REPORT

NOTE: The original page numbering has been maintained throughout this document.

of the

TOMATO GENETICS COOPERATIVE

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FOREWORD

The Tomato Genetics Cooperative is a group of researchers who share an interest in tomato genetics, and who have organized informally for the purpose of exchanging information, germplasm, and genetic stocks. The Report of the TGC is published annually and, in addition to reports of work in progress by members, it contains updates on materials available and of the tomato linkage maps. The research reports include work on such diverse topics as new traits or mutants isolated, new cultivars or germplasm developed, interspecific transfer of traits, studies of gene function or control and tissue culture.

As of May 1, 1996 TGC membership stood at 420 from 45 different countries. Requests for membership ($5.00 {US} per year) should be sent to Rich Zobel, 1005 Bradfield Hall, Cornell University, Ithaca NY 14853-1901. Suggestions for improvement or additions to the reports are always welcome.

Submission for the next report can be sent either to R. Zobel or M. Mutschler anytime before February 1, 1997 (submissions may be made on IBM or MacIntosh compatible discs with an included hard copy) or by e-mail (rz11@cornell.edu or mam13@cornell.edu). Names for new mutants, clones, and RFLPs should be submitted to the nomenclature committee c/o R. Zobel, in advance of publication.

Requests for seed stocks should be addressed to the respective suppliers

Cover Figure: Root system of a double homozygote from a cross between a lateral-less and an adventitious-less root mutant. See article by Zobel, R.W. "Basal Roots".

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RESEARCH REPORTS

Tomato Genotypes Resistant to <u>Phytophthora</u> <u>capsici</u>

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Problems in greenhouse tomato growing areas of Russia due to soil borne *Phytophthora species,* causal agents of foot, crown, fruit root, and necrotic lesions on foliage, have been sharply increasing in recent years. *Phytophthora* soil born species were found to be primary colonizers of tomato plant tissue, which is secondarily colonized by other fungi often masked by the presence of *Phytophthora. Phytophthora capsici* isolates, obtained from naturally infected tomato plants, were used in bio-assay to find resistant tomato forms. Tomato collection (125 patterns) was subjected to screening procedure on seedlings (1-2 true leaves). Seedlings were grown in sterile sand fertilized with Knops medium. Inoculation was performed by spraying of zoospores suspension (6000 zoospores per ml). Zoospores were obtained by chilling suspensions of sporangia harvested from oat agar at 10°C for 90 min. Infected material maintained at high humidity using *plastic covers and* incubated at 21-22°C with illumination (16 h daylength). High resistance was recorded for patterns with overall means of 85-100% and 50-85% viability of seedlings (table).

Tomato genotypes with high resistance to *P. capsici*

	SEEDLING VIABILITY
85-100%	50-85%
L. chilense (5031)*	*L. pimpinellifolium* (3731)
L. peruvianum v. humifusum (3967)	*L. pimpinellifolium* (3989)
L. Humboldtii (353/2)	*L. pimpinellifolium* (3990)
CRA-66 (13225)	F_1 (*L. peruvianum* (2020) x *L. Humboldtii (2884))*
Line 327-2B	F_1 (*L. chesmanii f. minor* (3969) x *L. chesmanii f. minor* (3969)
1.372 NISTIO, Moldova	Grushevidny (342)
1.349 NISTIO, Moldova	BU-12, Belarus (5085)
1.342 NISTIO, Moldova	

* Number in VIR catalogue, S. Petersburg, Russia

Tomato Genotypes Resistant to *<u>Phytophthora</u>* *<u>infestans</u>*

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A field study was conducted in Moscow Region in September-October 1990-1991 to evaluate tomato collection for resistance to *Phytophthora infestans* in naturally occurring late-blight epidemics. Screening of 800 genotypes, including wild species yielded samples (2%) which showed the greatest resistance to P. *infestans* on leaves, fruits and stems (disease severity less than 10%).

A list of tomato patterns with highest resistance to *P. infestans,* natural infestation in the Mytichi (Moscow Region) follows:

L hirsutum (5041)*
L pimpinellifolium (3731) West
Virginia 181-1-6-21 West
Virginia 139-1-2-1-1-1
West Virginia 700
West Virginia 63
Ottawa 30 (3919)
Hessoline, France
Heline, France
Juno (3215)
Droplet (4316)
1.132, Moldova
1.342, Moldova
BU-13, Belarus

* Number in VIR catalogue, S. Petersburg, Russia.

Tomato Genotypes Resistant to Phytophthora infestans and Phytophthora. capsici

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Mechanisms of pathogenesis of *Phytophthora capsici* and *P. infestans* are known to be different *Phytophthora capsici* produces great amount of maceric enzymes, causing soft root of host-plant tissue. *P. infestans* cause dry root. A screening of tomato collection (68 genotypes) in detached fruits bio-assay was performed to select resistant forms to both P. *infestans* and *P. capsici*. Fruits were inoculated with zoospore suspension 6000 zoospore, per ml. The results indicated slight differences in tomato resistance to these pathogens (Table 1).

Table 1. Tomato patterns with different level of resistance to *P. infestans* and *P. capsici*

Level of resistance	Accessions, %
High (0-1) to *P. infestans* and *P. capsici*	13
High (0-1) to *P. infestans* and susceptible (3-5) to *P. capsici*	9
High (0-1) to *P. capsici* and susceptible to *P. infestans* (3-5)	1.5
Susceptible (3-5) to *P. infestans* and *P. capsici*	86.5

List of the accessions with highest resistance to *P. capsici* and *P. infestans*:

L. peruvianum (2020)
L. peruvianum v. dentatum (3963)
L. Humboldtii (2884)
L. Humboldtii (2884) x L Humboldtii (353) Vishnevidny (342)
L. pimpinellifolium (3731)
L. pimpinellifolium (3990)
CRA-66
F2 (Xachmasskiy 18 ¡x *L. Humboldtii* (35312)

* Number in VIR catalogue, S. Petersburg, Russia

Screening tomato mutants for abnormalities in VA mycorrhizal symbiosi.

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Vesicular-arbuscular mycorrhizal (VAM) symbiosis is a mutualistic plant-fungal interaction that occurs in more than 80 % of extant plant species and that has also been shown in some of the earliest land plant fossils (Harley *and* Smith*,* 1983*;* Remy *et al*., 1994). Despite their extensive co-relationship, and although the fungal partner cannot yet be cultured in the absence of a plant, many plant species are not obligate symbionts. Thus, at least some of the plant genes that are required for successful establishment of the symbiosis are expected to be identifiable by mutation analysis. Until recently, virtually no molecular study of VAM had been attempted, due at least in part to the recalcitrance of the fungus to axenic culture. However, with the development of a rapid synchronous infection method (Rosewame et al., 1996), we have initiated several projects in this area of research.

Tomato plants are natural VAM hosts and show a reasonable growth response when infected (Rosewame et aL, 1996). In order to identify genes that might be important in the symbiosis, we have been screening a Fast Neutron mutagenised population of Rio Grande 76R, that had provided several distinct mutations in *Pto* and *Prf* (Salmeron et al., 1994), for altered VAM symbiosis. So far, from a preliminary screening of 209 families, we have identified 10 families which contain putative mutations in ability to form the symbiosis with the VAM fungus *Glomus mosseae*, and these are currently being further characterized.

In addition to the mutant population, we have screened several genetic marker stocks and root morphology mutants for their ability to form VAM symbioses. The accessions screened and their designated mutations are listed in Table 1. None of these stocks show any abnormality in infection morphology, as might be expected from the lack of host specificity demonstrated by the fungus.

Table 1. Genetic marker stocks showing normal VAM symbiosis morphology with *G. mosseae*.

Accession	Mutation(s)	Accession	Mutation(s)
LA 512	Chr 5 (*mc-tf-wt*)	LA 2464A	cv. White Beauty
LA 630	*um* (*aer-2; r, y; upg*)	LA 1103	Chr 7 (*var, not*)
LA 2504	Chr 10 (*u-h-t-nd-ag*)		
LA 1177	Chr. 12 (*alb-mua*)	LA 2802	cv. Globonnie *crt*
LA 1189	Chr. 6 (*pds-c*)	LA 2816	*brt*
LA 1430	Chr. 3 (*sy-bls-Ln-sf*)	LA 3205	*aer*
LA 1490	Chr. 1 (au^{+1}, *co, inv, dgt*)	LA 3206	*brt-2*
LA 1666	Chr 8 (*l-bu-dl-ae*)	LA 3207	*drt*
LA 1700	Chr. 2 (*wv-aa-d*)	LA 3353	Chr. 9 (*pct-ah-marm*)
LA 1794	*ri*	2-110	*wd*
LA 1796	*Rs, d, h*		

We are interested in screening biochemical mutants, such as those with altered root exudates, or mutants that have altered phosphate, photosynthate or micronutrient status, as these traits may play a direct role in establishment of a successful symbiosis. Collaborative interactions are of particular interest to us, and we would appreciate contact from anyone holding mutants of these types.

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Rosewame, G.M., Barker, S.J., Smith, S.E. 1996. In Preparation
Salmeron, J.M., Barker, S.J., Carland, F.M., Mehta, A.Y., Staskawicz, B.J. 1994. Plant Cell, 6, 511-520

Recovery of S-locus *homozygotes through wide hybridization in* L. peruvianum

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In our investigation of self-incompatibility in tomato we have sought to determine functional relationships among well characterized alleles in two divergent populations *of L peruvianum.* The alleles S_{m1} and S_{m2} (previously designated S_7 and S_6, Liang et al. *1994) are from LA2163* (provided by C.M. Rick) and their cDNA sequences have been cloned. The sequence of S_{m1} is 98% identical to another cloned allele S_3 which is derived from a line obtained from the State Dept. of Agriculture, Burnley, Victoria, Australia (Mau et al. 1986, Royo et al. 1994). S_{m2} has high homology to S_4 from the same population as S_3, based on DNA Southern hybridization (unpublished). DNA restriction fragments generated with Eco RI allow us to genotype individuals bearing these alleles (S_{m1}, 1.3 and 6.0 kb: S_{m2}, 0.6 and 4.2 kb, S_3, 3.5 and 6.2 kb; S_4 0.6 and approximately 18.5 kb). As with many *S-alleles of L* peruvianum, there is a conserved Eco Rl site within the coding region.

We made more than twenty attempts to cross $S_{m1}Sm_2$ X S_3S_4 (and reciprocal) but succeeded in getting poorly developed fruits filled primarily with tiny aborted seed. We obtained only eight viable seed and the seedlings did not appear to be hybrid but looked instead like the female parents. *Since these* materials are strongly self-incompatible, we did not emasculate the flowers prior to pollination. RFLP analysis revealed that these plants were a result of self-fertilization. In addition, we were able to recover individuals homozygous for each of the alleles. We suggest that these illegitimate selfs are a result of the mentor effect of the distantly related applied pollen (Knox et al. 1987). We have been previously unable to produce any selfed seed of LA2163 through standard bud-pollination, possibly because of the early expression of S-related proteins in developing flowers (Rivers and Bernatzky 1994).

We have used these inbred materials as pollen testers to determine relationships among *these* alleles. Crosses between the different populations are considered to be incompatible if the flowers abscise and compatible if fruits set (even though the seeds do not develop well). We conclude that $Sm_{,}$ and S_3 are functionally different alleles (i.e. compatible) but that S_{m2} and S_4, are the same alleles.

Literature Cited.

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Mau, S.L. et al., 1986. Planta 169:184-191.
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Segregation for a dominant male-sterility, Ms-57, in derivatives of S. lycopersicoides

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In various derivatives of *S.lycopersicoides,* we have frequently encountered partial male-sterility in early backcross generations. Such sterilities were often associated with other defects (e.g. reduced vigor, abortive inflorescence, deformed anthers, etc.), which rarely produced discrete phenotypic classes or monogenic segregations.

In backcross derivatives of one F, intergeneric hybrid (plant 90L4178-1 = *L. esculentum* cv. VF36 x *S.lycopersicoides* LA2951), clear cut segregation for male-sterile and male-fertile phenotypes was observed. The first generation in which this occurred was a BC_3 family (93L8235): of 11 plants, 7 were sterile, producing no detectable pollen, and 4 were fertile. The nature of the cross suggested the sterility was of a dominant nature, and the frequency of steriles was likewise consistent with the predicted 1:1 ratio (X2 = 0.5, not significant). Larger BC_4, and BC_5 populations produced a pooled segregation of 124 steriles 139 fertiles, results consistent with a monogenic dominant (X^2=0.75, not significant), for which we propose the gene symbol Ms-51. Surprisingly, the original F, plant was sufficiently male-fertile to permit direct backcrossing as stamina parent to VF36; this apparent lack of Ms-51 expression suggests the presence of a restorer gene(s) in the *S. lycopersicoides* genome.

Anthers of *Ms-51/*+ plants are noticeably thinner than normal, but not significantly shortened, hence stigmas are inserted, as in VF36. No detectable pollen can be collected by vibration or dissection of anthers. No mature pollen grains are observable under the microscope following squashing of anthers in acetocarmine; only very small immature or abortive grains or clumps of cells are seen. The phenotype *of Ms-51* is similar to that of *Ms-48* (Rick 1987), the only other dominant male-sterility described in tomato, suggesting they might be allelic.

Literature Cited

Rick, C.M. 1987. A dominant male sterility (Ms-48) gene. TGC 37:62.

Tolerance to <u>Botrytis</u> <u>cinerea</u> in L. <u>esculentum</u> x S. <u>lycopersicoides</u> hybrids.

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We know of no reports of resistance to gray mold (*Botrytis cinerea*) in tomato or its wild relatives, other than that of Farley et al. (1976). Observations made during regular seed increases of S. lycopersicoides at the C.M.R. TGRC suggested this species might be resistant or tolerant to stem infection by *B. cinerea*. Accordingly, we screened sesquidiploid and diploid *L esculentum x* S. lycopersicoides hybrids, representing accessions LA1964, LA2408, and LA2951 (Rick et al. 1986; Chetelat et al. 1989; Chetelat at al. unpublished, respectively), for resistance to gray mold.

B. cinerea attacks all the aboveground parts of the tomato plant, including leaves, stems and fruit; the stem lesions can girdle the shoot, leading to wilting and death. The intergeneric hybrids are generally sterile, and produce few fruits. For these reasons, we screened plants for reaction to stem infection by *B. cinerea.*

The method involves inoculation of *the* cut petiole. surfaces of stem cuttings with agar plugs containing *B. cinerea* mycelia. The cuttings are kept in boxes with vermiculite at 90-100% RH for 2 days, after which time the agar plugs are removed. Two isolates of *B. cinerea* were used: TI from tomato and DEL-11 from grape.

The first symptoms appeared as elliptical water-soaked lesions on the stem, the length of which were measured at 3 and 6 days, approximately. The lesions enlarged from 3 to 6 days in the susceptible *cultivar VF36, whereas no progression of the disease was seen on the S. lycopersicoides* hybrids. After 6 days, the average lesion length on VF36 was approximately 3 times greater than on cuttings from the diploid or sesquidiploid F, intergeneric hybrids.

Having obtained some evidence of tolerance in the parental hybrids, we have begun to screen derivatives from the backcrosses to *L. esculentum*. Several lines with apparent stem tolerance have been identified, some of which were also tolerant in a leaf injection assay.

ACKNOWLEDGMENTS

We are grateful to Of. Ann Powell (Mann Laboratory, UC-Davis) for providing *Botrytis* strains and for suggesting the inoculation technique.

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Farley, J. D., W. L. George and E.A. Kerr. 1976. Resistant to *Botrytis cinerea*. TGC 26:7.
Rick, C.M., J.W. DeVerna, R.T. Chetelat and M.A. Stevens. 1986. Meiosis in sesquidiploid hybrids of *Lycopersicon esculentum* and *Solanum lycopersicoides*. Proc. Natl. Acad. Sci. U.S.A. 83:3580-3583.

A new source of PVY resistance

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A total of 169 *Lycopersicon* accessions, including *L. esculentum, L pimpinellifolium, L. peruvianum, L. glandulosum and L. hirsutum* have been screened for reaction to potato virus Y (PVY) of the AVRDC. A new source of resistance to PVY was identified: AVRDC accession L3683 (*L hirsutum* PI 365904) from Ecuador. Inoculation was done mechanically, at the 2-3 leaf stage with strain PVY-0 and plants were evaluated visually and by ELISA at 14 and 42 days after inoculation. The susceptible check, *L esculentum* cv TK 70, inoculated at the same time was 100% susceptible at 14 days after inoculation, whereas 240 plants of L3683 were resistant (no symptoms, and ELISA negative) at 42 days after the inoculation. Seeds of L3683 were also sent to Australia (J.E. Thomas), Hawaii (J. Cho) and California (J. Kao) and to Thailand (K. Kruapan) for testing with local strains/isolates. In all locations, L3683 was resistant. This is interesting since the only other known PVY resistance source, *L. hirsutum* PI 247087 was found resistant to Taiwan and Australian isolates, but susceptible to the Hawaii and Thailand isolate. *F_1 plants* of CLN 236 (*L esculentum*) *x* L3683 were susceptible, suggesting that PVY resistance in L3683 is recessive. An inheritance study is underway.

Literature cited:

Thomas, J.E. 1981. Australas Plant Pathology, 10, 67-68.

A functional Cf-4 gene for resistance to Cladosporium fulvum Cke. is present in Cf-8 and Cf-11 lines

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In the history of tomato breeding for resistance to *Cladosporium fulvum* many genes have been identified and designated, *Cf-1* to *Cf-24*. Lindhout *et*. *al*. (1989) showed that there was no race that could distinguish between *Cf-4* and *Cf-8*. Moreover, it appeared that these genes were allelic and therefore indistinguishable (Gerlagh et. al., 1989). One of .the ancestors of the Cf-8 line (Ontario 7522) is Vantage, which is known to contain *Cf-4* from *Lycopersicon peruvianum* (Kerr, 1980; Bailey & Kerr, 1964). Lindhout *et al.* (1989) also characterized the *Cf-11* resistance gene by differential response upon inoculation with different races of *C. fulvum*. Remarkably, all races virulent on *Cf-11* from Ontario 7716 also were virulent on lines containing the *Cf-4* resistance gene. *Cf-11* is the result of a dominant mutation in the *Cf-4* containing breeding line Massachusetts #2, for this gene was found in 'an aberrant plant of the breeding line Massachusetts #2'. This plant was resistant to race 4, but susceptible to another race, which later appeared to be 2.3.4.11 (Kerr & Patrick, 1977). The *Cf-11* line was crossed to other (unknown) lines, resulting in Ontario 7716, which was used in later experiments.

Upon inoculation of different plant genotypes with the systemic virus PVX, expressing the avirulence gene *avr4,* Vantage, Moneymaker-*Cf-4* (MM *Cf-4*), Ontario 7522 and Ontario 7716 exhibited necrosis, indicating that these lines all contain an active *Cf-4* gene. Southern analysis with genomic DNA of these lines digested with *EcoRl, Bg/ll, Hindlll* and *EcoRV* and probed with a *Cf-4* or a *Cf-9* probe indicated that the patterns of MM *Cf-4*, Ontario 7522 and Ontario 7715 were identical and different from control lines.

In experiments using PCR primers derived from the DNA sequence of *Cf-9* no difference in PCR pattern between MM *Cf-4*, Ontario 7522 and Ontario 7716 was detected again. Later, specific PCR primers were designed, based on the sequence of Cf-4. When used at high annealing temperatures, no difference was found between these lines, also after digestion of the PCR products with *Bgl*ll, *Eco*RI, *Hin*cll, *Hind*lll and *Eco*RV, while they did differ from banding patterns of other lines used.

The experiments mentioned in this paper suggest the *presence of a* functional *Cf-4* gene in the *Cf-8* and *Cf-11* lines. The line *Cf-11* seems to harbour another gene, *Cf-11*, for which a corresponding avirulence gene exists. Because the *Cf-4* gene was already present in Massachusetts #2 and *Cf-11* was found in a plant of the same line (Kerr & Patrick, 1977) it seems that the genes were both transferred to Ontario 7716. In a report by Kanwar et al. (1980), Cf-l7 was mapped on chromosome 12. *But* several of the mapped genes in this report have been relocated later, e.g. *Cf-5* and *Cf-9* (Jones et al., 1995; BalintKurti *et al.*, 1994), so his data might be conspicuous. Furthermore, it seems very unlikely that Cf-8 can be on chromosome 9, since this gene is allelic to Cf-4 (Gerlagh et. al., 1989) and has the same function and DNA structure, as indicated above. Moreover, there is no evidence for the existence of a unique functional *Cf-8* gene, for no corresponding avirulence gene has been found. In conclusion, we propose not to use the designation *Cf-8* anymore, but *Cf-4* instead and indicate that Ontario 7716 harbours two genes: *Cf-4* and *Cf-11*.

ACKNOWLEDGMENTS

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Effects of starter phosphorus and nitrogen on the vegetative growth, yield and incidence of powdery mildew of tomato (Lycopersicon esculentum Mill.) *incited by* Leveillula taurica (Lev) *Am.*

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In the Sudan, tomato *Lycopersicon esculentum* Mill) is the second most important vegetable after onion. It is produced on large areas around big cities along the Nile and on seasonally flooded plains. It is a high value crop and fetches high prices especially when grown off-season. Powdery mildews are probably the most common, conspicuous, wide spread, and easily recognizable plant diseases affecting many kinds of plants.

