GENETIC CATALOGUING OF TOMATO GERMPLASM TOWARDS ISOLATION OF LINE(S) RESISTANT TO BACTERIAL WILT

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THESIS

Submitted in partial fulfilment of the requirement for the degree of

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Faculty of Agriculture
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DECLARATION

I hereby declare that the thesis entitled "Genetic cataloguing of tomato germplasm towards isolation of lines) resistant to bacterial wilt" is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title of any other University or Society.

Vellanikkara, 27th July, 1981.

CELINE, V.A.

CERTIFICATE

Certified that the thesis entitled "Genetic cataloguing of tomato germplasm towards isolation of lines) resistant to bacterial wilt" is a record of research work done independently by Miss. Celine, V.A. under my guidance and supervision and that it has not previously formed the basis for the award of any degree, fellowship or associateship to her.

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Vellanikkara, 27th July, 1981.

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CERTIFICATE

We, the undersigned members of the Advisory
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INTRODUCTION

INTRODUCTION

Tomato (Lycopersicon lycopersicum (L) Karst) is one of the most important fruit vegetables grown both in tropics and subtropics. It is affected by a conglomeration of parasitic and non-parasitic diseases. Bacterial wilt, caused by <u>Pseudomonas solanacearum</u> (E.F.Smith), is the most serious disease which has made cultivation of tomato impossible in certain acidic soils of the tropics. The attempts on disease management and control have not made substantial impact, necessitating the development of resistant lines to bacterial wilt. Luckily, two basic sources of resistance and a large array of resistant lines have been reported. The reports on susceptibility of reportedly resistant lines elsewhere have complicated the attempts on breeding for disease resistances.

Genetic cataloguing is the key and vital step

a priori to any disease resistance breeding programme.

The information bank generated in tomato through the

Reports of the Tomato Genetics Cooperative provide

adequate bases for such attempts. Genetic cataloguing

would also throw light on linkage/pleiotropism among

mendelian characters and disease resistance. This would

help in the screening and isolation of resistant lines both in the nursery and mainfield.

The reports on undesirable linkage between resistance and unfavoured marketable fruit characteristics present a gloomy picture to the breeders. This has necessitated detailed study on mendelian characters and their association, if any, with resistance.

Being a self pollinated crop, pureline selection is the ideal method to develop newer productive lines for characters essentially governed by additive gene action. Mass selection would help to cull out undesirable plant types. The efficiency of different methods of selection for economic characters in association with resistance needs to be investigated.

The present study was formulated with the following objectives

- 1. To catalogue the available tomato germplasm maintained in the department of Olericulture
- 2. To isolate, if any, line(s) resistant to bacterial wilt
- 3. To estimate realised selection response under pureline, mass and bulk methods of selection based on yield per se associated with resistance

REVIEW OF LITERATURE

REVIEW OF LITERATURE

A Genetic cataloguing

Genetic cataloguing would enable identification of line(s) based on distinct mprphological and mendelian characters. Identification of marker character(s) linked with/pleiotropic to disease resistance character would help in screening a large number of germplasm for source of resistance.

Reports of the Tomato Genetics Cooperative (1979, 1980) provide an uptodate information on genes, their reference and seed source in tomato. The information on mapped genetic loci of the crop has also been provided. The 81 characters thus listed were made use of to catalogue the present germplasm.

B Sources of resistance to bacterial wilt

Bacterial wilt remains the most important disease of tomato in warm humid tropics. The causal agent, <u>Pseudomonas solanacearum</u>, (a soil borne bacterium which prefer acidic soils) exists in several races. This has further complicated breeding for resistance to the

bacterium. The Annual Report of the School of Agriculture, North Carolina State College (1950-151) contains the first report on breeding for resistance to bacterial wilt in tomato. Lines with good field resistance to bacterial wilt have been developed. These lines had lesser fruit size resulting in low marketable returns. Greenhouse testing indicated higher susceptibility of young plants than old ones. Abeygunawardena and Siriwardena (1963) tested 49 hybrids and their parents for resistance to bacterial wilt. The North Carolina lines 1960 - 8, 1960 - 2a, 1962 - B2 and 1961 - 57 - 55 M and Masterglobe, Rahangala Selection II were observed more resistant. Los Banos strain which was reported resistent in Philippines was observed susceptible in Sri Lanka. This was the first indication of the presence of different races in P. solanacearum. Abeygunawardena and Siriwardena (1963) reported the efficiency of root inoculation studies to eliminate susceptible ones. The crosses involving the popular varieties of U.S.A., Manalucie and Floradel with a resistant stock from North Carolina resulted in the evolution of a few lines resistant to P. solanacearum (University of Florida, 1967). The four F7 lines from

a cross UPR 199 x Floralou showed good tolerance to P. solanacearum (IRAT, 1970). The local line 2 ASS was observed tolerant to bacterial wilt (Serere Research Station, 1970-71). Henderson and Jenkins (1971) reported resistance in Venus and Saturn to bacterial wilt. Akiba et al. (1972) reported resistance in three strains of tomato viz., 6582, 66 852 and 68 84. Daly (1973) confirmed the resistance in the North Carolina cultivars Venus and Saturn and in local lines III TRAT and OTB2. Chetia and Kakati (1973) reported some resistance to P. solanacearum in Oxheart under natural infection. Mew and Ho (1976) screened 43 varieties and lines. The line VC 8-1-2-1 was observed resistant regardless of inoculum density. Sunarjono et al. (1976) screened tomato varieties resulting in the isolation of AVRDC resistant. lines 15, 22 and 33. New F_8 tomato lines FP - 1, FP - 2and FP - 5 were selected for tolerance to bacterial wilt (University of Malaya, 1977). Sonada and Augustine (1977) isolated Hawaian selection 7997 as resistant out of 72 tomato lines screened against bacterial wilt. Sonoda (1977) further evaluated 121 lines and cultivars and observed tolerance in Venus and Saturn. Graham et al. (1977) observed resistance in VC-4. Badekar (1977) reported the resistance in VC 9-1 UG and VC 11-1 UG.

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). Sonoda et al. (1979) reported moderate tolerance in tomato accessions 102, 106, 135-1, 135-2, 14 and 123-1 in Fort Pierce.

C Genetics of resistance

Two primary sources of resistance have been reported (Russell, 1978). Louisiana Pink, being the first source of resistance, has been studied in detail. The Louisiana Pink source of resistance, also called as North Carolina type of resistance, is inherited recessively and controlled by polygenes (Singh, 1961). Graham and Yap (1976) conducted detailed variance component analysis of the parents, F1S, F2S, B1S and B2S of Cross between resistant line, VC4, and susceptible line, Walter. This study indicated a narrow sense heritability of 42% and a broad sense heritability of 53% with a degree of dominance of 75% for wilt resistance. Inheritance of resistance was observed mainly due to additive gene action. They suggested repeated selfing and selection followed by intercrossing of resistant

selections as the most efficient breeding procedure for wilt resistance. The polygenic resistance is modified by changes in temperature (Mew and Ho, 1977). Another factor which alters the resistance mechanism is the inoculum density of bacteria. Villareal and Lai (1978) supported the hypothesis of additive gene action in the inheritance of disease resistance.

A second type of resistance has been derived from the Eulycopersicon species Lycopersicon pimpinellifolium (PJ 127805 A) (Acosta et al., 1964; Mohanakumaran et al., 1969 and Roddick, 1974). Acosta et al. (1964) presented evidence for partial dominance for resistance in F₁ in early stage of growth. In mature plants, resistance appeared to be controlled by recessive genes.

