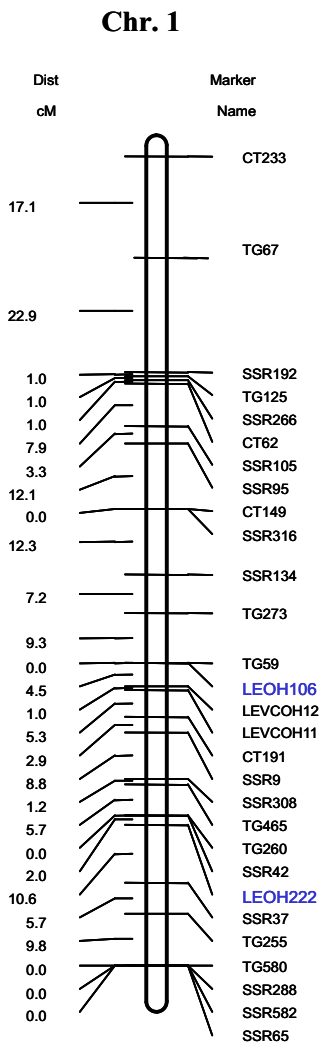
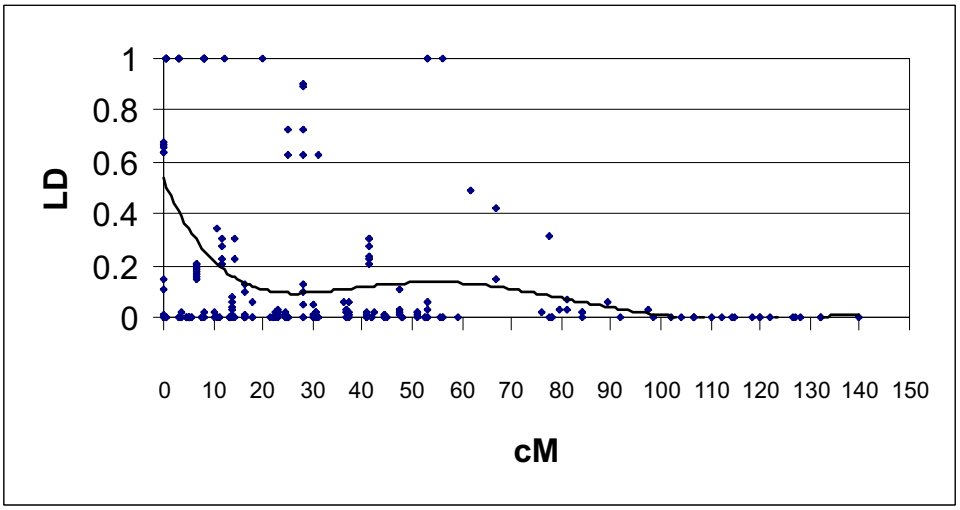
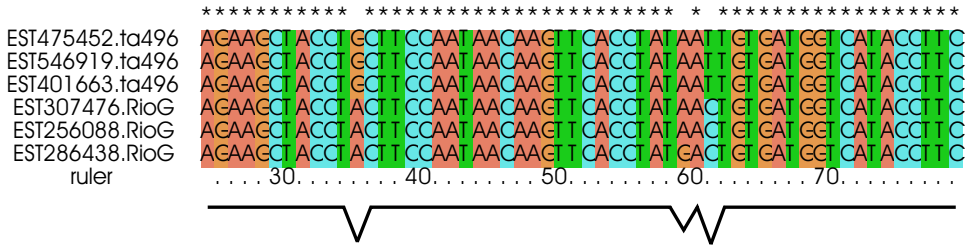
Report of the
Tomato Genetics Cooperative



SNP development and translational genomics research in tomato





Volume 55 *October 2005*

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

Table of Contents

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:

Jay W. Scott, Ph.D.
Gulf Coast Research & Education Center
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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.

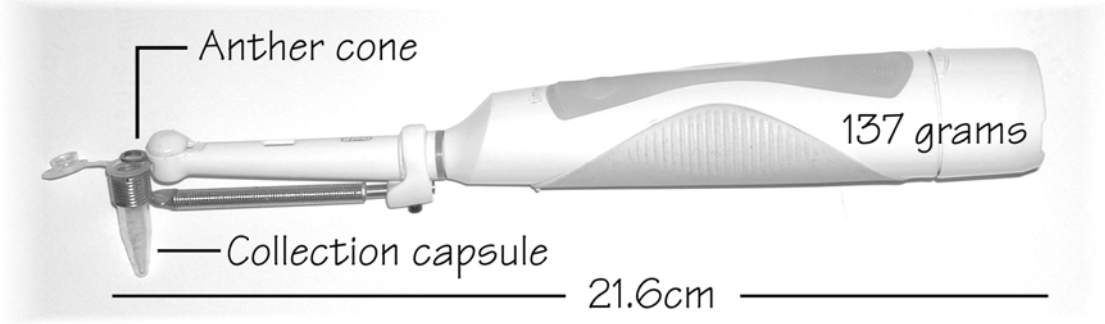
Evaluation data obtained will be according to CGC descriptors and codes and will be entered into GRIN by the crop curator. Funding for data entry into GRIN should be considered when developing proposals.

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?

TPB ~ BATTERY-POWERED TOMATO POLLEN COLLECTOR



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
Department of Horticulture and Crop Science, Ohio Agricultural Research and Development Center, The Ohio State University, 1680 Madison Avenue, Wooster, OH 44691-4096, email: francis.77@osu.edu

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

Song-Bin Chang and Stephen M. Stack
Department of Biology, Colorado State University, Fort Collins, CO 80523-1878

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.