In the Sudan, tomato is attacked by many plant diseases including powdery mildew which is caused by the Leveillula taurica (Mohamed Eljack, 1994). The disease is becoming very serious on tomato and some farmer's fields were completely destroyed. The disease development is influenced by many factors, among which is soil fertility (Wheeler, 1978). The objective of this study is to evaluate the effect of phosphorus and nitrogen on the vegetative growth, yield and incidence of powdery mildew in tomato.

The experiment was conducted at the University of Gezira farm on heavy clay soils with no pervious history of fertilization for the last ten years. Tomato "Strain B' seedlings were transplanted when three weeks old. Plants were spaced 30 cm apart and 120 cm between rows. Plot size was 6 x 6 meter and the sowing date was 15 December. The experimental design was factorial arrangement in a randomized complete block design. Starter fertilizer treatments consisted of three phosphorus rates and two nitrogen levels arranged in a 3 x 2 factorial and replicated four times. Phosphorus treatments equivalent to 0 and 20 lbs/acre were evaluated. Starter fertilizers salts were made in solution and applied as 250 ml directly on planting holes. The total number of plants was obtained for all treatments, three weeks after transplanting. Plants revealing symptoms of powdery mildew were counted at 15-day intervals throughout the experiment Counts of plants showing symptoms in each treatment were expressed as percentage of the total number. Irrigation was at weekly intervals (furrow irrigation) and hand weeding was carried out every three weeks.

Results in Table 1 show that, disease incidence generally increases with fertilizer dose. However, the role of phosphorus is more pronounced. This may be related to its effect on vigor as shown by the number of branches. Result in Table 2 show that the effect of Phosphorus fertilizer is more pronounced in the early yield. However, later on, this effect did not show. At 40 P, which is the highest phosphorus dose, addition of N - nitrogen seem to reduce the disease incidence.

Table 1: The effect of starter phosphorus and nitrogen on the vegetative growth and incidence of powdery mildew of tomato.

Treatments	Number of branches		mean Infection*
	25 Feb.	11 March	
0P 0N	0.22 c	2.05 d	1.81 c
0P 20N	0.62 c	2.88 d	9.75 bc
20P 0N	3.23 b	4.03 bc	21.94 bc
20P 20N	8.85 ab	4.25 b	41.97 ab
40P 0N	4.60 a	5.45 a	75.59 a
40P 20N	3.33 ab	4.70 ab	41.32 ab
			SE = ± (11.41)

*Data are transformed into $\sqrt{x+1}$. Means followed by different letters are significantly different according to Duncuns Multiple range test at P=0.01.

Table 2. The effect of starter phosphorus and nitrogen on yield and incidence of powdery mildew of tomato

Treatments		Mean weight of fruits kg/hectare*			Total yield	Mean Infection*
		Early yield	Mid yield	Late yield		
0P	0N	0.00 b	216.50 b	1271.20 a	1471.68 b	1.81 c
0P	20N	2.24 b	681.86 b	1715.05 a	2399.04 b	9.75 bc
20P	0N	114.58 ab	2773.46 a	1573.60 a	4563.99 a	21.94 ab
20P	20N	245.05 b	3207.68 a	1286.66 a	4742.08 a	41.97 ab
40P	0N	235.76 a	3473.46 a	1523.20 a	5790.39 a	75.59 a
40P	20N	205.86 a	2741.20 a	1584.80 a	4537.12 a	41.32 ab

Means followed by different letters are significantly different according to Duncuns Multiple range test at P = 0.01.

The results obtained show that plant vigor generally increases with fertilizers. The vegetative growth is mainly affected by the dose of phosphorus, also there is no interaction, between the phosphorus and the nitrogen. This finding is in full agreement with those obtained by other workers. White (1938), found that plant height, leaf area and the number of flowers produced increased in response to added nitrogen. Both growth and development may be restricted by an inadequate level of phosphorus applied, particularly at the high pH (Massey and Winsor, 1969). Phosphorus deficiency also reduced the number of flower buds formed and delayed antithesis (Menary and Staden-Van, 1976). In our results, high levels of phosphorus were found to be associated with more vigorous growth and higher disease levels. The increased vigor was reflected by the greater number of branches and higher early yields. The adverse effects of the disease on crop yield were clearly indicated by the lack of significant differences between fertilizer treatments in late-season yields. Incidence of powdery mildew is found to be affected by both phosphorus and nitrogen. At 40 P, which is the highest phosphorus dose, addition of N-nitrogen seem to reduce the disease incidence, suggesting that it is not only the phosphorus that affects the disease build-up but also the ration of P:N.

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Development of Interspecific Hybrids between Lycopersicon esculentum *and* L. peruvianum *var. humifusum and Introgression of Wild Type Invertase Gene into* L. esculentum.

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The strictest barriers hamper the development of the hybrid embryos of *L esculentum* and *L. peruvianum var. humifusum.* This study was carried out in order to produce interspecifc hybrids and their backcross progenies using the ovule selection method (Imanishi et al., 1985; Imanishi et al., 1993). Twenty-three hybrid plants (F,) were obtained from 67 fruits (Table 1). These F, plants were confirmed by the morphological and physiological resemblance of their traits (prostrate habit, slender stem, tiny leaf segment, high levels of anthocyanin, and the scent of Japanese pepper) to those of the pollen parent, *L. peruvianum* var. *humifusum* LA2153. The first backcross progeny (B1F1) obtained were 9 plants from 61 fruits. Many plants of the second backcross progeny (B_2F_1) were produced, of which 70% were self-compatible. Fruit weight and seeds per fruit of the B_2F_1, indicated *that* their traits were beginning to match those of the *L. esculentum.*

Table 1. Ovule culture for the development of the F_1, B_1F_1, and B_2F_1, generations in the Interspecific hybridization of *L. esculentum* and *L peruvianum* var. *humifusum*.

Cross Combinations	Generations	# of fruits	# of selected ovules	# of germinated ovules	# of germinated ovules per fruit
EP x LA2153	F_1	67	61	23	0.34
EP x F_1	B_1F_1	61	120	9	0.15
EP x B_1F_1	B_2F_1	-	129	18[1]	-

EP: *Lycopersicon esculentum* c.v. 'EarlyPink' LA2153: *L peruvianum var. humifusum*

[1] The rest of the ovules which did not germinate were dissected for the embryo culture which recovered a number of B_2F_1, plants.

PCR-diagnosis of the tomato acid invertase gene was performed by using one pair of primers (Harda et al., 1995) in order to confirm the introgression of the *L. peruvianum* type invertase gene into the B2F2 population. Twenty-three lines out of a total of 28 lines that were examined were found to be homozygous for the *L. esculentum* type gene (Table 2). The remaining five lines were found to be of mixed types, including the homozygous *L. esculentum* type, the homozygous *L. peruvianum* type, and the F_1 type gene plants. Seven homozygous L peruvianum type gene plants *were* selected out of a total of 263 B_2F_2 plants. The content of sucrose and hexoses of fruits was determined for each of the invertase - genotypes. The fruits of the homozygous *L. esculentum* type and the F_1 type plants accumulated mainly hexoses, glucose and fructose, while the homozygous *L peruvianum* type plants accumulated soluble sugars in the fruit primarily as sucrose (Fig. 1).

L. esculentum or B_2F_2 lines	Invertase gene plant: Homozygous *L. esculentum* type plant	Homogzyous *L. peruvianum* type plant	Heterozygous F_1 type plant	Total
Early Pink	1	0	0	1
Ogatazuiko	4	0	0	4
5,6,7,8,17,21,23, 24,25,26,24,28,3 4,36,40,51,52,56, 65,66,72	205	0	0	205
11	3	3	5	11
12	7	2	13	22
35	1	1	5	7
59	7	2	10	18
Total	18	7	22	58

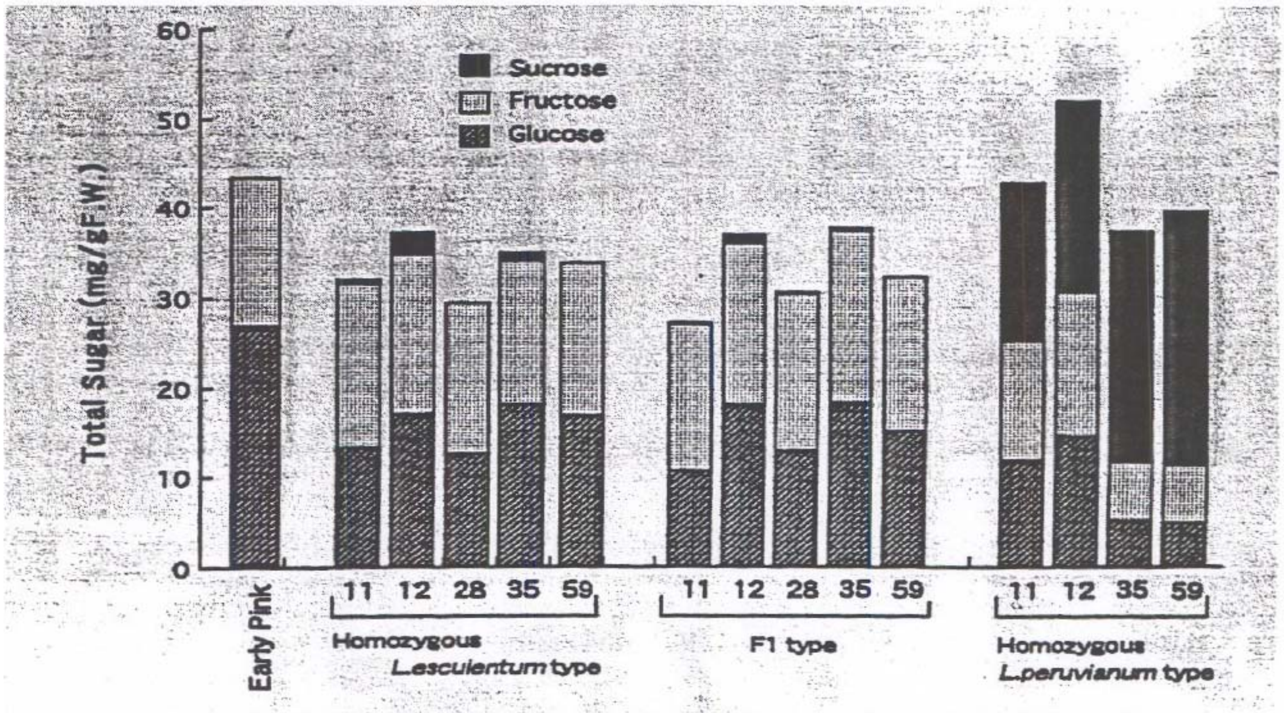

Fig.1 Fruit sugar content of the homozygous *L.esculentum* type, F1 type and homozygous *L.peruvianum* type plants in the mixed type lines (Nos. 11, 12, 28, 35 and 59) of the B1F1 generation.

Table 2. The introgression of *L. peruvianum* type invertase gene into *L esculentum* assessed by PCR in the second backcross generation (B2F2) of *L. esculentum* c.v. 'Early Pink' x *L. peruvianum* var. *humifusum* LA2153.

The present study reports the first case of the transfer of the *L. peruvianum* type invertase gene in B_2F_2 population, *L. esculentum*-equivalent tomato lines.

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Allelism tests: in is allelic to com, dp is allelic to dgt and pu-2 is allelic to al.

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During a study designed to integrate the classical and RFLP maps of the short arm of chromosome I (reported by Balint-Kurti *et al.* 1995), a number of markers that had been previously suggested to map to chromosome *1* were assessed. The phenotypes conferred by two of these markers, *in* (indiga, Stubbe 1958) and *dp* (drooping leaf, Yu and Yeager 1960), were found to resemble those conferred by two known chromosome *1* markers, *com* (complicata) and *dgt* (diageotropica), respectively. In a separate study comparing markers affecting anthocyanin production, the phenotype conferred by *pu-2* (pulvinata-2, Stubbe 1965) was found to resemble that conferred by *al* (anthocyanin loser). Experiments were carried out to determine the allelism or otherwise of these markers.

To test for allelism between *in* and *com*, the cross GCR703 *in-imb* x CLS3483 au^{tl}-com was performed and the F_1 progeny were found to be wild type for imb and au^{tl}, confirming the cross, but to have the indiga/complicata phenotype, indicating allelism between *in* and *com*. To test for allelism between *dp* and *dgt*, the cross LA2605 *scf-dp r-wf c gs marm a hp* x CLS4783 *dgt-rvt* was performed and the F_1 progeny were found to be wild type for *scf*, *c, a* and *rvt*, confirming the cross, but to have the drooping leaf/diageotropica phenotype, indicating allelism between *dp* and *dgt.* Finally, to test for allelism between pu^{-2} and *al*, the cross LA973 *pu-2 u* x GCR382 *al* u^+ was performed using LA973 as the female parent and the F_1, progeny were found to have the putida/anthocyanin loser phenotype, indicating allelism between *pu-2* and *al*, and to have non uniform fruit (u^+), confirming the cross.

Regardless of the order of precedence in the discovery and naming of these mutations, we suggest that the well known names com, dgt and al should be retained in preference to the more obscure names *in, dp* and *pu-2*, which should be altered to com^{in} dgt^{dp} and al^{pu-2}, to reflect both their origin and their location at the well mapped *com, dgt* and *al loci*, respectively.

Tomato stocks used

GCR stocks were obtained from John Maxon-Smith, HRI, Littlehampton, UK.

LA and 2-stocks were obtained from Charles Rick, Tomato Genetics Stock Centre, Davis CA, USA.
CLS3483= an F_3 Line derived from an au^{tl} com F_2 segregant of the cross CLS2531 au^{tl} Tm-2^2 x LA664 com
CLS2531= an F_3 line derived from an au^{tl} Tm-2^2 F_2 segregant of the cross 2-655A au^{l} x GCR758 *Tm*-2^2
CLS4783= an F_3 line derived from a *dgt rvt* F_2 segregant of the cross LA1186 au^{tl} *dgt inv scf* x LA1799 *rvt*

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The <u>rvt</u> *gene maps close to* <u>inv</u> *on the long arm of chromosome 1.*

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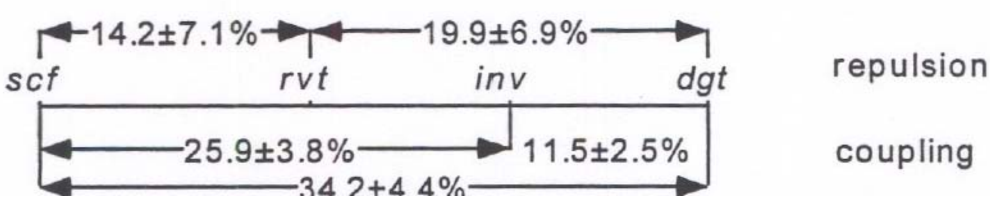
The *rvt* (red vascular tissue) gene has been suggested to lie on chromosome 1 (Kerr 1982 a, b, Kerr *et al.* 1988), but this has not been confirmed with respect to well mapped markers on chromosome 1. To test this location we crossed LA1799 *rvt* to the chromosome 1 tester line LA1186 au *scf inv dgt* and examined 189 F_2 progeny. The segregation data were as follows.

Phenotype					
au	scf	inv	dgt	rvt	number
+	+	+	+	+	56
+	+	+	+	rvt	37
+	+	+	dgt	+	6
+	+	inv	+	+	1
+	scf	+	+	+	16
au	+	+	+	+	11
+	+	+	dgt	rvt	1
+	scf	+	+	rvt	1
au	+	+	+	rvt	7
+	+	inv	dgt	+	14
+	scf	+	dgt	+	2
au	+	+	dgt	+	6
au	+	+	dgt	rvt	1
+	scf	inv	+	+	3
au	scf	+	+	+	7
+	scf	inv	dgt	+	11
au	scf	inv	dgt	+	9

The complete absence of inv rvt recombinants suggests that *rvt* is close to *inv.* This is confirmed by the occurrence of only one scf rvt recombinant and two dgt rvt recombinants which are wild type for dgt and scf, respectively, indicating that scf and dgt are close to, but on opposite sides of *rvt.* Analysis of these data using the maximum likelihood method of linkage estimation leads to the following map.



This analysis suggests that *rvt* is located between inv and scf. However, the recombination distances for *rvt* are based on an F_2 in repulsion phase and so are prone to error. Therefore the placement of *rvt* proximal to inv should be considered probable but tentative.

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FORL resistance in Tm-2 and $Tm\text{-}2^2$ lines from the TGRC stock.

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The linkage between the *Fr1* allele controlling the *Fusarium oxysporum f. sp*. radicis *lycopersici (=* FORL) resistance with the *Tm-2* or *$Tm\text{-}2^2$* allele for TMV resistance is frequent (Laterrot and Couteaudier, 1989. TGC Report N° 39 p 21). Many lines and commercial F_1, hybrids resistant to FORL have been found amoung the varieties carrying the *$Tm\text{-}2^2$* allele.

Recently we have tested the 10 accessions carrying the *Tm-2* or *$Tm\text{-}2^2$* alleles from the stock of the TGRC listed by Rick and Chetelat in TGC Report N° 44: 32-44 (1994). The test was realized with a french isolate of FORL, with 18 days-old plantlets. Five lines showing FORL resistance response were tested a second time using a second sample of seeds received like the first one from C.M. Rick. There was a problem of seed germination with the accession LA 3275 carrying *$Tm\text{-}2^2$* linked to *ah*. Only one plant was obtained, this plant was FORL resistant It is know that *ah* sometimes causes a poor seed germination (Laterrot, 1973. TGC Report N° 23 p 24).

The results of the 2 tests are presented in the table 1.

Table 1 : Results of the FORL tests (total of the 2 tests).

Accessions	Number of plants		
	Resistant	Susceptible	Total
LA 1791	24	-	24
LA 3264	-	10	10
LA 3265	-	9	9
LA 3268	-	7	7
LA 3270	16	-	16
LA 3273	29	-	29
LA 3274	-	10	10
LA 3275	1	-	1
LA 3292	27	-	27
LA 3297	7	6	13

Four accessions resistant to TMV are also resistant to FORL. These lines are carrying the following alleles of TMV resistance

LA 1791: *$Tm\text{-}2^2$* allele
LA 3270: *Tm-2* allele linked to nv LA 3273: *$Tm\text{-}2^2$* allele
LA 3292: *Tm-2* allele

Results are uncertain with LA 3275 (only I plant).
The line LA 3297 is in segregation for the *Fr1* allele.

Resistance to tobacco etch virus in <u>Lycopersicon</u> <u>hirsutum.</u>

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Tobacco etch virus (TEV) causes serious economic losses in Solanaceous crops. This potyvirus is commonly found on tomato an the east coast of Florida (Zitter, 1991). This virus is also present in South America (Zitter, 1991), Cuba (Fernandez, 1979), the Philippines (Xuan et al, 1987), Taiwan (Yoon et al, 1989), Thailand (Yoon et al, 1989), and Turkey (Yilmaz and Davis, 1985). TEV causes stunting on tomato plants and intense mottling on tomato leaves and fruits. In conditions of natural infection, the crop loss may be total if seedlings are infected just after transplanting (litter, 1991).

Sources of resistance or tolerance to TEV have been reported in *L. esculentum PI 183692* (Walter, 1956) and in Pt 166989 (Alexander, 1959), and in *L. hirsutum* PI 134417, PI 127827 (Alexander and Hoover, 1955), and PI 247087 (Hikida and Raymer, 1972). However, no tolerant or resistant tomato cultivars are available (Zitter, 1991). The following accessions were screened for resistance to TEV by artificial mechanical inoculations. Some of them were previously described resistant to potyviruses (TEV and/or potato virus Y):

Genotypes	described resistance or tolerance to potyviruses	literature cited
Lycopersicon esculentum		
Angela 18.1	PVY	Nagaï and Costa 1969
PI 126410	PVY	"
F_1 Sweet 100	PVY	Stobbs et al 1994
F_1 Sweet Million	PVY	"
F_1 Micro Tom	PVY	"
Lycopersicon hirsutum		
PI 134417	TEV	Alexander 1959
PI 247087	TEV	Hikida and Raymer 1972
	PVY	Thomas and Mac Grath 1988
Lycopersicon pennellii		
LA 716	-	
Lycopersicon peruvianum		
PI 128660	PVY	Nagaï and Costa 1969
Lycopersicon pimpinellifolium		
LA 1478	-	

The susceptible tomato controls were the INRA line Monalbo and its near isogenic line Momor resistant to TMV (*Tm-2*^{2}). Screening for resistance to tobacco etch virus has been realized in growth chamber at INRA-Avignon, during 1995. Twenty plants of each genotypes were inoculated with the strain of TEV called "CAA 10" and coming from California. The symptoms were scored 45 days after inoculation. In order to confirm visual reactions, DAS-ELISA tests were performed on each plant 45 days after inoculation.

Stunt of the plant, distortion and mosaic of the leaves were observed on all the plants of Momor, Monalbo, Angela 18.1, P1 126410, F, Sweet 100, F, Sweet Million, F, Micro Tom, PI 134417 and PI 128660. No symptoms were observed on PI 247087, LA 716 and LA 1478. Among the 12 tested genotypes TEV was detected in the upper noninoculated leaves of all the plants of 11 accessions by ELISA. No virus was detected by ELISA in the upper non inoculated leaves of *L. hirsutum* PI 247087.

