

Report of the Tomato Genetics Cooperative Number 55 – October 2005

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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 Tomato Genetics Cooperative 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 or tissue culture. Relevant work on other Solanaceous species is encouraged as well.

Paid memberships currently stand at approximately 120 from 25 countries. Requests for membership (per year) US \$15 to addresses in the US and US \$20 if shipped to addresses outside of the United States--should be sent to Dr. J.W. Scott, jwsc@ifas.ufl.edu (see address information in Announcements section.) Please send only checks or money orders. Make checks payable to the **University of Florida**. We are sorry but we are **NOT** able to accept cash or credit cards.

Cover Figure of chromosome 1 of tomato based on molecular markers that are polymorphic between two genotypes of cultivated tomato. Genomic markers for use in intraspecific crosses are being developed as the landscape of tomato breeding is rapidly changing. The possible role of the TGC in serving as a conduit for “translational” research to the user community is discussed in a feature article by David Francis who is participating in efforts to organize translational genomics in the *Solanaceae*.
- J.W. Scott

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From the editor

Greetings to the TGC membership from your Managing Editor at our new research center. We moved in last February. Last year I gave you an address for the center but afterwards the post office changed the address. My correct address and contact information is:

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This year's report is being mailed to you about five weeks late. Let's blame it on the move. Please accept my apologies and I hope we will be mailing next year's volume out in mid-September as we've done the last several years.

Gail Somodi continues to do most of the work keeping the TGC operation organized. John Petti is our webmaster who has been very busy with one of our major goals to get all the reports on the web and searchable by keyword using the Google search engine. Gail Somodi and Rosa Ayala have been assisting him with this detailed and omnipresent task. We hope to have all volumes searchable by the end of 2005. There is a lot of good information in the TGC so check the "Online volumes" section of our website <http://tgc.ifas.ufl.edu/> **[Note: this address has changed from last year]** to search topics of interest. You can also access all except the latest volume online (or will be able to do so shortly). The latest volume will be available one year after publication. Let us know (see my e-mail address above) of any problems you encounter so we can get them fixed.

We have a listserv of email addresses for TGC members, but when I used it in August I got a lot of failures due to incorrect addresses. If you did not receive a TGC email from me in August please send corrected email addresses so we can get you connected for our next email attempt. I promise not to spam you with too many but it is a good way to keep you informed.

Jay W. Scott
Managing Editor

UPCOMING MEETING**Tomato Breeders Roundtable and Tomato Quality Workshop, May 7-12, 2006, Tampa, FL, USA**

For registration information please contact:

Jay Scott
Address above
jwsc@ifas.ufl.edu
or

Jeff Brecht
Univ. of Florida
Horticultural Science Dept.
Gainesville, FL 32611-0690
jkb@ifas.ufl.edu

A website with meeting information is under construction but check later at:
<http://roundtable06.ifas.ufl.edu/>

GRANT OPPORTUNITY**USDA Funding for Tomato Germplasm Evaluation**

Funding will again be available from the USDA, ARS in FY 2006 for evaluation of tomato germplasm. Evaluation funding will be used on germplasm maintained in or destined for the National Plant Germplasm System (NPGS). Relevant NPGS germplasm includes the tomato collection maintained by USDA's Plant Genetic Resources Unit in Geneva, New York and the collection at the University of California, C.M. Rick Tomato Genetics Resource Center, Davis, California. Proposal guidelines are noted below.

All proposals will be evaluated on the need for evaluation data, national and/or regional interest in the problem, scientific soundness and feasibility of the proposal, the likelihood of success, germplasm to be screened, and the likelihood that data will be entered into NPGS databases and freely shared with the user community.

Proposals will be reviewed by the Tomato Crop Germplasm Committee (CGC) and applicable ad hoc reviewers and ranked in priority order for funding. Funding for successful proposals will be capped at \$15,000, so please plan accordingly.

The letter I received concerning this call stated, "All proposals will be evaluated according to the national need for evaluation data, the likelihood of success, and the likelihood that the data will be entered into GRIN and shared with the user community." Including this consideration should strengthen a proposal.

All proposals and CGC prioritization are forwarded to USDA for a final decision on funding. Multiple year projects are welcomed, but funding must be applied for each year and is subject to a progress review.

STANDARD EVALUATION PROPOSAL FORMAT FOR THE NPGS

- I. Project title, name, title, and e-mail address of evaluators.
- II. Significance of the proposal to U.S. agriculture.
- III. Outline of specific research to be conducted including the time frame involved—include the number of accessions to be evaluated
- IV. Funding requested, broken down item by item (**no overhead charges are permitted**).
- V. Personnel:
 - A. What type of personnel will be used to perform the research (e.g. ARS, state, industry scientist; postdoc; grad student, or other temporary help).
 - B. Where will the personnel work and under whose supervision.
- VI. Approximate resources contributed to the project by the cooperating institution (e.g. facilities, equipment, and funds for salaries).

Evaluation funding will be used on germplasm maintained in or destined for the National Plant Germplasm System (NPGS).

Evaluation proposals must be submitted through the Crop Germplasm Committee (CGC) for their approval. If more than one proposal is submitted, please rank them by priority. All proposals should follow the evaluation priorities established by the CGC.

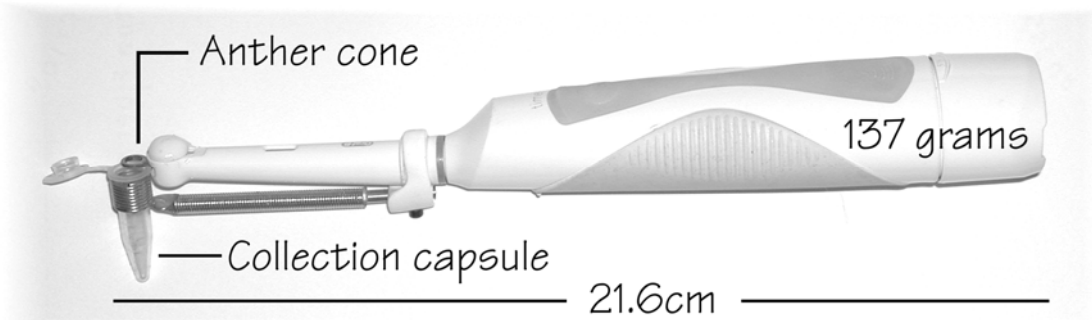
Evaluation data obtained will be according to CGC descriptors and codes and will be entered into GRIN by the crop curator. Funding for data entry into GRIN should be considered when developing proposals.

Evaluation proposals covering several descriptors, such as several diseases, should give the cost and time frame for each descriptor along with the combined cost. Funding may only be available to cover one of the traits to be evaluated.

PLEASE NOTE: Submission deadline: **November 30, 2005**. Electronic submission of proposals is encouraged. I can handle most word processing packages, at least through conversion. Please submit electronic files (PDF) to David M. Francis, Chair Elect of the Tomato Crop Germplasm Committee: francis.77@osu.edu.

DO YOU NEED A TOMATO POLLEN COLLECTOR?

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Total operating weight including 2 size AA DC batteries and a 0.5 ml disposable microfuge tube for pollen collection is ONLY 137 grams. A stainless steel loop protrudes from the working end of the TPB. Simply guide it through the foliage to a cluster of flowers and slip the loop around an anther cone. Gentle pressure on a conveniently-located water-tight rubber switch pad sets the loop in motion, shaking the flower gently but briskly at approximately 30 cycles per second. Usually, one hand is all you need to operate the device. The tube is held stationary by springs, isolating it from vibration so pollen falls into the tube and stays there! The TPB is constructed from plastic, rubber, and stainless steel so it is able to stand up to the harshest of field and greenhouse conditions. To learn more about the TPB or have one constructed for you, email johnmpetti@aol.com.

Translational Genomics and the *Solanaceae*

David Francis

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With several plant genome sequencing efforts complete, and tomato and potato genome sequencing efforts underway, there is reason to be optimistic that new information will benefit crop improvement efforts in the *Solanaceae* in general and tomato in particular. Large-scale genome sequencing projects are changing the fundamental organization of biological research. In plant science, new initiatives are emphasizing “translational genomics”. The word “translational” is borrowed from medical research in which it is understood to refer to the use of basic knowledge for applied outcomes, as in the “the process of translating discoveries in the laboratory into clinical interventions” (Minna and Gazdar, 1996 *Nature Med.* 2:974-975). Therefore, “translational genomics” implies the adaptation of information derived from genome technologies for crop improvement. Changes in research funding patterns necessitate a reexamination of traditional organizational frameworks and established institutions such as the Report of the Tomato Genetics Cooperative. While biological research has been revolutionized by genome sequencing efforts and allied technology (“Genomics”), agricultural research is undergoing a consolidation of commodity-focused research. Given these changes, we should ask “what role will the Report of the Tomato Genetics Cooperative play in future genome-based research efforts?”

Recent meetings highlight a need for applied scientists working on tomato genetics and breeding to consider organizational models that facilitate the application of genome technologies for applied goals. These meetings emphasize both the promise of new technology and the obstacles faced by plant breeders who hope to apply the results of genome sequencing projects to crop improvement. At the July 2005 ASHS meetings in Las Vegas, a workshop “Translational Genomics of Vegetable Crops” sponsored by the Vegetable Breeding Working Group was held. The purpose of the workshop was to raise awareness of translational research in the vegetable crops through an overview of current genome projects in the *Solanaceae* (<http://www.sgn.cornell.edu/>) and *Compositae* (<http://cpgdb.ucdavis.edu/>) and translational research for marker development, germplasm curation, and breeding. Following formal presentations a group discussion was held to initiate organizational efforts that may boost translational research in vegetable crops in general, and the *Solanaceae* in particular.

Several themes emerged during the course of the ASHS workshop discussion that are worth highlighting. First, “translational” research that makes use of genome sequencing information requires that we think about agricultural research from the point of view of taxonomic groups and DNA sequence homology rather than traditional commodity boundaries. To maximize the use of resources, a research community must be willing to work beyond traditional commodity divisions. Second, access to technology is limited by financial resources and remains a primary limitation in applying genome sequence data to crop improvement in vegetable crops. Resources are limited for the development of populations, the collection of meaningful phenotypic data, and

genotyping populations for selection. Third, there remains a paucity of markers that can be applied to most breeding populations. Although the role of protein and DNA-based molecular markers has long been established for selection and introgression, research has often focused on wide crosses and thus the available markers are tailored for this use. Even as we make dramatic progress in sequencing the tomato genome, there remains an insufficient number of polymorphic markers for application to intraspecific crop improvement efforts. Finally, in organizing and planning for large community-based efforts in translational genomics there must be a balance between achieving general goals and allowing sufficient resources to accomplish specific goals. For example, an effort coordinated around a general trait-based theme such as improving nutritional value would need to remain flexible enough to accommodate nutritional traits specific to individual crops. An effort that aimed to develop DNA-based markers that serve the need of multiple commodities must also meet the needs of individual market niches and breeding programs. A major research effort that helps discover polymorphic markers across species and within relevant germplasm pools appears to be emerging as a primary goal. Cost may be lowered and access to technology may be improved if the community can develop both a plan and infrastructure to share common reagents such as primers, DNA for a common panel of varieties, and other genotyping reagents. Information sharing that involves the collection of data in a common format and the development of tools that increase accessibility and ease of viewing will further strengthen research efforts and reduce duplication.

Models for organizing translational research are now emerging. The USDA/NRI Coordinated Agricultural Project (CAP) program offers one template. The applied plant genomics CAPs were initiated to bring together scientists and stakeholders with a shared vision and plan to facilitate translation of basic discoveries and technology. The goal is to create an inclusive community consisting of applied and basic, private and public researchers combined with participation of commodity groups, growers, and end users (http://www.csrees.usda.gov/funding/rfas/nri_applied_plant_genomics_cap.html). To maximize the use of resources, a research community must be willing to work beyond traditional divisions. It is unclear, however, where the new divisions should be established. A family based CAP focused on the *Solanaceae* would include potato, tomato, pepper, eggplant, and petunia. At the same time, there are advocates for a larger focus. For example, the "Asterid I" clade would include *Solanaceae* and *Rubiaceae* (including coffee) among other economically important plants. History has not supported the ability of such broad based efforts to organize for translational research. The first CAP was funded for rice in 2004. Other CAP planning efforts have not been able to transcend traditional divisions, perhaps due to resource limitation or due to unique needs for each commodity, and previous CAP planning efforts have reduced to single species. A major hurdle in developing an organizational structure that spans taxonomic groups will be the development of resources that serve a general need while providing capital to address individual needs. In the U.S., follow up meetings for a *Solanaceae* CAP (SolCAP) are scheduled for November 15, in Davis, CA, January at the Plant and Animal Genome Conference in San Diego, CA, and July 2006 at the Third *Solanaceae* Genome Workshop in Madison, Wisconsin.

As U.S. efforts develop, the European Union has launched an ambitious project focused on the *Solanaceae*. At the Second *Solanaceae* Genome Workshop held in

Ischia, Italy September 25-29, 2005, Dr. Willem Stiekema described the organizational structure of the European *Solanaceae* (EuSol) project, a 19 M Euro effort that emphasizes both tomato and potato. This large integrated effort is organized around three trait-based modules (organoleptic traits, health-based traits, and producer-processor traits). Modules focused on genetic resources, technology platforms and bioinformatics are integrated with the trait-based research efforts. Modules devoted to coordination and technology transfer complete the organizational model.

The following recommendations for organizing the tomato community follow from these models:

- Seek partners from other commodity groups in the *Solanaceae* and organize around taxonomic groups and DNA sequence homology rather than traditional commodity boundaries.
- Reduce duplication, both by dividing the workload and improving information exchange, in order to help leverage scarce resources and build community resources.
- Develop flexible tools that comprehensively sample variation in breeding populations including a core set of markers for use as anchors across species.
- Develop common panels of germplasm for screening new markers across and within species.
- Create bioinformatic platforms that allow access, updating, and sharing of data and information among all researchers in the community.
- Curate marker data in a common format so that database tables can be shared and expanded.
- Adopt trait-ontology approaches for the collection of phenotypic data in standardized formats and promote the development of phenotypic databases.

Given these recommendations, is there a role for the Report of the Tomato Genetics Cooperative to play in future genome-based research efforts? The issue of declining and or consolidating resources for the type of applied science reported in the TGC may lead to some pessimism about the future of the applied community. This pessimism is only warranted if we fail to learn from the emergence of genomic sciences and fail to recognize traditional strengths of the applied community and the TGC. There are reasons for applied researchers to be optimistic about the ability of traditional breeding to assimilate into these new models and to absorb the tools and information developed through genome sequencing efforts. We can recognize several fundamental changes that the “-omics” sciences have brought to biological research that are traditional strengths of plant breeding programs. The development and application of efficient assays to facilitate high throughput data collection (often referred to as “pipelines”) has been a part of traditional selection practices for some time. A difference between this activity, as conducted in breeding programs, and the parallel activity in genome sequencing projects has been the willingness to archive data in public databases open to all. As genome efforts gravitate to translational projects, the data generated by the applied community represents a resource. Our challenge is to adopt standard germplasm controls, standard data collection practices, and to identify resources for the collection and archiving of data in accessible databases. The publication of genetic data, tables of germplasm, and communication with the

research community are areas of traditional strengths for the Report of the Tomato Genetics Cooperative. In the future one role of the TGC may be as an applied conduit for genomics output. The TGC's efforts to make past and future volumes available and searchable through the website <http://tgc.ifas.ufl.edu/> , will provide a database (or links) to facilitate the sharing and use of translational resources as outlined above.

TGR4, a novel tomato centromere-specific retrotransposon

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Centromeres are sites on chromosomes where spindle microtubules attach to move chromosomes in mitosis and meiosis. In plants, centromere-specific DNA sequences consist of tandem repeats 150-180 bp in length and Ty3-Gypsy type long terminal repeat (LTR) retrotransposons (Jiang et al. 2003). In spite of the conserved nature of centromere function, the sequence of centromere repeats varies between different plant groups. Here we report a new Ty3-Gypsy type retrotransposon called TGR4 that is found exclusively in the centromeres of all tomato (*Solanum lycopersicum*) chromosomes. Fig. 1a illustrates fluorescent *in situ* hybridization (FISH) using TGR4 as a probe on a spread of the twelve tomato pachytene bivalents. The signals at the centromeres vary in brightness, implying differing numbers of the TGR4 sequence on different chromosomes.

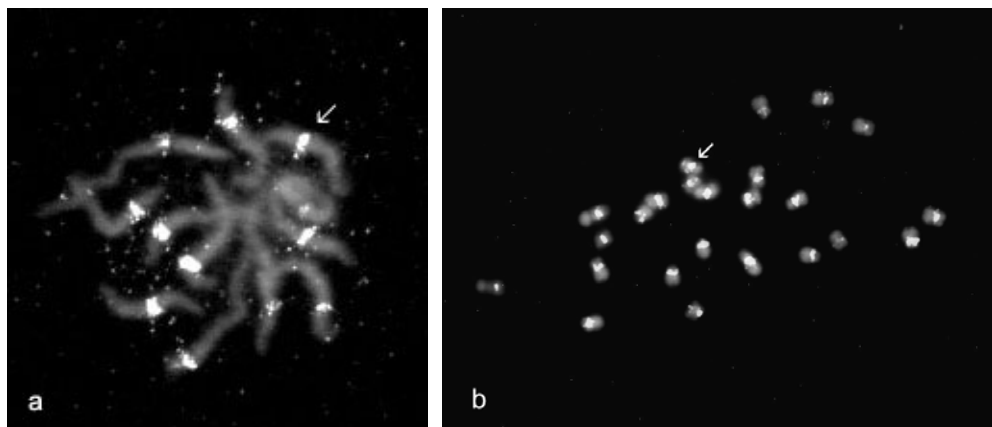


Figure 1. TGR4 loci after FISH (e.g., arrows) on (a) tomato (*Solanum lycopersicum* VFNT pachytene chromosomes and on (b) metaphase chromosomes of *S. chilense*.

When TGR4 is used as a probe for FISH on metaphase chromosome spreads from other solanaceous species, hybridization occurred exclusively at centromeres in members of the section Lycopersicon (Fig. 1b, Fig. 2). More distantly related solanaceous species, including *S. tuberosum*, showed no hybridization, suggesting that TGR4 arose in the common ancestor of the section Lycopersicon.

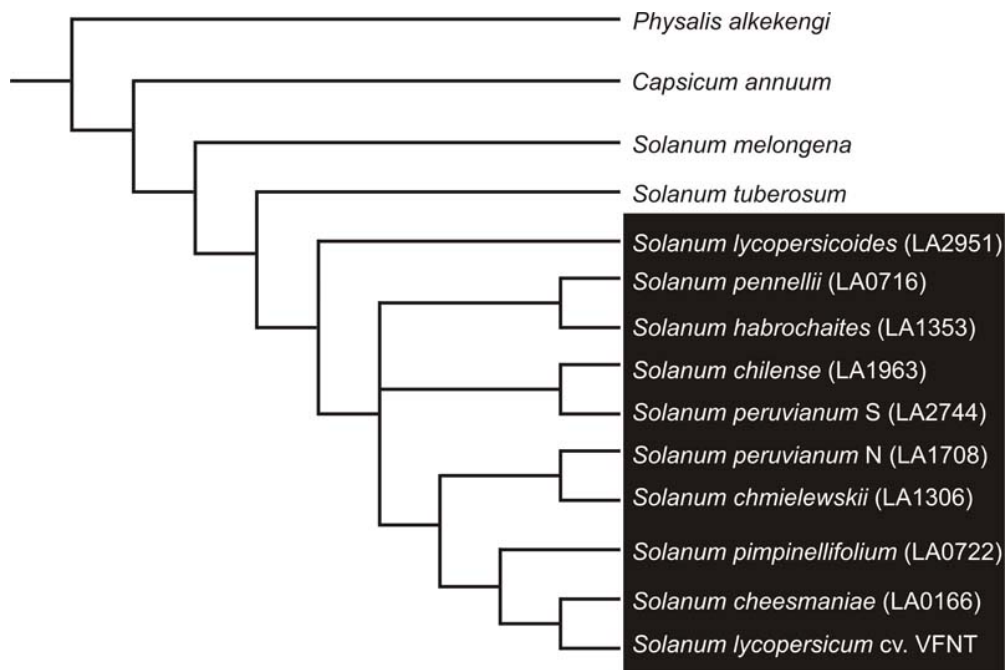


Figure 2. A combined phylogenetic tree based on Bohs and Olmstead, (1997) and Spooner *et al.* (2005). Among the species investigated above, the TGR4 centromere-specific retrotransposon is confined to the section *Lycopersicon* (black box).

Acknowledgements. Seeds were supplied by the Tomato Genetics Resource Center (TGRC) at the University of California at Davis. This research was supported by NSF grant DBI-0421634

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- Spooner D.M., Peralta I.E., and Knapp S. (2005) Comparison of AFLPs with other markers for phylogenetic inference in wild tomatoes [*Solanum* L. section *Lycopersicon* (Mill.) Wettst.]. *Taxon* 54:43-61.

Preliminary evaluation of LA1777 introgression lines for early blight resistance

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AVRDC-The World Vegetable Center, P.O. Box 42, Shanhua, Tainan 74151, Taiwan

Introduction

Early blight (EB) caused by *Alternaria solani*, is a serious disease of tomato in the tropics, particularly the mid-altitude areas of South Asia and southern and eastern sub-Saharan Africa. Defoliation and fruit lesions due to EB often lead to severe yield reductions, and fungicide costs for disease control can be prohibitive for small-scale farmers. High levels of EB resistance have been found in some accessions of *Lycopersicon hirsutum* (*Solanum habrochaites*) (Nash and Gardner, 1988; Foolad *et al.*, 2002). Using a growth room seedling screening technique, high levels of EB resistance were identified in *L. hirsutum* accession LA1777. LA1777 was also the donor parent of the *L. hirsutum* introgression line (IL) population developed by Monforte and Tanksley (2000) and made available through the TGRC. The objective of this study was to evaluate LA1777 ILs for EB resistance.

Materials and Methods

Two growth room EB experiments were conducted at AVRDC in 2004. Entries in the first experiment included 90 *L. hirsutum* ILs listed on pages 75-77 of TGC report 50 (2000), and parents of the IL population: LA1777 and E6203 (LA4024). Twenty ILs demonstrating relatively higher resistance in the first experiment were tested in a second experiment. In both experiments 10-12 plants per entry were evaluated. Foliar inoculation with a 2.5×10^4 conidia/ml suspension of pathogen isolate *A. solani*-1 from Taiwan was carried out on thirty-day-old plants. Plants were maintained at $23 \pm 1^\circ\text{C}$ and scored for disease severity rating (DSR) seven days after inoculation on the following scale: 0=no symptoms; 1=very few lesions per plant; 2=about 5 lesions per plant; 3=numerous lesions per leaf; 4=numerous lesions per leaf, coalescing lesions and leaf collapse. Data were analyzed according to a RCBD with experiments as replications.

LA1777 introgressions are defined by RFLP markers. Many PCR based tomato markers have been developed and mapped, and are publicly available from a variety of sources (*e.g.*, <http://www.sgn.cornell.edu/>, <http://hornbill.cspp.latrobe.edu.au/ssrdiscovery.html>). These resources enabled screening a set of genome-wide markers to identify polymorphic markers distinguishing LA1777 and LA4024. If the markers were informative, they were then screened on the ILs to delineate introgressed regions.

Results and Discussion

All entries in both experiments developed lesions although differences in DSR were evident. Mean DSR of most ILs in experiment 1 exceeded 3.7 and were dropped from experiment 2. None of the ILs demonstrated resistance comparable to LA1777 with a DSR of 1.0 (Table 1). Among IL, LA3913, LA3914, LA3916 and LA3970, all

with *L. hirsutum* introgressions on chromosome 1, and LA3922, LA3923, LA3924, and LA3971 and with *L. hirsutum* introgressions on chromosome 2 displayed partial EB resistance; however, variability in DSR scores within each of the above IL was apparent.

