Report

of the

Tomato Genetics Cooperative

Number 49 - October 1999

Department of Plant Breeding
252 Emerson Hall
Cornell University
Ithaca, NY 14853-1901

Foreword

The Tomato Genetics Cooperative, initiated in 1951, 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 contains reports of work in progress by members, announcements, and updates on linkage maps and materials available. The research reports include work on diverse topics such as new traits or mutants isolated, new cultivars or germplasm developed, interspecific transfer of traits, studies of gene function or control and tissue culture. Relevant work on other Solanaceous species is encouraged as well.

Membership currently stands at over 200 from 34 countries. Requests for membership (US$15 plus $5 shipping if international) should be sent to Theresa Fulton, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1901.

Cover photo taken by Charles M. Rick. Stem sections of tomato plants. Top: *grn*, below: + (isogenic control)

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From the editors

Please note the reinstatement of an Authors Index.

Deadline for submissions for the next report is June 1, 2000. Submissions received after this date will be accepted but not guaranteed publication in the current issue. As always, articles should be as concise as possible, 2 pages maximum. Submissions (preferably in Microsoft Word) should be sent to the managing editor as Macintosh or compatible diskettes (with an included hard copy), emailed as attachments, or uploaded by FTP.

Most images can be included, preferably TIFF or EPS, but also Pict, Photoshop, B/W photos, Excel tables, and other graphics. For more information and links to some past issues, see the renovated web site:

http://genome.cornell.edu/tgc

Managing Editor:

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Special thanks to Cynda Farnham, Doug Bingham, and the members of Steve Tanksley's group at Cornell University for help with mailings, editing, and general support!

Announcement: Tomato Breeders Roundtable and Tomato Disease Workshop

Organizing Committee:

David Francis, Ron Pitblado, Mark Ricker
The Ohio State University/OARDC
The University of Guelph/Ridgetown College
Heinz Canada

The 1999 Tomato Disease Workshop and Tomato Breeders Roundtable will take place December 2-3 and 3-5 at the Doubletree Hotel in Detroit, Michigan. Research, regional roundups, and current topics relevant to tomato breeding, disease resistance, fruit quality, genetics, and production will be discussed by industry and university participants.

Getting there
The Doubletree Hotel is located near to the Detroit International Airport. Shuttle Service from the Airport to the Hotel is available every 15 min.

Hotel Accommodations
Blocks of guest rooms have been reserved at the Doubletree Hotel ($99.00 plus tax) single or double occupancy. The Comfort Inn located next door also has rooms available.

For Additional Information:

David Francis
Ohio Agricultural Research & Development Center
1680 Madison Ave.
Wooster, OH 44691

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ANNOUNCEMENT: MOLECULAR MARKERS FOR CHARACTERIZING GENOTYPES AND IDENTIFYING CULTIVARS IN HORTICULTURE

MONTPELLIER , FRANCE
March 6, 7, 8, 2000

International Symposium under the aegis of the Commission Biotechnology of ISHS (International Society for Horticultural Science)
Organised by -Institut National de la Recherche Agronomique (INRA)
-Ecole Nationale Supérieure Agronomique (Agro Montpellier)
-Groupe d'Etude et de contrôle des Variétés et des Semences (GEVES)

Objectives of the Symposium

To provide opportunities for researchers of public institutes and private companies to exchange state of the art of methodologies and new knowledge on use and interest of molecular markers at the various steps of horticultural breeding (fruits, vegetables, ornamentals, medicinal and aromatic plants, tuber crops and grapevine).

Main topics of the symposium will deal with :
- Molecular characterization of biodiversity to study and manage genetic resources,
- Marker assisted selection (MAS),
- Identifying and distinguishing genotypes,
- Use of molecular markers as a complementary tool for Distinctness, Uniformity and Stability studies of cultivars (DUS),
- Comparison of molecular and morphological markers for estimating genetic distances between genotypes,
- Essential derivation,
- Appropriate statistical approaches for molecular characterization,
- Evaluation of genetic, sanitary and specific quality of propagated material.

This symposium will consecutively take place after a meeting held in Angers of « Biochemical and Molecular Techniques » workshop of UPOV (International Union for the Protection of new Varieties of Plants), and could therefore be an opportunity for a common discussion on molecular markers and protection rights.

Call for oral communications and posters

Authors of oral communications and posters should send a one page abstract of their communication by mail to
mmh@versailles.inra.fr before October 31st 1999.

Oral presentations and posters will be published in Acta Horticulturae if accepted by the Editorial Board. In this case, authors will receive instructions for preparing the full text of both oral communications or posters to be published in Acta Horticulturae.

The official language for scientific sessions will be English.

The symposium will be held in Montpellier, in the Ecole Nationale Supérieure Agronomique (Agro Montpellier) buildings which provide a conference room, poster

exhibition room and restaurant facilities. Montpellier is located in the South of France near the Mediterranean and can be reached from Paris within four hours by TGV (High Speed Train) or one hour by plane.
Many research institutes and agricultural colleges, gathered within Agropolis, as well as very important breeding companies and nurseries dealing with different aspects of Horticulture, are located in this area.

Deadline

Submission of abstracts : **October 31st 1999**
Registration : **November 30th 1999**

For more information, see: http://www.ensam.inra.fr/arbo/mmh.html

Station de Génétique et d'Amélioration des Plantes
Institut National de la Recherche Agronomique
Centre de Versailles-Grignon
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Construction of a deep-coverage BAC library from *Lycopersicon esculentum* cv. Heinz 1706

Budiman, M.A., Frisch, D.A., and Wing, R.A.

Clemson University Genomics Institute (CUGI), Clemson University, 100 Jordan Hall BOX 345780, Clemson, SC 29634-5708

Large insert genomic DNA libraries are essential for many genome-based applications from positional cloning to genome sequencing. We have recently completed the construction of a deep-coverage BAC library of the cultivated tomato-*Lycopersicon esculentum* cv. Heinz 1706. Heinz 1706 was selected because it is a recurrent parent of several NILs developed by Philouze et al. (1991) and is the jointed parent of a mapping population we developed to map *jointless-2*. Here we report a brief description of the library and how it will be provided to the plant community.

Tomato BAC library construction and characterization

The BAC library was constructed by size selecting *Hind* III partially digested tomato genomic DNA and ligating with pBeloBAC11 (kindly provided by H. Shizuya, Caltech), followed by electroporation into *E. coli*. White recombinant clones were robotically picked and arrayed into 336 384-well microtiter plates using the Q-BOT system (Genetix, UK). The library contains 129,000 clones with an average insert size of 117.5 kb based on a random sampling of 498 BAC clones (Figure 1). Based on a haploid genome size of tomato of 930 Mbp/C (Arumuganathan and Earle, 1991), the BAC library represents approximately 15 genome equivalents and thus over a 99 % probability of recovering any specific sequence of interest.

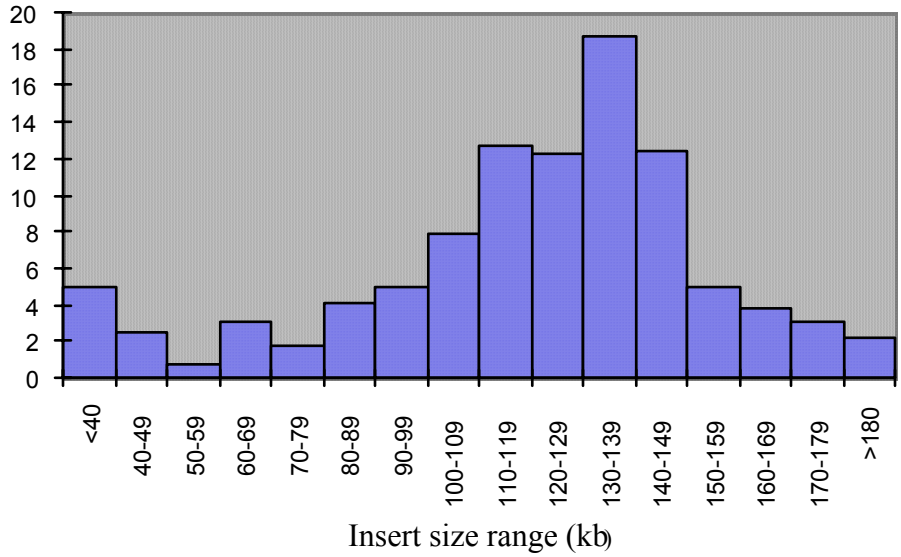

Figure 1. Insert size distribution of *Lycopersicon esculentum* BAC library based upon the analysis of 498 random BAC clones.

To determine empirically the genome coverage of the BAC library, we screened it with 5 single copy RFLP markers on chromosome 12 (kindly provided by S. Tanksley, Cornell University). Table 1 shows the result of the screening from the first three filters. In every case, at least 5 clones were identified.

Table 1. The average number of hits/probe for each filter (2.14 genome coverage/filter)

RFLP marker	No. of filters screened	Total No. of hits	Average No. of hits/filter	Expected No. of hits/filter
CD4	3	9	3	2.14
CD22	3	9	3	2.14
TG387	3	11	3.7	2.14
TG394	3	5	1.7	2.14
TG618	3	12	4	2.14
Total	15	46	3.06	2.14

BAC library access and distribution

The tomato BAC library was constructed with funds provided by the USDA NRI program and therefore is freely available to the research community. The library is made available through our BAC Resource Center at CUGI, either as a set of high density hybridization filters or individual clones (http://www.genome.clemson.edu). The BAC Resource Center has received NSF funding for the next five years to provide services to the genomics community.

The entire library is gridded onto seven 500 cm^2 Hybond N+ filters (Amersham, USA). Each filter contains 18,432 independent BAC clones plated in duplicate. The duplication pattern aids in clone identification and provides a positive control for each positive hybridization signal. Figure 2 shows an example of such a filter hybridized with the tomato marker CD22.

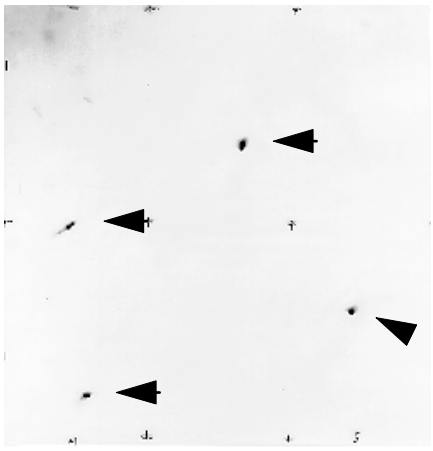

Figure 2. An autoradiograph of a filter hybridized with tomato CD22 resulting in 4 hits.

To obtain a set of filters for the BAC library and a detailed set of instructions for hybridization and clone identification please contact us individually at our email address (dfrisch@clemson.edu) or place your order on our web site. The filter sets are supplied ready to use in hybridization experiments, with colony lysis and cross-linking already performed. Each filter can be hybridized for 5-10 times. The complete set of filters costs $350 plus shipping (at our cost of $50/filter). Individual clones can be obtained at $5/clone plus shipping.

Literature cited

Arumuganathan, K. and Earle, E.D. (1991) Plant Mol Biol Rep 9: 208-219.
Philouze, J. (1991) Euphytica 56: 121-131.

Mae-1, a malic enzyme coding gene on chromosome 5

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Malic enzymes (MAE) are $NADP^+$-dependent malate dehydrogenases that catalyze the metabolism of malic acid to pyruvate. MAE activity is found in all plant organs, and increases during fruit development in many plants, where it is an important determinant of flavor. We were interested in studying MAE isozymes in tomato. Whereas four malate dehydrogenase genes (*Mdh-1, 2, 3, 4*) are known, of which several have been placed on the genetic map in interspecific mapping populations, the number and location of *Mae* genes has not been reported.

We first detected MAE polymorphisms in a F_1 *L. esculentum* cv. VF36 x *Solanum lycopersicoides* LA2951 hybrid and its backcross derivatives. This exceptionally wide cross has proven a rich source of isozyme variation, allowing the determination of map locations of several previously unmapped genes, including *Mdh-1* and *–4*, *Dia-1, -2, -3,* and *–4*, *Fdh-1*, and *Tpi-1* (Chetelat et al. 1997, and unpublished data). For the resolution of MAE isozymes, several starch gel electrophoresis buffer systems were tested, including sodium-borate/tris-citrate pH 7.8, citrate/histidine pH 7.0, and histidine-citrate pH 5.7 (Wendel & Weeden 1989). Of these, the pH 7.8 gel system produced the sharpest banding, yet failed to reveal a polymorphism between the parental species. In contrast, the pH 7.0 gel produced lower resolution electrophoregrams, but nonetheless revealed a putative polymorphism between the parental species. Of the plant tissues assayed, including stems, leaves, anthers, and roots, only roots produced satisfactory results under these gel conditions.

The allele of *S. lycopersicoides* was slightly retarded relative to that of *L. esculentum*, but due to their broad zone of activity, the two alleles overlapped in heterozygotes, producing an extended smear. The fact that active MAE is normally a tetramer (Weeden & Wendel 1989), would tend to make the bands in heterozygotes more difficult to resolve, since as many as 5 different combinations of subunits could be formed. Despite this inherent complexity, it seems likely that gel resolution could be substantially improved by further optimizations of the buffer systems. However, even under the electrophoresis conditions used, results for individual plants were reproducible and accurate genotyping was obtained, as indicated by progeny testing and analysis of flanking markers in later generations. A single band was observed in *L. esculentum* under all tested gel systems, suggesting MAE activity, at least in roots, is controlled by a single locus, herein designated *Mae-1.* Segregation for *Mae-1* was approximately normal in the BC_1 *L. esculentum* x *S. lycopersicoides* population (BC-LS), yielding 84 +/+ and 52 +/S plants, not significantly different from the expected 1:1 ratio (X^2 = 3.5). Linkage analysis using Mapmaker indicated the *Mae-1* locus was located on chromosome 5, between the RFLP markers TG379 and TG23 (Fig. 1).