D Information on linkage

Acosta (1964) reported a possible linkage between sp⁺, the factor for indeterminate growth habit and resistance to wilt caused by bacteria. Acosta et al.(1964) observed no association between the gene 'u' controlling uniform fruit colour and resistance to bacterial wilt. A few resistant selections had yellow gel round the seeds of ripening fruits. They could get no lines in resistant

group with fruits of commercial quality. Scientists at University of West Indies (1968-'69) based on the investigations on resistance to <u>P. solanacearum</u> indicated close linkage between recessive genes for resistance and genes for poor fruit characteristics. Kann and Laterot (1977) reported pleiotropism rather than linkage between resistant factors against <u>P. solanacearum</u> and <u>Fusarium oxysporum</u>.

E Biochemical basis of resistance

x - tomatine content was more in resistant parents and hybrids than in susceptible ones (Mohanakumaran, et al., 1969). A marked increase in α- tomatine content was observed in resistant lines following artificial inoculation than in susceptible ones. Roddick (1974) reported higher levels of the steroidal glycoalkaloid α- tomatine in the roots of L. pimpinellifolium cultivars resistant to P.solanacearum.

F Breeding methods

Continued selfing followed by selection and interplant hybridisation was suggested by Graham and Yap (1976) to develop resistant lines. Peter and Rai (1976) conducted detailed studies on genetic analysis of economic

traits in tomato. Locule number and plant height were reported to be more important characters of divergence in tomato and obviously governed by additive gene action. Information on variability and association among polygenic characters were collected by a number of workers (Singh et al., 1973; Peter and Rai, 1976; Prasad and Prasad, 1976; Singh et al., 1977; Nandpuri et al., 1977). Information on realised genetic response for different economic characters in association with resistance to bacterial wilt are rather limited.

MATERIALS AND METHODS

MATERIALS AND METHODS

The present study was conducted at the Instructional Farm of the College of Horticulture, Kerala Agricultural University, Trichur, during April-August 1980, May-September 1980, September-December 1980 and February-May 1981. The farm is located at an altitude of 22.25 m. and at 10° 32" N latitude and 76° 10" E longitude. The soil of the experimental site is deep, well drained, moderately acidic (pH = 5.1), medium clay loam and fairly rich in organic matter. The area enjoys a typical warm humid tropical climate. The soil is highly infested with Pseudomonas solanacearum resulting in high rate of crop damage when solanaceous vegetables are grown.

A. Experimental materials

The tomato germplasm maintained in the Department of Olericulture formed the basic experimental material for cataloguing and screening under field conditions. The source, pedigree and morphological description of the tomato lines are given in Table 3.1.

B. Experimental methods

1. Cataloguing

The 78 tomato lines were sown in raised beds during September 1980 and the seedlings were studied for qualitative characters as suggested in the Report of the Tomato Genetics Cooperative, May, 1980 (Table 3.2). The seedlings were classified into five distinct groups based on the spread and intensity of purple pigmentation as indicated below:

- a) completely free of anthocyanin
- b) upper part of the hypocotyl free of anthocyanin
- c) full hypocotyl region with anthocyanin
- d) hypocotyl and epicotyl with anthocyanin and
- e) hypocotyl, epicotyl, cotyledons and first leaves with anthocyanin

The seedlings were further classified into groups based on phyllotaxy as suggested by Bible (1976).

The seedlings were transplanted and they were 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. Estimation of response to selection

The line(s) showing resistance to bacterial wilt based on 'ooze test' was observed on individual plant basis and observations were recorded on plant height, primary branches per plant, days to first fruit set, days to first harvest, fruits per plant, marketable fruits per plant, locules per fruit, marketable fruit weight per plant and total fruit weight per plant. Elite plants were identified based on total fruit weight per plant and negligible or no incidence of cracking to generate progenies through mass selection (three plants out of 67), pureline (single elite plant) and the bulk. The progenies were later grown during February 1981 in a randomised block design with six replications. There were five rows of 12 plants per row in bulk and mass selected progenies and a single row for single plant selected progeny (pureline) in each replication. Every fifth row in each replication was planted with susceptible variety of tomato, Sioux, to study simultaneously the resistance/susceptibility of the above lines. Observations were recorded on plant height, primary branches per plant, days to first fruit set, days to first harvest, total fruits per plant, marketable fruits per plant, locules per fruit, percentage of small fruited plants (<20 g.), percentage of medium fruited plants

(20 to 40 g.) percentage of large fruited plants (>40 g.), percentage of plants without cracked fruits (zero per cent cracked fruits), percentage of plants with medium cracked fruits (>zero to 25 per cent cracked fruits), percentage of plants with highly cracked fruits (>25 per cent cracked fruits), marketable fruits per plant and total fruit weight per plant. The data were analysed as in randomised block design and later in completely randomised design as the variations due to replication were found to be non-significant.

Selection differential (S), selection response (R) and realised heritability (h²) for each polygenic character was computed as given by Falconer (1960).

3. Evaluation of field tolerance

The trials were carried out in soils known for high inoculum density of <u>Pseudomonas solanacearum</u>. The cropping was done in the same plot where the previous crop was tomato or a solanaceous vegetable. The lines under screening were grown along with known susceptible line (Sioux) to prove the inoculum potential of the soil.

4. Artificial inoculation

- 1. The soil where diseased plants were observed was used for growing the line(s) under screening.
- 2. Artificial inoculation was done as suggested by Winstead and Kelman (1952).

Table 3.1 The source, name, pedigree and morphological description of lines under screening.

Accession number	Source	Cultivar name	Pedigree	Important traits
LE 5	I.A.R.I.	Pusa Ruby	Improved Meeruthi x Sioux	Indeterminate, spreading, moderately ribbed fruit surface
LE 18	Pantnagar	AC 238	•	Indeterminate, large fruited
LE 23	Pantnagar	AC 259	-	-
LE 34	Pantnagar	11-5-2-3-1	HS102 x AC 142	Determinate, medium fruited
LE 40	Pantnagar	AC 111		Indeterminate, large fruited, smooth fruited
LE 44	A.I.C.V.I.P.	King Kig	-	-
LE 47	Pantnagar	11-2-74-3-1	HS 102 x AC 142	-
LE 69	I.A.R.I.	Pusa Early Dwarf	-	Semideterminate, moderately ribbed fruit surface
LE 71	Pan tnaga r	11-5-2-0-1	HS 102 x AC 142	Determinate, medium fruited

Table 3.1 (Contd.)

	ession ber	Source	Cultivar name	Pedigree	Important traits
LE	7 ¹ +	Pantnagar	. =		
LE	75	AVRDC, Taiwan	CL 8d-0-7-1 GS	VC 11-1-2-1B x Venus	Determinate, early bearing, heat tolerant, bacterial wilt resistant, nematode resistant
LE	78	AVRDC, Taiwan	CL 11d-0-2-2-0-3UG	VC 9-1-2-9B x Venus	Determinate, early bearing, heat tolerant, bacterial wilt resistant, nematode resistant
LE	7 9	AVRDC, Taiwan	CL 32d-0-1-19 GS	VC 9-1-2-3 x Venus	Indeterminate, early bearing, heat tolerant, bacterial wilt and nematode resistant
LE	82	AVRDC, Taiwan	CL 143-0-6-9 UG	VC 48-1 x Tamu Chico III	Determinate, early bearing, heat tolerant, bacterial wilt and nematode resistant
LE	84	AVRDC, Taiwan	LTGS	VC 48-1	Determinate, early bearing, heat tolerant, bacterial wilt and nematode resistant.

Table 3.1 (Contd.)