EB resistance in LA1777 is multigenic like that of *L. hirsutum* PI126445 (Foolad *et al.*, 2004). It is likely that EB QTL from LA1777 are located on chromosome 1 between TG607 and TG17, and chromosome 2 between TG353 and TG620 (Figure 1). Foolad *et al.* (2004) also mapped EB QTL on chromosomes 1 and 2 in the same region. However, IL with introgressions on chromosome 9 in our experiment showed no resistance while Foolad (2004) found a large EB QTL on chromosome 9 and additional QTLs on chromosomes 3, 5, 10, 11, and 12.

Several colleagues in India have agreed to evaluate resistant ILs and checks for reaction to local pathogen isolates. At AVRDC we intend to re-screen the resistant ILs and select the most resistant plants within ILs to determine if within-IL variability can be reduced. We will design and make crosses to combine chromosome 1 and 2 introgressions and determine if combining QTL improves resistance, and marker-assisted selection will aid this breeding objective.

LITERATURE CITED

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- Nash, A.F. and Gardner, R.G. 1988. Heritability of tomato early blight resistance derived from *Lycopersicon hirsutum* P.I. 126445. *J. Amer. Soc. Hort. Sci.* 113: 264-268.
- Tomato Genetics Cooperative. 2000. *L. hirsutum* introgression lines. TGC Rpt. 50: 75-77.

Table 1. Reactions of *L. hirsutum* introgression lines and parents to *Alternaria solani*, sorted by overall disease severity rating (DSR), AVRDC, 2004.

Entry	Chrom ¹	Experiment I					Experiment II					Overall			
		DSR ²					DSR					Mean	LSD ³		
		0	1	2	3	4	Mean	0	1	2	3	4	Mean		
LA1777		10					1.0	10					1.0	1.0	A
LA3922	2				6	5	3.5			9	3		2.3	2.9	B
LA3913	1				10	2	3.2			4	7	1	2.8	3.0	Bc
LA3914	1				7	4	3.4			5	5	2	2.8	3.1	Bcd
LA3941	5				10	2	3.2			1	9	1	3.0	3.1	Bcd
LA3923	2				10	2	3.2			2	7	3	3.1	3.1	Bcd
LA3929	3,8				5	7	3.6			6	4	2	2.7	3.1	Bcd
LA3970	1				7	5	3.4			1	7	4	3.3	3.3	bcde
LA3916	1				5	7	3.6			1	8	3	3.2	3.4	bcde
LA3924	2				5	7	3.6			2	5	5	3.3	3.4	bcde
LA3971	1				5	7	3.6			1	6	5	3.3		
														3.5	Cde
LA3972	2				6	6	3.5				3	9	3.8		
														3.6	De
LA3915	1				4	8	3.7				4	8	3.7		
														3.7	E
LA4024 (E6203)					3	9	3.8				5	7	3.6		
														3.7	E

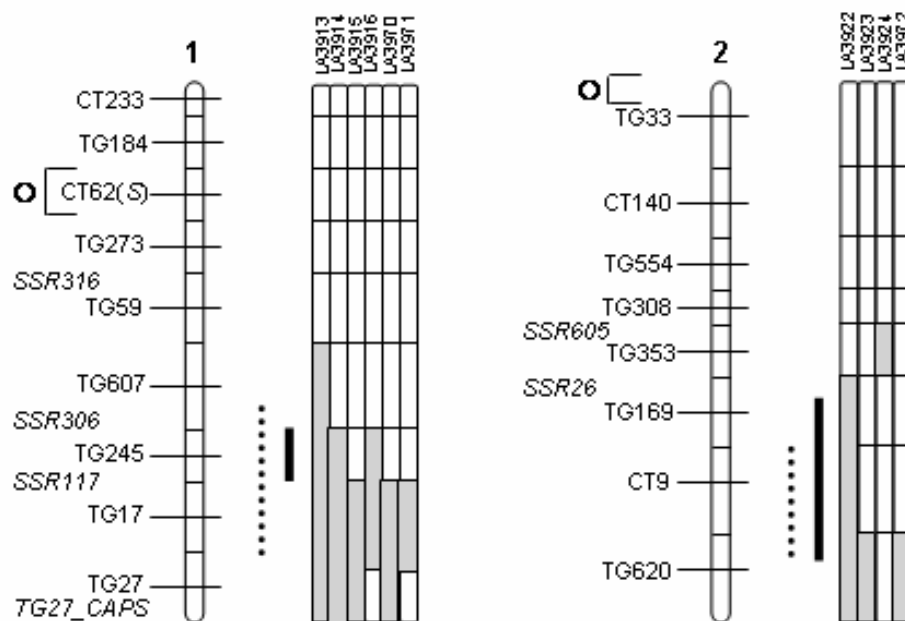
¹ Chrom is the chromosome containing the region introgressed from *L. hirsutum*

LA1777

² DSR: 0=no symptoms; 1=very few lesions per plant; 2=about 5 lesions per plant; 3=numerous lesions per leaf; 4=numerous lesions per leaf, coalescing lesions and leaf collapse

³ Mean separation by least significant difference at P=0.05.

Figure 1. Chromosomes 1 and 2 depicting *L. hirsutum* introgressions and putative EB QTL. RFLP markers next to the chromosomes delineate introgressions, SSR and CAPS markers offset in italics are PCR based markers that can be used to differentiate ILs. Putative EB QTL are indicated to the right of the chromosomes by dashed line (Foolad *et al.*), and solid line (AVRDC). The shaded bars to the far right of the chromosomes show individual introgressions.



Obtaining and characterization of interspecific hybrids *Lycopersicon esculentum* x *L. peruvianum* via embryo callus

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Lycopersicon peruvianum is a highly polymorphic, allogamous species and an abundant source of valuable genetic traits for tomato improvement – disease resistance, drought and salt tolerance, and high ascorbic acid levels in fruits (Doganlar et al., 1997). *L. peruvianum* comparatively rarely is included in a tomato breeding program because of crossability barriers with *L. esculentum* (Rick, 1979b). One of the ways of overcoming this incompatibility is *in vitro* plant regeneration from embryo callus (Thomas and Pratt, 1981, Cap et al., 1991, Demirel and Seniz, 1997).

Our purpose with this experimental work is obtaining F₁ hybrids between lines and cultivars of *L. esculentum* and accessions of *L. peruvianum* by embryo callus culture technique.

Material and methods

Plants from four accessions of *L. peruvianum* (№ 894750110, 894750235, 894750236 and 894750238) obtained from the botanical garden to the University of Nijmegen – The Netherlands, line №177 and variety Ideal of *L. esculentum* were grown under greenhouse conditions for the purposes of hybridization. *L. peruvianum* accessions were used as male parents for the crosses. Pollinations were made on newly emasculated buds, between 8 am and 12 noon. Fruits were harvested between 30 to 40 days after pollination and surface sterilized in 5% NaOCl. The excised embryos were cultivated on medium with macro- and microelements by Murashige and Skoog (1962) (MS), Gamborg et al., (1968) vitamins, 40 mg/l Glycine, 2.2 mg/l BAP, 1.6 mg/l IAA 20 g/l Sucrose, 0.7 % Agar and pH=5.8 before autoclaving. Petri dishes with embryos were incubated in growth chamber at 25°C ± 1°C, around 4000 lux and 16/8 h day/night. After the callus induction each explant with d=1.0-2.0cm were transferred on MS regeneration medium with 2 mg/l BAP and 0.2 mg/l IAA. Plant-regenerants were rooted on MS medium without growth regulators.

Results and Discussion

Fruits with embryos were obtained in early developing stage – torpedo shape from the crosses among the all parents. There weren't embryos in later developing – heart-shaped stage more often developing to the regenerants. The data in the Table 1 prove that fruits are formed in all eight hybrid combinations, but the embryos turned brown and died. In the period of 40 – 50 days after explantating of the 146 undeveloped embryos from the combination 177 x 894750235 callusogenesis was established in only 3 hybrid embryos, or in 2.05%. Twenty-one regenerants developed – one from the first, eight from the second and twelve from the third callus clone, respectively initiated from the 3 different embryos. The morphological

characteristics of the plants prove their hybrid origin – all of them possess the characteristics from the two parents. They were indeterminate, vigorous and with gray-green leaves with the exception of one plant formed in the third callus clone. This plant differs from the others mainly by very light green color of the leaves, slow vegetative growth and small size compared to the other plants. This could be attributed to the process of *in vitro* induced variation because of the regeneration by callus culture and the response of specific embryonic tissue to the culture conditions. Embryo callus culture gives an additional opportunity for broadening of the diversity in case of interspecific hybridization.

Table 1. Results of *in vitro* cultivation of hybrid embryos
L. esculentum x *L. peruvianum*

Genotype	Cultured embryos No.	Callusing via embryo culture		Obtained plants No.
		No.	%	
177 x 894750110	20	0	0.00	0
177 x 894750235	146	3	2.05	21
177 x 894750236	142	0	0.00	0
177 x 894750238	292	0	0.00	0
Ideal x 894750110	169	0	0.00	0
Ideal x 894750235	25	0	0.00	0
Ideal x 894750236	138	0	0.00	0
Ideal x 894750238	57	0	0.00	0
Total	989	3	0.30	21

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Development of tomato lines and hybrid F₁ varieties with complex resistance to viruses

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Cucumber mosaic (cucumovirus-CMV), tomato mosaic (tobamovirus-ToMV) and tomato spotted wilt (tospovirus-TSWV) are economically important plant viruses causing diseases of tomato crops in Bulgaria. These viruses cause significant losses of yield and quality in tomatoes in all production areas of Bulgaria.

Wild *Lycopersicon spp.* have gradually increased their importance as a source of genetic variability for tomato improvement. *L. peruvianum* and *L. chilense* are rich in gene resistance. Virus resistance has been reported in accessions of *L. peruvianum* and *L. chilense* (Maluf et al., 1991, Stamova et al., 1998)

The objective of our study was to develop direct and hybrid F₁ tomato varieties, resistant to economically important viruses.

Our work started with interspecific complex hybrids – { BC₃P₁ (cv. Merkury x *L. peruvianum* LA 462) x BC₃P₁ (cv. Merkury x *L. chilense* LA 1958)}. Plants were maintained in a growth chamber with a 14 h light cycle (25° C/ 18° C) and high relative humidity. The primary complex hybrid and lines were tested for resistance to ToMV, CMV and TSWV. ToMV inoculum was in 1:50(w/v) in water, CMV and TSWV - were 1:5(w/v) in cold 0.1M phosphate buffer pH=7 containing 0.5% sodium sulfite, 0.2% sodium diethyldithiocarbamate and 2% PVP. Inoculation was performed 3 times at 10 day intervals on about 20 plants per genotype, and on 10 positive and negative controls. Plants were scored visually for virus symptoms and those without symptoms were tested using ELISA (Clark and Adams, 1977) after 20 days post inoculation.

Results

Interspecies complex hybrid – {BC₃P₁(cv. Merkury x *L. peruvianum* LA 462) x BC₃P₁(Merkury x *L. chilense* LA 1958)} was hybridized with cv. 382 and cv. Merkury. The cultivars with good economic properties were selected.

Results from analyses of some of the selected lines are presented in Tables 1-3. The lines № 5, 15, 14-15 were ToMV resistant, № 2, 4, 6 were ToMV & CMV resistant and line№ 8 was ToMV & TSWV resistant.

Future work involves evaluation of combining ability, economic value and virus resistance of four F₁ hybrids.

Table. 1 -3 Reaction of tested tomato lines to virus inoculation with ToMV, CMV and TSWV.**ToMV**

Lines /controls	Analyses in 2002		Analyses in 2004		
	Number of plants tested	Number of healthy	Number of Plants tested	Number of healthy plants	Absorbance values of ELISA
№ 5	0	0	20	20	0,132 ± 0,076
№ 9*	0	0	25	21	0,110 ± 0,052
№15	19	16	17	17	0,119 ± 0,061
№ 15-14	0	0	21	21	0,112 ± 0, 088
Drujba S+	20	0	25	0	0,780 ± 0,045
Rila R-	18	14	34	30	0,115 ± 0,062
Balkan R-	16	15	20	16	0,123 ± 0,056

ToMV-CMV

Lines/ controls	Test in 2002		Test in 2004			
	Number of plants tested	Number of healthy Plants	Number of plants tested	Number of healthy plants	Absorbance values of ELISA	
					ToMV	CMV
№ 4	20	16	23	20	0.148 ± 0,085	0,059 ± 0,025
№ 6	0	0	25	21	0,148 ± 0,067	0,044 ± 0,016
Drujba S+	20	0	15	0	0,985 ± 0.076	-
№6 injected S+					-	0,652 ± 0,072

ToMV-TSWV

Lines, controls	Test in 2002		Test in 2004			
	Number of plants tested	Number of healthy Plants	Number of plants tested	Number of healthy plants	Absorbance values of ELISA	
					ToMV	TSWV
№ 8	25	12	20	15	0.079 ± 0,004	0,035 ± 0,009
R480 R	-	-	25	25	-	0,034 ± 0,004
Drujba S+	20	0	15	0	0,982 ± 0,075	-
K +						0,703 ± 0,035
K -						0,049 ± 0,009

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Tomato lines resistant to races T1 and T3 of *Xanthomonas vesicatoria* in Bulgaria

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Bacterial spot, caused by *Xanthomonas vesicatoria*, is one of the most destructive pathogens of tomato in Bulgaria. Despite extensive investigations, the breeding for resistance of tomato to bacterial spot is difficult. There were no known commercial resistant cultivars (Scott et al., 1991). Probably, one of the difficulties is the differences in the natural populations of *X. vesicatoria* in the world.

The natural population of *X. vesicatoria* in Bulgaria belongs to two pathotypes tomato, T, and pepper-tomato, PT, pathotype and races T1 and T3 of tomato pathotype. Race T1 is occurring in the narrow breeding fields only, while race T3 is dominant in many tomato fields in Bulgaria (Bogatzevska and Sotirova, 2000). Results from resistance of tomato lines to races T1 and T3 in Bulgaria are reported in this communication.

Tomato plants were inoculated with races T1 and T3 by the vacuum infiltration method (Bogatzevska, 1988), in plants with 5-6 true leaves. Inoculated plants were evaluated on the 0-4 scale of Sotirova and Beleva (1975) as follows: 0-lack of symptoms; 1-1 to 10 spots; 2-11 to 20 spots; 3-21 to 50 spots and 4-more than 50 spots per plant. The hypersensitive reaction (HR) was also evaluated. A series of lines were tested for resistance to race T1 and T3 of *X. vesicatoria*.

Tomato lines with some resistance to race T1 are presented in Table 1. All lines possessed more resistance to T1 than very susceptible control plants (cv. Ideal). These lines were rated from 1.07 to 2.00. HR was not observed among a great number of lines. HR in lines 3587, 3427 and 3998 was manifested. Nevertheless, these lines had high disease ratings and were not as resistant as the other lines. Although these lines possessed some resistance to T1 such resistance does not promise to be effective for tomato breeding.

Lines 1704, 2649, 3189, 3457 and 5804 with rating 1.38, 1.07, 1.43, 1.33 and 1.17, respectively showed relative resistance in comparison with the other lines (Table 1). Further, the testing of the lines has to continue to better characterize their response to bacterial spot.

Resistance to T1 is not explained by HR only. For example, lines 1704 and 5804 possessed relative resistance without appearance of HR.

All lines with exception of 5104 and 5204 produced HR after infection with race T3. They were much more resistant than very susceptible control plants, cv. Ideal (Table 2). More than 50% of plants from lines 3818, 3928, 3998 and 5904 showed hypersensitive reaction. These lines were rated < 1 and were designated as lines with good resistance (Table 2). Line 3808 showed high HR and was mainly symptomless. This line possesses the highest level of resistance among all investigated lines.

All examined lines in both Tables 1 and 2 were obtained by hybridization with wild tomato species. They possessed various levels of resistance. Line 1704, resistant to T3 and relatively resistant to T1, was derived by intercrossing between cv. Roma x *Lycopersicon pimpinellifolium*. Lines 3638, 3808, 3818, 3898, 3968, 3998, 6104 resistant to T3, lines 4804, 5104, 6204 relatively resistant to T3 and lines 2649, 3189, 3457, 5804 relatively resistant to T1 were derived from a cross (*Isogenic line gf* x *L. chilense*) x *L. peruvianum* var. *humifusum* followed by selection procedure for T1 and

T3 resistance. Line 3928 was resistant to T3, while line 5904 was resistant to T3 and relatively resistant to T1. In both lines wild species *L. hirsutum* f. *glabratum* was used in hybridization.

Lines resistant to both races were not observed. Many resistant lines were obtained with the participation of *L. chilense* and *L. peruvianum* var. *humifusum*. These wild species appeared to be good sources for of resistance to different races of *X. vesicatoria*.

Finally, lines 1704, 2649, 3189, 3457, 3638, 3808, 3818, 3898, 3928, 3998, 5804 and 5904, are the most attractive in searching for resistance to bacterial spot in Bulgaria. Further, the investigation should be continued for selection of the lines with high level of resistance to race T1 and T3.

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Table.1-Tomato lines resistant to race T1.

Lines	HR	Disease Severity (No. plants)					Mean score
		0	1	2	3	4	
L. 1704	-	2	11	11	-	-	1.38
L. 2304			20	16			1.44
L. 2649	14	-	-	16	-	-	1.07
L. 3189	16	-	-	18	8	-	1.43
L. 3427	10	4	2	24	16	2	1.83
L. 3457	6	4	4	13	2	1	1.33
L. 3467	12	-	10	16	8	2	1.54
L. 3587	12	4	3	19	11	11	1.97
L. 3998	12	-	10	8	18	2	1.76
L. 5104	-	-	-	25	-	-	2.00
L. 5204	-	-	9	12	-	-	1.57
L. 5504	-	-	6	14	2	-	1.82
L. 5804	-	-	20	4	-	-	1.17
L. 5904	-	-	17	14	6	-	1.70
L. 6204	-	-	2	13	1	-	1.94
Ideal-control	-	-	-	5	15	31	3.51

Table.2-Tomato lines resistant to race T3.

Lines	HR	Disease Severity (No. plants)					Mean Score
		0	1	2	3	4	
L. 1704	4	8	11	3	-	-	0.65
L. 1804	2	3	12	6	-	-	1.04
L. 1904	4	-	9	7	1	-	1.24
L. 3638	16	6	2	20	-	-	0.95
L. 3728	16	2	-	16	6	-	1.25
L. 3808	18	11	1	-	-	-	0.03
L. 3818	20	2	4	4	-	-	0.40
L. 3838	14	4	4	28	-	-	1.20
L. 3898	12	1	5	12	-	-	0.97
L. 3928	22	-	2	16	2	-	0.95
L. 3958	14	-	2	10	3	1	1.17
L. 3968	15	-	4	10	1	1	1.00
L. 3998	24	-	2	12	2	-	0.80
L. 4804	5	-	7	8	1	-	1.24
L. 5104	-	5	5	10	-	-	1.25
L. 5204	-	-	2	14	-	-	1.88
L. 5404	9	-	3	6	-	-	0.83
L. 5604	2	-	4	12	-	-	1.56
L. 5904	11	-	5	3	-	-	0.58
L. 6104	6	-	10	6	-	-	1.00
L. 6204	5	-	6	9	-	-	1.20
Ideal-control	-	-	-	2	9	40	3.75

Generation of transgenic tomato plants producing chimeric protein TBI-HBsAg

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Introduction

Viruses of the human immunodeficiency (HIV) and of hepatitis B (HBV) are causative agents for very dangerous diseases.

One of the most important goals in the fighting HIV-infection is the creation of an effective vaccine. On the special United Nations General Assembly devoted to the strategy of fighting against AIDS, the conclusion was formulated about the necessity of the activation of efforts in the development of the vaccine against HIV (Declaration of Commitment on HIV/AIDS, 2001).

The approach of the traditional viral vaccines was based on killing a virus or its weakening ("attenuating") so that immune responses were elicited to the viral antigens without the virus itself causing disease. But it became increasingly apparent that an attenuated HIV vaccine was still associated with safety risks.

The preventive defense from the infection with HBV is possible only by means of the immunization.

Recently one of the most promising directions in the creation of new types of vaccines had become the development of "edible" vaccines on the basis of transgenic plants, in the genome of which the target gene is encoded for the synthesis of antigenic proteins of agents of infective diseases.

"Edible" vaccines have advantages compared to other types of vaccines because they are not so expensive and they can be maintained and transported without "cold chain". The immunization occurs during eating of fruits, seeds or leaves of plants that are without the risk of contagiousness inherent to injection vaccines. By eating of the edible vaccine as an food additive, antigen proteins react with the mucous surface of the gastrointestinal tract activating a mucous type of immune defense and as a result the synthesis of antibodies are proceeded against the corresponding infection agent (Streatfield *et al.* 2003).

Up to this time several types of transgenic plants have been successfully generated which were considered as "edible" vaccines against viruses of rabies, food-and-mouth disease, hepatitis B and others. Plant cell walls play the role of microcapsules for the antigen packed in this way and allow the passage of antigens through the gastrointestinal tract (Streatfield *et al.* 2003).

The goal of the present work was the generation of transgenic tomato plants with the introduced target chimeric gene encoding the synthesis of a chimeric protein TBI-HBS composed from antigenic determinants of protective proteins HIV-1 and HBV. So the synthetic gene TBI encoded the chimeric peptide of 372 amino acids

named **T** and **B** cell epitope containing **I**mmunogene (Eroshkin *et al.*1993). This long peptide was built in the special protein-carrier HBSAg.

The study included the creation of a hybrid molecular agrobacterial vector admissible for the genetic plant transformation, the introduction of this vector into explants of tomato, obtaining of regenerants, the selection of transgenic plants on a selective medium with kanamycin, the confirmation of the integration of the target gene TBI-HBS and finding specific antigens of HIV and HBV in fruits from transgenic tomato.

Materials and methods

Construction of plasmids for plant transformation

The plasmid pBINPLUS/ARS (kindly provided by Dr Bill Belknap, USA) was used as a molecular vector after the insertion of the gene *TBI-HBS* encoding the synthesis of chimeric polyepitopic immunogen – artificial protein TBI compiled from 9 antigenic determinants ENV and GAG of HIV-1 and fused with them in open reading frame of the main antigenic protein HBsAg of HBV (Eroshkin *et al.*1993).

The target gene in the created hybrid plasmid pBINp35STBI-HBS#15 was placed under the cauliflower mosaic virus promoter p35S (Figure 1) with the signal sequence of the cauliflower mosaic virus for the polyA site at 3' end. The target gene *TBI-HBS*, with the sequence encoding the neomycinphosphotransferase (NPTII) driven by the promoter of the gene ubiquitin *ubi3*, was bordered by RB and LB regions of T-DNA (Figure 1). This provided delivery inside the agrobacterial binary vector system and the integration of this vehicle into the genome of the plant. The accuracy of the structure of the created hybrid plasmid was checked by the restriction analysis and by the sequence of the target gene.

Plant transformation and propagation

Lycopersicon esculentum cv Ventura was used for transformation. Tomato seeds were sterilized with 5% of commercial bleach for 10 min and washed with sterile tap water several times, then placed on agar medium supplemented with ½ MS salts (Murashige and Scoog, 1962) without sucrose for germination (“germination medium”). Explants of tomato were obtained from 14-15 day old seedlings. The transformation was done by pricking a needle loaded with cells of *Agrobacterium tumefaciens* LBA4404 (pBINp35STBI-HBS#15) inside the wound surface after removing the apex.

