INCORPORATION OF TWO MAIN SOURCES OF RESISTANCE TO BACTERIAL WILT IN F_1 GENERATION OF TOMATO *Lycopersicon lycopersicum* (L) KARST

By

I. SREE LATHA KUMARY

THESIS

Submitted in partial fulfilment of
the requirement for the degree of

Master of Science in Horticulture

Faculty of Agriculture
Kerala Agricultural University

Department of Horticulture (Olericulture)
COLLEGE OF HORTICULTURE
Vellanikkara, - Trichur
KERALA - INDIA

1983

DECLARATION

I hereby declare that the thesis entitled "Incorporation of two main sources of resistance to bacterial wilt in F_1 generation of tomato Lycopersicon lycopersicum (L) Karst" is a bonafide record of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associationship, fellowship or other similar title of any other University or Society.

Sreelatha
26/12/83

Vellanikkara,
26th, December, 1983.

I. SREELATHAKUMARY

CERTIFICATE

Certified that the thesis entitled "Incorporation of two main sources of resistance to bacterial wilt in F_1 generation of tomato Lycopersicon lycopersicum (L) Karst" is a record of research work done independently by Miss I. Sreelathakumary under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associationship to her.

P.K. Gopalakrishnan,
Chairman,
Advisory Committee

Vellanikkara,
26th, December, 1983.

Associate Dean,
College of Horticulture.

CERTIFICATE

We, the undersigned members of the Advisory Committee of Miss I. Sreelathakumary a candidate for the degree of Master of Science in Horticulture agree that the thesis entitled "Incorporation of two main sources of resistance to bacterial wilt in F_1 generation of tomato Lycopersicon lycopersicum (L) Karst" may be submitted by Miss I. Sreelathakumary in partial fulfilment of the requirement for the degree.

P.K. Gopalakrishnan,
Chairman.

K.V. Peter,
Member. 13/6/84

Abi Cheeran,
Member. 13/6/84

N. Ramachandran Nair,
Member.

ACKNOWLEDGEMENT

I wish to express my profound sense of gratitude and indebtedness to Dr. P.K. Gopalakrishnan, Associate Dean, College of Horticulture, Vellanikkara and Chairman of my Advisory Committee for his able guidance, critical suggestions and constant help throughout the investigation and in the preparation of manuscript.

I am greatly indebted to Dr. K.V. Peter, Professor and Head of the Department of Olericulture for his valuable advice, keen interest, constructive criticisms and for the proper guidance rendered for the preparation of manuscript.

I consider it as my privilege to express my heartfelt thanks and indebtedness to Dr. Abi Cheeran, Professor, Department of Plant Pathology and Sri. N. Ramachandran Nair, Associate Professor, Department of Agricultural Botany for their help during the study and for critically going through the manuscript.

I am also thankful to Sri. P.V. Prabhakaran and Sri. V.K.G. Unnithan, Associate Professors, Department of Agricultural Statistics for their help in the

statistical analysis.

Sincere thanks are due to the members of staff of Department of Olericulture for the help rendered by them at all stages of the present investigation.

I acknowledge all my friends for their most sincere cooperation and help rendered during the period of investigation.

I also acknowledge the Kerala Agricultural University for granting me the Junior Fellowship and National Bureau of Plant Genetic Resource, Rome for providing the photograph.

Sreelatha
26/12/83

I. SREELATHAKUMARY

CONTENTS

LIST OF TABLES

LIST OF FIGURE

Introduction

INTRODUCTION

Bacterial wilt, caused by Pseudomonas solanacearum (E.F. Smith), is the most serious disease of tomato (Lycopersicon lycopersicum (L) Karst) in Kerala. Conventional plant protection methods, are found ineffective to control the disease. Resistance breeding is then the obvious method, which would make possible the cultivation of tomato in the problematic tropical acidic soils. Two sources of resistance to bacterial wilt have been reported - one from North Cardina type of resistance and other derived from Lycopersicon pimpinellifolium (PI 127805A). Attempts to incorporate the above two sources of resistance in single variety(s) would be a worthwhile effort to develop multigenically resistant plant types with broad spectrum genetic base. The F_1 hybrids involving the above two sources of resistance and further their progenies, if developed, could give transgressive segregants with combined wilt resistance and wider adaptability.

Genetic cataloguing is a key and vital step taken a priori to any disease resistance breeding programme. Genetic cataloguing would identify

line(s) based on distinct morphological and mendelian characters. Information on linkage/pleiotropism existing between wilt resistance and morphological characters could act as aids in plant selections.

The present study was formulated with the following objectives.

1. To catalogue and document tomato lines, reported resistant to bacterial wilt.
2. To develop F_1 hybrids involving the two sources of resistance, Lycopersicon pimpinellifolium (PI 127805A) as male and Lycopersicon esculentum lines as female.
3. To evaluate the interspecific F_1 hybrids for heterosis and resistance to wilt.
4. To evaluate parental lines, F_1S and F_2 hybrids under field conditions to find out inheritance of combined wilt resistance.

Review of Literature

REVIEW OF LITERATURE

A. Genetic cataloguing

Genetic cataloguing is done *a priori* to any effective resistance breeding programme. It helps to evaluate plants for sources of resistance and identify marker character(s) linked with disease resistance. Information on genes, their reference and seed source in tomato were provided in the Reports of the Tomato Genetics Cooperative (1980).

B. Sources of resistance to bacterial wilt

Bacterial wilt, caused by *Pseudomonas solanacearum* is the most serious disease of tomato in many tropical, subtropical and warm temperate regions of the world. Breeding bacterial wilt resistant tomatoes by crossing wild tomato strains and commercial varieties was started at North Carolina Agricultural Experiment Station as early as in 1944 (Weaver, 1944). Crosses between Louisiana Pink and a *Lycopersicon esculentum* line, T 414 were considered to be promising sources of resistance to bacterial wilt. Aberdeen (1946) tested a number of tomato varieties for resistance to bacterial wilt in Australia and found that strains derived from Louisiana Pink were resistant in Queensland also.

Annual Report of the School of Agriculture, North Carolina State College (1950-51) contained reports on lines with good field resistance to bacterial wilt, but only a few bore fruits of marketable size. Testing in green house indicated higher susceptibility of young plants than old ones. Abeygunawardena and Siriwardena (1963) tested 49 tomato varieties and hybrids for resistance to bacterial wilt. The North Carolina lines 1960-8, 1960-2a, 1962-B2 and 1961-57-55M and varieties Masterglobe and Rahangala selection II were the most resistant. The Los Banos strain reported resistant in Phillippines was observed susceptible in Sri Lanka. This was the first indication of the presence of different races in Pseudomonas solanacearum. Acosta et al. (1964) observed bacterial wilt resistance in Lycopersicon pimpinellifolium (PI 127805A). Morton et al. (1966) conducted a study to find out the serological relationships of races 1, 2 and 3 of Pseudomonas solanacearum. They indicated races 2 and 3 were more closely related to each other than either was to race 1. The crosses involving the popular varieties of USA, Manalucie and Floradel with a resistant stock from North Carolina resulted in the evolution of a few

lines resistant to Pseudomonas solanacearum (University of Florida, 1967). The presence of certain plant parasitic nematode species in the soil could affect the susceptibility of tomato varieties to Pseudomonas solanacearum. Temiz (1968) reported susceptibility of bacterial wilt resistant varieties in the presence of nematodes. The local line 2 ASS was observed tolerant to Pseudomonas solanacearum (Serere Research Station, 1970-71). Henderson and Jenkins (1972) reported bacterial wilt resistance in Venus and Saturn, which had been derived from crosses among Louisiana Pink, Beltsville 3814, Pan America, Rutgers, Marglobe, STEP 174 and Manalucie at different levels. Akiba et al. (1972) reported high levels of resistance in three tomato introductions 65 S2, 66 S52 and 68 S4 from U.S.A. Daly (1973) confirmed resistance to bacterial wilt in Saturn, Venus and in local lines III IRAT and OTB2. In a screening programme involving 247 cultivars, two additional sources of resistance to Pseudomonas solanacearum, accessions 1737 and 1937 were isolated after being clip-inoculated in the seedling stage (AVRDC Tomato Report, 1975). New and Ho (1976) screened 43 varieties and lines and found that VC-8-1-2-1 was resistant regardless of inoculum density.

Sunarjono et al. (1976) screened tomato varieties and isolated the AVRDC resistant lines 15, 22 and 33. On the basis of pathogenicity 10 isolates of race 1 of Pseudomonas solanacearum were identified by Rath and Addy (1977). Sonoda and Augustine (1977) isolated Hawaian selection 7997 as resistant out of 72 tomato lines screened against bacterial wilt. Sonoda (1977) further evaluated 121 cultivars and lines of tomatoes in three tests in a field naturally infested with Pseudomonas solanacearum and observed resistance in Venus and Saturn. Graham et al. (1977) reported the resistance in VC-4. The line VC 48-1 was observed resistant to bacterial wilt in Taiwan (AVRDC, 1978). Of the 25 lines reported as being resistant, only the lines L 3972, L 3987 and CL 8d-0-7-1 were moderately resistant in Nigeria (IITA, 1978). Villareal and Lal (1978) inoculated three bacterial wilt resistant tomato varieties and their F_1S with a virulent isolate (group 12, isolate 2) and a weak isolate (group 16, isolate 17) of Pseudomonas solanacearum. They observed higher level of resistance in F_1S than in the cultivars. Eight AVRDC advanced breeding lines and 109 newly collected accessions were evaluated for resistance to bacterial wilt. Only two advanced breeding

lines (CL 1094-0-0-5-7-0 and CL 123-2-4) and four accessions (L1, L 4678, L 4681 and L 4712) had survival rates above 80% (AVRDC, 1979). Sunarjona (1980) reported the breeding lines AVRDC 33 and AVRDC 15 were resistant to Pseudomonas solanacearum. Hawaii 7996 was resistant to bacterial wilt under lowland conditions. Sonoda et al. (1980) reported strong and stable sources of resistance to Pseudomonas solanacearum in Hawaii 7997, CRA 66 and PI 126408. Ramachandran et al. (1980) evaluated 36 tomato varieties for sources of resistance to bacterial wilt under the warm humid tropical conditions of Kerala. They observed resistance in La Bonita and CL 32d-0-1-19 GS. Celine (1981) reported field tolerance to bacterial wilt in CL 32d-0-1-19 GS. Goth et al. (1983) used eight isolates of Pseudomonas solanacearum (race 1-K 60, A21, TFP 12, TFP 13, 126408-1 and Tifton 80-1; race 3- W82; race unknown - FF) collected from diverse locations to study the bacterial wilt resistance of selected tomato lines and cultivars. They reported that the line CL 32d-0-1-19 GS from AVRDC, Taiwan which was later named as LE 79 at Kerala Agricultural University, Vellanikkara, Trichur was resistant to three isolates K 60, 126408-1 and

Tifton 80-1 of race 1. The cultivar Venus was observed resistant to the isolate 126408-1 of race 1. Goth et al. (1983) reported effect of root knot nematode in bacterial wilt of tomato. They observed that bacterial wilt resistance in LE 79 was broken down when root knot nematode Meloidogyne incognita larvae were added (100/10 cm pot) at the time of inoculation with bacterial isolates. They suggested that Meloidogyne incognita should also be considered as a factor in the development of bacterial wilt resistant tomato germplasm.