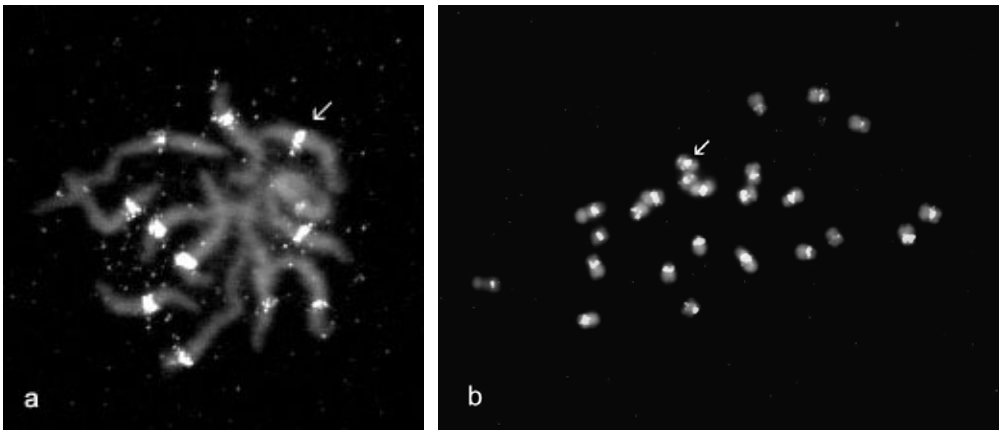


Figure 1. TGR4 loci after FISH (e.g., arrows) on (a) tomato (*Solanum lycopersicum* VFNT pachytene chromosomes and on (b) metaphase chromosomes of *S. chilense*.

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.

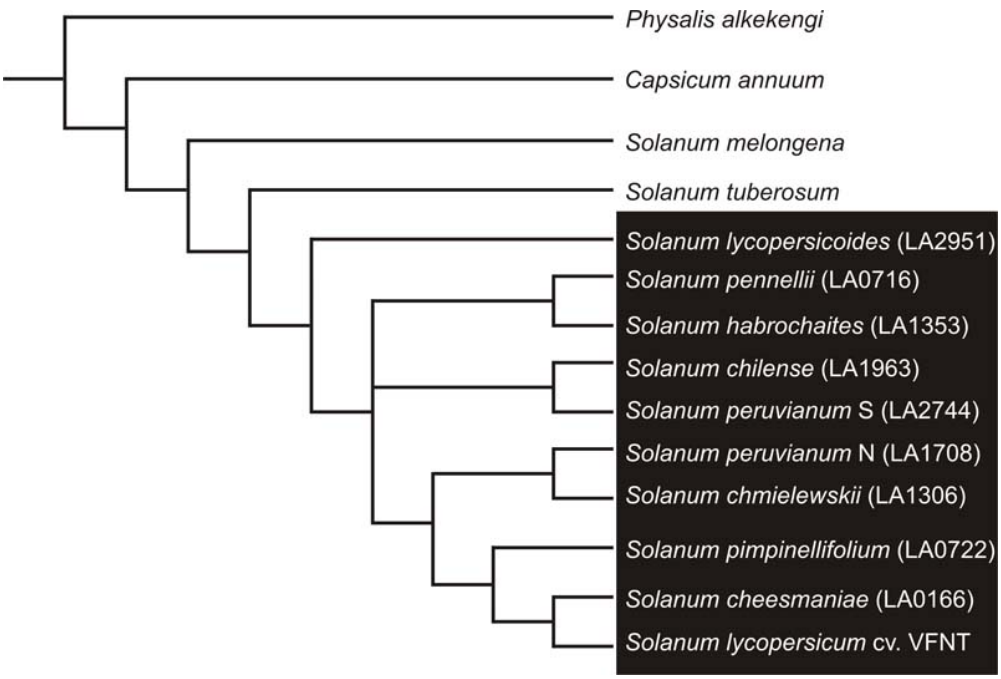


Figure 2. A combined phylogenetic tree based on Bohs and Olmstead, (1997) and Spooner *et al.* (2005). Among the species investigated above, the TGR4 centromere-specific retrotransposon is confined to the section *Lycopersicon* (black box).

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

References

Bohs L. and Olmstead R.G. (1997) Phylogenetic relationships in Solanum (Solanaceae) based on *ndhF* sequences. Systematic Botany 22:5-17.

Jiang J., Birchler J.A., Parrott W.A., and Dawe R.K. (2003) A molecular view of plant centromeres. Trends in Plant Science 8: 570-575.

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

Graham, E, Wang, TC, and Hanson, P
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 x 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±1°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.

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Monforte, A.J. and Tanksley, S.D. 2000. Development of a near isogenic and backcross recombinant inbred lines containing most of the *Lycopersicon hirsutum* genome in a *L. esculentum* background: a tool for gene mapping and gene discovery. Genome 43: 803-813.

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.

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

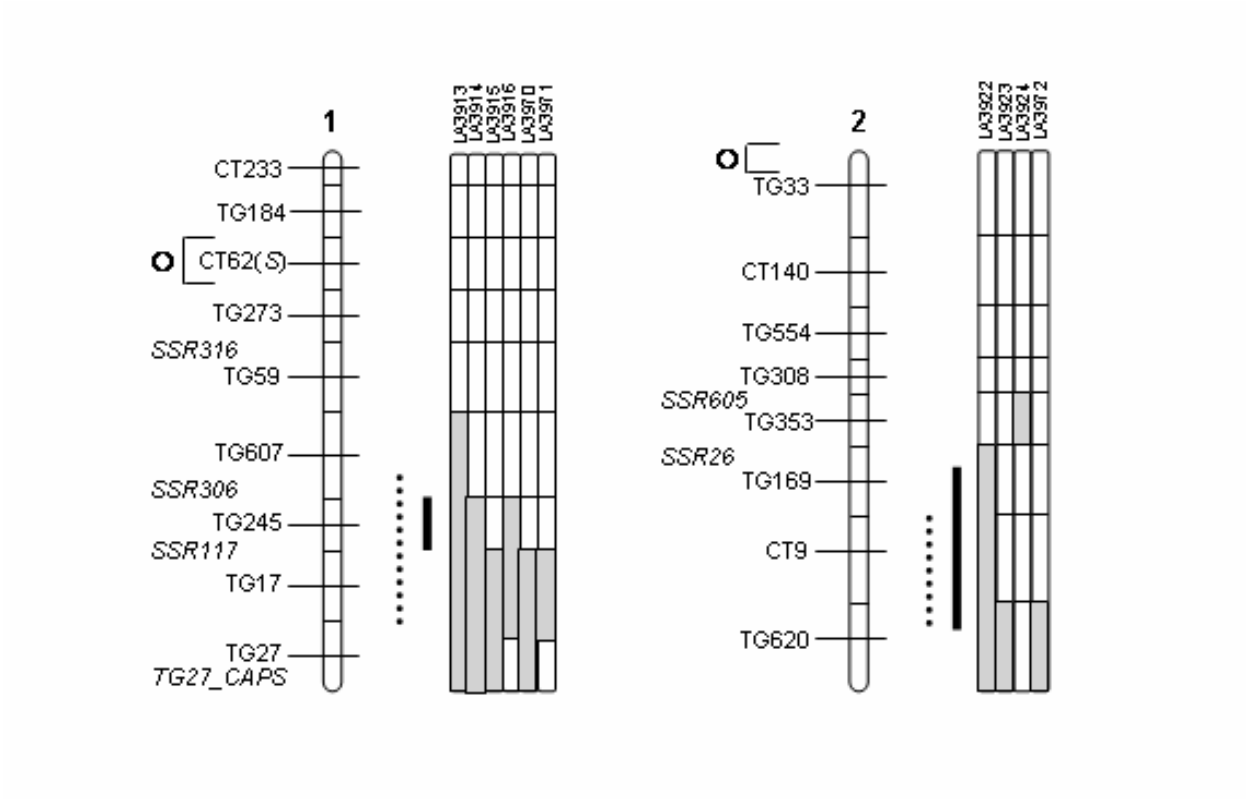
		Experiment I DSR[2]						Experiment II DSR						Overall	
Entry	Chrom[1]	0	1	2	3	4	Mean	0	1	2	3	4	Mean	Mean	LSD[3]
LA1777			10				1.0		10				1.0	1.0	A
LA3922	2				6	5	3.5			9	3		2.3	2.9	B
LA3913	1				10	2	3.2			4	7	1	2.8	3.0	Bc
LA3914	1				7	4	3.4			5	5	2	2.8	3.1	Bcd
LA3941	5				10	2	3.2			1	9	1	3.0	3.1	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					3	9	3.8				5	7	3.6		
(E6203)														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

