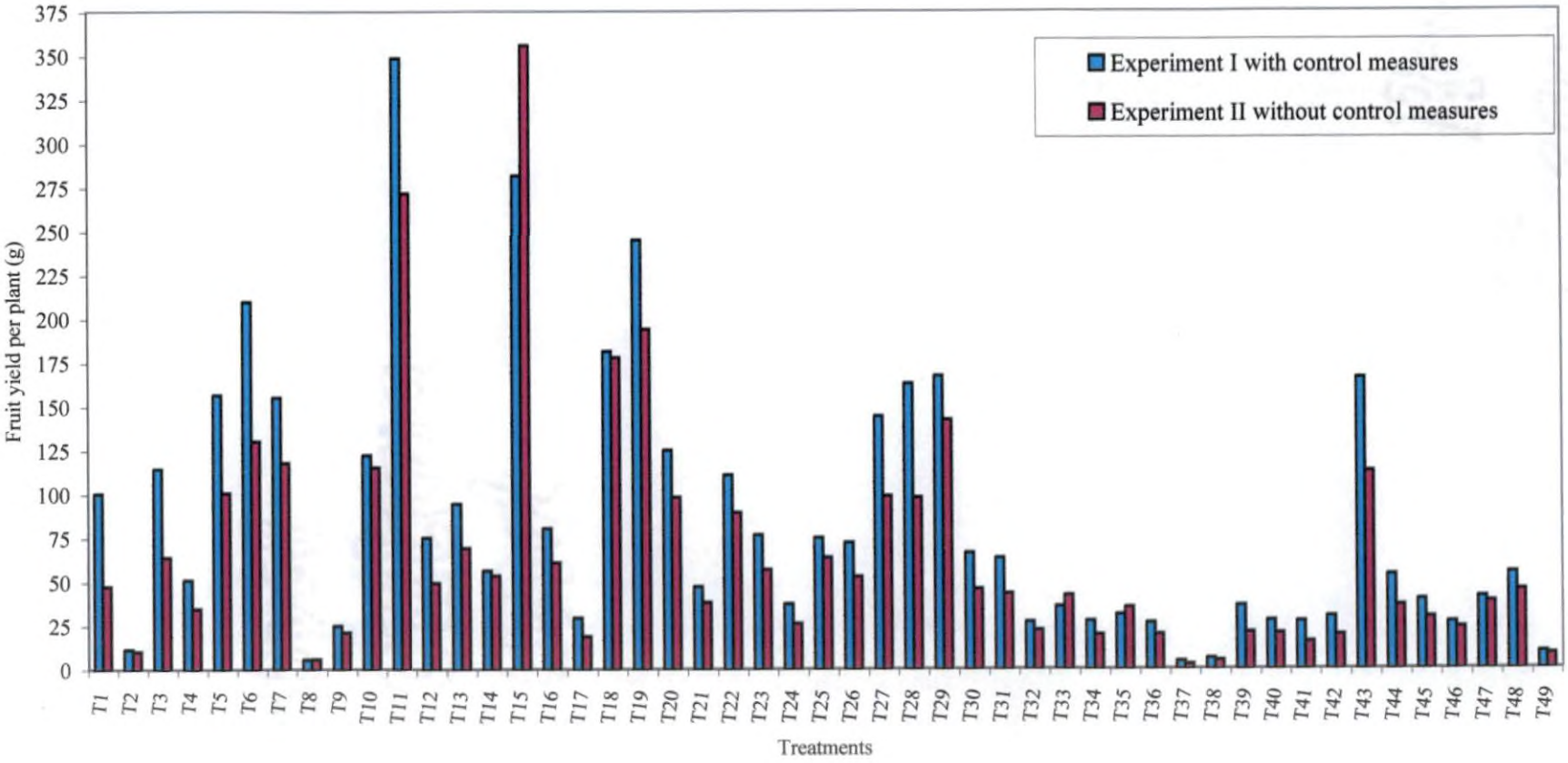


Fig. 9. Comparison of fruit yield per plant in Experiment I and II

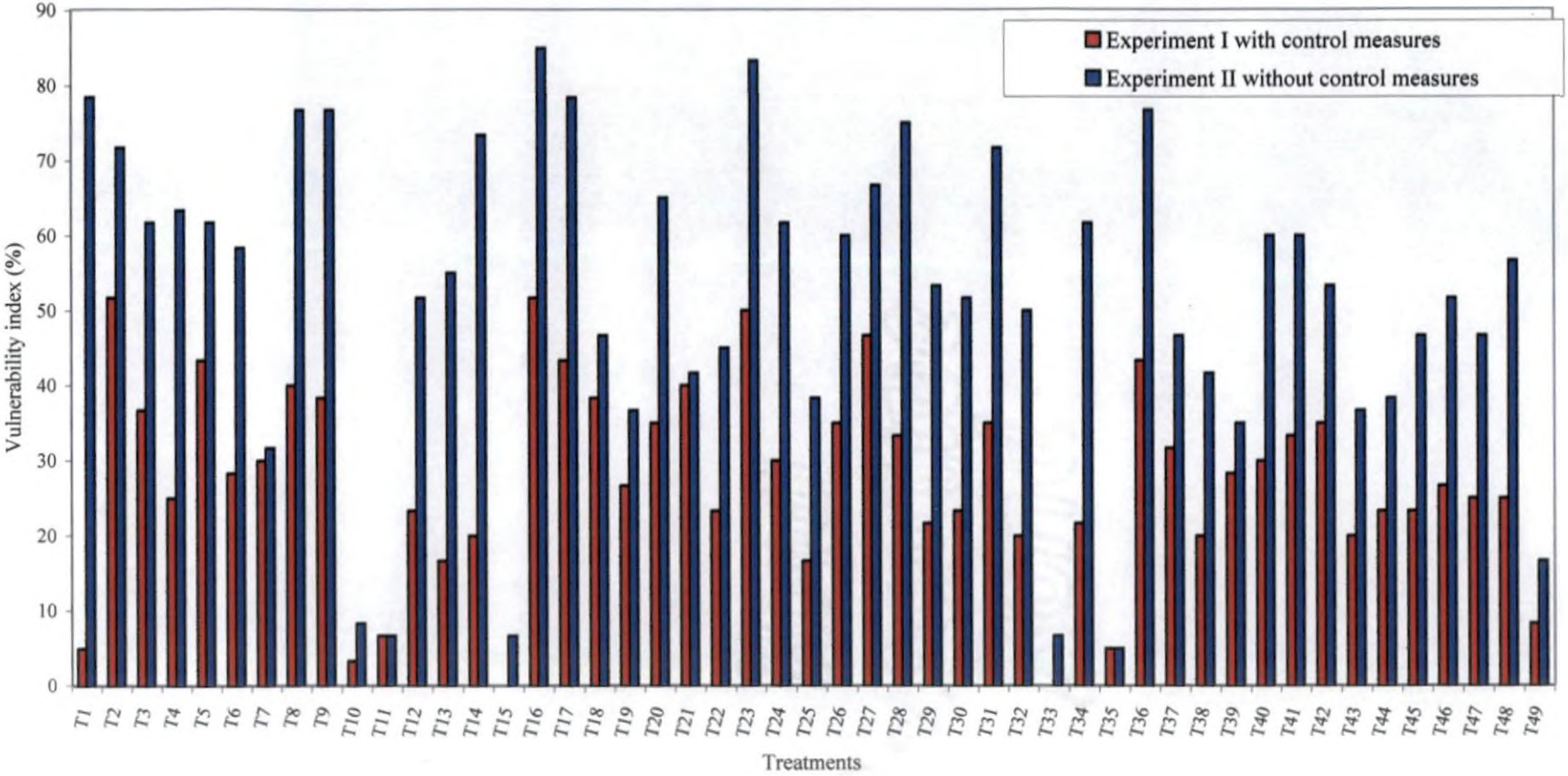


Fig. 10. Comparison of vulnerability index in Experiment I and II

terminal leaves were classified under the tolerant category (Plate 4). Fourteen genotypes fell under the susceptible class with the virus score ranging from 1 to 3 in most cases. This class included the genotypes with vulnerability index in the range 25.01 to 50.00. These accessions showed curling of terminal and adjacent lower leaves with some of them having blisters on leaves. A maximum of 29 genotypes were highly susceptible to the disease as evidenced by the high vulnerability index of more than 50.00.

4.2.2 Fruit Yield per Plant

The varieties varied significantly for yield per plant (Table 14). The highest yielding genotype was T_{15} (356.18 g). This was significantly superior to all other genotypes. The genotype T_{37} gave the lowest yield that was on par with 29 other genotypes.

4.2.3 Correlation Analysis

Table.15 Simple correlation between yield and vulnerability index of Experiments I and II

	Yield per plant in Experiment I (1)	Yield per plant Experiment II (2)	Vulnerability index in Experiment I (3)	Vulnerability index in Experiment II (4)
(1)	1.0000			
(2)	0.9770**	1.0000		
(3)	-0.2502	-0.3465**	1.0000	
(4)	-0.3507**	-0.4598**	0.7995**	1.0000

The yield per plant in Experiments I and II showed highly significant positive correlation. The vulnerability indices in the two experiments were also significantly and positively correlated with each

Kayamkulam local 4 (T_{33})

Kayamkulam local 3 (T_{35})

Plate 4. Leaf curl virus tolerant genotypes of bird chilli

other. The two traits showed the same trend in controlled and uncontrolled conditions. The yield per plant was negatively correlated with vulnerability index in both the experiments. Hence, greater susceptibility leads to reduction in yield.

4.3 MOLECULAR CHARACTERIZATION

The DNA isolation was done from the tender leaves of bird chilli, following the procedure of Rogowsky *et al.* (1991) with required modifications. The DNA yield of 49 genotypes and the initial purity of DNA are given in Table 16. It ranged from 90 ng/µl (T_{30} and T_{36}) to 4080 ng/µl (T_{49}) and 1.14 (T_9) to 2.45 (T_{17}) respectively.

The electrophoretic assay of DNA samples using agarose gel (0.8 %) revealed that the DNA samples isolated were intact and native without any shearing.

The PCR reaction mixture (25 µl) consisted of 25 ng template DNA, 2.5 µl 10x PCR buffer, 2.5 mM $MgCl_2$, 0.2M each of dATP, dCTP, dGTP and dTTP, 4pM primer and 0.6 units of Taq DNA polymerase. The programme consisted of an initial denaturation at 94° C for five minutes followed by 43 cycles of denaturation at 94°C for one minute, annealing at 35°C for one minute 30 seconds and extension at 72°C for two minutes. The synthesis step of the final cycle was extended further by five minutes. Finally the products of amplification were coded at 4°C.

Twenty four decamer primers (OPA, OPB, OPM, OPJ and OPK) were screened for their efficiency using the DNA isolated from T_{24} (Varkala local) as the representative sample. Out of 24 decamer primers, 13 yielded amplification products. There was no amplification with 11 primers. The total number of bands, number of faint bands and number of intense bands produced by the primers were recorded (Table 17). These primers produced 41 bands (average 1.71 bands per primer) of which 28 bands were polymorphic and 13 bands were monomorphic.

Table 16 DNA yield and initial purity in bird chilli

Genotype	DNA yield (ng/µl)	Purity
T_1	1530	1.55
T_2	1380	1.48
T_3	210	1.75
T_4	1950	1.31
T_5	2370	1.39
T_6	1320	1.29
T_7	120	1.33
T_8	360	1.71
T_9	990	1.14
T_{10}	630	1.50
T_{11}	1410	1.24
T_{12}	180	2.00
T_{13}	990	2.35
T_{14}	210	1.40
T_{15}	360	1.71
T_{16}	420	1.55
T_{17}	3750	2.45
T_{18}	120	1.33
T_{19}	210	1.75
T_{20}	660	2.00
T_{21}	750	1.32
T_{22}	1050	1.66
T_{23}	1020	1.89
T_{24}	1800	1.76
T_{25}	300	2.00
T_{26}	1500	1.51
T_{27}	720	1.50
T_{28}	120	1.33
T_{29}	720	1.60
T_{30}	90	1.50
T_{31}	2010	1.63
T_{32}	120	2.00
T_{33}	270	1.80
T_{34}	270	1.80
T_{35}	840	1.65
T_{36}	90	1.80
T_{37}	660	2.00
T_{38}	360	1.71
T_{39}	660	1.83
T_{40}	360	1.33
T_{41}	210	1.75
T_{42}	270	1.80
T_{43}	2970	1.59
T_{44}	3000	1.67
T_{45}	1410	1.51
T_{46}	780	1.85
T_{47}	270	1.29
T_{48}	1380	1.86
T_{49}	4080	1.86

Table 17. Primer associated banding pattern with the DNA of bird chilli genotype, Varkala local

Primer	Intense bands	Faint bands	Total number of bands
OPA-01	5	2	7
OPA-06	0	1	1
OPA-12	0	1	1
OPA-18	0	3	3
OPA-20	3	1	2
OPB-01	3	2	5
OPB-06	2	3	5
OPB-08	1	1	2
OPB-10	4	2	6
OPB-11	1	1	2
OPB-15	1	0	1
OPB-19	0	1	1
OPB-20	3	2	5
OPJ-01	0	1	0
OPJ-05	0	0	0
OPJ-08	0	0	0
OPJ-11	0	0	0
OPJ-18	0	0	0
OPK-06	0	0	0
OPK-15	0	0	0
OPK-16	0	0	0
OPK-19	0	0	0
OPK-20	0	0	0
OPM-02	0	0	0

Primer OPA-01 produced the highest number of bands (7 bands). Six bands were produced by OPB-10. OPB-01, OPB-06 and OPB-20 produced five bands each.

For further amplification only four primers were selected which produced good amplification and more number of polymorphic bands. Using these four primers, the DNA samples isolated from the 49 genotypes were amplified. The nucleotide sequences of primers used are given in Table 18.

Table 18 Nucleotide sequence of primers used for RAPD analysis

Primer	Sequence
OPA-01	CAGGCCCTTC
OPB-01	GTTTCGCTCC
OPB-06	TGCTCTGCCC
OPB-10	CTGCTGGGAC

The banding patterns of these four primers are given in Plates 5, 6, 7 and 8. The primer OPA-01 used in this analysis yielded 390 scorable bands with 49 genotypes. Number of bands per genotype varied from 0 to 14. The primers OPB-01, OPB-06 and OPB-10 yielded 190, 197 and 269 bands respectively.

4.3.1 Data Analysis

Reproducible bands were scored for their presence (+) or absence (-) for all the genotypes studied (Fig. 11, 12, 13 and 14). All the bands were polymorphic in nature for each of the four primers used for amplification. A genetic similarity matrix was constructed using the Jaccard's coefficient method (Table 19). The pair wise coefficient values varied from 0.04 (T_{31} and T_{43}) to 0.96 (T_{18} and T_{19}).