After the transformation the infected explants were subcultivated *in vitro* during 15-20 days on MS medium supplemented with (in mg/l): thiamine – 10, kinetin – 0.05, gibberellin – 0.2, indole butyric acid – 0.1, phytigel – 3, with the addition of 50 mg/l kanamycin and 200 mg/l cefotaxime for a thorough selection (“selection medium”) and to get rid of any *Agrobacterium* contamination.

Similar seedlings without the infection with *Agrobacterium* were nontransformed controls.

Northern dot blot hybridization

Total RNA was extracted from leaves and fruits from control and transgenic tomato plants by general methods which involved the extraction of the guanidinium thiocyanate homogenate with phenol-chloroform at reduced pH. As a probe, the

RT-PCR product of the 742 bp fragment was used and labeled with ^{32}P - α -ATP by using the kit RediPrime™ Random Prime labeling system (Amersham Pharmacia Bioscience, England). For dot blot, 25 μg total RNA in 10 μl water solution was denatured in 6 μl 20x SSC and 4 μl 37% formaldehyde at 60°C for 15 min following cooling on ice. Denatured RNA samples were transferred onto Hybond N+ nylon membranes (Amersham Pharmacia Bioscience, England) and probed with labeled ^{32}P - α -ATP 742 bp fragment of the gene TBI-HBS overnight at 42°C. Blots were washed first with a solution of 1x SSC, 0.1 % (w/v) SDS preheated to appropriate temperature and then with second wash solution of 0.1x SSC, 0.1 % SDS and exposed to X-Omat AR film for 7 days or used for measuring of radioactivity in the scintillation counter.

RT-PCR analysis was performed with the total RNA isolated with the same guanidinium thiocyanate method from cells of *Agrobacterium tumefaciens* LBA4404 (pBINp35STBI-HBS#15) by using of primers: forward GCCCATCGAAATCAAAGATACC-3' and reverse 5'-CCCAAAGACAGAGAAAATTGG-3', which primed the synthesis of a fragment of the gene TBI-HBS of 742 bp in size. Ready-to-Go RT-PCR Beads kit (Amersham Biosciences, England) was used for the synthesis of DNA of appropriate size 742 bp for preparation of the probe.

The thermocycler profile was 5 min hot start at 94°C, followed by 32 cycles as at 94°C for 1 min; 55°C for 1 min; and 72°C for 2 min. The cycle for final extension was at 72°C for 7 min. Electrophoresis was performed in 1.2% agarose gels using 1xTAE buffer.

Immunoassay analyses

The immunoassay (EIA) of TBI was carried out with the kit «Genscreen Plus HIV Ag/Ab» (BIO-RAD, France) for the detection of the antigen p24 HIV-1. The determination of the presence of the antigenic protein HBsAg conducted with the commercial kit «VectogepB-HBsAg-antigen-strip D0556 (VectorBest, Koltzovo, Novosibirsk region, Russia).

Samples preparation for EIA

For immunoassay with fresh fruits, the buffer was used which contained 50 mM Na phosphate, 150 mM NaCl, 1 mM EDTA, 0.3% Tween 20, 04 mM phenylmethylsulfonyl flouride pH 7.5. Two g of fresh materials were ground in a mortar and pestle in liquid nitrogen. To the melted material, 1 ml of buffer was added, centrifuged in the bench labtop centrifuge for 15 min at maximum speed and supernatant was used for EIA. One-half g of lyophilized material of fruits was ground in liquid nitrogen with the same buffer with the addition of 0.3% of Triton X-100, centrifuged and supernatant was used for EIA.

Results

Creation of transgenic plants of T₀ and T₁ generations

Seedlings transformed with the gene TBI-HBS were passed through the selection medium with the efficiency of the transformation of 1-5%. As a whole, approximately 2000 tomato explants were infected in the work.

After screening, the 26 regenerants of the T₀ generation that survived were rooted *in vitro*, then were transferred to pots with water for the acclimatization and then were placed in hydroponic vessels with soil or planted in soil beds for growing in the special isolated greenhouse until fruits developed. The insertion of the target gene

into the genome of leaves and fruits was confirmed by PCR analyses (Shchelkunov *et al.* 2004). When fruits appeared, some parts of both leaves and fruits were analyzed for the expression and appearance of antigens. Mature fruits were collected for seeds and for drying of fruit masses.

During the selection on the kanamycin-containing medium, nontransformed tomato seedlings did not form roots, had retarded growth and died.

In order to obtain the T₁ generation, seeds from mature fruits of the T₀ generation were taken up, sterilized, placed on the germination medium and 12 day old seedlings were obtained. Then these seedlings were derooted and transferred to the selection medium with the addition of 50 mg/l kanamycin. After 2 – 2.5 weeks on the selection medium with 50 mg/l kanamycin, explants with roots were picked up and transferred into glass jars with tap water for the acclimatization and further growing in soil. Selected plants were placed into special greenhouse to obtain fruits from tomato plants of the T₁ generation.

Characteristics of transgenic plants of the T₀ generation

Samples of total RNA were isolated from segments of developed leaves of 20 plants of the T₀ generation with the introduced gene TBI-HBS and from two plants with the “empty” plasmid without target gene TBI-HBS. Shown in Figure 2 is the pattern of dot blot hybridization of RNA samples isolated from leaves of the T₀ transgenic plants with ³²P-labeled PCR products from the plasmid pBINp35STBI-HBS *A. tumefaciens* strain LBA4404 used as a probe. Most of plants of the T₀ generation expressed mRNA having the homology with the PCR product probed.

Such a homology with RNA was not found from leaves of tomato plants infected with the plasmid pBINPLUS/ARS lacking the gene TBI-HBS.

Fruits harvested from selected transgenic tomato plants were screened with EIA for the detection of the antigen p24 HIV-1. Fruits from plant № 13 revealed the absorbance of 0.391 during the measuring at 492 nm with the spectrophotometer. This value was approximately the same in comparison with the standard blood serum of HIV-1 infected human which was equal to 0.379. Seeds from fruits of this individual EIA-positive plant №13 were used for obtaining of the T₁ generation.

From fruits of transgenic tomato plant № 13 117 seeds were obtained. Seeds were sterilized and placed onto ½ MS “germination” medium without sucrose. Ninety-one of 117 seeds germinated and gave quite normal seedlings which were then derooted and their explants without roots were placed onto “selection” medium with 50 mg/l kanamycin. Only 10 explants from 91 were able to form roots during two weeks on the “selection” medium. From them only 4 plants passed through the acclimatization and were placed in greenhouse for growth and fruit development. The data in the Table 1 shows the total harvest of fruits obtained from transgenic plants of line № 13.

Table 1. Weight and number of fruits produced by transgenic plants of the line # 13 of the T₁ generation during vegetation in greenhouse

Plant and construction	Weight, kg	Number of fruits
13(1) p35STBI-HBS	3.359	79
13(2) p35STBI-HBS	3.378	70
13(3) p35STBI-HBS	2.234	43
13(4) p35STBI-HBS	0.865	18

Northern dot blot hybridization of RNA from transgenic tomato of T₁ generation

The expression of the target gene TBI-HBS was confirmed by Northern dot blot hybridization (Figure 3) in RNA samples isolated from leaves, stems with roots, and fruits of transgenic tomato plants of the T₁ generation.

There was not any significant incorporation of the labeled probe in spots with 10 µg of RNA both from control fruits (columns 1-2) or with 20 µg of RNA from control leaves (columns 3-4).

But incorporation of the labeled probe was high in spots with 20 µg of RNA from transgenic leaves [columns 7-10, variants 13(1), 13(2), 13(3) and 13(4), correspondingly] or 25 µg of RNA from stems with roots [columns 11-12, variants 13(1) and 13(3), correspondingly] or 25 µg of RNA from fruits [columns 13-16, variants 13(1), 13(2), 13(3) and 13(4), correspondingly].

It seemed that there was the expression of the gene TBI-HBS in different parts of transgenic tomato plants of the T₁ generation.

Immunoassays

EIA was performed both in test systems for the presence of the antigenic peptide HBSAg (HBV) and antigen p24 (HIV), which was the evidence for the synthesis of the target chimeric protein TBI-HBS in fruits. There were observed a clonal diversity in the level of the production of the target polypeptide (Figures 4 and 5) that is characteristic of transgenic plants and perhaps dependent on the position effect of the integrated transgene in the plant genome. As a whole the activity in EIA of HBSAg (HBV) was looking higher than the activity of p24 of HIV-1. This might be possible because only one epitope p24 of HIV-1 was determined in comparison with several epitopes of HBS. But fruits of one plant № 13(4) (Figure 5) gave a dramatic rise of the activity of the p24 in HIV-1 immunoassay.

For the purpose of the preparation of the “edible vaccine”, transgenic tomato fruits were lyophilized and the activity in dried tomato mass was determined with EIA HBSAg.

In Figure 6 the data of determination of antigenic protein HBSAg in lyophilized material are presented. There was found a great activity of antigens in lyophilized material in fruits of all transgenic plants of the T₁ generation tested. The protein content of TBI-HBS in the tomato dried sample was in the range 0.7 ± 0.35 ng per mg of the dried material.

These dried materials were further used for feeding of animals in order to evaluate the rise of neutralizing antibodies to HIV-1 and HBV (Shchelkunov *et al.* 2005).

Discussion

The demonstration of the induction of immune responses was a key step in all experiments with plant-derived vaccines. Subunit HIV vaccine candidates produced by plants or by plant viruses have been administered in trials to experimental mice intraperitoneally, subcutaneously, intranasally or orally and in most cases immune responses have been recorded (Streatfield *et al.* 2003).

In the present study for the development of the effective and safe vaccine of the new generation, the multivalent synthetic peptide vaccine was developed with T and B cell epitopes of HIV-1 included in the connection with HBSAg.

In our work from 2000 tomato explants infected with the *Agrobacterium*

tumefaciens LBA4404 harboring p35STBI-HBS, only 26 plantlets survived after selection on the kanamycin containing MS agar medium. From these only one plant № 13 was chosen because of its positive response in primary screening during the testing of HIV-positive expressive p24 antigene. Nevertheless, almost all investigated tomato plants of the T₀ generation showed the homology of their total RNA with the labeled probe prepared on the RT-PCR product of the plasmid of p35STBI-HBS (Figure 2).

The expression of the gene TBI-HBS was demonstrated when the Northern dot blot hybridization was carried out with total RNA isolated from leaves, stems with roots and fruits of transgenic plants of the line №13 hybridized with the labeled probe made on the base of RT-PCR products of the plasmid of p35STBI-HBS (Figure 3).

Both antigenic protein HBSAg and p24 of HIV-1 were detected in leaves and fruits of transgenic tomato of the T₁ generation. Even levels of expression greatly varied in some plants material, most plants of the T₁ generation of the line №13 demonstrated the successful expression (Figures 4 and 5).

For more convenient storage and gavage of transgenic tomato fruits, masses of dried fruits were prepared and there were no significant losses of the antigenic protein HBSAg during drying (Figure 6) and hopefully antigenic epitopes of ENV and GAG in dried fruits. So the dried vaccine might be kept at low temperatures in the refrigerator for a long time without losing activity.

Immune responses have been recorded when serum blood and feces were analyzed after feeding with dried transgenic fruits as a powder in a mixture with water via catheter to experimental mice (Shchelkunov *et al.* 2005). The immune response in mucosa began earlier after the first feeding, and in serum blood both types of antibodies appeared only after the second feeding. The injection of DNA vaccine in part of experimental mice fed at first with fruit tomato mass induced the additional increase in antibodies but only to HIV in blood.

Generated transgenic tomato plants revealed the important interest for the creation on their base of the “edible” vaccine against HIV/AIDS and hepatitis B.

The work was conducted due to the financial support of the International Science and Technology Center (USA) (grant # 2176p).

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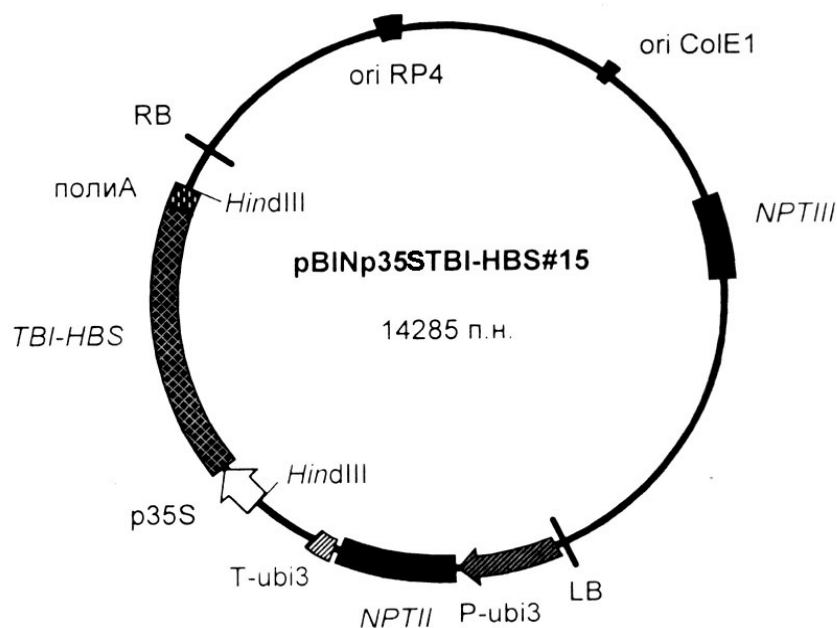


Figure 1

The scheme of the hybrid plasmid \ pBINp35STBI-HBS#15. p35S and polyA – promoter 35S RNA and the signal sequence of the polyadenylation of mRNA from the cauliflower mosaic virus. P-ubi3 and T-ubi3 – promoter and terminator from the gene ubi3. ori RP4, ori ColE1 – regions of the origin of the replication of plasmid RP4 и ColE1. NPTIII - the gene, giving the tolerance of bacterial cells to kanamycin. P-ubi3-NPTII- T-ubi3 – the hybrid gene, responsible for the tolerance of transformed plants to kanamycin.

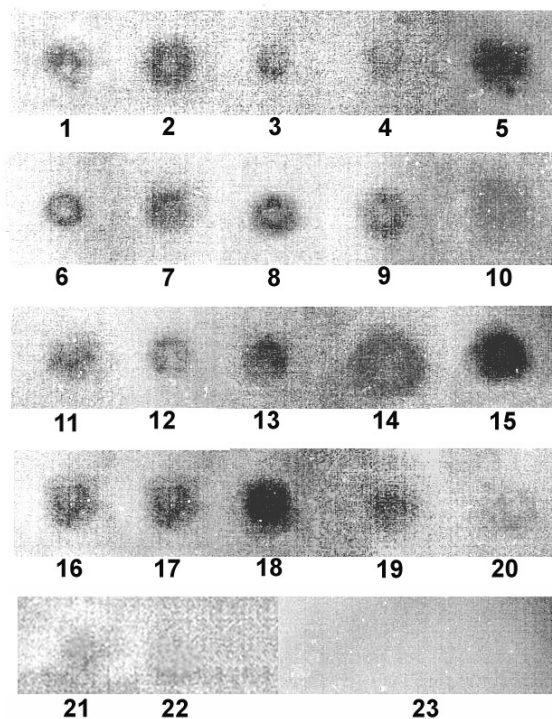


Figure 2.

Northern dot

loaded onto Hybond N+ membrane.

№№ 1-20 – RNA from leaves of transgenic tomato plants of T_0 generation.

№№ 21-22 – RNA from leaves of tomato plants of the T_0 generation transformed with an “empty” vector plasmid pBINPLUS/ARS.

№23 – hybridized membrane without loaded RNA.

blot with the total RNA

32P-ATP, cpm

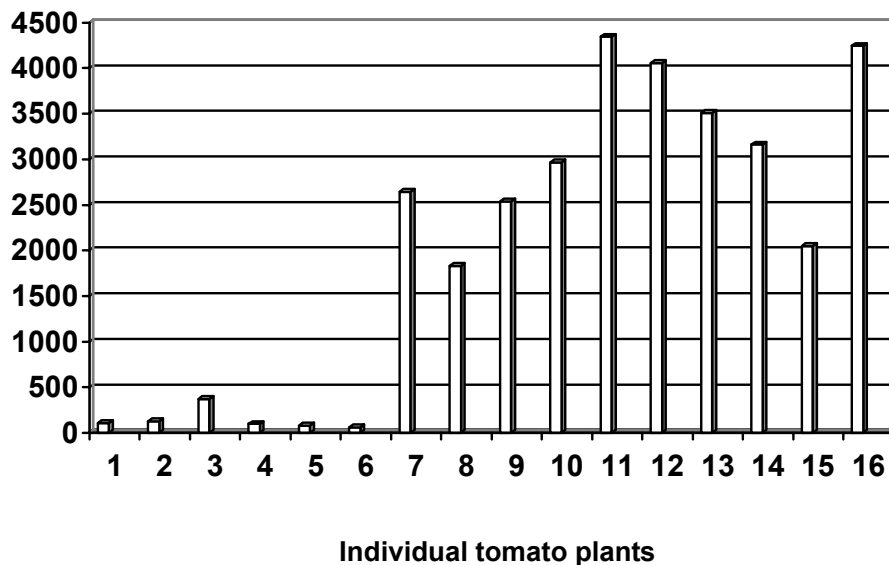


Figure 3.

Northern dot blot hybridization of total RNA from leaves, stems with roots and fruits with the probe of ^{32}P -RT-PCR product from total RNA of *Agrobacterium tumefaciens* LBA4404 with the cloned gene TBI-HBS in pBINPLUS/ARS.

Columns № 1-3 – RNA from leaves of nontransformed tomato plants.

Columns № 4-6 – RNA from fruit of nontransformed tomato plant.

Columns № 7 – 10 – RNA from leaves of transgenic tomato of the T₁ generation (20 µg per the line each) of lines ## 13(1), 13(2), 13(3) and 13(4).

Columns № 11 –12 – RNA from roots and stems of transgenic tomato of the T₁ generation (25µg per the line each) of lines ## 13(1) and 13(3).

Columns № 13 – 16 - RNA from fruits of transgenic tomato of the T₁ generation (25µg per the line each) of lines ## 13(1), 13(2), 13(3) and 13(4).

A492

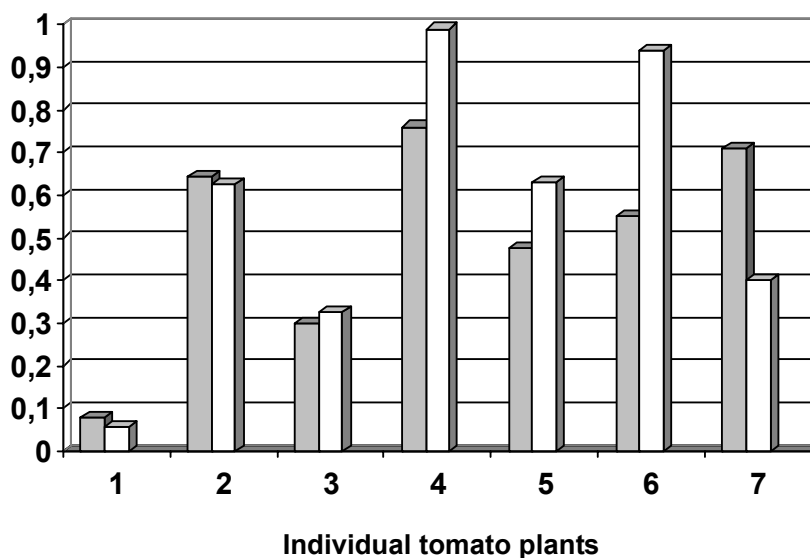


Figure 4.

The immunoassay of the presence of the protein HBSAg in fruits from nontransformed plant and transgenic lines ## 13 of tomato of the T₁ generation with the introduced gene TBI-HBS.

1 – serum blood of healthy human,

2 – serum blood of HBV-infected human,

3 – nontransformed fruit from market,

4 – 7 – fruits obtained from lines ## 13(1), 13(2), 13(3) and 13(4) of transgenic tomato plants of the T₁ generation.

Data of results are given in two replicates of independent experiments.

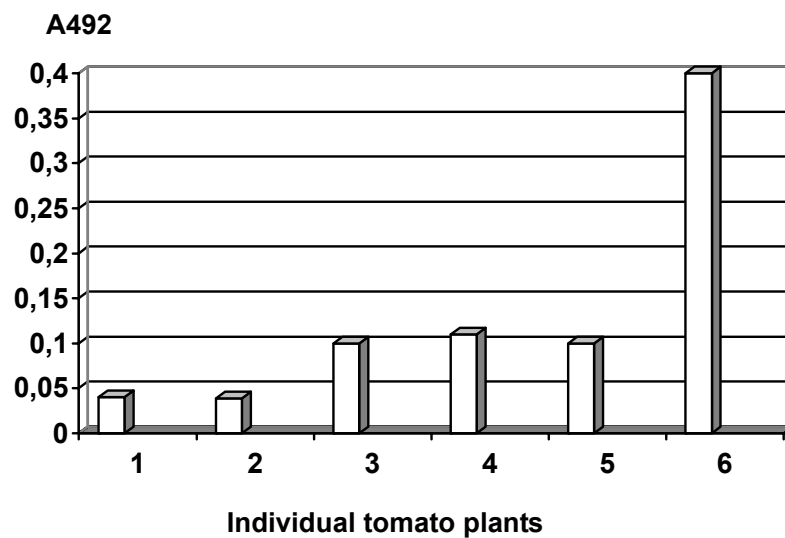


Figure 5.

The immunoassay of the presence of the antigen p24 in nontransformed fruit and transgenic fruits of tomato of the T₁ generation with the introduced gene TBI-HBS.

- 1 – the blood serum of the healthy human,
- 2 – fruit from nontransformed tomato plant,
- 3 – 6 - fruits from lines ##13(1), 13(2), 13(2 clone) and 13(4) of transgenic tomato plants of the T₁ generation.

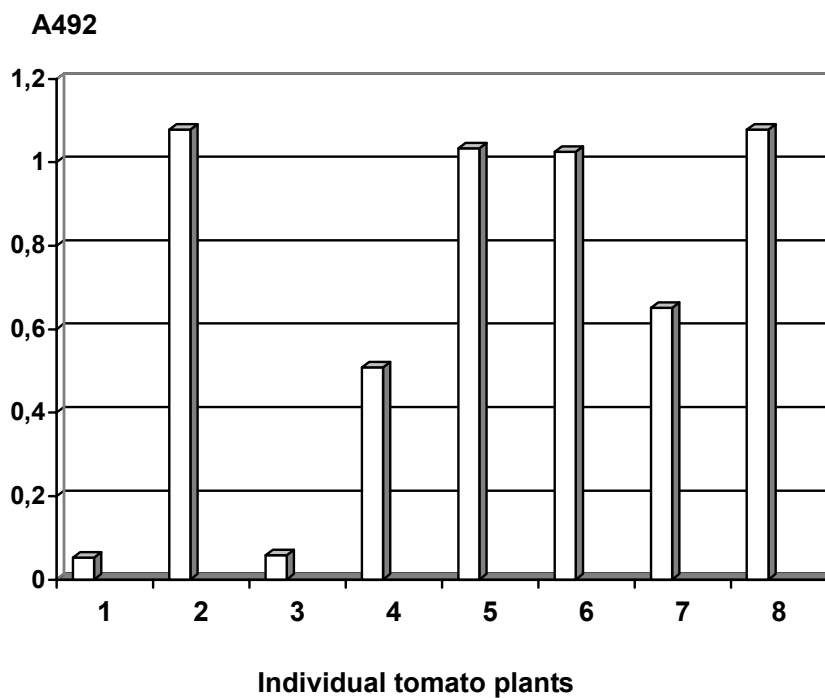


Figure 6.

The immunoassay of the presence of the antigenic protein HBSAg in dried fruit mass from nontransformed plant and from transgenic plants of lines # 13 of tomato of the T₁ generation with the introduced gene TBI-HBS.