Stanislava Grozeva, Velichka Rodeva, Zhivko Danailov*

Maritsa Vegetable Crops Research Institute, 4003 Plovdiv, Bulgaria
*Institute of Genetics "Akad.D.Kostoff", BAS, Sofia, Bulgaria
stanislava77@abv.bg; veliord@evrocom.net; zhivkodanailov@abv.bg

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 F_1 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 25ºC ± 1ºC, 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 F_1 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 F_1 tomato varieties, resistant to economically important viruses.

Our work started with interspecific complex hybrids –{ BC_3P_1 (cv. Merkury x *L. peruvianum* LA 462) x BC_3P_1 (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 – {BC_3P_1(cv. Merkury x *L. peruvianum* LA 462) x BC_3P_1 (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 F_1 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 became 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 gastroenteral 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, phytagel – 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 denaturated in 6 µl 20x SSC and 4 µl 37% formaldehyde at 60^{o}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^{o}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 GCCCATCGAAAT CAAAGATACC-3' and reverse 5'-CCCAAAGACAGAAGAAAATTGG-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^{0}C, followed by 32 cycles as at 94^{0}C for 1 min; 55^{0}C for 1 min; and 72^{0}C for 2 min. The cycle for final extention was at 72^{0}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 lyophylized 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 T_0 and T_1 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 T_0 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 T_1 generation, seeds from mature fruits of the T_0 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 T_1 generation.

Characteristics of transgenic plants of the T_0 generation

Samples of total RNA were isolated from segments of developed leaves of 20 plants of the T_0 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 T_0 transgenic plants with ^{32}P-labeled PCR products from the plasmid pBINp35STBI-HBS *A. tumefaciens* strain LBA4404 used as a probe. Most of plants of the T_0 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 T_1 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 T_1 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 T_1 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 T_1 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 T_1 generation.

Immunoassays

EIA was performed both in test systems for the presence of the antigenic peptide HBSAg (HBV) and antigene 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 then 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 lyophylized and the activity in dried tomato mass was determined with EIA HBSAg.

In Figure 6 the data of determination of antigenic protein HBSAg in lyophylized material are presented. There was found a great activity of antigens in lyophylized 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 T_0 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 T_1 generation. Even levels of expression greatly varied in some plants material, most plants of the T_1 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.

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Kopytina,T.V., Hammond, R. 2005. Studies of immunogenic properties of candidate edible vaccine against hepatitis B and human immunodeficiency viruses on the basis of transgenic tomato fruits. Doklady of Russian Academy of Sciences 401: 709-711.

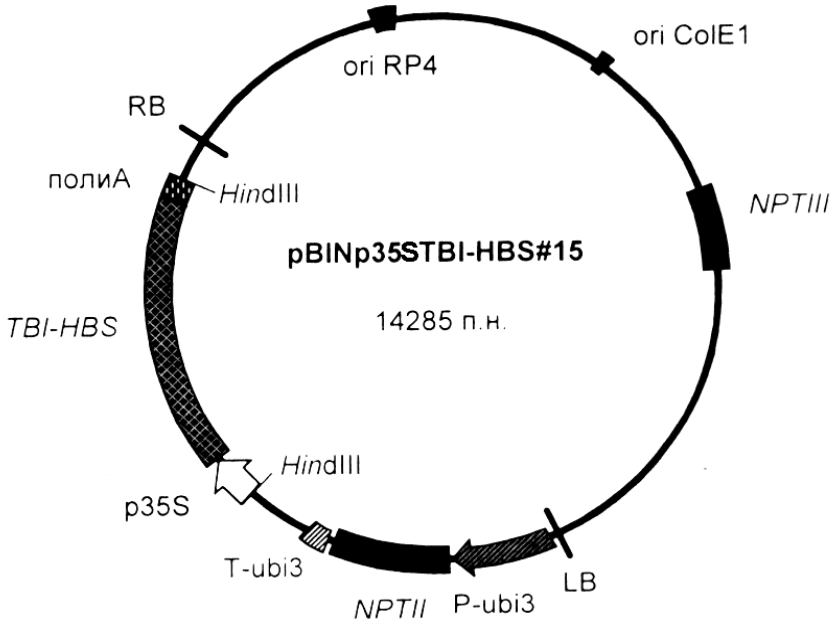

Figure 1

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.