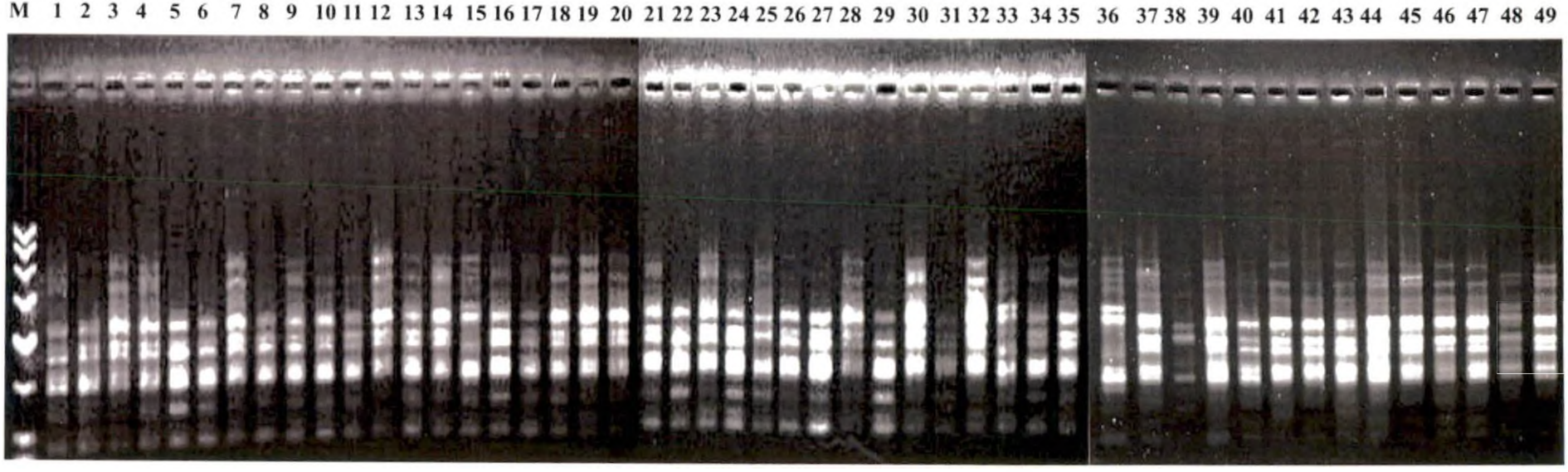


Plate 5. Amplification profiles of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPA-01

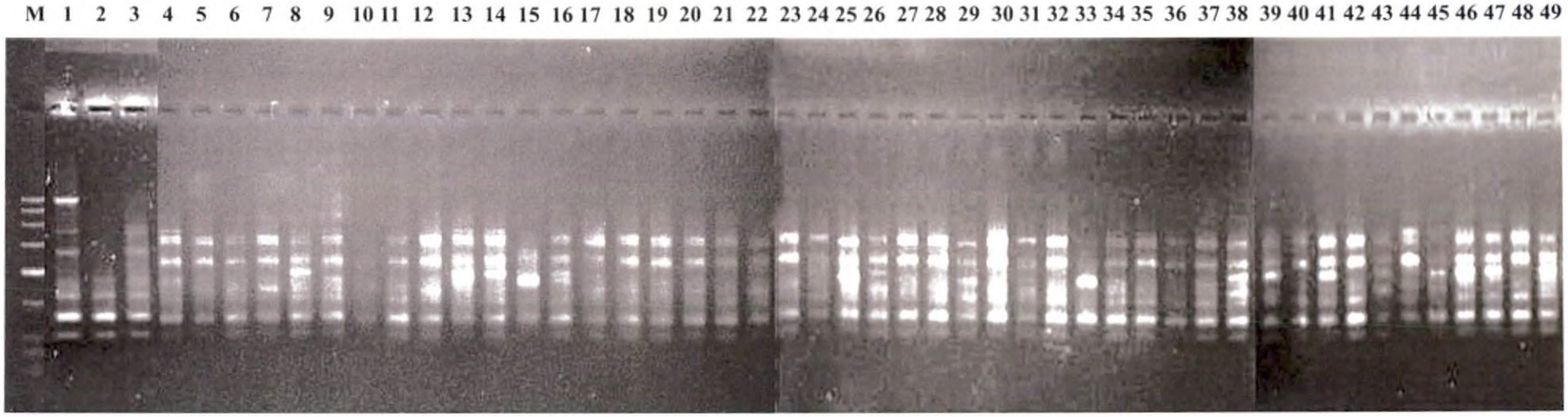


Plate 6. Amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-01

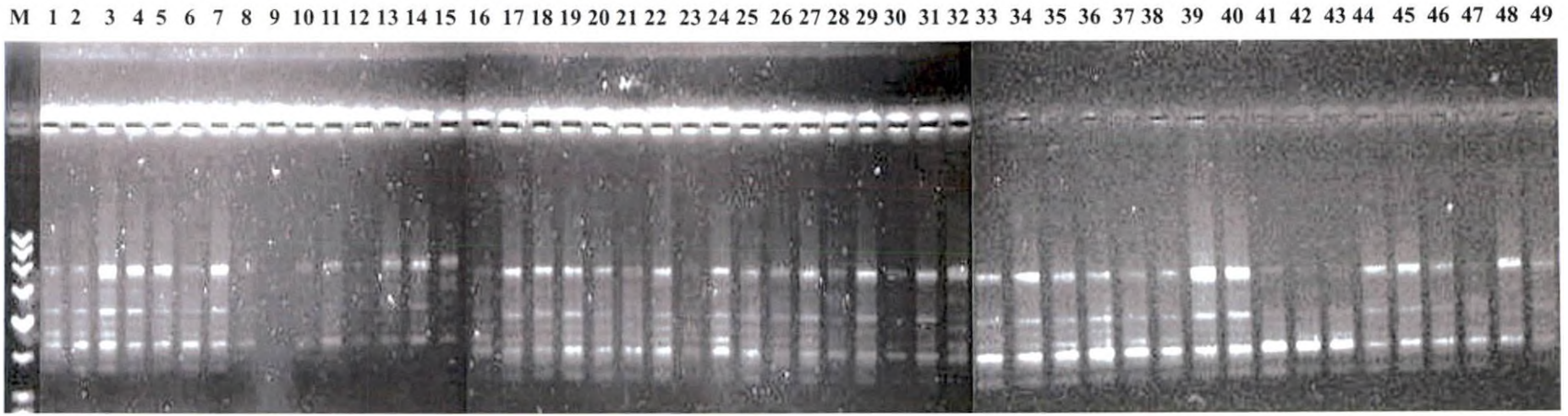


Plate 7. Amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-06

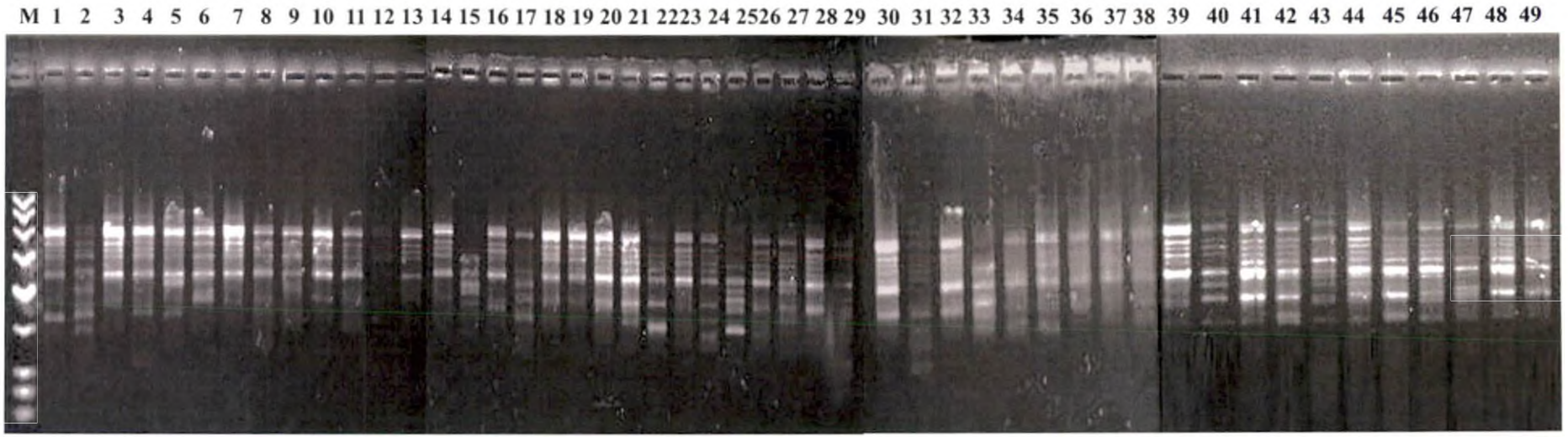


Plate 8. Amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-10

Fig. 11. Representation of amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPA-01

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	+	+	-	-	+	-	-	-	-	+	+	+	+	+	-	+	+	+	+	-	+	-	+	-	-	+	-	+	-	+	+	+	+	+	+	-	+	-	+	-	+	+	+	+	+	-	+
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
+	-	+	+	-	-	-	-	+	-	-	+	+	+	+	+	-	+	+	-	+	-	+	-	-	-	-	-	-	+	-	-	-	-	+	+	-	+	-	-	-	-	+	+	-	-	+	+
-	-	-	+	-	-	+	-	+	+	+	+	+	+	+	-	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-	-	+	-	+	-	+	-	+	+	+	+	+	+	+
-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-	-	+	-	-	+	+	+	+	-	+
-	-	-	-	-	-	-	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	+	+	-	+	-	+	+	-	+	+	+	-	-	-	+	-	+	+	+	+	+	-	-
+	+	+	+	+	+	+	-	+	-	-	-	-	-	-	-	-	-	+	+	+	-	-	-	-	-	+	+	-	+	-	+	-	-	+	+	+	-	+	+	+	+	+	+	+	+	+	-	+
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-
-	-	-	-	-	-	+	+	+	+	+	+	+	+	-	+	-	+	+	+	+	+	+	+	+	-	+	+	-	+	-	+	-	-	+	-	-	-	-	-	-	-	+	+	+	+	+	+	+
-	+	+	+	+	-	+	-	-	-	-	-	-	-	-	+	-	-	-	-	+	-	-	-	-	-	+	+	-	+	-	+	-	-	-	-	+	-	-	+	+	+	+	+	+	+	+	+	+
-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	-	+	+	+	+	+	-	+	-	-	-	-	+	-	+	+	+	+	+	+	+	+	+	+	+
-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	+	-	+	+	+	+	+	+	+	+	+	-	-
+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	-	-	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+
+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	-	+	-	+	-	-	+	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-
+	+	-	+	+	+	-	+	+	+	+	+	-	+	-	+	+	+	+	-	+	+	+	+	+	-	+	-	+	-	+	+	+	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-
+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	+	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	-	-	-	+	+	+	-	+	+	+	+	+	+	+	+	-	-	+	-	-	-	-	-	-	-	-	-	-

+ : Presence of band
- : Absence of band

Fig. 12. Representation of amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-01

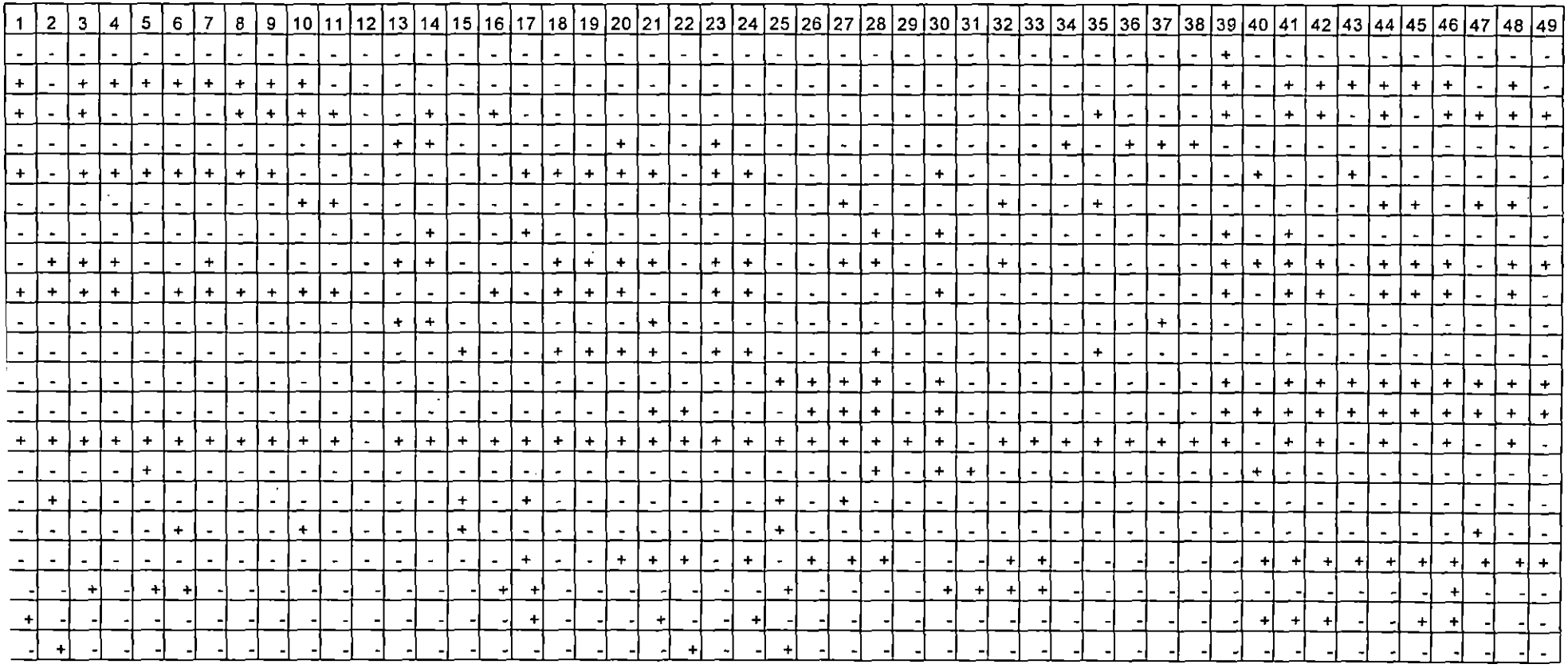
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	+	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-
+	-	+	+	+	+	+	+	+	-	+	+	+	+	-	+	+	+	+	+	+	-	+	+	+	+	+	+	-	+	+	+	-	-	+	-	+	+	-	+	+	+	-	+	-	+	+	+	+
-	-	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	-	+	+	-	+	+	+	+	+	+	-	+	-	+	+	+	+
-	-	-	-	-	-	-	+	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	+	+	-	+	-	-	-	+	+	+	-	+
-	-	-	-	-	-	+	+	+	-	-	-	-	-	+	-	+	+	+	-	-	-	-	-	-	+	-	+	+	+	-	+	+	+	-	-	+	+	-	-	-	+	+	-	+	-	-	-	-
+	+	+	-	-	-	-	+	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	-	+	-	+	+	-	-	+	-	-	+	+	-	-	-	+	+	+	+
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	-	-	-	-	-	-	-	-	-	-
+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	+	+	+	+	+	+	+
-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	+	-	-	+	-	-	-	+	+	+	+	+	+