All the genotypes previously described resistant or tolerant to TEV or PVY appear susceptible to our strain of TEV, except Pl 247087. This L hirsutum previously reported tolerant to TEV (Hikida and Raymer, 1972) appears to be highly resistant to TEV strain CAA 10. P1 247087 was also found resistant to two isolates coming from Cuba and one isolate coming from Turkey. This accession is also highly resistant to PVY (Thomas and Mac Grath, 1988 ; Legnani et al, 1996).

The inheritance of its resistance was studied in intraspecific crosses, F_2 (P1 134417 x P1 247087) and BC, (Pl 134417 x P1 247087) x Pl 247087. Thirty days after inoculation, segregation ratios (31 R:69S in F_2 and 52R:48S in BC,) fitted with the hypothesis of I recessive gene controlling the resistance to TEV in P1 247087,

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Crossing relationships between some accessions of L. pennellii and L. hirsutum.

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We have been combining some accessions with different insect resistance chemistries which has allowed the generation of some interspecific crossing information. The accessions utilized included LA 1265 and P1 126449 from *L. hirsutum* f. *glabratum*; LA1353, LA1777, LA386, and P1 127826 of *L. hirsutum* f. *typicum*; and LA 1340, LA 2560, and LA 1674 of *L*. *pennellii.* Plants *of* these accessions were grown in greenhouse beds between 24 Apr-28 May, 1995. Day/night temperatures during this time ranged from approximately 22-32/16-22 with the air being humid. There were 3 plants per accession used for crossing. The results are in Table 1. No fruit or seed was obtained from the *L. hirsutum* f. *glabratum/typicum* crosses. This is in contrast to the results of Martin (1962) who worked with a group of different crosses. Crosses of these L - h. glabratum accessions with L. pennellii were also very difficult. No fruit or seed were obtained from 111 crosses when L. *h. glabratum* was the female, and only 1 of 163 crosses had seed when *L pennellii* was the female. The crosses of *L. hirsutum* f. *typicum* and *L. pennellii* generally succeeded in both directions. An exception was that crosses with LA 1777 as the female parent did not result in any seed, while a small percentage of the reciprocal crosses produced seed. Also no seed was obtained from LA 386/LA 2560 crosses. The LA 386/LA 1674 cross only resulted in seed when the former was the female parent. According to Rick (1979) *L. pennellii* crosses unilaterally with *L. hirsutum*. Our data indicate *L. pennellii/L.h. typicum* crosses were successful bilaterally. Results could differ due to the accessions used and/or the environmental conditions under which the crossing is done. Our results do not make any definitive statement about these interspecific crosses, but do indicate the importance of the particular accessions used in such crossing. Researchers may wish to try crossing specific accessions under their own conditions rather than assuming that certain crosses or crossing directions will be unsuccessful.

Table 1. Pollination efficiency for interspecific crosses between *L. hirsutum* f. *glabratum, L hirsutum* f. *typicum, and L. pennelliI* at a Bradenton, Florida greenhouse, Spring 1995.

Cross[z]	Pollination (No.)	Fruit Set (No.)	Seeded Fruit (No.)	Seed (No.)	Seed/ Pollination (No.)	Germination[y] (%)
f. glabratum x f. typicum						
LA 1265 x LA 1353	9	0	0	0	0.0	-
LA 1265 x LA 1777	0	0	0	0	0.0	-
LA 1265 x LA 386	22	0	0	0	0.0	-
LA 1265 x PI 127826	17	0	0	0	0.0	-
PI 126449 x LA 1353	23	0	0	0	0.0	-
PI 126449 x LA 1777	52	0	0	0	0.0	-
PI 126449 x LA 386	31	0	0	0	0.0	-
PI 126449 x PI 127826	24	0	0	0	0.0	-
Total	178	0	0	0	0.0	
f. glabratum x L. pennelli						
LA 1265 x LA 2560	17	0	0	0	0.0	-
LA 1265 x LA 1340	25	0	0	0	0.0	-
LA 1265 x LA 1674	30	0	0	0	0.0	-
PI 126449 x LA 2560	15	0	0	0	0.0	-
PI 126449 x LA 1340	9	0	0	0	0.0	-
PI 126449 x LA 1674	15	0	0	0	0.0	-
Total	111	0	0	0	0.0	
L. pennellii x f. glabratum						
LA 2560 x LA 1265	11	0	0	0	0.0	-
LA 2560 x PI 126449	49	3	1	134	2.7	45
LA 1340 x LA 1265	81	2	0	0	0.0	-
LA 1340 x PI 126449	2	0	0	0	0.0	-
LA 1674 x LA 1265	0	0	0	0	0.0	-
LA 1674 x PI 126449	20	0	0	0	0.0	-
Total	163	5	2	134	0.8	
f. typicum x L. pennelli						
LA 1353 x LA 2560	21	7	4	22	1.1	60
LA 1353 x LA 1340	33	19	14	193	5.9	85

Cross[z]	Pollination (No.)	Fruit Set (No.)	Seeded Fruit (No.)	Seed (No.)	Seed/ Pollination (No.)	Germination[y] (%)
LA 1353 x LA 1674	13	8	6	106	8.2	95
LA 1777 x LA 2560	6	0	0	0	0.0	-
LA 1777 x LA 1340	22	14	0	0	0.0	-
LA 1777 x LA 1674	19	0	0	0	0.0	-
LA 386 x LA 2560	5	1	0	0	0.0	-
LA 386 x LA 1340	12	8	8	94	7.8	60
LA 386 x LA 1674	15	9	8	159	10.6	75
PI 127826 x LA 2560	28	14	13	213	7.6	70
PI 127826 x LA 1340	43	18	15	344	8.0	100
PI 127826 x LA 1674	39	6	6	129	3.3	70
Total	246	96	74	1260	5.1	
L. pennellii x f. *typicum*						
LA 2560 x LA 1353	21	9	6	94	4.5	60
LA 2560 x LA 1777	15	2	2	177	11.8	85
LA 2560 x LA 386	33	0	0	0	0.0	-
LA 2560 x PI 127826	17	5	2	178	10.5	70
LA 1340 x LA 1353	58	13	6	28	0.5	0
LA 1340 x LA 1777	19	4	1	22	0.1	20
LA 1340 x LA 386	36	5	1	4	0.1	25
LA 1340 x PI 127826	101	18	12	103	1.0	30
LA 1674 x LA 1353	37	16	5	38	1.0	30
LA 1674 x LA 1777	24	4	3	35	1.5	30
LA 1674 x LA 386	38	1	0	0	0.0	-
LA 1674 x PI 127826	20	5	2	19	1.0	0
Total	419	82	40	698	1.6	

[z]The accession listed first is the female.
[y]Based an 20 seeds per cross except for LA 1340 x LA 386 based on 4 seeds.

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Resistance to alfalfa mosaic virus in Lycopersicon hirsutum

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Alfalfa mosaic virus (AMV) is a virus with a widespread distribution and has been reported to infect more than 600 species of 250 genera belonging to 70 botanical families (Bellardi and Bertaccini, 1993). It is transmitted in non persistant manner by at least 22 aphid species (Edwardson and Christie, 1986).

Natural infections in tomato crops caused by AMV has been reported to occur in Australia (Halisky et al.,1960), in France (Marrow and Migliori, 1966), in Germany (Schmelzer, 1969), in Israel (Zimmermann et al., 1976), in Italy (Camele at al., 1991; Ragozzino, 1995) and in Japan (Okuda at *al., 1992).* In the Imperial Valley (California), losses of 10 to 15% has been reported in tomato fields (Rude, 1982).

No case of resistance to AMV is known in the *Lycopersicon* genus. Moreover, no tolerant tomato cultivars are available (Zitter, 1993). Screening for resistance to alfalfa mosaic virus has been realized in greenhouse at INRA-Avignon, during 1995. The following 10 accessions belonging to *5* species *of* the genus *Lycopersicon* were screened by mechanical inoculation tests

Lycopersicon esculentum var. *cerasiforme :*	WVa 136
Lycopersicon pimpinellifolium :	"hirsute"; ¯LA 121; WVa 700
Lycopersicon hirsutum f. *typicum* :	LA 1777
Lycopersicon hirsutum f. *glabratum* :	PI 247087 Australia; PI 134417; "Bruinsma"
Lycopersicon peruvianum :	"CMV sel. INRA"
Lycopersicon pennellii :	"Clayberg"

The susceptible tomato control was the INRA line "Momor", resistant to TMV (gene Tm-2^2).

Fifteen plants of 16 days old were inoculated with the isolate "LYH 1 " of AMV from a plant of *L. hirsutum* Pi 247087 which was found to be infected by AMV during a field test at the INRA-Avignon in the 1995. This isolate caused necrotic symptoms after inoculation on tomato plants. All the plants of each accession were checked visually for symptoms development and by DAS-ELISA tests, 15 and 30 days after inoculation.

No symptom was observed in the basal inoculated and in the upper non-inoculated leaves of all the plants of the 3 accessions of L. hirsutum : LA 1777, PI 134417 and "Bruinsma". Moreover, in the same plants, no virus was detected by ELISA tests in the upper leaves.

In all the plants of Momor and of the other 8 accessions, including *L. hirsutum* PI 247087, typical symptoms (local and systemic necrosis) were observed and AMV was detected by ELISA tests in the upper leaves of these plants. Further analysis could give more elucidations about the mechanisms and the inheritance of the resistance(s) in the 3 accessions of *L. hirsutum* found to be resistant to alfalfa mosaic virus.

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A single gene controls the hypersensitive response of Hawaii 7981 to race 3 (T3) of the bacterial spot pathogen.

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Presently three races of the bacterial spot pathogen *Xanthomonas campestris* pv. *vesicatoria* infect tomato. These are T1, T2, and T3 (Bouzar et aL, 1994). Hawaii 7998 is resistant to T1 with multigenic control of the hypersensitive reaction and field resistance (Wang et al., 1994). We recently reported that Hawaii 7981 had a hypersensitive response and a high level of field resistance to the T3 strain (Scott *et al.,* 1995). Plants of Hawaii 7981, Fla. 7060 (susceptible) and F_1, F_2, and BC generations derived from these two inbreds were injected with 10^8 cfu/ml of the T3 strain and rated for confluent necrosis at 24 and 48 hr after injection. This was done at 24 and 32°C. No confluent necrosis was expressed at 32°C. At 24°C (Table 1) 100% of Hawaii 7981, 54% of the backcross to Hawaii 7981, and 22% of the F_2 expressed confluent necrosis at 24 hr. At 48 hr 100% of the F, and the backcross to Hawaii 7981, 50% of the backcross to Fla. 7060, and 73% of the F_2 plants expressed hypersensitivity. The data support control of hypersensitivity to T3 from Hawaii 7981 by a single incompletely dominant gene. Two experiments suggest this gene plays a major role in field resistance (data not shown). We propose *Xv-3* as the symbol far this gene.

Table 1. Hypersensitive (Hr) responses at 24°C for Hawaii 7981, Fla. 7060, F_1, backcross, and F_2 generations at 24 and 48 hours and chi square tests for control by one genetic locus.

			24 Hours					48 Hours				
Genotype	Generation	Total Plants	Hr+ No.	Hr- No.	Hr+ (%)	X^2	p	Hr+ No.	Hr- No.	r+ (%)	X^2	p
Fla. 7060 (7060)	P_1	11	0	11	0	-	-	0	11	0	-	-
Hawaii 7981 (7981)	P_2	12	12	0	100	-	-	12	0	100	-	-
7060 x 7981	F_1	24	0	24	0	-	-	24	0	100	-	-
7060 (7060 x 7981)	BCP_1	48	0	48	0	-	-	24	24	50.0	0.0	1
7981 (7060 x 7981)	BCP_2	24	13	11	54.2	16	.9-.5	24	0	100	-	-
(7060 x 7981)-Bk	F_2	120	26	94	21.7	71	.5-.1	88	32	73.3	0.18	.9-.5

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Additional sources for resistance to Crown and Root Rot disease

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Fusarium oxysporum *f.sp. radicis-lycopersici* (FORL) causing Crown and Root Rot disease is very damaging in greenhouse and field tomato. The line IRB-301-31 derived from a cross with *L. peruvianum is* the only source for resistance to FORL that have been reported and used up to now (Yamakawa, 1978; Laterrot, 1988).

Within the Fuibright visit of the author a number of Bulgarian lines having different wild species in their genetic background were tested for resistance to FORL. Six numbers out of 54 totally screened inbred lines coming from the cross Ace x L. chilense back -crossed only once to the cultivated tomato, as well as two lines with *L. pennellii* in their pedigrees were found to be in segregation for resistance to FORL. Ten lines from crosses with *L. pimpinellifolium* and eight breeding lines with resistance to other diseases reported previously (Stamova, 1990), were proven again to be homozygous resistant. The resistance is dominantly inherited (Stamova, 1993).

To our knowledge this is the first report about resistance top FORL found in *L. chilense, L. pennellii* and *L. pimpinellifolium.* Allelic test between IRS-301-31 and some of the homozygous resistant lines are under way.

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Resistance to Tomato Spotted Wilt Virus

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The Tomato Spotted Wilt Virus (TSWV) has become a big problem for tomato crops in many regions. High level of resistance was reported in *L. peruvianum*, the resistance being controlled by partly dominant gene Sw-5 (Stevens et al., 1992). The same authors have later published resistance to 3 isolates of TSWN found in 20 *L. chilense* and 8 *L. peruvianum* accessions (Stevens et al., 1994).

In 1995 a number of lines from the breeding program for high D-carotene tomatoes (Manuelyan et al**.,** 1993) were tested for resistance to TSWV. All numbers under investigation have *L. chilense* in their pedigrees. The plants were mechanically inoculated in seedling stage. The inoculation was accomplished by rubbing the cotyledons of the plants previously dusted by carborundum, with an inoculum prepared from infected tomato leaves homogenized in cold inoculation buffer. The plants were inoculated twice. Visual symptoms were used as a criteria for evaluation of the plant reaction.

Two weeks after the inoculation the plants were evaluated and 40 lines out of 80 totally screened were found in segregation for resistance to TSWV. Ten lines showed more than 50% of the plants resistant to TSWV. Later on some of the plants selected as resistant developed typical symptoms for TSWV. The plants selected from 10 lines stayed symptomless till the end , when grown for seeds. The plants are vigorous, indeterminate, with middle size fruits.

Our results support those of Stevens et al. (1994) regarding TSWV resistance in L.chilense and also their suggestion that "other potential useful TSWV resistance genes probably exist within the genus Lycopersicon".

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I am grateful to Dr. A. Stevens and J. Kao for their good cooperation.

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Resistance to Pseudomonas syringae pv. tomato.

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Resistance to bacterial speck pathogen Pseudomonasd syringae pv. tomato (P.s.t.) race 0 is controlled by the single dominant gene Pto 1 /(Pitblado and Kerr, 1980) or Pto 2 (Pilowsky and Zutra, 1992). Lawton and Mac Neill (1986) in Canada and Bogatsevska et al. (1989) in Bulgaria have published about appearance of race 1 that is pathogenic on Pto I cultivars. Resistance to race 1 was found in L.chilense and L.pimpinellifolium (Stamova et al., 1990) and two novel genes Pto 3 and Pto 4 were identified in L.hirsutum var. glabratum, controlling resistance to the both races /Stockinger and Walling, 1994/.

In 1995 we screened for resistance to race 0, fifty seven lines having L.chilense, L.pennellii and L.pimpinellifolium in their pedigrees. No one line was found to be homozygous resistant but many lines segregated for resistance to race 0, some of them showing more than 50 % of the plants resistant to P.s.t. Lines coming from crosses with L.chilense differ in size and color of the fruits, indeterminant and determinant plant habit as well as resistance to other diseases. The results support our earlier finding (Stamova, 1990) about resistance to P.s.t. in L.chilense derivatives.

Line 341-94 derived from a cross with L. pennellii (unknown origin) was found to show 38% of the plants resistant to P.s.t. To our knowledge a few reports refer to the reaction of L.pennellii to P.s.t., except - that of Stockinger and Walling report susceptibility of L.pennellii LA 716 to race 0 and race 1.

Additional study is needed to clear up the independence or similarity of new found resistance and already known resistant genes.

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Oidium powdery mildew in California

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In 1978 Kontaxis and Van Maron reported powdery mildew as a new disease on tomatoes in the United States. The case referred to the disease caused by *Leveillula taurica,* which is now well controlled genetically by the gene *Lv* in the line Laurica, developed by Stamova and Yordanov (1990). Similar attacks of powdery mildew on tomatoes have occurred elsewhere in California, including Gilroy, San Juan Bautista and the San Diego region.

In the winter of 1995 we detected a "new powdery mildew" in our research greenhouses at Davis. The symptoms of the disease are quite different from those caused by *L. taurica*. Single white flour spots appear on the upper side of the leaves, then enlarge in size and the leaves collapse and dry up.

The fungus causing the "new powdery mildew" is easily distinguished from *L. taurica* which grows into the leaf and whose sporulation is visible on the lower side of the leaf. The new fungus grows on the epidermis, and its sporulation is visible on the upper side of the leaf. Unlike *L. taurica*, the new fungus also attacks stems and petioles. ,

Under natural infection in the greenhouse the new powdery mildew attacked leaves and stems of most *L. esculentum* lines growing at the time, however some derivatives of *L hirsutum* were symptomless.

A preliminary investigation showed that the size and shape of the conidiophores and conidia are different from L taurica and are typical of an *Oidium* state (Erisiphales). Mycelia are white and thin. Conidia are single and ellipsoid in shape, with average dimensions (LxW) of 37.87 µm (range 29.43-43.64) x 18.56 µm (range 12.66 - 21.31); germ-tubes are simple, cylindrical, and originate from one end or one side of the conidium.

In the late 1980's a powdery mildew appeared in Europe (Lindhout and Pet, 1990; Stamova et al., 1990) that causes these same symptoms and was designated by Noordeloos and Loerakker (1989) as *Oidium lycopersicum*.

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A tentative study of some Solanum relatives for disease resistance

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For some tomato diseases, no resistance is known, and for others resistance genes are ineffective against some pathogen strains. This situation led us to search for resistance in some genetically distant wild relatives, even if for the present they cannot be directly hybridized with the cultivated tomato. During the author's visit in the C. M. Rick TGRC in UC-Davis, the following species have been screened for resistance to some diseases: *S. sitiens* (accessions LA1974, LA2876, LA2877, LA2878, LA2885), S. ochrantum (LA2165, LA2682) and *S. juglandifolium* (LA2134, LA2788).

All of the above mentioned species were inoculated with a fern strain of cucumber mosaic virus (CMV). Plants of the susceptible cvs VF36 and Vendor-Tm2[a] showed heavy mosaic and shoe-string leaves, whereas no CMV symptoms were registered in *S. ochrantum* and *S. juglandifolium* accessions after inoculation. The same reactions were shown after inoculation with tomato spotted wilt virus (TSWV). Some of the *S. sitiens* were found to segregate for resistance to CMV in respect to stunting of the plants after inoculation. *S. sitiens* (LA1974) was uniformly susceptible after inoculation with 3 isolates of *Botrytis* cinerea from tomato, grape, and apple.

In the same greenhouse as these tests, a heavy natural infection was observed for an Oidium powdery mildew, apparently new for California. All of the aforementioned Solanum spp. showed resistance, and simultaneously the nearby normal cultivars suffered sporulation on leaves, petioles and stems.

Identification of co-dominant RAPD markers tightly linked to the tomato spotted wilt virus (TSWV) resistance gene Sw-5.

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The tomato *(Lycopersicon esculentum)* cultivar 'Stevens' contains a single dominant gene (Sw-5) (Stevens et al. 1992) originating from *L. peruvianum (van* Zijl et al. 1986) which confers resistance to tomato chlorotic spot virus (TCSV), ground ring spot virus (GRSV) and common strains of TSWV (Boiteux and Giordano 1993).

Restriction fragment length polymorphism (RFLP) analyses position Sw-5 on the long arm of chromosome 9 in the sub-telomeric region between CT71 and CT220 (Stevens, 1993; Stevens et al., 1995). We identified a randomly amplified polymorphic DNA (RAPD) primer (UBC primer #72 [GAG CAC GGG A]) which produces a 2.2 kilo base pair (kbp) polymorphic band linked to *Sw-5* in 89R, a tomato - breeding line developed at the University of Arkansas (UA). However, when this primer was tested in a Sw-5 segregating tomato population from the University of Florida (UF) the 2.2 kbp band was also found to be present in some breeding lines susceptible to TSWV (Stevens et al. 1996). These findings indicate this band has limited utility for marker-assisted selection in a broad range of breeding lines.