- 1 – serum blood from healthy human,
- 2 – serum blood from HBV-infected human,
- 3 – nontransformed dried fruits,
- 4 – 8 – dried masses of fruits from lines 13(1), 13(2), 13(2) derived clone, 13(3) and 13(4) of transgenic tomato plants of the T₁ generation.

An alternative source of resistance to Tomato Spotted Wilt Virus

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Present cultivars resistant to tomato spotted wilt virus (TSWV) use the *Sw-5* gene that was introgressed from *L. peruvianum* into the South African cultivar 'Stevens' (Stevens et al., 1992). However, strains of tospovirus that cause spotted wilt symptoms and that are virulent on the *Sw-5* gene have been reported (Cho et al., 1996; Latham and Jones, 1996; Thompson and van Zijl, 1996). Canady et al. (2001) reported spotted wilt resistance in primitive breeding lines derived from *L. chilense* accession LA 1938. These lines were originally selected for resistance to the begomovirus tomato mottle virus (ToMoV) (Scott et al., 1995). Since then further crossing was done with the lines reported by Canady and in 2002 BC₄F₂ generation lines were grown in a field with very low natural TSWV infection. Only nine plants looked like tomatoes without wild characteristics and these were selected in lieu of being able to select for TSWV resistance. After an unsuccessful field test in 2003 where there was no spotted wilt infection, a field test was conducted in 2004 where susceptible lines had about 50% infection. Seven selections were made from one of the nine lines selected previously which appeared to be homozygous resistant. About 120 plants each of these seven selections were grown on a grower farm in spring 2005 along with *Sw-5* resistant and susceptible control cultivars (Table 1). The susceptible controls had 57 and 69% infection while the resistant control had 1.5% infection. The 2004 selections turned out to be from a line that was not homozygous as 1 appeared susceptible, 3 segregated for resistance, and 3 were homozygous resistant (Table 1). The 3 segregating lines had 28, 29, and 34% infection. By adjusting the susceptible plants in the segregating lines based on the percentage escapes in the susceptible control (mean=63%) there were 45, 47, and 55% susceptible plants in the 3 lines, respectively. The former two had acceptable fits to a 9:7 digenic ratio but the latter had an unacceptable fit. More definitive work needs to be done to determine the number of genes conferring resistance. Given the ability to recover resistance from selections made in 2002 without disease pressure, it is evident that resistance is controlled by a small number of genes, probably one or two. There were low percentages of infected plants in all three homozygous resistant lines as there were for the resistant controls (one not shown in Table 1) with the *Sw-5* gene. The seven lines were similar in horticultural traits and showed no evidence of any *L. chilense* characteristics. Fruit were small to large (with more of the former than the latter), firm, crack resistant, and had smooth blossom scars (*n-4* gene).

Of particular interest with this material is that predecessor lines from the LA 1938 resistance source were recently found to have resistance to a Hawaiian strain of the virus that is virulent on *Sw-5* (Stevens, unpublished data). Studies are underway to insure that the 3 advanced lines reported above have resistance to this strain as did their predecessors. We also want to determine if the gene(s) that confer resistance to the strains that are controlled by *Sw-5* or those that overcome it are the same and/or different. Also, work is underway to find co-dominant molecular markers linked to the

resistance genes. Testing of this resistance against other tospovirus that are virulent on Sw-5 is also of interest.

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Table 1. Tomato spotted wilt disease incidence for seven lines derived from *L. chilense* LA1938 and control hybrids grown in South Georgia, Spring 2005, plus Chi-square test for goodness of fit to a two dominant gene model (9:7 ratio).

Genotype	Plants				Conclusion ^y	Chi-square	P
	Total (No.)	Healthy (No.)	Diseased (No.)	Diseased adjusted ^z			
9-1	126	89	37 (29) ^x	59 (47) ^x	Seg	0.485	.5-.1
9-2	127	126	1 (0.8)	----	R		
9-3	126	125	1 (0.8)	----	R		
9-4	125	39	86 (69)	----	S		
9-5	128	92	36 (28)	57 (45)	Seg	0.032	.9-.5
9-6	128	127	1 (0.8)	-----	R		
9-7	93	61	32 (34)	51 (55)	Seg	4.647	.05-.025
Crista	200	197	3 (1.5)	----	R - control		
Mt.	49	21	28 (57)	----	S - control		
Spring							

^z There was an average of 63% infection for the 2 susceptible genotypes 9-4 and Mt. Spring. Thus, the diseased plants in segregating lines were assumed to represent 63% of the actual number of susceptible plants and adjusted accordingly. Chi-square test is based on the adjusted numbers.

^y R = resistant, Seg = segregating, S = susceptible.

^x Percentage diseased plants in parentheses.

Sources of resistance to Pepino mosaic virus (PepMV) in tomato

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PepMV belongs to genus *Potexvirus*. It is transmitted mechanically by contact among plants and does not present specific vectors (Jones *et al.*, 1980). However, given the high efficiency in the mechanical transmission of this disease in tomato fields, adoption of preventive growing techniques has not stopped its fast spread in Spain and other countries. Typical symptoms include yellow mosaic, leaf puckering and distortion, and irregular fruit ripening, which reduces its market value. Furthermore, PepMV is associated with the collapse syndrome which is greatly affecting the tomato crops (Soler-Aleixandre *et al.*, 2005). This virus is found in the Spanish Mediterranean area and the Canary Islands. The greatest incidence of the disease occurs in the area of Murcia, causing losses between 20 and 40% of the total production (Soler *et al.*, 2000).

In order to identify sources of resistance to PepMV, a collection of 2 accessions of *Lycopersicon cheesmanii*, 11 of *L. chilense*, 13 of *L. esculentum*, 3 of *L. esculentum* var. *cerasiforme*, 47 of *L. hirsutum*, 9 of *L. pennellii*, 46 of *L. peruvianum* and 38 of *L. pimpinellifolium*, 1 of *Solanum basendopogon*, 1 of *S. canense*, 5 of *S. caripense*, 9 of *S. muricatum*, 1 of *S. ochrantum* and 1 of *S. pseudocapsicum* were screened.

We inoculated between 15 and 18 plants of each of these accessions with the PepMV isolate LE-2002. We scored the symptoms in a scale ranging from 0 to 4 (0, no symptoms; 1, mild symptoms; 2, moderate symptoms; 3, severe symptoms; 4, very severe symptoms or dead plant). Apical leaves were taken from each plant at 30 or 60 days after inoculation (DAI). These samples were analyzed with the DAS-ELISA technique (Clark and Adams, 1977). The absorbance value of the serological reaction was taken as an indirect estimator of the viral accumulation (Ding *et al.*, 1995). Plants were considered as infected (positive DAS-ELISA) if their absorbance was, at least, three times higher than the absorbance of control healthy plants.

All accessions corresponding to *L. cheesmanii*, *L. esculentum*, *L. esculentum* var. *cerasiforme*, *L. parviflorum* and *L. pennellii*, had 100% of plants with systemic infection, with moderate or severe symptoms and high viral accumulation (data not shown). The same behavior was observed in most of the accessions of *L. hirsutum*, *L. peruvianum* and *L. pimpinellifolium*. However, a reduction of symptoms and viral accumulation was observed in accession ECU-968 of *L. hirsutum*, CIAPAN-16 of *L. peruvianum* and ECU-693 of *L. pimpinellifolium* (Table 1). In *L. chilense*, 4 accessions showed 100% of plants with systemic infection, variable viral accumulation and mild symptoms; notwithstanding, in 7 accessions, between 30 and 90% of plants did not show symptoms and the virus could not be detected. The best behavior corresponded to accession LA-470 (Table 1). All plants inoculated of *Solanum basendopogon*, *S. canense*, *S. caripense* and *S. muricatum* were classified as susceptible. All plants of *S. ochrantum* accession ECU-335 presented systemic infection by PepMV (Table 1). However, symptoms were mild, viral accumulations low, and at 60 DAI only 13.3% of the plants remained systemically infected. No symptoms were observed in plants of the accession AN-CA-214 of *S. pseudocapsicum*, and all plants were DAS-ELISA negative.

These results suggest that *L. chilense* is the most promising species of genus *Lycopersicon* in the search of sources of resistance to PepMV, while the best behavior has corresponded to accessions ECU-335 of *S. ochrantum* and AN-CA-214 of *S. pseudocapsicum*. ECU-335 showed a steady reduction in the viral accumulation, at least in the upper parts of the plants. Accession AN-CA-214 has shown a total resistance to mechanical inoculation with PepMV. The identification of these sources of resistance may contribute to the development of new tomato varieties resistant to PepMV.

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Table 1.- Accessions with a better behavior against the mechanical inoculation with PepMV.

Accession	Mean symptoms index max. ^a	Mean maximum absorbance 1 ^b	Mean maximum absorbance 2 ^c	Absorbance index ^d	% infected plants
<i>L. chilense</i>					
LA-372	2.0	0.32	0.68	0.23	50.0
PER-551	1.0	0.68	0.79	0.26	100.0
LA-470	1.1	1.03	0.90	0.30	30.0
ECU-527	1.9	0.79	0.97	0.33	80.0
PER-522	0.9	1.08	1.08	0.36	100.0
PER-526	0.7	1.15	1.15	0.39	100.0
PER-542	1.0	1.18	1.18	0.39	100.0
LA-1968	3.5	2.28	2.35	0.79	83.3
LA-1971	3.2	2.31	2.61	0.87	88.2
LA-2762	2.6	2.34	2.71	0.91	92.3
LA-458	3.6	2.52	2.75	0.92	78.6
<i>L. hirsutum</i>					
ECU-968	1.2	0.60	0.60	0.20	100.0
<i>L. peruvianum</i>					
CIAPAN-16	0.5	0.60	0.70	0.23	77.8
<i>L. pimpinellifolium</i>					
ECU-693	1.5	1.62	1.62	0.54	100.0
<i>S. ochrantum</i>					
ECU-335	0.6	0.14	0.14	0.05	100.0/13.3 ^e
<i>S. pseudocapsicum</i>					
AN-CA-214	0.0	0.04	-	-	0.0
CONTROL					
Fortuna-C	3.2	2.98	2.98	1.00	100.0

^amean symptoms index measured in a 0 to 4 scale (0, no symptoms; 1, mild symptoms; 2, moderate symptoms; 3, severe symptoms; 4, very severe symptoms or dead plant).

^bmean value of the maximum absorbance for each plant.

^cmean value of the maximum absorbance for each infected plant.

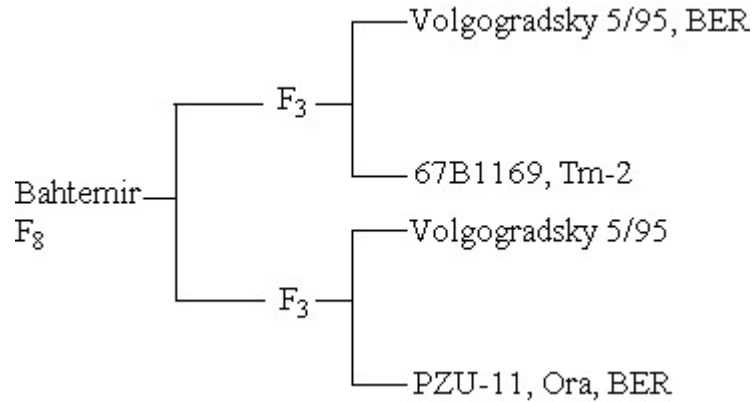
^dindex calculated as: Mean maximum absorbance 2 of each accession/Mean maximum absorbance of the susceptible control.

^epercentage of plants systemically infected at 30 DAI/percentage of plants systemically infected at 60 D

Y.I. Avdeyev, B.M. Scherbinin, A.Y. Avdeyev, L.M. Ivanova, O.P. Kigashpaeva
Russian varieties resistant to broomrape *Orobanche aegypticaca* Pers.

Bahtemir

Pedigree:



Characteristics:

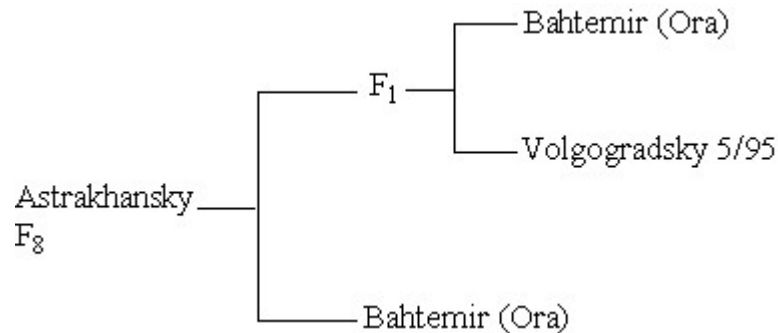
Fruit: red color round, 70-100 g by weight, 4-5 locular, *u*, soluble solids content is 5.91%, ascorbic acid 18 mg%

Plant: *sp, d*, 45-55 cm in height, *Ora*, BER, *Tm-2*, resistant to skin cracking (RSC)

Utility and maturity: middle-early, for fresh market and processing.

Astrakhansky

Pedigree:

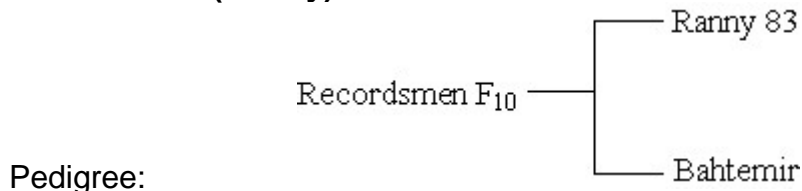


Characteristics:

Fruit: red color, rounded, 100-130 g in weight, 4-7 locular, *u*, soluble solids content is 5.2-5.6%, sugar content is 3.4-4.12%, ascorbic acid 18.2 mg%.

Plant: *sp, d*, about 70 cm in height, *Ora*, BER, *Tm-2*, RSC, tolerant to heat and *Alternaria solani*.

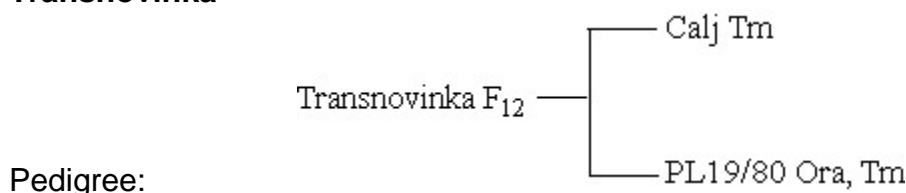
Utility and maturity: for middle and late seasons, fresh market and processing.

Recordsman (lunsky)**Characteristics:**

Fruit: red color, round, 80-120 g in weight , 4-5 locular, *u*, soluble solids content is 5.8%, sugar content is 3.15%, ascorbic acid 17-19 mg%.

Plant: *sp*, 50-65 cm in height, *Ora*, BER, TmV, RSC.

Utility and maturity: for early and middle seasons, fresh market and processing.

Transnovinka

Characteristics: red color, plummy-length form, 60-80 g in weight, 2-3 locular, very firm, has jointless pedicels (*j-2*), soluble solids content is 5.73%, sugar content is 2.91%, ascorbic acid 22.12 mg%.

Plant: *sp*, 70-90 cm in height, *Ora*, TmV, RSC.

Utility and maturity: for middle and late seasons of mechanical harvesting for processing, is suited for preparing whole-peel tomato products.

Urievsky**Characteristics:**

Urievsky was created from Bahtemir variety by 9-times every year selections of individual plants for highest bush and largest size of fruits. It has the length of main stem about 80 cm and fruits 120-150 g in weight. The rest complex of useful characteristics of Urievsky (*d*, *u*, rounded fruits, *Ora*, BER, TmV, RSC) are similar to initial variety except later maturity and fruits have more locules (4-6).

Utility and maturity: for middle and late seasons, fresh market and processing.

Revised List of Monogenic Stocks

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The following catalogue of 1,017 monogenic stocks (at 622 loci) is a revision of the previous list issued in TGC 52. (Lists of available wild species and miscellaneous genetic stocks were last updated in TGC 53 and TGC 54, respectively.) Certain obsolete or unavailable items have been deleted, newly acquired stocks have been added, inaccuracies corrected, and gene symbols revised to reflect allele tests or other information. This stock list includes only accessions we consider to be the primary sources for individual mutations: usually the original stock in which the mutation was first described, as well as any nearly isogenic lines into which it has been bred. Most mutant stocks are homozygous and true-breeding. However, seed of the male-steriles, homozygous-inviable mutants, and other stocks that are difficult or impossible to maintain as homozygotes, must be propagated via heterozygotes. In these cases, seed are provided in the form of segregating F₂ or BC populations.

Monogenic mutants acquired since the last edition of this stock list are: *bks*¹ and *bks*², seed testa mutants isolated by Bruce Downie; breeding lines containing *Ph-3*, a gene for resistance to *Phytophthora infestans*, bred into *L. esculentum* from *L. pimpinellifolium* by Peter Hanson; an indeterminate (*sp*⁺) isoline of M-82 donated by Dani Zamir; a stock of *Rg-1* for high efficiency regeneration from tissue culture, bred into *L. esculentum* from *L. peruvianum* by Maarten Koorneef; allozyme variants for the markers *Dia-2*, *Dia-3*, *Dia-4*, *Fdh-1*, and *Mae-1* transferred from *S. lycopersicoides*; stocks of the leaf vein mutant *obv* and its wild type (clear vein) allele.

Documented cases of allelism between mutants are incorporated into this list, and gene symbols revised accordingly. The mutant *dg* (dark green) was reported by Levin et al. (TAG 2003, 106: 454-460) to be an allele of *hp-2* (high pigment-2), and is herein designated *hp-2*^{dg}.

Additional information on individual stocks, including phenotypes, references, images, chromosomal locations, etc., can be obtained through our website (<http://tgrc.ucdavis.edu>). We ask that users report any problems they detect in our lines, such as aberrant segregation, incorrect phenotypes, unexpected variability, etc. TGC members are also encouraged to submit stocks of verified monogenic mutants not listed here to the TGRC for maintenance and distribution.

Table 1. List of monogenic stocks, sorted by gene symbol. For each locus, stocks containing the original mutant allele are listed first, followed by any additional alleles at the same locus ('prov' indicates a provisional allele). Older gene symbols (synonyms) for each allele are listed (^ indicates superscript). Each mutant is assigned to one or more phenotypic categories (Class), defined in Table 2 (** indicates the primary category for each allele). Background genotypes (Back.) of each stock are listed in abbreviated form, with full names given in Table 3. The origin of each mutation is specified as either spontaneous ('SPON'), or induced by chemical treatment ('CHEM') or irradiation ('RAD'). Isogenicity (Iso.) indicates whether the nonmutant control is available as an isogenic ('IL') or nearly isogenic ('NIL') line, or is nonisogenic ('NON').

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>a</i>		anthocyaninless	a1	A*	SPON	AC	NIL	LA3263
<i>a</i>		anthocyaninless	a1	A*	SPON	X	NON	LA0291
<i>a</i>	<i>prov2</i>	anthocyaninless	a	A*	CHEM	VF36	IL	3-414

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>a</i>	<i>prov3</i>	anthocyaninless	a	A*	CHEM	VF36	IL	3-415
<i>aa</i>		anthocyanin absent		A*	SPON	MD	IL	LA1194
<i>aa</i>		anthocyanin absent		A*	SPON	AC	NIL	LA3617
<i>Abg</i>		Aubergine		P*	SPON	X	NON	LA3668
<i>abi</i>		aborted inflorescence		M*	CHEM	CSM	NON	3-803
<i>Aco-1</i>	1	Aconitase-1		V*	SPON	pen	NON	LA2901
<i>Aco-1</i>	2	Aconitase-1		V*	SPON	pim	NON	LA2902
<i>Aco-1</i>	3	Aconitase-1		V*	SPON	pim	NON	LA2903
<i>Aco-2</i>	1	Aconitase-2		V*	SPON	pim	NON	LA2904
<i>Aco-2</i>	2	Aconitase-2		V*	SPON	chm	NON	LA2905
<i>acr</i>		acroxantha	acr1	D*JK	RAD	CR	IL	LA0933
<i>ad</i>		<i>Alternaria lternate</i> resistance		Q*	SPON	X	NON	LA1783
<i>Adh-1</i>	1	Alcohol dehydrogenase-1		V*	SPON	VCH	NON	LA2416
<i>Adh-1</i>	2	Alcohol dehydrogenase-1		V*	SPON	par	NON	LA2417
<i>Adh-1</i>	<i>n</i>	Alcohol dehydrogenase-1		V*	CHEM	MM	IL	LA3150
<i>Adh-2</i>	1	Alcohol dehydrogenase-2		V*	SPON	hir	NON	LA2985
<i>adp</i>		adpressa		K*J	RAD	CR	IL	LA0661
<i>adp</i>		adpressa		K*J	RAD	AC	NIL	LA3763
<i>adu</i>		adusta	adu1	H*K	RAD	CR	IL	LA0934
<i>ae</i>		entirely anthocyaninless	a332	A*	RAD	KK	IL	LA1048
<i>ae</i>		entirely anthocyaninless	a332	A*	RAD	CG	NIL	LA3018
<i>ae</i>		entirely anthocyaninless	a332	A*	RAD	AC	NIL	LA3612
<i>ae</i>	2	entirely anthocyaninless		A*	CHEM	UC82 B	IL	3-706
<i>ae</i>	<i>afr</i>	entirely anthocyaninless	afr, ap	A*	RAD	CT	IL	LA2442
<i>ae</i>	<i>prov3</i>	entirely anthocyaninless	ae	A*	CHEM	VCH	IL	3-620
<i>aeg</i>		aegrota		H*	RAD	CR	IL	LA0537
<i>aer</i>		aerial roots		R*	SPON	X	NON	LA3205
<i>aer-2</i>		aerial roots-2		R*	SPON	X	NON	LA2464A
<i>af</i>		anthocyanin free	a325	A*I	RAD	AC	NIL	LA3610
<i>af</i>		anthocyanin free	a325	A*I	RAD	RCH	IL	LA1049
<i>afe</i>		afertilis	afe1	N*CJK	RAD	RR	IL	LA0935
<i>afl</i>		albifolium	af	B*G	SPON	XLP	IL	2-367
<i>afl</i>		albifolium	af	B*G	SPON	AC	NIL	LA3572
<i>Aft</i>		Anthocyanin fruit	Af	P*	SPON	X	NON	LA1996
<i>ag</i>		anthocyanin gainer		A*	SPON	AC	NIL	LA3163
<i>ag</i>		anthocyanin gainer		A*	SPON	GS5	NON	LA0177
<i>ag</i>	2	anthocyanin gainer		A*	SPON	che	NON	LA0422
<i>ag</i>	2	anthocyanin gainer		A*	SPON	AC	NIL	LA3164
<i>ag</i>	<i>k</i>	anthocyanin gainer		A*	SPON	T5	IL	LA3149
<i>ag-2</i>		anthocyanin gainer-2		A*	SPON	AC	NIL	LA3711
<i>ah</i>		Hoffman's anthocyaninless	ao, a337	A*	SPON	OGA	IL	LA0260
<i>ah</i>	<i>prov3</i>	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-607
<i>ah</i>	<i>prov4</i>	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-628
<i>ah</i>	<i>prov5</i>	Hoffman's anthocyaninless	ah	A*	CHEM	VCH	IL	3-629
<i>ah</i>	<i>prov6</i>	Hoffman's anthocyaninless	ah	A*	SPON	PSN	IL	LA0352
<i>ah</i>	<i>prov7</i>	Hoffman's anthocyaninless	ah	A*	CHEM	MM	IL	3-343
<i>ai</i>		incomplete anthocyanin	a342	A*	RAD	KK	IL	LA1484
<i>ai</i>		incomplete anthocyanin	a342	A*	RAD	AC	NIL	LA3611
<i>ai</i>	2	incomplete anthocyanin	am, a340	A*	RAD	KK	IL	LA1485
<i>al</i>		anthocyanin loser	a2	A*	SPON	AC	NIL	LA3576
<i>alb</i>		albescens		G*C	SPON	AC	NIL	LA3729
<i>alb</i>	<i>prov2</i>	albescens	alb	G*C	CHEM	VCH	IL	3-625
<i>alc</i>		alcobaca		P*	SPON	X	NON	LA2529
<i>alc</i>		alcobaca		P*	SPON	RU	NIL	LA3134
<i>alu</i>		alutacea	alu1	C*K	RAD	CR	IL	LA0838
<i>an</i>		anantha	an^1, an^2, ca	L*N	RAD	CR	IL	LA0536
<i>ap</i>		apetalous		L*N	SPON	ESC	IL	2-009
<i>ap</i>		apetalous		L*N	SPON	AC	NIL	LA3673