Accession number	Source	Cultivar name	Pedigree	Important traits
LE 87	N.B.P.G.R.	La Bonita	•	
LE 88	T.N.A.U.	PKM - 1	sa	
LE 90	T.N.A.U.	Co-2	•	
LE 93	IIHR.Bangalore		-	-
LE 94	Takii & Co. Ltd., Kyoho, Japan	Master No.1	-	em-
LE 95	Takii & Co.Ltd., Kyoho, Japan	Hope No.1	-	; -
LE 97	AVRDC, Taiwan	CL 9-0-0-1	VC 11-1-2-1 B x Venus	-
le 98	AVRDC, Taiwan	CL 143-0-10-3	VC 48-1 x Tamu Chico II	.
LE 99	AVRDC, Taiwan	CL 123-2-4	ah TM - 2a x VC 8-1-2-1	- .
LE 101	AVRDC, Taiwan	CL 1591-5-0-1-6	F 63 - 19 x CL 11-0-2-1-	-0-2 -
LE 105	AVRDC, Taiwan	L1	VC 48-1	A
LE 106	AVRDC, Taiwan	L 387	White skin	
LE 107	ining	Tropic	_	We.

Table 3.1 (Contd.)

Accession number	Source	Cultivar name	Pedigree	Important traits
LE 108	Strocks Seed Ltd., Canada	New York Special	GB '	-
LE 111	Strocks Seed Ltd., Canada	Quinte	-	-
LE 114	Strocks Seed Ltd., Canada	Veepick VF 419 A	-	-
LE 117	Strocks Seed Ltd., Canada	Starshot 408	-	-
LE 118	Strocks Seed Ltd., Canada	Veepro 464 A	- -	≒
IE 119	Strocks Seed Ltd., Canada	Starfire	-	-
LE 121	Strocks Seed Ltd., Canada	Veeroma VF 418	.	-
LE 124	Strocks Seed Ltd., Canada	Basket Vee 326	-	-
IE 13 ¹ +	-	-	BWN 21 x HS 10	1 -
LE 158	Petro Seed Co. Inc.Calipso	-	-	<u>.</u>

Table 3.1 (Contd.)

Acces numbe	ssion	Source	Cultivar name	Pedigree	.Important traits
LE 1	160	AVRDC, Taiwan	VC 98-1	. •	
LE' 1	161	AVRDC, Taiwan	VC 48-1-1-2	-	.
LE 1	162	AVRDC, Taiwan	VC 8-1-2-1	_ -	
LE 1	163	AVRDC, Talwan	VC 9-1-UG	-	••••••••••••••••••••••••••••••••••••••
IE 1	164	AVRDC, Taiwan	VC 11-1 UG	_	-
IE 1	165	AVRDC, Taiwan	VC 2029	•	, -
LE 1	166	AVRDC, Taiwan	VC 8-1-2-1	-	-
LE 1	i6 7	AVRDC, Taiwan	VC 11-2-2-79	•	50
Le 1	68	AVRDC, Taiwan	(TR x VC 11-2)-2-1	•	alas
LE 1	169	AVRDC, Taiwan	(TR x VC 1+8-1)-11-2	•	-
le 1	70	AVRDC, Taiwan	Walter		· • .
LE 1	78	AVRDC, Taiwan	Florida MH	~	-
LE 1	172	AVRDC, Taiwan	Venus	Louisiana Pink x Beltsville 3814	Reported resistant to bacterial wilt
Le 1	173	AVRDC, Taiwan	Saturn	Louisiana Pink x Beltsville 3814	Reported resistant to bacterial wilt

Table 3.1 (Contd.)

Acc	ession ber	Source	Cultivar name	Pedigree	Important traits
LE	174	AVRDC, Taiwan	Galaxy	•	•
LE	175	AVRDC, Taiwan	Anahu	-	Reported resistant to nematodes
LE	176	AVRDC, Taiwan	Kewalo	,	
LE	177	AVRDC, Taiwan	White skin	-	· .
LE	178	AVRDC, Taiwan	Green Fruit	-	**
le	179	AVRDC, Taiwan	Tropic	· -	- `.
LE	180	AVRDC, Taiwan	Hotset	-	
IE	181	Herbrew Univ. of Jeruselem-Israel	Hosen - Elion	•	829
LE	182	Herbrew Univ. of Jeruselem-Israel	Game d	-	Indeterminate, oval fruited
LE	183	Holland	Mandel 502 VFNF - 1 - RS	80	-
LE	184	Holland	Monprecos RS	-	-
LE	185	Holland	Bonset F-IRS	-	-
Œ	186	Holland	Tobol (No.748) WFNF - IRS.	-	_

Table 3.1 (Contd.)

Acces numbe		Source	Cultivar name	Pedigree	Important traits
LE 1	187	Redwood City, Seed Co., California	Roma	Cas	Semideterminate, bushy, extrovert, deep yellow flowers, small smooth fruits, nipple tipped
LE 1	88	Redwood City Seed Co., California	Yellow Pear	@	
LE 1	189	Redwood City Seed Co., California	Red Cherry	**	•
LE 1	190	Redwppd City Seed Co., California	Beefsteak	-	, -
LE 1	191	Redwood City Seed Co., California	India River	-	•
LE 1	192	Redwood City Seed Co., California	Early Large Red		-
LE 1	193	NSC, New Delhi	Sioux	~	Indeterminate, large fruited
le 1	194	Hissar	HS-110	-	Determinate, large fruited
LE 1	195	Yates Co., Australia	Red Cloud	-	-
IE 1	196	Yates Co., Australia	Grosse Lisse	- ,	· _

Table 3.1 (Contd.)

Accession number	Source	Cultivar name	Pedigree	Important traits
LE 19 7	Yates Co., Australia	Rouge De Marmande	•	-
E 198	Vellayani	Local		-
E 199	Vellayani	Local	-	-
	÷			

Table 3.2 Seedling characters

Gene	Name	Phenotype	Locus	
	Monie	rneno type	Chromosome	Site
a	anthocyaninless	Completely anthocyaninless	11L ·	68
aw2	without anthocyanin ²	Completely free of anthocyanin		
atv	atroviolacea	Intense anthocyanin pigmentation	7L	
dkv	dark veined leaf	seedling leaves yellow green, veins, always draker green	-	
Fw	Furrowed	plant stunted, cotyledons deeply fur	rowed	
hp-2	•	high pigment -	11L	95
lg	light green	light green foliage colour	108	18
.1g ₂ ,	light green ₂	cotyledons light yellow, leaves pale	green	
^{1g} 3	light green3	cotyledins and leaves light green, cotyledons fade to yellow, mature plants pale green		
pg ₂	pale green			
pg ₃	pale green3	· .		
v	virescent	white seedlings turning to green		

L = long arm of chromosome

S = short arm of chromosome

Table 3.3 Juvenile characters

_			Locus		
Gene	Name	Phenotype	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	authocyanin reduced	young leave of older plants pigmented	2L	58	
au	aurea	bright yellow foliage	18	32	
aud	aurold	uniform yellow foliage	128		
oi.	bifurate	extreme stem fasciation	12L	97	
bip	bipinnata	highly divided leaves	2L	68	
br	brachytic	internodes shortened	15	0	
3	potate leaf	fewer leaf segments	6L	10 4	
clau	clausa	leaves subdivided, segment tip acute	¹ ts	0	
cpt	compact	habit compact, exceedingly branched	8r	1 6	
dp	drooping leaf	leaf drooping, elongate, dark, green stem weak, slender and prostrate			
е	entire	leaf segments few, mid vein distorted	f+T*	66	
fy	field yellow	bright yellow green foliage in the fiel	.đ		
'n	hair absent	large trichomes absent	10L	46	

Table 3.3 (Contd.)