A cDNA corresponding to a cytosolic malic enzyme, designated LeME2, was cloned from tomato (K. Franke and D. Adams unpublished). It hybridized to two or more restriction fragments on Southern blots, suggesting it is present in more than one copy in the tomato genome; one of these restriction fragments may correspond to the other malic enzyme gene (LeME1 = Genbank # AF001269) cloned from tomato, which

encodes a protein targeted to the chloroplast. In an F_2 *L. esculentum* cv. VF36 x *L. pennellii* LA716 population (F2-LP), the LeME2 probe segregated 12 +/+ : 35 +/P : 22 P/P, consistent with the expected 1:2:1 ratio (X^2= 2.9). LeME2 mapped to approximately the same region of chromosome 5, where it showed tight linkage to TG379 (Fig. 1). These results indicate the LeME2 cDNA and *Mae-1* isozyme locus very likely correspond to the same gene.

Although we haven't surveyed other *Lycopersicon* species for *Mae-1* polymorphism, we anticipate that in certain wide crosses this gene could provide a useful new isozyme marker for the long arm of chromosome 5.

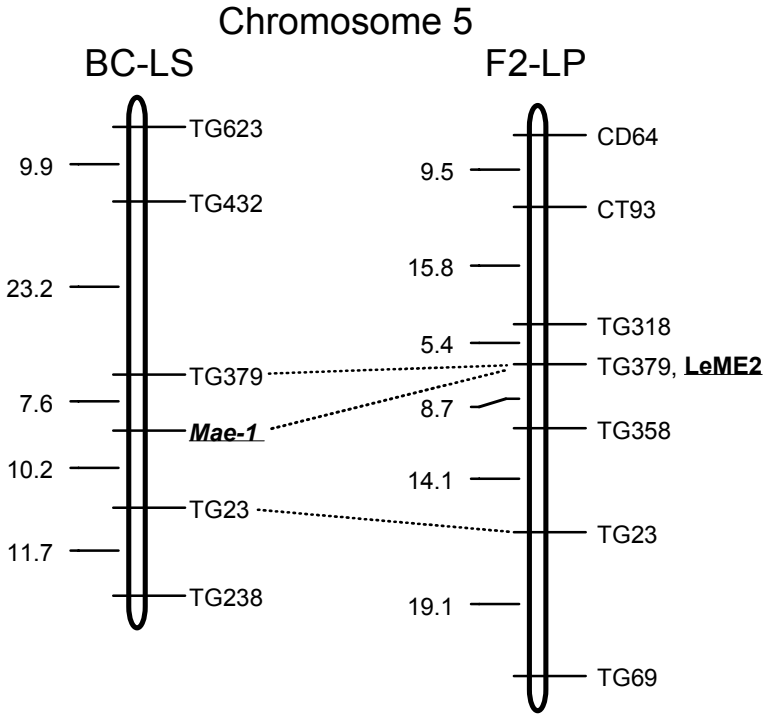

Figure 1. Genetic maps of chromosome 5, from BC_1 *L. esculentum* x *S. lycopersicoides* (BC-LS) and F_2 *L. esculentum* x *L. pennellii* (F2-LP) populations, showing the location of a malic enzyme gene determined through segregation of the isozyme (*Mae-1*) or cDNA (LeME2).

Literature cited:

Chetelat, R.T., P. Cisneros, L. Stamova, C.M. Rick. 1997. A male-fertile *Lycopersicon esculentum* x *Solanum lycopersicoides* hybrid enables direct backcrossing to tomato at the diploid level. Euphytica 95: 99-108.

Weeden, N.F., J.F. Wendel. 1989. Genetics of plant isozymes. In: D.E. Soltis & P.S. Soltis (eds) Isozymes in Plant Biology. Dioscorides Press, Portland. pp. 46-72.

Wendel, J.F., N.F. Weeden. 1989. Visualization and interpretation of plant isozymes. In: D.E. Soltis & P.S. Soltis (eds) Isozymes in Plant Biology. Dioscorides Press, Portland. pp. 5-45.

Mapping and introgression of a quantitative trait loci (QTL) for reduced stem scar size from *Lycopersicon pimpinellifolium*

Doganlar, S. and Tanksley, S.D.

Stem scar size, attachment site of fruit to the stem, is an important characteristic for both processing- and fresh market-type tomatoes. In processing-type varieties, a small stem scar size is desirable because fruit with small stem scars usually release better during harvest and peel more easily with less waste during processing. In addition, large stem scars may penetrate into the fruit and be visible as a "yellow eye" if the processed peeled fruit is whole or diced. However, varieties with very small stem scars are undesirable because the fruit may fall off the plant prematurely during mechanical harvesting. For fresh market tomatoes, stem scar size is mainly an appearance characteristic.

When a line having large stem scars is crossed with a line with small stem scars, F1 hybrids resemble the parent with small stem scars on the fruits. Therefore, it has been concluded that enlarged stem scars appeared to be controlled by one or more recessive genes.

In this study, a QTL controlling stem scar size was identified in a population of 216 BC2F4 lines derived from a cross between *L. esculentum* cv. M82 x *L. pimpinellifolium* (LA1589). Based on phenotypic and molecular marker analysis, the QTL was mapped to the bottom of chromosome 8 between CT265 and CT68. As further confirmation, 59 BC2F5 lines derived from BC2 plants that were heterozygous for these 2 markers were selected and grown in the greenhouse. Based on phenotypic and genotypic (CT265 and CT68) analysis of these 59 plants, CT265 showed a strong association ($P<0.0001$) with stem scar size. No significant association was seen for fruit weight. Therefore, CT265 can be used for marker assisted selection for reduced stem scars without sacrificing fruit weight.

Efficiency of using CAPs as an alternative and potentially automatable mapping system

Fulton, T.M., Xu, Y., Siew, F.L., Tanksley, S.D.

Cornell University, Plant Breeding Dept., 252 Emerson Hall, Ithaca, NY 14853

RFLP mapping has become the standard method of genetic mapping due to the advantages of reproducible, high quality results and the added bonus of information regarding copy number in the genome. However, this method also has the disadvantage of requiring the use of radioisotopes or hazardous chemicals, and contains steps that are not easily automatable. Therefore it does not hold much potential for scaling up.

PCR assays, on the other hand, can give results in much less time, and require no radioisotopes or chemicals, merely a thermal cycler and electrophoresis apparatus (Konieczny, 1993). This is especially advantageous for labs that may not be set up for radioisotope work. These assays have become a very useful technique, in particular, for screening large populations for disease resistance genes. Furthermore, the creation of automated pipettors and thermal cyclers has made it possible to greatly scale up the amount of samples that can be done simultaneously. Consequently, mapping by PCR has much more potential for automation and large scale use.

We are currently working on a project in the lab which includes mapping EST (expressed sequence tag) sequences by designing primers specific to the EST sequence. These sequences can then be mapped either by using the PCR amplified DNA as a radioactive probe on southerns or mapping the PCR band directly. For the reasons given above, it was of interest to us to test the efficiency of mapping strictly by PCR, especially in the event of potential future automation.

PCR bands derived from ESTs are rarely polymorphic, even among different species, with the resolution of typical agarose gels. However, polymorphisms called cleaved amplified polymorphisms (CAPs) can sometimes be uncovered by digesting the PCR products with restriction enzymes. The parents of our current mapping population are *Lycopersicon esculentum* M82 and the wild species *L. pennellii* LA716, two very divergent species, which have a very high level of polymorphism using RFLPs (>50%). Therefore, we set up a test of 9 sets of primers (Table 1), chosen randomly from those available in the lab, amplifying various sized inserts, digested with 10 different restriction enzymes (Table 2).

Table 3 shows the results of each sequence/enzyme combination. No particular enzyme or site bias seemed to be much more efficient at detecting polymorphisms. Overall, polymorphisms using any of the 10 enzymes could only be detected for 5 out of the 9 primer sets (55%) (these results may be a conservative estimate as the presence/absence of an extra band was not counted as a clear polymorphism). However, for all of the primer sets with amplicon sizes of 1 kb or more, a polymorphism could be identified with at least one enzyme. Therefore, although mapping by CAPs may be less efficient than RFLPs until automation is more readily available, the use of CAPs can be optimized by using sequences of 1 kb or higher.

Primer set	F sequence	R sequence
T20P8.A	AGATCAGCTCACCGAAGATCA	TGGCCATCATGACCTTAACA
T15B16.A	GGTGTTGGGAGATCCTGATG	CAACTGCCCAAATCCCTTTA
F4L23.19	TGGAGCGATTTGGTGTCTTTG	TGCAGTAGTCTGACCCTTCAACAAC
T13M11.A	GCAACAGTGAGCATGTCAAAA	CCAAGATTGCAATAGCAGCA
MJB24.A	ATCCAATCCAGCACAGGAAG	AAAGCAGGAGCATCGTTCAC
F4L23.20	ACCTGGTTTCCTTGGTGGTAGTG	CTTTAGTTCCTCAGCAGCCTTGAC

Table 1. Primer sequences, 5'-3'

Enzyme		cleavage site		CAPs detected		% success
Tru9I		TTAA		0/8		0%
Tsp509I		AATT		1/8		13%
RsaI		GTAC		2/9		22%
EcoRV		GATATC		1/9		11%
DraI		TTTAAA		1/9		11%
HaeIII		GGCC		0/9		0%
AluI		AGCT		0/9		0%
TaqI		TCGA		2/8		25%
MspI		CCGG		1/8		13%
HinfI		GANTC		1/8		13%

Table 2. Enzymes used and their success rate in identifying polymorphisms.

Literature cited:

Konieczny A, Ausubel FM (1993) A procedure for mapping *Arabidopsis* mutations using co-dominant ecotype-specific PCR-based markers. Plant J 4: 403-410

Primer set	uncut	Tru9I	Tsp509I	RsaI	EcoRV	DraI	HaeIII	AluI	TaqI	MspI	HinfI	Total
T20P8.A	1.9	N	Y(P)	Y?	Y	Y?(E)	N	Y(P)	N?	Y?	-	**1/9**
T15B16.A	1.8	N	Y(P)	Y	Y?(E)	N	N	N	Y	N	N	**2/10**
F4L23.19	1.7	N	N	Y	N	N	N	Y?(P)	N	Y	Y?	**2/10**
T13M11.A	1.4	N	Y	Y?	N	Y	N	N	N	N	N	**2/10**
MJB24.A	1.3	N	N	N	N	N	N	Y(E)	Y	N	Y	**2/10**
F4L23.20	0.6	N	N	N	N	N	N	N	N	N	N	**0/10**
T2P11.A	0.6	N	N	N	N	N	N	N	N	N	N	**0/10**
TOTALS		**0/6**	**1/7**	**2/7**	**1/7**	**1/7**	**0/7**	**0/7**	**2/7**	**1/7**	**1/7**	

Table 3. Results of PCR amplified sequences digested with restriction enzymes.
N = no polymorphism

- = no amplification

(s) = too small

? = unclear

(P) = pres/abs of P band

(E) = pres/abs of E

band = good polymorphism

Early appearance of word "tomate" in a Peruvian document

Holle, M.

International Potato Center, Apartado 1558, LIMA 100, Peru.

Note from the editor: Due to its historical nature, some of the following article is necessarily given in the original text (Spanish). Translation is given further on in the article, please persevere!

QUOTE from the document cited below (1):

Page 74. (Foja 527r):
Testigo: "En el dicho pueblo de Tucume (de la encomienda de Lorenzo de Zamudio vecino de la cibdad de Trujillo en veinte y nueve dias del mes de Abril de mil quinientos y ochenta anos) en este dia, mes y ano susu dicho el dicho don Juan Pozul presento por testigo en la dicha razon a don Andres Macza yndio alcalde deste dicho pueblo del cual tome y recebi juramento en forma de derecho so cargo del cual juramento prometio de dezir la verdad y siendo preguntado por el tenor de las perguntas del interrogatoryo en esta causa por su parte presentada dixo y declaro lo siguiente:"

Page 75. (Foja 257 v):
III A la tercera pregunta dixo que sabe e vio este testigo que el dicho rio les llevo a los dichos yndios las comidas que tenian para coger en sus chacras mayz y frisoles y otras legumbres y las dichas lluvias pudrieron lo que tenian guardado en sus casas y en otras partes de suerte que no fue nada de provecho y los yndios padecieron a esta causa gran hambre y necesidad porque no tenian que comer ni aun algarrova no tenian y asi fueron a Motupe y a outras partes a comprar mayz y muchos no tenian con que conprallo se mantenian con yervas del campo y TOMATES y esto dize a esta pregunta".

This is a legal document arisen from the testimony of Indians and Spaniards in 1580 after some torrential rains that occurred in the northern part of Peru. Witnesses answered a standard set of 14 questions in order to demonstrate their impossibility of paying taxes that year because the rains had destroyed their farm and their stored food. Huertas Vallejos suggests that this is the first written account or mention of what we know as a meteorological phenomenon called El Nino. In 1983 (405 years later) in the same area another Nino reoccurred.

A free translation into English would read like this:
Witness: In the aforesaid town of Tucume (of the encomineda owned by Lorenzo Zamudio, a neighbor of Trujillo, the 29th of April of 1580) Don Juan Pozul presented as a witness Don Andres Macza, Indian, mayor of this town, who swore in front of me to tell the truth and when asked the standard questionnaire said and declared the following:

Answer to question No III. The aforesaid river had taken the food from the fields where the aforesaid native Indians could harvest maize and phaseolus beans and other crops. The aforesaid rains rotted what they had stored in their houses and in other places. All this was now of no use. The Indians suffered great hunger and need, and because they had nothing left to eat, not even an algarroba bean, they went to Motupe and to other

places to buy maize and many did not have money to buy it. So they survived with wild herbs and TOMATOES. Thus did he answer this question.

(1) "Ecologia e Historia. Probanzas de indios y Espanoles referentes a las catastroficas lluvias de 1578 en los corregimentos de Trujillo y Sana. Francisco Alcocer, Escribano receptor. Version paleografica y comentarios de Lorenzo Huertas Vallejos. CES Solidaridad, Chiclayo, 1987.