Using both the OF and UA TSWV susceptible and resistant tomato lines, we conducted another search for RAPID markers. One RAPD primer (UBC primer #421 (ACG GCC CAC C]) detects a pair of co-dominant RAM markers linked to Sw-5. This primer produces a 0.94 kbp band (421R) from DNA in tomato lines with Sw-5. Susceptible *L. esculentum* plants lack the 421R band but contain a unique 0.90 kbp band. Both bands have been cloned and partially sequenced for construction of a pair of primers specific to just these two fragments. Sequence analyses indicate that the 0.94 and 0.90 kbp bands are allelic; consistent with segregation data. Our analysis of the interspecific population (*L. esculentum* (SAl x *L. pennellii* [LA716]) used to map Sw-5 (Stevens, 1993) suggest that the 0.94 and 0.90 kbp bands derive from the region between CT71 and CT220. In a population of >200 *L. esculentum* backcross plants segregating for Sw-5, we identified only two plants with probable crossover events between Sw-5 and the 0.94 kbp 421 R band. Additional analyses have determined that the TSWV resistance phenotype for these plants was incorrectly diagnosed. Thus, the genetic distance in *an L. esculentum* population is <1 cM between the 421 bands and Sw-5. We have found the specific primers to be highly reliable in a number of different buffers and amplification conditions. The co-dominant resistant and sensitive specific bands differ in size by 0.04 kbp. Therefore, care must be used in the selection of gel electrophoresis conditions in order to distinguish homozygous resistant, homozygous susceptible, and heterozygous plants.

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van Zijl, J.J.B., S.E. Bosch and C.P.J. Coetzee. 1986. Acta Hortic. 194:69-75.

Pto^h, an allele of Pto conferring resistance to Pseudomonas syringae pv. tomato (race 0) that is not associated with fenthion sensitivity

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Pto is a dominant gene on chromosome 5 conferring resistance to *Pseudomonas syringae pv. tomato* (race 0) (Pitblado and MacNeill 1983). It has also been shown that *Pto* confers susceptibility to the organophosphate insecticide, fenthion (Laterrot 1985, Laterrot and Moretti 1989). Recent molecular studies have shown that resistance to *Ps* pv tomato and susceptibility to fenthion is conferred not by a single gene, but two tightly linked and functionally similar genes (*Pto and Fen*) (Martin et al. 1994). Thus far there have been no reported successes in breaking the linkage between *Pto and Fen*.

Recently Laterrot and Moretti (1992) reported that several accessions of L hirsutum appear to be resistant both to *Ps* pv *tomato* and fenthion. In an attempt to test the genetic basis of Ps pv tomato resistance from *L. hirsutum*, a cross was made between a single individual of *L. hirsutum* PI134418 (shown to be resistance to Ps pv tomato and fenthion) and the cultivated processing line E6203 (susceptible to *Ps* pv *tomato* and resistant to fenthion). A single F, hybrid plant was backcrossed to E6203 and 20 BC_1 progeny, as well as resistant (Rio Grande-R) and susceptible (Rio Grande-S) controls, were screened for resistance to *Pst* race 0 strain PT11 (Martin et al. 1993) via a leaf inoculation assay. 4-6 week old seedlings were inoculated by dipping in a solution of 4×10^7 Pst colony forming units per ml, 10 mM $MgCl_2$, 0.05% L-77 Silwet (Union Carbide) dispersed in distilled water.

A wide range of reactions was observed in the BC1. Two plants displayed a susceptible reaction equivalent to the susceptible control. Eleven plants showed intermediate resistance (fewer lesions that the susceptible controls, but more lesions than the resistant controls). Seven plants displayed a resistance equivalent to the resistant controls. One of these highly resistant individuals was backcrossed again to E6203. In this generation the segregation for resistance was more clear cut. Twelve BC_2 progeny were screened: 10 were highly susceptible and 2 were highly resistant. Both highly resistant individuals were backcrossed again and a total of 11 BC_3 (94T693) progeny were screened with Pst . Only a single resistant individual was observed in the BC_3.

The single resistant BC3 plant (94T693-2) was both selfed and backcrossed to E6203 to produce BC_3F_2 (94T890) and BC4 (94989) populations. Individuals from both populations were screened with both *Pst* race *0* strain PT11 and, *P. syringae* race 1 strain T1 (Ronald et al. 1992) and fenthion. In addition, DNA from these plants were probed for RFLP segregation of the cloned *Pto* gene (CD186) (Martin et al. 1993). All plants showed resistance to fenthion and susceptibility to race 1 strain T1 (Ronald et al. 1992), The segregation results for reaction to *Pst* race *0* strain PT11 and for probing with the cloned *Pto* gene are summarized in Table I and 2.

Table 1. BC4 segregation for resistance to *Ps* pv. tomato race 0 and the cloned *Pto* gene (CD186)

		reaction to *Ps* pv. *tomato*	
		resistant	susceptible
CD186	+/+	0	16
(*Pto*)	+/h	10	0

Table 2. BC3F2 segregation for resistance to *Ps* pv. tomato race 0 and the cloned *Pto* gene (CD186)

		reaction to *P.s.* pv. *tomato*	
		resistant	susceptible
CD186	+/+	0	20
(*Pto*)	+/h	28	0
	h/h	13	0

Resistance to Pst race 0 and CD186 (cloned Pto gene from chromosome 5) showed perfect cosegregation in both the BC4 and BC3F2 populations indicating that race 0 resistance *from L hirsutum* P1134418 is likely allelic to *Pto*. We therefore designate the gene from *L. hirsutum* as Pto^h. Pto^h is similar to Pto in that it confers a dominant resistance to race 0 but is ineffective against race *1.* Pto^h differs from *Pto* in that it is not associated with fenthion susceptibility. The region of chromosome 5 containing the Pto^h gene showed skewed segregation in favor of the susceptible *(esculentum)* homozygotes in both the BC_4 (10 R/S:16 S/S) and the BC_3F_2 (13 RJR^- 28 R/S: 20 S/S) generations. The skewed segregation may be due to the interspecific origin of the Pto^h gene and may account for the high level of skewing towards susceptible types in the early backcross generations.

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Observation upon the comparative use of two isozyme loci in F, tomato hybrids

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In our previous work it was estimated that some isoenzyme molecular forms of the enzymes alchohol dexydrogenase and esterase may be used as genetic markers for tomato seed hybridity (TGC Report, 1993, No. 43, p. 50). These isoenzyme molecular forms later were sighted as locus Adh-1 and locus Est-1 (Compt. Rend. Acad. Bulg. Sci., 1993, No. 46, pp. 89, 97).

In this study we have compared the application of the two isozyme loci for F, tomato hybridity determination. 2113 individual seeds of tomato (*L. esculentum* Mill.) hybrids and their parental lines, taken from different lots and experimental stations in Bulgaria, were analyzed (Table 1). The enzyme extractions, the electrophoretic division on polyacrilamide gel and the isozyme visualization were carried out by our previous work.

Table 1. Parental and F_1 hybrid tomato cultivars, analyzed using *Adh-1* and *Est-1* loci

Hybrids	Observed Genotypes						Total seeds
	Adh-1			Est-1			
	P_1	F_1	P_2	P_1	F_1	P_2	
Maritsa 15	-	-	-	58	300	43	401
Maritsa 25	-	-	-	22	313	20	355
Kristi	36	152	36	36	152	36	448
Standard 69	38	242	36	38	242	36	632
Hybrid 80	-	-	-	25	133	19	177
Hybrid 82B	-	-	-	20	60	20	100
Total	74	394	72	199	1200	174	2113

The two loci for tomato hybridity identification were used only in Kristi and Standard 59 cultivars. These tomato hybrids were distinguished for their mother line which had the gene of make sterility: ms-35. The results showed complete comparison of the loci Est-1 and Adh-1 as markers of F_1 hybridity. In the other tomato hybrids that we have investigated, we were not able to use the locus Adh-1 because of lack of alternative isozymes in the parental lines. Therefore this locus wasn't applicable to prove F, hybridity in all tomato cultivars, i.e. its application was limited. As hybrid marker for the other tomato varieties we used only locus Est-1. There was no difference between the locus Est-1 expressions for the proving of F_1 hybridity in combinations both from different regions of the country and with different origin. The facts of great importance were the quicker esterase isozymes visualization and the cheaper chemicals for if.

The data of this research indicate some universality of locus Est-1 for proving F_1 tomato hybridity.

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Basal Roots

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For the last 100 years or so, plant scientists have been investigating plant root systems to improve growth, reduce sensitivity to stressful conditions, or improve tolerance to pathogens like nematodes, Fusarium, etc. During this time the plant anatomists characterized the plant root system as having three types of root: the radicle or tap-root which is the first to emerge, lateral roots (branches off other roots), and adventitious roots (roots originating from non-root, non-meristematic tissues). Because ail three types of root are virtually identical in their anatomy, root researchers assumed that they were also functionally (physiologically) equivalent - paradigm: *Although most plant root systems consist of three developmentally distinct types of root (radicle or tap root, lateral roots and adventitious roots), their virtually identical anatomy and morphology suggests that these three types are functionally (physiologically) equivalent.*

In the 1970's we hybridized the diageotropica (*dgt*) mutant with the rosette (*ro*) mutant and obtained the double homozygote shown on the cover of this issue of the TGC Reports. Since *dgt* does not develop lateral roots, and *ro* does not develop adventitious roots, the resulting homozygote should have had only a tap root - indeed this was the original intent. Morphologically, the segregating F_2 seedlings showed a ratio of 9:3:4 *(+:dgt.ro*) for shoot characteristics, and 3:1 *(+:dgt*) for root characteristics. The seedlings which were classified as *ro* segregated 3:1 *(+:dgt*) for the lateral-less characteristic of *dgt* - double homozygotes. When tested for adventitious rooting, none of the ro plants developed adventitious roots, and the double homozygotes did not develop lateral roots. The additional roots on the double homozygote have been termed 'Basal Roots" because of their location at the base of the hypocotyl (Zobel, 1975).

These results suggested that there were four types of root rather than the classical three. Further research with other plant species has confirmed the existence of four types, and evidence dating back to the 1800's (Weinhold, 1967) demonstrate the development of these basal roots on all plant species. This article is placed in this issue of the reports, because new data from our lab., with other species, demonstrates that these four types of root are functionally distinct as well as developmentally distinct. The following note describes a short experiment where we demonstrated the physiological distinctness of the tap, basal, and lateral roots of tomato in terms of nutrient uptake.

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Spatial and temporal characteristics *of* nutrient uptake; root type *differences*

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Using ion specific microelectrode technology (Toulemonde, 1992), we investigated the spatial and temporal characteristics of several different root-types on seedlings of cv. VFN8 (Zobel et al. 1992). We measured the rate of potassium (K*) uptake by tap roots at 7 and 14 days after germination and by basal roots at 14 days after germination. At 7 days the tap root was 8 cm long and at 14 days the basal roots were 8 cm long. We assn a that these roots are a developmentally similar when they are the same length. This may be an unwarranted assumption, but suffices for this study. We also measured Nitrate ($N0_3$) uptake in tap, basal and lateral roots in 7, 14, and 21 day old plants (same assumptions as before).
The results are shown in figures 1-3.

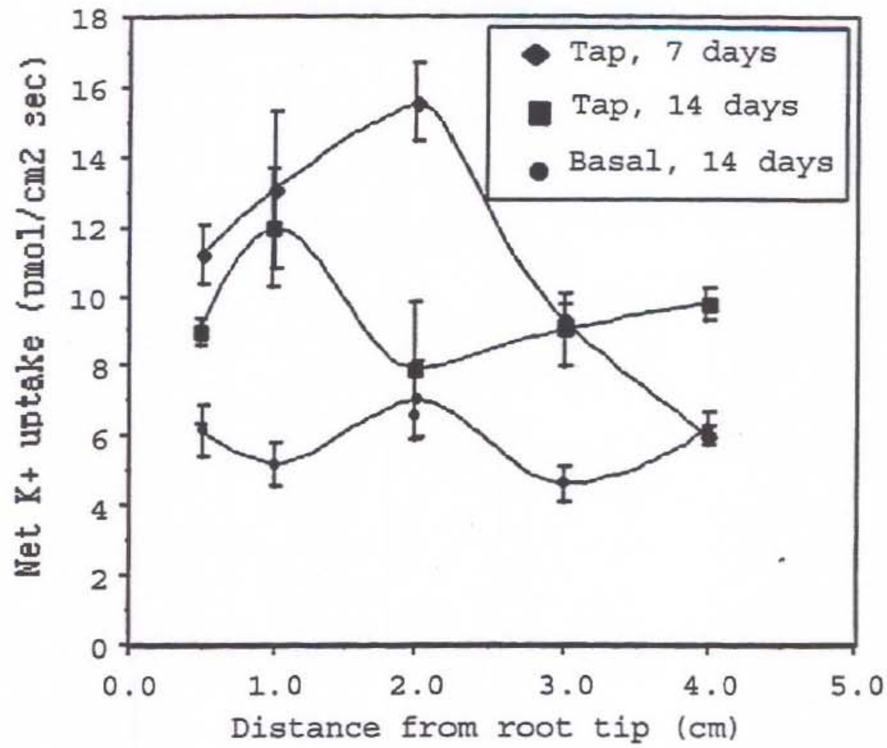

Figure 1. K+ uptake by tap and basal roots in 7 and 14 day old seedlings. (7 day tap roots = 8 cm long; 14 day tap roots = 15 cm long; basal roots in 14 day plants = 8 cm long) (Values are means, error bars represent SE. n=10 in tap roots at 7 days; n=9 in tap roots at 14 days; n=8 in basal roots at 14 days) (Modified from Toulemonde, 1992)

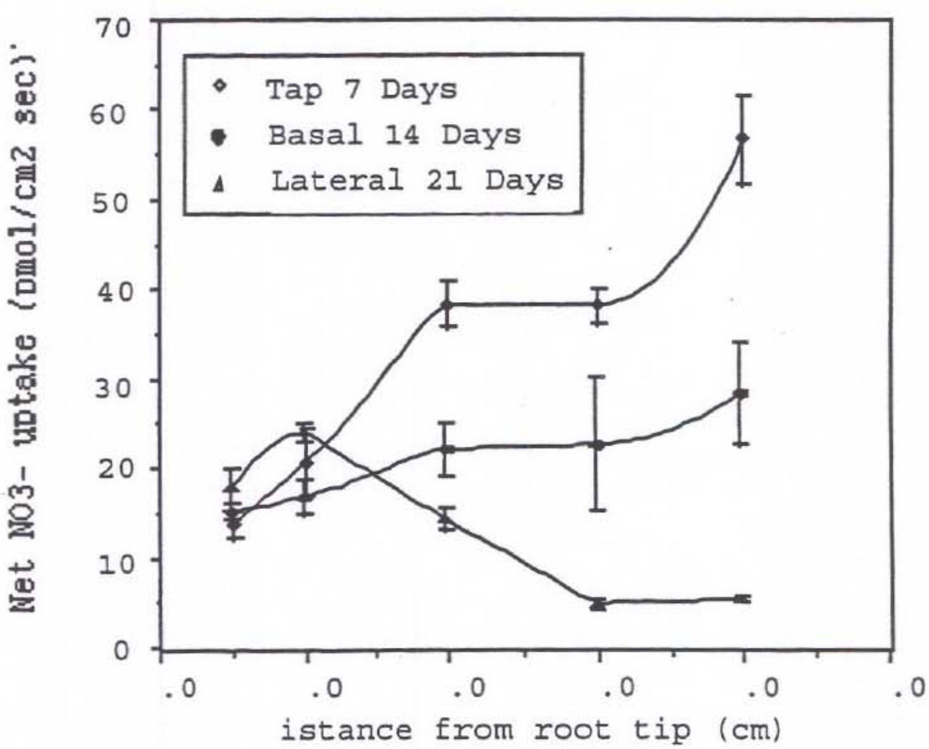

Figure 2. NO3- uptake by tap, basal and lateral roots of 7, 14 and 21 day old seedlings respectively. (8, 8, 6-8 cm long respectively) (Values are means, error bars represent SE. n=6 at 7, 14 & 21 days.) (Adapted from Toulemonde, 1992)

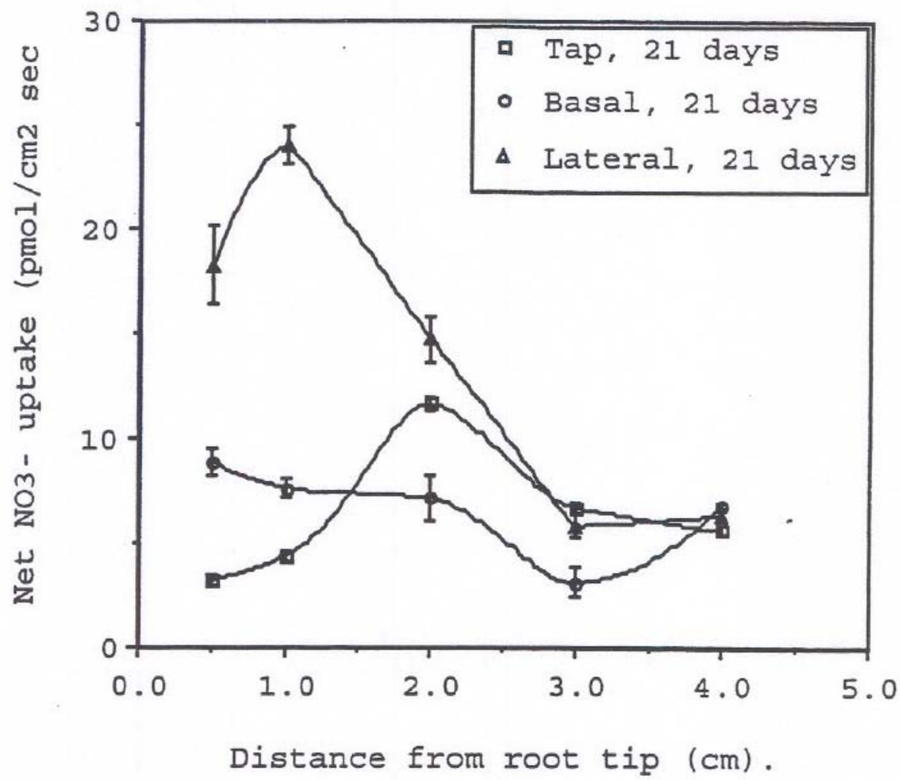

Figure 3. N03- uptake by tap, basal and lateral roots of 21 day old seedlings. (50,45, 6-8 cm respectively) (Values are means, error bars represent SE. n=5 in tap root; n=5 in basal roots; n=6 in lateral roots) (From Toulemonde, 1992)

It can be seen from these graphs that the different types of root have different spatial patterns of uptake (along the length of the root) as well as differential temporal patterns. With potassium uptake, the spatial pattern on the tap root changes from day 7 to day 14, with both being different than the basal root pattern. The absolute rate of potassium uptake for the tap root actually increases from day 7 to day 14. Similar responses are observed with nitrate uptake, except the pattern and rate of nitrate uptake for the tap root remains constant from day 7 to day 14 (data not shown). It appears that once the lateral rootshave begun to take up nitrate, both tap and basal roots reduce their rates to a lower rate which is commonwith the distal parts of the lateral roots.

This data suggests that different types of root differ in their functional characteristics as well as their developmental patterns. The demonstration that they are genetically distinct in terms of initiation (Zobel, 1975), combined with this demonstration of differential gene activity related to function suggests a need to evaluate root system function based on the separate root types existing in that root system.

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STOCK LIST

Laterrot. H
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Twenty-one near isogenic lines in Moneymaker type with different genes for disease resistances.

genes	lines	pedigree**
———	Moneymaker	———
Ve	Monalbo	Loran Blood x Eclaireur x 5 (Moneymaker)
Ve, aa	Monalbo verte	Spontaneous *anthocyanin absent* mutant
Mi	Monita	Anahu x Eclaireur x 5 (Moneymaker)
Ve, Mi	Motabo	Loran Blood x Eclaireur x 5 (Moneymaker) x Monita
Ve, I, I-2, Sm	Mobox	Walter 742-R1-3-3BK x 2 (Martarum = Marmande I. Mi) x 4 (Monalbo)
Ve, I, Mi	Mossol	from Mobox x Monita
Ve, I, I-2, Sm, Mi	Motelle*	from Mobox x Monita
Ve, pyl	Moboglan	Pannevis F1 02126K x 3 (Monalbo)
Ve, I, Pto	Movione	Ontario 7710 x 5 (Monalbo)
Tm-1	Mobaci	H.E.S. 5639-15 x Eclaireur x 5 (Moneymaker)
Mi, Tm-1	Motaci	from Monita x Mobaci
Ve, Frl, Tm-2	Mopérou	Moneymaker x (Saint-Pierre) x L. peruvianum PI 126926 line D4 x D5) x 2 (Saint-Pierre) x (Piertarum = Saint-Pierre I, Mi) x (Piéralbo = Saint-Pierre Ve) x 11 (Monalbo)
Ve, Frl, $Tm\text{-}2^2$	Momor	Alexander 630818 x 2 (Moneymaker) x 13 (Monalbo)
Ve, Frl	Mocis	from Monalbo x Momor
Ve, Frl, $Tm\text{-}2^2$*, aa*	Momor verte	from Momor x Monalbo verte
Ve, Frl, Tm-1, $Tm\text{-}2^2$	Mocimor	from Momor x Mobaci
Ve, Frl, $Tm\text{-}2^2$*, Sw-5*	Mospomor	Stevens x 5 (Momor)
Ve, I, Frl, $Tm\text{-}2^2$*, Sw-5*	Mospomorif	Stevens x 5 (Momor)
Ve, I, Sm, Frl, $Tm\text{-}2^2$*, Sw-5*	Mospomorist	Stevens x 5 (Momor)
Ve, I, I-2, Frl, Mi, pyl, $Tm\text{-}2^2$*, aa*	Mogéor	(Momor verte x Moboglan) x Motelle.