Fig. 13. Representation of amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-06

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49
-	-	-	-	-	-	-	-	-	-	-	-	+	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
-	-	-	-	-	-	-	-	-	-	+	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-
+	+	+	+	+	+	+	-	-	+	-	-	-	-	-	-	+	+	+	+	+	+	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-	+
-	-	-	-	-	-	-	-	-	-	-	-	-	+	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	-	+	-	+	-	+	+	+	+	+	+	+	+	+	-	-	-	+	+	+	-	-
+	+	+	+	+	+	+	-	-	-	-	-	-	-	-	+	+	+	+	+	-	+	-	+	+	-	+	-	+	-	-	-	+	+	+	+	-	-	+	+	+	-	-	+	-	-	-	-	-
+	+	+	+	+	+	+	-	-	-	+	-	-	+	-	+	+	+	+	+	+	+	-	+	+	-	+	-	-	-	-	-	+	+	+	+	+	+	+	-	-	+	+	+	-	+	+	-
+	+	+	+	+	+	+	+	-	-	-	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
-	+	+	-	-	-	-	-	-	-	-	-	-	-	-	+	+	+	+	+	+	-	+	+	-	+	-	-	-	-	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	-	-

+ : Presence of band
- : Absence of band

Fig. 14. Representation of amplification profile of the DNA of 49 bird chilli (*C. frutescens*) genotypes using the primer OPB-10



+ : Presence of band
- : Absence of band

	T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}	T_{15}	T_{16}	T_{17}	T_{18}	T_{19}	T_{20}	T_{21}	T_{22}	T_{23}	T_{24}	T_{25}
T_1	1.00																								
T_2	0.50	1.00																							
T_3	0.57	0.56	1.00																						
T_4	0.53	0.52	0.64	1.00																					
T_5	0.50	0.48	0.56	0.69	1.00																				
T_6	0.58	0.50	0.58	0.65	0.77	1.00																			
T_7	0.45	0.43	0.55	0.68	0.54	0.56	1.00																		
T_8	0.41	0.26	0.32	0.34	0.34	0.41	0.50	1.00																	
T_9	0.45	0.25	0.35	0.34	0.33	0.39	0.40	0.77	1.00																
T_{10}	0.28	0.21	0.19	0.33	0.21	0.31	0.36	0.49	0.52	1.00															
T_{11}	0.34	0.28	0.26	0.32	0.28	0.33	0.43	0.57	0.61	0.52	1.00														
T_{12}	0.21	0.14	0.17	0.33	0.23	0.24	0.40	0.41	0.52	0.35	0.53	1.00													
T_{13}	0.18	0.15	0.21	0.35	0.19	0.19	0.41	0.37	0.41	0.27	0.40	0.58	1.00												
T_{14}	0.25	0.19	0.25	0.38	0.23	0.24	0.39	0.40	0.43	0.31	0.54	0.52	0.71	1.00											
T_{15}	0.15	0.16	0.15	0.25	0.16	0.21	0.34	0.30	0.38	0.29	0.32	0.47	0.48	0.34	1.00										
T_{16}	0.39	0.32	0.43	0.45	0.41	0.43	0.52	0.54	0.46	0.33	0.52	0.50	0.44	0.52	0.37	1.00									
T_{17}	0.42	0.40	0.38	0.39	0.50	0.52	0.50	0.41	0.35	0.23	0.34	0.31	0.25	0.32	0.31	0.43	1.00								
T_{18}	0.44	0.42	0.48	0.60	0.42	0.48	0.74	0.48	0.52	0.34	0.46	0.50	0.45	0.47	0.43	0.55	0.59	1.00							
T_{19}	0.47	0.45	0.52	0.63	0.45	0.52	0.78	0.47	0.55	0.33	0.45	0.48	0.43	0.45	0.41	0.53	0.57	0.96	1.00						
T_{20}	0.36	0.39	0.50	0.52	0.39	0.45	0.70	0.35	0.39	0.27	0.38	0.35	0.41	0.39	0.30	0.42	0.50	0.74	0.78	1.00					
T_{21}	0.37	0.31	0.41	0.47	0.39	0.32	0.40	0.22	0.24	0.11	0.19	0.23	0.26	0.29	0.20	0.34	0.37	0.47	0.50	0.48	1.00				
T_{22}	0.26	0.32	0.22	0.24	0.28	0.24	0.25	0.16	0.12	0.19	0.17	0.12	0.09	0.14	0.10	0.27	0.34	0.32	0.31	0.33	0.43	1.00			
T_{23}	0.33	0.24	0.29	0.39	0.27	0.29	0.32	0.32	0.31	0.16	0.22	0.26	0.29	0.29	0.23	0.34	0.22	0.44	0.42	0.41	0.55	0.26	1.00		
T_{24}	0.42	0.36	0.34	0.40	0.36	0.38	0.41	0.33	0.29	0.21	0.27	0.19	0.19	0.23	0.17	0.35	0.47	0.53	0.52	0.55	0.65	0.50	0.62	1.00	
T_{25}	0.30	0.41	0.34	0.36	0.41	0.48	0.38	0.29	0.21	0.20	0.27	0.27	0.26	0.29	0.28	0.50	0.48	0.45	0.44	0.38	0.38	0.41	0.30	0.39	1.00
T_{26}	0.22	0.19	0.18	0.24	0.28	0.29	0.33	0.38	0.28	0.19	0.21	0.21	0.25	0.21	0.27	0.31	0.39	0.32	0.31	0.29	0.34	0.31	0.30	0.40	0.41
T_{27}	0.37	0.48	0.37	0.43	0.44	0.41	0.53	0.32	0.31	0.28	0.39	0.31	0.29	0.32	0.27	0.47	0.55	0.52	0.55	0.53	0.53	0.48	0.30	0.50	0.52
T_{28}	0.19	0.24	0.30	0.29	0.28	0.21	0.47	0.33	0.32	0.16	0.27	0.27	0.30	0.29	0.28	0.31	0.34	0.41	0.44	0.47	0.42	0.23	0.26	0.31	0.27
T_{29}	0.42	0.46	0.28	0.34	0.40	0.42	0.41	0.42	0.35	0.25	0.33	0.29	0.22	0.23	0.35	0.38	0.48	0.44	0.43	0.31	0.24	0.33	0.28	0.38	0.38
T_{30}	0.33	0.24	0.37	0.39	0.35	0.32	0.53	0.41	0.48	0.24	0.34	0.36	0.33	0.32	0.35	0.47	0.37	0.47	0.50	0.40	0.41	0.23	0.33	0.31	0.34
T_{31}	0.28	0.25	0.23	0.31	0.50	0.45	0.27	0.26	0.20	0.14	0.23	0.29	0.17	0.18	0.13	0.29	0.39	0.31	0.30	0.22	0.24	0.17	0.23	0.25	0.41
T_{32}	0.28	0.33	0.35	0.45	0.42	0.34	0.57	0.43	0.47	0.34	0.46	0.44	0.40	0.38	0.38	0.50	0.44	0.50	0.53	0.47	0.43	0.28	0.31	0.36	0.36
T_{33}	0.32	0.44	0.37	0.39	0.44	0.41	0.35	0.23	0.18	0.17	0.20	0.19	0.16	0.20	0.25	0.38	0.52	0.43	0.42	0.35	0.36	0.44	0.28	0.42	0.48
T_{34}	0.36	0.44	0.36	0.38	0.38	0.40	0.39	0.30	0.24	0.15	0.27	0.22	0.21	0.26	0.28	0.37	0.46	0.48	0.46	0.39	0.35	0.38	0.31	0.37	0.54
T_{35}	0.42	0.40	0.42	0.44	0.40	0.41	0.05	0.37	0.40	0.32	0.50	0.36	0.29	0.36	0.31	0.48	0.42	0.59	0.62	0.55	0.45	0.34	0.33	0.42	0.54
T_{36}	0.39	0.42	0.44	0.46	0.42	0.38	0.43	0.20	0.23	0.19	0.21	0.26	0.30	0.29	0.27	0.36	0.39	0.46	0.50	0.48	0.34	0.36	0.26	0.27	0.36
T_{37}	0.28	0.33	0.44	0.45	0.38	0.34	0.52	0.26	0.33	0.18	0.28	0.33	0.40	0.38	0.38	0.41	0.39	0.50	0.53	0.52	0.43	0.24	0.28	0.29	0.32
T_{38}	0.28	0.30	0.32	0.26	0.30	0.31	0.31	0.31	0.21	0.07	0.23	0.13	0.22	0.23	0.15	0.24	0.37	0.34	0.33	0.36	0.28	0.23	0.23	0.29	0.38
T_{39}	0.39	0.41	0.52	0.53	0.37	0.42	0.50	0.31	0.33	0.26	0.29	0.25	0.31	0.38	0.29	0.44	0.35	0.49	0.51	0.46	0.38	0.29	0.28	0.36	0.40
T_{40}	0.32	0.39	0.46	0.43	0.50	0.41	0.40	0.19	0.18	0.06	0.13	0.15	0.16	0.14	0.13	0.25	0.41	0.34	0.38	0.45	0.50	0.29	0.24	0.42	0.29
T_{41}	0.32	0.34	0.48	0.46	0.34	0.31	0.43	0.35	0.34	0.20	0.29	0.22	0.29	0.32	0.23	0.41	0.32	0.34	0.37	0.43	0.39	0.22	0.26	0.33	0.30
T_{42}	0.36	0.39	0.50	0.38	0.34	0.35	0.39	0.35	0.34	0.15	0.29	0.13	0.17	0.21	0.18	0.33	0.32	0.31	0.33	0.35	0.40	0.21	0.22	0.33	0.26
T_{43}	0.18	0.23	0.33	0.31	0.27	0.23	0.41	0.23	0.27	0.18	0.17	0.20	0.16	0.17	0.26	0.26	0.29	0.31	0.34	0.37	0.29	0.25	0.11	0.19	0.18
T_{44}	0.38	0.36	0.53	0.58	0.39	0.37	0.56	0.30	0.36	0.30	0.35	0.29	0.34	0.37	0.26	0.46	0.34	0.50	0.53	0.56	0.56	0.39	0.38	0.49	0.35
T_{45}	0.29	0.31	0.40	0.42	0.27	0.24	0.52	0.28	0.31	0.27	0.26	0.26	0.29	0.28	0.26	0.37	0.32	0.46	0.49	0.47	0.47	0.33	0.26	0.37	0.30
T_{46}	0.33	0.32	0.49	0.42	0.35	0.32	0.51	0.40	0.39	0.29	0.34	0.27	0.33	0.33	0.24	0.46	0.37	0.42	0.45	0.51	0.47	0.31	0.30	0.41	0.38
T_{47}	0.21	0.22	0.31	0.29	0.25	0.22	0.37	0.33	0.32	0.25	0.40	0.32	0.30	0.33	0.28	0.44	0.27	0.32	0.35	0.41	0.38	0.27	0.21	0.28	0.35
T_{48}	0.31	0.26	0.39	0.37	0.26	0.26	0.42	0.39	0.42	0.30	0.52	0.29	0.31	0.38	0.25	0.45	0.24	0.37	0.36	0.38	0.35	0.24	0.28	0.32	0.25
T_{49}	0.26	0.23	0.36	0.38	0.26	0.20	0.31	0.31	0.34	0.19	0.29	0.34	0.37	0.35	0.26	0.42	0.22	0.34	0.37	0.39	0.44	0.25	0.29	0.30	0.29

Table 19 Continued

	T_{26}	T_{27}	T_{28}	T_{29}	T_{30}	T_{31}	T_{32}	T_{33}	T_{34}	T_{35}	T_{36}	T_{37}	T_{38}	T_{39}	T_{40}	T_{41}	T_{42}	T_{43}	T_{44}	T_{45}	T_{46}	T_{47}	T_{48}	T_{49}
T_{26}	1.00																							
T_{27}	0.43	1.00																						
T_{28}	0.41	0.47	1.00																					
T_{29}	0.45	0.41	0.29	1.00																				
T_{30}	0.39	0.44	0.62	0.32	1.00																			
T_{31}	0.35	0.29	0.24	0.39	0.29	1.00																		
T_{32}	0.37	0.56	0.55	0.44	0.56	0.31	1.00																	
T_{33}	0.33	0.41	0.25	0.48	0.29	0.32	0.43	1.00																
T_{34}	0.38	0.40	0.28	0.63	0.31	0.37	0.38	0.59	1.00															
T_{35}	0.30	0.55	0.39	0.42	0.41	0.33	0.53	0.46	0.58	1.00														
T_{36}	0.21	0.39	0.23	0.33	0.26	0.23	0.33	0.50	0.50	0.44	1.00													
T_{37}	0.32	0.43	0.36	0.34	0.43	0.21	0.45	0.39	0.43	0.44	0.46	1.00												
T_{38}	0.39	0.28	0.29	0.36	0.24	0.32	0.26	0.31	0.55	0.37	0.33	0.50	1.00											
T_{39}	0.41	0.46	0.32	0.34	0.42	0.19	0.33	0.34	0.38	0.43	0.41	0.44	0.26	1.00										
T_{40}	0.33	0.50	0.38	0.31	0.32	0.32	0.34	0.31	0.30	0.32	0.29	0.39	0.26	0.38	1.00									
T_{41}	0.29	0.43	0.45	0.24	0.43	0.12	0.46	0.31	0.26	0.40	0.29	0.38	0.24	0.57	0.48	1.00								
T_{42}	0.33	0.44	0.42	0.27	0.36	0.14	0.38	0.27	0.30	0.32	0.21	0.42	0.36	0.46	0.50	0.67	1.00							
T_{43}	0.25	0.38	0.34	0.18	0.38	0.04	0.35	0.32	0.21	0.25	0.25	0.45	0.14	0.39	0.37	0.45	0.46	1.00						
T_{44}	0.35	0.64	0.42	0.26	0.48	0.16	0.50	0.37	0.29	0.49	0.39	0.50	0.23	0.65	0.44	0.62	0.51	0.37	1.00					
T_{45}	0.33	0.51	0.41	0.24	0.43	0.12	0.50	0.35	0.26	0.36	0.38	0.46	0.24	0.53	0.39	0.54	0.47	0.35	0.67	1.00				
T_{46}	0.38	0.51	0.50	0.29	0.51	0.21	0.59	0.32	0.28	0.44	0.31	0.46	0.32	0.53	0.44	0.73	0.61	0.48	0.66	0.68	1.00			
T_{47}	0.31	0.50	0.44	0.21	0.42	0.13	0.53	0.26	0.24	0.47	0.27	0.44	0.29	0.39	0.33	0.58	0.50	0.41	0.57	0.58	0.67	1.00		
T_{48}	0.32	0.47	0.41	0.26	0.43	0.13	0.45	0.16	0.21	0.35	0.17	0.37	0.26	0.44	0.30	0.50	0.62	0.55	0.58	0.50	0.59	0.58	1.00	
T_{49}	0.38	0.44	0.52	0.27	0.48	0.18	0.57	0.20	0.22	0.36	0.25	0.42	0.27	0.46	0.40	0.56	0.48	0.46	0.56	0.56	0.71	0.71	0.62	1.00