Tomato genotypes resistant to *Phytophthora infestans* and *Phytophthora capsici*

Ignatova S.I.[1], Gorshkova N.S.[1], Bagirova S.F.[2]

1. All- Russian Scientific Research Institute for Vegetable Crops Department of Plant Breeding, mail-box 15, Moscow 105215, Russia
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A screening of 68 tomato samples in detached fruits bio-assays were performed to select tomato forms resistant to both *P.infestans* and *P.capsici*. Fruits were inoculated with zoospore suspension in concentration 6000 zoospores per ml. Our results indicate 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	Patterns (%)
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 tomato patterns showing the highest resistance to both *P.capsici* and *P.infestans*:

L.peruvianum (2020, VIR)
L.peruvianum v. *dentatum* (3963, VIR)
L.*humboldtii* (2884, VIR)
[*L.humboldtii* (2884, VIR) x *L.humboldtii* (353, VIR)]
Vishnevidny (342, VIR)
L.pimpinellifolium (3731, VIR)
L.pimpinellifolium (3990, VIR)
CRA-66 (13225, VIR)
F_2 [Xachmasskiy x *L.humboldtii* (353/2, VIR)]

Tomato resistance to phytophthorosis in a protected crop

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In the recent seasons tomato diseases, caused by Phytophthora soilborne species, have become more severe in greenhouses in Moscow. More aggressive populations, which are capable of colonizing tomato roots, shoots, stems, foliage, fruits and of killing plants rapidly, seem to be involved. Disease symptoms have become more diverse and appear at earlier growth phases of tomato plants.

Strains of *Phytophthora capsici* isolated from diseased tomato plants were used in bio-assays to find resistant tomato samples. CRA-66 (accession number 13225, VIR) was found to be the most resistant against the pathogen. *L. pimpinellifolium* (accn 3930 and 3731,VIR), *L. chilense* (accn 5031, VIR), *L. peruvianum* v. *humifusum* (accn 3967, VIR), *L.humboldtii* (accn 353/2, VIR) showed a high resistance. Selected tomato lines, l-372, l-342, l-349 (NISTIO, Moldova), were also characterised by high resistance. These results were confirmed as well by the data obtained under natural epidemic conditions.

Tomato resistance to late blight in a protected crop in Moscow

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To evaluate tomato patterns on their resistance against new sexual populations of *Phytophthora infestans*, a field study was conducted at naturally occurring late-blight epidemics. Screening of 800 genotypes, including wild species, selected lines, and cultivated varieties, yielded the following tomato samples which showed the greatest resistance to *P.infestans*:

L.hirsutum, accession number 5041, VIR
L.pimpinellifolium, an 3731, VIR
West Virginia 181-1-6-2
West Virginia 139-1-2-1-1-1
West Virginia 700
Ottawa 30, an 3919, VIR
Hessoline, France, INRA
Heline, France, INRA
Juno, an 3215, VIR
Droplet, an 4316 VIR
I-132, Moldova
1-342, Moldova
BU-13, Belarus

Genetic mapping of the tomato *Epinastic* (*Epi*) locus

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The tomato *Epinastic* (*Epi*) mutation was originally characterized as a semi-dominant, single locus mutation resulting in leaf epinasty, vertical growth, minimal branching, and highly branched root structure (1,2). These effects are consistent with ethylene over-production or constitutive ethylene signaling (3). Although elevated ethylene biosynthesis has been reported in some tissues of the *Epi* mutant, treatment with inhibitors of ethylene biosynthesis or action had little effect on mutant phenotype, suggesting that *Epi* represents a lesion in ethylene signal transduction (4). The *Arabidopsis ctr1* mutant is also characterized by constitutive ethylene signal transduction, and the corresponding *CTR1* gene has been isolated and shown to have homology to the *Raf* family of protein kinases (5). We report here genetic mapping of the *Epi* locus as a first step for testing linkage with tomato CTR1-related sequences that represent candidates for the *EPI* gene, or alternately, for positional cloning of the *Epi* locus should none of the candidate genes co-segregate with *Epi*. While it is possible that *Epi* may represent a tomato homologue of the *Arabidopsis CTR1* gene, *Epi* alternatively may represent an ethylene signal transduction component whose *Arabidopsis* counterpart remains to be identified or does not exist.

Tomato cultivar VFN8 (*Epi/Epi*) was kindly provided by V. Ursin and crossed to the wild tomato relative *L. cheesmanii* (LA483; *epi/epi*) to facilitate RFLP mapping. Resulting F1 progeny were selfed and an F2 population of 962 plants was scored for the presence or absence of leaf epinasty. A total of 123 mutant individuals were identified (or approximately half the number expected for a recessive mutation). In this regard it is noteworthy that poor transmission of the recessive *Arabidopsis ctr1* mutant allele has also been reported (5). It is also important to note that we did not observe any effects of the mutant allele in the original F1 individuals, supporting the concept that the mutant phenotype results from a recessive allele, and in contrast to previous reports that *Epi* is semi-dominant (1,2). It is noteworthy that *L. cheesmanii* was used as the normal parent in the cross as opposed to *L. esculentum* parents in previous studies of *Epi* dominance, and thus that alleles derived from *L. cheesmanii* may have influenced the expression of the epinastic phenotype in heterozygous individuals. Finally, 14 of the F2 mutants have been tested in the F3 generation and all breed true for epinasty, suggesting homozygosity for the mutant allele.

To date only one ethylene signal transduction mutant resulting in constitutive ethylene signaling has been identified in *Arabidopsis* (*ctr1*; 5). We have isolated a cDNA from a tomato early ripening fruit library which hybridizes to the *Arabidopsis CTR1* gene at high stringency and have named this clone TCTR1 (6). A second tomato cDNA related to *CTR1* was isolated by others and named TCTR2 (7). We have previously mapped both TCTR1 and TCTR2 as RFLP markers to chromosomes 1 and 2 of tomato, respectively (6). Both cDNAs were also mapped in the subset of 123 mutant F2 progeny described above and both loci segregated in a 1:2:1 ratio within this sub-population indicating that the *TCTR* loci are not linked to *Epi* (data not shown).

RFLP Marker	Restriction Enzyme
TG574	DraI
TG65	BstnI
TG163	EcoRV
CT50	EcoRV
CT133	NdeI
CT173	AvaII

Table 1. Chromosome 4 RFLP markers and restriction enzyme yielding *L. esculentum* vs. *L. cheesmanii* RFLPs.

In order to place the *Epi* locus on the tomato genetic map pools of four "normal" and four "mutant" DNA pools were created by combining genomic DNA from 5 F2 individuals scored as normal or mutant with regards to leaf epinasty, respectively. 60 RFLP markers spanning the tomato genome and spaced at 20 - 40 cM intervals were selected from the tomato RFLP map (8) and hybridized to the pooled DNAs following digestion with the appropriate restriction enzyme for RFLP visualization. RFLP markers which yielded skewed hybridization to the *L. esculentum* allele in the "mutant" pools were potentially linked to the *Epi* locus. The first RFLP marker to demonstrate such skewing was CT50 which had been previously mapped to chromosome 4 (8). Several additional RFLP markers from chromosome 4 (TG65, TG574, CT133, TG16, CT173; see table 1) in addition to CT50 were scored in a population of 31 randomly chosen *L. esculentum* (*Epi*/Epi) X *L. cheesmanii* (*epi/epi*) F2 progeny (including 6 individuals demonstrating the epinastic leaf phenotype) resulting in placement of the *Epi* locus between CT133 and TG16 on tomato chromosome 4 (Figure 1).

In summary, the tomato *Epi* locus maps to chromosome 4 while two candidate cDNAs (TCTR1 and TCTR2) related to the *Arabidopsis CTR1* gene map to chromosome 2 and 1, respectively. Genetic localization of the *Epi* locus will facilitate candidate gene testing as additional putative *EPI* gene sequences become available. In addition, physical mapping of the *Epi* region of chromosome 4 will indicate the feasibility of positional cloning of the *EPI* gene.

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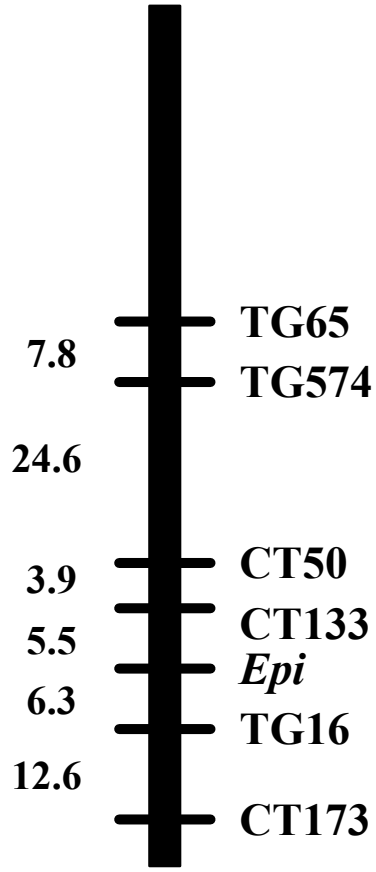

Figure 1. Genetic localization of the *Epi* locus on tomato chromosome 4. Linkage analysis was performed using Map-maker software (9).

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Second generation *L. pennellii* introgression lines and the concept of bin mapping

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The major challenge for the coming years is to develop approaches for tying together sequence information and biological functions. One framework for associating gene sequences and phenotypes is a genetic linkage map. This note introduces the concept of bin mapping in tomato that provides a rapid method for assigning a map position to DNA sequences.

Bin mapping is based on an introgression line (IL; Eshed and Zamir 1995) population that is composed of *L. esculentum* (cv. M82) lines each containing a single RFLP defined introgression from the green fruited species *L. pennellii* (LA 716). Each of the ILs is nearly isogenic to the cultivated tomato and together the lines provide complete coverage of the tomato genome. The ILs divide the tomato genome into bins each defined by a unique composition of genome coverage. Through probing of the IL membranes with DNA probes it is possible to associate sequences to specific bins. The high level of polymorphism at the DNA level between the two syntenic species, *L. esculentum* and *L. pennellii*, ensures high mapping efficiency and the perpetual nature of the population allows to accumulate mapping information from different research groups into a single database. A unique advantage of the ILs is the phenotypic variation that is unraveled in the different lines for simple Mendelian traits as well as for QTLs associated with fruit yield and quality.

In this communication we present a new generation of the IL population that is composed of 75 lines (compared to 50 lines in the previous generation) that partition the tomato genome into 107 mapping bins. The original IL map was based on a BC1 population map that included 375 markers while the new population is presented relative to the F2 RFLP map that includes more than 1500 markers that span 1274 cM (Tanksley et al. 1992). The orientation of the second generation population relative to the F2 map was achieved through probing of all the lines covering each of the chromosomes with all the markers indicated for this chromosome on the genetic map (Figure 1). A major focus in the probing was to use RFLP markers that map in the vicinity of the borders of the introgressed segments. The 107 bins partition the map into segments with an average size of 12 cM. In ten cases the introgression ends separated between cosegregating markers on the F2 map e.g. TG295 and TG326 on the southern end of IL1-2. All the ILs are homozygous for the corresponding *L. pennellii* introgressions except for IL8-1; this line is homozygous for the markers in the northern part of the introgression until CT92, but is heterozygous for the markers to the south until TG624. This is due to a gametophytic factor that maps to bin 8-C and is causing the elimination of male gametes containing the *L. pennellii* allele. It is also important to note that flowers of IL1-1 and IL1-2 have exerted stigmas and are prone to outcrossing; seed increase of these lines should be handled with care. The ILs provide an efficient tool for low resolution mapping of DNA clones to the tomato genome. High-resolution mapping can be achieved through analysis of F2 generations resulting from crosses of the targeted IL with M82. The syntenic relationships of tomato with potato and pepper make the ILs an efficient mapping resource for Solanaceae genetics.