*Coobtention INRA-Tunisie - INRA-France
** x (cultivar) = number of backcrosses with the specified cultivar
Preceding lists in TGC Report N° 37, 1987, p 91; TGC Report N° 43, 1993, p 79-80.

TGRC STOCK LISTS

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Miscellaneous Stocks (935 accessions total) are listed in TGC 44 (1994)
Wild Species Stocks (1,053 accessions total) are listed in TGC 45 (1995)

REVISED LIST OF MONOGENIC STOCKS

The following list of 950 monogenic stocks (at 603 loci) is a revision of the list issued in TGC 43. Certain obsolete or unavailable items have been deleted, newly acquired stocks have been added, and numerous inaccuracies corrected. Since the demand for isogenic and nearly-isogenic lines has increased, we solicited such stocks that were not present in the TGRC collection. We are particularly indebted to Practical Plant Genetics of Littlehampton, England which has continued to anually donate sets of NILs in the Ailsa Craig background, and to many other workers for supplying other stocks. We also thank Elizabeth Munro for reformatting and proofing this stock list.

For each monogenic stock, the following information is provided: *GENE* = gene symbol, *ALLELE* = allele symbol (provisional alleles are indicated by *prov#*, and first or unnamed alleles are indicated by --), *NAME* = gene name, *CLASS* = phenotypic class (see definition of classes in table at end of this stock list), *SOURCE* = source of mutation (*SPON* = spontaneous, *CHEM* = chemically induced, *RAD* = radiation-induced), *BACK* = background genotype (see definitions in table at end of stock list), *ISO* = isogenicity of gene in the given stock (*IL* = isogenic line, *NIL* = nearly isogenic line, *NON* = nonisogenic), and *ACC#* = accession number.

This stock list includes only accessions we consider to be "primary sources" for individual genes or alleles. In general, we have listed stocks in which the gene/allele is isogenic (usually the original mutation in a known background), as well as any nearly isogenic stocks (mainly in the Ailsa Craig, Rutgers or Moneymaker backgrounds). Most stocks are true-breeding except for male-steriles, other inherited sterilities, homozygous-inviable dominants, other mutants that are too difficult to maintain homozygous, etc., all of which are propagated via heterozygotes, usually as F_2's.

Phenotypic descriptions associated with each gene can be obtained from the SolGenes database, available via the World Wide Web at "http://probe.nalusda.gov" or via Gopher at "nightshade.cit.cornell.edu port 71". For further information on connecting to SolGenes, contact the curator, Clare Nelson at the Dept. of Plant Breeding and Biometry, Cornell University, Ithaca, NY 14853, or via Email at jcn5@cornell.edu. We will furnish other types of information on monogenic stocks upon request.

Members are urged to submit stocks of verified monogenic mutants not listed here to the TGRC

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
6Pgdh-2	*1*	*6-Phosphogluconate dehydrogenase-2*		*V**	*SPON*	*pen*	*NON*	*LA2991*
6Pgdh-3	*1*	*6-Phosphogluconate dehydrogenase-3*		*V**	*SPON*	*pen*	*NON*	*LA2434*
a	--	*anthocyaninless*	*a1*	*A**	*SPON*	*X*	*NON*	*LA0291*
a	--	*anthocyaninless*	*a1*	*A**	*SPON*	*AC*	*NIL*	*LA3263*
a	*prov2*	*anthocyaninless*	*a*	*A**	*CHEM*	*VF36*	*IL*	*3-414*
a	*prov3*	*anthocyaninless*	*a*	*A**	*CHEM*	*VF36*	*IL*	*3-415*
aa	--	*anthocyanin absent*		*A**	*SPON*	*MD*	*IL*	*LA1194*
aa	--	*anthocyanin absent*		*A**	*SPON*	*AC*	*NIL*	*LA3617*
Abg	--	*Aubergine*		*P**	*SPON*	*X*	*NON*	*LA3668*
abi	--	*aborted inflorescence*		*M**	*CHEM*	*CSM*	*NON*	*3-803*

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
Aco-1	1	Aconitase-1		V*	SPON	pen	NON	LA2901
Aco-1	2	Aconitase-1		V*	SPON	pim	NON	LA2902
Aco-1	3	Aconitase-1		V*	SPON	pim	NON	LA2903
Aco-2	1	Aconitase-2		V*	SPON	pim	NON	LA2904
Aco-2	2	Aconitase-2		V*	SPON	chm	NON	LA2905
acr	–	acroxantha	acr1	D*JK	RAD	CR	IL	LA0933
ad	–	Alternaria alternata resistance		Q*	SPON	X	NON	LA1783
Adh-1	1	Alcohol dehydrogenase-1		V*	SPON	VCH	NON	LA2416
Adh-1	2	Alcohol dehydrogenase-1		V*	SPON	par	NON	LA2417
Adh-1	n	Alcohol dehydrogenase-1		V*	CHEM	MM	IL	LA3150
Adh-2	1	Alcohol dehydrogenase-2		V*	SPON	hir	NON	LA2985
adp	–	adpressa		K*J	RAD	CR	IL	LA0661
adp	–	adpressa		K*J	RAD	AC	NIL	LA3763
adu	–	adusta	adu1	H*K	RAD	CR	IL	LA0934
ae	–	entirely anthocyaninless	a332	A*	RAD	KK	IL	LA1048
ae	–	entirely anthocyaninless	a332	A*	RAD	CG	NIL	LA3018
ae	–	entirely anthocyaninless	a332	A*	RAD	AC	NIL	LA3612
ae	2	entirely anthocyaninless		A*	CHEM	UC82B	IL	3-706
ae	afr	entirely anthocyaninless	afr, ap	A*	RAD	CT	IL	LA2442
ae	prov3	entirely anthocyaninless	ae	A*	CHEM	VCH	IL	3-620
aeg	–	aegrota		H*	RAD	CR	IL	LA0537
aer	–	aerial roots		R*	SPON	X	NON	LA3205
aer-2	–	aerial roots-2		R*	SPON	X	NON	LA2464A
af	–	anthocyanin free	a325	A*I	RAD	RCH	IL	LA1049
af	–	anthocyanin free	a325	A*I	RAD	AC	NIL	LA3610
Af.	–	Anthocyanin fruit		P*	SPON	chi	NON	LA1996
afe	–	afertilis	afe1	N*CJK	RAD	RR	IL	LA0935
afl	–	albifolium	af	B*G	SPON	XLP	IL	2-367
afl	–	albifolium	af	B*G	SPON	AC	NIL	LA3572
ag	–	anthocyanin gainer		A*	SPON	GS 5	NON	LA0177
ag	–	anthocyanin gainer		A*	SPON	AC	NIL	LA3163
ag	2	anthocyanin gainer		A*	SPON	che	NON	LA0422
ag	2	anthocyanin gainer		A*	SPON	AC	NIL	LA3164
ag	k	anthocyanin gainer		A*	SPON	T5	IL	LA3149
ag-2	–	anthocyanin gainer-2		A*	SPON	AC	NIL	LA3711
ah	–	Hoffman's anthocyaninless	ao, a337	A*	SPON	OGA	IL	LA0260
ah	prov2	Hoffman's anthocyaninless	ah	A*	CHEM	MM	IL	3-302
ah	prov3	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-607
ah	prov4	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-628
ah	prov5	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-629
ah	prov6	Hoffman's anthocyaninless	ah	A*	SPON	PSN	IL	LA0352
ah	prov7	Hoffman's anthocyaninless	ah	A*	CHEM	MM	IL	3-343
ai	–	incomplete anthocyanin	a342	A*	RAD	KK	IL	LA1484
ai	–	incomplete anthocyanin	a342	A*	RAD	AC	NIL	LA3611
ai	2	incomplete anthocyanin	am, a340	A*	RAD	KK	IL	LA1485
al	–	anthocyanin loser	a2	A*	SPON	AC	NIL	LA3576
alb	–	albescent		G*C	SPON	AC	NIL	LA3729
alb	prov2	albescent	alb	G*C	CHEM	VCH	IL	3-625

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
alc	--	alcobaca		P*	SPON	X	NON	LA2529
alc	--	alcobaca		P*	SPON	RU	NIL	LA3134
alu	--	alutacea	alu1	C*K	RAD	CR	IL	LA0838
an	--	anantha	an:1, an:2, ca	L*N	RAD	CR	IL	LA0536
ap	--	apetalous		L*N	SPON	ESC	IL	2-009
ap	--	apetalous		L*N	SPON	AC	NIL	LA3673
apl	--	applanata		J*K	RAD	LU	IL	LA0662
apn	--	albo-punctata		G*BJK	CHEM	VF36	IL	3-105
Aps-1	1	Acid phosphatase-1		V*	SPON	VCH	NIL	LA1811
Aps-1	2	Acid phosphatase-1		V*	SPON	chm	NON	LA1812
Aps-1	n	Acid phosphatase-1		V*	SPON	pim	NON	LA1810
Aps-2	1	Acid phosphatase-2		V*	SPON	SM	NON	LA1814
Aps-2	2	Acid phosphatase-2		V*	SPON	che	NON	LA1815
Aps-2	3	Acid phosphatase-2		V*	SPON	par	NON	LA1816
Aps-2	n	Acid phosphatase-2		V*	SPON	che	NON	LA1813
are	--	anthocyanin reduced		A*	CHEM	VF36	NON	3-073
Asc	--	Alternaria stem canker resistance		Q*	SPON.	X	NON	LA2992
at	--	apricot		P*	SPON	X	NON	LA0215
at	--	apricot		P*	SPON	RU	NIL	LA2998
at	--	apricot		P*	SPON	AC	NIL	LA3535
atn	--	attenuata	at	E*AJK	RAD	RR	IL	LA0587
atv	--	atroviolacium		A*	SPON	AC	NIL	LA3736
au	(1s)	aurea	au:2, au, brac	C*B	RAD	CR	IL	LA0538
au	--	aurea		C*B	RAD	AC	NIL	LA3280
au	6	aurea	yg:6, yg-6, yo	C*B	SPON	RCH	IL	LA1486
au	6	aurea	yg:6, yg-6, yo	C*B	SPON	AC	NIL	LA2929
au	tl	aurea		C*B	SPON	VF145	IL	2-655A
au	w	aurea	w616	C*B	SPON	MM	IL	LA2837
aus	--	austera		J*KT	RAD	LU	IL	LA2023
aut	--	aureata		C*F	SPON	X	NON	LA1067
aut	--	aureata		C*F	SPON	AC	NIL	LA3166
auv	--	aureate virescent		F*C	CHEM	VF36	IL	3-075
avi	--	albovirens	avi1	C*BGN	RAD	CR	IL	LA0936
aw	--	without anthocyanin	aba, ab, a179	A*	SPON	per	NON	LA0271
aw	--	without anthocyanin	aba, ab, a179	A*	SPON	AC	NIL	LA3281
aw	prov3	without anthocyanin	aw	A*	CHEM	VF36	IL	3-121
aw	prov4	without anthocyanin	aw	A*	CHEM	VCH	NON	3-603
aw	prov5	without anthocyanin	aw	A*	CHEM	VCH	NON	3-627
B	--	Beta-carotene		P*	SPON	hir	NON	LA2374
B	--	Beta-carotene		P*	SPON	RU	NIL	LA3000
bc	--	bicolor	bi	U*JKT	RAD	CR	IL	LA0588
bi	--	bifurcate inflorescence		M*	SPON	X	NON	LA1786
bip	--	bipinnata		J*	RAD	LU	IL	LA0663
bip	--	bipinnata		J*	RAD	AC	NIL	LA3765
bip	prov2	bipinnata	bip	J*	CHEM	VCH	IL	3-602
bk	--	beaked		O*	SPON	X	NON	LA0330
Bk-2	--	Beaked-2		O*	SPON	X	NON	LA1787
bl	--	blind		K*	SPON	X	NON	LA0059

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
bl	2	blind	to:2	K*	SPON	LU	IL	LA0980
bls	--	baby lea syndrome	alm	A*K	SPON	X	NON	LA1004
bls	--	baby lea syndrome	alm	A*K	SPON	AC	NIL	LA3167
bls	prov2	baby lea syndrome	bls	A*K	CHEM	VCH	IL	3-610
Bnag-1	1	Beta N acetyl-D glucosamindase-1		V*	SPON	pen	NON	LA2986
br	--	brachytic		K*	SPON	X	NON	LA2069
brt	--	bushy root		R*	SPON	X	NON	LA2816
brt-2	--	bushy root-2		R*	SPON	X	NON	LA3206
bs	--	brown seed		S*	CHEM	AC	NIL	LA2935
bs-2	--	brown seed-2		S*	SPON	PLB	IL	LA1788
bs-4	--	brown seed-4		S*	RAD	MM	IL	LA1998
btl	--	brittle		J*Y	SPON	X	NON	LA1999
bu	--	bushy	fru	K*JM	SPON	X	NON	LA0897
bu	--	bushy	fru	K*JM	SPON	AC	NIL	LA2918
bu	ab	bushy	fru:ab	K*JM	RAD	RR	IL	LA0549
bu	cin	bushy	cin	K*JM	SPON	HSD	IL	LA1437
bu	cin-2	bushy	cin-2	K*JM	SPON	HSD	IL	LA2450
bu	hem	bushy	fru:hem	K*JM	RAD	CR	IL	LA0604
bul	--	bullata		C*JK	RAD	CR	IL	LA0589
buo	--	bullosa	buo1	J*O	RAD	pim	IL	LA2000
c	--	potato leaf		J*	SPON	AC	NIL	LA3168
c	int	potato leaf	int	J*	RAD	CR	IL	LA0611
c	int	potato leaf	int	J*	RAD	AC	NIL	LA3728A
c	prov2	potato leaf	c	J*	CHEM	MM	IL	3-345
c	prov3	potato leaf	c	J*	CHEM	VCH	IL	3-604
c	prov4	potato leaf	c	J*	CHEM	VCH	IL	3-609
c	prov5	potato leaf	c	J*	CHEM	VCH	IL	3-626
c	prov6	potato leaf	c	J*	CHEM	VCH	IL	3-631
car	--	carinata		J*DLO	RAD	CR	IL	LA0539
car-2	--	carinata-2	car2	J*K	RAD	pim	IL	LA2001
cb-2	--	cabbage leaf-2		J*K	SPON	X	NON	LA2002
cb-2	--	cabbage leaf-2		J*K	SPON	AC	NIL	LA3169
Cf-1	--	Cladosporium fulvum resistance-1	Cf, Cf1, Cfsc	Q*	SPON	X	NON	LA2443
Cf-1	2	Cladosporium fulvum resistance-1	Cf-4, Cf4	Q*	SPON	X	NON	LA2446
Cf-1	2	Cladosporium fulvum resistance-1	Cf-4, Cf4	Q*	SPON	MM	NIL	LA3045
Cf-1	3	Cladosporium fulvum resistance-1	Cf-5, Cf5	Q*	SPON	X	NON	LA2447
Cf-1	3	Cladosporium fulvum resistance-1	Cf-5, Cf5	Q*	SPON	MM	NIL	LA3046
Cf-2	--	Cladosporium fulvum resistance-2	Cf2, Cfp1	Q*	SPON	X	NON	LA2444
Cf-2	--	Cladosporium fulvum resistance-2	Cf2, Cfp1	Q*	SPON	MM	NIL	LA3043
Cf-3	--	Cladosporium fulvum resistance-3	Cf3, Cfp2	Q*	SPON	X	NON	LA2445
Cf-3	--	Cladosporium fulvum resistance-3	Cf3, Cfp2	Q*	SPON	MM	NIL	LA3044
Cf-6	--	Cladosporium fulvum resistance-6		Q*	SPON	X	NON	LA2448
Cf-7	--	Cladosporium fulvum resistance-7		Q*	SPON	X	NON	LA2449
Cf-9	--	Cladosporium fulvum resistance-9		Q*	SPON	MM	NIL	LA3047
cg	--	congesta	cg1	K*J	RAD	RR	IL	LA0831
ch	--	chartreuse		L*	SPON	PSN	IL	2-253
ch	--	chartreuse		L*	SPON	AC	NIL	LA3720
ci	--	cincta	ci1	K*	RAD	CR	IL	LA0938

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
cit	–	citriformis		O*JK	RAD	RR	IL	LA2024
cjf	–	confunctiflora		L*N	SPON	PTN	IL	LA1056
ck	–	corky fruit		O*	SPON	X	NON	LA2003
cl-2	–	cleistogamous-2	cl2	L*N	SPON	SM	IL	2-185
cla	–	clara		C*A	RAD	LU	IL	LA0540
clau	–	clausa	ff, vc	J*LO	RAD	LU	IL	LA0591
clau	–	clausa	ff, vc	J*LO	RAD	X	NON	LA0719
clau	–	clausa	ff, vc	J*LO	RAD	AC	NIL	LA3583
clau	ff	clausa		J*LO	SPON	VFSM	IL	2-505
clau	prov2	clausa	clau	J*LO	SPON	VFSM	IL	LA0509
clau	vc	clausa		J*LO	SPON	X	NON	LA0896
cls	–	clarescens		C*K	RAD	RR	IL	LA2025
clt	–	coalita		J*	RAD	LU	IL	LA2026
cm	–	curly mottled		G*JNO	SPON	PCV	NON	LA0272
cm	–	curly mottled		G*JNO	SPON	AC	NIL	LA2919
cma	–	commutata		K*DHJ	RAD	RR	IL	LA2027
cn	–	cana	ca	D*K	RAD	RR	IL	LA0590
co	–	cochlearis		J*D	RAD	CR	IL	LA0592
coa	–	corrotundata	coa1	J*KLT	RAD	CR	IL	LA0940
com	–	complicata		K*J	RAD	CR	IL	LA0664
con	–	convalescens		E*FK	RAD	CR	IL	LA0541
con	–	convalescens		E*FK	RAD	AC	NIL	LA3671
cor	–	coriacea		K*J	RAD	CR	IL	LA0666
cpa	–	composita	cpa1	M*K	RAD	RR	IL	LA0833
cpt	–	compact		K*EJ	RAD	XLP	IL	2-377
cpt	–	compact		K*EJ	RAD	AC	NIL	LA3723
Cri	–	Crispa		H*JU	RAD	CR	IL	LA0667
Crk	–	Crinkled		J*T	SPON	X	NON	LA1050
crt	–	cottony-root		R*	SPON	RCH	NON	LA2802
cta	–	contaminata	cta1	K*HJN	RAD	RR	IL	LA0939
ctt	–	contracta		K*J	RAD	LU	IL	LA2028
Cu	–	Curl		J*KT	SPON	STD	IL	LA0325
Cu	–	Curl		J*KT	SPON	AC	NIL	LA3740
cu-2	–	curl-2	cu2	J*	RAD	CT	IL	LA2004
cu-3	–	curl-3		J*KT	SPON	pim	IL	LA2398
cul	–	culcitula		K*U	RAD	RR	IL	LA2029
cur	–	curvifolia		J*EK	RAD	RR	IL	LA0668
cv	–	curvata	cu	K*JT	RAD	LU	IL	LA0593
cv	2	curvata	acu	K*JT	RAD	CR	IL	LA0660
cva	–	conversa		K*D	RAD	CR	IL	LA0665
cvl	–	convoluta	cvl1	K*J	RAD	RR	IL	LA0830
Cvx	–	Convexa		J*	SPON	X	NON	LA1151
d	–	dwarf	rob:imm	K*JT	SPON	STN	NIL	LA0313
d	–	dwarf	rob:imm	K*JT	SPON	FB	NIL	LA3022
d	–	dwarf	rob:imm	K*JT	SPON	GRD	NIL	LA3031
d	cr	dwarf	rob:crisp	K*JT	SPON	CR	IL	LA0570
d	im	dwarf		K*JT	RAD	CR	IL	LA0571
d	prov2	dwarf	d	K*JT	CHEM	VCH	IL	3-623