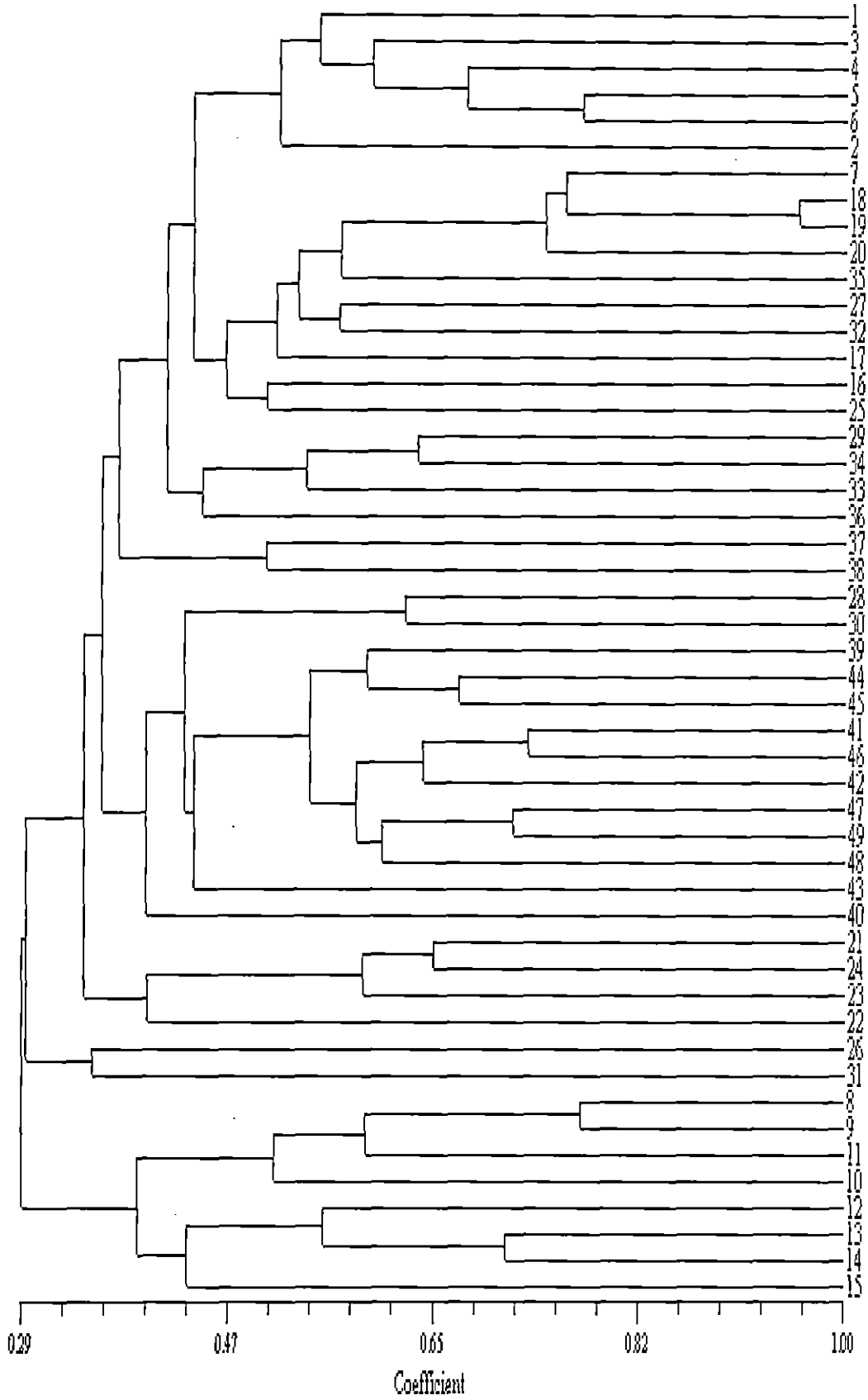


Fig. 15. Dendrogram for 49 bird chilli (*C. frutescens*) genotypes based on the RAPD analysis

Based on the scores the genotypes were divided into different clusters and a dendrogram was drawn. In the dendrogram, if a vertical line is drawn at 0.29 similarity coefficient, 49 genotypes were grouped into two clusters. The largest cluster consisted of 41 genotypes (Cluster I), while the other included the remaining eight genotypes (Cluster II). The high yielding genotypes T_{11} and T_{15} came in cluster II and the leaf curl tolerant genotypes T_{35} and T_{33} in the other (Cluster I).

Discussion

5. DISCUSSION

Spices including chillies are in use to augment colour, taste and flavour of foods. They are used both at domestic and industrial level in different forms like fresh, dried or other processed products. Bird chilli (*Capsicum frutescens*) is known for its pungency, but its cultivation is limited to the homestead gardens. Besides possessing a number of medicinal and culinary properties it has been reported to possess multiple disease resistance also. This property can be utilized in breeding programmes to develop disease resistant or tolerant and high yielding genotypes of chilli through interspecific hybridization.

In the study, chilli leaf curl disease is given emphasis. Genotypes collected from different sources were evaluated for yield and component characters and screened for leaf curl virus resistance. The genotypes were characterized using RAPD also.

The results of the study are discussed below.

5.1 EXPERIMENT I

5.1.1 Assessment of Variability and Genetic Parameters for Yield and Morphological Characters

The phenotypic variation present in a population with respect to various characters gives the basic idea of the extent of variability .

In the present investigation, all the 14 characters under study showed a wide range of variation (Table 2). This was further confirmed by analysis of variance in which significant differences were observed for all the characters.

Number of fruits per plant showed the greatest range of variation. The genotype T_{29} (Kolanchery local) produced the highest number of fruits followed by T_{19} (Meenachil local), T_{11} (Karumukku local), T_{28}

(Elvanthitta local), T_6 (Thavanur local 1), T_{18} (Irumbuzhi local) and T_1 (Parasuvaikkal local 1). T_{37} (Mulleria local) produced the least number of fruits per plant followed by T_8 (Ambalavayal local 1), T_{38} (Edneer local) and T_{25} (Ambalavayal local 3). High variability was observed for fruit yield per plant, number of secondary branches, plant spread and plant height. This was in accordance with Singh and Singh (1976a), Arya and Saini (1977), Ramkumar *et al.* (1981), Nair *et al.* (1984a), Adamu and Ado (1988), Ahmed *et al.* (1990) and Khurana *et al.* (2003). Days to first flowering and number of seeds per fruit showed high variability and were supported by the findings of Acharya *et al.* (1992), Choudhary *et al.* (1985). Gopalakrishnan *et al.* (1985) and Verma *et al.* (1998). Their report also supported the wide variation in fruit length, fruit girth and average fruit weight. Hundred seed weight also showed high variability. Dwivedi and Bhandari (1999) expressed similar view with respect to 1000-seed weight in chilli.

5.1.2 Classification of Genotypes

Grouping of genotypes into different classes based on their mean values helps to identify the phenotypically superior genotypes for each character.

Fifteen genotypes with days to first flowering less than the mean were included in the better class (Table 3). Nine genotypes each were included in the better category for plant height and number of primary branches. Fifteen and 17 genotypes each were having the number of secondary branches and plant spread higher than the mean, which were coming in the better class.

The better class consisted of 15 genotypes for number of fruits per plant.

Seven genotypes with individual fruit weight higher than the mean were included in the better class while it consisted of 11 genotypes for fruit yield per plant.

Ten, eleven and nine genotypes respectively were included in the better class for fruit length, pedicel : fruit ratio and fruit width.

The better class consisted of 16 and 10 genotypes for 100-seed weight and number of seeds per fruit respectively.

In the case of vulnerability index based on leaf curl virus score, only two genotypes viz., T_{15} (Thavanur local 3) and T_{33} (Kayamkulam local 4) were coming in the better class.

The genotypes T_{15} (Thavanur local 3), T_{11} (Karumukku local), T_{19} (Meenachil local), T_{23} (Mallassery local) and T_{33} (Kayamkulam local 4) fell in the better class while T_{17} (Vamanapuram local), T_{38} (Edneer local), T_{36} (Kayamkulam local 1), T_{37} (Mulleria local), T_{40} (Puthige local) and T_{49} (Paadi local) were included in the poor class for most of the characters.

5.1.3 Components of Variability

The estimates of variances *viz.*, phenotypic, genotypic and environmental variance will give a better idea of the extent of variation in genotypes which is the key for improvement through selection.

High estimates of phenotypic and genotypic variances were observed for number of fruits per plant followed by fruit yield per plant, plant spread and number of secondary branches (Table 4). This result was supported by the observations by Arya and Saini (1977), Ramalingam and Murugarajendran (1977) and Elangovan *et al.* (1981). But the variances were low for 100-seed weight, followed by pedicel : fruit ratio, individual fruit weight, fruit width, fruit length and number of primary branches. This was in accordance with the reports by Vijayalakshmi *et al.* (1989). The values of genotypic variance were close to the phenotypic variance in almost all the characters, suggesting the predominance of

genetic component over environmental effect on its phenotype. Ahmed *et al.* (1990) also expressed a similar view with respect to all the characters studied in a set of 64 chilli lines.

5.1.4 Coefficient of Variation

The comparison of variation among different characters studied is possible only if they are unit free. Unlike the estimates of variance, the coefficient of variation provides an excellent basis for such a comparison.

The phenotypic coefficient of variation (PCV) ranged from 8.77 for days to first flowering to 98.79 for fruit yield per plant. In addition to fruit yield per plant, high estimates of PCV were also noticed for individual fruit weight, number of fruits per plant and number of secondary branches (Table 4 and Fig.4). This is in accordance with the reports by Nair *et al.* (1984a), Rani (1996), Jabeen *et al.* (1999) and Nandadevi and Hosamani (2003a).

Number of seeds per fruit and vulnerability index also showed high estimates of PCV.

The genotypic coefficient of variation (GCV) describes the inherent genetic variation. The highest value of GCV estimate was obtained for individual fruit weight followed by fruit yield per plant and fruit number per plant. This was supported by the studies of Arya and Saini (1976), Gopalakrishnan *et al.* (1987), Nandi (1993), Jabeen *et al.* (1999) and Rathod *et al.* (2002a). GCV was also high for number of seeds per fruit and vulnerability index, indicating the inheritance of these characters.

A major portion of PCV was contributed by GCV for characters like days to first flowering, fruit length , fruit width and 100-seed weight suggesting that the observed variation was mainly due to genetic factors (Fig. 4). Pitchaimuthu and Pappiah (1992) also reported a close association between the estimates of phenotypic and genotypic coefficients of variation for several characters in chilli. However,

comparatively high values of environmental coefficient of variation was observed for days to first flowering, plant height, number of primary branches, number of fruits per plant, fruit yield per plant, pedicel : fruit ratio and vulnerability index indicating the greater influence of environment on these characters. This was supported by the findings of Vijayalakshmi *et al.* (1989) and Gopalakrishnan *et al.* (1985).

5.1.5 Heritability and Genetic Advance

Selection acts on genetic differences and the benefits from selection for a particular trait depend on its heritability (Allard, 1960). Burton (1952) suggested that variability together with heritability estimates would give the extent of advance to be expected by selection. Hence, it will be appropriate to combine variability and heritability components along with genetic advance to be used in selection programme. Genetic advance indicates the progress that can be expected as a result of selection on a particular population. It is the measure of genetic gain under selection (Singh and Narayanan, 1993).

Present investigation revealed high heritability values for all the characters (Table 4 and Fig. 5). Genetic advance values as per cent of mean were high for all the characters except days to first flowering for which it was moderate.

Many workers have reported high heritability coupled with high genetic advance for different characters in chilli.

Singh and Singh (1977a) observed high values of heritability and genetic advance for number of fruits per plant, number of branches, plant height and yield per plant in chilli.

Bavaji and Murthy (1982) noticed high heritability coupled with high genetic advance for branches per plant, fruit length, 50 fruit weight and number of fruits per plant. High heritability and genetic advance were reported by Shah *et al.* (1986) for plant height and number of fruits per

plant, Das *et al.* (1989) for yield per plant, Depestre *et al.* (1989a) for fruit number per plant and yield. Sahoo *et al.* (1989) reported high heritability and genetic advance for yield per plant, number of fruits per plant and weight of ten dry fruits. Das and Choudhary (1999a) obtained very high heritability for fruit length, fruit number, fruit weight and yield. Similar results were reported by Munshi and Behera (2000).

Moderate genetic advance was obtained only for days to first flowering. This result was supported by Nair *et al.* (1984b), who reported high heritability along with low genetic advance for days to flower and number of primary branches.

High heritability values for all the traits confirmed negligible influence of environment. High heritability coupled with high genetic advance indicates that the traits are controlled by additive gene action which make selection very effective. According to Johnson *et al.* (1955b) high heritability coupled with high genetic advance will be a more reliable criterion for selection than selection based on heritability alone.

5.1.6 Association of Characters

5.1.6.1 Correlation Coefficient Analysis

Being a polygenic trait, yield is a complex character that is dependent on several component characters and there exists relationship among these component characters. Correlation analysis provides a reliable estimate on the nature, extent and direction of relation and thus aids selection process. Improvement of characters with high correlation to yield can lead to significant increase in yield.

In general, the genotypic correlation coefficients were higher than phenotypic correlation coefficient for all the characters studied. Low phenotypic correlation might be due to the masking or modifying effect of the environment on the phenotypic expression of the characters (Johnson *et al.*, 1955b). But, the difference between the two types of correlation

coefficients was relatively low for most of the characters and indicated negligible influence of environment (Dewey and Lu, 1959) on the relationship of characters at genotypic level and hence selection could be based on phenotypic performance itself.

Fruit yield per plant had positive genotypic correlation with plant height, number of primary branches, number of secondary branches, plant spread, fruit number per plant, individual fruit weight, fruit length, fruit width, 100-seed weight and number of seeds per fruit while the genotypic correlation of yield was negative and significant with pedicel: fruit ratio. (Table 6).