C. Genetics of resistance

Two primary sources of resistance to bacterial wilt were reported (Russell, 1978). The first being North Carolina type of resistance, expressed by derivatives of Louisiana Pink was inherited as a recessive character and controlled by polygenes (Singh, 1961). Graham and Yap (1976) conducted a variance component analysis of parents, F_1S, F_2S, BC_1S and BC_2S of a cross between a resistant line VC_4 and a susceptible line Walter. Wilt resistance showed a narrow sense heritability of 42%, broad sense heritability of 53% and a degree of

dominance of 75%. The polygenic resistance in tomato was observed modified by changes in temperature (Mew and Ho, 1977). Another factor which determined the disease resistance was inoculum density. Villareal and Lal (1978) also supported the hypothesis of additive gene action for the inheritance of disease resistance.

A second type of resistance was reported in Lycopersicon pimpinellifolium (PI 127805A) by many workers (Acosta et al., 1964; Mohanakumaran et al., 1969 and Roddick, 1974). Acosta et al. (1964) observed that the resistance derived from Lycopersicon pimpinellifolium was partially dominant in the seedling stage. In mature plants, resistance was controlled by recessive gene.

D. Information on linkage

Acosta (1964) reported a possible linkage between Sp^{+} the gene for indeterminate plant habit and bacterial wilt resistance. Acosta et al. (1964) observed no association between the gene 'U' controlling immature fruit colour and resistance to bacterial wilt. A few resistant selections had a yellow gel round the seeds of ripening fruits, but none of the resistant selections had fruits of

commercial size. Investigations on resistance to Pseudomonas solanacearum indicated close linkage between recessive genes for resistance and genes for poor fruit characteristics (University of West Indies, 1968-69). Celine (1981) reported yellow gel around the seeds of resistant line LE 79 (CL 32d-0-1-19 GS).

E. Biochemical basis of resistance

Mohanakumaran et al. (1968) reported higher content of steroidal glycoalkaloid α-tomatin in resistant parents and hybrids. After inoculation a greater increase in tomatin content was observed in resistant varieties. Roddick (1974) also reported higher levels of α-tomatin in roots of Lycopersicon pimpinellifolium cultivars, resistant to Pseudomonas solanacearum than in susceptible cultivars.

F. Variability studies

Success of any crop improvement programme depends largely on the genetic variability of the crop. Srivastava and Sachan (1973) reported that the genotypic, phenotypic and environmental coefficients of variation were the highest for fruits/bunch and

the lowest for peduncle length in tomato varieties they studied. Heritability in broad sense was the highest (88.25%) for total soluble solids. Heritability and expected genetic advance were reported to be high (74.19% and 43.35 respectively) for fruit weight. Singh et al. (1973) recorded high heritability associated with high genetic variability for plant height, locules/fruit, fruit width, days to flower and yield/plant which are mainly due to additive gene effects. Parthasarathy et al. (1976) observed wide range of variability for all the characters they studied in tomato. They observed high heritability for all characters except stem girth (28.9%) and the highest value was recorded for fruit size (97.69%). Expected genetic advance was low for yield (1.17) and primary branches/plant (4.02) while it was maximum for average fruit weight (124.33). The genetic gain was found to be quite high for yield (129.50), fruit size (131.56) and average fruit weight (175.31). Prasad and Prasad (1977) reported that the genotypic and phenotypic coefficients of variation were high for plant height, leaves/plant, primary branches/plant and fruits/plant. Heritability was more than 50% for all characters they studied.

Nandapuri et al. (1977) observed that fruits/plant was the most variable character. Heritability estimates were high for plant height, days to maturity, fruit size and yield/plant. Fruit size, fruits/plant and yield had the higher values of expected genetic advance indicating considerable scope for selection.

H. Heterosis as a function of genetic distance

Genetic distance existing between parental lines in a hybrid has frequently been related to the expression of heterosis in different crop plants. Genetic divergence study in tomato by Peter and Rai (1976) revealed that genetic and geographic divergence were not related. Genetic divergence was mostly expressed by characters such as locules/fruit and plant height. Khanna and Mishra (1977) studied 50 varieties of tomato to estimate the taxonomic distance among them using the Mahalanobis D^2 statistic. The varieties were grouped into ten clusters on the basis of intracluster and intercluster distances with respect to plant height, fruits/plant, branches/plant, locules/fruit, days to first flower, total soluble solids and fruit yield. Total soluble solids,

locules/fruit and fruits/plant were found to be the major determinants of D^2 value. Higher heterotic values were observed in intercluster hybrids than in intracluster hybrids particularly for yield. Rajanna et al. (1977) reported a quadratic relationship between the extent of heterozygote advantage and genetic divergence. They suggested that selection of parents for hybridization on the basis of plant height, locules/fruit, and nodes to first inflorescence would lead to the selection of genetically divergent materials. Peter and Rai (1978) could not work out an optimum genetic distance between parents for maximum exploitation of heterosis in tomato.

H. Interspecific heterosis

Intervarietal heterosis for total yield/plant, average fruit weight, fruits/plant, days to first fruit set, days to first harvest and plant height were reported by many workers (Kolhe, 1970; Mittal et al., 1974 and Virdelwala et al., 1981). Saakjan (1967) and Choudhary and Khanna (1972) reported heterosis for fruit size. Heterosis for yield/plant was observed by Kolhe (1970) and

Choudhary and Khanna (1972). Heterosis for fruits/plant were observed by Saakjan (1967) and Shevelen (1977). Avdeev (1974) reported negative heterosis for maturity. Mittal et al. (1974) examined 14 hybrids involving seven selected lines and two male parents to investigate the extent of heterosis in various crosses. Pronounced heterosis was observed in many F_1 hybrids for early yield than for total yield. Fruits/plant and fruit weight were observed to be the main component characters of yield. Heterosis over better and the best check for yield were observed in pear-shaped tomato by Sidhu et al. (1981). Virdelwala et al. (1981) observed heterosis for total yield/plant, average fruit weight, fruits/plant, days to first set and maturity. But no hybrid showed significant heterosis over better parents. Reports on interspecific heterosis are rather limited in tomato.

Materials and Methods

MATERIALS AND METHODS

The experiments were conducted at the Instructional Farm of the College of Horticulture, Kerala Agricultural University, Trichur, during August-December, 1982, January-May, 1983 and July-October, 1983. The farm is located at an altitude of 22.25 m and at 10°32" N latitude and 76°11" E longitude. The soil of the experimental site is deep, well drained and moderately acidic with a pH of 5.1. The area enjoys a typical warm humid tropical climate. The soil is highly infested with the bacteria Pseudomonas solanacearum resulting heavy cfop damage in solanaceous vegetables.

A. Materials

The materials for the study comprised of lines derived from the two reported sources of resistance to bacterial wilt. The first being North Carolina type of resistance, expressed by ten derivatives of Louisiana Pink, included LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212, LE 213, LE 214 and LE 217 (Table 3.1). A few of the above lines were reported resistant to bacterial wilt in diverse geographical areas. The second type of resistance

has been derived from the Eulycopersicon species Lycopersicon pimpinellifolium (PI 127805A) and is accessed as LE 218.

B. Experimental Methods

1. Cataloguing

a. Seedling characters

The eleven parental lines were sown in raised beds during August, 1982 and the seedlings were observed for qualitative characters as given in the Report of the Tomato Genetics Cooperative, May, 1980 (Table 3.2). The seedlings were further classified into five distinct groups based on the spread and intensity of purple pigmentation.

i. Completely free of anthocyanin
ii. Upper part of the hypocotyl free of anthocyanin
iii. Full hypocotyl region with anthocyanin
iv. Hypocotyl and epicotyl with anthocyanin, and
v. Hypocotyl, epicotyl, cotyledens and first leaves with anthocyanin

Seedlings were again grouped based on phyllotaxy as suggested by Bible (1976).

b. Juvenile and adult plant characters

The seedlings were transplanted and observed for juvenile and adult plant characters as suggested in

the Report of the Tomato Genetics Cooperative, May, 1980 (Tables 3.3 and 3.4).

2. Development of F_1 hybrids

F_1 hybrids were developed through hand emasculation and pollination using Lycopersicon pimpinellifolium (PI 127805A) as male line and Caroline type of resistance as female lines. The 10 hybrids thus developed were catalogued as per the Report of Tomato Genetics Cooperative, May, 1980 and also grouped based on phyllotaxy and spread and intensity of purple pigmentation.

3. Evaluation of F_1 hybrids for heterosis and resistance to bacterial wilt

The 11 parental lines and 10 F_1 hybrids derived formed the materials for this experiment. They were grown during January-May 1983 in a randomised block design with three replications. The parental lines and F_1S were randomised separately within each block. The susceptible line Pusa Ruby was grown all around the field to check for the incidence of wilt. LE 79 was used as resistant standard check. There were 20 plants/line/replication both in parents and F_1S. The spacing given was 75 x 45 cm. The trial was conducted in the field where the previous crop was

tomato and the field was known for disease susceptibility and inoculum potential.

4. Evaluation for combined wilt resistance

Evaluation for resistance to bacterial wilt was done by taking observations on number of plants wilted at 15 days interval. The occurrence of bacterial wilt was confirmed through ooze test in each of the wilted plants. The disease rating was done as per the scale suggested by Sitaramaiah, et al. (1981) - 1 = Immune (0% plants wilted); 2 = Highly resistant (1 to 10% plants wilted); 3 = Moderately resistant (11 to 50% plants wilted); 4 = Moderately susceptible (51 to 70% plants wilted) and 5 = Highly susceptible (71 to 100% plants wilted).

5. Statistical analysis

Five disease free plants were randomly selected in each line and hybrid and observations were recorded on days to first flower, days to first harvest, plant height, branches/plant, locules/fruit, fruits/plant, average fruit weight and fruit yield. Observations were also made on the incidence of root knot nematode after uprooting plants and recorded as low (≤25 nodules/plant), medium (>25≤50 nodules/plant)

and high (>50 nodules/plant). Data on different quantitative characters were subjected to statistical analysis. The analysis of variance technique suggested by Fisher (1954) was employed and useful genetic parameters were estimated. Different components of variation were derived using the following analytical format.

Sources of variation	df	Mean squares	
		observed	expected
Total	rv - 1	TMS	σ^2_t
Replications	r - 1	RMS	$\sigma^2_e+r\sigma^2_g+rv\sigma^2_b$
Genotypes	v - 1	GMS	$\sigma^2_e+r\sigma^2_g$
Error	(r-1) (v-1)	EMS	σ^2_e

where σ^2_e = Environmental variance

σ^2_g = Genotypic variance

σ^2_b = Block variance

a. Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation were calculated by the formula suggested by Burton (1952).

Phenotypic coefficient of variation (pcv) = $\frac{\sigma p \times 100}{\bar{x}}$

where σp = Phenotypic standard deviation

$\bar{x}$ = Mean of the character under study

Genotypic coefficient of variation (gcv) = $\frac{\sigma g \times 100}{\bar{x}}$

where σg = Genotypic standard deviation

$\bar{x}$ = Mean of the character under study

b. Heritability

Heritability in broad sense (h^2b) was estimated by the formulae suggested by Allard (1960).

$$h^2b = \frac{\sigma^2 g}{\sigma^2 p}$$

where $\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

c. Expected genetic advance at 5% intensity of selection was calculated by the formulae suggested by Allard (1960).