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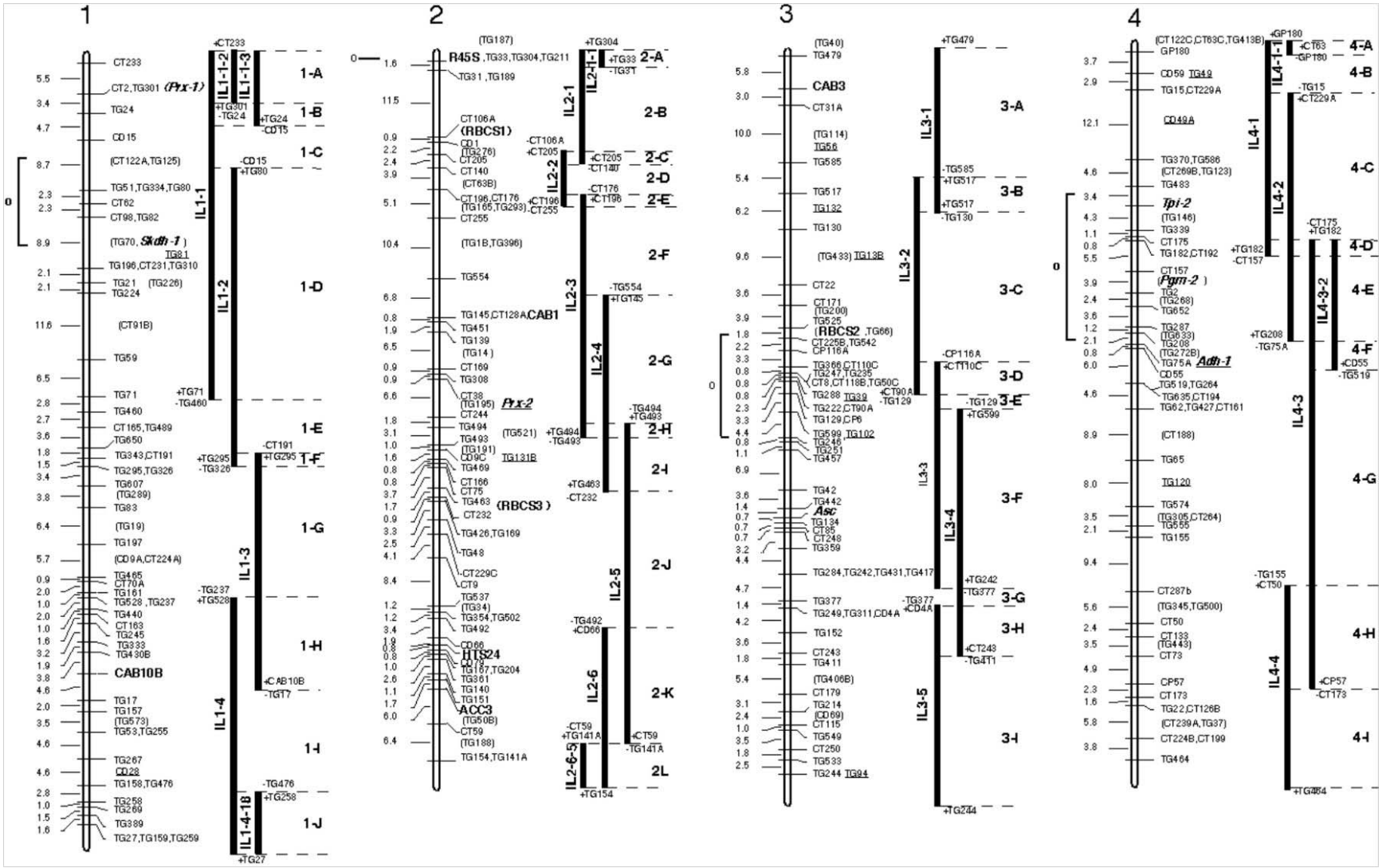
Figure 1. Chromosomal locations, sizes and identities of the 75 *L. pennellii* ILs and the derived mapping bins. For each IL, the positive markers that flank the introgressed segment are indicated with + and the closest marker that is not present in the introgressed segment is indicated by -.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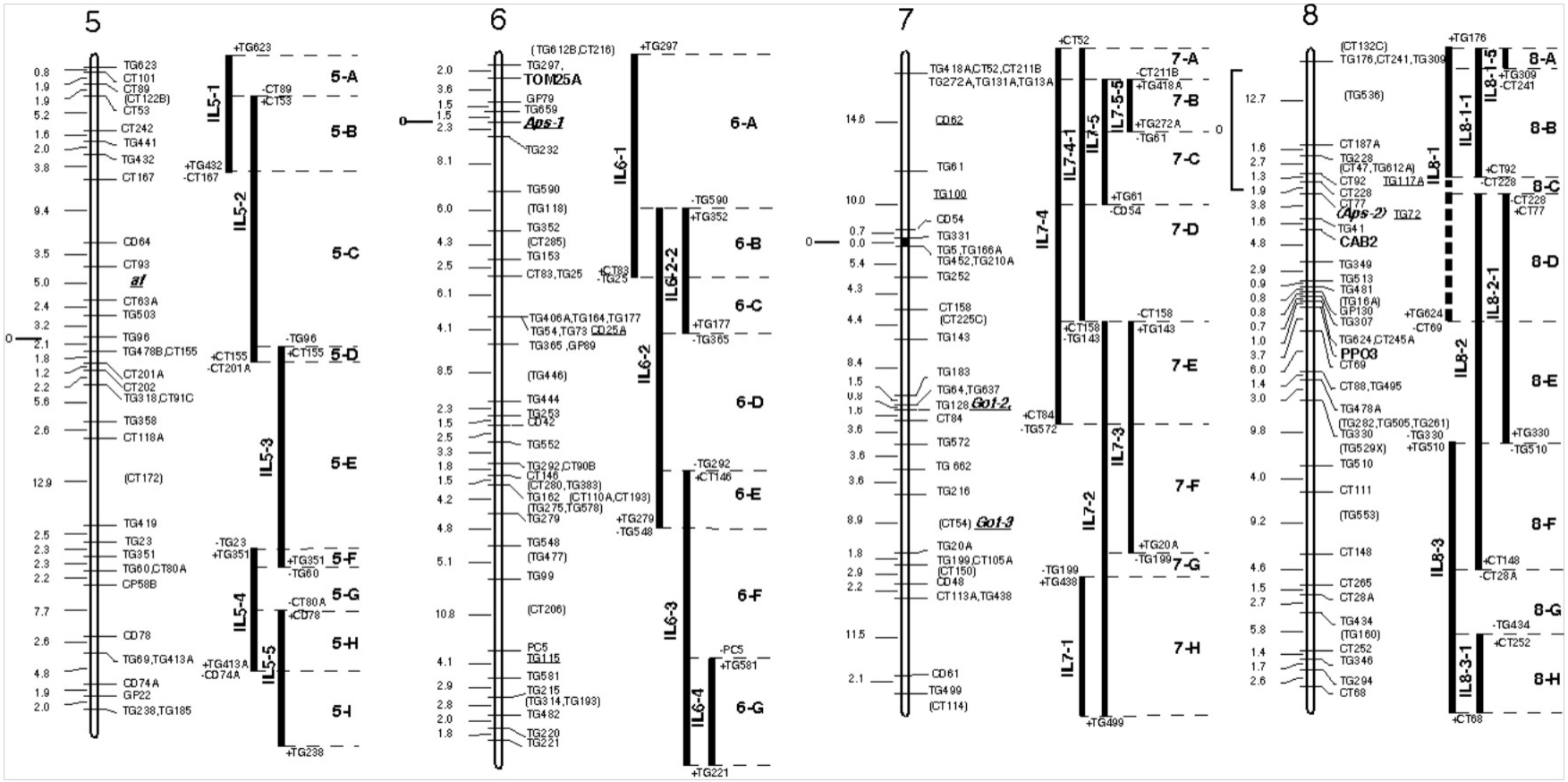
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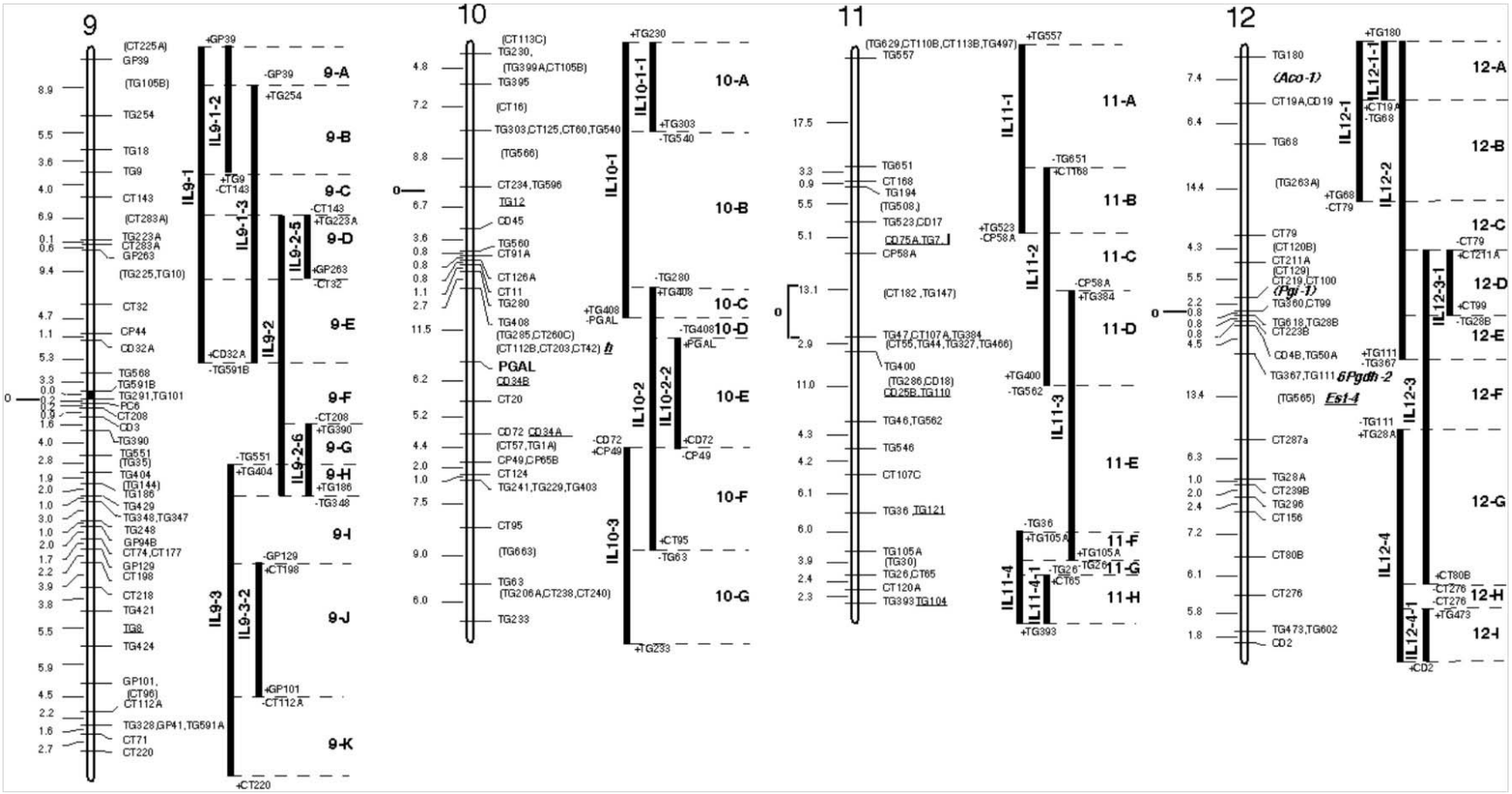
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12-E
12-F
12-G
12-H
12-I
(Aco-1)
6Pgdh-2
Est1-4
Pgi-1

Evaluation of somaclones of tomato under tropical conditions

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Most of the focus of crop improvement in our country has been based fundamentally on selection practised on indigenous varieties, the introduction of exotic varieties and the hybridisation of the two types. In recent years new techniques have been incorporated for the creation of genetic variability, and agricultural biotechnology holds much promise in the development of horticultural cultivars (Gómez and Depestre, 1992).

Starting from the variety Campbell-28, (C-28) belonging to the *Lycopersicon esculentum* cv. Mill, grown under conditions of cultivation in vitro, the somaclones selected were SC-7, SC-8, SC-10, SC-36, SC-37, (for their good characteristics) all coming from the same callus, obtained from the National Institute of Agricultural Sciences (INCA); and the behaviour of these and the donor were analysed in the third generation.

Variables of agricultural interest, the internal quality of the fruit, as well as the disease incidence under our conditions were evaluated. In Table 1 the analysis of variance of the characters of agricultural interest is shown, and data given for the internal quality of the fruits, where there were significant differences between the genotypes studied for the polar and equatorial diameter, and the mass average of the fruits. In the results of the test of multiple ranges of Duncan for these characters it was observed that the greater values were for SC-36, C-28 SC-37, which do not show significant differences among each other.

Table 1 also shows significant differences between genotypes for the total soluble solids and content of vitamin C. The results of the test of multiple ranges of Duncan (Table 1), show that the cultivar containing greater soluble solids was SC-10, followed by C-28, SC-36 and SC-7, with no significant differences between them; for the content of vitamin C, the somoclones SC-8, SC-10, and C-28 gave the best results.

Table 2 presents the response of the above genotypes to the diseases in this study. It was observed that all the somaclones presented resistance to the *Phytophthora infestans* virus, however only SC-8 and SC-37 were resistant to *Xanthomonas vesicatoria*. Another aspect of supreme interest is the tolerance of the fields of SC-37 and SC-8 to *Alternaria solani*, *Phytophthora parasitica*, and also to *Xanthomonas vesicatoria*. In the end, SC-37 displayed better behaviour in the field in the face of the evaluated disease.

These results show the feasibility of the use of somaclonal variation as an alternative method in the programs of improvement of the cultivation of tomato, with this example demonstrating the potential use in improving complex characters such as disease resistance.

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Table 1. Results of the analysis of variance and test of multiple ranges of Duncan to the 5%.

Components of agricultural interest

Genotype	Diameter (cm) polar	Diameter (cm) equator	fresh mass (g)	Number of fruits	Yield/ plant (kg)
SC-10	4.63 ab	5.90 b	80.68 cd	7.12	0.79
SC-8	4.47 bc	5.83 b	87.90 bc	7.00	0.58
SC-7	4.27 c	5.87 b	73.52 d	13.85	1.01
SC-36	4.87 a	6.53 a	102.42a	9.54	0.98
SC-37	4.73 ab	6.53 a	98.39 ab	7.94	0.76
C-28	4.80 a	6.43 a	101.32 a	7.12	0.72
Esx	0.08**	0.17*	4.00**	2.27 [ns]	0.18 [ns]

Components of the internal fruit quality

Genotype	Acidity (%)	Total Soluble.Solids (%)	Vitamin C ([mg]/ 100g)	Dry Matter (%)
SC-10	0.42	5.06 a	16.07 a	5.06
SC-8	0.37	4.33 b	13.99 abc	4.34
SC-7	0.46	4.64 ab	12.98 bcd	4.64
SC-36	0.38	4.75 ab	11.70 cd	4.75
SC-37	0.41	4.45 b	10.88 d	4.45
C-28	0.37	4.76 ab	15.45 ab	4.77
Esx	0.02 [ns]	0.13*	0.89*	0.18 [ns]

Values followed by the same letters are not significantly different at $p < 0.05$

Table 2. Behaviour of the genotypes under diseases evaluated

Disease	C-28	SC-36	SC-7	SC-8	SC-37	SC-10
Alternaria solani	-	-	-	-	X	-
Phytophthora infestans	X	X	X	X	X	X
Phytophthora parasitica	-	-	-	-	X	-
Stemphylium solani	-	-	-	-	-	-
Xanthomonas vesicatoria	-	-	-	X	X	-
Virus	X	X	X	X	X	X

X = Tolerant - = not tolerant

Granulosa (*grn*) a new epidermal trichome marker

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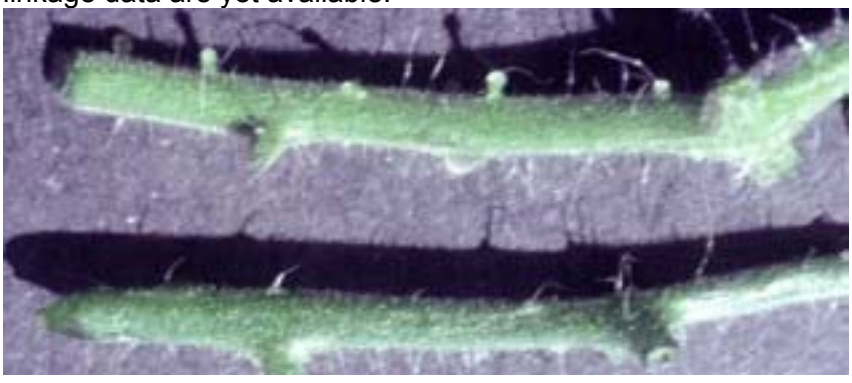
This mutant (3-804), induced by EMS in cv. Castlemart, was first identified in 1981, contemporary with cactiflora (*ccf*). In the initial M2 the segregation was 8 normal and one granulosa, the latter strikingly distinct, not only for the hair trait but also for very retarded growth and chlorosis, manifest particularly in a yellow-green virescence.