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
d	provcr-2	dwarf	d:cr	K*JT	CHEM	VF36	IL	3-420
d	provcr-3	dwarf	d:cr	K*JT	CHEM	VF36	IL	3-422
d	x	dwarf		K*JT	SPON	SPZ	IL	LA0160
d	x	dwarf		K*JT	SPON	PCV	NON	LA1052
d-2	--	dwarf-2	rob2, rob II, d2	K*N	RAD	RR	IL	LA0625
dc	--	decomposita	dc1	J*	RAD	RR	IL	LA0819
dd	--	double dwarf	d:xx	K*J	SPON	X	NON	LA0810
de	--	declinata		K*JU	RAD	RR	IL	LA0594
deb	--	debilis		H*BCJ	RAD	CR	IL	LA0542
deb	--	debilis		H*BCJ	RAD	AC	NIL	LA3727
dec	--	decumbens		K*R	RAD	LU	IL	LA0669
def	--	deformis		J*LN	RAD	RR	IL	LA0543
def	--	deformis		J*LN	RAD	AC	NIL	LA3749
def	2	deformis	vit	J*	RAD	CR	IL	LA0634
def-2	--	deformis		J*LN	RAD	AC	NIL	LA2920
Del	--	Delta		P*	SPON	AC	NIL	LA2921
Del	--	Delta		P*	SPON	RU	NIL	LA2996A
deli	--	deliquescens		K*CJ	RAD	RR	IL	LA0595
dep	--	deprimata		T*J	RAD	CR	IL	LA0544
depa	--	depauperata		K*CJ	RAD	RR	IL	LA0596
depa	--	depauperata		K*CJ	RAD	AC	NIL	LA3725
det	--	detrimentosa		C*KF	RAD	RR	IL	LA0670
det	2	detrimentosa		C*KF	RAD	RR	IL	LA0820
dg	--	dark green		T*	SPON	MP	IL	LA2451
dg	--	dark green		T*	SPON	WA	NIL	LA3011
dgt	--	diageotropica	lz-3	K*QR	SPON	VFN8	IL	LA1093
Dia-2	1	Diaphorase-2		V*	SPON	pen	NON	LA2987
Dia-3	1	Diaphorase-3		V*	SPON	lyc	NON	LA3345
dil	--	diluta		D*JK	RAD	CR	IL	LA0545
dil	--	diluta		D*JK	RAD	AC	NIL	LA3728
dim	--	diminuta		A*DK	RAD	LU	IL	LA0597
dim-2	--	diminuta-2	dim2	A*K	RAD	AC	NIL	LA3170
dis	--	discolor		D*F	RAD	CR	IL	LA0598
div	--	divaricata		C*AJK	RAD	CR	NON	LA0671
dl	--	dialytic		I*LN	SPON	SM	IL	2-069
dl	--	dialytic		I*LN	SPON	AC	NIL	LA3724
dlb	--	dilabens	dlb1	C*JK	RAD	CR	IL	LA0829
dm	--	dwarf modifier	d2	K*	SPON	X	NON	LA0014
dmd	--	dimidiata		K*JU	RAD	LU	IL	LA2033
dmt	--	diminutiva		K*	CHEM	VF36	IL	3-007
dp	--	drooping leaf		J*KT	RAD	CT	IL	LA2526
dps	--	diospyros		P*	SPON	che	NON	LA1016
dpy	--	dumpy		K*J	SPON	X	NON	LA0811
dpy	--	dumpy		K*J	SPON	AC	NIL	LA3171
dpy	prov2	dumpy	dpy	K*J	CHEM	VCH	IL	3-630
dpy	prov3	dumpy	dpy	K*J	SPON	ANAHU	IL	LA1053
drt	--	dwarf root		R*	CHEM	X	IL	LA3207
ds	--	dwarf sterile		N*K	SPON	EPK	IL	2-247

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
ds	--	dwarf sterile		N*K	SPON	AC	NIL	LA3767
dt	--	dilatata	dt1	C*JK	RAD	CR	IL	LA0828
dtt	--	detorta		J*K	RAD	LU	IL	LA2030
du	--	dupla		J*KU	RAD	LU	IL	LA2034
dv	--	dwarf virescent		F*D	SPON	X	NON	LA0155
e	--	entire	b	J*	SPON	AC	NIL	LA2922
e	prov3	entire	e	J*	CHEM	VCH	IL	3-616
eca	--	echinata		K*	RAD	RR	IL	LA2035
el	--	elongated	e	O*	SPON	AC	NIL	LA3738
ele	--	elegans		E*JK	RAD	CR	IL	LA0546
ele	2	elegans	ang	E*JK	RAD	CR	IL	LA0586
elu	--	eluta		E*K	RAD	LU	IL	LA0547
em	--	emortua	em1	H*K	RAD	RR	IL	LA0827
en	--	ensiform		J*	SPON	X	NON	LA1787
ep	--	easy peeling		O*	RAD	MM	IL	LA1158
ep	--	easy peeling		O*	RAD	AC	NIL	LA3616
epi	--	epinastic		J*K	SPON.	VFN8	IL	LA2089
er	--	erecta		K*JT	RAD	CR	IL	LA0600
era	--	eramosa	era1	B*JK	RAD	CR	IL	LA0850
Est-1	1	Esterase-1		V*	SPON	pim	NON	LA1818
Est-1	1	Esterase-1		V*	SPON	cer	IL	LA2415
Est-1	2	Esterase-1		V*	SPON	pim	NON	LA1819
Est-1	3	Esterase-1		V*	SPON	pim	NON	LA1820
Est-1	4	Esterase-1		V*	SPON	par	NON	LA1821
Est-1	5	Esterase-1		V*	SPON	pen	NON	LA2419
Est-1	n	Esterase-1		V*	SPON	pim	NON	LA1817
Est-2	1	Esterase-2		V*	SPON	pen	NON	LA2420
Est-3	1	Esterase-3		V*	SPON	par	NON	LA2421
Est-4	1	Esterase-4		V*	SPON	par	NON	LA2422
Est-4	2	Esterase-4		V*	SPON	pim	NON	LA2423
Est-4	4	Esterase-4		V*	SPON	PCV	NON	LA2425
Est-4	5	Esterase-4		V*	SPON	pim	NON	LA2426
Est-4	6	Esterase-4		V*	SPON	pim	NON	LA2427
Est-4	7	Esterase-4		V*	SPON	cer	NON	LA2428
Est-4	8	Esterase-4		V*	SPON	pim	NON	LA2429
Est-5	1	Esterase-5		V*	SPON	pen	NON	LA2430
Est-6	1	Esterase-6		V*	SPON	pen	NON	LA2431
Est-7	1	Esterase-7		V*	SPON	par	NON	LA2432
Est-7	2	Esterase-7		V*	SPON	pen	NON	LA2433
Est-8	1	Esterase-8		V*	SPON	pen	NON	LA2988
ete	--	extenuata	ete1	K*JN	RAD	CR	IL	LA0942
ex	--	exserted stigma		L*N	SPON	SM	IL	2-191
exl	--	exilis	ex	D*JK	RAD	CR	IL	LA0601
exs	--	excedens	exs1	K*J	RAD	CR	IL	LA0852
f--		fasciated fruit		O*L	SPON	ESC	NON	LA0517
fD		fasciated fruit		O*L	RAD	PCV	NON	LA0767
fa	--	falsiflora	fa1	M*N	RAD	RR	IL	LA0854
fcf	--	fucatifolia	fcf1	D*CK	RAD	CR	IL	LA0945

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
fd	--	flecked dwarf		G*DK	RAD	BK	NON	LA0873
fd	--	flecked dwarf		G*DK	RAD	AC	NIL	LA3750
Fdh-1	1	Formate dehydrogenase-1		V*	SPON	pen	IL	LA2989
fe	--	fertilis		J*LO	RAD	LU	IL	LA0672
fgv	--	fimbriate gold virescent		F*CJ	SPON	VF36	IL	LA1143
fir	--	firma		K*JM	RAD	CR	IL	LA0602
fl	--	fleshy calyx		O*	SPON	hir	NON	LA2372
fla	--	flavescens		D*JK	RAD	LU	IL	LA0548
fla	--	flavescens		D*JK	RAD	AC	NIL	LA3565
flav	--	flavida		C*	RAD	LU	IL	LA0603
flc	--	flacca		K*HW	RAD	RR	IL	LA0673
flc	--	flacca		K*HW	RAD	AC	NIL	LA3613
fld	--	flaccida	fld1	K*HJT	RAD	RR	IL	LA0943
fle	--	flexifolia	fle1	A*J	RAD	AC	NIL	LA3764
fli	--	filiform inflorescence		M*LN	SPON	X	NON	LA1790
fn	--	finely-netted		D*	RAD	PSP	IL	LA2005
fn	--	finely-netted		D*	RAD	X	NON	LA2481
fr	--	frugalis		K*JT	RAD	CR	IL	LA0674
frg	--	fragilis	frg1	D*CJK	RAD	CR	IL	LA0864
Frs	--	Frosty spot	Nec	H*	SPON	chi	NON	LA2070
frt	--	fracta		K*JT	RAD	LU	IL	LA2038
fsc	--	fuscatinervis	dkv	E*	SPON	VF145	IL	LA0872
ft	--	fruiting temperature		O*	SPON	X	NON	LA2006
fu	--	fusiformis		C*JK	RAD	CR	IL	LA0605
fua	--	fucata	fua1	E*K	RAD	CR	IL	LA0944
fug	--	fulgida	fug1	E*BK	RAD	RR	IL	LA0946
ful	--	fulgens		E*	RAD	CR	IL	LA0550
ful	2	fulgens	ful1:2	E*	RAD	RR	IL	LA0843
ful-3	--	fulgens-3		E*	SPON	VF36	IL	LA1495
fus	--	fulgescens		E*	RAD	LU	IL	LA2039
Fw	--	Furrowed		J*KN	SPON	PSN	IL	LA0192
Fw	--	Furrowed		J*KN	SPON	AC	NIL	LA3300
fx	--	flexa		K*	RAD	LU	IL	LA2037
fy	--	field yellow		E*	SPON	AC	NIL	LA3295
ga	--	galbina	ga1	D*BE	RAD	CR	IL	LA0836
gas	--	gamosepala	gas1	D*JL	RAD	RR	IL	LA0947
gbl	--	globula		K*JU	RAD	LU	IL	LA2032
Ge	c	Gamete eliminator		N*	SPON	CR	IL	LA0533
Ge	p	Gamete eliminator		N*	SPON	PSN	NON	LA0012
gf	--	green flesh		P*	SPON	PCV	NON	LA2071
gf	--	green flesh		P*	SPON	RU	NIL	LA2999
gf	--	green flesh		P*	SPON	AC	NIL	LA3534
gfl	--	globular flower		L*	SPON	X	NON	LA2984
gh	--	ghost	ab	B*G	SPON	SM	IL	LA0295
gh-2	--	ghost-2		C*G	CHEM	SX	IL	LA2007
gi	--	gibberosa		J*K	RAD	RR	IL	LA2040
gib-1	--	gibberellin deficient-1		K*Y	CHEM	MM	IL	LA2893
gib-2	--	gibberellin deficient-2		K*Y	CHEM	MM	IL	LA2894

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
gib-3	--	gibberellin-deficient-3		K*Y	CHEM	MM	IL	LA2895
gib-3	x	gibberellin-deficient-3		K*Y	CHEM	X	NON	LA2993
gl	--	glauca		J*F	RAD	CR	IL	LA0675
glau	--	glaucescens		E*JK	RAD	CR	IL	LA0606
glb	--	blobularis		K*CJ	RAD	RR	IL	LA0677
glc	--	glaucophylla		D*JK	RAD	RR	IL	LA0676
glf	--	globiformis	glf1	K*M	RAD	CR	IL	LA0948
glg	--	galapagos light green		D*	SPON	che	NON	LA1059
glm	--	glomerata		K*	RAD	LU	IL	LA2031
glo	--	globosa		K*	RAD	CR	IL	LA0551
glo	2	globosa	inx, intro	K*	RAD	LU	IL	LA0612
glo	2	globosa	inx, intro	K*	RAD	AC	NIL	LA3618
glu	--	glutinosa	glu1	O*P	RAD	RR	IL	LA0842
gm	--	gamosepalous		L*	RAD	SX	IL	LA2008
Got-1	1	Glutamate oxaloacetate transaminase-1		V*	SPON	pim	NON	LA1822
Got-1	2	Glutamate oxaloacetate transaminase-1		V*	SPON	pim	NON	LA1823
Got-2	1	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1825
Got-2	2	Glutamate oxaloacetate transaminase-2		V*	SPON	che	NON	LA1826
Got-2	3	Glutamate oxaloacetate transaminase-2		V*	SPON	par	NON	LA1827
Got-2	4	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1828
Got-2	n	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1824
Got-3	1	Glutamate oxaloacetate transaminase-3		V*	SPON	pim	NON	LA1830
Got-3	2	Glutamate oxaloacetate transaminase-3		V*	SPON	pim	NON	LA1831
Got-3	3	Glutamate oxaloacetate transaminase-3		V*	SPON	par	NON	LA1832
Got-3	n	Glutamate oxaloacetate transaminase-3		V*	SPON	che	NON	LA1829
Got-4	1	Glutamate oxaloacetate transaminase-4		V*	SPON	par	NON	LA1834
Got-4	2	Glutamate oxaloacetate transaminase-4		V*	SPON	pim	NON	LA1835
Got-4	n	Glutamate oxaloacetate transaminase-4		V*	SPON	cer	NON	LA1833
Gp	--	Gamete promoter		N*	SPON	per	NON	LA1791
Gr	--	Green ripe	gr	P*	SPON	X	NON	LA2453
gra	--	gracilis		K*J	RAD	CR	IL	LA0607
grc	--	gracillama	grc1	E*JK	RAD	RR	IL	LA0950
grf	--	grandifructa	grf1	K*O	RAD	LU	IL	LA0951
grl	--	gracilenta	grl1	E*JK	RAD	RR	IL	LA0949
gro	--	grossa		J*DK	RAD	LU	IL	LA2041
gs	--	green stripe		P*	SPON	GSM	IL	LA0212
gs	--	green stripe		P*	SPON	AC	NIL	LA3530
h	--	hairs absent	H	I*	SPON	X	NON	LA0154
h	--	hairs absent	H	I*	SPON	AC	NIL	LA3172
he	--	heteroidea		D*JK	RAD	CR	IL	LA0679
Hero	--	Heterodera rostochieusi's resistance		Q*	SPON	pim	NON	LA1792
hg	--	heterogemma	hg1	K*M	RAD	CR	IL	LA0837
hi	--	hilara		K*DJT	RAD	CR	IL	LA0952
hl	--	hairless		I*X	SPON	AC	NIL	LA3556
hl	2	hairless	cal, cal1	I*X	RAD	CR	IL	LA0937
hl	prov3	hairless	hl	I*X	CHEM	VCH	IL	3-095
hl	prov4	hairless	hl	I*X	CHEM	VCH	IL	3-126
hl	prov5	hairless	hl	I*X	CHEM	VCH	IL	3-605

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
hp	--	high pigment	hp1, hp2, bs, dr	P*T	SPON	X	NON	LA0279
hp	--	high pigment	hp1, hp2, bs, dr	P*T	SPON	RU	NIL	LA3004
hp	--	high pigment	hp1, hp2, bs, dr	P*T	SPON	SM	NIL	LA3006
hp	--	high pigment	hp1, hp2, bs, dr	P*T	SPON	AC	NIL	LA3538
Hr	--	Hirsute		I*	SPON	CT	IL	LA0895
Hrt	--	Hirtum		I*	SPON	X	NON	LA0501
ht	--	hastate		J*L	SPON	SM	IL	2-295
hy	--	homogeneous yellow		E*	SPON	cer	NON	LA1142
hy	--	homogeneous yellow		E*	SPON	AC	NIL	LA3308
I	--	Immunity to Fusarium: race O		Q*	SPON	VD	NIL	LA3025
I	--	Immunity to Fusarium: race O		Q*	SPON	GRD	NIL	LA3042
I-2	--	Immunity to fusarium: race 2		Q*	SPON	MM	NIL	LA2821
ic	--	inclinata		J*CK	RAD	RR	IL	LA0682
ica	--	icana		B*JK	RAD	RR	IL	LA2042
icn	--	incana		B*F	SPON	X	NON	LA1009
icn	--	incana		B*F	SPON	AC	NIL	LA3173
ics	--	incisifolia		J*	SPON	PTN	IL	LA1054
ics	--	incisifolia		J*	SPON	AC	NIL	LA3713
id	--	indehiscens		L*JO	RAD	RR	IL	LA0684
ida	--	inordinata		K*JT	RAD	RR	IL	LA2043
Idh-1	1	Isocitrate dehydrogenase-1		V*	SPON	hir	NON	LA2906
ig	--	ignava		D*K	RAD	CR	IL	LA0608
ig	--	ignava		D*K	RAD	AC	NIL	LA3752
im	--	impatiens	im1	K*UW	RAD	RR	IL	LA0863
imb	--	imbecilla		E*DK	SPON	CR	IL	LA0552
imb	--	imbecilla		E*DK	SPON	AC	NIL	LA3566
imp	dia	impedita		E*K	SPON	CR	IL	LA0680
imp	eg	impedita		E*K	SPON	CR	IL	LA0681
in	--	indiga		K*DJ	RAD	CR	IL	LA0610
in	--	indiga		K*DJ	RAD	AC	NIL	LA3715
ina	--	inflexa	ina1	K*	RAD	LU	IL	LA0840
ina	--	inflexa	ina1	K*	RAD	AC	NIL	LA3732
inc	--	incurva		K*J	RAD	CR	IL	LA0609
inc	--	incurva		K*J	RAD	AC	NIL	LA3730
inf	--	informa		J*K	RAD	CR	IL	LA0553
inf	--	informa		J*K	RAD	AC	NIL	LA3726
ini	--	inquieta	ini1	I*DJK	RAD	RR	IL	LA0953
ino	--	involuta	ino1	K*	RAD	CR	IL	LA0954
ins	--	inconstans	ins1	K*	RAD	RR	IL	LA0841
inv	--	invalida		F*EJK	RAD	CR	IL	LA0554
inv	--	invalida		F*EJK	RAD	AC	NIL	LA3439
Ip	--	Intense pigment		P*	SPON	VF145	NIL	LA1563
irr	--	irregularis		J*CT	RAD	CR	IL	LA0613
irr	--	irregularis		J*CT	RAD	AC	NIL	LA3747
ita	--	inquinata	ita1	H*G	RAD	RR	IL	LA0839
j	--	jointless	lf	M*	SPON	FB	NIL	LA3023
j	--	jointless	lf	M*	SPON	GRD	NIL	LA3033
j-2	--	jointless-2	j2	M*	SPON	che	NON	LA0315

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
j-2	in	jointless-2	j2:in	M*	SPON	X	NON	LA0756
Jau	—	Jaundiced		E*	SPON	AC	NIL	LA3174
jug	—	jugata		K*LO	RAD	CR	IL	LA0555
jug	2	jugata	jug1:2	K*LO	RAD	LU	IL	LA0834
l	—	lutescent	g	C*	SPON	AC	NIL	LA3717
l	2	lutescent	rub	C*	RAD	LU	IL	LA0572
l	prov3	lutescent	l	C*	SPON	ROMA	IL	2-491
l	prov4	lutescent	l	C*	SPON	EPK	NIL	LA3009
l-2	—	lutescent-2	l-3, l2	C*Y	SPON	LRD	IL	LA0643
l-2	—	lutescent-2	l-3, l2	C*Y	SPON	AC	NIL	LA3581
La	—	Lanceolate		J*	SPON	PCV	NON	LA0335
lae	—	laesa		H*JK	RAD	RR	IL	LA0685
lan	—	languida		D*F	RAD	RR	IL	LA2044
lap	—	lamprochlora	lap1	J*K	RAD	RR	IL	LA0955
lat	—	lata		K*	RAD	CR	IL	LA0556
le	—	lembiformis	le1	K*ACJR	RAD	RR	IL	LA0956
lep	—	leprosa	lep1	H*K	RAD	RR	IL	LA0957
lg	—	light-green	lme	D*	SPON	AC	NIL	LA3175
lg-5	—	light green-5	lg5, lm, fy, yt	D*	SPON	X	NON	LA0757
lg-5	—	light green-5	lg5, lm, fy, yt	D*	SPON	AC	NIL	LA3176
li	—	limbrata		J*	RAD	LU	IL	LA2045
Ln	—	Lanata		I*	CHEM	VF36	IL	3-071
Ln	G	Lanata		I*	CHEM	FLD	NON	LA3127
lop	—	longipes	lop1	J*DK	RAD	CR	IL	LA0958
Lpg	—	Lapageria		J*LNT	SPON	VF36	IL	2-561
Lpg	—	Lapageria		J*LNT	SPON	AC	NIL	LA3739
ls	—	lateral suppresser		K*LN	SPON	AMB	IL	LA0329
ls	—	lateral suppresser		K*LN	SPON	X	NON	LA2892
lt	—	laeta	lt1	E*DK	RAD	CR	IL	LA0835
ltf	—	latifolia		J*	CHEM	VF36	IL	3-035A
lu	—	luteola		L*	RAD	LU	IL	LA0686
luc	—	lucida		C*F	RAD	CR	IL	LA0557
lur	—	lurida	lur1	E*D	RAD	RR	IL	LA0959
lut	—	lutea		E*F	RAD	CR	IL	LA0558
lut	—	lutea		E*F	RAD	AC	NIL	LA3714
Lv	—	Leveillula taurica resistance		Q*	SPON	X	NON	LA3118
Lv	—	Leveillula taurica resistance		Q*	SPON	X	NON	LA3119
Lx	—	Lax		J*	SPON	LK	NON	LA0505
Lx	—	Lax		J*	SPON	AC	NIL	LA3177
lyr	—	lyrate		J*NO	SPON	PCV	NON	LA0763
lyr	—	lyrate		J*NO	SPON	AC	NIL	LA2923
lz	—	lazy		K*	RAD	AC	NIL	LA3762
lz-2	—	lazy-2		K*	CHEM	SM	NIL	LA2924
lz-2	—	lazy-2		K*	CHEM	AC	NIL	LA3710
m	—	mottled		K*	RAD	AC	NIL	LA3568
m-2	—	mottled-2	m2, mo, md	F*D	RAD	AC	NIL	LA3574
ma	—	macrocarpa		J*O	RAD	LU	IL	LA0687
mac	—	maculata	mac1	H*K	RAD	CR	IL	LA0960