Genetic Advance (R) = $i.h^2.\sigma p$

where i = 2.06 at 5% intensity of selection

h^2 = Heritability

σp = Phenotypic standard deviation

d. Genetic gain = $\frac{R}{\bar{x}} \times 100$ (Johnson *et al.*, 1955)

where R = Expected genetic advance

$\bar{x}$ = Mean of the character under study

e. Analysis of genetic divergence through metroglyph method

Anderson (1957) proposed this method to study the pattern of morphological variation in parents and hybrids. In the present study 11 genotypes were analysed in a replicated trial and from the data mean tables were prepared. Two most variable characters viz., fruit weight and plant height were selected. Fruit weight was taken along the x - axis and plant height on the y - axis. The means of y - values were plotted against the means of x-values for each genotype. A particular genotype was thus represented by a glyph on the graph.

The other characters viz., locules/fruit and disease score were represented by rays on the glyph, the rays for same character having the same position on each glyph. The range of variation in each character was represented by different length of rays ie., a genotype having low values for the character will have a small ray. Thus the length of the ray is either short, medium or long depending on the magnitude of values.

f. Estimation of genetic distance among 11 lines

The genetic distance was calculated considering

the following characters.

x_1. Days to first fruit set

x_2. Plant height

x_3. Fruit weight

x_4. Locules/fruit

The method suggested by Mahalanobis (1928) was used to estimate the total D^2 between the lines with x_1, x_2, x_3 and x_4 as the multiple measurements available on each line and d_1, d_2, d_3 and d_4 as $x_1^{-1} - x_1^{-11}$, $x_1^{-2} - x_1^{-11}$, $x_1^{-3} - x_1^{-11}$, ... $x_4^{-9} - x_4^{-11}$, $x_4^{-10} - x_4^{-11}$ respectively being the differences in the means of above 11 lines. Mahalonobis D^2 statistic is defined as:

$$D^2 = b_1d_1 + b_1d_2 + b_3d_3 + b_4d_4$$

Here the b_i values were estimated such that ratio of variance between populations to variance within populations was maximised. In terms of variances and covariances the $D^2 = wij\ (x_1^{-1} - x_1^{-2})\ (x_j^{-1} - x_j^{-2})$, where wij is the inverse of estimated variance covariance matrix.

From the data variances and covariances were calculated using linear model. From these estimates a dispersion table was prepared. Using '$\wedge$' statistic which in turn utilized wilk's criteria, a simultaneous test of differences between mean values of a number of correlated variables was done (Rao, 1948).

$$\wedge = \frac{/W/}{/S/} = \frac{/\text{Determinant of error matrix}/}{/\text{Determinant of error + variety matrix}/}$$

Significance of $\wedge$ was tested using chisquare test with appropriate degrees of freedom. Since the variables were highly correlated, they were transformed using pivotal condensation method. The parental lines were grouped into different clusters using Tocher Method (Singh and Choudhary, 1979).

g. The general combining ability effect of male parent LE 218 was estimated as the average performance of the line in hybrid combinations.

h. Heterosis

The interspecific F_1 hybrid vigour was estimated using the formulae (Hayes et al., 1956 and

Briggle, 1963).

$$\text{Heterobeltiosis} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

$$\text{Relative heterosis} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

$$\text{Standard heterosis} = \frac{\overline{F}_1 - \text{Mean of check variety}}{\text{Mean of check variety}} \times 100$$

where $\overline{F}_1$ = Mean performance of F_1

$\overline{BP}$ = Mean performance of Better Parent

$\overline{MP}$ = Mean performance of Mid Parent

Significance of heterosis was tested using students 't' test with $n_1 + n_2 - 2$ degrees of freedom.

$$t = \frac{/ hi /}{SE(hi)}$$

where hi = heterosis using i^{th} method

Standard errors of the heterosis were calculated by the formulae:

Standard error of Heterobeltiosis

$$SE = \sqrt{\frac{\sigma^2 F_1}{n_1} + \frac{\sigma^2 BP}{n_2}}$$

where $\sigma^2 F_1$ = F_1 variance

$\sigma^2 BP$ = Better parental variance

n_1 = Number of F_1 plants

n_2 = Number of better parental plants

Standard error of relative heterosis is

$$SE = \sqrt{\frac{\sigma^2 F_1}{n_1} + \frac{1}{4}\left[\frac{(\sigma^2 p_1}{n_2} + \frac{\sigma^2 p_2)}{n_3}\right]}$$

where $\sigma^2 p_1$ = Maternal parental variance

$\sigma^2 p_2$ = Paternal parental variance

n_1 = Number of F_1 plants

n_2 = Number of maternal plants

n_3 = Number of paternal plants

Standard error of standard heterosis is

$$SE = \sqrt{\frac{\sigma^2 F_1}{n_1} + \frac{\sigma^2 S_p}{n_2}}$$

where $\sigma^2 F_1$ = F_1 variance

$\sigma^2 S_p$ = Standard parental variance

n_1 = Number of F_1 plants

n_2 = Number of standard parental plants

6. Inheritance of combined wilt resistance

Parental lines, F_1S and F_2S were grown during June-October 1983 to study inheritance of combined bacterial wilt resistance. There were 10 plants each in parental lines, 10 to 20 plants in F_1S and 25 to 75 plants in F_2S. Observations were recorded from each and every plant and data were analysed as suggested by Panse and Sukhatme (1978).

Table 3.1. The source, name and pedigree of lines under evaluation

Accession number	Name	Pedigree	Source
Lycopersicon esculentum			
LE 206	CL-9-0-0-1-30-4	VC-11-1-2-1B/Saturn	AVRDC Taiwan
LE 207	CL-123-2-4-1	ah-Tm-20/VC-8-1-2-1	"
LE 208	CL-143-0-10-3-1-2	VC-48-1-/Tamu chico III	"
LE 209	CL-1104-0-0-71-4-2	VC-9-1 Ug/Saturn/ah Tm-2a/ VC 11-1Ug	"
LE 210	CL-1131-00-38-40	VC 48-1/Tamu chico III/ah Tm-2a/VC-11-1-ug	"
LE 211	CL-1351-1-6	Carorich/VC 11-1-ug/VC 11-1 ug BC_2 /// (ah-Tm-2a/VC-8-1-2-1)-4-4-0	"
LE 212	CL-1351-1-9	Carorich/VC 11-1-ug/VC-11-1-ug BC_2 (ah-Tm-2a/VC-8-1-2-98/ VC 9-1-2-98)	"
LE 213	CL-1219-0-6-2	71-483N/VC 9-1-2-9B//VC 9-1-2-9 B///VC9-1-2-9 B	"

Contd.....

Table 3.1. contd.....

Accession number	Name	Pedigree	Source
Lycopersicon esculentum			
LE 214	CL-948-0-20-2	KL 1/VC-11-3-4//1339/ Ottawa 66 (F_3)	AVRDC Taiwan
LE 217	Louisiana Pink	E.C 143572 (PI 270196)	"
LE 79	CL-32d-0-1-19GS	VC 9-1-2-3/Venus	"
LE 5	Pusa Ruby	Improved Meeruti/Sioux	IARI, New Delhi
Lycopersicon pimpinellifolium			
LE 218	PI 127805A	E.C. 143573	University of California, USA

Table 3.2. Gene list of seedling characters

Gene	Name	Phenotype	Locus	
			Chromosome	Site
a	anthocyaninless	Completely anthocyaninless	IIL	68
aw_2	without anthocyanin^2	Completely free of anthocyanin		
atv	atroviolacea	Intense anthocyanin pigmentation	7L	
dkv	dark veined leaf	Seedling leaves yellow green, veins, always darker green		
Fw	Furrowed	Plant stunted, cotyledons deeply furrowed		
hp-2		High pigment	IIL	95
lg	light green	Light green foliage colour	IOS	18
lg_2	light green$_2$	Cotyledons light yellow leaves pale green		
lg_3	light green$_3$	Cotyledons and leaves light green, cotyledons fade to yellow, mature plants pale green		
pg_2	pale green$_2$			
pg_3	pale green$_3$			
v	virescent	White seedlings turning to green		

L = Long arm of chromosome

S = Short arm of chromosome

Table 3.3. Gene list of Juvenile characters

Gene	Name	Phenotype	Locus	
			Chromosome	Site
acu	accumbens	Leaves and pinnae shortly stalked, leaf surface furrowed, older leaves strongly bend downwards		
aer	aerial roots	Adventitious roots on the stem from soil level to considerable height above		
al	anthocyanin loser	Pigmented only at nodes later	8L	67
are	anthocyanin reduced	Young leaves of older plants pigmented	2L	58
au	aurea	Bright yellow foliage	1S	32
aud	auroid	Uniform yellow foliage	12S	
bi	bifurkate	Extreme stem fasciation	12L	97
bip	bipinnate	Highly divided leaves	2L	68
br	brachytic	Internodes shortened	1S	0
c	potato leaf	Fewer leaf segments	6L	104
clau	clausa	Leaves subdivided, segment tip acute	4S	0
cpt	compact	Habit compact, exceedingly branched	8L	16
dp	drooping leaf	Leaf drooping, elongate, dark green stem weak, slender and prostrate		
e	entire	Leaf segments few, mid vein distorted	4L	66

Contd.....

Table 3.3. contd.....

Gene	Name	Phenotype	Locus	
			Chromosome	Site
fy	field yellow	Bright yellow green foliage in the field		
h	hair absent	Large trichomes absent	10L	46
Hr	hirsute	Long hairs on adaxial leaf surface	8L	46
Hrt	hirtum	Increased density of larger trichomes	7L	
lg	light green	Light green foliage colour	10S	18
ni	nitida	Leaves long petioled, pinnae deeply cut	8L	45
od	odourless	Herbage with little or no volatiles	3	
pg_2	pale $green_2$			
pg_3	pale $green_3$			
sf	solanifolia	Pinnae entire, epiculate, concave	3L	111
tp	tripinnate	Plant retarded, leaves tripinnately compound	8L	22
vi	villous	Stem very hairy	10	
wd	wilty dwarf	Plants stunted, leaves grey green droop if drought stressed	9S	20
wt	wilty	Leaf margins curl adaxially	SL	55
wo	wooly	All parts densely pubescent	2L	46
yg_2	yellow-$green_2$	Foliage uniformly yellow green	12S	

Table 3.4. Gene list of Adult plant characters

Gene	Name	Phenotype	Locus	
			Chromosome	Site
ap	apetalous	Most or part of corolla lacking	11	114
at	apricot	Fruit flesh colour	5	-
bk	beaked	Fruit stylar end pointed	2L	38
bl	blind	Stem terminate in first inflorescence	11L	75
bs	brown seeds	Endosperm brown	1S	17
bu	bushy	Inflorescences and internodes fore-shortened	8L	18
ch	chartreuse	Corolla greenish yellow	8L	28
ck	corky fruit	Fruit wall splits	—	—
cl-2	cleistogamous-2	Flowers open only slightly	6L	113
el	elongated fruits	—	—	—
ex	exserted	—	—	—
f	fasciated	Fruits fasciated, many loculed	11L	95
f^D	fasciated	—	—	—
fl	fleshy calyx	—	—	—
Fs	fruit stripe	Broad distal stripe as in Lycopersicon hirsutum	10S	11
g	grooved	—	—	—
gf	green fruit	Chlorophyll persists in the fruit locules	8L	44
gs	green stripe	Unripe fruit with radial green stripes	7S	5
hp	high pigment	Fruit pigments intensified	12S	—
Ip	intense pigmentation	Dark pigmentation of the fruit both in ripe and unripe stages.	—	—

Contd.....