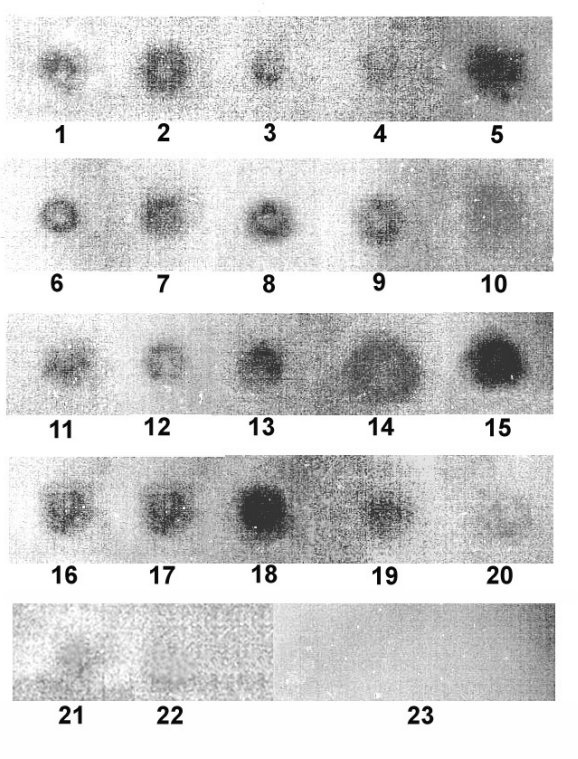

Figure 2.
Northern dot blot with the total RNA loaded onto Hybond N+ membrane.
№№ 1-20 – RNA from leaves of transgenic tomato plants of T_0 generation.
№№ 21-22 – RNA from leaves of tomato plants of the T_0 generation transformed with an "empty" vector plasmid pBINPLUS/ARS.
№23 – hybridized membrane without loaded RNA.

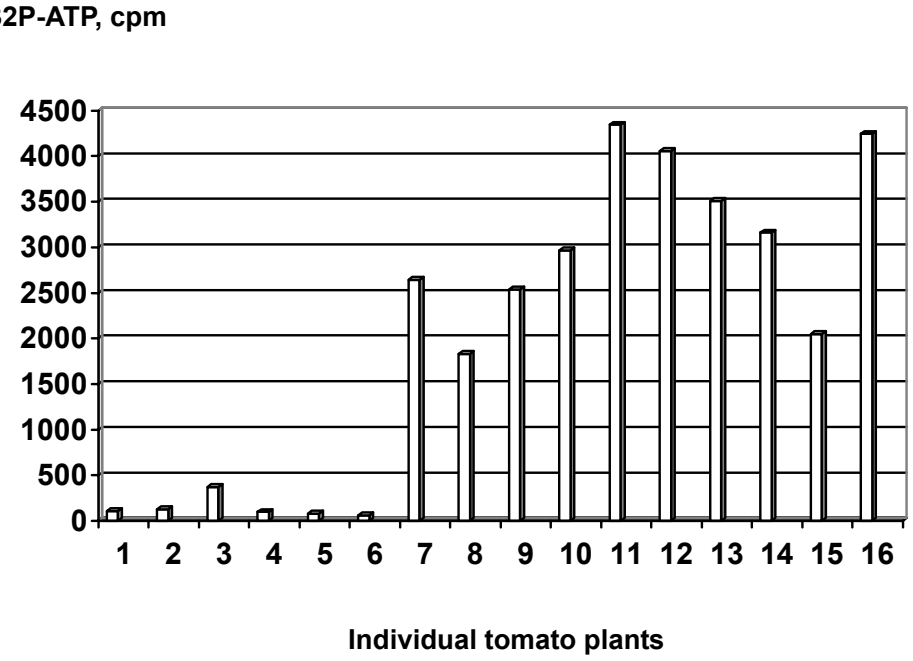

Figure 3.
Northern dot blot hybridization of total RNA from leaves, stems with roots and fruits with the probe of ^{32}P-RT-PCR product from total RNA of *Agrobacterium tumefaciens* LBA4404 with the cloned gene TBI-HBS in pBINPLUS/ARS.

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 T_1 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 T_1 generation (25µg per the line each) of lines ## 13(1) and 13(3).
Columns № 13 – 16 - RNA from fruits of transgenic tomato of the T_1 generation (25µg per the line each) of lines ## 13(1), 13(2), 13(3) and 13(4).

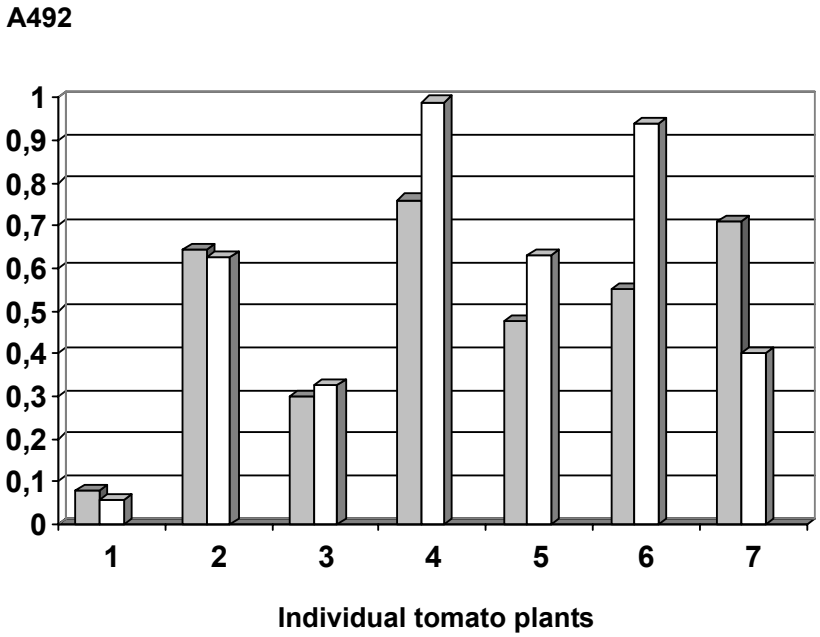

Figure 4.
The immunoassay of the presence of the protein HBSAg n fruits from nontransformed plant and transgenic lines ## 13 of tomato of the T_1 generation with the introduced gene TBI-HBS.

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 T_1 generation.