Positive genotypic correlation of yield with plant height was reported by Ahmed *et al.* (1997), Rani (1997) and Khurana *et al.* (2003).

Bavaji and Murthy (1982), Kaul and Sharma (1989), Rani (1995) and Das and Choudhary (1999b) reported significant positive correlation of fruit yield per plant with number of primary branches. The studies by Ghai and Thakur (1987), Rani (1997) and Jose and Khader (2002) also were the same. Jose and Khader (2002) also reported positive correlation of yield with number of fruits per plant, individual fruit weight, fruit length , fruit width and 100-seed weight, and this supported the present study. Ibrahim *et al.* (2001) also observed positive correlation of yield per plant with fruit length and fruit width. Positive correlation of plant spread with fruit yield was in accordance with the study by Ali (1994).

In contrary to the present findings, He *et al.* (1989) observed negative correlation of yield with fruit length, and Aliyu *et al.* (2000) noticed that yield was negatively correlated with plant height.

According to the study conducted, yield per plant showed negative correlation with days to first flowering. Rao *et al.* (1981), Bhagyalakshmi *et al.* (1990) and Warade *et al.* (1996) reported similar results. But,

Sundaram and Ranganathan (1978), Meshram (1987) and Rathod *et al.* (2002b) reported positive association of yield with days to flowering.

Pedicel : fruit ratio and vulnerability index also had negative correlation with yield and hence had a negative effect on yield. It is appropriate to do selection against these characters for improving the yield.

The interrelationships of component characters were also analysed. Days to first flowering was negatively correlated with most of the characters studied except plant height and vulnerability index. The positive correlation of the character with plant height and vulnerability index was very low and non-significant. Mini (2003) and Philip (2004) found negative association of days to flowering with most of the characters.

Highly significant and positive correlation of number of primary branches was observed with number of secondary branches, plant spread and number of fruits per plant. This was supported by the findings of Ahmed *et al.* (1997) and Ibrahim *et al.* (2001). These four characters were found to have significant positive correlation with yield and hence selection for these characters would indirectly benefit the yield.

The strong positive correlation of fruit length with fruit weight was observed as reported by Kumar *et al.* (2003). But, individual fruit weight had negative association with number of fruits per plant. This was in accordance with the report of Munshi *et al.* (2000) that individual fruit weight had positive correlation with fruit length and negative correlation with fruit number.

Vulnerability index showed negative association with most of the characters. This clearly indicates that susceptibility to the disease can adversely affect the vegetative and reproductive growth of the plant.

5.1.7 Path Coefficient Analysis

The association pattern between traits can at times be misleading because it may not indicate the actual effect of one character upon another. Path analysis can be a tool here that provides information on the real nature of association of several yield related characters contributing to yield, by separating the genotypic correlation into direct and indirect effects.

Number of fruits per plant and individual fruit weight had high and positive direct effect on fruit yield per plant while that of vulnerability index of leaf curl virus was high and negative.

Number of primary branches had significantly high positive correlation with yield, but the direct effect was low and negative (Table 8 and Fig. 7). So, the high correlation effect might be due to indirect effect via other characters especially number of fruits per plant. Sundaram and Ranganathan (1978) also had the same observation.

Number of secondary branches had high positive correlation with yield and its direct effect on yield was positive and low. Number of fruits per plant contributed indirectly to the correlation. Nair *et al.* (1984b) reported that number of secondary branches had positive direct effect on yield.

Plant spread showed low positive direct effect on yield. However, the trait contributed indirectly via number of fruits per plant. Legesse *et al.* (1999) found positive direct effects of canopy width on yield. .

Number of fruits per plant had the highest positive direct effect on yield. Its correlation with yield was also high and positive. Hence, direct selection for number of fruits per plant would effectively improve the fruit yield per plant *i.e.*, the correlation represents a true relationship between the two traits. Rao *et al.* (1981), Solanki *et al.* (1986) and Kaul and Sharma (1989) supported this result with their findings. Number of fruits

per plant exerted low negative indirect effect on yield via most of the characters such as number of primary branches, individual fruit weight, pedicel: fruit ratio and number of seeds per fruit. Korla and Rastogi (1977) found negative indirect effect via average fruit weight.

The direct effect of individual fruit weight was positive and higher than its genotypic correlation with yield. Rao and Chhonkar (1981), Depestre *et al.* (1989c), Das and Choudhary (1999b), Munshi *et al.* (2000) and Mini (2003) also observed high and positive direct effect of fruit weight on yield.

Fruit length had low positive direct effect on yield and a high positive correlation with it. The positive correlation was due to the indirect effect via individual fruit weight. Solanki *et al.* (1986) and Sarma and Roy (1995) also reported positive direct effect of length of fruit on yield.

Characters fruit width and number of seeds per fruit had low negative direct effect on yield. However, both had high positive indirect influence on yield via individual fruit weight. Aliyu *et al.* (2000) reported the direct positive effect of these characters on yield.

Pedicel : fruit ratio also had negative direct effect on yield. Vulnerability index had low positive direct effect and high negative correlation with yield. So, selection is to be done against long pedicel and susceptibility of the plant to the disease.

Hundred seed weight had low positive direct effect and high positive correlation on yield.

The residual value was low indicating that most of the important characters contributing to yield were included in the study. Rao and Chhonkar (1981) and Munshi *et al.* (2000) also observed low residual value in their study.

Based on correlation and path analysis studies, it could be concluded that selection for number of fruits per plant and individual fruit weight might lead to increase in yield. Similarly selection for shorter pedicel and lesser vulnerability index also could be beneficial.

5.1.8 Selection Index

Selection index involving several yield related characters will be more efficient in identifying the superior genotypes. Use of selection index also provides scope for greater efficiency in increasing yield through selection rather than straight selection for yield alone.

In the present study, selection index was constructed based on fruit yield per plant and 11 other characters that had significantly high correlation with yield (Table 9).

Many of the high yielding and superior genotypes such as T_{19} (Meenachil local), T_{29} (Kolanchery local), T_{11} (Karumukku local), T_6 (Thavanur local I) and T_{18} (Irumbuzhi local) were found to have high selection indices while low yielding types like T_{37} (Mulleria local), T_{38} (Edneer local) and T_{49} (Paadi local) were having low selection indices, indicating the efficiency of the technique in identifying the superior genotypes. This may be due to the inclusion of several economically important yield related characters in computing the selection index. Singh and Singh (1976b), Gill *et al.* (1977), Singh and Singh (1977a), Sundaram *et al.* (1979) and Jose (2001) also used selection index for discrimination of genotypes. It was also noted that many of the genotypes with high selection index fell under the 'better' class and the genotypes with low selection index under 'poor' class with respect to the mean values for yield per plant.

5.1.9 Genetic Divergence Analysis

A knowledge of genetic divergence between genotypes helps to identify suitable parents from a population. Mahalanobis D^2 statistics was

found to be a powerful tool to assess the degree of relationship among the genotypes and to group them into different clusters. This could provide a dependable means for identifying genetically divergent parents to be used in breeding programmes.

Forty-nine accessions were grouped into five clusters with varying number of genotypes in each cluster (Table 10). The genotypes with minimum divergence got clustered together. Cluster I with 29 genotypes was the largest and clusters IV and V containing one genotype each were the smallest.

Cluster I had most of the genotypes included in the 'better' and 'average' class for number of fruits per plant and fruit yield per plant. It also had the highest cluster mean for number of fruits per plant, the character which showed maximum genotypic correlation with yield. This shows its superiority with respect to yield and yield related characters (Table 11).

Cluster II showed maximum cluster means for pedicel : fruit ratio and vulnerability index both of which negatively affect the yield of the plant. Its minimum cluster mean for fruit yield per plant support this view.

Cluster III had the highest cluster mean for number of primary branches and plant spread and its vulnerability index value was considerably high.

Genotypes included in Cluster III were scattered in all the three class *i.e.*, poor, average and better class and its cluster mean for fruit yield per plant was near to the average performance. Genotypes in clusters IV and V had average performance with respect to yield per plant.

It was noted that the clustering pattern was in agreement with the phenotypic classification based on mean values of genotypes for yield per plant. In brief, Cluster I included the superior genotypes, while Cluster II was poor in performance. Clusters III, IV and V stood at the average level.

The intercluster distance (D) was maximum between clusters I and III suggesting that these were the most divergent clusters (Table 12 and Fig. 8). Clusters III and IV were genetically closer, indicated by the low value of intercluster distance.

High intracluster distance indicated high degree of variability within that cluster offering scope for improvement by various selection methods. In this study, Cluster I containing 29 genotypes had the highest intracluster distance.

In general, intercluster distances were much higher than the intra cluster values, suggesting that there was homogeneity among the genotypes included in a cluster while heterogeneity existed between clusters.

5.2 EXPERIMENT II

5.2.1 Screening for Leaf Curl Virus Resistance

Among the 49 genotypes, T_{35} (Kayamkulam local 3) showed the lowest value of vulnerability index and was on par with T_{33} (Kayamkulam local 4), T_{11} (Karumkukku local), T_{15} (Thavanur local 3), T_{10} (Mangalapuram local) and T_{49} (Padi local) (Table 13). These genotypes were highly tolerant to leaf curl as indicated by the low value of vulnerability index. The genotypes T_{16} (Ambalavayal local 2), T_{23} (Mallassery local) and T_1 (Parasuvaikkal local) and T_{17} (Vamanapuram local) were the most susceptible ones to leaf curl as they recorded the highest values of vulnerability index.

The genotypes were classified into tolerant, susceptible and highly susceptible based on their vulnerability index values. Six genotypes *viz.*, T_{10} (Mangalapuram local), T_{11} (Karumukku local), T_{15} (Thavanur local 3), T_{33} (Kayamkulam local 4), T_{35} (Kayamkulam local 3) and T_{49} (Paadi local) showed high tolerance to the disease. They exhibited mild symptoms such as slightly curling of a few terminal leaves for some

plants. The susceptible class consisted of 14 genotypes with many of them showing curling of terminal and adjacent leaves and presence of blisters on leaves. Remaining 29 genotypes were included in the highly susceptible class. Many of them showed curling of terminal and adjacent leaves and presence of blisters on leaves. Two genotypes *viz.*, T_{16} (Ambalavayal local 2) and T_{23} (Mallassery local) were highly susceptible to the disease with severe curling of leaves and stunting of plants. In some cases, small clusters of leaves were produced due to the proliferation of axillary buds.

There was no genotype showing immunity to the disease. However, the genotypes included in the tolerant category could be considered as fairly resistant to the disease.

5.2.2 Comparison of Yield in Experiment I (with control measures) and Experiment II (without control measures)

Comparison of yield per plant of the two experiments revealed that yield reduction in tolerant genotypes was comparatively lesser than that in susceptible genotypes (Table 14).

The correlations between yield and vulnerability index of both experiments were worked out (Table 15). The high positive correlation between yield per plant in experiments I and II suggested that the high yielding genotypes produced good yields under controlled and uncontrolled conditions while the low yielding ones produced low yields under both situations. Vulnerability index also showed a similar trend as indicated by the high positive correlation. This led to the conclusion that there was an inherent genetic difference among the genotypes with respect to yield potential and reaction to leaf curl virus.

Vulnerability index was negatively correlated with yield per plant in both the experiments indicating that greater susceptibility to the disease leads to reduction in yield.

Based on the variability and screening studies, it was concluded that the superior genotypes with high yield *viz.*, Karumukku loal, Thavanur local 3, Meenachal I local and Thavanur local 1 can be used as parents in hybridization programme. Among these genotypes Karumukku local and Thavanur local 3 showed leaf curl virus tolerance also. Ranking based on selection index also showed that Karumukku local, Meenachil local and Thavanur local 1 were superior to others and hence they can be selected as parents in hybridization programme to evolve high yielding and disease tolerant varieties.

5.3 MOLECULAR CHARACTERISATION

Detection of polymorphism at DNA level is used for estimation of genetic diversity, similarity and/or characterizing cultivars. In the present study an attempt was made to determine the extent of relationship among the 49 genotypes of chilli using random primers.

Four promising primers identified through screening *viz.*, OPA-01, OPB-01, OPB-06 and OPB-10 were used for amplification of the genomic DNA. The genotypes were grouped into different clusters based on the similarity coefficient. There were two clusters at 0.29 similarity coefficient. The genotypes which were divided into different clusters as per Mahalanobis D^2 analysis were grouped into the same cluster in the dendrogram.

Summary

6. SUMMARY

The study entitled "Screening for leaf curl virus disease complex resistance, genetic evaluation and molecular characterisation of bird chilli (*Capsicum frutescens* L.)" was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram during 2003-2004 with the objective of estimating the genetic diversity including yield and resistance to leaf curl virus in a collection of 49 bird chilli genotypes. The data for the investigation were collected from two field experiments.

In experiment I, 49 genotypes of bird chilli, collected from various agro climatic zones of south India, were evaluated for yield and its component characters in Randomised Block Design with three replications. Observations were recorded on 16 characters *viz.*, days to first flowering, plant height, number of primary branches, number of secondary branches, plant spread, number of fruits per plant, individual fruit weight, fruit yield per plant, fruit length, pedicel : fruit ratio, fruit width, 100-seed weight, number of seeds per fruit, vulnerability index calculated on the basis of leaf curl virus disease scoring and two qualitative characters viz., leaf pubescence and fruit colour at intermediate stage.

The important findings of the present study are summarized below.

Significant differences among the genotypes for all the 16 characters studied indicated high variability among genotypes. Karumukku local was the highest yielder while the lowest yielders included Mulleria local followed by Ambalavayal local 1 and Edneer local. On the basis of number of fruits per plant, Kolanchery local was the highest producer followed by Meenachil local and Karumukku local. Mulleria local produced the least number of fruits.

The genotypic variance values were close to the phenotypic variances for almost all the characters, suggesting the predominance of genetic component over environmental effect.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) also showed a similar trend. A major portion of PCV was contributed by GCV especially for characters like days to first flowering, fruit length, fruit width and 100-seed weight suggesting that the observed variation was mainly due to the genetic factors and the environmental effect was less.

All the traits exhibited high heritability. Genetic advance as per cent of mean was found to be high for all the characters except days to first flowering, suggesting additive gene action for these traits.

Correlation analysis indicated that most of the character combinations had higher genotypic correlation coefficient than phenotypic, though both were in the same direction. Environmental correlation coefficients were the lowest. Yield per plant exhibited significant positive association with number of fruits per plant, individual fruit weight, fruit length, fruit width, 100-seed weight and number of seeds per fruit, while negative correlation with days to first flowering, pedicel : fruit ratio and vulnerability index.

Path coefficient analysis revealed that number of fruits per plant and individual fruit weight had high positive direct effect on yield. The negative direct effects were low. The low residual value (0.2926) indicated that the characters considered in path analysis could explain the major portion of the variation in yield.