Table 3.4. contd.....

Gene	Name	Phenotype	Locus	
			Chromosome	Site
j	jointless	Pedicel jointless, inflorescence leafy	11S	28
lu	luteola	Corolla light green	—	—
mc	macrocalyx	Sepals and inflorescence leafy	5S	—
n	nipple tip	At stylar end of the fruit	5	—
nor	non ripening	Fruit ripening greately retarded	10S	—
Nr	Never ripe	Fruit ripen slowly to dull orange	9	—
o	ovate	Fruits elongate	2L	55
p	peach	Fruit surface dull, more hairy	2L	67
pst	persistent style	Developing into beak	7S	5
pat	parthenocarpic fruits	Seedless fruits	—	—
rl	radial	Cracking resistance of fruits	—	—
r_2	yellow fruit,flesh,	lighter yellow flowers	—	—
rin	ripening inhibitor	Fruits ripen very slowly to yellow	5S	0
s	compound cluster	Inflorescence strongly proliferated	2L	30
sp	self pruning	Determinate habit	6L	—
spf	superpuff	Extremely puffy, hollow locules and bell pepper shaped fruits	—	—
ss	spong seed	Smooth, but spongy seed	—	—
u	uniform ripening	Unripe fruits lack bicolour pigmentation	10S	14
ye	yellow calyx when fruit ripens		—	—

Results

RESULTS

Data collected in the present study were statistically analysed and are presented under the following heads.

1. Genetic cataloguing
2. Evaluation for resistance to bacterial wilt
3. Inheritance of combined wilt resistance
4. Somatic analysis of parents and hybrids
5. Estimation of genetic divergence
6. Estimation of interspecific heterosis

1. Genetic cataloguing

Eleven parental lines and ten F_1 hybrids of tomato were genetically catalogued in seedling stage (Table 4.1a), juvenile stage (Table 4.1b) and adult plant stage (Table 4.1c) during August, 1982 and January, 1983. The main distinguishing feature among lines in the seedling stage was the stem and petiole colour and also the absence/presence of stem hairs. Lycopersicon pimpinellifolium (LE 218) could be easily distinguished from Lycopersicon esculentum (LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212, LE 213, LE 214 and LE 217) in the seedling stage for its narrow leaves, smooth thin and slender stem. The distinct character of

Lycopersicon esculentum was its plant texture. All the F_1 hybrids had a few hairs on the stem. Genetic cataloguing in the juvenile stage indicated that all the lines and hybrids had normal leaves except the line LE 210 in which potato leaf (cc) was noticed. The 11 tomato lines were indeterminate ($S_p^{\pm}$) in their growth habit. The seeds were observed covered by a yellow gel in all the lines. The line LE 210 was nipple tipped (nn) and ovate fruited (OO) with persistant style (pst pst). The twenty-one genotypes were normal fruited ($f^{\pm}$) non-grooved ($g^{\pm}$) with jointed pedicel ($j^{\pm}$) and uniform ripening (uu).

In the seedling stage, they were critically studied for intensity and spread of anthocyanin pigmentation, which varied greatly. Based on this character, seedlings were grouped into five classes (Table 4.1d). The lines LE 207 and LE 210 were observed completely free of anthocyanin (aa). All other lines and hybrids had intense anthocyanin pigmentation. The seedlings were further observed for arrangement of leaves-Phyllotaxy (Table 4.1e). Only one line LE 212 had right phyllotaxy, while all others had left phyllotaxy.

Table 4.1a. Genetic cataloguing of tomato lines and F_1 hybrids in seedling stage

LE 206	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $lg\frac{2}{3}-$, $pg\frac{3}{3}-$, pg^+_2-, v^+-
LE 207	aa, aw^2aw^2, atv^+-, dkv^+-, fw^+-, $hp\text{-}2^+-$, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 208	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 209	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 210	aa, aw^2aw^2, atv^+-, dkv^+-, fw^+-, $hp\text{-}2^+-$, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 211	a^+-, aw^{2+}, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 212	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 213	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 214	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 217	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 206 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 207 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 208 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 209 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 210 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 211 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 212 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 213 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 214 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-
LE 217 x LE 218	a^+-, $aw^{2+}-$, atvatv, dkv^+-, fw^+-, hp-2 hp-2, lg^+-, $lg\frac{2}{2}-$, $lg\frac{3}{3}-$, $pg\frac{2}{2}-$, $pg\frac{3}{3}-$, v^+-

Table 4.1b. contd.....

LE 213 x LE 218	acu^{+}-, aeraer, al^{+}-, areare, au^{+}-, aud^{+}-, bi^{+}-, bipbip, br^{+}-, c^{+}-, clausclaus, cpt^{+}-, dp^{+}-, e^{+}-, fy^{+}-, hh, Hr^{+}-, Hrt^{+}-, lg^{+}-, ni^{+}-, od^{+}-, pg$\frac{1}{2}$-, pg$\frac{1}{3}$-, sf^{+}-, tp^{+}-, vi^{+}-, wd^{+}-, wt^{+}-, wo^{+}-, yg$\frac{1}{2}$
LE 214 x LE 218	acu^{+}-, aeraer, al^{+}-, areare, au^{+}-, aud^{+}-, bi^{+}-, bipbip, br^{+}-, c^{+}-, clausclaus, cpt^{+}-, dp^{+}-, e^{+}-, fy^{+}-, hh, Hr^{+}-, Hrt^{+}-, lg^{+}-, ni^{+}-, od^{+}-, pg^{+}-, pg^{+}-, sf^{+}-, tp^{+}-, vi^{+}-, wd^{+}-, wt^{+}-, wo^{+}-, yg$\frac{1}{2}$
LE 217 x LE 218	acu^{+}-, aeraer, al^{+}-, areare, au^{+}-, aud^{+}-, bi^{+}-, bipbip, br^{+}-, c^{+}-, clausclaus, cpt^{+}-, dp^{+}-, e^{+}-, fy^{+}-, hh, Hr^{+}-, Hrt^{+}-, lg^{+}-, ni^{+}-, od^{+}-, pg$\frac{1}{2}$-, pg$\frac{1}{3}$-, sf^{+}-, tp^{+}-, vi^{+}-, wd^{+}-, wt^{+}-, wo^{+}-, yg$\frac{1}{2}$

Table 4.1c contd.....

LE 210 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, ip^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r2–, rin^{+}–, s^{+}–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}
LE 211 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, lp^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r^{+}–, rin^{+}–, s2–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}
LE 212 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, lp^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r2–, rin^{+}–, s^{+}–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}
LE 213 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, lp^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r2–, rin^{+}–, s^{+}–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}
LE 214 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, lp^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r2–, rin^{+}–, sl^{+}–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}
LE 217 x LE 218	ap^{+}–, at^{+}–, bk^{+}–, bl^{+}–, bs^{+}–, bu^{+}–, ch^{+}–, ck^{+}–, cl-2^{+}–, el^{+}–, ex^{+}–, f^{+}–, f^{D+}–, fl^{+}–, fs^{+}–, g^{+}–, gf^{+}–, gs^{+}–, hp^{+}–, lp^{+}–, j^{+}–, lu^{+}–, mc^{+}–, n^{+}–, nor^{+}–, Nr^{+}–, o^{+}–, p^{+}–, pst^{+}–, pat^{+}–, rl^{+}–, r2–, rin^{+}–, s^{+}–, sp^{+}–, spf^{+}–, ss^{+}–, u^{+}–, ye^{+}

Table 4.1d. Classification of tomato lines and hybrids based on intensity and spread of anthocyanin pigment in seedling stage

Classes*				
1	2	3	4	5
LE 207	LE 208	LE 206		
LE 210	LE 217	LE 209		
		LE 211		
	LE 207 x LE 218	LE 212	LE 208 x LE 218	
		LE 213		
		LE 214		
		LE 218		
		LE 206 x LE 218		
		LE 209 x LE 218		
		LE 210 x LE 218		
		LE 211 x LE 218		
		LE 212 x LE 218		
		LE 213 x LE 218		
		LE 214 x LE 218		
		LE 217 x LE 218		

* 1. Seedlings completely free of anthocyanin
  2. Seedlings where upper part of the hypocotyl region free of anthocyanin
  3. Seedlings where full hypocotyl region has anthocyanin
  4. Seedlings where hypocotyl and epicotyl region have anthocyanin
  5. Seedlings where hypocotyl, epicotyl, cotyledons and first leaf have anthocyanin

Table 4.1e. Classification of tomato lines and hybrids based on phyllotaxy

Left	Right
LE 206	LE 212
LE 207	
LE 208	
LE 209	
LE 210	
LE 211	
LE 213	
LE 214	
LE 217	
LE 218	
LE 206 x LE 218	
LE 207 x LE 218	
LE 208 x LE 218	
LE 209 x LE 218	
LE 210 x LE 218	
LE 211 x LE 218	
LE 212 x LE 218	
LE 213 x LE 218	
LE 214 x LE 218	
LE 217 x LE 218	

2. Evaluation for resistance to bacterial wilt

Eleven parental lines and ten F_1 hybrids were further evaluated under field conditions to test disease reaction (Table 4.1). There was 100% disease incidence in the susceptible check Pusa Ruby confirming presence of high bacterial inoculum in the test field. Lines found to be highly resistant were LE 214 (score = 2) and LE 217 (score = 2). The highly susceptible line was LE 218 (score = 5). Moderate resistance (score = 3) was observed in remaining parental lines LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212 and LE 213 and in a few F_1S LE 206 x LE 218, LE 207 x LE 218, LE 214 x LE 218 and LE 217 x LE 218. No line was observed immune to bacterial wilt.

Parental lines and F_1 hybrids were further evaluated for resistance to nematode by counting root nodules/plant at the end of cropping season (120 days after transplanting) (Table 4.3). The line LE 207 had the minimum nodules/plant (14). The Lycopersicon pimpinellifolium (LE 218) had 19 nodules/plant. The interspecific F_1 hybrid (LE 207 x LE 218) had only 16 nodules/plant. More than 50 nodules/plant were observed in lines

Table 4.2. Evaluation of tomato lines and hybrids for resistance/susceptibility to bacterial wilt

Genotypes	No. of plants	Juvenile stage		Adult stage		Total	Score*
		plants wilted	% of plants wilted	plants wilted	% of plants wilted		
LE 206	60	8	13.28	10	16.6	29.88	3
LE 207	60	3	4.98	12	19.92	24.90	3
LE 208	60	10	16.6	19	31.54	48.14	3
LE 209	60	4	6.64	16	26.56	33.20	3
LE 210	60	5	8.30	13	21.58	29.88	3
LE 211	60	5	8.30	17	28.22	36.52	3
LE 212	60	3	4.98	6	9.96	14.94	3
LE 213	60	3	4.98	6	9.96	14.94	3
LE 214	60	2	3.32	4	6.64	9.96	2
Louisiana pink (LE 217)	60	1	1.66	0	0	1.66	2
LE 218	60	18	29.88	25	41.60	71.48	5
Pusa Ruby	300	193	64.33	107	35.67	100.00	5
Crosses							
LE 206 x LE 218	60	7	11.62	15	24.90	36.52	3
LE 207 x LE 218	60	12	19.92	18	29.88	49.80	3
LE 208 x LE 218	60	8	13.28	25	41.50	54.78	4
LE 209 x LE 218	60	17	28.22	16	26.56	54.78	4

Contd.....