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

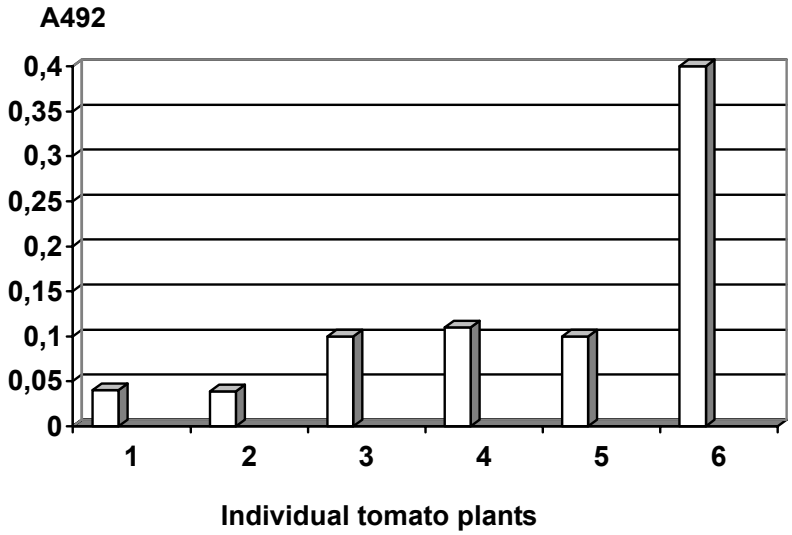

Figure 5.
The immunoassay of the presence of the antigen p24 in nontransformed fruit and transgenic fruits of tomato of the T_1 generation with the introduced gene TBI-HBS.

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 T_1 generation.

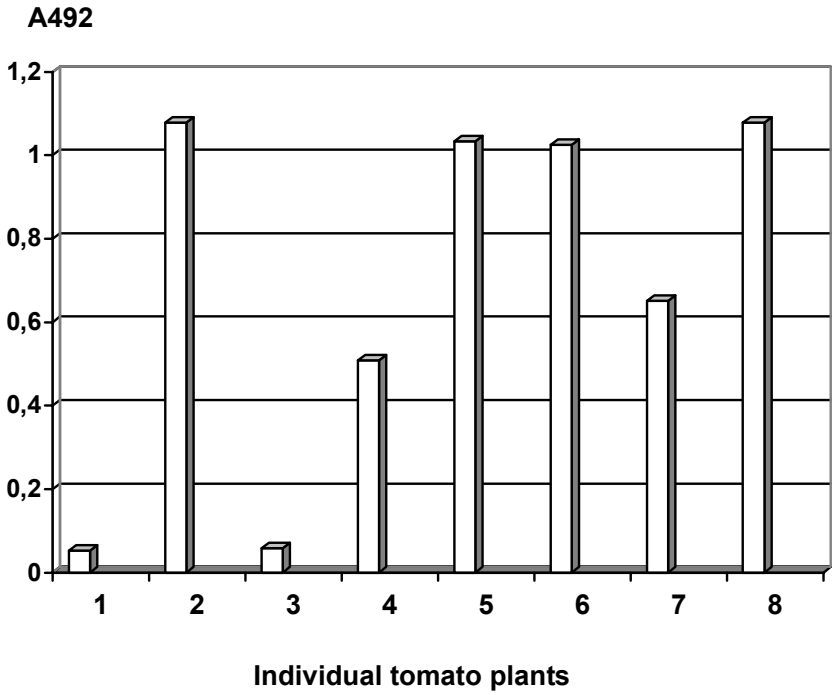

Figure 6.
The immunoassay of the presence of the antigenic protein HBSAg in dried fruit mass from nontransformed plant and from transgenic plants of lines # 13 of tomato of the T_1 generation with the introduced gene TBI-HBS.

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 T_1 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 BC_4F_2 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).

	Plants						
Genotype	Total (No.)	Healthy (No.)	Diseased (No.)	Diseased adjusted[z]	Conclusion[y]	Chi-square	P
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. Spring	49	21	28 (57)	----	S - control		

[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
L. chilense					
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
L. hirsutum					
ECU-968	1.2	0.60	0.60	0.20	100.0
L. peruvianum					
CIAPAN-16	0.5	0.60	0.70	0.23	77.8
L. pimpinellifolium					
ECU-693	1.5	1.62	1.62	0.54	100.0
S. ochrantum					
ECU-335	0.6	0.14	0.14	0.05	100.0/13.3[e]
S. pseudocapsicum					
AN-CA-214	0.0	0.04	-	-	0.0
CONTROL					
Fortuna-C	3.2	2.98	2.98	1.00	100.0

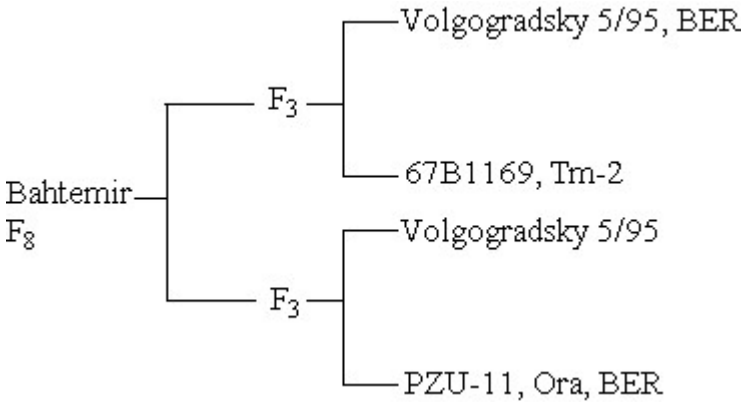
[a]mean symptoms index measured in a 0 to 4 scale (0, no symptoms; 1, mild symptoms; 2, moderate symptoms; 3, severe symptoms; 4, very severe symptoms or dead plant).
[b]mean value of the maximum absorbance for each plant.
[c]mean value of the maximum absorbance for each infected plant.
[d]index calculated as: Mean maximum absorbance 2 of each accession/Mean maximum absorbance of the susceptible control.
[e]percentage 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 aegyptiaca* Pers.

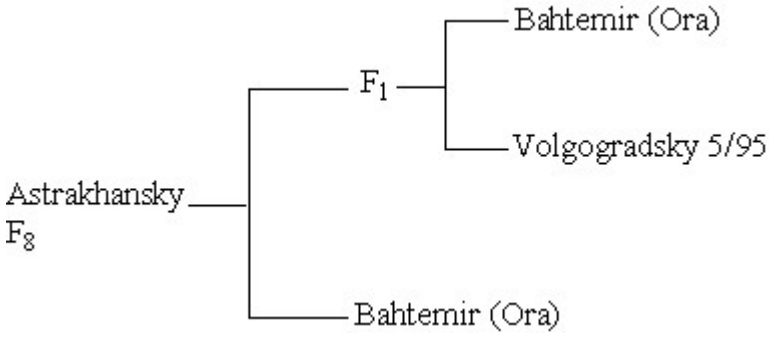
Bahtemir

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

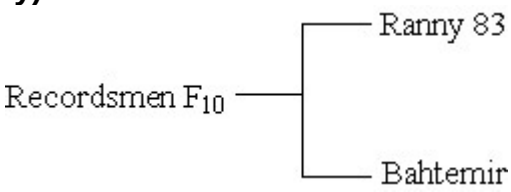


Pedigree:

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)

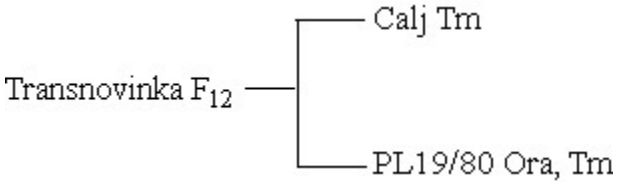
Pedigree:



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

Pedigree:



Characteristics: red color, plumy-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 F_2 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. #
a		anthocyaninless	a1	A*	SPON	AC	NIL	LA3263
a		anthocyaninless	a1	A*	SPON	X	NON	LA0291
a	*prov2*	anthocyaninless	a	A*	CHEM	VF36	IL	3-414

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

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

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

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

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
d	*cr*	dwarf	rob^crisp	K*JT	RAD	CR	IL	LA0570
d	*im*	dwarf	rob^imm	K*JT	RAD	CR	IL	LA0571
d	*prov2*	dwarf	d	K*JT	CHEM	VCH	IL	3-623
d	*provcr-2*	dwarf	d^cr	K*JT	CHEM	VF36	IL	3-420
d	*provcr-3*	dwarf	d^cr	K*JT	CHEM	VF36	IL	3-422
d	*x*	dwarf		K*JT	SPON	SPZ	IL	LA0160
d	*x*	dwarf		K*JT	SPON	VAN	NIL	LA3902
d	*x*	dwarf		K*JT	SPON	PCV	NON	LA1052
d	*x*	dwarf		K*JT	SPON	AC	NIL	LA3615
d-2		dwarf-2	rob2, rob II, d2	K*N	RAD	RR	IL	LA0625
dc		decomposita	dc1	J*	RAD	RR	IL	LA0819
dd		double dwarf	d^xx	K*J	SPON	X	NON	LA0810
de		declinata		K*JU	RAD	AC	NIL	LA3742
de		declinata		K*JU	RAD	RR	IL	LA0594
deb		debilis		H*BCJ	RAD	AC	NIL	LA3727
deb		debilis		H*BCJ	RAD	CR	IL	LA0542
dec		decumbens		K*R	RAD	LU	IL	LA0669
def		deformis		J*LN	RAD	RR	IL	LA0543
def		deformis		J*LN	RAD	AC	NIL	LA3749
def	*2*	deformis	vit	J*	RAD	CR	IL	LA0634
def-2		deformis		J*LN	RAD	AC	NIL	LA2920
Del		Delta		P*	SPON	AC	NIL	LA2921
Del		Delta		P*	SPON	RU	NIL	LA2996A
Del		Delta		P*	SPON	M82	NON	LA4099
deli		deliquescens		K*CJ	RAD	RR	IL	LA0595
dep		deprimata		T*J	RAD	CR	IL	LA0544
depa		depauperata		K*CJ	RAD	RR	IL	LA0596
depa		depauperata		K*CJ	RAD	AC	NIL	LA3725
det		detrimentosa		C*KF	RAD	RR	IL	LA0670
det	*2*	detrimentosa		C*KF	RAD	RR	IL	LA0820
Df		Defoliator		Y*H	SPON	par	NON	LA0247
dgt		diageotropica	lz-3	K*R	SPON	VFN8	IL	LA1093
dgt	*dp*	diageotropica	dp	J*KT	RAD	CT	IL	LA2526
Dia-2	*1*	Diaphorase-2		V*	SPON	pen	NON	LA2987
Dia-2	*2*	Diaphorase-2		V*	SPON	VF36	NIL	LA4232
Dia-3	*1*	Diaphorase-3		V*	SPON	X	NON	LA3345
Dia-3	*1*	Diaphorase-3		V*	SPON	VF36	NIL	LA4269
Dia-4	*1*	Diaphorase-4		V*	SPON	VF36	NIL	LA4284
dil		diluta		D*JK	RAD	CR	IL	LA0545
dil		diluta		D*JK	RAD	AC	NIL	LA3728
dim		diminuta		A*DK	RAD	LU	IL	LA0597
dim-2		diminuta-2	dim2	A*K	RAD	AC	NIL	LA3170
dis		discolor		D*F	RAD	CR	IL	LA0598
div		divaricata		C*AJK	RAD	CR	NON	LA0671
div		divaricata		C*AJK	RAD	AC	NIL	LA3818
dl		dialytic		I*LN	SPON	SM	IL	2-069
dl		dialytic		I*LN	SPON	AC	NIL	LA3724
dl	*S*	dialytic	Dl^s	L*N	SPON	VF36	NIL	LA3906
dlb		dilabens	dlb1	C*JK	RAD	CR	IL	LA0829
dm		dwarf modifier	d2	K*	SPON	X	NON	LA0014
dmd		dimidiata		K*JU	RAD	LU	IL	LA2033
dmt		diminutiva		K*	CHEM	VF36	IL	3-007
dps		diospyros		P*	SPON	X	NON	LA1016
dpy		dumpy		K*J	SPON	X	NON	LA0811
dpy		dumpy		K*J	SPON	AC	NIL	LA3171
dpy	*prov2*	dumpy	dpy	K*J	CHEM	VCH	IL	3-630
dpy	*prov3*	dumpy	dpy	K*J	SPON	ANU	IL	LA1053
drt		dwarf root		R*	CHEM	X	NON	LA3207
ds		dwarf sterile		N*K	SPON	EPK	IL	2-247