Selection indices were constructed based on the 12 characters studied and the genotypes were ranked based on that. High yielding and superior genotypes like Meenachil local, Kolanchery local, Karumukku local, Thavanur local 1 and Irumbuzhi local had high selection indices,

while low yielding genotypes like Mulleria local, Edneer local and Paadi local were having low selection indices.

Genotypes were grouped into five clusters considering 12 characters, each cluster with varying number of genotypes. Cluster I with 29 genotypes was the largest one and clusters IV and V were the smallest with only one genotype each. Intercluster distance was maximum between clusters I and III while intracluster distance was maximum in Cluster I. The intercluster distances were much higher than the intracluster distances.

In the experiment II, the 49 genotypes were screened for leaf curl virus resistance in a field experiment in Randomised Block Design with three replications. Observations were taken on yield per plant and virus scoring (based on which vulnerability index was calculated).

Significant differences were observed among genotypes for yield and vulnerability index. Five genotypes were found to be tolerant to leaf curl virus while 14 genotypes were susceptible and the remaining 30 were highly susceptible to the disease.

Comparison of yield and vulnerability index in both the experiments showed that reduction in yield was less in tolerant varieties than in susceptible ones. The performance of Karumukku local, Thavanur local 3 and Meenachil local was comparable under controlled and uncontrolled conditions. Correlation analysis showed negative association of yield with vulnerability index in both the experiments indicating that susceptibility to the disease leads to a reduction in yield.

RAPD technique was used to characterize the genotypes at the molecular level. Decamer primers were screened for their efficiency using the DNA isolated from Varkala local (T_{24}) as the representative sample. Out of the 24 primers used for screening, 13 yielded amplification products. RAPD analysis of all the 49 samples was performed using the

random primers OPA-01, OPB-01, OPB-06 and OPB-10 and the genotypes were characterized using Jaccard's similarity coefficient analysis and dendrogram was constructed to cluster the genotypes. The high yielding genotypes were clustered into one group and the leaf curl virus tolerant genotypes into the other.

The superior genotypes identified in the study can be used to develop high yielding, leaf curl virus tolerant varieties of chilli through interspecific hybridization.

References

7. REFERENCES

Acharya, L., Sahu, G.S. and Mishra, R.S. 1992. Genetic variability in chilli. *Environ. Ecol.* 10 : 723-725

Acharyya, P. 2002. Screening of progenies of different cross combinations of *Capsicum* spp. against leaf curl incidence. *Environ. Ecol.* 20 : 576-571

Acharyya, P., Joshi, A.K. and Rajput, C.B.S. 2002. Studies on variability and character association for different traits in six generations of the cross 'LCA 301 x Punjab Lal' (*Capsicum annuum* L.) under two environments with respect to leaf curl complex. *Capsicum Eggplant Newsl.* 21: 60-63

Adamu, S.U. and Ado, S.G. 1988. Genotypic variability in fruit characteristics of pepper (*Capsicum* spp.). *Capsicum Newsl.* 7: 46

*Adetula, O.A. 2005. Genetic diversity in Capsicum germplasm lines using RAPD markers. *Plant and Animal Genomes XIII Conference, January 15-19*, Town and Country Convention Centre, San Diego

Ado, S.G., Samarawira, I. and Olarewaju, J.D. 1987. Evaluation of local accessions of pepper (*Capsicum annuum*) at Samaru, Nigeria. *Capsicum Newsl.* 6: 17-18

Ahmed, N., Nayeema, J. and Tanki, M.I. 1997. Character association in hot pepper (*Capsicum annuum* L.). *Capsicum Eggplant Newsl.* 16:68-71

Ahmed, N., Tanki, M.I. and Bhat, M.Y. 1990. Genetic variability in Kashmiri chilli (*Capsicum annuum* L.). *Veg. Sci.* 17 : 217-220

Ajith, P.M. 2004. Genetic analysis of yield and resistance to anthracnose in chilli(*Capsicum annuum* L.). Ph.D thesis, Kerala Agricultural University, Thrissur, 181 p.

Albejo, M.D. 1999. Screening of pepper cultivars for resistance to pepper leaf curl virus. *Capsicum Eggplant Newsl.* 18: 69-72

*Ali, S.A. 1994.Correlation of yield characters with yield in different chilli genotypes. *Bharatiya Krishi Anusandhan Patrika* 9: 81-83

Aliyu, L., Ahmed, M.K. and Magaji, M.D. 2000. Correlation and multiple regression analysis between morphological characters and components of yield in pepper (*Capsicum annuum* L.). *Crop Res.* 19: 318-323

Allard, R.W.1960.*Principles of Plant Breeding*. John Wiley and Sons, New York, 485p

Amin, P.W. 1979. Leaf curl disease of chilli pepper in Maharashtra, India. *PANS* 25: 131-134

Arora, S.K., Pandita, M.L., Pratap, P.S., Malik, Y.S., Mehra, R., Dhawan, P. and Gandhi, S.K. 1996. Hisar Vijay and Hisar Shakti – two new varieties of chilli. *Haryana agric. Univ. J. Res.* 26: 227-233

*Arya, P.S. and Saini,S.S.1976.Genetic variability and correlation studies in bell peppers. *Indian J.agric.Res.*10: 223-228

Arya, P.S. and Saini, S.S. 1977. Variability studies in pepper (*Capsicum* spp. L.) varieties. *Indian J. Hort.* 34 (4): 415-421

Ayyar, T.V.R., Subbiah, M.S. and Krishnamurthi, P.S. 1935. The leaf curl disease of chillies caused by thrips in the Guntur and Madras tracts. *Madras agric. J.* 23: 403-410

Bai, D.I.S., Chandramony, D. and Nayar, N.K. 1987. Genetic variability in red pepper. *Indian J. agric. Sci.* 57: 941-942

Bal, S.S., Singh, J. and Dhanju, K.C. 1995. Genetics of resistance to mosaic and leaf curl viruses in chilli (*Capsicum annuum* L.). *Indian J. Virol.* 11: 77-79

*Ballester, J. and Vincento, M.C. 1998. Determination of F_1 hybrid seed purity in pepper using PCR based markers. *Euphytica* 103: 223-226

*Baruah, S.J.N. and Baruah, M. 2004. Bird's eye chilli-a forex earner for North East. *Spice India* 17(4): 40-43

Bavaji, J. N. and Murthy, N. S. 1982. Selection indices for yield components in chilli (*Capsicum annuum* L.). *S. Indian Hort.* 30: 17-21

Berry, S.K. 2003. Chillies, hot, hotter, hottest. *Processed Fd. India* 6 (3) : 21-29

Bhagyalakshmi, P.V., Ravishankar, C., Subrahmanyan, D. and Babu, V.G. 1990. Study on heritability, genetic advance and character association in chilli (*Capsicum annuum* L.). *S. Indian Hort.* 38: 15-17

Bos, L. 1982. Crop losses caused by viruses. *Adv. Virus Res.* 2: 31-57

Bosland, P.W. 1994. Chillies: History, cultivation and uses. *Spices, Herbs and Edible Fungi* (ed. Charalambour, G.). Elsevier Publishers, New York, pp. 347-366

Bosland, P.W. 2000. Sources of curly top virus resistance in *Capsicum*. *Hort. Technol.* 35: 1321-1322

Brar, S.S., Rewal, H.S., Singh, D., Singh, H. and Hundal, J.S. 1989. Screening of indigenous germplasm of chilli against virus diseases in the south western region of Punjab. *Pl. Dis. Res.* 4: 180

Brown, J.K., Idris, A.M. and Fletcher, D.C. 1993. Sonaloa tomato leaf curl virus, a news described gemini virus of tomato and pepper in west coastal Mexico. *Pl. Dis.* 77: 1262

*Burton,G.W.1952 .Quantitative inheritance in grasses. *Proc. Int. Grassld. Congr.* 6:227-283

Chaim, A.B. and Paran, I. 2000. Genetic analysis of quantitative traits in pepper (*Capsicum annuum* L.). *J. Am. Soc. Hort. Sci.* 125: 66-70

*Chao, Y.W., Park, D.Y. and Suh, K.H. 1998. Pepper (*Capsicum annuum* L.) cultivar identification and seed purity test by random amplified polymorphic DNAs (RAPDs) and phosphoglucomutase isozyme. *RDA J. hort. Sci.* 40: 15-23 (Korean)

Chatterjee, R., Kohli, U.K. and Chatterjee, R. 2001. Correlation and path coefficient analysis in bell pepper (*Capsicum annuum* L.). *Hort. J.* 14: 51-55

Choudhary, M.L., Singh, R. and Mandal, G. 1985. Genetic studies in chilli (*Capsicum annuum* L.). *S. Indian Hort.* 33 (5): 302-306

*Chouvey, V.K., Choudhary, M.L. and Saha, B.C. 1986. Correlation and path analysis in chilli. *Bangladesh Hort.* 14: 9-13

*Dalmon, A. and Marchoux,G .2000. *Tomato yellow leaf curl virus host* plants. *Phytoma* 527: 14-17

Das, P.R., Maurya, K.R. and Saha, B.C. 1989. Genetic variability in chilli. *Res. Develop. Rep.* 6: 144-148

Das, S. and Choudhary, D.N. 1999a. Genetic variability in summer chilli (*Capsicum annuum* L.). *J. Appl. Biol.* 9 (1): 8-10

Das, S. and Choudhary, D.N. 1999b. Studies on correlation and path analysis in summer chilli (*Capsicum annuum* L.). *J. appl. Biol.* 9 (1): 5-7

*Depestre, T., Gomez, O. and Espinosa, J. 1989a. Components of variability and genetic advance in red pepper. *Ciencia y Tecnica en la Agricultura, Hortalizas, Papa, Granos y Fibras* 8: 91-95

*Depestre, T., Gomez, O. and Espinosa, J. 1989b. Study of correlation in red pepper progenies. *Ciencia y Tecnica en la Agricultura, Hortalizas, Papa, Granos y Fibras* 8: 67-71

Depestre, T., Gomez, O. and Espinosa, J. 1989c. Path coefficient analysis in sweet pepper. *Capsicum Newsl.* 19 : 37-39

Devi, D.S. and Arumugam, R. 1999. Genetics of yield components in F_1 generation of chillies (*Capsicum annuum* L.). *Crop Res.* 18: 112-114

Dewey, D.R. and Lu, K.H. 1959.A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518

Dhanraj, K.S. and Seth, M.L. 1968. Enations in *Capsicum annuum* L. germplasm by a new strain of leaf curl virus. *Indian J. Hort.* 25: 70-71

Dhanraj, K.S., Seth, M.L. and Bansal,H.C.1968.Reactions of certain chilli mutants and varieties to leaf curl virus. *Indian Phytopath.* 21:342-343

Dimova, D. and Panaystov, V. 1999. Path coefficient analysis of some quantitative fruit characters in different pepper cultivars. *Pl. Breed. Seed Sci.* 43: 15-19

Doshi, K.M. 2003. Genetic architecture of chilli (*Capsicum annuum* L.). *Capsicum Eggplant Newsl.* 22: 33-36

Dwivedi, N.K. and Bhandari, D.C. 1999. Collecting *Capsicum annuum* L. germplasm in Rajasthan, India. *Pl. Genet. Resour. Newsl.* 119: 56-58

Elangovan, M., Suthanthirapandian, I.R. and Sayed, S. 1981. Genetic variability in certain metric traits of *Capsicum annuum* L. *S. Indian Hort.* 29: 224-225

Fan, M.J., Wang, J.Y., Lo, S.F., Shu, T.R. and Engle, I.M. 2001. Analysis of the genetic diversity of *Capsicum* spp. (Pepper) using random amplified polymorphic DNA analysis. *J. agric. Res. China* 50: 29-42

Fernando, H.E. and Peiris, J.W.L. 1957. Investigations on the chilli leaf curl complex and its control. *Trop. Agric.* 113: 305-323

*Fisher, R.H. 1936. The use of multiple measurements in taxonomic problems. *Ann. Eugen.* 7: 179-188

Fugro, P.A. 2000. Role of organic pesticides and manures in management of some important chilli diseases. *J. Mycol. Pl. Path.* 30: 96-97

Gandhi, S.K., Maheswari, S.K. and Arora, S.K. 1995. Pepper lines resistant to leaf curl virus disease. *Pl. Dis. Res.* 10: 180-181

*Garcia, B.F., Salinas, G.G.E., Pozo, C.O., Reyes, V.H., Ramirez, M.N.. Lopez, S.J.A., Aguirre, B.M. and Salazar, S.O. 2002. Estimation of genetic distances among green pepper (*Capsicum annuum* L.) lines using RAPD markers and its relationship with heterosis. *Proc. Sixteenth int. Pepper Conf. – Tampico, 10-12 November 2002*, Tamaulipas, Mexico, pp. 1-4

Ghai, T.R. and Thakur, M.R. 1987. Variability and correlation studies in an intervarietal cross of chilli. *Punjab hort. J.* 27 (1-2): 80-83

Gill, H.S., Asawa, B.M., Thakur, P.C. and Thakur, T.C. 1977. Correlation, path coefficient and multiple regression analysis in sweet pepper. *Indian J. agric. Sci.* 47: 408-410

Gill, H.S., Thakur, P.C., Asawa, B.M. and Thakur, T.C. 1982. Diverstiy in sweet pepper. *Indian J. agric. Sci.* 52 : 159-162

Gogoi, D. and Gautam, B.P. 2002. Variability, heritability and genetic advance in chilli. *Agric. Sci. Digest* 22 : 102-104

*Gonzalez, G., Tsyplenkiv, A., Alonso, X., Rodriguez, D. and Font, C. 1993. Tomato yellow leaf curl virus (ToYLCV) in Cuba. *Revista-de-Proteccion-Vegatal* 8: 79-88

Gopalakrishnan, T.R., Gopalakrishnan, P.K. and Peter, K.V. 1987. Variability in a set of chilli lines. *Agric. Res. J. Kerala* 25 : 1-4

Gopalakrishnan, T.R., Nair, C.S.J., Joseph, S. and Peter, K.V. 1985. Studies on yield attributes in chilli. *Indian Cocoa Arecanut Spices J.* 8 : 72-73

Grube, R.C., Yiping, Z., Murphy, J.F., Loaiza-Figueoa, F., Lackney, V.K., Provvidenti, R. and Jain, M.K. 2000. New source of resistance to cucumber mosaic virus in *Capsicum frutescens*. *Plant Dis.* 84: 885-891

*Gupta, C.R. and Yadav, R.D.S. 1984. Genetic variability and path analysis in chilli (*Capsicum annuum* L.). *Genetica-Agraria* 38 : 425-432

*He, X.M., Wang, M., Marinkovic, N., Miladinovic, Z., Stevanovic, D., Gvozdenovic, D.J. and Jankulovski, D.1989. Correlation and path coefficient analysis of fruit characters in sweet pepper. *EUCARPIA VIIth Meeting on Genetics and Breeding on Capsicum and Eggplant, 27-30 June 1989.* Krazujevac, Yugoslavia, pp. 31-35

Hiremath, K.G. and Mathapati, S.N. 1977. Genetic variability and correlation studies in *Capsicum annuum* L. *Madras agric. J.* 64 : 170-173

Huang, S.W., Zhang, B.X., Guo, J.Z., Yang, G.M., Zhu, D.W., Du, M.Z. and Yang, J.E. 2001. Establishment of an efficient RAPD protocol in pepper and its application in genetic purity testing of F_1 seeds. *Acta Hort. Sinica* 28: 77-79

Ibrahim, M., Ganiger, V.M. and Yenjerappa, S.T. 2001. Genetic variability, heritability, genetic advance and correlation studies in chilli. *Karnataka J. agric. Sci.* 14: 784-787

*Ilbi, H. 2003. RAPD markers assisted varietal identification and genetic purity test in pepper, *Capsicum annuum*. *Scientia Hort.* 97: 211-218

Jabeen, N., Ahmad, N. and Tanaki, M.I. 1998. Genetic variability in hot pepper (*Capsicum annuum* L.). *Agric. Sci. Digest* (Karnal) 18 : 23-26

Jabeen, N., Ahmed, N. and Tanaki, M.I. 1999. Genetic variability in hot pepper (*Capsicum annuum* L.). *Appl. Biol. Res.* 1: 87-89

*Jaccard, P. 1908. Nouvelles researches sur la la distribution florale. *Bull. Soc. Vaudoise des Sci. Naturelles* 44: 223-270

Jadhav, M.G., Dhumal, S.A., Burli, A.V. and Moro, S.M. 2000. Phulesai (GCH-8) a new rainfed chilli variety. *J. Maharashtra agric. Univ.* 25: 110-112

Jain, J.P. 1982. *Statistical Techniques in Quantitative Genetics.* Tata McGraw Hill Co., New Delhi, 281 p.