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>apl</i>		applanata		J*K	RAD	LU	IL	LA0662
<i>apn</i>		albo-punctata		G*BJK	CHEM	VF36	IL	3-105
<i>Aps-1</i>	1	Acid phosphatase-1		V*	SPON	VCH	NIL	LA1811
<i>Aps-1</i>	2	Acid phosphatase-1		V*	SPON	chm	NON	LA1812
<i>Aps-1</i>	<i>n</i>	Acid phosphatase-1		V*	SPON	pim	NON	LA1810
<i>Aps-2</i>	1	Acid phosphatase-2		V*	SPON	SM	NON	LA1814
<i>Aps-2</i>	2	Acid phosphatase-2		V*	SPON	che	NON	LA1815
<i>Aps-2</i>	3	Acid phosphatase-2		V*	SPON	par	NON	LA1816
<i>Aps-2</i>	<i>n</i>	Acid phosphatase-2		V*	SPON	che	NON	LA1813
<i>are</i>		anthocyanin reduced <i>Alternaria</i> stem canker resistance		A*	CHEM	VF36	NON	3-073
<i>Asc</i>		apricot		Q*	SPON	X	NON	LA3528
<i>at</i>		apricot		P*L	SPON	X	NON	LA0215
<i>at</i>		apricot		P*L	SPON	RU	NIL	LA2998
<i>at</i>		apricot		P*L	SPON	AC	NIL	LA3535
<i>atn</i>		attenuata	at	E*AJK	RAD	RR	IL	LA0587
<i>atn</i>		attenuata	at	E*AJK	RAD	AC	NIL	LA3829
<i>atv</i>		atroviolacium		A*	SPON	VF36	NON	LA0797
<i>atv</i>		atroviolacium		A*	SPON	AC	NIL	LA3736
<i>au</i>		aurea		C*B	RAD	AC	NIL	LA3280
<i>au</i>	(1s)	aurea	au^2, au, brac	C*B	RAD	CR	IL	LA0538
<i>au</i>	6	aurea	yg^6, yg-6, au^yg-6, yo	C*B	SPON	RCH	IL	LA1486
<i>au</i>	6	aurea	yg^6, yg-6, au^yg-6, yo	C*B	SPON	AC	NIL	LA2929
<i>au</i>	<i>tl</i>	aurea		C*B	SPON	VF145	IL	2-655A
<i>au</i>	<i>w</i>	aurea	w616	C*B	CHEM	MM	IL	LA2837
<i>aus</i>		austera		J*KT	RAD	LU	IL	LA2023
<i>aut</i>		aureata		C*F	SPON	X	NON	LA1067
<i>aut</i>		aureata		C*F	SPON	AC	NIL	LA3166
<i>auv</i>		aureate virescent		F*C	CHEM	VF36	IL	3-075
<i>avi</i>		albovirens	avi1	C*BGN	RAD	CR	IL	LA0936
<i>aw</i>		without anthocyanin	aba, ab, a179	A*	SPON	X	NON	LA0271
<i>aw</i>		without anthocyanin	aba, ab, a179	A*	SPON	AC	NIL	LA3281
<i>aw</i>	<i>prov3</i>	without anthocyanin	aw	A*	CHEM	VF36	IL	3-121
<i>aw</i>	<i>prov4</i>	without anthocyanin	aw	A*	CHEM	VCH	NON	3-603
<i>aw</i>	<i>prov5</i>	without anthocyanin	aw	A*	CHEM	VCH	NON	3-627
<i>B</i>		Beta-carotene		P*	SPON	X	NON	LA2374
<i>B</i>		Beta-carotene		P*	SPON	RU	NIL	LA3000
<i>B</i>		Beta-carotene		P*	SPON	E6203	NIL	LA3898
<i>B</i>		Beta-carotene		P*	SPON	O8245	NON	LA3899
<i>B</i>	<i>c</i>	Beta-carotene	og^c,Crn,Cr,cr n-2,cr-2	P*L	SPON	PCV	NON	LA0806
<i>B</i>	<i>c</i>	Beta-carotene	og^c,Crn,Cr,cr n-2,cr-2	P*L	SPON	AC	NIL	LA3179
<i>B</i>	<i>og</i>	Beta-carotene	og	L*P	SPON	chi	NON	LA0294
<i>B</i>	<i>og</i>	Beta-carotene	og	L*P	SPON	X	NON	LA4026
<i>B</i>	<i>og</i>	Beta-carotene	og	L*P	SPON	X	NON	LA4025
<i>B</i>	<i>og</i>	Beta-carotene	og	L*P	SPON	PSN	NIL	LA0348
<i>B</i>	<i>og</i>	Beta-carotene	og	L*P	SPON	X	NON	LA0500
<i>bc</i>		bicolor	bi	U*JKT	RAD	CR	IL	LA0588
<i>Bco</i>		Brilliant corolla		L*	SPON	VF36	NON	LA4261
<i>bi</i>		bifurcate inflorescence		M*	SPON	X	NON	LA1786
<i>bip</i>		bipinnata		J*	RAD	LU	IL	LA0663
<i>bip</i>		bipinnata		J*	RAD	AC	NIL	LA3765
<i>bip</i>	<i>prov2</i>	bipinnata	bip	J*	CHEM	VCH	IL	3-602
<i>bk</i>		beaked		O*	SPON	X	NON	LA0330
<i>Bk-2</i>		Beaked-2		O*	SPON	X	NON	LA1787
<i>bks</i>		black seed	bks1-1	S*A	RAD	X	NON	LA4290
<i>bks</i>	2	black seed	bks1-2	S*A	RAD	X	NON	LA4291

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>bl</i>		blind		K*	SPON	AC	NIL	LA3745
<i>bl</i>		blind		K*	SPON	X	NON	LA0059
<i>bl</i>	2	blind	to^2	K*	SPON	LU	IL	LA0980
<i>bl</i>	to	blind	to	K*JLO	RAD	CR	IL	LA0709
<i>bls</i>		baby lea syndrome	alm	A*K	SPON	X	NON	LA1004
<i>bls</i>		baby lea syndrome	alm	A*K	SPON	AC	NIL	LA3167
<i>bls</i>	prov2	baby lea syndrome	bls	A*K	CHEM	VCH	IL	3-610
<i>Bnag-1</i>	1	Beta-N-acetyl-D-glucosaminidase-1		V*	SPON	pen	NON	LA2986
<i>br</i>		brachytic		K*	SPON	X	NON	LA2069
<i>brt</i>		bushy root		R*	SPON	X	NON	LA2816
<i>brt-2</i>		bushy root-2		R*	SPON	X	NON	LA3206
<i>bs</i>		brown seed		S*	CHEM	AC	NIL	LA2935
<i>bs-2</i>		brown seed-2		S*	SPON	PLB	IL	LA1788
<i>bs-4</i>		brown seed-4		S*	RAD	MM	IL	LA1998
<i>btl</i>		brittle stem		J*Y	SPON	X	NON	LA1999
<i>bu</i>		bushy	fru	K*JM	SPON	X	NON	LA0897
<i>bu</i>		bushy	fru	K*JM	SPON	AC	NIL	LA2918
<i>bu</i>	ab	bushy	fru^ab	K*JM	RAD	RR	IL	LA0549
<i>bu</i>	cin	bushy	cin	K*JM	SPON	HSD	IL	LA1437
<i>bu</i>	cin-2	bushy	cin-2	K*JM	SPON	HSD	IL	LA2450
<i>bu</i>	hem	bushy	fru^hem	K*JM	RAD	CR	IL	LA0604
<i>bul</i>		bullata		C*JK	RAD	CR	IL	LA0589
<i>buo</i>		bullosa	buo1	J*O	RAD	pim	IL	LA2000
<i>c</i>		potato leaf		J*	SPON	AC	NIL	LA3168
<i>c</i>	int	potato leaf	int	J*	RAD	CR	IL	LA0611
<i>c</i>	int	potato leaf	int	J*	RAD	AC	NIL	LA3728A
<i>c</i>	prov2	potato leaf	c	J*	CHEM	MM	IL	3-345
<i>c</i>	prov3	potato leaf	c	J*	CHEM	X	IL	3-604
<i>c</i>	prov4	potato leaf	c	J*	CHEM	VCH	IL	3-609
<i>c</i>	prov5	potato leaf	c	J*	CHEM	VCH	IL	3-626
<i>c</i>	prov6	potato leaf	c	J*	CHEM	VCH	IL	3-631
<i>car</i>		carinata		J*DLO	RAD	CR	IL	LA0539
<i>car-2</i>		carinata-2	car2	J*K	RAD	pim	IL	LA2001
<i>cb</i>		cabbage		J*K		AC	NIL	LA3819
<i>cb-2</i>		cabbage leaf-2		J*K	RAD	AC	NIL	LA3169
<i>cb-2</i>		cabbage leaf-2		J*K	RAD	X	NON	LA2002
<i>ccf</i>		cactiflora		N*LO	CHEM	CSM	IL	3-805
<i>Cf-1</i>		<i>Cladosporium fulvum</i> resistance-1	Cf, Cf1, Cfsc	Q*	SPON	X	NON	LA2443
<i>Cf-1</i>	3	<i>Cladosporium fulvum</i> resistance-1	Cf-5, Cf5	Q*	SPON	X	NON	LA2447
<i>Cf-1</i>	3	<i>Cladosporium fulvum</i> resistance-1	Cf-5, Cf5	Q*	SPON	MM	NIL	LA3046
<i>Cf-2</i>		<i>Cladosporium fulvum</i> resistance-2	Cf2, Cfp1	Q*	SPON	X	NON	LA2444
<i>Cf-2</i>		<i>Cladosporium fulvum</i> resistance-2	Cf2, Cfp1	Q*	SPON	MM	NIL	LA3043
<i>Cf-3</i>		<i>Cladosporium fulvum</i> resistance-3	Cf3, Cfp2	Q*	SPON	X	NON	LA2445
<i>Cf-3</i>		<i>Cladosporium fulvum</i> resistance-3	Cf3, Cfp2	Q*	SPON	MM	NIL	LA3044
<i>Cf-4</i>		<i>Cladosporium fulvum</i> resistance-4	Cf-8, Cf4, Cf-1^2	Q*	SPON	X	NON	LA2446
<i>Cf-4</i>		<i>Cladosporium fulvum</i> resistance-4	Cf-8, Cf4, Cf-1^2	Q*	SPON	MM	NIL	LA3045
<i>Cf-4</i>		<i>Cladosporium fulvum</i> resistance-4	Cf-8, Cf4, Cf-1^2	Q*	SPON	AC	NIL	LA3267
<i>Cf-6</i>		<i>Cladosporium fulvum</i> resistance-6		Q*	SPON	X	NON	LA2448
<i>Cf-7</i>		<i>Cladosporium fulvum</i> resistance-7		Q*	SPON	X	NON	LA2449

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>Cf-9</i>		<i>Cladosporium fulvum</i> resistance-9		Q*	SPON	MM	NIL	LA3047
<i>cfa</i>		conferta	cfa1	K*		LU	NON	LA0832
<i>cg</i>		congesta	cg1	K*J	RAD	RR	IL	LA0831
<i>ch</i>		chartreuse		L*	SPON	PSN	IL	2-253
<i>ch</i>		chartreuse		L*	SPON	AC	NIL	LA3720
<i>ci</i>		cincta	ci1	K*	RAD	CR	IL	LA0938
<i>cit</i>		citriformis		O*JK	RAD	RR	IL	LA2024
<i>cjf</i>		conjunctiflora		L*N	SPON	PTN	IL	LA1056
<i>ck</i>		corky fruit		O*	SPON	X	NON	LA2003
<i>cl-2</i>		cleistogamous-2	cl2	L*N	SPON	SM	IL	2-185
<i>cla</i>		clara		C*A	RAD	LU	IL	LA0540
<i>clau</i>		clausa	ff, vc	J*LO	RAD	LU	IL	LA0591
<i>clau</i>		clausa	ff, vc	J*LO	RAD	X	NON	LA0719
<i>clau</i>		clausa	ff, vc	J*LO	RAD	AC	NIL	LA3583
<i>clau</i>	<i>ff</i>	clausa		J*LO	SPON	VFSM	IL	2-505
<i>clau</i>	<i>ics</i>	clausa	ics	J*	SPON	PTN	IL	LA1054
<i>clau</i>	<i>ics</i>	clausa	ics	J*	SPON	AC	NIL	LA3713
<i>clau</i>	<i>prov2</i>	clausa	clau	J*LO	SPON	X	IL	LA0509
<i>clau</i>	<i>vc</i>	clausa		J*LO	SPON	X	NON	LA0896
<i>cls</i>		clarescens		C*K	RAD	RR	IL	LA2025
<i>clt</i>		coalita		J*	RAD	LU	IL	LA2026
<i>cm</i>		curly mottled		G*JNO	SPON	PCV	NON	LA0272
<i>cm</i>		curly mottled		G*JNO	SPON	AC	NIL	LA2919
<i>cma</i>		commutata		K*DHJ	RAD	RR	IL	LA2027
<i>Cmr</i>		Cucumber mosaic resistance		Q*	SPON	X	NON	LA3912
<i>cn</i>		cana	ca	D*K	RAD	RR	IL	LA0590
<i>co</i>		cochlearis		J*D	RAD	CR	IL	LA0592
<i>coa</i>		corrotundata	coa1	J*KLT	RAD	CR	IL	LA0940
<i>com</i>		complicata		K*J	RAD	CR	IL	LA0664
<i>com</i>	<i>in</i>	complicata	in	K*DJ	RAD	CR	IL	LA0610
<i>com</i>	<i>in</i>	complicata	in	K*DJ	RAD	AC	NIL	LA3715
<i>con</i>		convalescens		E*FK	RAD	CR	IL	LA0541
<i>con</i>		convalescens		E*FK	RAD	AC	NIL	LA3671
<i>cor</i>		coriacea		K*J	RAD	AC	NIL	LA3743
<i>cor</i>		coriacea		K*J	RAD	CR	IL	LA0666
<i>cpa</i>		composita	cpa1	M*K	RAD	RR	IL	LA0833
<i>cpt</i>		compact		K*EJ	SPON	XLP	IL	2-377
<i>cpt</i>		compact		K*EJ	SPON	AC	NIL	LA3723
<i>Cri</i>		Crispa		H*JU	RAD	CR	IL	LA0667
<i>Crk</i>		Crinkled		J*T	SPON	X	NON	LA1050
<i>crt</i>		cottony-root		R*	SPON	RCH	NON	LA2802
<i>cta</i>		contaminata	cta1	K*HJN	RAD	RR	IL	LA0939
<i>ctt</i>		contracta		K*J	RAD	LU	IL	LA2028
<i>Cu</i>		Curl		J*KT	SPON	STD	IL	LA0325
<i>Cu</i>		Curl		J*KT	SPON	AC	NIL	LA3740
<i>cu-2</i>		curl-2	cu2	J*	RAD	CT	IL	LA2004
<i>cu-3</i>		curl-3		J*KT	SPON	pim	NON	LA2398
<i>cul</i>		culcitula		K*U	RAD	RR	IL	LA2029
<i>cur</i>		curvifolia		J*EK	RAD	RR	IL	LA0668
<i>cv</i>		curvata	cu	K*JT	RAD	LU	IL	LA0593
<i>cv</i>	<i>2</i>	curvata	acu	K*JT	RAD	CR	IL	LA0660
<i>cva</i>		conversa		K*D	RAD	CR	IL	LA0665
<i>cvl</i>		convoluta	cvl1	K*J	RAD	RR	IL	LA0830
<i>Cvx</i>		Convexa		J*	SPON	X	NON	LA1151
<i>d</i>		dwarf		K*JT	SPON	FB	NIL	LA3022
<i>d</i>		dwarf		K*JT	SPON	GRD	NIL	LA3031
<i>d</i>		dwarf		K*JT	SPON	STN	NIL	LA0313
<i>d</i>	<i>b</i>	dwarf		K*JTL	SPON	RR	IL	LA3865

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>d</i>	<i>cr</i>	dwarf	rob [^] crisp	K*JT	RAD	CR	IL	LA0570
<i>d</i>	<i>im</i>	dwarf	rob [^] imm	K*JT	RAD	CR	IL	LA0571
<i>d</i>	<i>prov2</i>	dwarf	d	K*JT	CHEM	VCH	IL	3-623
<i>d</i>	<i>provcr-2</i>	dwarf	d [^] cr	K*JT	CHEM	VF36	IL	3-420
<i>d</i>	<i>provcr-3</i>	dwarf	d [^] cr	K*JT	CHEM	VF36	IL	3-422
<i>d</i>	<i>x</i>	dwarf		K*JT	SPON	SPZ	IL	LA0160
<i>d</i>	<i>x</i>	dwarf		K*JT	SPON	VAN	NIL	LA3902
<i>d</i>	<i>x</i>	dwarf		K*JT	SPON	PCV	NON	LA1052
<i>d</i>	<i>x</i>	dwarf		K*JT	SPON	AC	NIL	LA3615
<i>d-2</i>		dwarf-2	rob2, rob II, d2	K*N	RAD	RR	IL	LA0625
<i>dc</i>		decomposita	dc1	J*	RAD	RR	IL	LA0819
<i>dd</i>		double dwarf	d [^] xx	K*J	SPON	X	NON	LA0810
<i>de</i>		declinata		K*JU	RAD	AC	NIL	LA3742
<i>de</i>		declinata		K*JU	RAD	RR	IL	LA0594
<i>deb</i>		debilis		H*BCJ	RAD	AC	NIL	LA3727
<i>deb</i>		debilis		H*BCJ	RAD	CR	IL	LA0542
<i>dec</i>		decumbens		K*R	RAD	LU	IL	LA0669
<i>def</i>		deformis		J*LN	RAD	RR	IL	LA0543
<i>def</i>		deformis		J*LN	RAD	AC	NIL	LA3749
<i>def</i>	2	deformis	vit	J*	RAD	CR	IL	LA0634
<i>def-2</i>		deformis		J*LN	RAD	AC	NIL	LA2920
<i>Del</i>		Delta		P*	SPON	AC	NIL	LA2921
<i>Del</i>		Delta		P*	SPON	RU	NIL	LA2996A
<i>Del</i>		Delta		P*	SPON	M82	NON	LA4099
<i>deli</i>		deliquescens		K*CJ	RAD	RR	IL	LA0595
<i>dep</i>		deprimata		T*J	RAD	CR	IL	LA0544
<i>depa</i>		depauperata		K*CJ	RAD	RR	IL	LA0596
<i>depa</i>		depauperata		K*CJ	RAD	AC	NIL	LA3725
<i>det</i>		detrimentosa		C*KF	RAD	RR	IL	LA0670
<i>det</i>	2	detrimentosa		C*KF	RAD	RR	IL	LA0820
<i>Df</i>		Defoliator		Y*H	SPON	par	NON	LA0247
<i>dgt</i>		diageotropica	lz-3	K*R	SPON	VFN8	IL	LA1093
<i>dgt</i>	<i>dp</i>	diageotropica	dp	J*KT	RAD	CT	IL	LA2526
<i>Dia-2</i>	1	Diaphorase-2		V*	SPON	pen	NON	LA2987
<i>Dia-2</i>	2	Diaphorase-2		V*	SPON	VF36	NIL	LA4232
<i>Dia-3</i>	1	Diaphorase-3		V*	SPON	X	NON	LA3345
<i>Dia-3</i>	1	Diaphorase-3		V*	SPON	VF36	NIL	LA4269
<i>Dia-4</i>	1	Diaphorase-4		V*	SPON	VF36	NIL	LA4284
<i>dil</i>		diluta		D*JK	RAD	CR	IL	LA0545
<i>dil</i>		diluta		D*JK	RAD	AC	NIL	LA3728
<i>dim</i>		diminuta		A*DK	RAD	LU	IL	LA0597
<i>dim-2</i>		diminuta-2	dim2	A*K	RAD	AC	NIL	LA3170
<i>dis</i>		discolor		D*F	RAD	CR	IL	LA0598
<i>div</i>		divaricata		C*AJK	RAD	CR	NON	LA0671
<i>div</i>		divaricata		C*AJK	RAD	AC	NIL	LA3818
<i>dl</i>		dialytic		I*LN	SPON	SM	IL	2-069
<i>dl</i>		dialytic		I*LN	SPON	AC	NIL	LA3724
<i>dl</i>	S	dialytic	DI's	L*N	SPON	VF36	NIL	LA3906
<i>dlb</i>		dilabens	dlb1	C*JK	RAD	CR	IL	LA0829
<i>dm</i>		dwarf modifier	d2	K*	SPON	X	NON	LA0014
<i>dmd</i>		dimidiata		K*JU	RAD	LU	IL	LA2033
<i>dmt</i>		diminutiva		K*	CHEM	VF36	IL	3-007
<i>dps</i>		diospyros		P*	SPON	X	NON	LA1016
<i>dpy</i>		dumpy		K*J	SPON	X	NON	LA0811
<i>dpy</i>		dumpy		K*J	SPON	AC	NIL	LA3171
<i>dpy</i>	<i>prov2</i>	dumpy	dpy	K*J	CHEM	VCH	IL	3-630
<i>dpy</i>	<i>prov3</i>	dumpy	dpy	K*J	SPON	ANU	IL	LA1053
<i>drt</i>		dwarf root		R*	CHEM	X	NON	LA3207
<i>ds</i>		dwarf sterile		N*K	SPON	EPK	IL	2-247