Gene	Neme	Phenotype	Locus	
			Chromosome	Site
Hr	Hirsute	long hairs on adaxial leaf surface	8L	46
Hrt	Hirtum	increased density of larger trichomes	7 L	
lg	light green	light green foliage colour	108	18
ni	nitida	leaves long petioled, pinnae deeply cut	8 1	45
od Pg ₂ Pg ₃	Odourless palegreen-2 palegreen-3	herbage with little or no volatiles	3.5 m	
sf	solanifolia	pinnae entire, epiculate, concave	3L	111
tp	tripinnate	plant retarded; leaves tripinnately compound	8 T	22
٧i	villous	stem very hairy	10	
wd	wilty dwarf	plants stunted, leaves grey green, droop if drought stressed	98	20
wt	wilty	leaf margins curl adaxially	5 L	55
Wo	Woolly	all parts densely pubescent	2L	46
уg ₂	yellow-green	foliage uniformly yellow green	128	

Table 3.4 Adult plant characters

Gene	Name	Phenotype Chromos	Locus	
			ome	Site
ap	apetalous.	most or part of corolla lacking	11	114
at	apricot	fruit flesh colour	5	-
bk	beaked	fruit stylar end pointed	2Γ	38
b1	blind	stem terminate in first inflorescence	11 L	75
bs	brown seeds	endosperm brown	1\$	17
bu	bushy	inflorescences and intermodes fore-shortened	8 L	18
ch	chartreuse	corolla greenish yellow	8L	28
ck	corky fruit	fruit wall splits	-	_
cl-2	cleistogamous-2	flowers open only slightly	, 6 L	113
el	elongated fruits	🖛 💛 ,	-	-
ex	exserted	- ;	.	- -
f_	fasciated	fruits fasciated, many loculed	11L	95
$\mathbf{f}^{\mathtt{D}}$	fasciated	-	-	**
fl	fleshy calyx		_	-
Fs	Fruit stripe	broad distal stripe as in Lycoperaicon hirsutum	108	11
g	grooved	· ·	-	45
gf	green fruit	chlorophyll persist in the fruit locules	8L	1 1)
gs	green stripe	unripe fruit with radial green stripes	7S	5
hp	high pigment	fruit pigments intensified	128	-
Ip	Intense pigmentation	dark pigmentation of the fruit both in ripe and unripe stages	-	de

Table 3.4 (Contd.)

Can -	Name	The same having	Locus	
Gene		Phenotype	Chromosome	Site
j	jointless	pedicel jointless, inflorescence leafy	118	28
lu	luteola	corolla light green	1	-
ac	macrocalyx	sepals and inflorescence leafy	5 s	-
n	nipple tip	at stylar end of the fruit	5	-
nor	Mon ripening	fruit ripening greatly retarded	108	•
Vr	Never ripe	fruit ripen slowly to dull orange	· 9	-
)	ovate	fruits elongate	2 L	55
ָ	peach	fruit surface dull, more hairy	2L	67
est	persistent style	developing into beak	7s	5
pat	parthenocarpic fruits	seedless fruits	-	-
1	radial cracking resista	-	-	
·2	yellow fruit flesh, lig	ghter yellow flowers	-	-
rin	ripening inhibitor	fruits ripen very slowly to yellow	5 S	0 -
3	Compound cluster	inflorescence strongly proliferated	2L	30
sp	selfpruning	determinate habit	6 L	-
spf	superpuff	extremely puffy, hollow locals, and bell pepper shaped fruits	-	-
ss	spong seed	smooth, but spongy seed	*	-
1	uniform ripening	unripe fruits lack bicolour pigmentation	1 08	14
7 0	yellow calyx	when fruit ripens	_	_

RESULTS

EXPERIMENTAL RESULTS

The data collected were analysed and are presented under the following sub-heads

- A Cataloguing
- B Estimation of response to selection
- C Evaluation for field tolerance to bacterial wilt
- D Artificial inoculation for testing resistance
- E Chemical analysis of resistant line

A Cataloguing

Seventyeight lines germinated and genetic cataloguing of the plants was done in the seedling stage (Table 4.1.a) and juvenile stage (Table 4.1.b). The line IE 79 was studied for adult plant characters (Table 4.1.c).

In the nursery, the seedlings were critically studied for intensity and spread of purple colour which varied greatly. The purple colour character was partitioned into five groups (Table 4.2). The lines IE 186 and IE 196 were observed completely free of anthocyanin. The line IE 79 had its hypocotyl, epicotyl, cotyledons and first leaf purple pigmented - when observation was taken 18 days after sowing.

The 78 lines were further classified into two groups - right and left - based on phyllotaxy (Table 4.3).

B. Estimation of response to selection

The line IE 79 survived the onslaught of bacterial wilt. The population was studied for nine polygenic characters - plant height, primary branches per plant, days to first fruit set, days to first harvest, fruits per plant, marketable fruits per plant, locules per fruit, marketable fruit weight per plant and total fruit weight per plant. The statistical properties of IE 79 population indicated that the population was a normal one for characters plant height, primary branches per plant, days to first fruitset, days to first fruit harvest, marketable fruits per plant and locules per fruit (Table 4.4). The averages - mean, median and mode - coincided for the above characters and thus justified the properties of normally distributed plant population.

The progenies derived from the population based on mass selection (intensity of selection 4.47%), single plant selection (pureline) and bulk selection were grown in a randomised block design with six replications. The data were analysed as per completely randomised design due to non-significance of the variation due to blocking (Table 4.5).

The progenies developed through the above three methods of selection were significantly different for plant height and days to first fruit set. No significant difference was observed among the progenies developed through the three methods of selection for primary branches per plant, days to first fruit harvest, total fruits per plant, marketable fruits per plant, locules per fruit, percentage of small fruited plants, medium fruited plants and large fruited plant, percentage of plants with no cracked fruits, medium cracked fruits and highly cracked fruits, marketable fruit weight, and total fruit weight.

Mean performances of the population selected plants and selected elite single plant and their respective progenies for 15 polygenic characters are presented in Table 4.6. The progenies derived through mass selection was superior to progenies through bulking for days to first fruit set, days to first harvest, fruits per plant, marketable fruits per plant and marketable fruit weight per plant. The progenies developed through pureline selection were superior to those developed through bulking for days to fruit set, days to first harvest, marketable fruit weight per plant, percentage of large fruited plants and percentage of plants with cracked fruits. The bulk

progenies were superior to those developed by mass and pureline selection for higher locules per fruit, total percentage of medium fruited plants and total fruit weight.

The values of selection differential (S), selection response (R) and realised heritability (h2) for 10 polygenic characters are presented in Table 4.7. The selection response through mass selection was positive for primary branches per plant and locules per fruit. The selection response through pureline selection was positive for primary branches per plant and locules per fruit. Selection response through bulk was positive for plant height and primary branches per plant. The realised heritability was very high (0.88) for days to first harvest indicating thereby the scope of going for selection to develop still The selection responses were obviously earlier lines. negative through bulk (-25.99), mass (-13.31) and pureline (-20.45) selection for days to first harvest.

C. Evaluation for field tolerance to bacterial wilt

Six independent trials were conducted to evaluate resistance of the line under field conditions (Table 4.8). Wilting, where coze test was positive, was more in juvenile stage as compared to one observed in adult stage.

Percentage of plants wilted ranged from 1.11 per cent during February-May 1981 to 46.91 per cent in September-December 1980 observed during juvenile stage. Percentage wilting ranged from zero during September-December 1980 and February-May 1981 to 1.34 during April-August 1980 in the adult plant stage.

D Artificial inoculation for testing resistance

1. Screening using infected soil as potting mixture

Out of 30 seedlings of LE 79 transplanted in pots where the soil was taken from the diseased field, no seedlings wilted.

2. Screening for wilt resistance through artificial inoculation

All the ten plants of LE 79 wilted within one week after inoculation along with the susceptible line.

E Chemical analysis of the resistant line

The fruits of LE 79 collected from progenies developed through bulking, mass selection and pureline selection were analysed for total soluble solids, ascorbic acid and pH. Total soluble solid content as read by Brix ranged from 3 to 6 with an average of five in progeny

developed through mass selection and ranged from 4 to 5 in progeny developed through pureline selection. Ascorbic acid content ranged from 16.45 to 29.61 mg/100 g in progeny developed through bulking, 18.06 to 40.20 mg/100g in progeny developed through mass selection and 18.38 to 33.03 mg/100 g in progeny developed through pureline selection. The pH of the fruits ranged from 5.8 to 6.0.