The main point of interest in *grn* is the unusual modification of the large epidermal trichomes (Luckwill's type I). In the catalog of normal *esculentum* hair types, these large multicellular trichomes are the most conspicuous. Their main column or stem consists of a series of 8-12 elongate cells arranged end-to-end, totaling 2-3 mm, easily visible to the naked eye. It surmounts a rounded mound of a few to many cells, well detailed at low magnification, but well distinguished without magnification if differentially pigmented with anthocyanin as in the *pennellii*-derived punctate (*pun*) mutation. The multicellular or "cushion" bases of *grn* are greatly expanded --up to 1-2 mm in diameter (see illustration below). The net effect is a "granular", roughened surface of stems, pedicels, and leaf bases. This trait alone serves to distinguish + from *grn* unequivocally, but strongly reinforced by pleiotropic differences in vigor and chlorophyll intensity.

Segregation of a series of *M3* families is summarized below:

Pedigree No.	Phenotypic segregation	
	+	*grn*
94L666	11	3
667	15	0
668	11	4
669	12	2
670	0	15
671	11	3
672	15	0

In these and other F2 segregating families the totals are 69+ : 19 *grn*, deviating only slightly from the expected 66+ : *22 grn*. The limited data are thus consistent with monogenic recessive determination. The seed yield of the parent of fam. #670 was high enough to justify hopes that this mutant is sufficiently fertile to be a useful seedling marker. No linkage data are yet available.



Pto allele from a *L. hirsutum* line that is resistant to bacterial speck disease encodes a protein that interacts with AvrPto

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In common with *Lycopersicon pimpinellifolium*, the source of the *Pto* resistance gene, some accessions of *Lycopersicon hirsutum* var. *glabratum* are resistant to strains of *Pseudomonas syringae* pv. *tomato* (*Pst*) which express the avirulence gene *avrPto* (Lawson and Summers 1984). We confirmed that bacterial speck disease resistance in *L. hirsutum* line PI134418 is *avrPto*-specific and introgressed it into the susceptible *L. esculentum* cultivar TA209 (Tanksley et al., 1996). The introgression involved six backcrosses to the *L. esculentum* parent and a final selfing in order to create the homozygous resistant line 96T133-3. Throughout the backcrossing, *Pst(avrPto)* resistance segregated with an RFLP detected by the cloned *Pto* gene and mapped to the same location on chromosome five corresponding to the *Pto* locus in *L. pimpinellifolium* (Tanksley et al., 1996). These data raised the likely possibility that a member of the *Pto* gene family is responsible for conferring *Pst(avrPto)* resistance in *L. hirsutum* PI134418.

We constructed a cDNA library from 96T133-3, probed it with the *Pto* gene and isolated four classes of *Pto*-like genes. The cDNAs were named *hirPto1*, *hirPto2*, *hirPto3*, and *hirPto4* and they encode predicted protein kinases that are 95%, 79%, 78%, and 77% identical to the *L. pimpinellifolium* Pto protein, respectively, at the amino acid level.

Genetic and molecular evidence indicates that physical interaction of Pto with the AvrPto protein is required for resistance to *Pst*(*avrPto)* (Scofield et al. 1996; Tang et al., 1996). In addition, previous studies indicated that a threonine residue at position 204 in the activation segment of Pto determines recognition specificity for AvrPto (Frederick et al. 1998). Thr-204 is required for interaction with AvrPto in the yeast two-hybrid system and the residue is also required for *Pto* to elicit a hypersensitive response when co-expressed with *avrPto* in *Nicotiana benthamiana*. An adjacent leucine residue at position 205 is not required, but it appears to enhance the ability of Pto to interact with AvrPto (Frederick et al. 1998). Of the four genes cloned from 96T133-3, only *hirPto1* and *hirPto2* encode proteins containing a threonine 204 in the activation segment and only *hirPto1* contains a leucine at the 205 position (Figure 1).

We tested the ability of the *L. hirsutum* Pto-like proteins to interact with the avirulence protein AvrPto in the yeast two-hybrid system. All four *hirPto* cDNAs were cloned into the two-hybrid bait vector, pEG202, and transformed into yeast strain EGY48 that contained the *lacZ* reporter plasmid pSH18-34. After confirming that none of the bait constructs activated the *lacZ* gene on their own, the strains were transformed with an *avrPto* prey plasmid. Based on activation of the *lacZ* gene, these experiments indicated that only the protein encoded by *hirPto1* was able to physically interact with AvrPto (Figure 2).

These genetic and molecular data, suggest that *hirPto1* is responsible for conferring resistance in *L. hirsutum* PI134418 to *Pst(avrPto)*.

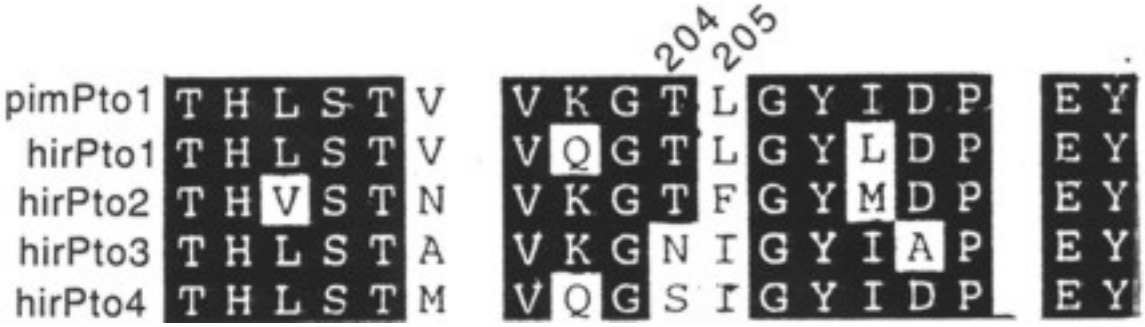

Figure 1. Alignment of part of the activation segment of the Pto and hirPto proteins. Positions of threonine 204 and leucine 205 of the Pto kinase are indicated

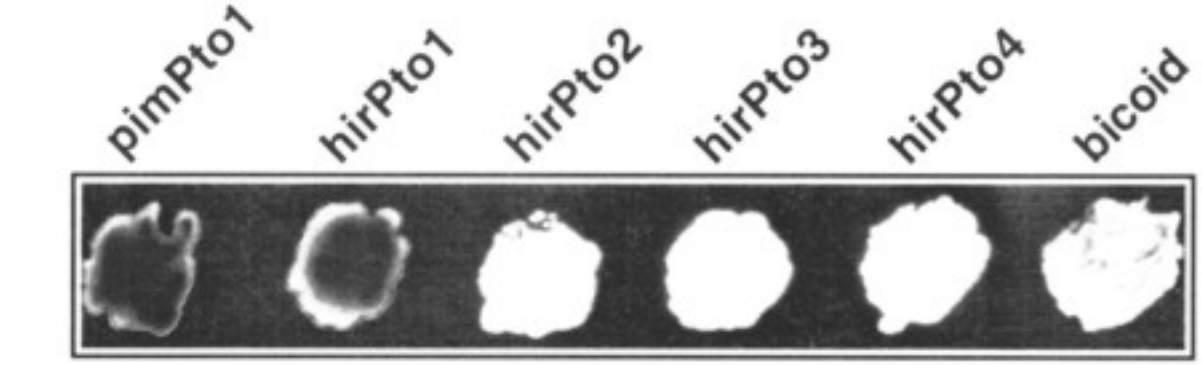

Figure 2. Yeast two-hybrid analysis demonstrated a physical interaction between hirPto1 protein and the AvrPto protein. Yeast strains containing the indicated "bait" proteins were transformed with an *avrPto* prey plasmid. Darker color indicates a physical interaction between the bait and prey proteins.

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An update to a 1998 TGC Report

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In TGC Report v. 48, p. 55: in Stoeva P., et al. "Resistance to TSWV in transgenic tomato varieties" we reported that full or partial resistance to TSWV was established in R1-R3 progenies from selected resistant primary tomato transformants carrying the *MnSOD* gene from *N. plumbaginifolia* and in R1 -R2 progenies from selected resistant primary transformants carrying the TSWV nucleoprotein (Np) gene. Further analysis (PCR analysis with specific primers for both transgenes and Southern blot analysis with the Np gene probe) has demonstrated the presence of the TSWV Np gene in all studied resistant transgenic plants. A technical mistake in primary seed material is assumed.

The influence of magnetic pulsation on the genetic variability of tomato

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There is much data in the scientific literature on the effective influence of magnetic fields on the germination of plant seeds (Saktheeswari, Hussain, 1995; Aksenov et al., 1996), plant growth (Namba, 1996; Yano et al., 1997), drought resistance (Suven et al., 1992), and plant yields (Pietruszewski, 1993; Gabrielian, 1996), but the question of the influence of magnetic pulsation on the genetic variability of plants is also very important.

The tomato F1 hybrids between Mo628 and Likurich were exposed to a low-frequency magnetic field ("CEF" device) using patented methods (RU 2083074 C1, 1997), where Mo628 (*L. esculentum*) is a multimarker mutant line homozygous for recessive linked markers on chromosomes 4 (*ful,e / ful,e*), and 11 (*hl,a / hl,a*). Marker *ful* (4, 24) is associated with yellow leaf colour at the growing points; *e* (4, 66) - serrated leaves with curved central vein; *hl* (11, 48) - hairless plant; *a* (11, 68) - lack of anthocyanin in the hypocotyl, stem and leaves of seedling (Tanksley, Mutschler, 1989). Likurich is a commercial tomato variety. Three time exposures (1, 4 and 8 hours) using wetted seeds, pre-meiotic buds (1st cluster), and also their combined action were studied. Ten F1 plants of each variant were examined. The collecting of F2 seeds for assessment of the crossing-over frequency was carried out separately on each of the plants and fruits of the first cluster. Recombination frequency (rf) was estimated by maximum likelihood method for each fruit of a plant and on the variants in whole (Fisher, 1958; Bailey, 1961). Statistical analysis was performed on an IBM PC compatible computer using the software package "BIOSTAT" (Preygel, 1986).

The F1 plants were grown in the greenhouse. During the growth of the vegetation we observed that 7% of the F1 had a very interesting phenomenon - mottled regions that were probably a consequence of mitotic crossing over which took place in the somatic tissue of the tomato (Photo 1-2). The stem of the plant usually has hairs and anthocyanin but here there appeared a region without hairs or anthocyanin. This is a consequence of the transition of recessive mutant genes to the homozygous state as a result of mitotic crossing over. Quite possibly the cause of the phenomenon was the magnetic field as usually this is a very infrequent event.

The analysis of recombination frequencies has shown the disposition towards an increase of crossing over frequency in both segments simultaneously with increasing magnetic field exposure. But only at 8 hours treatment (seeds + buds) was the difference statistically significant at the 5% level (Table 1) in comparison with the control for the chromosome 4 segment (*ful-e*).

Table 1. Crossing over frequency in the *ful-e* and *hl-a* segments of the hybrid F1 of tomato at the different variant of magnetic field treatment.

Variants of the experiment	ful-e (chromosome 4)		hl-a (chromosome 11)	
	Number F2s	rf	Number F2s	rf
Control	666	32.07±2.27	666	15.45±1.55
Seeds – 1 h.	920	33.42±1.98	920	17.63±1.41
Seeds – 4 h.	1445	32.23±1.55	1445	16.85±1.10
Seeds – 8 h.	2265	34.79±1.29	2265	16.03±0.85
Buds – 1 h.	898	32.89±2.11	898	17.75±1.52
Buds – 4 h.	842	33.87±2.08	842	17.31±1.46
Buds – 8 h.	1117	33.49±1.98	1117	16.93±1.38
Seeds + buds –1h.	648	33.19±2.56	648	15.13±1.69
Seeds + buds – 4 h.	795	31.54±2.21	795	13.85±1.43
Seeds + buds – 8 h.	309	38.27±3.68*	309	16.38±2.34

Note: * - rf significantly differs from the control at the $P < 0.5$

Conclusions:
1. These results show that the process of tomato meiosis is highly protected from the influence of a low-frequency magnetic field, in contrast to the somatic tissues.
2. The recombination effects occur only at longer-lasting and probably stronger physical properties of a magnetic field than what were applied in this experiment.
3. In the case of using a low-frequency magnetic field for irradiating seeds or seedlings of hybrids F1 (as a stimulating agent), the appearance of chimeric plants is possible.

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Variability of crossing over frequency in high- & low heterosis F_1 hybrids of tomato under continued exposure to low temperatures

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Introduction

Induced recombinogenesis is of great practical importance for plant breeding as an effective method of increasing genotype diversity in the progeny (Elliot, 1961; Zhuchenko, Korol, 1985; Zhuchenko, 1988).

The change in temperature was one of the first methods for experimental recombinogenesis (Dishler, 1983). The choice of this agent is not casual, as temperature is the basic limiting factor of environment, and also its use is simple and accessible.

In previous studies of effects of a thermal factor action on recombination, as a rule, short stresses were applied or the conditions of an external environment were used at the expense of a variation by terms of sowing, but in this case the temperature conditions were changed both in a hothouse, and in the field (Mock, 1973; Zhuchenko, Korol, 1985; Zhuchenko, Uschapovski, 1989).