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

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

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

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

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

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

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

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pct		polycot		J*KLMS	SPON	MM	NON	LA2896
pcv		polychrome variegated		G*BDJ	SPON	X	NON	LA1199
pdc		pudica		K*JT	CHEM	VF36	IL	3-047
pds		phosphorus deficiency syndrome	Ph-oid	A*CY	SPON	X	NON	LA0813
pdw		pale dwarf		V*	SPON	X	NON	LA2457
pdw		pale dwarf		V*	SPON	X	NON	LA2490
pe		sticky peel		O*	SPON	X	NON	LA0759
pen		pendens		J*C	RAD	CR	IL	LA0694
pen		pendens		J*C	RAD	AC	NIL	LA3293
per		perviridis		A*KT	RAD	RR	IL	LA0564
pet		penetrabile	pet-2, pet2	K*J	RAD	CR	IL	LA0971
Pgdh-2	*1*	6-Phosphogluconate dehydrogenase-2		V*	SPON	pen	NON	LA2991
Pgdh-3	*1*	6-Phosphogluconate dehydrogenase-3		V*	SPON	pen	NON	LA2434
Pgi-1	*1*	Phosphoglucoisomerase-1		V*	SPON	pen	NON	LA2435
Pgi-1	*2*	Phosphoglucoisomerase-1		V*	SPON	par	NON	LA2436
Pgm-1	*1*	Phosphoglucomutase-1		V*	SPON	hir	NON	LA2437
Pgm-2	*1*	Phosphoglucomutase-2		V*	SPON	pen	NON	LA2438
Ph		*Phytophthora infestans* resistance	PiT, TR1	Q*	SPON	X	NON	LA2009
Ph-2		*Phytophthora infestans* resistance		Q*	SPON	UC82	NIL	LA3151
Ph-2		*Phytophthora infestans* resistance		Q*	SPON	MNB	NIL	LA3152
Ph-3		*Phytophthora infestans* resistance		Q	SPON	CLN2264	NON	LA4285
Ph-3		*Phytophthora infestans* resistance		Q	SPON	CLN2264	NON	LA4286
pi		pistillate		L*N	SPON	SM	IL	2-137
pi-2		pistillate-2		N*LM	CHEM	CSM	IL	3-802
pic		picta		H*C	RAD	CR	IL	LA0620
pl		perlucida	pl1	D*CJ	RAD	CR	IL	LA0867
pl		perlucida	pl1	D*CJ	RAD	AC	NIL	LA3296
pla		plana		D*CK	RAD	CR	IL	LA0695
pli		plicata		K*ABJ	RAD	LU	IL	LA0696
pli		plicata		K*ABJ	RAD	AC	NIL	LA3672
pm		praematura	pm1	Z*CJK	RAD	RR	IL	LA0855
Pn		Punctate		A*I	SPON	X	NON	LA0812
Pn		Punctate		A*I	SPON	AC	NIL	LA3089
pol		polylopha		K*JO	RAD	LU	IL	LA0697
pp		polyphylla	pp1	J*D	RAD	RR	IL	LA0860
ppa		purpurea		A*	RAD	LU	IL	LA2054
pr		propeller		J*	RAD	X	NON	LA0326
pr		propeller		J*	RAD	AC	NIL	LA2925
prc		procumbens		K*CJ	RAD	CR	IL	LA0698
pre		pressa		K*J	RAD	RR	IL	LA2053
pro		procera		J*Z	RAD	AC	NIL	LA3283
pro		procera		J*Z	RAD	CR	IL	LA0565
prt		protea	prt1	C*JK	RAD	CR	IL	LA0972
prun		prunoidea		O*J	RAD	LU	IL	LA0566
Prx-1	*1*	Peroxidase-1		V*	SPON	pim	NON	LA1837
Prx-1	*2*	Peroxidase-1		V*	SPON	pim	NON	LA1838
Prx-1	*3*	Peroxidase-1		V*	SPON	pim	NON	LA1839
Prx-1	*4*	Peroxidase-1		V*	SPON	chm	NON	LA1840
Prx-1	*5*	Peroxidase-1		V*	SPON	pim	NON	LA1841
Prx-1	*n*	Peroxidase-1		V*	SPON	pim	NON	LA1836
Prx-2	*1*	Peroxidase-2		V*	SPON	cer	NON	LA1843
Prx-2	*3*	Peroxidase-2		V*	SPON	pim	NON	LA1845
Prx-2	*n*	Peroxidase-2		V*	SPON	pim	NON	LA1842

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

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

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
sfa	*2*	sufflaminata	par	C*AEK	RAD	CR	IL	LA0969
sft		single flower truss		M*	SPON	PTN	IL	LA2460
sh		sherry		P*	RAD	CX	IL	LA2644
sha		short anthers		L*N	CHEM	ROMA	IL	LA2013
si		sinuata		E*JK	RAD	AC	NIL	LA3728B
si		sinuata		E*JK	RAD	RR	IL	LA0993
sig-1		signal transduction-1	JL1	Y*	CHEM	CSM	IL	LA3318
sig-2		signal transduction-2	JL5	Y*	CHEM	CSM	IL	LA3319
sit		sitiens		W*HJKY	RAD	RR	IL	LA0574
Skdh-1	*1*	Shikimic acid dehydrogenase-1		V*	SPON	pen	NON	LA2439
sl		stamenless		L*N	SPON	AC	NIL	LA3816
sl		stamenless		L*N	SPON	X	NON	LA0269
sl	*cs*	stamenless	cs, sl^5, sl5	L*N	SPON	ONT	IL	LA1789
sl-2		stamenless-2	sl2	L*N	SPON	X	NON	LA1801
slx		serrate lax leaf		J*	SPON	PCV	NON	LA0503
Sm		*Stemphyllium* resistance		Q*	SPON	X	NON	LA1802
Sm		*Stemphyllium* resistance		Q*	SPON	MM	IL	LA2821
sn		singed		I*	SPON	CX	IL	LA2015
snt		Snout	sn	O*	SPON	X	NON	LA0499
so		soluta		J*	RAD	LU	IL	LA2058
Sod-1	*1*	Superoxide dismutase-1		V*	SPON	pen	NON	LA2909
Sod-2	*1*	Superoxide dismutase-2		V*	SPON	pen	NON	LA2910
sp		self-pruning		K*	SPON	TT	NON	LA0154
sp		self-pruning		K*	SPON	VF36	NON	LA0490
sp		self-pruning		K*	SPON	GRD	NIL	LA3133
sp	+	self-pruning		K*	SPON	M82	NIL	LA4287
sp	*prov2*	self-pruning		K*	RAD	VCH	IL	LA2705
spa		sparsa		E*BK	RAD	CR	IL	LA0703
spe		splendida	spe1	C*K	RAD	RR	IL	LA0977
sph		sphaerica		K*T	RAD	AC	NIL	LA3744
sph		sphaerica		K*T	RAD	CR	IL	LA0704
Spi	*2*	Sympodial index		K*	SPON	pen	NON	LA0716
spl		splendens	spl1	C*DJ	RAD	LU	IL	LA0821
spl		splendens	spl1	C*DJ	RAD	AC	NIL	LA3282
squa		squarrosa		D*KU	RAD	LU	IL	LA0627
sr		slender stem	sm	J*KU	RAD	CT	IL	LA1803
ss		spongy seed		S*	RAD	AC	NIL	LA3619
sta		stabilis		K*	RAD	RR	IL	LA2060
ste		sterilis		J*DKN	RAD	CR	IL	LA0705
stri		stricta		J*K	RAD	LU	IL	LA0575
stu		stunted		J*	SPON	X	NON	LA2461
su		suffulta		C*JM	RAD	LU	IL	LA0628
su	*2*	suffulta	exa	C*JM	RAD	RR	IL	LA0853
su	*3*	suffulta	di	C*J	RAD	CR	IL	LA0599
su	*ni*	suffulta	di^ni, ni	C*J	RAD	CR	IL	LA0616
sua		suffusa		D*CK	RAD	RR	IL	LA0707
sub		subtilis		J*K	RAD	LU	IL	LA0576
suc		succedanea		C*JK	RAD	CR	IL	LA0706
sucr		sucrose accumulator	TIV1	P*	SPON	H100	NIL	LA4104
suf		sufflava		D*	RAD	CR	IL	LA0577
suf		sufflava		D*	RAD	AC	NIL	LA3569
sup		superba		K*JT	RAD	RR	IL	LA2061
Sw-5		Spotted wilt resistance-5		Q*	SPON	X	NON	LA3667
sy		sunny	ye	F*CE	RAD	AC	NIL	LA3553
syv		spotted yellow virescent		F*CG	SPON	PCV	NON	LA1096
t		tangerine		P*L	SPON	X	NON	LA0030
t		tangerine		P*L	SPON	RU	NIL	LA3002
t		tangerine		P*L	SPON	AC	NIL	LA3183
t	*v*	tangerine		P*L	RAD	CX	IL	LA0351