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<i>ds</i>		dwarf sterile		N*K	SPON	AC	NIL	LA3767
<i>dt</i>		dilatata	dt1	C*JK	RAD	CR	IL	LA0828
<i>dt</i>		detorta		J*K	RAD	LU	IL	LA2030
<i>du</i>		dupla		J*KU	RAD	LU	IL	LA2034
<i>dv</i>		dwarf virescent		F*D	SPON	X	NON	LA0155
<i>e</i>		entire	b	J*	SPON	AC	NIL	LA2922
<i>e</i>	<i>prov3</i>	entire	e	J*	CHEM	VCH	IL	3-616
<i>eca</i>		echinata		K*	RAD	RR	IL	LA2035
<i>el</i>		elongated	e	O*	SPON	AC	NIL	LA3738
<i>ele</i>		elegans		E*JK	RAD	CR	IL	LA0546
<i>ele</i>		elegans		E*JK	RAD	AC	NIL	LA3825
<i>ele</i>	2	elegans	ang	E*JK	RAD	CR	IL	LA0586
<i>elu</i>		eluta		E*K	RAD	LU	IL	LA0547
<i>em</i>		emortua	em1	H*K	RAD	RR	IL	LA0827
<i>em</i>		emortua	em1	H*K	RAD	AC	NIL	LA3817
<i>en</i>		ensiform		J*	SPON	X	NON	LA1787
<i>ep</i>		easy peeling		O*	RAD	MM	IL	LA1158
<i>ep</i>		easy peeling		O*	RAD	AC	NIL	LA3616
<i>Epi</i>		Epinastic		J*K	SPON	VFN8	IL	LA2089
<i>er</i>		erecta		K*JT	RAD	CR	IL	LA0600
<i>era</i>		eramosa	era1	B*JK	RAD	CR	IL	LA0850
<i>Est-1</i>	1	Esterase-1		V*	SPON	cer	IL	LA2415
<i>Est-1</i>	1	Esterase-1		V*	SPON	pim	NON	LA1818
<i>Est-1</i>	2	Esterase-1		V*	SPON	pim	NON	LA1819
<i>Est-1</i>	3	Esterase-1		V*	SPON	pim	NON	LA1820
<i>Est-1</i>	4	Esterase-1		V*	SPON	par	NON	LA1821
<i>Est-1</i>	5	Esterase-1		V*	SPON	pen	NON	LA2419
<i>Est-1</i>	<i>n</i>	Esterase-1		V*	SPON	pim	NON	LA1817
<i>Est-2</i>	1	Esterase-2		V*	SPON	pen	NON	LA2420
<i>Est-3</i>	1	Esterase-3		V*	SPON	par	NON	LA2421
<i>Est-4</i>	1	Esterase-4		V*	SPON	par	NON	LA2422
<i>Est-4</i>	2	Esterase-4		V*	SPON	pim	NON	LA2423
<i>Est-4</i>	4	Esterase-4		V*	SPON	PCV	NON	LA2425
<i>Est-4</i>	5	Esterase-4		V*	SPON	pim	NON	LA2426
<i>Est-4</i>	6	Esterase-4		V*	SPON	pim	NON	LA2427
<i>Est-4</i>	7	Esterase-4		V*	SPON	cer	NON	LA2428
<i>Est-4</i>	8	Esterase-4		V*	SPON	pim	NON	LA2429
<i>Est-5</i>	1	Esterase-5		V*	SPON	pen	NON	LA2430
<i>Est-6</i>	1	Esterase-6		V*	SPON	pen	NON	LA2431
<i>Est-7</i>	1	Esterase-7		V*	SPON	par	NON	LA2432
<i>Est-7</i>	2	Esterase-7		V*	SPON	pen	NON	LA2433
<i>Est-8</i>	1	Esterase-8		V*	SPON	pen	NON	LA2988
<i>ete</i>		extenuata	ete1	K*JN	RAD	CR	IL	LA0942
<i>ex</i>		exserted stigma		L*N	SPON	SM	IL	2-191
<i>exl</i>		exilis	ex	D*JK	RAD	CR	IL	LA0601
<i>exs</i>		excedens	exs1	K*J	RAD	CR	IL	LA0852
<i>f</i>		fasciated fruit		O*L	SPON	ESC	NON	LA0517
<i>f</i>	<i>D</i>	fasciated fruit		O*L	SPON	PCV	NON	LA0767
<i>fa</i>		falsiflora	fa1	M*N	RAD	RR	IL	LA0854
<i>fcf</i>		fucatifolia	fcf1	D*CK	RAD	CR	IL	LA0945
<i>fd</i>		flecked dwarf		G*DK	RAD	BK	NON	LA0873
<i>fd</i>		flecked dwarf		G*DK	RAD	AC	NIL	LA3750
<i>Fdh-1</i>	1	Formate dehydrogenase-1		V*	SPON	pen	IL	LA2989
<i>Fdh-1</i>	2	Formate dehydrogenase-1		V*	SPON	VF36	NIL	LA4238
<i>fe</i>		fertilis		J*LO	RAD	LU	IL	LA0672
<i>fer</i>		fe inefficient		B*		X	NON	LA2994
<i>fgv</i>		fimbriate gold virescent		F*CJ	SPON	VF36	IL	LA1143
<i>fir</i>		firma		K*JM	RAD	CR	IL	LA0602
<i>fl</i>		fleshy calyx		O*	SPON	X	NON	LA2372

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<i>fla</i>		flavescens		D*JK	RAD	LU	IL	LA0548
<i>fla</i>		flavescens		D*JK	RAD	AC	NIL	LA3565
<i>flav</i>		flavida		C*	RAD	LU	IL	LA0603
<i>flc</i>		flacca		W*HJY	RAD	RR	IL	LA0673
<i>flc</i>		flacca		W*HJY	RAD	AC	NIL	LA3613
<i>fld</i>		flaccida	fld1	K*HJT	RAD	RR	IL	LA0943
<i>fle</i>		flexifolia	fle1	A*J	RAD	AC	NIL	LA3764
<i>fn</i>		finely-netted		D*	RAD	PSP	IL	LA2005
<i>fr</i>		frugalis		K*JT	RAD	CR	IL	LA0674
<i>frg</i>		fragilis	frg1	D*CJK	RAD	CR	IL	LA0864
<i>fri</i>	1	far red light insensitive		AY*	CHEM	MM	IL	LA3809
<i>Frl</i>		FORL resistance	Fr1, Fr-1	Q*	SPON	VGB	NON	LA3841
<i>Frl</i>		FORL resistance	Fr1, Fr-1	Q*	SPON	AC	NIL	LA3273
<i>Frs</i>		Frosty spot	Nec	H*	SPON	X	NON	LA2070
<i>frt</i>		fracta		K*JT	RAD	LU	IL	LA2038
<i>fsc</i>		fuscatinervis	dkv	E*	SPON	VF145	IL	LA0872
<i>ft</i>		fruiting temperature		O*	SPON	X	NON	LA2006
<i>fu</i>		fusiformis		C*JK	RAD	AC	NIL	LA3070
<i>fu</i>		fusiformis		C*JK	RAD	CR	IL	LA0605
<i>fua</i>		fucata	fua1	E*K	RAD	CR	IL	LA0944
<i>fug</i>		fulgida	fug1	E*BK	RAD	RR	IL	LA0946
<i>ful</i>		fulgens		E*	RAD	CR	IL	LA0550
<i>ful</i>	2	fulgens	ful1^2	E*	RAD	RR	IL	LA0843
<i>ful-3</i>		fulgens-3		E*	SPON	VF36	IL	LA1495
<i>fus</i>		fulgescens		E*	RAD	LU	IL	LA2039
<i>Fw</i>		Furrowed		J*KN	SPON	AC	NIL	LA3300
<i>Fw</i>		Furrowed		J*KN	SPON	PSN	IL	LA0192
<i>fx</i>		flexa		K*	RAD	LU	IL	LA2037
<i>fy</i>		field yellow		E*	SPON	VF36	IL	2-565
<i>fy</i>		field yellow		E*	SPON	AC	NIL	LA3295
<i>ga</i>		galbina	ga1	D*BE	RAD	CR	IL	LA0836
<i>ga</i>		galbina	ga1	D*BE	RAD	AC	NIL	LA3828
<i>gas</i>		gamosepala	gas1	D*JL	RAD	RR	IL	LA0947
<i>gbl</i>		globula		K*JU	RAD	LU	IL	LA2032
<i>Ge</i>	c	Gamete eliminator		N*	SPON	CR	NON	LA0533
<i>Ge</i>	p	Gamete eliminator		N*	SPON	PSN	NON	LA0012
<i>gf</i>		green flesh		P*	SPON	RU	NIL	LA2999
<i>gf</i>		green flesh		P*	SPON	AC	NIL	LA3534
<i>gf</i>		green flesh		P*	SPON	PCV	NON	LA2071
<i>gfl</i>		globular flower		L*	SPON	X	NON	LA2984
<i>gh</i>		ghost	ab	B*G	SPON	SM	IL	LA0295
<i>gh-2</i>		ghost-2		C*G	CHEM	SX	IL	LA2007
<i>gi</i>		gibberosa		J*K	RAD	RR	IL	LA2040
<i>gib-1</i>		gibberellin deficient-1		K*Y	CHEM	MM	IL	LA2893
<i>gib-2</i>		gibberellin deficient-2		K*Y	CHEM	MM	IL	LA2894
<i>gib-3</i>		gibberellin-deficient-3		K*Y	CHEM	MM	IL	LA2895
<i>gib-3</i>	x	gibberellin-deficient-3		K*Y	CHEM	X	NON	LA2993
<i>gl</i>		glauca		J*F	RAD	CR	IL	LA0675
<i>glau</i>		glaucescens		E*JK	RAD	CR	IL	LA0606
<i>glb</i>		globularis		K*CJ	RAD	RR	IL	LA0677
<i>glc</i>		glaucophylla		D*JK	RAD	RR	IL	LA0676
<i>glf</i>		globiformis	glf1	K*M	RAD	CR	IL	LA0948
<i>glg</i>		galapagos light green		D*	SPON	X	NON	LA1059
<i>glm</i>		glomerata		K*	RAD	LU	IL	LA2031
<i>glo</i>		globosa		K*	RAD	CR	IL	LA0551
<i>glo</i>	2	globosa	inx, intro	K*	RAD	LU	IL	LA0612
<i>glo</i>	2	globosa	inx, intro	K*	RAD	AC	NIL	LA3618
<i>glu</i>		glutinosa	glu1	O*P	RAD	RR	IL	LA0842
<i>gm</i>		gamosepalous		L*	RAD	SX	IL	LA2008

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<i>Got-1</i>	1	Glutamate oxaloacetate transaminase-1		V*	SPON	pim	NON	LA1822
<i>Got-1</i>	2	Glutamate oxaloacetate transaminase-1		V*	SPON	pim	NON	LA1823
<i>Got-2</i>	1	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1825
<i>Got-2</i>	2	Glutamate oxaloacetate transaminase-2		V*	SPON	che	NON	LA1826
<i>Got-2</i>	3	Glutamate oxaloacetate transaminase-2		V*	SPON	par	NON	LA1827
<i>Got-2</i>	4	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1828
<i>Got-2</i>	<i>n</i>	Glutamate oxaloacetate transaminase-2		V*	SPON	pim	NON	LA1824
<i>Got-3</i>	2	Glutamate oxaloacetate transaminase-3		V*	SPON	pim	NON	LA1831
<i>Got-3</i>	3	Glutamate oxaloacetate transaminase-3		V*	SPON	par	NON	LA1832
<i>Got-3</i>	<i>n</i>	Glutamate oxaloacetate transaminase-3		V*	SPON	che	NON	LA1829
<i>Got-4</i>	1	Glutamate oxaloacetate transaminase-4		V*	SPON	par	NON	LA1834
<i>Got-4</i>	2	Glutamate oxaloacetate transaminase-4		V*	SPON	pim	NON	LA1835
<i>Got-4</i>	<i>n</i>	Glutamate oxaloacetate transaminase-4		V*	SPON	cer	NON	LA1833
<i>Gp</i>		Gamete promoter		N*	SPON	AC	NIL	LA3273
<i>gq</i>		grotesque		L*O	SPON	X	NON	LA0137
<i>Gr</i>		Green ripe	gr	P*	SPON	X	NON	LA2453
<i>gra</i>		gracilis		K*J	RAD	CR	IL	LA0607
<i>grc</i>		gracillama	grc1	E*JK	RAD	RR	IL	LA0950
<i>grf</i>		grandifructa	grf1	K*O	RAD	LU	IL	LA0951
<i>grl</i>		gracilentia	grl1	E*JK	RAD	RR	IL	LA0949
<i>grn</i>		granulosa		I*	CHEM	CSM	IL	3-804
<i>gro</i>		grossa		J*DK	RAD	LU	IL	LA2041
<i>gs</i>		green stripe		P*	SPON	GSM	IL	LA0212
<i>gs</i>		green stripe		P*	SPON	AC	NIL	LA3530
<i>h</i>		hairs absent	H	I*	SPON	AC	NIL	LA3172
<i>h</i>		hairs absent	H	I*	SPON	X	NON	LA0154
<i>he</i>		heteroidea		D*JK	RAD	CR	IL	LA0679
<i>Hero</i>		<i>Heterodera rostochiensis</i> resistance		Q*	SPON	X	NON	LA1792
<i>hg</i>		heterogemma	hg1	K*M	RAD	CR	IL	LA0837
<i>hi</i>		hilara		K*DJT	RAD	CR	IL	LA0952
<i>hl</i>		hairless		I*X	SPON	AC	NIL	LA3556
<i>hl</i>	2	hairless	cal, cal1	I*X	RAD	CR	IL	LA0937
<i>hl</i>	<i>prov3</i>	hairless	hl	I*X	CHEM	VCH	IL	3-095
<i>hl</i>	<i>prov4</i>	hairless	hl	I*X	CHEM	VCH	IL	3-126
<i>hl</i>	<i>prov5</i>	hairless	hl	I*X	CHEM	VCH	IL	3-605
<i>hl-2</i>		hairless-2	hl^prov6	I*X	CHEM	VF36	NON	3-417
<i>hp-1</i>		high pigment-1	hp, hp1, hp2, bs, dr	P*TA	SPON	AC	NIL	LA3538
<i>hp-1</i>		high pigment-1	hp, hp1, hp2, bs, dr	P*TA	SPON	X	NON	LA0279
<i>hp-1</i>		high pigment-1	hp, hp1, hp2, bs, dr	P*TA	SPON	RU	NIL	LA3004
<i>hp-1</i>	<i>w</i>	high pigment-1		P*TA	CHEM	GT	IL	LA4012
<i>hp-2</i>		high pigment-2	hp	P*TA	CHEM	MM	NON	LA4013
<i>hp-2</i>		high pigment-2	hp	P*TA	CHEM	SM	NIL	LA3006
<i>hp-2</i>	<i>dg</i>	high pigment-2	dg	P*AT	SPON	MP	IL	LA2451

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>hp-2</i>	<i>dg</i>	high pigment-2	dg	P*AT	SPON	MP	NIL	LA3005
<i>hp-2</i>	<i>j</i>	high pigment-2	hp	P*T	SOMA	MM	NON	LA4014
<i>Hr</i>		Hirsute		I*	SPON	X	IL	LA0895
<i>Hrt</i>		Hirtum		I*	SPON	X	NON	LA0501
<i>ht</i>		hastate		J*L	SPON	SM	IL	2-295
<i>hy</i>		homogeneous yellow		E*	SPON	cer	NON	LA1142
<i>hy</i>		homogeneous yellow		E*	SPON	AC	NIL	LA3308
<i>I</i>		Immunity to <i>Fusarium</i> wilt race 0		Q*	SPON	VD	NIL	LA3025
<i>I</i>		Immunity to <i>Fusarium</i> wilt race 0		Q*	SPON	GRD	NIL	LA3042
<i>I-2</i>		Immunity to <i>Fusarium</i> wilt race 2		Q*	SPON	MM	NIL	LA2821
<i>I-3</i>		Immunity to <i>Fusarium</i> race 3		Q*	SPON	X	NON	LA4026
<i>I-3</i>		Immunity to <i>Fusarium</i> race 3		Q*	SPON	X	NON	LA4025
<i>ic</i>		inclinata		J*CK	RAD	RR	IL	LA0682
<i>ica</i>		icana		B*JK	RAD	RR	IL	LA2042
<i>icn</i>		incana		B*F	SPON	X	NON	LA1009
<i>icn</i>		incana		B*F	SPON	AC	NIL	LA3173
<i>id</i>		indehiscens		L*JO	RAD	RR	IL	LA0684
<i>ida</i>		inordinata		K*JT	RAD	RR	IL	LA2043
<i>ldh-1</i>	<i>1</i>	Isocitrate dehydrogenase-1		V*	SPON	hir	NON	LA2906
<i>ig</i>		ignava		D*K	RAD	CR	IL	LA0608
<i>ig</i>		ignava		D*K	RAD	AC	NIL	LA3752
<i>im</i>		impatiens	im1	K*UW	RAD	RR	IL	LA0863
<i>imb</i>		imbecilla		E*DK	SPON	CR	IL	LA0552
<i>imb</i>		imbecilla		E*DK	SPON	AC	NIL	LA3566
<i>imp</i>	<i>dia</i>	impedita		E*K	SPON	CR	IL	LA0680
<i>imp</i>	<i>eg</i>	impedita		E*K	SPON	CR	IL	LA0681
<i>ina</i>		inflexa	ina1	K*	RAD	AC	NIL	LA3732
<i>ina</i>		inflexa	ina1	K*	RAD	LU	IL	LA0840
<i>inc</i>		incurva		K*J	RAD	CR	IL	LA0609
<i>inc</i>		incurva		K*J	RAD	AC	NIL	LA3730
<i>inf</i>		informa		J*K	RAD	CR	IL	LA0553
<i>inf</i>		informa		J*K	RAD	AC	NIL	LA3726
<i>ini</i>		inquieta	ini1	I*DJK	RAD	RR	IL	LA0953
<i>ino</i>		involuta	ino1	K*	RAD	CR	IL	LA0954
<i>ins</i>		inconstans	ins1	K*	RAD	RR	IL	LA0841
<i>inv</i>		invalida		F*EJK	RAD	CR	IL	LA0554
<i>inv</i>		invalida		F*EJK	RAD	AC	NIL	LA3439
<i>lp</i>		Intense pigment		P*	SPON	VF145	NIL	LA1500
<i>lp</i>		Intense pigment		P*	SPON	VF145	NIL	LA1563
<i>irr</i>		irregularis		J*CT	RAD	CR	IL	LA0613
<i>irr</i>		irregularis		J*CT	RAD	AC	NIL	LA3747
<i>ita</i>		inquinata	ita1	H*G	RAD	RR	IL	LA0839
<i>j</i>		jointless	lf	M*	SPON	GRD	NIL	LA3033
<i>j</i>		jointless	lf	M*	SPON	FB	NIL	LA3023
<i>j-2</i>		jointless-2	j2	M*	SPON	PSN	NON	LA0315
<i>j-2</i>		jointless-2	j2	M*	SPON	O8245	NON	LA3899
<i>j-2</i>	<i>in</i>	jointless-2	j2 ⁱⁿ	M*	SPON	X	NON	LA0756
<i>Jau</i>		Jaundiced		E*	SPON	AC	NIL	LA3174
<i>jug</i>		jugata		K*LO	RAD	CR	IL	LA0555
<i>jug</i>	<i>2</i>	jugata	jug1 [^] 2	K*LO	RAD	LU	IL	LA0834
<i>l</i>		lutescent	g	C*	SPON	AC	NIL	LA3717
<i>l</i>	<i>2</i>	lutescent	rub	C*	RAD	LU	IL	LA0572
<i>l</i>	<i>prov3</i>	lutescent	l	C*	SPON	ROMA	IL	2-491
<i>l</i>	<i>prov4</i>	lutescent	l	C*	SPON	EPK	NIL	LA3009
<i>l-2</i>		lutescent-2	l-3, l2	C*Y	SPON	LRD	IL	LA0643
<i>l-2</i>		lutescent-2	l-3, l2	C*Y	SPON	AC	NIL	LA3581
<i>La</i>		Lanceolate		J*	SPON	PCV	NON	LA0335
<i>lae</i>		laesa		H*JK	RAD	RR	IL	LA0685
<i>lan</i>		languida		D*F	RAD	RR	IL	LA2044

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<i>lap</i>		lamprochlora	lap1	J*K	RAD	RR	IL	LA0955
<i>lat</i>		lata		K*	RAD	CR	IL	LA0556
<i>le</i>		lembiformis	le1	K*ACJR	RAD	RR	IL	LA0956
<i>lep</i>		leprosa	lep1	H*K	RAD	RR	IL	LA0957
<i>lg</i>		light-green	lme	D*	SPON	X	NON	LA1156
<i>lg</i>		light-green	lme	D*	SPON	AC	NIL	LA3175
<i>lg-5</i>		light green-5	lg5, lm, fy, yt	D*	SPON	X	NON	LA0757
<i>lg-5</i>		light green-5	lg5, lm, fy, yt	D*	SPON	AC	NIL	LA3176
<i>li</i>		limbrata		J*	RAD	LU	IL	LA2045
<i>Ln</i>		Lanata		I*	CHEM	VF36	IL	3-071
<i>Ln</i>	G	Lanata		I*	CHEM	FLD	IL	LA3127
<i>lop</i>		longipes	lop1	J*DK	RAD	CR	IL	LA0958
<i>Lpg</i>		Lapageria		J*LNT	SPON	VF36	IL	2-561
<i>Lpg</i>		Lapageria		J*LNT	SPON	AC	NIL	LA3739
<i>ls</i>		lateral suppresser		K*LN	SPON	AMB	NON	LA0329
<i>ls</i>		lateral suppresser		K*LN	SPON	X	NON	LA2892
<i>ls</i>		lateral suppresser		K*LN	SPON	AC	NIL	LA3761
<i>ls</i>	2	lateral suppresser		K*LN		PRI	NIL	LA3901
<i>lt</i>		laeta	lt1	E*DK	RAD	CR	IL	LA0835
<i>ltf</i>		latifolia		J*	CHEM	VF36	IL	3-035A
<i>lu</i>		luteola		L*	RAD	LU	IL	LA0686
<i>luc</i>		lucida		C*F	RAD	CR	IL	LA0557
<i>lur</i>		lurida	lur1	E*D	RAD	RR	IL	LA0959
<i>lut</i>		lutea		E*F	RAD	CR	IL	LA0558
<i>lut</i>		lutea		E*F	RAD	AC	NIL	LA3714
<i>Lv</i>		<i>Leveillula taurica</i> resistance		Q*	SPON	X	NON	LA3118
<i>Lv</i>		<i>Leveillula taurica</i> resistance		Q*	SPON	X	NON	LA3119
<i>Lx</i>		Lax		J*	SPON	LK	NON	LA0505
<i>Lx</i>		Lax		J*	SPON	AC	NIL	LA3177
<i>lyr</i>		lyrate		J*NO	SPON	PCV	NON	LA0763
<i>lyr</i>		lyrate		J*NO	SPON	AC	NIL	LA2923
<i>lz</i>		lazy		K*	RAD	AC	NIL	LA3762
<i>lz-2</i>		lazy-2		K*	CHEM	SM	NIL	LA2924
<i>lz-2</i>		lazy-2		K*	CHEM	AC	NIL	LA3710
<i>m</i>		mottled		G*J	RAD	AC	NIL	LA3568
<i>m-2</i>		mottled-2	m2, mo, md	F*D	RAD	AC	NIL	LA3574
<i>ma</i>		macrocarpa		J*O	RAD	LU	IL	LA0687
<i>mac</i>		maculata	mac1	H*K	RAD	CR	IL	LA0960
<i>mad</i>		marcida	mad1	T*K	RAD	CR	IL	LA0961
<i>Mae-1</i>		Malic enzyme-1		V*	SPON	VF36	NIL	LA4251
<i>mar</i>		marcescens		T*K	RAD	LU	NON	LA0688
<i>marm</i>		marmorata		G*D	RAD	CR	IL	LA0559
<i>marm</i>	2	marmorata	marm1^2	G*D	RAD	CR	IL	LA0844
<i>mc</i>		macrocalyx		L*M	SPON	X	NON	LA0159
<i>mcn</i>		maculonecrotic		G*H*CF	CHEM	VF36	IL	3-045
<i>mcr</i>		multicolor		B*CH	RAD	LU	IL	LA2047
<i>mcs</i>		macrosepala		L*J	RAD	LU	IL	LA2046
<i>Mdh-1</i>	1	Malate dehydrogenase-1		V*	SPON	X	NON	LA3344
<i>Mdh-1</i>	1	Malate dehydrogenase-1		V*	SPON	VF36	NIL	LA4243
<i>Mdh-4</i>	1	Malate dehydrogenase-4		V*	SPON	VF36	NIL	LA4283
<i>Me</i>		Mouse ears		J*K	SPON	RU	IL	LA0324
<i>Me</i>		Mouse ears		J*K	SPON	AC	NIL	LA3552
<i>med</i>		mediocris	med1	K*	RAD	CR	IL	LA0962
<i>mel</i>		melongenoida	mel1	O*K	RAD	LU	IL	LA0963
<i>mgn</i>		marginal necrotic		H*C	CHEM	VF36	IL	3-025
<i>Mi</i>		<i>Meloidogyne incognita</i> resistance		Q*	SPON	VFN8	NON	LA1022
<i>Mi</i>		<i>Meloidogyne incognita</i> resistance		Q*	SPON	MM	NIL	LA2819
<i>Mi-3</i>		<i>Meloidogyne incognita</i>		Q*	SPON	per	NON	LA3858