The temperature influences are usually accompanied by a recombinogenic effect (Dishler, 1983), however, the degree of response largely depends on the genotype (Straub, 1938; Wilson, 1959). Such differences, apparently, are caused by peculiarities both in the genetic control system of vegetative development (*F*), and in the system determining recombination (*R*), and also their interaction at each particular genotype. Also it is important to note, that the increase of morphometric parameters at heterosis, as a rule, is accompanied by increase of organism's fitness (Mather, Jinks, 1985) and probably it is related to the higher “buffer” ability of its *F* system in relation to *R*.

Therefore the problem was to determine how the cultivation of F_1 tomato hybrids under constant subextreme temperature conditions for a long time would influence the recombination system depending upon the level of hypothetical heterosis on morphometric traits of the hybrids.

Materials and methods.

Four F_1 hybrids heterozygous for the markers *ful-e* (chromosome 4) and *hl-a* (chromosome 11) and differing (by a factor of 2.5 to 5 under optimal conditions) in the degree of hypothetical heterosis (HH) for plant height and the sum of lengths of the first two true leaves were examined (Ursul, 1992). Hypothetical heterosis (HH) was estimated as:

$$HH = [(F_1 - P) / P] \times 100\%, \text{ where } P = (P_1 + P_2) / 2.$$

These had been derived from crosses of the multimarker line Mo628 (*L. esculentum*) with two varieties and two wild species: Nevsky — high heterosis (116%, ↑); Breakaday — low heterosis (24%, ↓); *L. es*. var. *racemigerum* — high heterosis (82%, ↑); *L. cheesmanii* — low heterosis (31%,↓).

The plants were grown in pots. At the stage of 3 true leaves they were placed into growth chambers KTLK-1250 «ILKA» under the following conditions: light intensity was 15000±100 lux, the day lighting was 13 hours, air humidity was 65%, 75% of field water capacity in the soil, the temperature regime was 17°C (day) and 15°C (at night) in the treatment variant and 25°C (day) and 23°C (at night) in the control.

The experiment was continued until fruits were set in the first two racemes, following which the plants were returned to optimal conditions. During all the experiment every three days for all plants a quantity of true leaves and opened flowers were taken. The collecting of seed-bearing F_2 fruits (for determination of a crossing-over frequency) was carried out separately on each plant, from the fruit of the first two inflorescences.

Recombination frequency (rf) was estimated by maximum likelihood method for each fruit of a plant and on the variants in whole (Fisher, 1958; Bailey, 1961). The estimation of *rf* values and the errors for each variant was made taking into account the number of genotypes, values of their *rf* and error for each of them separately. Thus we applied the formulas to account for an error of *rf* with the count of heterogeneity between replications (Urbah, 1964; Kendall, Stuart, 1966).

Statistical processing of the received results was carried out with application of Student and $Õ^2$ criteria (Rokitski, 1973). Statistical analysis was performed on an IBM PC compatible computer using the software packages BIOSTAT, (Preygel, 1986).

Results and discussion.

The effect of temperature on a plant is caused both by its direct influence on metabolism of premeiotic and meiotic cells, and indirectly, by the change in metabolic processes in the whole organism (Zhuchenko, 1988; Zhuchenko, Korol, 1985). It is thought that in the first case temperature touches on the function of the recombination system being a component of the genetic system of population adaptation (*R*-system), and in the second on the system of control of vegetative development and reverse physiological reactions of an organism to the change of environment (system of individual adaptation or *F* — System) (Zhuchenko, 1988). In both cases the fluctuation of temperature is transferred to sporogenous tissue, in which all necessary processes proceed for the realization of a crossing-over. And as the enzymes participating in crossing-over, as well as the majority of other cellular enzymes, have a temperature optimum, any deflection from it will be accompanied by alterations in enzymatic reactions (Alexandrov, 1975) and result in a change of conditions of the crossing-over process.

It is logical to note that temperature influences on a plant at the beginning is direct and a bit later it gets indirect. The short-term influences (temperature shock) will render direct influence on metabolism of the sporogenous tissue, while the long term temperature processing, on the contrary, will result in essential rearrangements of metabolism, down to the switching on of processes of morpho-anatomical and physiological and biochemical adaptation (Kuperman, 1984), the results of which will probably have an effect on the conditions of the crossing-over process.

It is important that in natural conditions the wild populations are usually subject not only to short-term shock influences of critical temperatures (for example, spring frosts), which are mainly considered in the scientific literature, but also rather long changes in small and/or subextreme values of temperature, that occur as a rule with long-term climatic changes and with colonization by species of new ecological niche.

During all of the experiment high-heterosis F_1 hybrids had an advantage both in growth rate and in generative development, in comparison to low heterosis hybrids or with hybrids where complete absence of heterosis was reported. As for recombination, the first thing observed in the experiment was a significant increase in crossing over frequency in all hybrids and within both segments in question in the treatment, the difference being statistically significant for the *hl-a* segment (Table 1). A similar reaction of tomatoes, only with short-term stresses, was mentioned in another article (Gavrilenko, 1984).

It is well-known that temperature lowering reduces the speed of biochemical reactions, thus increasing the duration of cycles and phases of various physiological processes (Alexandrov, 1975; 1985), and consequently the duration of conjugation, synapsis, crossing-over etc. Therefore it is supposed that recombination reactions to low temperature consists in an increase in the number of DNA breakages kept in pachytene, accessible to an exchange, at the expense of an avoidance of their reparation (Lu, Chiu, 1976). This assumption also explains well the high stage-specific influence of low temperature treatment (Lu, 1975).

By considering the effect separately in high and low-heterosis hybrids, the tendency for a stronger reaction to such influences in the former rather than in the latter (Table 1), especially in a segment *hl-a,* is obviously visible. In both investigated pairs the frequency of crossing-over was higher in case of high-heterosis hybrids.

It is essential that low temperature, acting on reparation of one-strand breakages in pachytene, can simultaneously result in a delay or avoidance of DNA reparation synthesis, together with regeneration complementation of molecular heterozygosity sites. The correction in sites of molecular heterozygosity is an absolutely necessary condition for a normal end to a recombination event, without it the products of an exchange will be nonviable (Lu, Chiu, 1976). Therefore the result of low temperature suppression of two types of reparations in pachytene, can be negative: under long processing, the increase of potential sites of crossing over will be compensated for by the reduction of vitality of incorrect products of an exchange.

This suggests that under equal conditions of induction of recombination frequency by means of low temperature, it is possible that a higher reparation ability of high heterosis hybrids results in less elimination of recombinant classes of gametes and/or zygotes, and thus to the better functioning of their metabolic systems; thus, long-term influences of low temperature can play an important role. This was strongly supported by persistence of heterosis in the high heterosis hybrids, the difference in the degree of heterosis between the former and the low heterosis hybrids becoming even larger towards the end of the experiment.

Thus the long action of low substress temperature also has highly effective recombinogenetic effects, and a higher reaction to an induction of crossing-over frequency is characteristic of high heterosis F_1 hybrids of tomato.

It is probable that high heterosis F_1 hybrids in contrast to low heterosis ones provide less elimination of recombinant classes of gametes and/or zygotes owing to more harmonious functioning of their metabolic systems under long-term influence of low temperature.

We believe that this effect merits further in depth investigation. However, even now it can be suggested that a more effective selection background can be performed in F_2 populations produced from F_1 high-heterosis.

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Table 1.

Crossing over frequency in the segments *ful-e*, *hl-a* at high- (↑) and low heterosis (↓) hybrids F_1 of tomato under extreme and optimum conditions of cultivation.

Hybrids F_1: Mo628 (P_1) with two varieties and wild species (P_2)	ful – e (chromosome 4)				hl – a (chromosome 11)			
	No F_2	Control	Treatment	Δ rf	No F_2	Control	Treatment	Δ rf
Breakaday (↓)	1784	34.22 ±1.44	37.17 +1.80	2.95	1245	17.61 +1.01	22.60 +1.38	4.99**
Nevsky (↑)	971	32.38 ±1.89	37.28 +1.79	4.90	1265	18.21 +1.40	26.31 +1.48	8.10***
L. rasemigerum (↑)	1006	34.17 ±1.92	38.12 +2.63	3.95	603	17.03 +1.32	25.05 +2.09	8.02**
L. cheesmanii (↓)	810	30.53 +2.01	35.92 +1.94	5.39	1038	15.39 +1.40	20.43 +1.43	5.04*

Note: *, **, *** - *rf* under the treatment significantly differs from that of control at $P < 0.05$, 0.01, and 0.001, respectively.

Characterization of two *N*-suppressor mutants in tomato

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The *N* gene confers resistance to tobacco mosaic virus (TMV) in tobacco. It is hypothesized that *N* constitutes an early component of a signal transduction pathway which results in the hypersensitive response (HR), systemic acquired resistant (SAR), and pathogen inhibition.

N confers a temperature sensitive hypersensitive response in tobacco and transgenic *NN* tomato (Whitham et al, 1996). At temperatures below 28°C, *N* functions normally; HR lesions develop and TMV movement is restricted to sites of inoculation. At temperatures above 28˚C, the *N*-mediated HR is suppressed and TMV moves systemically in the plant. HR is restored when TMV inoculated plants are shifted from high temperatures to temperatures below 28˚C, resulting in massive cell death which kills the plant. The ability to reconstruct the temperature sensitive-mediated resistance response in tomato demonstrates that all the components necessary for *N*-mediated resistance are conserved in tomato, making it an ideal genetic system to isolate and study components of the *N* signal transduction pathway. We have identified two mutants that suppress the *N* gene function in tomato.

Materials and Screen Used To Isolate *N*-Suppressor Mutants
Materials: Our *NN* transgenic tomato line contains three, linked copies of *N*, which reduces the possibility of isolating a mutation in *N* . We have generated two different M2 mutagenized seed populations for our screen: one pool is EMS mutagenized, and the other is fast neutron mutagenized.

Screen: *N*-mediated resistance to TMV in tobacco and transgenic *NN* tomato is reversibly inactivated at elevated temperatures. We have exploited this temperature sensitive property of *N* to isolate mutants using a temperature shift assay developed in our lab (fig 1). In a screen using the temperature shift assay, plants bearing a mutation in the *N*-mediated resistance response will survive the screen, while plants able to mount a normal resistance response will die. We have used this screen to isolate both EMS and fast neutron *N*-suppressor mutants.

EMS Induced *N*-Suppressor Mutants: 250,00 M2 EMS mutagenized, *NN* tomato seed were screened using the temperature shift assay outlined in Figure 1. Sixty survivors were isolated; 21 were putative *N*-suppressor mutants. All 21 lines share a similar “partial resistance” phenotype (Fig 2a). Partial resistance is characterized as simultaneous development of HR lesions and mosaic symptoms in the upper leaves of the plant. Mutant line B201 was chosen for further characterization and mapping.

EMS induced partial resistant mutant line B201 cannot contain virus to initial site of inoculation, despite development of HR lesions: Plants were hand inoculated with TMV at room temperature and monitored for their response to TMV. Seven days post TMV inoculation (dpi), plants from the mutant line B201 and wild-type *NN* control plants developed normal HR lesions on the inoculated leaves with no signs of mosaic or HR on the upper, uninoculated leaves. At 60 dpi, B201 plants developed the partial resistance phenotype, while the wild type *NN* control remained healthy. Protein was isolated from the upper, uninoculated leaves and, using an antibody against the TMV coat protein, virus was detected in the leaves of B201 plants but not in

Fig 1: Seedling Lethal Screen. *N* resistance is inactivated at 32?C, which allows the virus to spread systemically. After shifting to 24?C, seedlings with a functional *N* pathway undergo HR in every cell where virus is present, killing the plant.

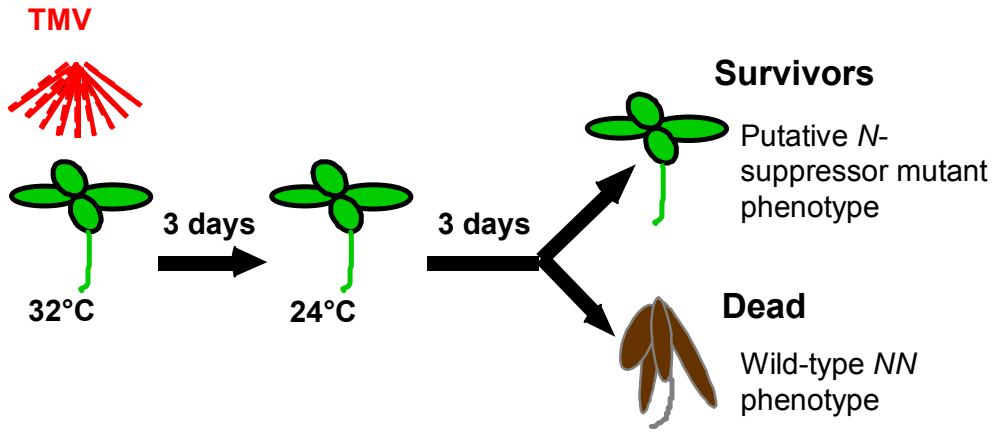
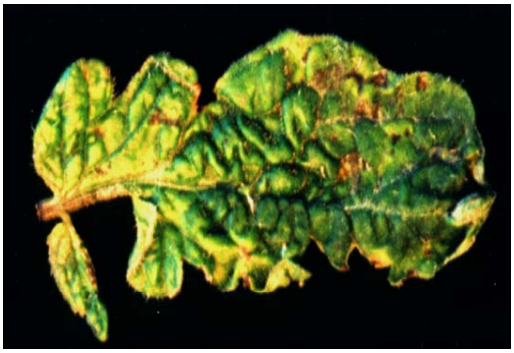


Fig 2: Two *N*-Suppresor Mutant Phenotypes. A) The EMS induced mutant B201 is partially resistant to TMV. This mutant develops both HR and mosaic symptoms on the same leaf. B) The fast-neutron induced mutant is susceptible to TMV. This mutant develops mosaic symptoms even though it contains the *N* transgenes.