Jayasankar, S., Irulappan, I. and Arumugam, R. 1987. Association analysis in the segregating generation of hot pepper. *S. Indian Hort.* 35 : 202-205

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955a. Estimation of genetic and environmental variability in soybean. *Agric. J.* 47: 314-318

Johnson, H.W., Robinson, H.F.and Comstock, R.E. 1955b. Genotypic and phenotypic correlations in soybean and their implications in selection.*Agron.J.* 47:477-483

Jose, L. 2001. Genetic variability in chilli (*Capsicum annuum* L.) with emphasis to reaction to leaf curl virus. M.Sc. (Ag.) thesis, Kerala Agricultural University, Thrissur, 118 p.

Jose, L. and Khader, K.M.A. 2002. Correlation and path coefficient analysis in chilli (*Capsicum annuum* L.). *Capsicum Eggplant Newsl.* 21: 56-59

Joshi, S. and Singh, B. 1983. Genotypic and phenotypic paths to fruit yield in sweet pepper (*Capsicum annuum* L.). *Prog. Hort.* 15 : 222-225

Kang, B.C., Kim, K.T., Kim, D.S. and Oh, D.G. 1997. Random amplified polymorphic DNA analysis of *Capsicum annuum*. *J. Korean Soc. hort. Sci.* 38: 39-42

Karad, S.R., Raikar, G.R. and Navale, P.A. 2002. Genetic divergence in chilli. *J. Maharashtra agric. Univ.* 27: 143-145

Kataria, G.J., Pandya, H.M. and Vaddoria, M.A. 1997. Genetic variability, heritability and genetic advance of various phylogenic traits in capsicum. *Gujarat agric. Univ. Res. J.* 22: 18-21

KAU. 2003. *Package of Practices Recommendations: Crops.* 12th edition. Kerala Agricultural University, Thrissur. 278p

Kaul, B.L. and Sharma, P.P. 1989. Correlation and path coefficient analysis studies in bell pepper (*C. annuum* L.). *S. Indian Hort.* 37 : 16-18

Khodawe, B.D. and Taley, Y.M. 1978. Note on the role of *Hemitarsonemus latus* Banks in chilli leaf curl. *Indian J. agric. Sci.* 48: 55-56

Khurana, D.S., Singh, P. and Hundal, J.S. 2003. Studies on genetic diversity for growth, yield and quality traits in chilli (*Capsicum annuum* L.). *Indian J. Hort.* 60: 277-282

Konai, M. and Nariani, T.K. 1980. Reaction of different chilli varieties and *Capsicum* spp. to mosaic and leaf curl viruses. *Indian Phytopah.* 33: 155

Korla, B.N. and Rastogi, K.B. 1977. A research note on path coefficient analysis in chilli. *Punjab Hort. J.* 17 (3-4): 155-156

Kumar, B.K., Munshi, A.D., Subodh, J., Charanjit, K., Joshi, S. and Kaur, C. 2003 .Correlation and path coefficient analysis for yield and biochemical characters in chilli. *Capsicum Eggplant Newsl.* 22: 67-70

Kumar, B.P., Sankar, C.R. and Subramanyan, D. 1993. Variability, heritability and genetic advance in the segregating generations of chilli (*Capsicum annuum* L.). *Capsicum Eggplant Newsl.* 20: 38-41

Kumar, R., Rai, N. and Lakpale, N. 1999. Field reaction of some chilli genotypes for leaf curl virus in Chhattisgarh region of India. *Orissa J. Hort.* 27: 100-102

Lanteri, S., Acquadro, A., Quagliotti, L. and Portis, E. 2003. RAPD and AFLP assessment of genetic variation in a landrace of pepper (*Capsicum annuum* L.) grown in North-West Italy. *Genet. Resour. Crop Evol.* 50: 723-735

Lefebvre, V., Goffinet, B., Chauvet, J.C., Caromel, B., Signoret, P., Brand, R. and Palloix, A. 2001. Evaluation of genetic distances between pepper inbred lines for cultivar protection purposes : comparison of AFLP, RAPD and phenotypic data. *Theo. appl. Genet.* 102: 741-750

*Legesse, G., Zelleke, A. and Bejiga, G. 1999. Character association and path analysis of yield and its components in hot pepper (*Capsicum annuum* L.). *Acta Agron. Hungarica* 47 : 391-396

Lim, S.H., Pen-Teg, P., Lee, Y. and Jin-Goh, C. 1999. RAPD analysis of some species in the genus *Vanda* (Orchidaceae). *Ann. Bot.* 83: 193-196

Lush, J.L. 1940. Intra-size correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. Am. Soc. Anim. Prod.* 33: 293-301

Ma, Y.Q., Liu, Z.M. and Zou, X.X. 2003. An RAPD analysis for pepper germplasm resources. *J. Hunan agric. Univ.* 29: 120-123

Mallapur, C.P. 2000. Screening of chilli genotypes against thrips and mites. *Insect Environ.* 5: 154-155

Memane, S.A., Joi, M.B. and Kale, P.N. 1987. Screening of chilli cultivars against leaf curl complex. *Curr. Res. Reptr.* 3: 98-99

Meshram, L.D. 1987. Studies on genetic variability and correlation in chilli. *PKV Res. J.* 11: 104-106

Miller, D.A., Williams, V.C., Robinson, H.P. and Comstock, R.E. 1958. Estimates of genotypic and environmental variances and covariances in upland cotton and their implication in selection. *Agron. J.* 5: 126-131

Mini, S. 2003. Genetic variability and characterisation in wax type chilli (*Capsicum annuum* L.). M.Sc. (Ag.) thesis, Kerala Agricultural University, Thrissur, 82 p.

*Miranda, J.E.C. de., Costa, C.P.da and Cruz, C.D. 1988. Genotypic, phenotypic and environmental correlations among fruit and plant traits in sweet pepper (*Capsicum annuum* L.). *Revista Brasileira de Genetica* 11 : 457-468

Mishra, A., Sahu, S.S. and Mishra, P.K. 2001. Variability in fruit characters of chilli. *Orissa J. Hort.* 29: 107-109

Mishra, M.D., Raychaudhuri, S.P. and Jha, A. 1963. Virus causing leaf curl of chilli (*Capsicum annuum* L.). *Indian J. Microbiol.* 3: 73-76

Mishra, Y.K., Ghildiyal, P.C., Solanki, S.S. and Joshi, R.P. 1998. Correlation and path coefficient analysis in sweet pepper (*Capsicum annuum* L.). *Recent Hort.* 4: 123-126

Munshi, A.D. and Behera, T.K. 2000. Genetic variability, heritability and genetic advance for some traits in chillies (*Capsicum annuum* L.). *Veg. Sci.* 27: 39-41

Munshi, A.D. and Sharma, R.K. 1996. Field screening of chilli germplasm against leaf curl complex. *Ann. Pl. Protec. Sci.* 4: 85-94

Munshi, A.D., Behera, T.K., Gyanendra, S.J. and Singh, G. 2000. Correlation and path coefficient analysis in chilli. *Indian Hort.* 57: 157-159

Muthuswamy, A. 2004. Genetic analysis of yield and leaf curling resistance in chilli (*Capsicum annuum* L.). Ph.D thesis, Kerala Agricultural University, Thrissur, 139 p.

Nair, M.C. and Menon, M.R. 1983. *Diseases of Crop Plants of Kerala.* Kerala Agricultural University, Thrissur, 251 p.

Nair, P.M., George, M.K., Mohanakumaran, N., Nair, V.G. and Saraswathy, P. 1984a. Studies on correlation and path analysis in *Capsicum annuum* L. *S. Indian Hort.* 32: 212-218

Nair, P.M., George, M.K. and Nair, V.G. 1984b. Estimation of variability and genetic parameters in chillies. *Indian Cocoa Arecanut Spices J.* 7 : 115-117

Naitam, N.R., Patangrao, D.A. and Deshmukh, S.D. 1990. Resistance responses of chilli cultivars to leaf curl. *PKV Res. J.* 14: 206-207

Nandadevi and Hosamani, R.M. 2003a. Variability, correlation and path analysis in Kharif grown chilli (*Capsicum annuum* L.) genotypes for different characters. *Capsicum Eggplant Newsl.* 22: 43-46

Nandadevi and Hosamani, R.M. 2003b. Estimation of heterosis, combining ability and *per se* performance in summer grown chilli (*Capsicum annuum* L.) for yield and resistance to leaf curl complex. *Capsicum Eggplant Newsl.* 22: 59-62

Nandi, A. 1993. Genetic variability in chilli (*Capsicum annuum* L.). *Indian Cocoa Arecanut Spices J.* 16:104-105

Nawalagatti, C.M., Chetti, M.B. and Hiremath, S.M. 1999. Biochemical basis of murda complex resistance in chilli (*Capsicum annuum* L.) genotypes. *S. Indian Hort.* 47: 310-312

Nene, Y.L. 1972. A survey of viral diseases of pulse crops in Uttar Pradesh. Final Technical Report. G.B.P.U.A.T., Pant Nagar, 191 p.

*Oliviera, V.R., Casali, V.W.D., Cruz, C.D., PeTeira, P.R.G. and Braccini, L.E. 1999. Genetic diversity in sweet pepper (*Capsicum annuum* L.). *Horticultura Brasileira* 17: 19-24

Pandian, R.S. and Sivasubramanian, V. 1978. Flowering and its relation to some yield components and earliness index in chillies. *Madras agric. J.* 65: 234-336

Panse, V.G. and Sukhatme, P.V. 1967. *Statistical Methods for Agricultural Workers.* Indian Council of Agricultural Research, New Delhi, 359 p.

*Paran, I., Aftergoot, E. and Shifriss, C. 1998. Variation in *Capsicum annuum* revealed by RAPD and RFLP markers. *Euphytica* 99: 167-173

Pawade, S.B., Sontake, M.B., Shinde, N.N. and Borikar, S.T. 1995. Studies on correlation and path analysis for some characters in local chilli (*Capsicum annuum* L.) types from Nagpur district. *PKV Res. J.* 19: 93-94

Peter, K.V. and Mac Collum, G.D. 1984. Pollen stigma compatibility in direct and reciprocal crosses of *Capsicum* species. *J. Hered.* 75: 70

Peter, K.V., Nybe, E.V. and Thanuja, T.V. 2004. *Future Prospects.* The Hindu Survey of Indian Agriculture, 184 p.

Philip, B.2004. Genetic improvement and molecular characterization of paprika (*Capsicum annuum* L.) genotypes. Ph.D thesis, Kerala Agricultural University, Thrissur, 150 p.

Pitchaimuthu, M. and Pappiah, C.M. 1992 .Studies on variability in chilli. *S. Indian Hort.*40: 109-110

Pitchaimuthu, M. and Pappiah, C.M. 1995. Heritability studies in chilli. *J. Maharashtra agric. Univ.* 20: 348-350

*Prince, J.P., Lackney, V.K., Angeles, C., Blauth, J.R. and Kyle, M.M. 1995. A survey of DNA polymorphism within the genus capsicum and the fingerprinting of pepper cultivars. *Genome* 38: 224-231

Prince, J.P., Loaiza, F.F. and Tanksley, S.D. 1992. Restriction fragment length polymorphism and genetic distance among Mexican accessions of capsicum. *Genome* 35: 725-732

Rajamony, L., More, T.a., Seshadri, V.S. and Varuna, A.1990.Reaction of muskmelon collections to cucumber green mottle mosaic virus. *Phytopathology* 29: 239-224

Rajput, J.C., Palve, S.B. and Patil, B.P. 1991. Varietal evaluation of red chillies for yield and quality in Konkan region of Maharashtra. *Indian Cocoa Arecanut Spices J.* 14: 107-108

Ramalingam, R.S. and Murugarajendran, C. 1977. Genotypic and phenotypic variability in quantitative characters in *Capsicum annuum* L. *Madras agric. J.* 64: 675-676

Ramkumar, P.V., Sriramachandramurthy, N. and Durgaprasad, M.M.K. 1981. Genetic variability, correlation and discriminant function in chilli. *Indian J. agric. Sci.* 51: 723-725

Rani, P.U. 1995. Correlation and regression studies in chilli (*Capsicum annuum* L.). *S. Indian Hort.* 43: 14-17

Rani, P.U. 1996. Fruit seed weight and seed number and their relationship with other characters in chilli. *Madras agric. J.* 83: 259-264

Rani, P.U. 1997. Association of morphological and quality parameters with fruit yield and their relationship in chilli (*Capsicum annuum* L.). *Karnataka J. agric. Sci.* 10: 78-85

Rani, P.U. and Singh, D.P. 1996. Variability, heritability and genetic advance in chilli (*Capsicum annuum* L.). *J. Res. ANGRAU* 24: 1-8

Rani, P.U.and Usha, R.P. 1996. Studies on fruit weight and its related characters in chilli (*Capsicum annuum* L.). *Int. J. trop. Agric.* 14: 123-130

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research.* John Wiley and Sons, New York, 390 p.