Table 4.1.a Seedling characters

IE 75
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+} , lg^{+} , pg^{+} , pg^{+} , pg^{+} , v^{+} .

LE 78
$$a^+$$
-, atv^+ -, av^{2+} -, dkv^+ -, Fv^+ -, $hp-2^+$ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 79
$$a^+$$
-, av^2 --, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_3^+ -, v^+ -

IE 82
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 84
$$a^+$$
, atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp-2^+$, $1g^+$, $1g^+_2$, $1g^+_3$, pg^+_2 , pg^+_3 , v^+

IE 87
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$, $1g^{+}_{3}$, pg^{+}_{3} , pg^{+}_{3} , pg^{+}_{3} , v^{+}

IE 88
$$a^+-$$
, atv^+- , $aw^{2+}-$, dkv^+- , Fw^+- , $hp-2^+-$, $1g^+-$, $1g^+_2-$, $1g^+_3-$, pg^+_2- , pg^+_3- , v^+-

LE 90
$$a^+$$
-, av^2 --, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg^+ -, lg^+ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 93
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 95
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$, $1g^{+}_{3}$, pg^{+}_{2} , pg^{+}_{3} , v^{+}

LE 97
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$, $1g^{+}_{3}$, pg^{+}_{2} , pg^{+}_{3} , v^{+}

LE 98
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 99
$$a^{+}$$
-, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, lg^{+} -, lg^{+} -, pg^{+}_{3} -, v^{+} -

IE 101
$$a^{+}$$
, av^{2} , av^{2} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+} , lg^{+} , pg^{+} , pg^{+} , v^{+}

IE 105
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g^+_2$ -, $1g^+_3$ -, pg^+_2 -, pg^+_3 -, v^+ -

LE 106
$$a^+$$
-, atv^+ -, av^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg^+ -, lg^+ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 107
$$a^{+}$$
, av^{2+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+}_{3} , lg^{+}_{3} , pg^{+}_{2} , pg^{+}_{3} , v^{+}

IE 108
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 111
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+} , pg^{+} , pg^{+} , pg^{+} , v^{+}

LE 114
$$a^+$$
, atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp-2^+$, lg^+ , lg^+_2 , lg^+_3 , pg^+_2 , pg^+_3 , v^+ .

LE 117 a^+ , atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp-2^+$, lg^+ , lg^+_2 , lg^+_3 , pg^+_2 , pg^+_3 , v^+ .

LE 118 a^+ , atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp-2^+$, lg^+ , lg^+_2 , lg^+_3 , pg^+_2 , pg^+_3 , v^+ .

LE 119
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+}_{3} , pg^{+}_{3} , pg^{+}_{3} , v^{+}

IE 121
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 124
$$a^+$$
, atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp-2^+$, lg^+ , lg_2^+ , lg_3^+ , pg_2^+ , pg_3^+ , v^+

LE 134
$$a^+$$
, atv^+ , aw^{2+} , dkv^+ , Fw^+ , $hp=2^+$, $lg^+=$, lg_2^+ , lg_3^+ , pg_2^+ , pg_3^+ , $v^+=$

LE 158
$$a^+-$$
, atv^+- , $aw^{2+}-$, dkv^+- , Fw^+- , $hp-2^+-$, lg^+- , lg_2^+- , lg_3^+- , pg_2^+- , pg_3^+- , v^+-

LE 160
$$a^{+}$$
-, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, $1g^{+}$ -, $1g^{+}$ -, pg^{+}_{3} -, pg^{+}_{3} -, v^{+} -

LE 161
$$a^{+}$$
-, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, $1g^{+}$ -, $1g_{3}^{+}$ -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+} -

IE 162
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 163	a^{+} -, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, lg^{+} -,
	$1g_2^+ -, 1g_3^+ -, pg_2^+ -, pg_3^+ -, v^+$
IE 164	a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$,
	$1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -
IE 165	a^{+} -, atv^{+} -, av^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, lg^{+} -,
	$1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -
IE 166	a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
	lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -
LE 167	a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$,
	$1g_2^+ -, 1g_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -$
IE 168	a^{+} -, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, lg^{+} -,
	$1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -
le 169	a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
	$1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -
IE 170	a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, $1g^{+}$,
	$1g_2^+ -, 1g_3^+ -, pg_2^+ -, pg_3^+ -, v^+$
LE 171	a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
	$lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -$
IE 172	a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
	lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 173
$$a^{+}-$$
, $atv^{+}-$, $aw^{2+}-$, $dkv^{+}-$, $Fw^{+}-$, $hp-2^{+}-$, $1g^{+}-$, $1g^{+}-$, $1g^{+}-$, $1g^{+}-$, $pg^{+}-$, $pg^{+}-$, $pg^{+}-$, $v^{+}-$

LE 174 $a^{+}-$, $atv^{+}-$, $aw^{2+}-$, $dkv^{+}-$, $Fw^{+}-$, $hp-2^{+}-$, $1g^{+}-$,

- LE 177 a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+} , pg^{+}_{3} , pg^{+}_{3} , v^{+}
- IE 178 a^{+} -, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, $1g^{+}$ -, $1g_{2}^{+}$ -, $1g_{3}^{+}$ -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+} -
- LE 179 a^+- , atv^+- , $aw^{2+}-$, dkv^+- , Fw^+- , $hp-2^+-$, lg^+- , lg_2^+- , lg_3^+- , pg_2^+- , pg_3^+- , v^+-
- LE 180 a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+}_{3} , pg^{+}_{2} , pg^{+}_{3} , pg^{+}_{3} , v^{+} .
- IE 181 a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+}_{3} , pg^{+}_{2} , pg^{+}_{3} , v^{+}
- IE 182 a^{+} , atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+} , lg^{+} , pg^{+} , pg^{+} , pg^{+} , v^{+} .