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
mad	–	marcida	mad1	T*K	RAD	CR	IL	LA0961
mar	–	marcescens		T*K	RAD	LU	NON	LA0688
marm	–	marmorata		G*D	RAD	CR	IL	LA0559
marm	2	marmorata	marm1:2	G*D	RAD	CR	IL	LA0844
mc	–	macrocalyx		L*M	SPON	X	NON	LA0159
mcn	–	maculonecrotic		G*H*CF	CHEM	VF36	IL	3-045
mcr	–	multicolor		B*CH	RAD	LU	IL	LA2047
mcs	–	macrosepala		L*J	RAD	LU	IL	LA2046
Mdh-1	2	Malate dehydrogenase-1		V*	SPON	lyc	NON	LA3344
Mdh-4	1	Malate dehydrogenase-4		V*		pen	NON	LA2990
Me	–	Mouse ears		J*K	SPON	RU	IL	LA0324
Me	–	Mouse ears		J*K	SPON	AC	NIL	LA3552
med	–	mediocris	med1	K*	RAD	CR	IL	LA0962
mel	–	melongenoida	mel1	O*K	RAD	LU	IL	LA0963
mgn	–	marginal necrotic		H*C	CHEM	VF36	IL	3-025
Mi	–	Meloidogyne incognita resist.		Q*	SPON	VFN8	NON	LA1022
Mi	–	Meloidogyne incognita resist.		Q*	SPON	MM	NIL	LA2819
mic	–	microcarpa	mic1	D*GLO	RAD	CR	IL	LA0845
mn	–	minuta	mi	K*CJ	RAD	CR	IL	LA0614
mon	–	monstrosa		K*J	RAD	CR	IL	LA0615
mor	–	morata	mor1	E*K	RAD	RR	IL	LA0848
ms-02	–	male-sterile-2	ms2	N*	SPON	PSN	IL	2-031
ms-03	–	male-sterile-3	ms3	N*	SPON	SM	IL	2-032
ms-05	–	male-sterile-5	ms5	N*	SPON	SM	IL	2-039
ms-06	–	male-sterile-6	ms6	N*	SPON	SM	IL	2-044
ms-07	–	male-sterile-7	ms7	N*	SPON	SM	IL	2-089
ms-09	–	male-sterile-9	ms9	N*	SPON	SM	IL	2-121
ms-10	–	male-sterile-10	ms10	N*	SPON	SM	IL	2-132
ms-10	35	male-sterile-10	ms-35, ms35	N*	SPON	VF11	IL	2-517
ms-10	36	male-sterile-10	ms-36	N*	SPON	VF36	IL	2-635
ms-11	–	male-sterile-11	ms11	N*	SPON	SM	IL	2-152
ms-12	–	male-sterile-12	ms12	N*	SPON	SM	IL	2-161
ms-13	–	male-sterile-13	ms13	N*	SPON	SM	IL	2-165
ms-14	–	male-sterile-14	ms14	N*	SPON	ERL	IL	2-175
ms-15	–	male-sterile-15	ms15	N*	SPON	SM	IL	2-193
ms-15	26	male-sterile-15	ms26, ms-26	N*	SPON	VE	IL	2-327
ms-15	47	male-sterile-15	ms-47	N*	SPON	UC82B	NIL	2-837
ms-16	–	male-sterile-16	ms16	N*	SPON	PRT	IL	LA0062
ms-17	–	male-sterile-1	ms17	N*	SPON	ACE	IL	2-225
ms-18	–	male-sterile-18	ms18	N*	SPON	H255	IL	2-233
ms-23	–	male-sterile-23	ms23	N*	SPON	EPK	IL	2-273
ms-24	–	male-sterile-24	ms24	N*	SPON	EPK	IL	2-277
ms-25	–	male-sterile-25	ms25	N*	SPON	RTVF	IL	2-313
ms-27	–	male-sterile-27	ms27	N*	SPON	VE	IL	2-331
ms-28	–	male-sterile-28	ms28	N*	SPON	XLP	IL	2-355
ms-29	–	male-sterile-29	ms29	N*	SPON	CPC#2	IL	2-423
ms-30	–	male-sterile-30	ms30	N*	SPON	SM	IL	2-455
ms-31	–	male-sterile-31	ms31	N*	SPON	VF6	IL	2-461

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
ms-32	--	male-sterile-32	ms32	N*	SPON	cer	NON	LA0359
ms-32	--	male-sterile-32	ms32	N*	SPON	MNB	NIL	LA2712
ms-32	--	male-sterile-32	ms32	N*	SPON	M167	NIL	LA2713
ms-32	--	male-sterile-32	ms32	N*	SPON	M168	NIL	LA2714
ms-32	--	male-sterile-32	ms32	N*	SPON	POR	NIL	LA2715
ms-33	--	male-sterile-33	ms33	N*	SPON	VF11	IL	2-511
ms-34	--	male-sterile-34	ms34	N*	SPON	VF11	IL	2-513
ms-38	--	male-sterile-38	ms38	N*	SPON	VF36	IL	2-539
ms-38	40	male-sterile-38	ms-40	N*	SPON	VF36	IL	2-553
ms-39	--	male-sterile-39		N*	SPON	VF36	IL	2-549
ms-44	--	male-sterile-44		N*	CHEM	SM	IL	LA2090
ms-45	--	male-sterile-45		N*	SPON	VFN8	IL	2-659
ms-46	--	male-sterile-46		N*	SPON	VFN8	IL	2-681
Ms-48	--	Male-sterile-48		N*	CHEM	CSM	IL	2-839
Ms-48	--	Male-sterile-48		N*	CHEM	VF36	NIL	LA3191
Ms-48	--	Male-sterile-48		N*	CHEM	TVD	NIL	LA3192
Ms-48	--	Male-sterile-48		N*	CHEM.	MR20	NIL	LA3193
Ms-48	--	Male-sterile-48		N*	CHEM	N28	NIL	LA3194
Ms-48	--	Male-sterile-48		N*	CHEM	T338	NIL	LA3195
Ms-48	--	Male-sterile-48		N*	CHEM	TR44	NIL	LA3196
Ms-48	--	Male-sterile-48		N*	CHEM	TR51	NIL	LA3197
Ms-48	--	Male-sterile-48		N*	CHEM	T5	NIL	LA3198
Ms-48	--	Male-sterile-48		N*	CHEM	VCH	NIL	LA3199
Ms-48	--	Male-sterile-48		N*	CHEM	spVCH	NIL	LA3200
ms-49	--	male-sterile-49		N*	SPON	per	NON	LA1161
ms-50	--	male sterile-50		N*	RAD	T5	IL	LA3149
mt	--	midget		K*N	SPON	NRT	IL	LA0282
mta	--	mutata	mta1	K*EFJ	RAD	RR	IL	LA0965
mts	--	mortalis	mts1	K*JM	RAD	RR	IL	LA0849
mu	--	multinervis		D*J	RAD	CR	IL	LA0690
mu	--	multinervis		D*J	RAD	AC	NIL	LA3573
mu	3	multinervis	rv-3	D*J	CHEM	VF36	IL	3-033
mua	--	multifurcata	mua1	K*M	RAD	CR	IL	LA0851
muf	--	multifolia		J*DK	RAD	RR	IL	LA0689
mult	--	multiflora		M*	RAD	CR	IL	LA0560
mup	--	multiplicata	mup1	M*L	RAD	RR	IL	LA0846
mut	--	mutabilia	mut1	K*DT	RAD	RR	IL	LA0866
muv-2	--	multivalens-2	mus1	C*FJK	RAD	CR	IL	LA0964
muv-2	--	multivalens-2	mus1	C*FJK	RAD	AC	NIL	LA3758
mux	--	multiplex	mux1	L*KM	RAD	CR	IL	LA0847
n	--	nipple-tip	nt	O*	SPON	X	NON	LA2353
n	--	nipple-tip	nt	O*	SPON	X	NON	LA2370
na	--	nana		K*J	RAD	CR	IL	LA0561
nc	--	narrow cotyledons		J*	SPON	AC	NIL	LA3178
nd	--	netted	m-4	F*	RAD	AC	NIL	LA3584
ndw	--	necrotic dwarf		H*JK	SPON	X	NON	LA3142
ne	--	necrotic		H*	SPON	X	NON	LA2350
neg	--	neglecta		H*DK	RAD	CR	IL	LA0562

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
neg	–	neglecta		H*DK	RAD	AC	NIL	LA3746
neg	ne-2	neglecta	ne-2, ne2	H*DK	RAD	CT	IL	LA2454
neg	ne-2	neglecta	ne-2, ne2	H*DK	RAD	X	NON	LA2489
neg	ne-2	neglecta	ne-2, ne2	H*DK	RAD	AC	NIL	LA3621
Nir-1	1	Nitrate reductase-1		V*	SPON	pen	IL	LA2908
nor	–	non-ripening		P*	SPON	X	NON	LA1793
nor	–	non-ripening		P*	SPON	RU	NIL	LA3013
nor	–	non-ripening		P*	SPON	AC	NIL	LA3770
not	–	notabilis		W*EHJY	RAD	LU	IL	LA0617
not	–	notabilis		W*EHJY	RAD	AC	NIL	LA3614
Nr	–	Never ripe		P*	SPON	PSN	IL	LA0162
Nr	–	Never ripe		P*	SPON	RU	NIL	LA3001
Nr	–	Never ripe		P*	SPON	AC	NIL	LA3537
Nr-2	–	Never ripe-2		P*	SPON	X	NON	LA2455
nv	–	netted virescent		E*F	SPON	per	NON	LA0786
o	–	ovate		O*	SPON	AC	NIL	LA3377
O.	1	Oval	ol	O*	SPON'	X	NON	LA0271
ob	–	obscura		T*K	RAD	RR	IL	LA0691
obl	–	oblate fruit		O*	RAD	MM	IL	LA1159
oc	–	ochroleuca		G*BK	RAD	RR	IL	LA0692
Od	–	Odorless		K*	SPON	PCV	NON	LA0292
og	–	old gold		P*L	SPON	chi	NON	LA0294
og	–	old gold		P*L	SPON	PSN	NIL	LA0348
og	c	old gold	Crn,Cr,crn-2,cr-	P*L	SPON	PCV	NON	LA0806
og	c	old gold	Crn,Cr,crn-2,cr-	P*L	SPON	AC	NIL	LA3179
oli	–	olivacea		J*KU	RAD	AC	NIL	LA3722
op	–	opaca		D*CF	RAD	CR	IL	LA0618
op	–	opaca		D*CF	RAD	AC	NIL	LA3567
opa	–	opacata	opa1	E*K	RAD	CR	IL	LA0966
or	–	ordinata		D*F	RAD	RR	IL	LA2048
Ora	–	Orobanche aegyptica resistance		Q*	SPON	X	NON	LA2530
os	–	oligosperma	os1	K*JT	RAD	CR	IL	LA0868
ovi	–	oviformis	ovi1	J*O	RAD	LU	IL	LA0967
p	–	peach		O*I	SPON	X	NON	LA2357
pa-2	–	parva-2	pa1, pa2	K*J	RAD	CR	IL	LA0970
pal	–	pallida		D*L	RAD	CR	IL	LA0563
pap	–	paupercula		J*W	RAD	RR	IL	LA2050
pas	–	pallescens	pas1	D*K	RAD	CR	IL	LA0968
pat	–	parthenocarpic fruit		S*	CHEM	ROMA	IL	LA2013
pat-2	–	parthenocarpic fruit-2		S*	SPON	X	NON	LA2413
pau	–	pauper		K*	RAD	CR	NON	LA0877
pct	–	polycot		J*KLM	SPON	MM	NON	LA2896
pcv	–	polychrome variegated		G*BDJ	SPON	X	NON	LA1199
pdc	–	pudica		K*JT	CHEM	VF36	IL	3-047
pds	–	phosphorus deficiency	Ph-oid	A*CY	SPON	X	NON	LA0813
pdw	–	pale dwarf		V*	SPON	X	NON	LA2457
pdw	–	pale dwarf		V*	SPON	X	NON	LA2490
pe	–	sticky peel		O*	SPON	X	NON	LA0759

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
pen	--	pendens		J*C	RAD	CR	IL	LA0694
pen	--	pendens		J*C	RAD	AC	NIL	LA3293
per	--	perviridis		A*KT	RAD	RR	IL	LA0564
pet	--	penetrabile	pet-2, pet2	K*J	RAD	CR	IL	LA0971
Pgi-1	1	Phosphoglucoisomerase-1		V*	SPON	pen	NON	LA2435
Pgi-1	2	Phosphoglucoisomerase-1		V*	SPON	par	NON	LA2436
Pgm-1	1	Phosphoglucomutase-1		V*	SPON	hir	NON	LA2437
Pgm-2	1	Phosphoglucomutase-2		V*	SPON	pen	NON	LA2438
Ph	--	Phytophthora infestans race resistance	PiT, TR1	Q*	SPON	X	NON	LA2009
Ph-2	--	Phytophthora infestans resistance		Q*	SPON	UC82	NIL	LA3151
Ph-2	--	Phytophthora infestans resistance		Q*	SPON	MNB	NIL	LA3152
pi	--	pistillate		L*N	SPON	SM	IL	2-137
pi-2	--	pistillate-2		N*LM	CHEM	CSM	IL	3-802
pic	--	picta		H*C	RAD	CR	IL	LA0620
pl	--	perlucida	pl1	D*CJ	RAD	CR	IL	LA0867
pl	--	perlucida	pl1	D*CJ	RAD	AC	NIL	LA3296
pla	--	plana		D*CK	RAD	CR	IL	LA0695
pli	--	plicata		K*ABJ	RAD	LU	IL	LA0696
pli	--	plicata		K*ABJ	RAD	AC	NIL	LA3672
pm	--	praematura	pm1	Z*CJK	RAD	RR	IL	LA0855
Pn	--	Punctate		A*	SPON	pen	NON	LA0812
Pn	--	Punctate		A*	SPON	AC	NIL	LA3089
pol	--	polylopha		K*JO	RAD	LU	IL	LA0697
Pox	--	Poxed fruit		P*	SPON	X	NON	LA2366
pp	--	polyphylla	pp1	J*D	RAD	RR	IL	LA0860
ppa	--	purpurea		A*	RAD	LU	IL	LA2054
pr	--	propeller		J*	RAD	X	NON	LA0326
pr	--	propeller		J*	RAD	AC	NIL	LA2925
prc	--	procumbens		K*CJ	RAD	CR	IL	LA0698
pre	--	pressa		K*J	RAD	RR	IL	LA2053
pro	--	procera		J*Z	RAD	CR	IL	LA0565
pro	--	procera		J*Z	RAD	AC	NIL	LA3283
prt	--	protea	prt1	C*JK	RAD	CR	IL	LA0972
prun	--	prunoidea		O*J	RAD	LU	IL	LA0566
Prx-1	1	Peroxidase-1		V*	SPON	pim	NON	LA1837
Prx-1	2	Peroxidase-1		V*	SPON	pim	NON	LA1838
Prx-1	3	Peroxidase-1		V*	SPON	pim	NON	LA1839
Prx-1	4	Peroxidase-1		V*	SPON	chm	NON	LA1840
Prx-1	5	Peroxidase-1		V*	SPON	pim	NON	LA1841
Prx-1	n	Peroxidase-1		V*	SPON	pim	NON	LA1836
Prx-2	1	Peroxidase-2		V*	SPON	cer	NON	LA1843
Prx-2	3	Peroxidase-2		V*	SPON	pim	NON	LA1845
Prx-2	n	Peroxidase-2		V*	SPON	pim	NON	LA1842
Prx-3	1	Peroxidase-3		V*	SPON	pim	NON	LA1847
Prx-3	2	Peroxidase-3		V*	SPON	pim	NON	LA1848
Prx-3	a1	Peroxidase-3		V*	SPON	chm	NON	LA1849
Prx-3	n	Peroxidase-3		V*	SPON	pim	NON	LA1846
Prx-4	1	Peroxidase-4		V*	SPON	pim	NON	LA1850

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GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
Prx-4	10	Peroxidase-4		V*	SPON	cer	NON	LA1859
Prx-4	11	Peroxidase-4		V*	SPON	pim	NON	LA1860
Prx-4	12	Peroxidase-4		V*	SPON	pim	NON	LA1861
Prx-4	13	Peroxidase-4		V*	SPON	pim	NON	LA1862
Prx-4	14	Peroxidase-4		V*	SPON	pim	NON	LA1863
Prx-4	15	Peroxidase-4		V*	SPON	pim	NON	LA1864
Prx-4	17	Peroxidase-4		V*	SPON	pim	NON	LA1866
Prx-4	18	Peroxidase-4		V*	SPON	pim	NON	LA1867
Prx-4	19	Peroxidase-4		V*	SPON	pim	NON	LA1868
Prx-4	2	Peroxidase-4		V*	SPON	pim	NON	LA1851
Prx-4	20	Peroxidase-4		V*	SPON	cer	NON	LA1869
Prx-4	21	Peroxidase-4		V*	SPON	pim	NON	LA1870
Prx-4	22	Peroxidase-4		V*	SPON	pim	NON	LA1871
Prx-4	23	Peroxidase-4		V*	SPON	pim	NON	LA1872
Prx-4	3	Peroxidase-4		V*	SPON	pim	NON	LA1852
Prx-4	4	Peroxidase-4		V*	SPON	chm	NON	LA1853
Prx-4	5	Peroxidase-4		V*	SPOŃ	chm	NON	LA1854
Prx-4	6	Peroxidase-4		V*	SPON	par	NON	LA1855
Prx-4	7	Peroxidase-4		V*	SPON	STN	NON	LA1856
Prx-4	8	Peroxidase-4		V*	SPON	pim	NON	LA1857
Prx-4	9	Peroxidase-4		V*	SPON	pim	NON	LA1858
Prx-7	1	Peroxidase-7		V*	SPON	pim	NON	LA1873
Prx-7	2	Peroxidase-7		V*	SPON	pim	NON	LA1874
Prx-7	n	Peroxidase-7		V*	SPON	pim	NON	LA1875
ps	--	positional sterile	va	L*N	SPON	JBR	IL	LA0063
ps	prov2	positional sterile	ps	L*N	SPON	PSN	IL	2-303
ps-2	--	positional sterile-2		L*N	SPON	X	NON	LA2010
ps-2	--	positional sterile-2		L*N	SPON	VRB	IL	LA3631
psa	--	perspicua		D*J	RAD	LU	IL	LA2051
pst	--	persistent style		O*	SPON	ESC	IL	2-005
pt	--	petite		D*	RAD	AC	NIL	LA3768
pta	--	partiaria		J*	RAD	RR	IL	LA2049
ptb	--	protuberant		O*	SPON	che	NON	LA1017
ptb	--	protuberant		O*	SPON	che	NON	LA1018
Pto	--	Pseudomonas tomato resistance		Q*	SPON	X	NON	LA2396
Pto	--	Pseudomonas tomato resistance		Q*	SPON	RG	NIL	LA3342
Pto	--	Pseudomonas tomato resistance		Q*	SPON	MM	NIL	LA3472
Pto	2	Pseudomonas tomato resistance		Q*	SPON	RH13	NON	LA3129
Pto-2	--	Pseudomonas tomato resistance-2		Q*	SPON	pim	NON	LA2934
Pts	--	Petroselinum leaf		J*	SPON	VF36	NIL	LA2532
pu	--	pulvinata	pul	K*J	RAD	RR	IL	LA0621
pu	2	pulvinata	pu2	K*J	RAD	CR	IL	LA0973
pum	--	pumila		K*	RAD	CR	IL	LA0567
pun	--	punctata	pun1	J*DGKT	RAD	RR	IL	LA0974
pur	--	purilla		K*C	RAD	CR	NON	LA0568
px	--	praecox	px1	K*JOZ	RAD	LU	IL	LA0856
py	--	pyramidalis		K*CJT	RAD	RR	IL	LA2055
pyl	--	Pyrenochaeta lycopersici resistance	py	Q*	SPON	per	NON	LA2531A