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

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

Gene	Allele	Locus name	Synonyms	Class	Origin	Back.	Iso.	Acc. #
yg-9		yellow-green-9		E*	SPON	C28	IL	LA2708
yv		yellow virescent		E*	SPON	AC	NIL	LA3554
yv		yellow virescent		E*	SPON	SM	IL	LA0055
yv	*2*	yellow virescent	vel^2, vel1^2	E*	RAD	CR	IL	LA0981
yv	*3*	yellow virescent	vel	E*	RAD	CR	IL	LA0631
yv	*ms*	yellow virescent		E*N		X		LA3907
yv-2		yellow virescent-2		E*	SPON	AC	NIL	LA3190
yv-4		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.#
A-1	A-1	LA0818
AC	Ailsa Craig	LA2838A
ACE	Ace	LA0516
ALA	Alabama	n/a
AMB	Antimold-B	LA3244
ANU	Anahu	LA3143
BK	Budai Korai	n/a
BOD	Break O'Day	LA1499
C255	Cal 255	LA0198
C28	Campbell 28	LA3317
cer	*L. esc*. var. *cerasiforme*	many
CG	Chico Grande	LA3121
che	*L. cheesmanii*	many
chi	*L. chilense*	many
chm	*L. chmielewskii*	many
CR	Condine Red	LA0533
CRGL	Craigella	LA3247
CSM	Castlemart	LA2400
CT	Chatham	n/a
CX	Canary Export	LA3228
E6203	E-6203	LA4024
EPK	Earlipak	LA0266
ERL	Earliana	LA3238
ESC	Early Santa Clara	LA517
FB	Fireball	LA3024
FEY	First Early	n/a
FLD	Flora-Dade	LA3242
GRD	Gardener	LA3030
GSM	Gulf State Market	LA3231
H100	Hunt 100	LA3144
hir	*L. hirsutum*	many
HSD	Homestead 24	LA3237
JBR	John Baer	LA1089
KK	Kokomo	LA3240
LGPL	Large Plum	LA3203
LK	Laketa	LA0505
LRD	Long Red	LA3232
LU	Lukullus	LA0534
lyc	*S. lycopersicoides*	many
M167	Montfavet 167	LA2713
M168	Montfavet 168	LA2714
MD	Marmande	LA1504
MGB	Marglobe	LA0502
MM	Moneymaker	LA2706
MNB	Monalbo	LA2818
MP	Manapal	LA2451
NRT	Norton	n/a
O8245	Ohio 8245	n/a
OGA	Ohio Globe A	LA1088
ONT	Ontario	n/a
par	*L. parviflorum*	many
PCV	primitive cultivar	n/a

Back.	Genotype name	Acc.#
pen	*L. pennellii*	many
per	*L. peruvianum*	many
pim	*L. pimpinellifolium*	many
PLB	Pieralbo	n/a
POR	Porphyre	LA2715
PRI	Primabel	LA3903
PRN	Prairiana	LA3236
PRT	Pritchard	LA3233
PSN	Pearson	LA0012
PSP	Prospero	LA3229
PTN	Platense	LA3243
RCH	Red Cherry	LA0337
RG	Rio Grande	LA3343
RH13	Rehovot 13	LA3129
RNH	Rouge Naine Hative	n/a
ROMA	Roma	n/a
ROVF	Roma VF	n/a
RR	Rheinlands Ruhm	LA0535
RSWT	Roumanian Sweet	LA0503
RTVF	Red Top VF	LA0276
RU	Rutgers	LA1090
SCZ	Santa Cruz	LA1021
SM	San Marzano	LA0180
spVCH	VFNT Cherry (sp)	LA2705
SPZ	San Pancrazio	n/a
STD	Stokesdale	LA1091
STN	Stone	LA1506
STR24	Start 24	LA3632
SX	Sioux	LA3234
T338	UC-T338	LA2939
T-5	UC-T5	LA2399
TGR	Targinnie Red	LA3230
TVD	Vendor (Tm-2a)	LA2968
UC82	UC-82B	LA1706
VCH	VFNT Cherry	LA1221
VD	Vendor	LA3122
VE	Van's Early	n/a
VF11	VF-11	LA0744
VF145	VF-145 78-79	LA1222
VF36	VF-36	LA0490
VF6	VF-6	LA0743
VFN8	VFN-8	LA1022
VFSM	VF San Marzano	n/a
VGB	Vagabond	LA3246
VRB	Vrbikanske nizke	LA3630
VTG	Vantage	LA3905
WA	Walter	LA3465
X	unknown or hybrid	n/a
XLP	XL Pearson	n/a

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