Table 4.2. contd.....

Genotypes	No. of plants	Juvenile stage		Adult stage		Total	Score*
		plants wilted	% of plants wilted	plants wilted	% of plants wilted		
LE 210 x LE 218	60	18	29.88	15	24.90	54.78	4
LE 211 x LE 218	60	17	28.22	16	26.56	54.78	4
LE 212 x LE 218	60	14	23.24	19	31.54	54.78	4
LE 213 x LE 218	60	11	18.26	22	36.52	54.78	4
LE 214 x LE 218	60	10	16.6	16	26.56	43.16	3
Louisiana pink x LE 218	60	13	21.58	6	9.96	31.54	3

* 1. Immune 0% wilt
2. Highly resistant 1 - 10% wilt
3. Moderately resistant 11 - 50% wilt
4. Moderately susceptible 51 - 70% wilt
5. Highly susceptible 71 - 100% wilt

Table 4.3. Evaluation of parental lines and F_1 hybrids for intensity of nematode induced root nodules

Intensity of nematode induced root nodules		
Low	Medium	High
LE 207 (14)	LE 206 (32)	LE 210 (71)
LE 218 (19)	LE 208 (37)	LE 212 (68)
LE 207 x LE 218 (16)	LE 209 (35)	LE 213 (52)
LE 208 x LE 218 (21)	LE 211 (38)	LE 214 (64)
LE 209 x LE 218 (23)	LE 206 x LE 218 (28)	LE 217 (56)
LE 211 x LE 218 (22)	LE 210 x LE 218 (47)	
LE 213 x LE 218 (24)	LE 212 x LE 218 (42)	
LE 217 x LE 218 (18)	LE 214 x LE 218 (38)	

Low = < 25 nodules/plant
Medium = >25 <50 nodules/plant
High = >50 nodules/plant

LE 210 (71), LE 212 (68), LE 213 (52), LE 214 (64) and LE 217 (56). The interspecific F_1 hybrids fall in the low (<25) and medium (>25<50) groups.

3. Inheritance of combined wilt resistance

The 11 parental lines, 10 F_1 hybrids and 10 F_2S were grown in a known diseased field during June-October, 1983 and data were collected on plants wilted. Bacterial wilt was confirmed through ooze test. The data were analysed for inheritance of combined wilt resistance (Table 4.4). A complementary type of gene action involving two separate gene systems was found responsible for resistance. The gene system operating in resistant line of Lycopersicon esculentum was notated as r_2r_2 and that of in Lycopersicon pimpinellifolium as r_1r_1. The presence of wilted plants in the parental lines was considered to calculate expressivity of the respective recessive genes imparting resistance. When expressivity of recessive genes was considered, four out of ten crosses substantiated a complementary and hypostatic type of digenic recessive gene system. When expressivity was assumed 100% the complementary and hypostatic type of digenic recessive system could be explained in all the ten crosses.

4. Somatic analysis of parental lines and hybrids

Analysis of variance showed significant variation among the eleven parental lines for days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit, fruits/plant, average fruit weight and fruit yield (Table 4.5). The mean squares due to hybrids were significant for all the above characters except days to first fruit harvest and fruit weight. Variance due to parents versus hybrids was significant for all the characters. Mean performance of parental lines and hybrids were given in Table 4.6. Maximum fruit yield was recorded in line LE 217 (1291.67 g) followed by LE 214 (874.47 g). Lines LE 214 (14 days) and LE 213 (14 days) were the earliest. Maximum plant height (120.83 cm) and branches/plant (8) were observed in LE 218. The hybrid LE 211 x LE 218 had maximum number of fruits (119) followed by LE 217 x LE 218 (104).

Mean, range, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic gain of characters under study are presented in Table 4.7. Maximum range was

Table 4.5. General analysis of variance

Sources of variation	df	Mean squares			
		Days to first flower	Days to first fruit harvest	Plant height (cm)	Branches/ plant
Replications	2	17.65**	202.98**	45.69	2.81**
Genotypes	20	119.36**	256.46**	1227.98**	2.57**
Parents	10	59.03**	119.56**	1244.69**	3.62**
Hybrids	9	3.21**	9.54	682.41**	1.46*
Parents vs Hybrids	1	1767.96**	3847.74**	5970.90**	2.17*
Error	40	0.92	8.22	115.92	0.53

* P = 0.05

** P = 0.01

Contd.....

Table 4.5. contd.....

Sources of variation	df	Mean squares			
		Locules/ fruit	Fruits/ plant	Fruit weight (g)	Fruit yield (g)
Replications	2	0.10	1910.91**	7.34	81547.70**
Genotypes	20	0.95**	3194.87**	523.14**	205471.07**
Parents	10	0.95**	829.44**	409.67**	256286.78**
Hybrids	9	0.29**	977.07**	2.31	41071.81**
Parents vs Hybrids	1	6.97**	46809.37**	15.64**	1176907.42**
Error	40	0.084	191.06	4.05	10684.77

** P = 0.01

Table 4.6. Mean performance of 11 tomato lines and 10 F_1 hybrids

Genotypes	Characters			
	Days to first flower	Days to first harvest	Plant height (cm)	Branches/ plant
Lycopersicon esculentum				
LE 206	17.40	56.27	60.33	4.27
LE 207	18.20	59.33	55.40	3.27
LE 208	23.33	57.67	49.53	4.93
LE 209	16.60	53.07	52.27	5.20
LE 210	17.93	54.53	59.07	4.33
LE 211	18.53	56.20	51.33	5.87
LE 212	13.60	52.80	70.53	5.00
LE 213	13.80	54.20	60.40	5.07
LE 214	20.20	56.67	71.93	4.67
LE 217	23.20	60.13	79.80	5.27
Lycopersicon pimpinellifolium				
LE 218	6.50	36.67	120.83	7.67
LE 206 x LE 218	6.67	37.67	97.40	5.47
LE 207 x LE 218	6.40	38.87	72.33	4.40
LE 208 x LE 218	6.47	37.00	68.73	4.80
LE 209 x LE 218	6.53	41.67	76.67	5.47
LE 210 x LE 218	6.00	39.13	76.80	4.87
LE 211 x LE 218	6.07	37.87	83.27	5.60
LE 212 x LE 218	6.80	36.40	79.47	5.00
LE 213 x LE 218	7.60	37.60	84.67	5.60
LE 214 x LE 218	9.07	38.93	106.33	6.33
LE 217 x LE 218	8.47	41.60	116.2	6.67
Sem ±	0.55	1.66	6.22	0.42
CD (P = 0.05)	1.58	4.73	17.76	1.20

Contd.....

Table 4.6. contd.....

Genotypes	Characters			
	Locules/ fruit	Fruits/ plant	Fruit weight (g)	Fruit yield (g)
Lycopersicon esculentum				
LE 206	2.57	20.87	27.83	571.53
LE 207	3.47	26.33	30.70	572.07
LE 208	2.73	19.20	21.76	449.80
LE 209	2.53	25.80	23.23	594.13
LE 210	2.57	20.47	17.00	340.60
LE 211	3.00	21.87	15.46	352.13
LE 212	2.90	33.13	18.60	689.73
LE 213	2.40	32.13	21.43	669.20
LE 214	3.30	29.87	35.53	874.47
LE 217	4.07	31.73	47.96	1291.67
Lycopersicon pimpinellifolium				
LE 218	2.07	78.67	3.13	232.67
LE 206 x LE 218	2.07	70.87	4.06	243.00
LE 207 x LE 218	2.03	63.07	3.70	234.53
LE 208 x LE 218	2.17	62.07	3.00	205.00
LE 209 x LE 218	2.33	80.20	3.13	283.07
LE 210 x LE 218	2.03	94.53	3.50	363.93
LE 211 x LE 218	2.00	118.93	3.33	401.07
LE 212 x LE 218	2.00	85.93	3.30	272.93
LE 213 x LE 218	2.07	95.4	3.30	280.93
LE 214 x LE 218	2.37	80.67	4.63	421.87
LE 217 x LE 218	3.00	103.87	5.86	591.53
Sem ±	0.17	7.98	1.16	59.68
CD	0.48	22.81	3.32	170.57

(P = 0.05)

Table 4.7. Mean, range, genotypic (gcv) and phenotypic coefficient of variation (pcv), heritability (h^2) genetic advance and genetic gain in the eleven tomato lines and ten F_1 hybrids

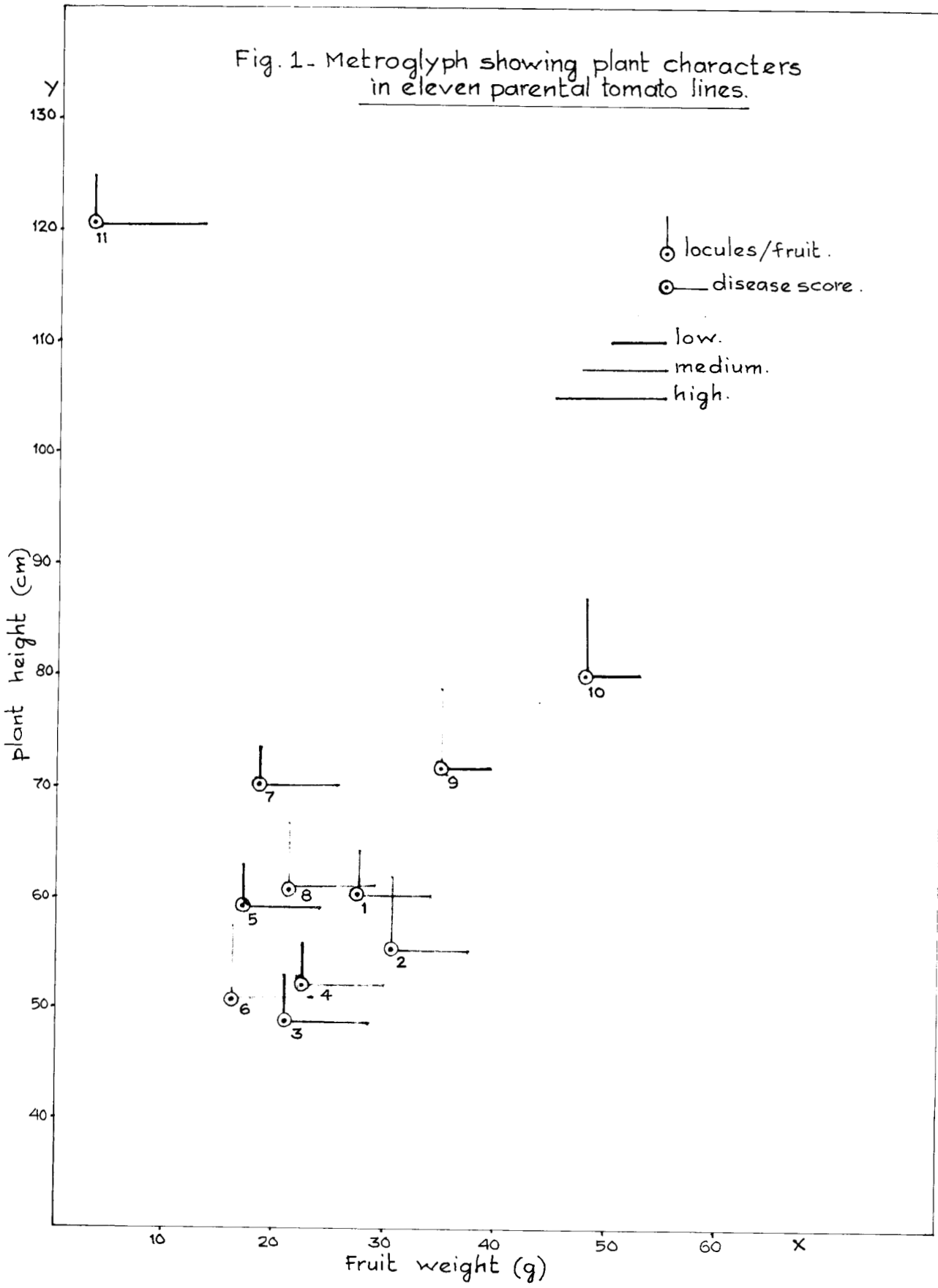
Characters	Mean	Range	gcv	pcv	h^2	Genetic advance	Genetic gain
Days to first flower	12.06 ± 0.55	5 - 29	52.07	52.70	0.97	12.65	104.89
Days to first fruit harvest	46.86 ± 1.66	33 - 73	19.41	20.35	0.90	17.67	37.70
Plant height (cm)	75.77 ± 6.22	43 -146	25.40	29.11	0.76	34.41	45.41
Branches/plant	5.22 ± 0.42	2 - 8	15.79	21.07	0.56	1.26	24.13
Locules/fruit	2.55 ± 0.17	2 - 6	21.17	23.85	0.78	0.96	37.64
Fruits/plant	56.90 ± 7.98	11 -230	55.61	60.68	0.83	59.01	103.70
Fruit weight (g)	14.31 ± 1.16	2 - 61	91.92	92.99	0.97	26.57	185.67
Fruit yield (g)	473.13 ± 58.68	56 -1659	53.85	58.11	0.85	481.48	101.76