Rao, P.V. and Chhonkar, V.S. 1981. Correlation and path coefficient analysis in chilli. *Indian J. agric. Sci.* 51: 857-860

Rao, V.V.R., Jaisvani, B.G. and Asawa, B.M. 1981. Factor analysis in chilli. *Indian J. agric. Sci.* 51: 225-228

Rathod, R.P., Deshmukh, D.T., Ghode, P.B. and George, V.S. 2002b. Correlation and path analysis studies in chilli (*Capsicum annuum* L.). *Haryana J. Hort.Sci.*31: 141-143

Rathod, R.P., Deshmukh, D.T., Sable, N.H. and Rathod, N.G. 2002a. Genetic variability studies in chilli (*Capsicum annuum* L.). *J. Soils Crops* 12: 210-212

Ray, S. and Sarkar, P.K. 2001. A histopathological study of viral leaf curl syndrome in chilli. *J. Interacad.* 5 (1): 71-73

Reddy, B.S., Thammaiah, N., Nandihali, B.S., Dharmatti, P.R. and Patil, R.V. 2000. Performance of chilli genotypes under Ghataprabha command area of northern part of Karnataka. *J. Maharashtra agric. Univ.* 25: 73-74

Reina, J., Morilla, G. and Bejarano, E.R. 1999. First report of *Capsicum annuum* plants infected by tomato leaf curl virus. *Pl. Dis.* 83: 1176

Rishi, N. and Dhawan, P.1988.Field reaction of chilli germplasm to different viral diseases. *Pl. Dis. Res.*3: 69-70

Robinson, H.F., Comstock, R.E. and Harvey, P.H. 1949. Estimates of heritability and degree of dominance in corn. *Agron. J.* 14: 352-359

Rodriguez, J.M., Berke, T., Engle, L. and Nienhuis, J. 1999. Variation among and within capsicum species revealed by RAPD markers. *Theo. appl. Genet.* 99: 147-156

Rogowsky, I.M., Mamning, S., Lin, J.Y. and Langridy, P. 1991. Small scale isolation of total DNA from cereals. *Genome* 34: 88-95

Sahoo, S. C., Mishra, S. N. and Mishra, R. S. 1990. Genetic variation in F_2 generation of red pepper (*Capsicum annuum* L.). *Indian J. agric. Sci.* 60: 834–835

Sahoo, S.C. Mishra, S.N. and Mishra, R.S. 1989. Variability in F_2 generation in a diallel cross of chilli. *S. Indian Hort.* 37 (6): 348-349

Samretwanich, K., Cheimsombat, P., Kittipakorn, K. and Ikegami, M. 2000. A new gemini virus associated with a yellow leaf curl disease of pepper in Thailand. *Pl. Dis.* 84: 1047

Sangar, R.B.S., Katwale, T.R., Saraf, R.K. and Parihar, M.S. 1988. Field screening of chilli varieties to viral diseases in Madhya Pradesh. *Farm Sci. J.* 3: 69-71

Sarma, R.N. and Roy, A. 1995. Variation and character association in chilli (*Capsicum annuum* L.). *Ann. agric. Res.* 16 (2): 179-183

Senapati, B.K., Sahu, P.K. and Sarkar, G. 2003. Genetic divergence in chilli. *Crop Res.* 26: 314-317

Shah, A., Lal, S.D. and Pant, C.C. 1986. Variability studies in chilli. *Prog. Hort.* 18: 270-272

*Silbernagel, M.J. and Jafri, A.M. 1974. Temperature effects on curly top resistance in *Phaseolus vulgaris*. *Phytopathology* 64: 825-827

Singh, A. and Singh, H.N. 1976a. Genetic divergence in chilli. *Indian J. Genet.* 36: 425-430

Singh, A. and Singh, H.N.1976b. Studies on selection indices in chilli. *Indian J. agric.* Res.10: 179-184

Singh, A. and Singh, H.N. 1977a. Note on heritability, genetic advance and minimum number of genes in chilli. *Indian J. agric. Sci.* 47: 260-262

Singh, A. and Singh, H.N. 1977b. Discriminany function in chilli (*Capsicum annuum* L.). *Madras agric. J.* 64:777-779

Singh, A.K. and Singh, A. 1998. Genetic studies of phylogenic traits in chilli (*Capsicum annuum* L.). *Crop Res.* (Hisar) 15 (1): 61-62

Singh, G.P., Maurya, K.R., Prasad, B. and Sinha, A.K. 1994. Genetic variability in *Capsicum annuum* L. *J. Appl. Biol.* 4: 19-22

Singh, J. 1993. Improvement of chillies. *Vegetable Crops* (eds. Chadha, K.L. and Kalloo, G.). Malhotra Publishing House, New Delhi, pp. 69-86

*Singh, J. and Kaur, S. 1986. Present status of hot pepper breeding for multiple disease resistance in Punjab. *Sixth Meeting on Genetics and Breeding on Capsicum and Eggplant*. Zaragoza, Spain, Servicio de Invertigation Agaria, pp. 111-114

Singh, P. and Narayanan, S.S.1993. *Biochemical Techniques in Plant Breeding*. Kalyani Publishers, New Delhi, 187 p.

Singh, S.J. 1973. Reaction of chilli varieties (*Capsicum* sp.) to mosaic and leaf curl virus under field conditions. *Indian J. Hort.* 30: 444-447

Singh, S.J., Sastry, K.S. and Sastry, K.S.M. 1979. Combining leaf curl virus in chilli. *Indian Hort.* 24: 9

Singh, U.C., Singh, R. and Nagaich, K.N. 1998. Reaction of some promising chilli varieties against major insect pests and leaf curl disease. *Indian J. Ent.* 60: 181-183

*Sitthiwong, K., Matsui, T. and Sukprakarn, S. 2005. Classification of pepper (*C. annuum* L.) accessions by RAPD analysis. *Biotechnology* 4: 305-309

Sivanathan, P. 1982. Epidemiology of chilli leaf curl disease in Sri Lanka. *Trop. Agricst* 138: 99-109

Smith, F.H. 1937. A discriminant function for plant selection. *Ann. Eugen.* 7: 240-250

Solanki, S.S., Saxena, P.K. and Pandey, I.C. 1986. Genotypic and phenotypic paths to fruit yield in chilli (*Capsicum annuum* L.). *Prog. Hort.* 18 (3-4): 227-229

Sreelathakumari, I. and Rajamony, L. 2002. Variability, heritability and correlation studies in chilli (*Capsicum* spp.) under shade. *Indian J. Hort.* 59 (1): 77-83

Subashri, S. and Natarajan, S. 1999. Studies on association of characters in F_2 generation of chilli (*Capsicum annuum* L.). *S. Indian Hort.* 47: 218-219

Sundaram, A. and Ranganathan, C.R. 1978. Path analysis in chilli (*Capsicum annuum* L.). *Madras agric. J.* 65: 401-403

Sundaram, A., Ranganathan, C.R. and Ramalingam, R.S. 1979. Selection criteria in chilli (*Capsicum annuum* L.). *Madras agric. J.* 66 (3): 177-179

*Tae, J.Y. and Hyo, G.P. 1998. Optimisation of random amplified polymorphic DNA analysis procedure for *Capsicum annuum* L. *Korean J. Breed.* 30 (2): 204-211

*Tavares, M., Melo, A.M.de and Suvittaro, W.B. 1999. Direct and indirect effects and canonical correlations of agronomic traits on sweet pepper yield. *Bragautia* 58 (1): 41-47

Tewari, V.P. 1977. Jwala boosts chilli yields. *Indian Fmg.* 27.(7): 21

Tewari, V.P. 1983. Work on breeding of chillies. Indian Agricultural Research Institute, *Indian Cocoa Arecanut Spices J.* 7: 6-7

Tewari, V.P. 1991. A multipurpose perennial chilli Pusa Sadabahar. *Indian Hort.* 35: 29-31

Tewari, V.P. and Anand, G.P.S. 1977. Incorporation of virus resistance in improved chillies. *Madras agric. J.* 64: 822-823

Tewari, V.P. and Viswanath, S.M. 1986. Breeding for multiple virus resistance in red pepper (*Capsicum annuum* L.). *Capsicum Newsl.* 5: 49

*Tewari, V.P. and Viswanath, S.M. 1988. Note on breeding for resistance in chillies-today and tomorrow. *New Botanist* 15 (2-3): 185-186

Todovora, V.Y., Pevicharova, G.T. and Todorov, Y.K. 2003. Correlation studies for quantitative characters in red pepper cultivars for grinding (*Capsicum annuum* L.). *Capsicum Eggplant Newsl.* 22: 63-66

*Vallejo, C.F.A., Ceballos, L.H. and Agudelo, A.E. 1997. Genetic analysis of a diallelic population of sweet pepper (*Capsicum annuum* L.). *Acta Agron.* 47: 25-36

Varalakshmi, B. and Haribabu, K. 1991. Genetic divergence, heritability and genetic advance in chilli (*Capsicum annuum* L.). *Indian J. Genet.* 51 (2): 174-178

*Veerappa, D.B. 1982. Studies on relative performance of different genotypes of sweet pepper (*Capsicum annuum* L. var. grossum Sendt). *Thesis Abstr.* 8: 381-382

Verma, S.K., Pant, K.C. and Muneem, K.C. 1998. Evaluation of chilli germplasm. *Indian J. Pl. Genet. Resour.* 11 (2): 237-239

Vijayalakshmi, Y., Rao, M. R., Reddy, E. N. and Murthy, N.S.R.C. 1989. Genetic variability in some quantitative characters of chilli. *Indian Cocoa Areacanut Spices J.* 12 (3): 84-86

Votava, E.J. and Bosland, P.W. 2001. Genetics diversity of *Capsicum pubescens* revealed via RAPD analysis. *Capsicum Eggplant Newsl.* 20: 60-63

Wang, J.J. and Fan, M.J. 1998. Comparison on microsatellite DNA and random amplified polymorphic DNA markers for germplasm identification of *Capsicum annuum*. *J. agric. Res. China* 47: 267-282

Wang, J.J., Fan, M.J. and Lo, S.F. 1997. Genetic diversity within capsicum evaluated by random amplified polymorphic DNA (RAPD) markers. *J. agric. Res. China* 46: 314-328

Wang, J.Y., Fan, M.J., Lo, S.F. and Liu, S.Y. 1996. Study on the molecular markers of capsicum wild / domesticated species using random amplified polymorphic DNA analysis. *J. agric. Res. China* 45: 370-381

Warade, S.D., Dhumal, M.M. and Shinde, K.G. 1996. Correlation studies in chilli. *J. Maharashtra agric. Univ.* 21: 55-57

Williams, J.G., Kubelik, A.R., Livak, K.J., Rafalski, J.A. and Tingey, S.V. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. *Nucleic Acid Res.* 18: 6531-6535

Wright, S. 1954. The interpretation of multivariate systems. *Statistics and Mathematics in Biology* (eds. Kempthorne, O., Bancroft, T.A., Gowen, J.W. and Lush, J.L.). State University Press, Iowa, pp. 11-13

*Wyrzykowska, M., Pazytula, M., Zieminska, J. and Pala, J. 2000. Quantitative traits and their correlation in sweet paprika (*Capsicum frutescens*) Kambi introduced into the pod larie region of Poland. VO golnopolskie Sympozjum "Genetyka ilosciowa roslin uprawnych". Ladek Zdroj, Polsha, 24-26 Maja 1999. *Bull. Inst. Hodowli Aklim. Roslin* 216 (2): 463-468 (Polish)

---

*Original not seen

SCREENING FOR LEAF CURL VIRUS DISEASE COMPLEX RESISTANCE, GENETIC EVALUATION AND MOLECULAR CHARACTERIZATION OF BIRD CHILLI (*Capsicum frutescens* L.)

NICEY MATHEW

Abstract of the
Thesis submitted in partial fulfilment of the requirement
for the degree of

Master of Science in Agriculture

Faculty of Agriculture
Kerela Agricultural University, Thrissur

2006

Department of Plant Breeding and genetics
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM - 695 522

ABSTRACT

The investigation entitled "Screening for leaf curl virus disease complex resistance, genetic evaluation and molecular characterisation of bird chilli (*C. frutescens* L.)" was conducted at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, Thiruvananthapuram during 2003-2005. The data for the investigation were collected from two field experiments, each laid out in Randomized Block Design with three replications. The second experiment was conducted without taking any control measures against leaf curl virus disease.

The 49 genotypes included in the study showed significant difference for all the 14 biometric characters. They all showed high heritability coupled with high genetic advance except days to first flowering for which the genetic advance was moderate. The maximum values for phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for fruit yield per plant and individual fruit weight respectively and the minimum values for days to first flowering.

Fruit yield per plant was positively correlated with number of fruit per plant, number of secondary branches, plant spread, 100-seed weight, number of primary branches, number of seeds per fruit, individual fruit weight, fruit length, fruit width and plant height. Path analysis revealed high positive direct effect of individual fruit weight and number of fruits per plant on yield per plant. Hence selection for these characters can improve the yield.

The 49 genotypes were grouped into five clusters based on Mahalanobis D^2 statistic. Cluster I was the largest with 29 genotypes while clusters IV and V had only one genotype each. Clusters II and III

had 11 and eight genotypes respectively. Cluster I was found to be superior to the other clusters with respect to the desirable characters.

The genotypes were ranked based on the selection indices. High yielding and superior genotypes had high selection indices while low yielding genotypes were having low selection indices.

Field screening of 49 genotypes for leaf curl virus resistance (experiment II) showed that five genotypes were highly tolerant to the disease while 14 genotypes were susceptible and 30 were highly susceptible.

Comparison of yield and vulnerability index in both the experiments showed that reduction in yield was less in tolerant varieties than in susceptible varieties. The yield performance of Karumukku local, Thavanur local 3 and Meenachil local were comparable under controlled and uncontrolled conditions.

Correlation analysis showed negative association of yield with vulnerability index in both experiments indicating that susceptibility to the disease leads to reduction in yield.

The high yielding and leaf curl tolerant types identified from the study can be used as parents in crop improvement programme to evolve high yielding, leaf curl tolerant varieties.

RAPD analysis was performed using the random primers OPA-01, OPB-01, OPB-06 and OPB-10 and the 49 genotypes were characterized using Jaccard's similarity coefficient analysis and a dendrogram was constructed to cluster the genotypes. The high yielding genotypes T_1 (Karumukku local) and T_{15} (Thavanur local 3) came in the same cluster (cluster II) while the leaf curl virus tolerant genotypes T_{35} (Kayamkulam local 3) and T_{33} (Kayamkulam local 4) came in the other cluster (Cluster I).