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a^{+}, atv<sup>+</sup>-, av^{2+}-, dkv^{+}-, Fw^{+}-, hp-2^{+}-, lg^{+}-,
LE 183
              1g2 -, 1g3 -, pg2 -, pg3 -, v+-
              a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
IE 184
             1g2 -, 1g3 -, pg2 -, pg3 -, v+-
IE 185 at-, atv-, aw2+-, dkv+-, Fw+-, hp-2+-, 1g^+-,
             1g_{2}^{+} -, 1g_{3}^{+} -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+}
             at-, atvt-, aw2+-, dkvt-, Fwt-, hp-2t-, lgt-,
IE 186
             1g_{2}^{+} -, 1g_{3}^{+} -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+}
             a^{+}, atv^{+}, av^{2+}, dkv^{+}, Fw^{+}, hp-2^{+}, lg^{+},
IE 187
             1g_{2}^{+} -, 1g_{3}^{+} -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+}
             at-, atv-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
IE 188
             1g2 -, 1g3 -, pg2 -, pg3 -, v+-
             a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
IE 189
             1g_2^+ -, 1g_3^+ -, pg_2^+ -, pg_3^+ -, v^+-
             a^{+}, atv^{+}, aw^{2+}, dkv^{+}, Fw^{+}, hp-2^{+}, lg^{+},
IE 190
             1g<sub>2</sub> -, 1g<sub>3</sub> -, pg<sub>2</sub> -, pg<sub>3</sub> -, v<sup>+</sup>-
             a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
LE 191
             1g_{2}^{+} -, 1g_{3}^{+} -, pg_{2}^{+} -, pg_{3}^{+} -, v_{-}^{+}
             a+-, atv+-, aw2+-, dkv+-, Fw+-, hp-2+-, lg+-,
LE 192
             1g_{2}^{+} -, 1g_{3}^{+} -, pg_{2}^{+} -, pg_{3}^{+} -, v^{+}
```

IE 193
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g^+_2$ -, $1g^+_3$ -, pg^+_2 -, pg^+_3 -, v^+ -

IE 194
$$a^+$$
-, atv^+ -, av^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, lg^+ -, lg_2^+ -, lg_3^+ -, pg_2^+ -, pg_3^+ -, v^+ -

IE 195
$$a^{+}$$
, atv^{+} , aw^{2+} , dkv^{+} , Fw^{+} , $hp-2^{+}$, lg^{+} , lg^{+}_{3} , pg^{+}_{2} , pg^{+}_{3} , v^{+}

LE 196
$$a^+$$
-, atv^+ -, aw^{2+} -, dkv^+ -, Fw^+ -, $hp-2^+$ -, $1g^+$ -, $1g_2^+$ -, $1g_3^+$ -, pg_2^+ -, pg_3^+ -, v^+ -

LE 197
$$a^+-$$
, atv^+- , $aw^{2+}-$, dkv^+- , Fw^+- , $hp-2^+-$, lg^+- , lg_2^+- , lg_3^+- , pg_2^+- , pg_3^+- , v^+-

LE 198
$$a^+-$$
, atv^+- , $aw^{2+}-$, dkv^+- , Fw^+- , $hp-2^+-$, lg^+- , lg_2^+- , lg_3^+- , pg_2^+- , pg_3^+- , v^+-

IE 199
$$a^{+}$$
-, atv^{+} -, aw^{2+} -, dkv^{+} -, Fw^{+} -, $hp-2^{+}$ -, lg^{+} -, lg^{+} -, pg^{+} -, pg^{+} -, v^{+} -

Table 4.1.b Juvenile characters*

- LE 5 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 18 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, bi⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- IE 23 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip bip, br⁺-, c⁺-, clau clau, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 34 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-

^{*} Observations were not recorded for the lines wilted very early.

- LE 40 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 44 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 47 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 74 acu⁺-, aer aer, al⁺-, are are, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, 1g⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-

- LE 75 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 78 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 79 acu⁺-, aer aer, al⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, hi⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 82 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bl⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-

- LE 84 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 87 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 88 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 90 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy^{*}-, h⁺-, Hr⁺-, Hr⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-

- LE 93 acut-, aer aer, alt-, aut-, aud-, bit-, bipt-, brt-, ct-, claut-, cptt-, dkvt-, dpt-, et-, fyt-, ht-, Hrt-, lgt-, nit-, Odt-, pgt-, pgt-, sft-, tpt-, vlt-, wdt-, wtt-, Wot-, ygt-
- LE 94 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-,
 pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg₂⁺-
- LE 95 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy^{*}-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 97 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-

- LE 98 acu⁺-, aer aer, al⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 99 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dpt⁻-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 101 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-,
 pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg₂⁺-
- LE 105 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-

- LE 106 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-,
 pg⁺₂ -, pg⁺₃ -, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg⁺₂ -
- IE 107 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h^{*}-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 108 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 121 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br br, c c, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e e, fy⁺-, h h, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺- sf sf, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-

- LE 160 acu⁺-, aer aer, al⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 161 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺_, or⁺-, e⁺-, clau⁺-, cpt⁺-, dkv⁺-, dpt⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, lg⁺-, ni⁺-, Od^{*}-,
 pg⁺₂ -, pg⁺₃ -, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg⁺₂ -
- LE 162 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hrt⁺-, Hrt⁺-, 1g⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 163 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dp⁺-, dkv⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, lg⁺-, ni ni, Od⁺-, pg₂⁺-,
 pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-,
 yg₂⁺-

- LE 164 acu⁺-, aer aer, al⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-
- LE 165 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 166 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-,
 pg⁺₂ -, pg⁺₃ -, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg⁺₂ -
- LE 167 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₄⁺-

- LE 170 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-, bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hr⁺-, 1g⁺-, ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-, wo⁺-, yg₂⁺-
- LE 182 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, 0d⁺-,
 pg⁺₂ -, pg⁺₃ -, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg⁺₂ -
- LE 184 acu⁺-, aer⁺-, al⁺-, are⁺-, au⁺-, aud⁺-, bi⁺-,
 bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-, dp⁺-,
 e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-, ni⁺-, Od⁺-,
 pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-, vi⁺-, wd⁺-, wt⁺-,
 Wo⁺-, yg₂⁺-



LE 186 acu⁺-, aer aer, al⁺-, au⁺-, aud⁺-, bi⁺-,
bip⁺-, br⁺-, c⁺-, clau⁺-, cpt⁺-, dkv⁺-,
dp⁺-, e⁺-, fy⁺-, h⁺-, Hr⁺-, Hrt⁺-, lg⁺-,
ni⁺-, Od⁺-, pg₂⁺-, pg₃⁺-, sf⁺-, tp⁺-,
vi⁺-, wd⁺-, wt⁺-, Wo⁺-, yg₂⁺-

Table 4.1.c Adult plant characters

LE 79 ap⁺-, at⁺-, bk⁺-, bl⁺-, bs⁺-, bu⁺-, ch⁺-, ck ck, cl-2⁺-, el⁺-, ex ex, f⁺-, f^D+-, fl⁺-, Fs⁺-, g⁺-, gf⁺-, gs⁺-, hp⁺-, Ip⁺-, j⁺-, lu lu, mc⁺-, n⁺-, nor⁺-, Nr⁺-, o⁺-, p⁺-, pst⁺-, rl⁺-, rl⁺-, rl⁺-, rin⁺-, s⁺-, spf⁺-, ss⁺-, u⁺-, ye⁺-

Table 4.2 Classification of tomato lines based on intensity and spread of anthocyanin pigment in seedling stage

ı		Classes*		
1	2	3	ýŧ	5
LE 186	LE 69	IE 31+	LE 5	IE 23
LE 196	LE 95	IE 40	le 18	LE 78
	IE 107	TE 1774	LE 71	LE 79
	LE 11 9	LE 47	LE 74	IE 1 65
	LE 160	le 82	IE 75	LE 174
	le 185	IE 93	IE 84	LE 175
·	LE 193	LE 97	IE 87	LE 177
	LE 194	IE 101	LE 88	LE 178
	IE 199	LE 106	IE 90	LE 180
		LE 118	IE 94	-
		LE 164	IE 98	
		LE 1 66	IE 99	
		IE 167	IE 105	
		LE 172	IE 108	•