A. EMS induced *N*-suppresor mutant line B201 is partially resistant to TMV

B. Fast Neutron induced *N*-suppresor mutant is susceptible to TMV

the leaves of the wild-type *NN*-tomato control. This suggests the mutation in B201 does not affect the cell death pathway leading to HR, but does affect the pathway(s) responsible for *N*-mediated viral inhibition.

Partial resistant phenotype in line B201 is due to a single, recessive mutation: Line B201 was crossed to wild-type VF36::*NN* tomato, as well as crossed to the near-isogenic TMV sensitive line VF36. F1's from these crosses were inoculated with TMV, and all responded with a wild-type HR and were able to inhibit virus spread, suggesting the mutation is recessive and not a mutation in *N*. F2 seed generated from these crosses were screened for their response to TMV. The phenotype is segregating as a single, recessive mutation.

Mapping of the Partial Resistant Mutation in B201 is in progress: The F2 progeny created by crossing line B201 to *L. pennellii* has been generated. The mutant phenotype is scorable in the F2 mapping population, and we are currently in the process of mapping the gene.

Fast Neutron-Induced *N*-Suppressor Mutant: Approximately 40,000 fast-neutron mutagenized M2 *NN* tomato seed have been screened to date. One fully-susceptible mutant has been isolated so far. This mutant develops normal mosaic symptoms (Fig 2b). Preliminary southern blot analysis confirms all *N* transgenes are intact. This mutant has been crossed to VF36, and the F1 from this cross have been inoculated with TMV. All F1 progeny are resistant to TMV, suggesting the mutation responsible for the fully susceptible phenotype is recessive. Analyses of the F2 progeny are underway.

We are continuing to screen our fast-neutron mutagenized population for new mutant classes/loci. With enough mutants isolated, we hope to identify most of the components necessary for *N*-mediated TMV resistance. Characterization of these mutants and study of the relationship between the components will help us to better understand the molecular mechanism(s) behind the disease resistance response. This study will also provide us an opportunity to look for an alternative way to manipulate the pathway to generate a broad spectrum and durable resistance to improve the health and productivity of the plants.

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Putative developmental mutants isolated from EMS and fast neutron mutagenized seed pools

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Our lab is primarily concerned with disease resistance; however, during our screen for disease resistance mutants, we isolated three putative developmental mutants from our EMS mutagenized and fast neutron mutagenized seed populations. We present these plants here with brief descriptions, so that any lab who is interested may obtain these lines from us for further study. All mutants are from a VF36 background, and are transgenic for the *N* TMV disease resistance gene.

Line	Mutagen	Description	Conferred to next Generation?
NST10	EMS	Putative leaf mutant. Variegated green/yellow patterns on leaves resembling mosaic-disease symptoms, even though plant is not infected with virus. Is not impaired in TMV resistance. Sets fruit, but has reduced fertility.	Yes
NST43	EMS	Dwarfed/small in stature. May have reduced number of trichomes. Appears to have increased rate of senescence in leaves. Fruit set does not appear to be affected.	Yes
FN3/1	Fast Neutron	"Cabbage/kale" mutant: Leaves are packed close together along the main stem of the plant and all stems of leaves/leaflets are very thick. Leaflets are tightly curled under. Plant does set fruit, but seed has not been collected yet.	Not determined

Potential limitations with using rhodamine B for the quantification of epicuticular acylsugars

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Control of insect pests is an important factor in tomato production. The acylsugars produced by the wild tomato *L. pennellii* mediate that species resistance to a number of important pests of tomato, including potato aphid, green peach aphid, leaf miner, fruit worm, army worm, and silverleaf whitefly. The goal of this project is the transfer of the acylsugar-mediated pest resistance to horticulturally acceptable varieties of cultivated tomato. The breeding program has progressed through 5 backcross generations, using for selection an acylsugar assay (Goffreda et al. 1990) that is based on Nelson's copper reagent. This assay measures acylsugars by measuring the total sugar content of the acylsugars produced.

Lin and Wagner (1994) suggested that the affinity of rhodamine B for acylsugars could be used to detect and quantify acylsucroses and acylglucoses. We developed a miniprep protocol based on their paper to rapidly screen large segregating populations for individuals accumulating acylsugars. The assay is essentially that of Lin and Wagner (1994), downscaled to permit the test to be run in Elisa plates. The Rhodamine-based assay does not give separate estimations of acylsucroses & acylglucoses, but it has several advantages over the Nelson-based assay. The Rhodamine assay has a much greater sensitivity to lower levels of acylsugars than the Nelson-based acylsugar assay. As a result, the Rhodamine-based assay can be used at a younger stage of plant development than possible using previous methods. In addition, the rhodamine assay only requires approximately 1/3 the labor and 1/3 the supplies cost of the Nelson's-based acylsugar assay. Also, rhodamine B does not detect free sugars, greatly reducing the background.

It was soon apparent, however, that the measurement of acylsugars using the Rhodamine B assay is biased in some way. The acylsugars of four segregating populations originating from interspecific crosses between *L. pennellii* and *L. esculentum* were quantified using both the Nelson's copper reagent and rhodamine assays. In all cases, a characteristic bifurcation in the data was seen, such that two intersecting lines were present when the Nelson's-calculated acylsugar quantities were plotted against the Rhodamine-calculated acylsugar quantities from the same samples. Furthermore, some plants that were positive for acylsugar production according to the Nelson-based assay were negative for acylsugars according to the Rhodamine- based assay. This result suggested that the Rhodamine and Nelson-based assays were not detecting all of the same compounds, or not measuring them equally. The Nelson's copper reagent assay's ability to detect acylsugars involves a color-yielding reaction that takes place between the sugar moiety and the assay reagents (Goffreda et al., 1990). The basis of the rhodamine B assay detection of acylsugars is less clear, but it has been suggested that the Rhodamine is lipophilic, causing it to associate with organic compounds (Lin and Wagner, 1994). Because rhodamine B appears to be less discriminating, the reason for the bifurcation seen with the segregating populations could be that: 1) Rhodamine B is detecting non-acylsugar epicuticular compounds extracted with the acylsugars in sample collection or 2) Rhodamine B is measuring the various types of acylsugars differently based on differences in sugar moiety, fatty acid chain length, or the number of fatty acids attached to the sugar moiety of the acylsugar.

In 1998/1999 we tested the rhodamine assay for types of bias, to determine the nature and levels of risk in reliance on this method. Because rhodamine B is used as a dye for detection of a number of compounds, including lipids, we could use compounds analogous to acylsugars to test for bias in the

binding of rhodamine. One such series of compound were free fatty acids of the types found in acylsugars. Glycerols esterified to fatty acids from C4 to C10, the range of chain lengths found in acylsugars of *L. pennellii* were also used as test compounds. The tests of rhodamine B binding to free fatty acids indicates that this test could be strongly biased depending on fatty acid chain length (Table 1). The assay's response is very strong in fatty acids of C7 and greater, but weak to non-existent in fatty acids shorter than C7. The Rhodamine B assay was similarly affected by fatty acid chain length in tests on diacylglycerols; however, diacylglycerols with shorter fatty acids appeared to have greater affinity for Rhodamine B than free fatty acids of the same length (data not shown). Since the relative levels of the different fatty acids present in acylsugars varies with genotype, the bias for fatty acid chain length could result in false negatives or in errors in estimation of relative acylsugar levels among genotypes when the Rhodamine B assay is used.

Table 1. Average absorbence values from Rhodamine binding to increasing amounts of different fatty acids.

Concentration	**.003M**	**.045M**	**.067M**	**.1M**	**.15M**	**.224M**	**.335M**	**.5M**	**.045M**
propionic acid (C3)	0.01	0.01	0.01	0.01	0.00	0.01	0.00	0.01	0.01
isobutyric acid (C4)	0.01	0.01	0.01	0.02	0.01	0.03	0.03	0.05	0.01
2-methylbutyric acid (C4)	0.01	0.01	0.02	0.02	0.03	0.06	0.11	0.23	0.01
n-valeric acid (C5)	0.01	0.01	0.01	0.02	0.03	0.06	0.26	0.53	0.01
3-methyl-n-valeric acid (C6)	0.01	0.01	0.02	0.04	0.10	0.21	0.23	0.79	0.01
heptanoic acid (C7)	0.21	0.44	1.00	1.71	2.00	2.00	2.00	2.00	0.44
octanoic acid (C8)	>2.00,	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00
8-methylnonanoic acid (C10)	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00
decanoic acid (C10)	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00	>2.00

Since these results suggested that chain length biases were the basis for the discrepancies between the results of the Nelson's and Rhodamine B-based tests, gas chromatograph analysis was performed of the fatty acids in acylsugars from nearly 40 different plants representing both regression lines from a segregating population. However, the fatty acid profiles of the plants surveyed were very complex, since each plant produces a mixture of acylsugars rather than a single acylsugar. The results did not permit comparison of acylsugar type and differential response to the Nelson and Rhodamine based tests. A valid comparison would require use of individual acylsugars separated by HPLC.

There is clearly a difference in the acylsugar detecting abilities of the Nelson's copper reagent and Rhodamine B assays, resulting in underestimation of acylsugar production by some plants or in false negatives. The bias in estimating levels of acylsugars is most critical when ranking acylsugar-

accumulating plants to select for the best plants to use in a breeding program. The bias would also be important if the type of acylsugar underestimated by the Rhodamine assay were particularly important for acylsugar efficiency or effectiveness. False negatives would be important if it is necessary to detect every acylsugar producing plant in a population.

Despite the bias in the Rhodamine B assay there could be instances in which the assay would be of value. An example is its use in our 1998 winter greenhouse survey. Since the Rhodamine B assay can be performed on younger plants, we grew a very large initial populations (filling the greenhouse even as small plants), used the Rhodamine assay in a preliminary screen and reduced the populations size to that the greenhouse could contain as mature plants by saving only the positive plants. The plants saved were then screened by the Nelson's copper reagent assay at 15 weeks to determine relative acylsugar levels. We, no doubt, eliminated acylsugar-producing plants in the first screen due to false negatives common in the Rhodamine test, however all of the plants which indicated as being positive by the Rhodamine-based test were also positive by the Nelson-based assay. This approach allowed us to maximize the number of acylsugar-accumulating plants recovered in that generation in a restricted area of greenhouse space. The use of the Rhodamine test did not eliminate the need to use the Nelson-based assay.

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TGRC STOCK LISTS

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Miscellaneous Stocks (1,192 accessions total) are listed in TGC 47 (1997)
Wild Species Stocks (1,106 accessions total) are listed in TGC 48 (1998)

REVISED LIST OF MONOGENIC STOCKS

The following list of 978 monogenic stocks (at 607 loci) is a revision of the list issued in TGC 46. Certain obsolete or unavailable items have been deleted, newly acquired stocks have been added, and numerous inaccuracies corrected. This year we are again indebted to John Maxon-Smith (Practical Plant Genetics) for many additional NILs in the Ailsa Craig background, as well as to Henri-Laterrot and C. Caranta (INRA) for stocks of *Is* and FORL-resistance, John Stommel (USDA-ARS) for stocks of *B*, and to Maarten Koornneef (Wageningen Agricultural University) for *fri* and *tri* mutants.

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 table at end of stock list; *=primary class), *SOURCE* = source of mutation (*SPON* = spontaneous, *CHEM* = chemically induced, *RAD* = radiation-induced), *BACK* = background genotype (see 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. For each mutation, we have attempted to list the original source, in which it is usually isogenic in a known background, as well as any nearly isogenic stocks into which it has been bred. Most stocks are homozygous and true-breeding. The exceptions are male-steriles (available as BC or F_2 populations), other inherited sterilities, homozygous-inviable dominants, and other mutants that are too difficult to maintain as homozygotes, hence are propagated via heterozygotes (usually as F_2's).

Detailed information on each monogenic stock, including phenotypic descriptions, references, images, map locations, colleague addresses, etc., can be obtained through the TGRC website at http://tgrc.ucdavis.edu, or through the SolGenes database at http://genome.cit.cornell.edu/solgenes/welcome.html.

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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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
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	CR	IL	LA0537
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
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	X	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-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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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
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
atn	--	attenuata	*at*	E*AJK	RAD	AC	NIL	LA3829
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,*	C*B	SPON	RCH	IL	LA1486
au	6	aurea	*yg:6, yg-6,*	C*B	SPON	AC	NIL	LA2929
au	tl	aurea		C*B	SPON	VF145	IL	2-655A
au	w	aurea	*w616*	C*B	CHEM	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	X	NON	LA2374

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
B	--	Beta-carotene		P*	SPON	RU	NIL	LA3000
B	--	Beta-carotene		P*	SPON	FM6	NIL	LA3898
B	--	Beta-carotene		P*	SPON	OHO	NON	LA3899
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
bl	--	blind		K*	SPON	AC	NIL	LA3745
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	--	cabbage		J*K		AC	NIL	LA3819
cb-2	--	cabbage leaf-2		J*K	RAD	X	NON	LA2002

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
cb-2	--	cabbage leaf-2		J*K	RAD	AC	NIL	LA3169
ccf	--	cactiflora		N*LO	CHEM	CSM	IL	3-805
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
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	X	NON	LA0719
clau	--	clausa	*ff, vc*	J*LO	RAD	AC	NIL	LA3583
clau	--	clausa	*ff, vc*	J*LO	RAD	LU	IL	LA0591
clau	ff	clausa		J*LO	SPON	VFSM	IL	2-505
clau	ics	clausa	*ics*	J*	SPON	PTN	IL	LA1054
clau	ics	clausa	*ics*	J*	SPON	AC	NIL	LA3713
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	AC	NIL	LA2919
cm	--	curly mottled		G*JNO	SPON	PCV	NON	LA0272
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