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		resistance-3						
<i>mic</i>		microcarpa	mic1	D*GLO	RAD	CR	IL	LA0845
<i>mn</i>		minuta	mi	K*CJ	RAD	CR	IL	LA0614
<i>mn</i>		minuta	mi	K*CJ	RAD	AC	NIL	LA3082
<i>mon</i>		monstrosa		K*J	RAD	CR	IL	LA0615
<i>mon</i>		monstrosa		K*J	RAD	AC	NIL	LA3826
<i>mor</i>		morata	mor1	E*K	RAD	RR	IL	LA0848
<i>ms-2</i>		male-sterile-2	ms2	N*	SPON	PSN	IL	2-031
<i>ms-3</i>		male-sterile-3	ms3	N*	SPON	SM	IL	2-032
<i>ms-5</i>		male-sterile-5	ms5	N*	SPON	SM	IL	2-039
<i>ms-6</i>		male-sterile-6	ms6	N*	SPON	SM	IL	2-044
<i>ms-7</i>		male-sterile-7	ms7	N*	SPON	SM	IL	2-089
<i>ms-9</i>		male-sterile-9	ms9	N*	SPON	SM	IL	2-121
<i>ms-10</i>		male-sterile-10	ms10	N*	SPON	SM	IL	2-132
<i>ms-10</i>	35	male-sterile-10	ms-35, ms35	N*	SPON	VF11	IL	2-517
<i>ms-10</i>	36	male-sterile-10	ms-36	N*	SPON	VF36	IL	2-635
<i>ms-11</i>		male-sterile-11	ms11	N*	SPON	SM	IL	2-152
<i>ms-12</i>		male-sterile-12	ms12	N*	SPON	SM	IL	2-161
<i>ms-13</i>		male-sterile-13	ms13	N*	SPON	SM	IL	2-165
<i>ms-14</i>		male-sterile-14	ms14	N*	SPON	ERL	IL	2-175
<i>ms-15</i>		male-sterile-15	ms15	N*	SPON	SM	IL	2-193
<i>ms-15</i>	26	male-sterile-15	ms26, ms-26	N*	SPON	VE	IL	2-327
<i>ms-15</i>	47	male-sterile-15	ms-47	N*	SPON	UC82 B	NIL	2-837
<i>ms-16</i>		male-sterile-16	ms16	N*	SPON	PRT	IL	LA0062
<i>ms-17</i>		male-sterile-17	ms17	N*	SPON	ACE	IL	2-225
<i>ms-18</i>		male-sterile-18	ms18	N*	SPON	C255	IL	2-233
<i>ms-23</i>		male-sterile-23	ms23	N*	SPON	EPK	IL	2-273
<i>ms-24</i>		male-sterile-24	ms24	N*	SPON	EPK	IL	2-277
<i>ms-25</i>		male-sterile-25	ms25	N*	SPON	RTVF	IL	2-313
<i>ms-27</i>		male-sterile-27	ms27	N*	SPON	VE	IL	2-331
<i>ms-28</i>		male-sterile-28	ms28	N*	SPON	XLP	IL	2-355
<i>ms-29</i>		male-sterile-29	ms29	N*	SPON	CPC2	IL	2-423
<i>ms-30</i>		male-sterile-30	ms30	N*	SPON	SM	IL	2-455
<i>ms-31</i>		male-sterile-31	ms31	N*	SPON	VF6	IL	2-461
<i>ms-32</i>		male-sterile-32	ms32	N*	SPON	cer	NON	LA0359
<i>ms-32</i>		male-sterile-32	ms32	N*	SPON	MNB	NIL	LA2712
<i>ms-32</i>		male-sterile-32	ms32	N*	SPON	M167	NIL	LA2713
<i>ms-32</i>		male-sterile-32	ms32	N*	SPON	M168	NIL	LA2714
<i>ms-32</i>		male-sterile-32	ms32	N*	SPON	POR	NIL	LA2715
<i>ms-33</i>		male-sterile-33	ms33	N*	SPON	VF11	IL	2-511
<i>ms-34</i>		male-sterile-34	ms34	N*	SPON	VF11	IL	2-513
<i>ms-38</i>		male-sterile-38	ms38	N*	SPON	VF36	IL	2-539
<i>ms-38</i>	40	male-sterile-38	ms-40	N*	SPON	VF36	IL	2-553
<i>ms-39</i>		male-sterile-39		N*	SPON	VF36	IL	2-549
<i>ms-44</i>		male-sterile-44		N*	CHEM	SM	IL	LA2090
<i>ms-45</i>		male-sterile-45		N*	SPON	VFN8	IL	2-659
<i>ms-46</i>		male-sterile-46		N*	SPON	VFN8	IL	2-681
<i>Ms-48</i>		Male-sterile-48		N*	CHEM	VF36	NIL	LA3191
<i>Ms-48</i>		Male-sterile-48		N*	CHEM	VCH	NIL	LA3199
<i>Ms-48</i>		Male-sterile-48		N*	CHEM	CSM	IL	2-839
<i>Ms-48</i>		Male-sterile-48		N*	CHEM	T5	NIL	LA3198
<i>Ms-48</i>		Male-sterile-48		N*	CHEM	TVD	NIL	LA3192
<i>ms-49</i>		male-sterile-49		N*	SPON	per	NON	LA1161
<i>ms-50</i>		male sterile-50		N*	RAD	T5	IL	LA3149
<i>mt</i>		midget		K*N	SPON	NRT	NON	LA0282
<i>mta</i>		mutata	mta1	K*EFJ	RAD	RR	IL	LA0965
<i>mts</i>		mortalis	mts1	K*JM	RAD	RR	IL	LA0849
<i>mu</i>		multinervis		D*J	RAD	CR	IL	LA0690

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<i>mu</i>		multinervis		D*J	RAD	AC	NIL	LA3573
<i>mu</i>	3	multinervis	rv-3	D*J	CHEM	VF36	IL	3-033
<i>mua</i>		multifurcata	mua1	K*M	RAD	CR	IL	LA0851
<i>muf</i>		multifolia		J*DK	RAD	RR	IL	LA0689
<i>mult</i>		multiflora		M*	RAD	CR	IL	LA0560
<i>mup</i>		multiplicata	mup1	M*L	RAD	RR	IL	LA0846
<i>mut</i>		mutabilia	mut1	K*DT	RAD	RR	IL	LA0866
<i>muv-2</i>		multivalens-2	mus1	C*FJK	RAD	AC	NIL	LA3758
<i>muv-2</i>		multivalens-2	mus1	C*FJK	RAD	CR	IL	LA0964
<i>mux</i>		multiplex	mux1	L*KM	RAD	CR	IL	LA0847
<i>n</i>		nipple-tip	nt	O*	SPON	X	NON	LA2353
<i>n</i>		nipple-tip	nt	O*	SPON	X	NON	LA2370
<i>na</i>		nana		K*J	RAD	CR	IL	LA0561
<i>nc</i>		narrow cotyledons		J*	SPON	AC	NIL	LA3178
<i>nd</i>		netted	m-4	F*	RAD	AC	NIL	LA3584
<i>ndw</i>		necrotic dwarf		H*JK	SPON	X	NON	LA3142
<i>ndw</i>		necrotic dwarf		H*JK	SPON	M82	NIL	LA4061
<i>ne</i>		necrotic		H*	SPON	X	NON	LA2350
<i>ne</i>		necrotic		H*	SPON	AC	NIL	LA3084
<i>neg</i>		neglecta		H*DK	RAD	CR	IL	LA0562
<i>neg</i>		neglecta		H*DK	RAD	AC	NIL	LA3746
<i>neg</i>	<i>ne-2</i>	neglecta	ne-2, ne2	H*DK	RAD	AC	NIL	LA3621
<i>neg</i>	<i>ne-2</i>	neglecta	ne-2, ne2	H*DK	RAD	X	NON	LA2489
<i>neg</i>	<i>ne-2</i>	neglecta	ne-2, ne2	H*DK	RAD	CT	IL	LA2454
<i>Nir-1</i>	1	Nitrate reductase-1		V*	SPON	pen	IL	LA2908
<i>nor</i>		non-ripening		P*	SPON	X	NON	LA1793
<i>nor</i>		non-ripening		P*	SPON	RU	NIL	LA3013
<i>nor</i>		non-ripening		P*	SPON	AC	NIL	LA3770
<i>not</i>		notabilis		W*JY	RAD	LU	IL	LA0617
<i>not</i>		notabilis		W*JY	RAD	AC	NIL	LA3614
<i>Nr</i>		Never ripe		P*	SPON	PSN	IL	LA0162
<i>Nr</i>		Never ripe		P*	SPON	RU	NIL	LA3001
<i>Nr</i>		Never ripe		P*	SPON	AC	NIL	LA3537
<i>Nr-2</i>		Never ripe-2		P*	SPON	X	NON	LA2455
<i>nv</i>		netted virescent		E*F	SPON	X	NON	LA0786
<i>o</i>		ovate		O*	SPON	AC	NIL	LA3543
<i>O</i>	1	Oval	ol	O*	SPON	X	NON	LA0271
<i>ob</i>		obscura		T*K	RAD	RR	IL	LA0691
<i>obl</i>		oblate fruit		O*	RAD	MM	NIL	LA1159
<i>obv</i>		obscuravenosa		U*X	SPON	M82	NON	LA3475
<i>obv</i>	+	obscuravenosa		U*X	SPON	M82	NON	LA4057
<i>oc</i>		ochroleuca		G*BK	RAD	RR	IL	LA0692
<i>Od</i>		Odorless		I*	SPON	PCV	NON	LA0292
<i>oli</i>		olivacea		K*U	RAD	AC	NIL	LA3722
<i>op</i>		opaca		D*CF	RAD	CR	IL	LA0618
<i>op</i>		opaca		D*CF	RAD	AC	NIL	LA3567
<i>opa</i>		opacata	opa1	E*K	RAD	CR	IL	LA0966
<i>or</i>		ordinata		D*F	RAD	RR	IL	LA2048
<i>Ora</i>		<i>Orobanche aegyptica</i> resistance		Q*	SPON	X	NON	LA2530
<i>os</i>		oligosperma	os1	K*JT	RAD	CR	IL	LA0868
<i>ovi</i>		oviformis	ovi1	J*O	RAD	LU	IL	LA0967
<i>p</i>		peach		O*I	SPON	X	NON	LA2357
<i>pa-2</i>		parva-2	pa1, pa2	K*J	RAD	CR	IL	LA0970
<i>pal</i>		pallida		D*L	RAD	CR	IL	LA0563
<i>pap</i>		paupercula		J*W	RAD	RR	IL	LA2050
<i>pas</i>		pallescens	pas1	D*K	RAD	CR	IL	LA0968
<i>pat</i>		parthenocarpic fruit		S*	CHEM	ROMA	IL	LA2013
<i>pat-2</i>		parthenocarpic fruit-2		S*	SPON	X	NON	LA2413
<i>pau</i>		pauper		K*	RAD	CR	NON	LA0877

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<i>pct</i>		polycot		J*KLMS	SPON	MM	NON	LA2896
<i>pcv</i>		polychrome variegated		G*BDJ	SPON	X	NON	LA1199
<i>pcd</i>		puddica		K*JT	CHEM	VF36	IL	3-047
<i>pds</i>		phosphorus deficiency syndrome	Ph-oid	A*CY	SPON	X	NON	LA0813
<i>pdw</i>		pale dwarf		V*	SPON	X	NON	LA2457
<i>pdw</i>		pale dwarf		V*	SPON	X	NON	LA2490
<i>pe</i>		sticky peel		O*	SPON	X	NON	LA0759
<i>pen</i>		pendens		J*C	RAD	CR	IL	LA0694
<i>pen</i>		pendens		J*C	RAD	AC	NIL	LA3293
<i>per</i>		perviridis		A*KT	RAD	RR	IL	LA0564
<i>pet</i>		penetrabile	pet-2, pet2	K*J	RAD	CR	IL	LA0971
<i>Pgdh-2</i>	1	6-Phosphogluconate dehydrogenase-2		V*	SPON	pen	NON	LA2991
<i>Pgdh-3</i>	1	6-Phosphogluconate dehydrogenase-3		V*	SPON	pen	NON	LA2434
<i>Pgi-1</i>	1	Phosphoglucoisomerase-1		V*	SPON	pen	NON	LA2435
<i>Pgi-1</i>	2	Phosphoglucoisomerase-1		V*	SPON	par	NON	LA2436
<i>Pgm-1</i>	1	Phosphoglucomutase-1		V*	SPON	hir	NON	LA2437
<i>Pgm-2</i>	1	Phosphoglucomutase-2		V*	SPON	pen	NON	LA2438
<i>Ph</i>		<i>Phytophthora infestans</i> resistance	PiT, TR1	Q*	SPON	X	NON	LA2009
<i>Ph-2</i>		<i>Phytophthora infestans</i> resistance		Q*	SPON	UC82	NIL	LA3151
<i>Ph-2</i>		<i>Phytophthora infestans</i> resistance		Q*	SPON	MNB	NIL	LA3152
<i>Ph-3</i>		<i>Phytophthora infestans</i> resistance		Q	SPON	CLN22 64	NON	LA4285
<i>Ph-3</i>		<i>Phytophthora infestans</i> resistance		Q	SPON	CLN22 64	NON	LA4286
<i>pi</i>		pistillate		L*N	SPON	SM	IL	2-137
<i>pi-2</i>		pistillate-2		N*LM	CHEM	CSM	IL	3-802
<i>pic</i>		picta		H*C	RAD	CR	IL	LA0620
<i>pl</i>		perlucida	pl1	D*CJ	RAD	CR	IL	LA0867
<i>pl</i>		perlucida	pl1	D*CJ	RAD	AC	NIL	LA3296
<i>pla</i>		plana		D*CK	RAD	CR	IL	LA0695
<i>pli</i>		plicata		K*ABJ	RAD	LU	IL	LA0696
<i>pli</i>		plicata		K*ABJ	RAD	AC	NIL	LA3672
<i>pm</i>		praematura	pm1	Z*CJK	RAD	RR	IL	LA0855
<i>Pn</i>		Punctate		A*I	SPON	X	NON	LA0812
<i>Pn</i>		Punctate		A*I	SPON	AC	NIL	LA3089
<i>pol</i>		polylopha		K*JO	RAD	LU	IL	LA0697
<i>pp</i>		polyphylla	pp1	J*D	RAD	RR	IL	LA0860
<i>ppa</i>		purpurea		A*	RAD	LU	IL	LA2054
<i>pr</i>		propeller		J*	RAD	X	NON	LA0326
<i>pr</i>		propeller		J*	RAD	AC	NIL	LA2925
<i>prc</i>		procumbens		K*CJ	RAD	CR	IL	LA0698
<i>pre</i>		pressa		K*J	RAD	RR	IL	LA2053
<i>pro</i>		procera		J*Z	RAD	AC	NIL	LA3283
<i>pro</i>		procera		J*Z	RAD	CR	IL	LA0565
<i>prt</i>		protea	prt1	C*JK	RAD	CR	IL	LA0972
<i>prun</i>		prunoidea		O*J	RAD	LU	IL	LA0566
<i>Prx-1</i>	1	Peroxidase-1		V*	SPON	pim	NON	LA1837
<i>Prx-1</i>	2	Peroxidase-1		V*	SPON	pim	NON	LA1838
<i>Prx-1</i>	3	Peroxidase-1		V*	SPON	pim	NON	LA1839
<i>Prx-1</i>	4	Peroxidase-1		V*	SPON	chm	NON	LA1840
<i>Prx-1</i>	5	Peroxidase-1		V*	SPON	pim	NON	LA1841
<i>Prx-1</i>	<i>n</i>	Peroxidase-1		V*	SPON	pim	NON	LA1836
<i>Prx-2</i>	1	Peroxidase-2		V*	SPON	cer	NON	LA1843
<i>Prx-2</i>	3	Peroxidase-2		V*	SPON	pim	NON	LA1845
<i>Prx-2</i>	<i>n</i>	Peroxidase-2		V*	SPON	pim	NON	LA1842

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>Prx-3</i>	1	Peroxidase-3		V*	SPON	pim	NON	LA1847
<i>Prx-3</i>	2	Peroxidase-3		V*	SPON	pim	NON	LA1848
<i>Prx-3</i>	a1	Peroxidase-3		V*	SPON	chm	NON	LA1849
<i>Prx-3</i>	n	Peroxidase-3		V*	SPON	pim	NON	LA1846
<i>Prx-4</i>	1	Peroxidase-4		V*	SPON	pim	NON	LA1850
<i>Prx-4</i>	10	Peroxidase-4		V*	SPON	cer	NON	LA1859
<i>Prx-4</i>	11	Peroxidase-4		V*	SPON	pim	NON	LA1860
<i>Prx-4</i>	12	Peroxidase-4		V*	SPON	pim	NON	LA1861
<i>Prx-4</i>	13	Peroxidase-4		V*	SPON	pim	NON	LA1862
<i>Prx-4</i>	14	Peroxidase-4		V*	SPON	pim	NON	LA1863
<i>Prx-4</i>	15	Peroxidase-4		V*	SPON	pim	NON	LA1864
<i>Prx-4</i>	17	Peroxidase-4		V*	SPON	pim	NON	LA1866
<i>Prx-4</i>	18	Peroxidase-4		V*	SPON	pim	NON	LA1867
<i>Prx-4</i>	19	Peroxidase-4		V*	SPON	pim	NON	LA1868
<i>Prx-4</i>	2	Peroxidase-4		V*	SPON	pim	NON	LA1851
<i>Prx-4</i>	20	Peroxidase-4		V*	SPON	cer	NON	LA1869
<i>Prx-4</i>	21	Peroxidase-4		V*	SPON	pim	NON	LA1870
<i>Prx-4</i>	22	Peroxidase-4		V*	SPON	pim	NON	LA1871
<i>Prx-4</i>	23	Peroxidase-4		V*	SPON	pim	NON	LA1872
<i>Prx-4</i>	3	Peroxidase-4		V*	SPON	pim	NON	LA1852
<i>Prx-4</i>	4	Peroxidase-4		V*	SPON	chm	NON	LA1853
<i>Prx-4</i>	5	Peroxidase-4		V*	SPON	chm	NON	LA1854
<i>Prx-4</i>	6	Peroxidase-4		V*	SPON	par	NON	LA1855
<i>Prx-4</i>	7	Peroxidase-4		V*	SPON	STN	NON	LA1856
<i>Prx-4</i>	8	Peroxidase-4		V*	SPON	pim	NON	LA1857
<i>Prx-4</i>	9	Peroxidase-4		V*	SPON	pim	NON	LA1858
<i>Prx-7</i>	1	Peroxidase-7		V*	SPON	pim	NON	LA1873
<i>Prx-7</i>	2	Peroxidase-7		V*	SPON	pim	NON	LA1874
<i>Prx-7</i>	n	Peroxidase-7		V*	SPON	pim	NON	LA1875
<i>ps</i>		positional sterile	va	L*N	SPON	JBR	IL	LA0063
<i>ps</i>	<i>prov2</i>	positional sterile	ps	L*N	SPON	PSN	IL	2-303
<i>ps-2</i>		positional sterile-2		L*N	SPON	X	NON	LA2010
<i>ps-2</i>		positional sterile-2		L*N	SPON	VRB	IL	LA3631
<i>ps-2</i>		positional sterile-2		L*N	SPON	STR24	NON	LA3632
<i>psa</i>		perspicua		D*J	RAD	LU	IL	LA2051
<i>pst</i>		persistent style		O*	SPON	ESC	IL	2-005
<i>pt</i>		petite		D*	RAD	AC	NIL	LA3768
<i>pta</i>		partitaria		J*	RAD	RR	IL	LA2049
<i>ptb</i>		protuberant		O*	SPON	X	NON	LA1018
<i>ptb</i>		protuberant		O*	SPON	X	NON	LA1017
<i>Pto</i>		<i>Pseudomonas syringae</i> pv tomato resistance		Q*	SPON	X	NON	LA2396
<i>Pto</i>		<i>P. syringae</i> pv tomato resistance		Q*	SPON	RG	NIL	LA3342
<i>Pto</i>		<i>P. syringae</i> pv tomato resistance		Q*	SPON	MM	NIL	LA3472
<i>Pto</i>	2	<i>P. syringae</i> pv tomato resistance		Q*	SPON	RH13	NON	LA3129
<i>Pto</i>	<i>Pto-2</i>	<i>P. syringae</i> pv tomato resistance	Pto-2	Q*	SPON	pim	NON	LA2934
<i>Pts</i>		Petroselinum		J*	SPON	VF36	NIL	LA2532
<i>pu</i>		pulvinata	pul	K*J	RAD	RR	IL	LA0621
<i>pu</i>	2	pulvinata	pu2	K*J	RAD	CR	IL	LA0973
<i>pum</i>		pumila		K*	RAD	CR	IL	LA0567
<i>pum</i>		pumila		K*	RAD	AC	NIL	LA3741
<i>pun</i>		punctata	pun1	J*DGKT	RAD	RR	IL	LA0974
<i>pur</i>		purilla		K*C	RAD	CR	NON	LA0568
<i>px</i>		praecox	px1	K*JOZ	RAD	LU	IL	LA0856
<i>py</i>		pyramidalis		K*CJT	RAD	RR	IL	LA2055
<i>pyl</i>		<i>Pyrenochaeta lycopersici</i>	py, py-1	Q*	SPON	X	NON	LA2531A