observed for fruit yield (56 g to 1659 g), followed by fruits/plant (11 to 230). Days to first flower and fruit weight also had wide range (5 to 29) and (2 to 61) respectively. Estimates of coefficient of variation revealed that the characters fruit weight (pcv = 92.99%), fruits/plant (pcv = 60.68%) and fruit yield (pcv = 58.1%) showed high values of phenotypic coefficient of variation. The highest genotypic coefficient of variation was recorded for fruit weight (gcv = 92.99%) followed by fruits/plant (gcv = 55.61%) and fruit yield (gcv = 53.85%). Both the characters fruit weight and days to first flower had high heritability values of 0.97 closely followed by days to first fruit harvest (0.90), fruit yield (0.85) and fruits/plant (0.83). Genetic advance, per se was high for fruit yield (481.48) whereas genetic advance as percentage of mean was high for fruit weight (185.67).

5. Estimation of genetic divergence

The eleven parental lines were pictorially represented through metroglyphs (Fig. 1) considering plant height, fruit weight, locules/fruit and disease score. The arrangement and form of metroglyphs indicated genetic similarity among

Fig. 1- Metroglyph showing plant characters in eleven parental tomato lines.



LE 206, LE 208, LE 209, LE 210, LE 212 and LE 213. The line LE 217 and LE 218 had separate and distinct metroglyphs.

Genetic distance existing between parental lines in a hybrid has frequently been related to the expression of heterosis in different crop plants. The correlated variables days to first flower, plant height, locules/fruit and fruit weight were transformed into uncorrelated variables using coefficients of 'X' in an equation of uncorrelated linear function of 'Y' (Table 4.8). The genetic distance (D^2) between Lycopersicon pimpinellifolium and ten lines of Lycopersicon esculentum were then calculated (Table 4.9). A maximum distance of 449.87 was estimated between lines LE 217 and LE 218. The line LE 212 was the closest to LE 218 (D^2 = 159.96). Percentage contribution of component characters to total genetic divergence is given in Table 4.10. Days to first flower contributed maximum (45.45) towards genetic divergence, followed by fruit weight (32.73) and plant height (12.73). Based on D^2 values, the eleven parental lines were grouped into three clusters. Cluster I was the largest containing nine lines LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212, LE 213 and LE 214. Cluster II and III consisted of solitary genotypes LE 217 and LE 218 respectively (Table 4.11).

Table 4.8. Coefficient of x in the uncorrelated linear function of y

$$y_1 = \frac{x_1}{\sqrt{4.33}} = 0.4805\, x_1$$

$$y_2 = \frac{-1.1732\, x_1 + 1x_2}{\sqrt{24.1002}} = -0.2389\, x_1 + 0.2037\, x_2$$

$$y_3 = \frac{-0.0149x_1 + 0.0068x_2 + 1x_3}{\sqrt{0.0987}} = -0.0474\, x_1 + 0.0216\, x_2 + 3.1837\, x_3$$

$$y_4 = \frac{0.1126\, x_1 + 0.1864\, x_2 - 2.4914\, x_3 + 1x_4}{\sqrt{5.5223}} = 0.0479\, x_1 + 0.0793\, x_2 - 1.060\, x_3 + 0.426\, x_4$$

Table 4.9. Genetic distance (D^2) between *Lycopersicon pimpinellifolium* and ten lines of *Lycopersicon esculentum*

Lines	Genetic distance (D^2)
LE 206 and LE 218	283.43
LE 207 and LE 218	329.43
LE 208 and LE 218	367.15
LE 209 and LE 218	301.81
LE 210 and LE 218	265.78
LE 211 and LE 218	324.74
LE 212 and LE 218	159.96
LE 213 and LE 218	219.33
LE 214 and LE 218	309.68
LE 217 and LE 218	449.87

Table 4.10. Percentage contribution of component characters to total genetic divergence in the materials under study

Characters	Days to first flower	Plant weight	Locules/ fruit	Fruit weight	Total
Number of times appearing first in ranking	25	7	5	18	55
% contribution	45.45	12.73	9.09	32.73	100

Table 4.11. Grouping of eleven tomato lines into clusters based on D^2 value

Clusters	lines
I	LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212, LE 213 and LE 214
II	LE 217
III	LE 218

6. Interspecific heterosis

General combining ability effects of Lycopersicon pimpinellifolium (LE 218) as the average performance in hybrid combinations were given in Table 4.12. The parents versus hybrids mean squares were significant for days to first flower, days to first harvest, plant height, branches/plant, locules/fruit, fruits/plant, fruit weight and fruit yield. Significant negative interspecific heterosis was observed for days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit and fruits/plant. Interspecific heterosis was not significant for fruit yield (Table 4.13). The hybrid LE 210 x LE 218 flowered six days after transplanting. LE 214 x LE 218 flowered 10 days after transplanting. All the ten F_1 hybrids were earlier to the female Lycopersicon esculentum lines. The hybrid LE 217 x LE 218 had maximum fruit weight (5.86 g) compared to 3.12 g in LE 218 and 47.96 g in LE 217. A maximum of three locules/fruit was observed in LE 217 x LE 218. The hybrid LE 217 x LE 218 had an yield of 591.53 g/plant while LE 217 and 218 yielded 1.29 kg/plant and 232.66 g/plant respectively.

Table 4.12. General combining ability of Lycopersicon pimpinellifolium (LE 218)

Characters	gca
Days to first flower	6.95
Days to first fruit harvest	38.48
Plant height (cm)	109.91
Branches/plant	5.61
Locules/fruit	2.19
Fruits/plant	84.86
Average fruit weight (g)	3.70
Fruit yield (g)	320.95

Table 4.13. Mean performance of 11 tomato lines

Parents	Days to first flower	Days to first harvest	Plant height (cm)	Branches/ plant	Locules/ fruit	Fruits/ plant	Fruit weight (g)	Fruit yield (g)
LE 206	17.40	56.26	60.33	4.26	2.56	20.86	27.83	571.53
LE 207	18.20	59.33	55.40	3.26	3.46	26.33	30.70	572.06
LE 208	20.33	57.66	49.53	4.93	2.73	19.20	21.76	449.80
LE 209	16.60	53.06	52.26	5.20	2.53	25.80	23.23	594.13
LE 210	17.93	54.53	59.06	4.33	2.56	20.46	17.00	340.60
LE 211	18.53	56.20	51.33	5.86	3.00	21.86	15.46	352.13
LE 212	13.60	52.80	70.53	5.00	2.90	33.13	18.60	689.73
LE 213	13.80	54.20	60.40	5.06	2.40	32.13	21.43	669.20
LE 214	20.20	56.66	71.93	4.66	3.30	29.86	35.53	874.46
LE 217	23.20	60.13	79.80	5.26	4.06	31.73	47.96	1291.66
LE 218	6.50	36.66	120.83	7.66	2.06	78.66	31.13	232.66
LE 79	39.00	70.00	68.00	6.00	3.33	35.00	35.00	1370.00
CD (P = 0.05)	1.58	4.73	17.06	1.20	0.48	27.81	3.32	170.57

Table 4.13. Contd.....

Hybrids	Mean	Fruit weight (g)			Mean	Fruit yield (g)		
		Hetero-beltiosis	Relative heterosis	Standard heterosis		Hetero-beltiosis	Relative heterosis	Standard heterosis
LE 206 x LE 218	4.06	-85.41**	-73.77**	-88.4**	243.00	-57.48	-39.57	-82.26
LE 207 x LE 218	3.70	-87.95**	-78.13**	-89.43**	234.53	-59.00	-41.71	-82.88
LE 208 x LE 218	3.00	-86.21**	-75.90**	-91.43**	205.00	-54.42	-39.92	-85.04
LE 209 x LE 218	3.13	-86.53**	-76.25**	-91.06**	283.06	-52.36	-31.53	-79.34
LE 210 x LE 218	3.50	-79.41**	-65.24**	-90.00**	363.93	6.85	26.97	-73.44
LE 211 x LE 218	3.33	-78.46**	-64.19**	-90.84**	401.06	13.89	37.16	-70.73
LE 212 x LE 218	3.30	-82.26**	-69.64**	-90.57**	272.93	-60.43	-40.82	-80.08
LE 213 x LE 218	3.30	-84.60**	-73.13**	-90.57**	280.93	-58.02	-37.70	-79.49
LE 214 x LE 218	4.63	-86.97**	-76.05**	-86.77**	421.86	-51.72	-23.79	-69.21
LE 215 x LE 218	5.86	-87.78**	-77.06**	-83.26**	591.53	-54.20	-22.39	-56.82
CD (P = 0.05)	3.32				170.57			

* P = 0.05

** P = 0.01

Discussion

DISCUSSION

Bacterial wilt caused by Pseudomonas solanacearum is the most serious disease which has made cultivation of tomato impossible in certain acidic soils of the tropics. Attempts on disease management and control have not made any substantial impact till date. This has necessitated the development of resistant lines to bacterial wilt. Two distinct sources of resistance - one derived from Louisiana Pink (North Carolina source) and the other from PI 127805A, (Lycopersicon pimpinellifolium) have been reported (Russell, 1978). The present investigation was carried out to incorporate the above two known sources of resistance in F_1 hybrids and then their integration in succeeding generation. An effective breeding programme for wilt resistance essentially consisted of collection of germplasm, cataloguing of the lines thus collected, evaluation for resistance and improving the line thus isolated through appropriate breeding methods.