* 1 Seedlings completely free of anthocyanin

2 Seedlings with upper part of the hypocotyl region free of anthocyanin

3 Seedlings with full hypocotyl region with anthocyanin 4 Seedlings with hypocotyl and epicotyl region with anthocyanin

Seedlings with hypocotyl, epicotyl, cotyledons and first leaf with anthocyanin

Table 4.2 (Contd.)

Classes							
1	2		3		l _t .	5	
		1E	179	LE	114		
		IE	181	LE	117		
		TE.	183	LE	111		
		Œ	184	IE	121		
		IE	188	LE	124		
		LE	189	LE	158		
•	-	IH	190	Œ	161		
		<u>L</u> E	192	IE	162		
		LE	195	Œ	163		
	,	LE	197	LE	1 68		
		IE	198	TE	169		
•				LE	170		
				IE	171		
				LE	173		
		•		ĬE	176		
				LE	182	·	
			,	LE	185		
	,			LE	187		
				LE	191		

Table 4.3 Classification of tomato seedlings based on phyllotaxy

Class	30 .	Class	ses
Left	Right	Left	Right
LE 18	LE 5	LE 165	LE 161
LE 23	LE 44	le 166	IE 164
TE 31+	IE 47	LE 167	LE 168
IE 40	LE 69	IE 169	LE 170
LE 71	LE 74	LE 173	IE 171
IE 75	LE 79	LE 174	IE 172
IE 78	IE 84	LE 176	LE 175
LE 82	LE 90	LE 177	LE 178
IE 87	LE 93	LE 179	LE 180
LE 88	LE 97	LE 182	IE 181
IE 94	LE 99	IE 183	LE 185
LE 95	IE 101	IE 184	LE 186
I E 98	IE 105	IE 188	LE 187
LE 106	IE 107	IE 189	LE 188
LE 111	LE 108	IE 191	LE 190
IE 121	LE 114	LE 192	LE 195
IE 124	LE 117	LE 193	IE 196
LE 158	LE 118	LEE 194	LE 197
LE 162	LE 11 9	LE 199	LE 198
IE 163	IE 160		

Table 4.4 Statistical properties of the base population of LE 79

Characters	Range	Mean	Median	Mode	Standard deviation	Coefficient of variation
Plant height (cm)	50-125	70.74 ± 2.2	23 71	71	17.00	24.04
Primary branches per plant	1-8	3.97 ± 0.1	19 4	1 +	1.43	35.96
Days to first fruit set	3 4- 82	58.82 ± 1.4	+3 58	50	11.52	19.58
Days to first fruit harvest	66-113	94.36 ± 1.5	53 94	94	10.94	11.59
Fruits per plant	2 - 53	17.02 ± 2.0	07 14	3	14.37	84.43
Marketable fruits per plant	1-48	14-25 ± 1.8	36 9	7	12.88	90.43
Locules per fruit	2 - 6	3.69 ± 0.1	10 . 4	1.	0.69	18.71
Marketable fruit weight per plant (g)	39-1541	517.79 ± 58.5	52 ¼ 1 0	79	405.43	78.30
Total fruit weight per plant (g)	39-1485	445.53 ± 54.5	58 351	-	378.13	84.87

Table 4.5 General analysis of variance

<u> </u>					Mean squ	ares			
Sources of variation	df	Plant height (cm)	Primary branches per plant	Days to first fruit set	Days to first fruit harvest	Total fruits per plant	Market- able fruits per plant	Locules per fruit	Small fruited plants (%)
Methods of selection	2	223.18*	0.29	23.35*	13.10	52.77	23.46	0.08	345.23
Error	12	49.59	0.25	2.19	6-40	18.64	17.21	0.03	92.70

''		•	<u> </u>	•	Mean squares	- · · · · · · · · · · · · · · · · · · ·	 	
Sources of variation	₫₽	Medium fruited plants (%)	Large fruited plants (%)	Plants with no cracked fruits (%)	Plants with medium cracked fruits (%)	Plants with highly cracked fruits (%)	ble fruit	er weight
Methods of selection	2	19.49	214.77	0.86	38.71	609.79	¥ 4 38.91	1719.88
Error	12	96.74	131.60	52.25	9 2.41	181.07	31495.78	34140.21

Table 4.6 Mean performance of base population, selected plants, single plant and their respective progenies

Characters	:	Mean		_ CD
	Bulk	Mass	Pureline	(P=0.05)
Plant height (cm)	72.00 (70.74)		59•12 (74•00)	9.70
Primary branches per plant	4.46 (3.97)	4.68 (4.67)	4.20 (4.00)	-
Days to first fruit set	37.20 (58.86)	36.10 (48.00)	33.60 (56.00)	2.04
Days to first fruit harvest	68.37 (94.36)	65.99 (76.00)	66.55 (87.00)	-
Fruits per plant	16.32 (17.02)	19•51 (박• 00)	12 . 99 (53 . 00)	-
Marketable fruits per plant	13.01 (14.25)	15.98 (39.67)	11. 7 7 (48.00)	-
Locules per fruit	3.65 (3.69)	3.63 (3.33)	3.42 (3.00)	
Small fruited plants (%)	8.35 (12.50)	22.73 (9.00)	5.00 (0.00)	-
Medium fruited plants ² (%)	74.94 (68.75)	73.15 (100.00)	71.00 (100.00)	alpui»
Large fruits plants (%)	16.90 (18.75)	4.27 (0.00)	2½.00 (0.00)	-

Data in parentheses indicate the mean performance of population, selected plants and single plant

- 1 Plants with average fruit weight less than 20 g
- 2 Plants with average fruit weight of 20 40 g
- 3 Plants with average fruit weight more than 40 g

Table 4.6 (Contd.)

Characters	Mean	ı	CD		
	Bulk	Mass	Pureline (P =	0.05)	
Plants without cracked fruits (%)	43.45 (50.00)		43.85 (0.00)	•	
Plants with medium cracked fruits 5 (%)	3 ⁴ •39 (29•17)	35.49 (66.67)	37.58 (100.00)	-	
Plants with highly cracked fruits 6(%)	28.73 (20.83)	27.06 (0.00)	22.14 (0.00)		
Marketable fruit weight per plant (g)		391.87 (1156.67)	433.50 (1118.00	-	
Total fruit weight per plant (g)	507.00 (51 7. 79)	485.27 (1296.33)	470.10 (1325.00)		

⁴ Plants with zero per cent cracked fruits

⁵ Plants with >0 - 25 per cent cracked fruits

⁶ Plants with more than 25 per cent cracked fruits

Table 4.7 Values of selection differential (S), selection response (R) and realised heritability (h2)

Characters		S	R	h ^{2*}
Plant height (cm)	В		1.26	
	M	2.26	-10.52	-
	P	3.26	-1 4.88	-
CD (P = 0.05)			9.70	
Primary branches per plant	В		0.50	-
	M	0.70	0.01	0.10
	P	0.04	0.36	
CD (P = 0.05)			-	
Days to first fruit set	В		-21.60	
	M	-10.80	-11.90	-
	P	- 2.80	-22.40	#¢#
CD (P = 0.05)			2.49	
Days to first fruit harvest	В		-25.99	
•	M	-15.05	-13.99	0.88
	P.	- 7.36	-20.45	
CD (P = 0.05)			3.62	

^{*} Negative values and values exceeding one are omitted

B = Bulk

M = Mass

P = Pureline

Table 4.7 (Contd.)

Characters		s,	R	h ^{2*}
Potal fruits per plant	В		-0.70	-
	M	26.98	-24.49	
	P	35.98	- 40.01	-
CD (P = 0.05)			7.71	
Marketable fruits per plant	В		-1.24	-
	M	25.42	- 23.68	-
	P	33•75	-36.23	
CD (P = 0.05)			4.57	
Locules per fruit	В		-0.01+	
,	M	-0.36	0.30	-
	P	-0.69	0.42	-
CD (P = 0.05)		` • • • • • • • • • • • • • • • • • • •	0.22	
Marketable fruit weight	В	•	- 69.96	
per plant (g)	M	771.13	- 764 . 79	-
	P	672.40	-684.60	-
. CD (P = 0.05)		•	।।। 0.19	,
Total fruit weight per	В	•	- 10•79	
plant (g)	M	778.54	* -	•
	P P	807.21		
	•	00/121	• •	
CD (P = 0.05)		4	53.65	

Table 4.8 Resistance of IE 79 under field conditions

T)	managa datau		Juvenile stage		Adult stage	
Popu	lation	Number of plants	plants wilted	% of plants wilted	Plants wilted	% of plants wilted
Base population 1		81	38	46.91	0	0
Progenie	_s 2	•			•	
_	Mass	360	5	1.38	- , O	.0
	Bulk	360	5	1.11	0	0
	Pureline	72	2	2.77	0	0
	Bulk ³	1185	45	3.79	13	1.14
	Bulk ^l t	1781	143	8.02	22	1.3 ¹
	Bulk ⁵	306	. 52	16.99	0	0
	Bulk ⁶	54 1	•	-	٠ 4.	0.73

1	September	_	December	1980
2	February	_	May	1981
3	April	-	August	1980
4	April	÷	A ugust	1980
5	September	-	December	1980
6	Mav	_	September	1980

DISCUSSION

DISCUSSION

Bacterial wilt caused by Pseudomonas solanacearum is the most serious disease of tomato The cultivation of in the acidic soils of Kerala. the crop has become impossible due to the incidence of this kighly appreciated disease. Any attempt to evolve a line tolerant/resistant to this disease would be highly appreciated. The present investigation was carried out to identify a line (s) tolerant/resistant to bacterial wilt. An effective breeding programme for wilt resistance essentially consists of collection of germplasm, cataloguing of the lines thus collected, screening for resistance, improving the line thus isolated through appropriate breeding methods and finally evaluating its yield potential for the economic cultivation of the crop.

Germplasm collection

Tomato lines reported tolerant/resistant to bacterial wilt were collected from AVRDC, Taiwan. The lines were CL 8d-0-7-1 GS, CL 11d-0-2-2-0-3 UG, CL 32d-0-1-19 GS, CL 143-0-6-9 UG, L 1 GS, Venus and

Saturn. La Bonita an introduction made by N.B.P.G.R., New Delhi showing tolerance to wilt was also included. Lines whose tolerance/resistance were not previously evaluated also formed the germplasm evaluated.

Genetic cataloguing

The Report of the Tomato Genetics Cooperative. 1980 provides 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. Asosta (1964) reported that the resistant lines to bacterial wilt are all indeterminate, indicating a possible relation between sp+- the gene for indeterminate growth habit and resistance to wilt. He noticed yellow gel around the seeds in a few of the resistant lines. The present study could identify the line IE 79 (CL 32 d-0-1-19 GS) with tolerance to bacterial wilt. The detailed genetic cataloguing of the line revealed high content of anthocyanin in the seedling stage, indeterminate growth habit, yellow gel around the seed, green shouldered and non-uniform coloured fruits. The above observation