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		resistance						
<i>r</i>		yellow flesh		P*	SPON	RU	NIL	LA2997
<i>r</i>		yellow flesh		P*	SPON	C37	NIL	LA3003
<i>r</i>		yellow flesh		P*	SPON	AC	NIL	LA3532
<i>r</i>	(2s)	yellow flesh	r ³ , r-2, r2	P*	RAD	RR	IL	LA2056
<i>r</i>	prov4	yellow flesh	r	P*	SPON	PSN	IL	2-141
<i>r</i>	prov5	yellow flesh	r	P*	SPON	EPK	IL	LA0353
<i>ra</i>		rava		D*CIJK	RAD	CR	IL	LA0569
<i>ra</i>	2	rava	gri	D*CIJK	RAD	RR	IL	LA0678
<i>rd</i>		reduced		K*	SPON	X	NON	LA2459B
<i>re</i>		reptans		K*	RAD	RR	IL	LA0624
<i>rela</i>		relaxata		K*D	RAD	CR	IL	LA0622
<i>rela</i>		relaxata		K*D	RAD	AC	NIL	LA3757
<i>rep</i>		repens		K*J	RAD	CR	IL	LA0623
<i>rep-2</i>		repens-2		K*J	RAD	LU	IL	LA2057
<i>res</i>		restricta	res1	C*ADJK	RAD	AC	NIL	LA3756
<i>res</i>		restricta	res1	C*ADJK	RAD	RR	IL	LA1085
<i>Rg-1</i>		Regeneration-1			SPON	GT	NON	LA4136
<i>ri</i>		ridged	rl	J*R	RAD	X	NON	LA1794
<i>ri</i>		ridged	rl	J*R	RAD	AC	NIL	LA3180
<i>ria</i>		rigidula	ria1	C*JKT	RAD	CR	IL	LA0825
<i>ria</i>	2	rigidula	ria1^2	C*JKT	RAD	LU	IL	LA0975
<i>rig</i>		rigida		C*K	RAD	CR	IL	LA0699
<i>rig</i>	2	rigida	pca, pca1	C*K	RAD	LU	IL	LA0822
<i>rig-2</i>		rigida-2		C*K	RAD	AC	NIL	LA3716
<i>rin</i>		ripening inhibitor		P*	SPON	X	NON	LA1795
<i>rin</i>		ripening inhibitor		P*	SPON	RU	NIL	LA3012
<i>rin</i>		ripening inhibitor		P*	SPON	AC	NIL	LA3754
<i>rl</i>		radial cracking resistance	ra	O*	SPON	AC	NIL	LA3092
<i>ro</i>		rosette		K*	RAD	X	NON	LA0270
<i>roa</i>		rotundata	roa1	J*DK	RAD	CR	IL	LA0976
<i>rot</i>		rotundifolia		J*K	RAD	AC	NIL	LA3751
<i>rot</i>		rotundifolia		J*K	RAD	RR	IL	LA0700
<i>Rs</i>		Root suppressed		R*	RAD	X	NON	LA1796
<i>rt</i>		potato virus Y resistance		Q*	SPON	SCZ	IL	LA1995
<i>rtd</i>		retarded dwarf		J*K	SPON	X	NON	LA1058
<i>ru</i>		ruptilis		J*D	RAD	CR	IL	LA0626
<i>ru</i>		ruptilis		J*D	RAD	AC	NIL	LA3440
<i>ru</i>	prov2	ruptilis	ru	J*D	CHEM	VF36	IL	3-081
<i>rust</i>		rustica		K*J	RAD	LU	IL	LA0573
<i>rust</i>		rustica		K*J	RAD	AC	NIL	LA3766
<i>rv-2</i>		reticulate virescent-2		D*C	CHEM	SX	IL	LA2011
<i>rv-4</i>		reticulate virescent-4		G*	SPON	X	NON	LA1496
<i>rvt</i>		red vascular tissue		X*	SPON	X	NON	LA1799
<i>s</i>		compound inflorescence		M*	SPON	X	NON	LA0330
<i>s</i>		compound inflorescence		M*	SPON	AC	NIL	LA3181
<i>sa</i>		sphacelata	sa1	H*CK	RAD	CR	IL	LA0865
<i>sar</i>		squarulosa	sar1	K*	RAD	CR	IL	LA0978
<i>scf</i>		scurfy		J*	SPON	PCV	NON	LA0767
<i>scl</i>		seasonal chlorotic lethal		C*	SPON	X	NON	LA1007
<i>sd</i>		sundwarf		K*	SPON	X	NON	LA0015
<i>sd</i>		sundwarf		K*	SPON	AC	NIL	LA3182
<i>Se</i>		<i>Septoria lycopersici</i> resistance		Q*	SPON	X	NON	LA1800
<i>sem</i>		semiglobosa		K*JT	RAD	CR	IL	LA0701
<i>ses</i>		semisterilis	ses1	C*DKN	RAD	LU	IL	LA0826
<i>sf</i>		solanifolia		J*LO	SPON	PSN	IL	2-311
<i>sf</i>		solanifolia		J*LO	SPON	AC	NIL	LA3674
<i>sf</i>	wl	solanifolia	wl, wr	J*LO	CHEM	ROMA	IL	LA2012
<i>sfa</i>		sufflaminata	sfa1	C*AEK	RAD	RR	IL	LA0862

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<i>sfa</i>	2	sufflaminata	par	C*AEK	RAD	CR	IL	LA0969
<i>sft</i>		single flower truss		M*	SPON	PTN	IL	LA2460
<i>sh</i>		sherry		P*	RAD	CX	IL	LA2644
<i>sha</i>		short anthers		L*N	CHEM	ROMA	IL	LA2013
<i>si</i>		sinuata		E*JK	RAD	AC	NIL	LA3728B
<i>si</i>		sinuata		E*JK	RAD	RR	IL	LA0993
<i>sig-1</i>		signal transduction-1	JL1	Y*	CHEM	CSM	IL	LA3318
<i>sig-2</i>		signal transduction-2	JL5	Y*	CHEM	CSM	IL	LA3319
<i>sit</i>		sitiens		W*HJKY	RAD	RR	IL	LA0574
<i>Skdh-1</i>	1	Shikimic acid dehydrogenase-1		V*	SPON	pen	NON	LA2439
<i>sl</i>		stamenless		L*N	SPON	AC	NIL	LA3816
<i>sl</i>		stamenless		L*N	SPON	X	NON	LA0269
<i>sl</i>	cs	stamenless	cs, sl ⁴ , sl ⁵	L*N	SPON	ONT	IL	LA1789
<i>sl-2</i>		stamenless-2	sl2	L*N	SPON	X	NON	LA1801
<i>slx</i>		serrate lax leaf		J*	SPON	PCV	NON	LA0503
<i>Sm</i>		<i>Stemphyllium</i> resistance		Q*	SPON	X	NON	LA1802
<i>Sm</i>		<i>Stemphyllium</i> resistance		Q*	SPON	MM	IL	LA2821
<i>sn</i>		singed		I*	SPON	CX	IL	LA2015
<i>snt</i>		Snout	sn	O*	SPON	X	NON	LA0499
<i>so</i>		soluta		J*	RAD	LU	IL	LA2058
<i>Sod-1</i>	1	Superoxide dismutase-1		V*	SPON	pen	NON	LA2909
<i>Sod-2</i>	1	Superoxide dismutase-2		V*	SPON	pen	NON	LA2910
<i>sp</i>		self-pruning		K*	SPON	TT	NON	LA0154
<i>sp</i>		self-pruning		K*	SPON	VF36	NON	LA0490
<i>sp</i>		self-pruning		K*	SPON	GRD	NIL	LA3133
<i>sp</i>	+	self-pruning		K*	SPON	M82	NIL	LA4287
<i>sp</i>	prov2	self-pruning		K*	RAD	VCH	IL	LA2705
<i>spa</i>		sparsa		E*BK	RAD	CR	IL	LA0703
<i>spe</i>		splendida	spe1	C*K	RAD	RR	IL	LA0977
<i>sph</i>		sphaerica		K*T	RAD	AC	NIL	LA3744
<i>sph</i>		sphaerica		K*T	RAD	CR	IL	LA0704
<i>Spi</i>	2	Sympodial index		K*	SPON	pen	NON	LA0716
<i>spl</i>		splendens	spl1	C*DJ	RAD	LU	IL	LA0821
<i>spl</i>		splendens	spl1	C*DJ	RAD	AC	NIL	LA3282
<i>squa</i>		squarrosa		D*KU	RAD	LU	IL	LA0627
<i>sr</i>		slender stem	sm	J*KU	RAD	CT	IL	LA1803
<i>ss</i>		spongy seed		S*	RAD	AC	NIL	LA3619
<i>sta</i>		stabilis		K*	RAD	RR	IL	LA2060
<i>ste</i>		sterilis		J*DKN	RAD	CR	IL	LA0705
<i>stri</i>		stricta		J*K	RAD	LU	IL	LA0575
<i>stu</i>		stunted		J*	SPON	X	NON	LA2461
<i>su</i>		suffulta		C*JM	RAD	LU	IL	LA0628
<i>su</i>	2	suffulta	exa	C*JM	RAD	RR	IL	LA0853
<i>su</i>	3	suffulta	di	C*J	RAD	CR	IL	LA0599
<i>su</i>	ni	suffulta	di ⁿⁱ , ni	C*J	RAD	CR	IL	LA0616
<i>sua</i>		suffusa		D*CK	RAD	RR	IL	LA0707
<i>sub</i>		subtilis		J*K	RAD	LU	IL	LA0576
<i>suc</i>		succedanea		C*JK	RAD	CR	IL	LA0706
<i>sucr</i>		sucrose accumulator	TIV1	P*	SPON	H100	NIL	LA4104
<i>suf</i>		sufflava		D*	RAD	CR	IL	LA0577
<i>suf</i>		sufflava		D*	RAD	AC	NIL	LA3569
<i>sup</i>		superba		K*JT	RAD	RR	IL	LA2061
<i>Sw-5</i>		Spotted wilt resistance-5		Q*	SPON	X	NON	LA3667
<i>sy</i>		sunny	ye	F*CE	RAD	AC	NIL	LA3553
<i>syv</i>		spotted yellow virescent		F*CG	SPON	PCV	NON	LA1096
<i>t</i>		tangerine		P*L	SPON	X	NON	LA0030
<i>t</i>		tangerine		P*L	SPON	RU	NIL	LA3002
<i>t</i>		tangerine		P*L	SPON	AC	NIL	LA3183
<i>t</i>	v	tangerine		P*L	RAD	CX	IL	LA0351

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<i>ta</i>		tarda		D*JK	RAD	CR	IL	LA0708
<i>tab</i>		tabescens		E*HJK	RAD	RR	IL	LA0629
<i>tab</i>		tabescens		E*HJK	RAD	AC	NIL	LA3734
<i>tc</i>		turbinate corolla		L*K	CHEM	SM	IL	LA2017
<i>te</i>		terminata	te1	K*LMO	RAD	LU	IL	LA0861
<i>tem</i>		tempestiva	tem1	K*DJ	RAD	CR	IL	LA0979
<i>ten</i>		tenuis		Y*DK	RAD	AC	NIL	LA3748
<i>ten</i>		tenuis		Y*DK	RAD	CR	IL	LA0578
<i>tf</i>		trifoliolate	ct, tri	J*KN	SPON	X	NON	LA0512
<i>tf</i>	2	trifoliolate	tri	J*KN	RAD	CR	IL	LA0579
<i>ti</i>		tiny plant		K*	SPON	X	NON	LA1806
<i>tl</i>		thiaminless		Y*C	SPON	X	NON	LA0758
<i>tl</i>		thiaminless		Y*C	SPON	AC	NIL	LA3712
<i>Tm</i>		Tobacco mosaic virus resistance		Q*	SPON	X	NON	LA2369
<i>Tm-2</i>		Tobacco mosaic virus resistance-2	Tm2	Q*	SPON	VD	NIL	LA3027
<i>Tm-2</i>	a	Tobacco mosaic virus resistance-2	Tm-2^2	Q*	SPON	VD	NIL	LA3028
<i>Tm-2</i>	a	Tobacco mosaic virus resistance-2	Tm-2^2	Q*	SPON	MM	NIL	LA3310
<i>Tm-2</i>	a	Tobacco mosaic virus resistance-2	Tm-2^2	Q*	SPON	AC	NIL	LA3769
<i>tmf</i>		terminating flower		K*M	SPON	X	NON	LA2462
<i>tn</i>		tenera		K*U	RAD	LU	IL	LA2062
<i>tp</i>		tripinnate leaf		J*K	RAD	X	IL	LA0895
<i>tp</i>		tripinnate leaf		J*K	RAD	AC	NIL	LA3184
<i>Tpi-2</i>	1	Triosephosphate isomerase-2		V*	SPON	pen	NON	LA2440
<i>tr</i>		truncata	tr1	D*CJK	RAD	CR	IL	LA0710
<i>tri</i>	1	temporarily red light insensitive		AKY*	CHEM	GT	IL	LA3808
<i>trs</i>		tristis		J*	CHEM		NON	3-057
<i>Ty-1</i>		TYLCV resistance		Q*	SPON	X	NIL	LA3473
<i>u</i>		uniform ripening	u1	P*	SPON	LRD	IL	LA0643
<i>u</i>		uniform ripening	u1	P*	SPON	GRD	NIL	LA3035
<i>u</i>		uniform ripening	u1	P*	SPON	AC	NIL	LA3247
<i>u</i>	G	uniform ripening		P*	SPON	VF36	NON	LA1018
<i>ub</i>		umbraculiformis		J*K	RAD	LU	IL	LA2063
<i>uf</i>		uniflora		M*	SPON	PTN	IL	LA1200
<i>uf</i>		uniflora		M*	SPON	AC	NIL	LA2936
<i>ug</i>		uniform gray-green	u2	P*	SPON	OGA	IL	LA0021
<i>ug</i>		uniform gray-green	u2	P*	SPON	AC	NIL	LA3539
<i>ul</i>		upright leaf		K*	SPON	X	NON	LA2463
<i>um</i>		umbrosa		K*JRT	RAD	CR	IL	LA0630
<i>um</i>		umbrosa		K*JRT	RAD	AC	NIL	LA3733
<i>uni</i>		unicaulis		K*	RAD	CR	IL	LA0580
<i>up</i>		upright pedicel		L*	SPON	FLD	IL	LA2397
<i>upg</i>		upright growth		K*	SPON	X	NON	LA2464A
<i>v-2</i>		virescent-2	v2	F*D	SPON	X	NON	LA2465
<i>v-2</i>		virescent-2	v2	F*D	SPON	AC	NIL	LA3185
<i>v-3</i>		Virescent-3	V3	F*B	RAD	X	NON	LA2707
<i>va</i>	dec	varia		F'E	RAD	CR	IL	LA0581
<i>va</i>	dec	varia		F'E	RAD	AC	NIL	LA3669
<i>va</i>	virg	varia		F'E	RAD	CR	IL	LA0582
<i>var</i>		variabilis		D*EK	RAD	CR	IL	LA0583
<i>Ve</i>		<i>Verticillium</i> resistance		Q*	SPON	GRD	NIL	LA3038
<i>Ve</i>		<i>Verticillium</i> resistance		Q*	SPON	AC	NIL	LA3277
<i>Ve</i>		<i>Verticillium</i> resistance		Q*	SPON	MM	NIL	LA2818
<i>ven</i>		venosa		J*BDK	RAD	LU	IL	LA0888
<i>ven</i>		venosa		J*BDK	RAD	AC	NIL	LA3564
<i>ver</i>		versicolor	yv-4, ver1	G*C	RAD	CR	IL	LA0632

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>ves</i>		versiformis	ves1	J*P		pim	IL	LA0859
<i>ves-2</i>		versiformis-2	vf	C*JK	RAD	LU	IL	LA1078
<i>vg</i>		vegetative		L*N	SPON	AC	NIL	LA2916
<i>vga</i>		virgulta	vga1	D*EFK	RAD	RR	IL	LA0858
<i>vi</i>		villous		I*	SPON	X	NON	LA0759
<i>vio</i>		violacea		D*A	RAD	LU	IL	LA0633
<i>vio</i>		violacea		D*A	RAD	AC	NIL	LA3734A
<i>vir</i>		viridis		T*J	RAD	CR	IL	LA0585
<i>vlg</i>		virescent light green		F*D	CHEM	VF36	IL	3-128
<i>vms</i>		variable male-sterile		N*L	SPON	SM	IL	2-219
<i>vo</i>		virescent orange		F*CP	SPON	RU	NIL	LA2995
<i>vo</i>		virescent orange		F*CP	SPON	ROVF	IL	LA1435
<i>vra</i>		viridula	vra1	D*JK	RAD	CR	IL	LA0857
<i>vt</i>		vieta		J*CFK	RAD	LU	IL	LA2064
<i>w</i>		wiry		J*LN	RAD	CX	NON	LA0274
<i>w-3</i>		wiry-3	w3, w2	J*LN	RAD	FEY	NON	LA1498
<i>w-4</i>		wiry-4	w4	J*LN	SPON	PSN	IL	2-237
<i>w-6</i>		wiry-6		J*	RAD	RR	IL	LA2065
<i>Wa</i>		White anthers		L*	SPON	VF36	NIL	LA3906
<i>wd</i>		wilty dwarf		R*K	SPON	SM	IL	2-110
<i>wf</i>		white flower		L*	RAD	X	NON	LA0023
<i>wf</i>		white flower		L*	RAD	AC	NIL	LA3575
<i>Wlt</i>		Wilty		W*	SPON	LGPL	NON	LA3203
<i>Wo</i>		Wooly		I*	SPON	AC	NIL	LA3186
<i>Wo</i>		Wooly		I*	SPON	X	IL	LA0053
<i>Wo</i>	<i>m</i>	Wooly		I*	SPON	RU	IL	LA0258
<i>Wo</i>	<i>m</i>	Wooly		I*	SPON	AC	NIL	LA3718
<i>Wo</i>	<i>mz</i>	Wooly		I*	SPON	VF145	IL	LA1908
<i>Wo</i>	<i>v</i>	Wooly		I*	SPON	RU	IL	LA1531
<i>Wo</i>	<i>v</i>	Wooly		I*	SPON	AC	NIL	LA3560
<i>wt</i>		wilty		J*W	SPON	X	NON	LA0030
<i>wv</i>		white virescent		F*B	SPON	AC	NIL	LA3187
<i>wv</i>		white virescent		F*B	SPON	X	NON	LA0659
<i>wv-2</i>		white virescent-2		F*B	SPON	X	NON	LA1150
<i>wv-3</i>		white virescent-3		F*B	SPON	X	NON	LA1432
<i>x</i>		gametophytic factor		N*	SPON	X	NON	LA2348
<i>Xa</i>		Xanthophyllic		C*	SPON	X	NON	LA2470
<i>Xa</i>		Xanthophyllic		C*	SPON	AC	NIL	LA3579
<i>Xa-2</i>		Xanthophyllic-2	Xa2, A	C*	RAD	X	NON	LA4134
<i>Xa-2</i>		Xanthophyllic-2	Xa2, A	C*	RAD	X	NON	LA2471
<i>Xa-2</i>		Xanthophyllic-2	Xa2, A	C*	RAD	AC	NIL	LA3188
<i>Xa-3</i>		Xanthophyllic-3	Xa3	C*	RAD	CR	IL	LA2472
<i>Xa-3</i>		Xanthophyllic-3	Xa3	C*	RAD	AC	NIL	LA3430
<i>xan-2</i>		xantha-2	xan2	C*	RAD	AC	NIL	LA3759
<i>xan-4</i>		xantha-4	xan4	C*	RAD	AC	NIL	LA3760
<i>y</i>		colorless fruit epidermis		P*	SPON	OGA	NON	LA1088
<i>y</i>		colorless fruit epidermis		P*	SPON	AC	NIL	LA3189
<i>yg-2</i>		yellow-green-2	yc, yg282, yg2	E*	RAD	AC	NIL	LA3551
<i>yg-2</i>		yellow-green-2	yc, yg282, yg2	E*	RAD	KK	IL	LA2469A
<i>yg-2</i>	<i>aud</i>	yellow-green-2	yg-2 ^r , aud	E*	SPON	AC	NIL	LA3165
<i>yg-2</i>	<i>aud</i>	yellow-green-2	yg-2 ^r , aud	E*	SPON	X	NON	LA1008
<i>yg-3</i>		yellow-green-3	yg3, yg330, ye	E*	RAD	KK	NIL	LA2926
<i>yg-4</i>		yellow-green-4	yg4, yl, yg333	E*J	RAD	KK	NIL	LA2927
<i>yg-4</i>		yellow-green-4	yg4, yl, yg333	E*J	RAD	AC	NIL	LA3731
<i>yg-5</i>		yellow-green-5	yw, yg388, yg5	E*	RAD	AC		LA2928B
<i>yg-5</i>		yellow-green-5	yw, yg388, yg5	E*	RAD	RCH	NIL	LA2928
<i>yg-5</i>		yellow-green-5	yw, yg388, yg5	E*	RAD	AC	NIL	LA2928A

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
<i>yg-9</i>		yellow-green-9		E*	SPON	C28	IL	LA2708
<i>yv</i>		yellow virescent		E*	SPON	AC	NIL	LA3554
<i>yv</i>		yellow virescent		E*	SPON	SM	IL	LA0055
<i>yv</i>	2	yellow virescent	vel ² , vel1 ²	E*	RAD	CR	IL	LA0981
<i>yv</i>	3	yellow virescent	vel	E*	RAD	CR	IL	LA0631
<i>yv</i>	<i>ms</i>	yellow virescent		E*N		X		LA3907
<i>yv-2</i>		yellow virescent-2		E*	SPON	AC	NIL	LA3190
<i>yv-4</i>		yellow virescent-4		E*	SPON	AC	NIL	LA3570

Table 2. Definition of phenotypic class symbols listed in Table 1.

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

Table 3. Definition of abbreviations used for background genotypes in Table 1, and their corresponding accession numbers (n/a = not available).

Back.	Genotype name	Acc.#	Back.	Genotype name	Acc.#
A-1	A-1	LA0818	pen	<i>L. pennellii</i>	many
AC	Ailsa Craig	LA2838A	per	<i>L. peruvianum</i>	many
ACE	Ace	LA0516	pim	<i>L. pimpinellifolium</i>	many
ALA	Alabama	n/a	PLB	Pieralbo	n/a
AMB	Antimold-B	LA3244	POR	Porphyre	LA2715
ANU	Anahu	LA3143	PRI	Primabel	LA3903
BK	Budai Korai	n/a	PRN	Prairiana	LA3236
BOD	Break O'Day	LA1499	PRT	Pritchard	LA3233
C255	Cal 255	LA0198	PSN	Pearson	LA0012
C28	Campbell 28	LA3317	PSP	Prospero	LA3229
cer	<i>L. esc. var. cerasiforme</i>	many	PTN	Platense	LA3243
CG	Chico Grande	LA3121	RCH	Red Cherry	LA0337
che	<i>L. cheesmanii</i>	many	RG	Rio Grande	LA3343
chi	<i>L. chilense</i>	many	RH13	Rehovot 13	LA3129
chm	<i>L. chmielewskii</i>	many	RNH	Rouge Naine Hative	n/a
CR	Condine Red	LA0533	ROMA	Roma	n/a
CRGL	Craigella	LA3247	ROVF	Roma VF	n/a
CSM	Castlemart	LA2400	RR	Rheinlands Ruhm	LA0535
CT	Chatham	n/a	RSWT	Roumanian Sweet	LA0503
CX	Canary Export	LA3228	RTVF	Red Top VF	LA0276
E6203	E-6203	LA4024	RU	Rutgers	LA1090
EPK	Earlipak	LA0266	SCZ	Santa Cruz	LA1021
ERL	Earliana	LA3238	SM	San Marzano	LA0180
ESC	Early Santa Clara	LA517	spVCH	VFNT Cherry (sp)	LA2705
FB	Fireball	LA3024	SPZ	San Pancrazio	n/a
FEY	First Early	n/a	STD	Stokesdale	LA1091
FLD	Flora-Dade	LA3242	STN	Stone	LA1506
GRD	Gardener	LA3030	STR24	Start 24	LA3632
GSM	Gulf State Market	LA3231	SX	Sioux	LA3234
H100	Hunt 100	LA3144	T338	UC-T338	LA2939
hir	<i>L. hirsutum</i>	many	T-5	UC-T5	LA2399
HSD	Homestead 24	LA3237	TGR	Targinnie Red	LA3230
JBR	John Baer	LA1089	TVD	Vendor (Tm-2a)	LA2968
KK	Kokomo	LA3240	UC82	UC-82B	LA1706
LGPL	Large Plum	LA3203	VCH	VFNT Cherry	LA1221
LK	Laketa	LA0505	VD	Vendor	LA3122
LRD	Long Red	LA3232	VE	Van's Early	n/a
LU	Lukullus	LA0534	VF11	VF-11	LA0744
lyc	<i>S. lycopersicoides</i>	many	VF145	VF-145 78-79	LA1222
M167	Montfavet 167	LA2713	VF36	VF-36	LA0490
M168	Montfavet 168	LA2714	VF6	VF-6	LA0743
MD	Marmande	LA1504	VFN8	VFN-8	LA1022
MGB	Marglobe	LA0502	VFSM	VF San Marzano	n/a
MM	Moneymaker	LA2706	VGB	Vagabond	LA3246
MNB	Monalbo	LA2818	VRB	Vrbikanske nizke	LA3630
MP	Manapal	LA2451	VTG	Vantage	LA3905
NRT	Norton	n/a	WA	Walter	LA3465
O8245	Ohio 8245	n/a	X	unknown or hybrid	n/a
OGA	Ohio Globe A	LA1088	XLP	XL Pearson	n/a
ONT	Ontario	n/a			
par	<i>L. parviflorum</i>	many			
PCV	primitive cultivar	n/a			

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