Germplasm collection

Tomato lines reported resistant to bacterial wilt were collected from AVRDC, Taiwan and University of California, USA. The lines LE 206, LE 207, LE 208,

LE 209, LE 210, LE 211, LE 212, LE 213, LE 214 and LE 217 were collected from AVRDC, Taiwan and LE 218 from University of California, USA.

Genetic cataloguing

The Report of the Tomato Genetics Cooperative, 1980 contained an exhaustive list of genes which could be used for cataloguing the germplasm. This might reveal marker character(s) associated with tolerance/resistance to bacterial wilt. The marker character thus identified could be used in screening in seedling stage, juvenile stage or even in adult plant stage of the crop. Acosta (1964) reported that the resistant lines to bacterial wilt are all indeterminate, indicating a possible relationship between Sp^{+}_{-} the gene for indeterminate growth habit and resistance to wilt. He also noticed yellow coloured gel around the seeds of resistant lines. In the present study also it is observed that all the resistant lines are indeterminate in growth habit with yellow gel around the seeds.

Bible (1976) reported a positive relationship between right hand leaf orientation and better performance in tomato. In the present case, seedlings of tomato were observed for arrangement of leaves. Only one line (LE 212) had right phyllotaxy, while

all others had left phyllotaxy.

Screening of twenty-one genotypes under field conditions indicated that no line is immune (score = 1) to bacterial wilt as per the cfiterion of Sitaramaiah et al. (1981). The lines LE 214 and LE 217 exhibited high field resistance (score = 2). Moderate resistance (score=3) was observed in LE 206, LE 207, LE 208, LE 209, LE 210, LE 211, LE 212 and LE 213. All the F_1 hybrids were scored 3/4 indicating moderate resistance/moderate susceptibility.

Inheritance of combined wilt resistance

The first source of resistance (North Carolina type) expressed by derivatives of Louisiana Pink is inherited as a recessive character and is controlled by polygenes (Singh, 1961). Second type of resistance was derived from Lycopersicon pimpinellifolium Acosta et al. (1964) reported resistance derived from Lycopersicon pimpinellifolium is partially dominant in the seedling stage. In mature plant, resistance is controlled by recessive genes. The present study notated the gene system operating in resistant line of Lycopersicon esculentum as r_2r_2 and that in Lycopersicon pimpinellifolium as r_1r_1. Analysis of inheritance of combined wilt resistance indicated a

complementary and hypostatic type of digenic recessive gene system as responsible for combined wilt resistance. The two genes responsible for resistance are observed located in different locii. This observation of complementary and hypostatic type of gene action could be effectively utilised to synthesise resistant lines possessing r_1r_1 and r_2r_2 gene systems.

Information on variability and its components are vital to any plant improvement programme. Genetic advance expected in succeeding generations depends considerably on variability of the base population and heritability of the character under study (Allard, 1960).

Twenty-one tomato genotypes were significantly different for yield and its component characters days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit, fruits/plant, fruit weight and fruit yield. The high level of significance of the differences among genotypes indicated that the differences were due to genetic reasons. In the present study, it was seen that the range of variation for almost all characters was large, particularly in respect of fruit yield (56 g to 1659 g), fruits/plant (11 to 230) and

plant height (43 cm to 146 cm). This showed that the available population had sufficient amount of variation for most of the characters studied for which selection could be practiced. Parthasarathy et al. (1976) showed that a wide range of variation was present in tomato for many of the characters he considered for improvement.

The magnitude of variance as such did not reveal the relative amount of variability as ascertained through coefficient of variation. High genotypic coefficient of variation indicated that genotypic variability for the character was high and enabled to compare with that present in other characters. The values of genotypic and phenotypic coefficient of variation indicated high estimates for fruit weight (91.92 and 92.99), fruits/plant (55.61 and 60.68), fruit yield (53.85 and 58.11) and days to first flower (52.07 and 52.70). This suggested that there was a high degree of genetic variability in the crop for these characters as compared to others, and therefore these could be utilised in the crop improvement programme.

The heritable portion of the variation could be found out with the help of heritability estimates. Burton (1952) had suggested that genotypic coefficient of variation together with heritability

estimates would give the best picture of the amount of progress to be expected by selection. Results of the investigations now undertaken clearly indicated that all characters except branches/plant had high heritability. Heritability estimate was the highest for fruit weight and days to first flower (0.97 each). Characters days to first fruit harvest (0.90), plant height (0.76), locules/fruit (0.78), fruits/plant (0.83) and fruit yield (0.85) also showed high values of heritability. Hence these economic characters could be improved by selection, because of the fact that, high heritability indicated the effectiveness with which selection of genotypes could be based on phenotypic performance (Johnson et al. 1955a). Among the characters studied branches/plant showed lowest heritability estimate (0.56) thus limiting the scope of selection for this character.

In the present study, the genetic advance was estimated as absolute for a character and also as the percentage of mean (genetic gain) for comparing different characters. The genetic gain estimate was maximum for fruit weight (185.67) which was followed by days to first flower (104.89) and fruit yield (101.76). These characters were also observed

to have high heritability in addition to high genetic gain values which might be attributed to the additive gene effects (Panse, 1957). This showed that there was sufficient scope for the improvement of this character. Days to first fruit harvest eventhough having high heritability estimate (0.90) the expected genetic advance as percentage of mean was found to be low (37.70). This was attributed to the action of non additive genes which included dominance and epistasis. (Panse, 1957). Hence selection had limited scope for improving days to first fruit harvest.

Genetic distance existing between parental lines in a hybrid has frequently been related to the expression of heterosis in different crop plants. Marked negative heterosis was observed for many of the quantitative characters days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit, fruits/plant and fruit weight in many F_1 hybrids. Maximum negative heterosis was observed for fruit weight and days to first flower. No significant heterosis was observed for fruit yield. Being interspecific hybrids, the importance of heterosis per se was limited and the scope for commercial utilization was hence negligible.

Based on D^2 values, eleven genotypes were grouped into three clusters. Genotypes with closely related values were grouped into one cluster indicating wider differences, between the clusters than within the clusters. Cluster III having only one line Lycopersicon pimpinellifolium (LE 218) was different from other clusters in respect of mean performance for days to first flower, plant height, locules/fruit and fruit weight. The characters days to first flower (45.45%) and fruit weight (32.73%) contributed maximum towards genetic divergence. Among the ten Lycopersicon esculentum lines, LE 212 was the closest to Lycopersicon pimpinellifolium (D^2 = 159.96), followed by LE 213 (219.33) and LE 210 (D^2 = 265.78).

The study revealed that a recessive digenic complementary and hypostatic type of gene system were involved in the inheritance of combined wilt resistance. The line LE 217 with the maximum fruit weight of 47.96 g had score 2 indicating high field resistance. The existence of negative relative heterosis for fruit weight in all the F_1 hybrids caused concern in the development of large fruited lines with combined wilt resistance. The F_2 lines possessing combined wilt resistance are being progressed.

Summary

SUMMARY

The study "Incorporation of two main sources of resistance to bacterial wilt in F_1 generation of tomato, Lycopersicon Lycopersicum (L) Karst" was conducted to find out inheritance of combined resistance to bacterial wilt (Pseudomonas solanacearum) and generate useful variability for further selection. The experiment was laid out during August-November, 1982, January-May 1983 and June-October 1983 at the Instructional Farm of College of Horticulture.

2. The experimental materials consisted of ten lines of known sources of wilt resistance possessing "North Carolina type" of gene system and one line (PI 127805A) possessing Lycopersicon pimpinellifolium type of gene system. Ten interspecific F_1 hybrids were generated between the above two distinct resistant sources and they were evaluated under field conditions for disease reaction. The interspecific F_1 heterosis was estimated for days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit, fruit weight, fruits/plant and fruit yield. The F_1S were selfed to generate F_2S. The parental lines, F_1S and F_2S were further grown in diseased plots to estimate inheritance of combined resistance.

3. The F_1 hybrids were all earlier and exhibited significant negative heterosis for days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit and fruit weight.

4. The inheritance studies indicated that there are separate gene systems responsible for resistance in the two sources of wilt resistance. A complementary and hypostatic recessive gene action was observed responsible for the combined disease resistance. The complete susceptibility of F_1S conclusively proved the recessive type of gene action involved in the inheritance of resistance.

5. The genetic distance (D^2) was calculated between Lycopersicon pimpinellifolium (LE 218) and ten lines of Lycopersicon esculentum to find out genetic similarity/dissimilarity. The line LE 217 was observed farthest to LE 218 (D^2 = 159.96). Attempt was also made to relate heterosis with genetic divergence.

6. The line LE 217 with large fruit size (47.96 g) had a disease score of two, indicating high field resistance.

7. Screening for nematode resistance indicated that all the lines are susceptible to nematode.

8. The F_2 lines observed free from bacterial wilt are being progressed for further selection.

References

REFERENCES

*Aberdeen, J.E.C. 1946. Experiments in the control of bacterial wilt of tomatoes in South Eastern Queensland. Bul. Dept. Agr. Queensland 30: 1-5.

Abeygunawardena, D.V.W. and Siriwardena, A.A.P. 1963. Studies on resistance in tomato to bacterial wilt. Trop. Agr. 119: 55-66.

Acosta, J.C. 1964. Genetic analysis of bacterial wilt resistance and certain other characters in a tomato cross Lycopersicon esculentum x Lycopersicon pimpinellifolium. Diss. Abs. 25: Order No. 64-2645. P. 746.

Acosta, J.C., Gilbert, J.C. and Quinon, V.L. 1964. Heritability of bacterial wilt resistance in tomato. Proc. Amer. Soc. hort. Sci. 84: 455-462.

*Akiba, F., Riberio, R. Del., Sudo, S.O., Robbs, C.F. and Kimura, O. 1972. Evaluation of the performance of introduced tomato lines in relation to Brazilian isolates of Pseudomonas solanacearum, the causal agent of bacterial wilt. Arq. do Inst. Biol. 39(4): 243-250.

Allard, R.W. 1969. Principles of Plant Breeding. 1st ed. pp. 75-99. John Wiley and Sons, London.

*Anderson, E. 1957. A semigraphical method for the analysis of complex problems. Proc. Natn. Acad. Sci. Wash. 43: 923-927.

*Annual Report of Agriculture, 1950-51. Agriculture astride the century. Ann. Rpt. 96 p. School of Agriculture, North Carolina State College.

*Avdeev, Yu. I. 1974. Heterosis and combining ability in tomato varieties in Astrakhan Province. Referat Zh. 10 (55): 202 (Cf. Plant Breeding Abs. 47: 1773).

AVRDC, 1975. Tomato Report. pp 25-28. Asian Vegetable Research and Development Centre, Taiwan.

AVRDC, 1978. Progress Report for 1977. 90 p. Asian Vegetable Research and Development Centre, Taiwan.

AVRDC, 1979. Progress Report for 1978. 36 p. Asian Vegetable Research and Development Centre, Taiwan.

Bible, B.B. 1976. Non equivalence of left handed and right handed phyllotaxy in tomato and pepper. Hort Sci. 11 (6): 601-602.

*Briggle, L.W. 1963. Heterosis in wheat. A review. Crop Sci. 3: 407-412.

*Burton, G.W. 1952. Quantitative inheritance in grasses. Proc. 6th Inst. Grsald. Cong. 1: 277-283.

Celine, V.A. 1981. Genetic cataloguing of tomato germplasm towards isolation of line(s) resistant to bacterial wilt. M.Sc. (Hort.) thesis submitted to Kerala Agricultural University, Vellanikkara.