concurs with the findings of Acosta (1964) and further points out the possibility of a relationship between resistance and high content of anthocyanin in the seedling stage, green shouldered and non-uniform coloured fruits. If there exists a relationship between resistance and green shouldered and non-uniform coloured fruits, there remains need for an effective breeding programme to delink the characters. Green shouldered and non-uniform coloured fruits are undesirable characters during marketing.

Genetic improvement of the tolerant/resistant line

Scientists at University of West Indies (1968-169) reported close linkage between recessive genes for resistance and genes for poor fruit characteristics. The line LE 79 isolated for field tolerance had also poor fruit characteristics like small fruit size (average fruit weight 30.42 g) which needs to be further improved. This is in conformation with the results reported from University of West Indies (1968-169) and University of Hawaii (1951). Being a self-pollinated crop conventional breeding methods like pureline selection and mass selection were initially done to upgrade the fruit size of the line, keeping resistance intact. The efficiency of different methods

of selection was compared with progressing the generation through bulking. Significant differences due to the three methods of selection were observed /frutteet only for plant height and days to first/ `The initial criteria of selection both in pureline and mass selection methods were fruit yield and absence of cracking. Selection based exclusively on fruit yield and absence of cracking may have been responsible for nonsignificant differences due to different methods of selection with respect to other polygenic characters. A trait-wise selection making use of discriminant function equations would have been more appropriate in such situations. The Realised heritability was higher (0.88) for days to fruit harvest indicating considerable scope for selection of early line(s) in the tolerant/resistant line identified.

Evaluation for field tolerance/resistance of the line

The line IE 79 observed "not affected from" bacterial wilt in the initial evaluation trial was grown separately in diseased plots in six independent trials. These trials indicated field tolerance of the line. To confirm the tolerance under artificial conditions, the seedlings were transplanted in pots filled with earth from known and confirmed diseased plots. Here again, the

seedlings withstood the test of tolerance. artificial inoculation technique as suggested by Winstead and Kelman (1952) caused susceptible reaction in the line under test. Mew and Ho (1976) found that certain tomatoes showed an uncertain degree of susceptibility to bacterial wilt when they were exposed to high inoculum densities; differences in inoculum density may, therefore, explain the differences in the expression The resistance of bacterial wilt can of resistance. wary with the temperature as reported by Krausz and Therefore, the susceptibility of the Thurston (1975). resistant line, IE 79, under artificial inoculation may be attributed to the fact that the inoculum density and temperature can alter the disease resistance.

SUMMARY

SUMMARY

- 1. One hundred and sixtyfive lines of tomato collected from different sources were sown during September 1980 to isolate line(s) resistant/tolerant to bacterial wilt. Genetic cataloguing of available lines was also attempted.
- 2. Seventyeight lines germinated were critically examined for seedling characters as given in the Report of the Tomato Genetics Cooperative, 1980. The line IE 79 had its hypocotyl, epicotyl, cotyledons and the first leaf purple pigmented, as observed 18 days after sowing.
- 3. The line LE 79 survived the onslaught of bacterial wilt. The statistical properties of LE 79 population indicated that the population was a normal one for plant height, primary branches per plant, days to first fruit set, days to first fruit harvest, marketable fruits per plant and locules per fruit.
- 4. An attempts was made to improve the fruit size and productivity of the line (IE 79) through pureline selection and mass selection. A comparison of the effectiveness of the above methods with bulking was also

made. The progeny developed through pureline selection were superior to those developed through bulking for days to fruit set, days to first fruit harvest, marketable fruit weight per plant, percentage of large fruited plants and percentage of plants with cracked fruits. The selection response obtained through mass selection was positive for primary branches/plant and locules/fruit. The realised heritability was very high (0.88) for days to first fruit harvest indicating thereby the scope of going for selection to develop still earlier lines.

- 5. The tolerance/resistance of the line IE 79 was further evaluated in six independent trials. The percentage of plants susceptible ranged from zero to 1.34 per cent (adult plant stage) indicating a case of tolerance.
- 6. Under artificial inoculation as proposed by Winstead and Kelman (1952), the line LE 79 became susceptible as any other susceptible line. This may possibly be due to high inoculam density in artificial inoculation.

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* Originals not seen

APPENDIX



GENETIC CATALOGUING OF TOMATO GERMPLASM TOWARDS ISOLATION OF LINE(S) RESISTANT TO BACTERIAL WILT

BY CELINE, V. A.

ABSTRACT OF THE THESIS

Submitted in partial fulfilment of the requirement for the degree of

Master of Science in Horticulture

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Kerala Agricultural University

1

Department of Horticulture (Olericulture)

COLLEGE OF HORTICULTURE

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ABSTRACT

Bacterial wilt caused by <u>Pseudomonas solanacearum</u> is the single disease causing the greatest damage in tomato grown in the acidic soils of Kerala. Isolation of a line(s) tolerant/resistant would be a worthwhile attempt which would have considerable impact on tomato production in Kerala. An experiment was planned and carried out during 1980-181 in the College of Horticulture, Vellanikkara to isolate tolerant/resistant line to bacterial wilt.

Seventy eight lines collected from different sources where genetically catalogued as per the Reports of the Tomato Genetics Cooperative, 1980. Field screening indicated the tolerance of one line, LE 79 (CL &M-32d-0-1-19 GS) received from AVRDC, Taiwan. This line had indeterminate growth habit, green shouldered and medium sized fruits and the seeds covered by yellow gel.

The line was grown in the field continuously for six seasons to confirm the tolerance/resistance. The susceptibility ranged from zero per cent to 1.34 per cent in the adult plant stage.

Breeding methods like pureline and mass selection were adopted to improve the fruit size and other characters

of the resistant line. Genetic information like realised heritability were gathered for plant height, primary branches per plant, days to first fruit set, days to first fruit harvest, fruits per plant, marketable fruits per plant, locules per fruit, marketable fruit weight per plant and total fruit weight per plant.

The tolerance/resistance was tested using soils from susceptible plots. Here again, LE 79 showed freedom from disease infection. The artificial inoculation proposed by Winstead and Kelman (1952) caused susceptibility in the resistant line. This may probably be due to high inoculum density which alter the disease resistance.