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cor	--	coriacea		K*J	RAD	AC	NIL	LA3743
cpa	--	composita	*cpa1*	M*K	RAD	RR	IL	LA0833
cpt	--	compact		K*EJ	SPON	XLP	IL	2-377
cpt	--	compact		K*EJ	SPON	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	FB	NIL	LA3022
d	--	dwarf	*rob:imm*	K*JT	SPON	GRD	NIL	LA3031
d	--	dwarf	*rob:imm*	K*JT	SPON	STN	NIL	LA0313
d	b	dwarf		K*JTL	SPON	RR	IL	LA3865
d	cr	dwarf	*rob:crisp*	K*JT	RAD	CR	IL	LA0570
d	im	dwarf		K*JT	RAD	CR	IL	LA0571
d	prov2	dwarf	*d*	K*JT	CHEM	VCH	IL	3-623
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	VAN	NIL	LA3902
d	x	dwarf		K*JT	SPON	AC	NIL	LA3615
d	x	dwarf		K*JT	SPON	PCV	NON	LA1052
d	x	dwarf		K*JT	SPON	SPZ	IL	LA0160
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
de	--	declinata		K*JU	RAD	AC	NIL	LA3742
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

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def-2	--	deformis	J*LN	RAD	AC	NIL	LA2920	
Del	--	Delta		P*	SPON	RU	NIL	LA2996A
Del	--	Delta		P*	SPON	AC	NIL	LA2921
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
Df	--	Defoliator		Y*H	SPON	par	NON	LA0247
dg	--	dark green		T*	SPON	MP	IL	LA2451
dg	--	dark green		T*	SPON	WA	NIL	LA3011
dgt	--	diageotropica	*lz-3*	K*R	SPON	VFN8	IL	LA1093
Dia-2	1	Diaphorase-2		V*	SPON	pen	NON	LA2987
Dia-3	1	Diaphorase-3		V*	SPON	X	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
div	--	divaricata		C*AJK	RAD	AC	NIL	LA3818
dl	--	dialytic		I*LN	SPON	SM	IL	2-069
dl	--	dialytic		I*LN	SPON	AC	NIL	LA3724
dl	s	dialytic		L*N	SPON	VF36	NIL	LA3906
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	X	NON	LA1016
dpy	--	dumpy		K*J	SPON	AC	NIL	LA3171
dpy	--	dumpy		K*J	SPON	X	NON	LA0811
dpy	prov2	dumpy	*dpy*	K*J	CHEM	VCH	IL	3-630
dpy	prov3	dumpy	*dpy*	K*J	SPON	ANU	IL	LA1053
drt	--	dwarf root		R*	CHEM	X	IL	LA3207
ds	--	dwarf sterile		N*K	SPON	EPK	IL	2-247
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	--	elegans		E*JK	RAD	AC	NIL	LA3825
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
em	--	emortua	*em1*	H*K	RAD	AC	NIL	LA3817
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	cer	IL	LA2415

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
Est-1	1	Esterase-1		V*	SPON	pim	NON	LA1818
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
f	D	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
fd	--	flecked dwarf		G*DK	RAD	BK	NON	LA0873

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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	X	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
fn	--	finely-netted		D*	RAD	X	NON	LA2481
fn	--	finely-netted		D*	RAD	PSP	IL	LA2005
fr	--	frugalis		K*JT	RAD	CR	IL	LA0674
Frl	--	FORL resistance	*Fr1, Frl*	Q*	SPON	AC	NIL	LA3273
Frl	--	FORL resistance	*Fr1, Frl*	Q*	SPON	VGB	NON	LA3841
frg	--	fragilis	*frg1*	D*CJK	RAD	CR	IL	LA0864
fri	--	far red light insensitive		--		MM	IL	LA3809
Frs	--	Frosty spot	*Nec*	H*	SPON	X	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	AC	NIL	LA3300
Fw	--	Furrowed		J*KN	SPON	PSN	IL	LA0192
fx	--	flexa		K*	RAD	LU	IL	LA2037
fy	--	field yellow		E*	SPON	AC	NIL	LA3295
ga	--	galbina	*ga1*	D*BE	RAD	CR	IL	LA0836
ga	--	galbina	*ga1*	D*BE	RAD	AC	NIL	LA3828
gas	--	gamosepala	*gas1*	D*JL	RAD	RR	IL	LA0947
gbl	--	globula		K*JU	RAD	LU	IL	LA2032
Ge	c	Gamete eliminator		N*	SPON	CR	NON	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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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
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	X	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	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
gq	--	grotesque		L*O	SPON	X	NON	LA0137
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	AC	NIL	LA3530
gs	--	green stripe		P*	SPON	GSM	IL	LA0212
h	--	hairs absent	*H*	I*	SPON	X	NON	LA0154
h	--	hairs absent	*H*	I*	SPON	AC	NIL	LA3172

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
he	--	heteroidea	D*JK	RAD	CR	IL	LA0679	
Hero	--	Heterodera rostochiensis 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
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	X	NON	LA0279
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 0		Q*	SPON	VD	NIL	LA3025
I	--	Immunity to Fusarium: race 0		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
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	AC	NIL	LA3715
in	--	indiga		K*DJ	RAD	CR	IL	LA0610
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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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	PSN	NON	LA0315
j-2	--	jointless-2	*j2*	M*	SPON		NON	LA3899
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	IL	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	NON	LA0329
ls	--	lateral suppresser		K*LN	SPON	AC	NIL	LA3761
ls	--	lateral suppresser		K*LN	SPON	X	NON	LA2892
ls	2	lateral suppresser		K*LN		PRI	NIL	LA3901
lt	--	laeta	*lt1*	E*DK	RAD	CR	IL	LA0835
ltf	--	latifolia		J*	CHEM	VF36	IL	3-035A

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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	AC	NIL	LA3177
Lx	--	Lax		J*	SPON	LK	NON	LA0505
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
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
Mi-3	--	Meloidogyne incognita-3		Q*	SPON	per	NON	LA3858
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
mon	--	monstrosa		K*J	RAD	AC	NIL	LA3826
mor	--	morata	*mor1*	E*K	RAD	RR	IL	LA0848
ms-2	--	male-sterile-2	*ms2*	N*	SPON	PSN	IL	2-031
ms-3	--	male-sterile-3	*ms3*	N*	SPON	SM	IL	2-032
ms-5	--	male-sterile-5	*ms5*	N*	SPON	SM	IL	2-039

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
ms-6	--	male-sterile-6	*ms6*	N*	SPON	SM	IL	2-044
ms-7	--	male-sterile-7	*ms7*	N*	SPON	SM	IL	2-089
ms-9	--	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-17	*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
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	TR44	NIL	LA3196
Ms-48	--	Male-sterile-48		N*	CHEM	spVCH	NIL	LA3200
Ms-48	--	Male-sterile-48		N*	CHEM	VCH	NIL	LA3199
Ms-48	--	Male-sterile-48		N*	CHEM	T5	NIL	LA3198
Ms-48	--	Male-sterile-48		N*	CHEM	TR51	NIL	LA3197
Ms-48	--	Male-sterile-48		N*	CHEM	N28	NIL	LA3194
Ms-48	--	Male-sterile-48		N*	CHEM	MR20	NIL	LA3193

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
Ms-48	--	Male-sterile-48		N*	CHEM	TVD	NIL	LA3192
Ms-48	--	Male-sterile-48		N*	CHEM	VF36	NIL	LA3191
Ms-48	--	Male-sterile-48		N*	CHEM	CSM	IL	2-839
Ms-48	--	Male-sterile-48		N*	CHEM	T338	NIL	LA3195
ms-49	--	male-sterile-49		N*	SPON	per	NON	LA1161
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	AC	NIL	LA3746
neg	--	neglecta		H*DK	RAD	CR	IL	LA0562
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	AC	NIL	LA3770
nor	--	non-ripening		P*	SPON	X	NON	LA1793
nor	--	non-ripening		P*	SPON	RU	NIL	LA3013
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	X	NON	LA0786
o	--	ovate		O*	SPON	AC	NIL	LA3543
O	1	Oval	*ol*	O*	SPON	X	NON	LA0271

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
ob	--	obscura	T*K	RAD	RR	IL	LA0691	
obl	--	oblate fruit		O*	RAD	MM	NIL	LA1159
oc	--	ochroleuca		G*BK	RAD	RR	IL	LA0692
Od	--	Odorless		K*	SPON	PCV	NON	LA0292
og	--	old gold		L*P	SPON	PSN	NIL	LA0348
og	--	old gold		L*P	SPON	chi	NON	LA0294
og	--	old gold		L*P	SPON	unk	NON	LA0500
og	c	old gold	*Crn,Cr,crn-2,cr-*	P*L	SPON	AC	NIL	LA3179
og	c	old gold	*Crn,Cr,crn-2,cr-*	P*L	SPON	PCV	NON	LA0806
oli	--	olivacea		--	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 syndrome	*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
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 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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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*I	SPON	AC	NIL	LA3089
Pn	--	Punctate		A*I	SPON	X	NON	LA0812
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	AC	NIL	LA2925
pr	--	propeller		J*	RAD	X	NON	LA0326
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
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

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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*	SPON	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
ps-2	--	positional sterile-2		L*N	SPON	STR24	IL	LA3632
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	X	NON	LA1017
ptb	--	protuberant		O*	SPON	X	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
pum	--	pumila		K*	RAD	AC	NIL	LA3741
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	X	NON	LA2531A
r	(2s)	yellow flesh	*r:3, r-2, r2*	P*	RAD	RR	IL	LA2056
r	--	yellow flesh		P*	SPON	RU	NIL	LA2997

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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	AC	NIL	LA3756
res	--	restricta	*res1*	C*ADJK	RAD	RR	IL	LA1085
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	RU	NIL	LA3012
rin	--	ripening inhibitor		P*	SPON	AC	NIL	LA3754
rin	--	ripening inhibitor		P*	SPON	X	NON	LA1795
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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
sd	--	sundwarf		K*	SPON	X	NON	LA0015
sd	--	sundwarf		K*	SPON	AC	NIL	LA3182
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
si	--	sinuata		E*JK	RAD	AC	NIL	LA3728B
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	--	stamenless		L*N	SPON	AC	NIL	LA3816
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
sph	--	sphaerica		K*T	RAD	AC	NIL	LA3744
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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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
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	X	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	X	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	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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
tr	--	truncate	*tr1*	D*CJK	RAD	CR	IL	LA0710
tri	--	temporarily red light insensitive		--		GT	IL	LA3808
trs	--	tristis		J*	CHEM		NON	3-057
Ty-1	--	TYLCV resistance		Q*	SPON	X	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	AC	NIL	LA2936
uf	--	uniflora		M*	SPON	PTN	IL	LA1200
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
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	AC	NIL	LA3185
v-2	--	virescent-2	*v2*	F*D	SPON	X	NON	LA2465
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 VF	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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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
Wa	--	white anthers		L*	SPON	VF36	NIL	LA3906
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
wv-3	--	white virescent-3		F*B	SPON	X	NON	LA1432
x	--	gametophytic factor		N*	SPON	X	NON	LA2348
Xa	--	Xanthophyllic		C*	SPON	AC	NIL	LA3579
Xa	--	Xanthophyllic		C*	SPON	X	NON	LA2470
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	AC	NIL	LA3551
yg-2	--	yellow-green-2	*yc, yg282, yg2*	E*	RAD	KK	IL	LA2469A
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-5	--	yellow-green-5	*yw, yg388, yg5*	E*	RAD	AC	NIL	LA2928A
yg-5	--	yellow-green-5	*yw, yg388, yg5*	E*	RAD	AC	NIL	LA2928B
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

GENE	ALLELE	NAME	SYNONYM	CLASS	SOURCE	BACK	ISO	ACC#
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

CLASS	DESCRIPTION
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 modifications: augmentation, reduction, distortion, elimination
J	Leaf form and size
K	Plant habit and size
L	Flower form and color
M	Inflorescence (exclusive of L)
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

BACK	GENOTYPE	ACC#
6203	FM6203	
AC	Ailsa Craig	LA2838A
Ace	Ace	LA0516
ALA	Alabama	
AMB	Antimold-B	LA3244
ANU	Anahu	LA3143
BK	Budai Korai	
BOD	Break O'Day	LA1499
C28	Campbell 28	LA3317
cer	L. esc. var.	
CG	Chico Grande	LA3121
che	L. cheesmanii	
chi	L. chilense	
chm	L. chmielewskii	
CR	Condine Red	LA0533
CRGL	Craigella	LA3247
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	Flora-Dade	LA3242
GRD	Gardener	LA3030
GSM	Gulf State Market	LA3231
H100	Hunt 100	LA3144
hir	L. hirsutum	
HSD	Homestead 24	LA3237
JBR	John Baer	LA1089
KK	Kokomo	LA3240
LGPL	Large Plum	
LK	Laketa	LA0505
LRD	Long Red	LA3232
LU	Lukullus	LA0534
lyc	S. lycopersicoides	
M167	Montfavet 167	LA2713
M168	Montfavet 168	LA2714

MD	Marmande	LA1504
MGB	Marglobe	LA0502
MM	Moneymaker	LA2706
MNB	Monalbo	LA2818
MP	Manapal	LA2451
MR20	UC-MR20	LA2937
N28	UC-N28	LA2938
NRT	Norton	
OGA	Ohio Globe A	LA1088
OHO	Ohio 8245	
ONT	Ontario	
par	L. parviflorum	
PCV	Primitive Cultivar	
pen	L. pennellii	
per	L. peruvianum	
pim	L. pimpinellifolium	
PLB	Pieralbo	
POR	Porphyre	LA2715
PRI	Primabel	LA3903
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
spVCH	VFNT Cherry (sp)	LA2705
SPZ	San Pancrazio	
STD	Stokesdale	LA1091
STN	Stone	LA1506
STR24	Start 24	LA3632
SX	Sioux	LA3234
T-5	T-5	LA2399
T338	UC-T338	LA2939
TGR	Targinnie Red	LA3230
TR44	UC-TR44	LA2940

TR51	UC-TR51	LA2941
TVD	Vendor (Tm-2a)	LA2968
UC82	UC-82B	LA3772
VCH	VFNT Cherry	LA1221
VD	Vendor	LA3122
VE	Van's Early	
VF11	VF-11	LA0744
VF145	VF-145 78-79	LA1222
VF36	VF-36	LA0490
VFN8	VFN-8	LA1022
VGB	Vagabond	LA3246
VRB	Vrbikanske nizke	LA3630
VTG	Vantage	LA3905
WA	Walter	LA3465
X	Unknown or hybrid	
XLP	XL Pearson	

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