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GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
r	(2s)	yellow flesh	r:3, r-2, r2	P*	RAD	RR	IL	LA2056
r	--	yellow flesh		P*	SPON	RU	NIL	LA2997
r	--	yellow flesh		P*	SPON	C37	NIL	LA3003
r	--	yellow flesh		P*	SPON	AC	NIL	LA3532
r	prov4	yellow flesh	r	P*	SPON	PSN	IL	2-141
r	prov5	yellow flesh	r	P*	SPON	EPK	IL	LA0353
ra	--	rava		D*CIJK	RAD	CR	IL	LA0569
ra	2	rava	gri	D*CIJK	RAD	RR	IL	LA0678
rd	--	reduced		K*	SPON	X	NON	LA2459B
re	--	reptans		K*	RAD	RR	IL	LA0624
rela	--	relaxata		K*D	RAD	CR	IL	LA0622
rela	--	relaxata		K*D	RAD	AC	NIL	LA3757
rep	--	repens		K*J	RAD	CR	IL	LA0623
rep-2	--	repens-2		K*J	RAD	LU	IL	LA2057
res	--	restricta	res1	C*ADJK	RAD	RR	IL	LA1085
res	--	restricta	res1	C*ADJK	RAD	AC	NIL	LA3756
ri	--	ridged	rl	J*R	RAD	X	NON	LA1794
ri	--	ridged	rl	J*R	RAD	AC	NIL	LA3180
ria	--	rigidula	ria1	C*JKT	RAD	CR	IL	LA0825
ria	2	rigidula	ria1:2	C*JKT	RAD	LU	IL	LA0975
rig	--	rigida		C*K	RAD	CR	IL	LA0699
rig	2	rigida	pca, pca1	C*K	RAD	LU	IL	LA0822
rig-2	--	rigida-2		C*K	RAD	AC	NIL	LA3716
rin	--	ripening inhibitor		P*	SPON	X	NON	LA1795
rin	--	ripening inhibitor		P*	SPON	RU	NIL	LA3012
rin	--	ripening inhibitor		P*	SPON	AC	NIL	LA3754
ro	--	rosette		K*	RAD	X	NON	LA0270
roa	--	rotundata	roa1	J*DK	RAD	CR	IL	LA0976
rot	--	rotundifolia		J*K	RAD	RR	IL	LA0700
rot	--	rotundifolia		J*K	RAD	AC	NIL	LA3751
Rs	--	Root suppressed		R*	RAD	X	NON	LA1796
rt	--	potato Y virus resis.		Q*	SPON	SCZ	IL	LA1995
rtd	--	retarded dwarf		J*K	SPON	X	NON	LA1058
ru	--	ruptilis		J*D	RAD	CR	IL	LA0626
ru	--	ruptilis		J*D	RAD	AC	NIL	LA3440
ru	prov2	ruptilis	ru	J*D	CHEM	VF36	IL	3-081
rust	--	rustica		K*J	RAD	LU	IL	LA0573
rust	--	rustica		K*J	RAD	AC	NIL	LA3766
rv-2	--	reticulate virescent-2		D*C	CHEM	SX	IL	LA2011
rvt	--	red vascular tissue		X*	SPON	X	NON	LA1799
s	--	compound inflorescence		M*	SPON	X	NON	LA0330
s	--	compound inflorescence		M*	SPON	AC	NIL	LA3181
sa	--	sphacelata	sa1	H*CK	RAD	CR	IL	LA0865
sar	--	squarrulosa	sar1	K*	RAD	CR	IL	LA0978
scf	--	scurfy		J*	SPON	PCV	NON	LA0767
scl	--	seasonal chlorotic lethal		C*	SPON	X	NON	LA1007
sd	--	sundwarf		K*	SPON	X	NON	LA0015
sd	--	sundwarf		K*	SPON	AC	NIL	LA3182

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
Se	--	Septoria lycopersici resistance		Q*	SPON	X	NON	LA1800
sem	--	semiglobosa		K*JT	RAD	CR	IL	LA0701
ses	--	semisterilis	ses1	C*DKN	RAD	LU	IL	LA0826
sf	--	solanifolia		J*LO	SPON	PSN	IL	2-311
sf	--	solanifolia		J*LO	SPON	AC	NIL	LA3674
sf	wl	solanifolia	wl, wr	J*LO	CHEM	ROMA	IL	LA2012
sfa	--	sufflaminata	sfa1	C*AEK	RAD	RR	IL	LA0862
sfa	2	sufflaminata	par	C*AEK	RAD	CR	IL	LA0969
sft	--	single flower truss		M*	SPON	PTN	IL	LA2460
sh	--	sherry		P*	RAD	CX	IL	LA2644
sha	--	short anthers		L*N	CHEM	ROMA	IL	LA2013
si	--	sinuata		E*JK	RAD	RR	IL	LA0993
sig-1	--	signal transduction mutant-1	JL1	Y*	CHEM	CSM	IL	LA3318
sig-2	--	signal transduction mutant-2	JL5	Y*	CHEM	CSM	IL	LA3319
sit	--	sitiens		W*HJKY	RAD	RR	IL	LA0574
Skdh-1	1	Shikimic acid dehydrogenase-1		V*	SPON	pen	NON	LA2439
sl	--	stamenless		L*N	SPON	X	NON	LA0269
sl	cs	stamenless	cs, sl:5, sl5	L*N	SPON	ONT	IL	LA1789
sl-2	--	stamenless-2	sl2	L*N	SPON	X	NON	LA1801
slx	--	serrate lax leaf		J*	SPON	PCV	NON	LA0503
Sm	--	Stemphyllium resistance		Q*	SPON	X	NON	LA1802
Sm	--	Stemphyllium resistance		Q*	SPON	MM	IL	LA2821
sn	--	singed		I*	SPON	CX	IL	LA2015
so	--	soluta		J*	RAD	LU	IL	LA2058
Sod-1	1	Superoxide dismutase-1		V*	SPON	pen	NON	LA2909
Sod-2	1	Superoxide dismutase-2		V*	SPON	pen	NON	LA2910
sp	--	self-pruning		K*	SPON	X	NON	LA0154
sp	--	self-pruning		K*	SPON	X	NON	LA0490
sp	--	self-pruning		K*	SPON	GRD	NIL	LA3133
sp	prov2	self-pruning		K*	RAD	spVCH	IL	LA2705
spa	--	sparsa		E*BK	RAD	CR	IL	LA0703
spe	--	splendida	spe1	C*K	RAD	RR	IL	LA0977
sph	--	sphaerica		K*T	RAD	CR	IL	LA0704
Spi	2	Sympodial index		K*	SPON	pen	NON	LA0716
spl	--	splendens	spl1	C*DJ	RAD	LU	IL	LA0821
spl	--	splendens	spl1	C*DJ	RAD	AC	NIL	LA3282
squa	--	squarrosa		D*KU	RAD	LU	IL	LA0627
sr	--	slender stem	sm	J*KU	RAD	CT	IL	LA1803
ss	--	spongy seed		S*	RAD	AC	NIL	LA3619
sta	--	stabilis		K*	RAD	RR	IL	LA2060
ste	--	sterilis		J*DKN	RAD	CR	IL	LA0705
stri	--	stricta		J*K	RAD	LU	IL	LA0575
stu	--	stunted		J*	SPON	X	NON	LA2461
su	--	suffulta		C*JM	RAD	CR	IL	LA0628
su	2	suffulta	exa	C*JM	RAD	RR	IL	LA0853
su	3	suffulta	di	C*J	RAD	CR	NON	LA0599
su	ni	suffulta	di:ni, ni	C*J	RAD	CR	IL	LA0616
sua	--	suffusa		D*CK	RAD	RR	IL	LA0707

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
sub	–	subtilis		J*K	RAD	LU	IL	LA0576
suc	–	succedanea		C*JK	RAD	CR	IL	LA0706
suf	–	sufflava		D*	RAD	CR	IL	LA0577
suf	–	sufflava		D*	RAD	AC	NIL	LA3569
sup	–	superba		K*JT	RAD	RR	IL	LA2061
Sw-5	–	Spotted wilt resistance-5		Q*	SPON	AC	NIL	LA3667
sy	–	sunny	ye	F*CE	RAD	AC	NIL	LA3553
syv	–	spotted yellow virescent		F*CG	SPON	PCV	NON	LA1096
t	–	tangerine		P*L	SPON	X	NON	LA0030
t	–	tangerine		P*L	SPON	AC	NIL	LA3183
t	v	tangerine		P*L	RAD	CX	IL	LA0351
t	v	tangerine		P*L	RAD	RU	NIL	LA3002
ta	–	tarda		D*JK	RAD	CR	IL	LA0708
tab	–	tabescens		E*HJK	RAD	RR	IL	LA0629
tab	–	tabescens		E*HJK	RAD	AC	NIL	LA3734
tc	–	turbinate corolla		L*K	CHEM	SM	IL	LA2017
te	–	terminata	te1	K*LMO	RAD	LU	IL	LA0861
tem	–	tempestiva	tem1	K*DJ	RAD	CR	IL	LA0979
ten	–	tenuis		Y*DK	RAD	CR	IL	LA0578
ten	–	tenuis		Y*DK	RAD	AC	NIL	LA3748
tf	–	trifoliate	ct, tri	J*KN	SPON	X	NON	LA0512
tf	2	trifoliate	tri	J*KN	RAD	CR	IL	LA0579
ti	–	tiny plant		K*	SPON	X	NON	LA1806
tl	–	thiaminless		Y*C	SPON	AC	NIL	LA3712
Tm	–	Tobacco-mosaic virus resis.		Q*	SPON	chi	NON	LA2369
Tm-2	–	Tobacco-mosaic virus resis.-2	Tm2	Q*	SPON	VD	NIL	LA3027
Tm-2	a	Tobacco-mosaic virus resis.-2	Tm-2:2	Q*	SPON	per	NON	LA1791
Tm-2	a	Tobacco-mosaic virus resis.-2	Tm-2:2	Q*	SPON	VD	NIL	LA3028
Tm-2	a	Tobacco-mosaic virus resis.-2	Tm-2:2	Q*	SPON	MM	NIL	LA3310
Tm-2	a	Tobacco-mosaic virus resis.-2	Tm-2:2	Q*	SPON	AC	NIL	LA3769
tmf	–	terminating flower		K*M	SPON	X	NON	LA2462
tn	–	tenera		K*U	RAD	LU	IL	LA2062
to	–	torosa		K*JLO	RAD	CR	IL	LA0709
tp	–	tripinnate leaf		J*K	RAD	CT	IL	LA0895
tp	–	tripinnate leaf		J*K	RAD	AC	NIL	LA3184
Tpi-2	1	Triosephosphate isomerase-2		V*	SPON	pen	NON	LA2440
tr	–	truncata	tr1	D*CJK	RAD	CR	IL	LA0710
Ty-1	–	TYLCV resistance		Q*	SPON	M82	NIL	LA3473
u	–	uniform ripening	u1	P*	SPON	LRD	IL	LA0643
u	–	uniform ripening	u1	P*	SPON	GRD	NIL	LA3035
u	–	uniform ripening	u1	P*	SPON	AC	NIL	LA3247
ub	–	umbraculiformis		J*K	RAD	LU	IL	LA2063
uf	–	uniflora		M*	SPON	PTN	IL	LA1200
uf	–	uniflora		M*	SPON	AC	NIL	LA2936
ug	–	uniform gray-green	u2	P*	SPON	OGA	IL	LA0021
ug	–	uniform gray-green	u2	P*	SPON	AC	NIL	LA3539
ul	–	upright leaf		K*	SPON	X	NON	LA2463
um	–	umbrosa		K*JRT	RAD	CR	IL	LA0630

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
um	--	umbrosa		K*JRT	RAD	AC	NIL	LA3733
uni	--	unicaulis		K*	RAD	CR	IL	LA0580
up	--	upright pedicel		L*	SPON	FLD	IL	LA2397
upg	--	upright growth		K*	SPON	X	NON	LA2464A
v-2	--	virescent-2	v2	F*D	SPON	X	NON	LA2465
v-2	--	virescent-2	v2	F*D	SPON	AC	NIL	LA3185
v-3	--	virescent-3	V3	F*B	SPON	PSN	IL	LA2707
va	dec	varia		F*E	RAD	CR	IL	LA0581
va	dec	varia		F*E	RAD	AC	NIL	LA3669
va	virg	varia		F*E	RAD	CR	IL	LA0582
var	--	variabilis		D*EK	RAD	CR	IL	LA0583
Ve	--	Verticillium resistance		Q*	SPON	MM	NIL	LA2818
Ve	--	Verticillium resistance		Q*	SPON	GRD	NIL	LA3038
Ve	--	Verticillium resistance		Q*	SPON	AC	NIL	LA3277
ven	--	venosa		J*BDK	RAD	LU	IL	LA0888
ven	--	venosa		J*BDK	RAD	AC	NIL	LA3564
ver	--	versicolor	yv-4, ver1	G*C	RAD	CR	IL	LA0632
ves-2	--	versiformis-2	vf	C*JK	RAD	LU	IL	LA1078
vg	--	vegetative		L*N	SPON	AC	NIL	LA2916
vga	--	virgulta	vga1	D*EFK	RAD	RR	IL	LA0858
vi	--	villous		I*	SPON	X	NON	LA0759
vio	--	violacea		D*A	RAD	LU	IL	LA0633
vio	--	violacea		D*A	RAD	AC	NIL	LA3734A
vir	--	viridis		T*J	RAD	CR	IL	LA0585
vlg	--	virescent light green		F*D	CHEM	VF36	IL	3-128
vms	--	variable male-sterile		N*L	SPON	SM	IL	2-219
vo	--	virescent orange		F*CP	SPON	ROMA	IL	LA1435
vo	--	virescent orange		F*CP	SPON	RU	NIL	LA2995
vra	--	viridula	vra1	D*JK	RAD	CR	IL	LA0857
vt	--	vieta		J*CFK	RAD	LU	IL	LA2064
w	--	wiry		J*LN	RAD	CX	NON	LA0274
w-3	--	wiry-3	w3, w2	J*LN	RAD	FEY	NON	LA1498
w-4	--	wiry-4	w4	J*LN	SPON	PSN	IL	2-237
w-6	--	wiry-6		J*	RAD	RR	IL	LA2065
wd	--	wilty dwarf		R*K	SPON	SM	IL	2-110
wf	--	white flower		L*	RAD	AC	NIL	LA3575
Wlt	--	Wilty		W*	SPON	LGPL	NON	LA3203
Wo	--	Wooly		I*	SPON	X	IL	LA0053
Wo	--	Wooly		I*	SPON	AC	NIL	LA3186
Wo	m	Wooly		I*	SPON	RU	IL	LA0258
Wo	m	Wooly		I*	SPON	AC	NIL	LA3718
Wo	mz	Wooly		I*	SPON	VF145	IL	LA1908
Wo	v	Wooly		I*	SPON	RU	IL	LA1531
Wo	v	Wooly		I*	SPON	AC	NIL	LA3560
wt	--	wilty		J*W	SPON	X	NON	LA0030
wv	--	white virescent		F*B	SPON	X	NON	LA0659
wv	--	white virescent		F*B	SPON	AC	NIL	LA3187
wv-2	--	white virescent-2		F*B	SPON	X	NON	LA1150

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
wv-3	--	*white virescent-3*		*F*B*	*SPON*	*X*	*NON*	*LA1432*
x	--	*gametophytic factor*		*N**	*SPON*	*X*	*NON*	*LA2348*
Xa	--	*Xanthophyllic*		*C**	*SPON*	*X*	*NON*	*LA2470*
Xa	--	*Xanthophyllic*		*C**	*SPON*	*AC*	*NIL*	*LA3579*
Xa-2	--	*Xanthophyllic-2*	*Xa2, A*	*C**	*RAD*	*X*	*NON*	*LA2471*
Xa-2	--	*Xanthophyllic-2*	*Xa2, A*	*C**	*RAD*	*AC*	*NIL*	*LA3188*
Xa-3	--	*Xanthophyllic-3*	*Xa3*	*C**	*RAD*	*CR*	*IL*	*LA2472*
Xa-3	--	*Xanthophyllic-3*	*Xa3*	*C**	*RAD*	*AC*	*NIL*	*LA3430*
xan-2	--	*xantha-2*	*xan2*	*C**	*RAD*	*AC*	*NIL*	*LA3759*
xan-4	--	*xantha-4*	*xan4*	*C**	*RAD*	*AC*	*NIL*	*LA3760*
y	--	*colorless fruit epidermis*		*P**	*SPON*	*AC*	*NIL*	*LA3189*
yg-2	--	*yellow-green-2*	*yc, yg282, yg2*	*E**	*RAD*	*KK*	*IL*	*LA2469A*
yg-2	--	*yellow-green-2*	*yc, yg282, yg2*	*E**	*RAD*	*AC*	*NIL*	*LA3551*
yg-2	*aud*	*yellow-green-2*	*yg-2:r, aud*	*E**	*SPON*	*X*	*NON*	*LA1008*
yg-2	*aud*	*yellow-green-2*	*yg-2:r, aud*	*E**	*SPON*	*AC*	*NIL*	*LA3165*
yg-3	--	*yellow-green-3*	*yg3, yg330, ye*	*E**	*RAD*	*KK*	*NIL*	*LA2926*
yg-4	--	*yellow-green-4*	*yg4, yl, yg333*	*E*J*	*RAD*	*KK*	*NIL*	*LA2927*
yg-4	--	*yellow-green-4*	*yg4, yl, yg333*	*E*J*	*RAD*	*AC*	*NIL*	*LA3731*
yg-5	--	*yellow-green-5*	*yw, yg388, yg5*	*E**	*RAD*	*RCH*	*NIL*	*LA2928*
yg-9	--	*yellow-green-9*		*E**	*SPON*	*C28*	*IL*	*LA2708*
yv	--	*yellow virescent*		*E**	*SPON*	*SM*	*IL*	*LA0055*
yv	--	*yellow virescent*		*E**	*SPON*	*AC*	*NIL*	*LA3554*
yv	*2*	*yellow virescent*	*vel:2, vel1:2*	*E**	*RAD*	*CR*	*IL*	*LA0981*
yv	*3*	*yellow virescent*	*vel*	*E**	*RAD*	*CR*	*IL*	*LA0631*
yv-2	--	*yellow virescence-2*		*E**	*SPON*	*AC*	*NIL*	*LA3190*
yv-4	--	*yellow virescence-4*		*E**	*SPON*	*AC*	*NIL*	*LA3570*

Phenotypic Class List

A	Anthocyanin modifications: intensification, reduction, elimination
B	Chlorophyll deficiency: white or whitish
C	Chlorophyll deficiency: yellow or yellowish
D	Chlorophyll deficiency: light, grey, or dull green
E	Chlorophyll deficiency: yellow-green
F	Virescent: chlorophyll deficiency localized at growing point
G	Variegation, flecking or striping
H	Leaf necrosis
I	Hair modificatins: augmentation, reduction, distortion, elimination
J	Leaf form and size
K	Plant habit and size
L	Flower form and color
M	Inflorescence (exclusive of 12)
N	Sterility: any condition leading to partial or complete unfruitfulness
O	Fruit form and surface texture
P	Fruit color and flavor, ripening modification
Q	Disease resistance
R	Root modification
S	Seed
T	Foliage color: dark
U	Foliage color, miscellaneous: olive, brown, blue-green
V	Allozyme variant
W	Overwilting stomatal defect
X	Vascular modification
Y	Nutritional or hormonal disorder
Z	Precocious development

Key to Background Genotypes

ABBREV	GENOTYPE	ACC#
AC	Ailsa Craig	LA2838A
ALA	Alabama	
AMB	Antimold-B	LA3244
BK	Budai Korai	
BOD	Break O'Day	LA1499
CG	Chico Grande	LA3121
CR	Condine Red	LA0533
CSM	Castlemart	LA2400
CT	Chatham	
CX	Canary Export	LA3228
EPK	Earlipak	LA0266
ERL	Earliana	LA3238
ESC	Early Santa Clara	LA517
FB	Fireball	LA3024
FEY	First Early	
FLD	Floridade	LA3242
GRD	Gardner	LA3030
GSM	Gulf State Market	LA3231
HSD	Homestead 24	LA3237
JBR	John Baer	LA1089
KK	kokomo	LA3240
LGPL	Large Plum	LA3203
LK	Laketa	LA0505
LRD	Long Red	LA3232
LU	Lukullus	LA0534
M167	Montfavet 167	LA2713
M168	Montfavet 168	LA2714
MD	Marmande	LA1504
MGB	Marglobe	LA0502
MM	Moneymaker	LA2706
MNB	Monalbo	LA2818
MP	manapal	LA2451
NRT	Norton	
OGA	Ohio Globe A	LA1088
ONT	Ontario	
PCV	Primitive Cultivar	
PLB	Pieralbo	
POR	Porphyre	LA2715

ABBREV	GENOTYPE	ACC#
PRN	Prairiana	LA3236
PRT	Pritchard	LA3233
PSN	Pearson	LA0012
PSP	prospero	LA3229
PTN	Platense	LA3243
RCH	Red Cherry	LA0337
RH13	Rehovot 13	LA3129
RNH	Rouge Naine Hative	
RR	Rheinlands Ruhm	LA0535
RSWT	Roumanian Sweet	LA0503
RTVF	Red Top VF	LA0276
RU	Rutgers	LA1090
SCZ	Santa Cruz	LA1021
SM	San Marzano	LA0180
spVEH	VFNT Cherry (sp)	LA2705
SPZ	San pancrazio	
STD	Stokesdale	LA1091
STN	Stone	LA1506
SX	Sioux	LA3234
TGR	Targinnie Red	LA3230
TVD	Vendor (Tm-2a)	La2968
U82	UC-82B	LA2801
VCH	VFNT Cherry	LA1221
VD	Vendor	LA3122
VE	Van's Early	
WA	Walter	LA3465
X	Unknown or Hybrid	
XLP	XL Pearson	

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Univ. of New South Wales	DS6044 - Biomedical Library - SZ Serial		Sydney 2052		AUSTRALIA
University of California	Agricultural Library	40 Giannini Hall	Berkeley	CA	94720
University of Minnesota	St. Paul Campus Libr.	1984 Buford Avenue	St. Paul	MN	55108
University of New Hampshire	Library Serials Dept.	18 Library Way	Durham	NH	03824
University of Stellenbosch	University Library	Private Bag 5036	Stellenbosch 7600		SOUTH AFRICA
Vegetable and Ornamental	Plant Res. Inst Librar.	Private Bag X293	Pretoria 0001		SOUTH AFRICA
Purdue University Libraries	(1ABZ1288) CDM - Kardex	1535 Stewart Center	West Lafayette	IN	47907
J.S. Gericke Library		PO Box 830661	Birmingham	AL	35283-0661
Swets Subscription Service	440 Creamery Way, Suite A		Exton	PA	19341
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