Choudhary, R.C. and Khanna, K.R. 1972. Exploitation of heterosis in tomato: yield and its components. South Indian Hort. 20: 59-65.

*Daly, P. 1973. Studies of 3 tomato varieties tolerant to Pseudomonas solanacearum. Agron. Trop. 28 (1): 23-83.

Fisher, R.A. 1954. Statistical Methods for Research Workers. 12th ed. pp. 54-62. Oliver and Boyd Ltd., London.

Goth, R.W., Peter, K.V. and Webb, R.E. 1983. Effect of root knot nematode on bacterial wilt of tomato. Phytopathology, 73 (5): 966.

*Graham, K.M. and Yap, T.C. 1976. Studies on bacterial wilt. I. Inheritance of resistance to Pseudomonas solanacearum in tomato. Malayasian Agr. Res. 57 (1): 1-8.

*Graham, K.M., Tan, H., Chong, K.Y., Yap, T.C. and Vythilingam, S. 1977. Breeding tomatoes for lowlands of Malaysia. Res. Pub. Malaysian App. Biol. 1: 34.

Hayes, H.K.,Immer, F.A. and Smith, D.C. 1956. Methods of Plant Breeding. 1st ed. pp. 52-66. Hill Book Company. Inc. New York.

Henderson, W.R. and Jenkins, S.F. 1972. Venus and Saturn: two new tomato varieties combining desirable horticultural features with Southern bacterial wilt resistance. Bul. Agr. Expt. Sta. North Carolina State Univ., 444, 13 p.

*IITA. 1978. Ann. Rpt. Vi, 130 p. International Institute of Tropical Agriculture, Ibadan, Nigeria.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in Soybeans. Agron. J. 47 (6): 314-318.

*Khanna, K.R. and Mishra, C.H. 1977. Divergence and heterosis in tomato. SABRAO J. 9 (1): 43 - 50.

Kolhe, A.K. 1970. Possibilities and extent of exploitation of hybrid vigour in tomato. Res. J. Mahatma Phule Agr. Univ. 1: 54-61.

*Mahalanobis, P.C. 1928. A statistical study at Chinese head measurement. J. Asiatic Soc. Bengal. 25: 301-377.

*Mew, T.W. and Ho, W.C. 1976. Varietal resistance to bacterial wilt in tomato. Plant Dis. Reporter 60 (3): 264-268.

Mew, T.W. and Ho, W.C. 1977. Effect of soil temperature on resistance to tomato cultivars to bacterial wilt Phytopathology, 67 (7): 907-911.

Mittal, R.K., Singh, H.N., Singh, R.R. and Singh, J.B. 1974. Heterosis in tomato. Indian J. Genet. 34 (3): 333-337.

Mohanakumaran, N., Gilbert, J.C. and Buddenhagen, I.W. 1969. Relationship between tomatin and bacterial wilt resistance in tomato. Phytopathology. 59 (1): 14.

*Morton, D.J., Dukes, P.D. and Jenkins, S.F. 1966. Serological relationship of races 1,2 and 3 of Pseudomonas solanacearum. Plant Dis. Reporter 50: 275-277.

Nandpuri, K.S., Kanwar, J.S. and Lal, R. 1977. Variability, pathanalysis and discriminant function selection in tomato. Haryana J. Res. 1 (2): 98-103.

Panse, V.G. and Sukhatme, P.V. 1978. Statistical methods for agricultural workers. 3rd ed. pp. 80-87. Indian Council of Agricultural Research, New Delhi.

Parthasarathy, V.A., Anand, N. and Irulappan, J. 1976. Genetic variability in tomato. Indian J. agr. Res. 10 (2): 133-135.

Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. Indian J. Genet. 17 : 318-329.

Peter, K.V. and Rai, B. 1976. Genetic divergence in tomato. Indian J. Genet. 36 (3): 379-384.

Peter, K.V. and Rai, B. 1976. Potentialities for genetic improvement of yield and yield components on elite tomato germplasm. Pantnagar J. Res. 1 (2): 98-103.

Prasad, A. and Prasad, R. 1977. Variability and correlation studies in tomato. Indian J. agr. Sci. 47 (2): 77-80.

Rajanna, A., Lal, G. and Peter, K.V. 1977. Heterozygote advantage as a function of genetic divergence in tomato. Indian J. agr. Sci. 47 (9): 434-437.

Ramachandran, C., Gopalakrishnan, P.K. and Peter, K.V. 1988. Personnel communication.

Rao, C.R. 1948. The utilization of multiple measurement in problems of biological classification. J. Roy. Stat. Soc. 10: 159-203.

Rath, P.K. and Addy, S.K. 1977. Variation in Pseudomonas solanacearum causing bacterial wilt of tomato. Indian Phytopath. 39 (4): 502-505.

Report of the Tomato Genetics Cooperative, 1980. Department of vegetable crops, University of California, Davis, California. 30: 2-17.

Roddick, J.G. 1974. The steroiodal glycoalkaloid α-tomatine. Phytochemistry, 13 (1): 9-25.

Russell, G.E. 1978. Plant Breeding for Pest and disease Resistance. 1st ed. pp. 190-193. Buttenworths, London.

*Sakjan, G.A. 1967. Heterosis in the yield of tomatoes in relation to the choice of parental pairs. Referat Zh. 7 (55): 24 (Cf. Plant Breeding Abs. 39: 6133).

*Serere Research Station, 1970-71. Ann. Rpt. Part I & II Serere Research Station. (cf. Plant Breeding Abs. 44 (10): 6459).

*Shevelen, N.E. 1977. Weight and number of fruits in hybrid and in the seed progeny of tomato grafts. Referat Zh. 7 (55): 93 (cf. Plant Breeding Abs. 49: 5296).

Sidhu, A.S., Dixit, J. and Bhutani, R.D. 1981. Heterosis and combining ability in pear-shaped tomato. Haryana agr. Univ. J. Res. XI (1): 1-7.

*Singh, K. 1961. Inheritance of North Carolina type of bacterial wilt resistance in tomato. Lycopersicon esculentum L. M.Sc. thesis submitted to University of Hawaii, Honolulu.

Singh, R.R., Mital, R.K. and Singh, H.N. 1973. Note on the variability studies in some intervarietal crosses of tomato. Progve. Hort. 5 (2): 55-59.

Singh, R.K. and Choudhary, B.D. 1979. Biometrical methods in quantitative genetic analysis. 1st ed. pp. 215-221. Kalyani Publications, Ludhiana.

Sitaramaiah, K., Singh, R.S., Vishwakarma, S.N. and Dubey, G.S. 1981. Brinjal cultivars resistant to Pseudomonas wilt. Indian Phytopath. 34 (1): 113.

*Sonoda, R.M. 1977. Behaviour of tomato lines selected for resistance to Southern bacterial wilt in a field infested with the pathogen. Res. Rpt. 8 p. Agricultural Research Centre, Fort Pierce.

*Sonoda, R.M. and Augustine, J.J. 1977. Reaction of tomato lines selected for resistance to Southern bacterial wilt in a field infested with the Pathogen. Res. Rpt. 5 p. Agricultural Research Centre, Fort Pierce.

*Sonoda, R.M., Augustine, J.J. and Volin, R.B. 1980. Bacterial wilt of tomato in Florida: history, status, and sources of resistance. Proc. Fla. State Hort. Soc. 92: 100-102.

Srivastava, L.S. and Sachan, S.C.P. 1973. Genetic parameters, correlation coefficients and path coefficient analysis in tomato. Indian J. agr. Sci. 43 (6): 606-607.

*Sunarjona, H., Hartininysih, M.G. and Sahat, S. 1976. Adaptability of some tomato varieties in the lowland. Penelitian Hort. 4 (4): 3-11.

*Sunarjono, H. 1980. Increasing tomato production, disease resistant varieties show promise. Indonesian Agr. Res. Devlpmt. J. 2 (1): 5-7.

*Temiz, K. 1968. Investigations on the role of plant parasitic nematodes in the infection of tomato varieties with Pseudomonas solanacearum. Yalova Bahce Kulturleri Arastirma ve Egitim Merkezi Dergisi, 1 (2): 17-18.

*University of Florida, 1967. Ann. Rpt. for the fiscal year ending June 30, 414 p. Agricultural Experiment Station, University of Florida.

*University of West Indies, 1968-69. Rpt. Fac. Agr. pp. 55 + 15 + 112 + 6 + 23 + 62 + 3 + 8, University of West Indies.

Villareal, R.L. and Lal, S.H. 1978. Reaction of three tomato cultivars, their F_1's and three-way crosses to two isolates of bacterial wilt (Pseudomonas solanacearum). Hort. Sci. 13 (3): 366.

Virdelwala, H.A., Nandpuri, K.S. and Singh, S. 1981. Heterosis and combining ability in tomato. Veg. Sci. 8 (2): 120-131.

*Weaver, J.G. 1944. Seeking a tomato resistant to bacterial wilt. Res. Farm. N.C. Prg. Rpt. 1. p. 11.

* Originals not seen

INCORPORATION OF TWO MAIN SOURCES OF RESISTANCE TO BACTERIAL WILT IN F_1 GENERATION OF TOMATO *Lycopersicon lycopersicum* (L) KARST

By

I. SREE LATHA KUMARY

ABSTRACT OF THE THESIS

Submitted in partial fulfilment of
the requirement for the degree of

Master of Science in Horticulture

Faculty of Agriculture
Kerala Agricultural University

Department of Horticulture (Olericulture)
COLLEGE OF HORTICULTURE
Vellanikkara, - Trichur
KERALA - INDIA

1983

ABSTRACT

Bacterial wilt of tomato caused by Pseudomonas solanacearum (E.F. Smith) is a serious disease causing considerable damage in crops grown in the acidic soils of Kerala. Development of resistant variety(s) could be a worthwhile attempt which would have considerable impact on tomato production in Kerala. Experiments were planned and carried out during 1981-82 at the Instructional Farm of College of Horticulture, Vellanikkara, Trichur, to incorporate two reported sources of resistance in F_1 hybrids and then to find out inheritance of combined resistance to bacterial wilt.

Two distinct sources of resistance one derived from Louisiana Pink possessing North Carolina type of gene system and the other from PI 127805A possessing Lycopersicon pimpinellifolium type of gene system were made use in the present study. Interspecific F_1 hybrids were produced between the above two sources of resistance. The F_1S were selfed to generate F_2S. Parental lines, F_1S, F_2S were further grown to evaluate the inheritance of combined wilt resistance in a field which was known for disease susceptibility and inoculum potential.

The inheritance studies indicated a complementary and hypostatic type of digenic recessive gene system responsible for combined wilt resistance.

Interspecific F_1 heterosis was estimated. Significant negative interspecific heterosis was observed for days to first flower, days to first fruit harvest, plant height, branches/plant, locules/fruit and fruit weight. Genetic distance (D^2) was calculated to find out genetic similarity/dissimilarity between Lycopersicon pimpinellifolium (LE 218) and ten lines of Lycopersicon esculentum. The line LE 217 was observed farthest to Lycopersicon pimpinellifolium (D^2 = 449.87). The line LE 212 was the closest to Lycopersicon pimpinellifolium (D^2 = 159.96). The line LE 217 had a disease score of two indicating high field resistance. The tomato lines were further evaluated for incidence of nematadol root knots and observed that all the lines were susceptible to nematode.

The F_2 lines possessing combined wilt resistance are being progressed for further study.