

Report of the Tomato Genetics Cooperative



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Foreword

The Tomato Genetics Cooperative, initiated in 1951, is a group of researchers who share and 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 the Solanaceous species is encouraged as well.

Paid memberships currently stand at approximately 101 from 19 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@ufl.edu. 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. The woodcut of "Poma aurea" or "Goldapffel" (Solanum lycopersicum) from Matthioli (1586), a German edition edited not by Matthioli, but by the German herbalist Joachim Camerarius. This copy has been hand-colored, but the flowers were left unpainted, presumably because their color was not known. Reproduced with permission of the Natural History Museum Botany Library. Photo provided by Dr. Iris Peralta. See her feature article where the recent changes in tomato nomenclature are discussed. -J.W. Scott

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From the Editor:

Greetings to the TGC membership! This is the fourth volume from your present Managing Editor and the first for my new TGC assistant Dolly Cummings. Dolly has been invaluable in all phases of the TGC operation and you would not be reading this if not for her stellar efforts. I do want to thank John Petti and Gail Somodi who so ably assisted this effort in the past. My contact information is the same as last year except for a small change in my email:

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We are back to a September mailing and hope to keep on this schedule in the future. Since I started as Managing Editor, I have asked for tomato researchers to clear the naming of genes and gene symbols through the Tomato Genetics Cooperative. Roger Chetelat as chair of the gene list committee can then easily insure that the nomenclature rules are properly followed. In this volume we finally have officially named two genes, both for TYLCV resistance (*Ty-2* and *Ty-3*). I hope this will be the start of a trend. Also note that Volume 56 includes figures in color, a first for the ever-improving TGC!

One of my major TGC objectives over the past several years has been to have all the TGC volumes electronically available on line and searchable by keyword. This has proven to be a rather involved task, but we are making progress. By the time you read this all volumes should be available on line in both .pdf and .html formats (**see our website <http://tgc.ifas.ufl.edu/> click Online Volumes**). All volumes are not yet keyword searchable but we hope they will be in the not too distant future. The volumes that are presently keyword searchable are listed on the website.

Thank you to all who sent in reports this year. Please consider sending reports for future volumes as it is the lifeblood of the TGC. Reports on varietal releases and on crops closely related to tomato are encouraged. Special thanks to Iris Peralta and colleagues who provided our feature article on tomato nomenclature. Some are using *Lycopersicon* and some are using *Solanum* in the literature and this article may help you decide which system you want to use.

If you have a change in your contact information please send me an email so we can keep our records up to date and keep you abreast of the latest from the TGC. Best wishes in your endeavors for 2006-2007.

Jay W. Scott
Managing Editor

UPCOMING MEETINGS

- 🍅 21st Annual Tomato Disease Workshop, November 9- 10, 2006, Fletcher, NC.
<http://www.ces.ncsu.edu/fletcher/events/2006-11-tomato-disease/index.html>
- 🍅 4th International Bemisia & Whitefly Genomics Workshop, December 3-8, 2006, Duck Key, FL
<http://conference.ifas.ufl.edu/bemisia/>
- 🍅 4th Solanaceae Genome Workshop 2007, Jeju Island, Korea.
<http://www.solanaceae2007.org>
- 🍅 2nd International Symposium on Tomato Disease, October 8-12, 2007
<http://www.2istd.ege.edu.tr/index.html>
- 🍅 Tomato Breeders Roundtable, late October or November 2007, Penn State U.
Contact Majid Foolad for information: mrf5@psu.edu

GRANT OPPORTUNITY**Request for Proposals for Tomato Germplasm Evaluation**

Funding is expected to be available again in fiscal year 2007 for evaluation of tomato germplasm. Proposals must be submitted through the Crop Germplasm Committee (CGC). 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. Evaluation priorities established by the CGC (Table 1) will provide review criteria. When all other factors are equal, preference for funding will be given to supporting those proposals forwarded by CGCs that have not received prior funding. Proposals will be reviewed by the CGC and forwarded to the USDA for consideration. Proposals Must be returned to the CGC Chair by October 27 so that reviews and rankings, can be forwarded to the USDA in Beltsville by November 17, 2006.

Because of limited funds, the USDA cannot support all proposals submitted. Consequently, please be very frugal in your request for funds. In recent years, the USDA has capped budget allocations in the range of \$15,000-\$18,000 per project annually.

The proposal format is outlined below. Please submit proposals electronically as a PDF file to David Francis, CGC Chair, francis.77@osu.edu.

- I. Project title and name, title 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. Budgets should follow USDA form ARS454 as funding will be in the form of a specific cooperative agreement. No overhead charges are permitted.
- V. Personnel:
 - A. What type of personnel will perform the research (e.g. ARS, State, or industry scientist; postdoc; grad student, or other temporary help).

- B. Where will 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).

Table 1. Crop Germplasm Committee Priorities for Tomato

Type	Priority	Description
Bacterial Diseases	High	Bacterial canker
Bacterial Diseases	High	Bacterial spot
Bacterial Diseases	Medium	Bacterial soft rot (post harvest)
Bacterial Diseases	Medium	Bacterial Speck
Bacterial Diseases	Low	Bacterial Wilt
Fungal Diseases	High	Verticillium wilt race 2
Fungal Diseases	High	Target Spot
Fungal Diseases	High	Corky root
Fungal Diseases	Medium	Late blight
Fungal Diseases	Medium	Phytophthora root rot
Fungal Diseases	Medium	Fruit rots
Fungal Diseases	Low	Target spot
Fungal Diseases	Low	Powdery mildew
Viral Disease	High	Pepino mosaic virus
Viral Disease	High	Non-spotted wilt tospoviruses
Viral Disease	High	Marchites manchada syn Sinolva necrosis
Viral Disease	Medium	gemini viruses
Viral Disease	Medium	Spotted wilt
Viral Disease	Medium	CMV
Viral Disease	Low	Beet curly top virus
Viral Disease	Low	PVY
Insect screening Protocols	High	Silverleaf whitefly
Insect screening Protocols	High	Nematodes, heat stable
Insect screening Protocols	Medium	Aphids
Insect screening Protocols	Medium	Psyllid insects
Stress	High	Cold tolerance
Stress	High	Heat tolerance
Stress	Medium	Salinity tolerance
Stress	Medium	Color disorders
Horticultural	High	Soluble solids
Horticultural	High	Flavor (define components)
Horticultural	Medium	Antioxidants/nutritional content
Horticultural	Medium	Color
Horticultural	Medium	Sugar type
Horticultural	Medium	Peelability/dicing
Horticultural	Medium	Viscosity
Horticultural	Low	Blossom-end smoothness
Horticultural	Low	Fruit chilling tolerance
Genetic Resources	High	Genotyping to define core collections
Genetic Resources	High	Phenotypic characterization of segregating populations

NOMENCLATURE FOR WILD AND CULTIVATED TOMATOES

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An efficient way to communicate ideas about our world is to build a common language, including scientific names of biological organisms that are named according a Latin binomial nomenclature first used for all plants by Linnaeus (1753). In binomial nomenclature a name is composed of two parts, the first refers to the genus and the second, often called the epithet, refers to the species, followed by the author(s) of the name. Species epithets can refer to striking characteristics of the plant (e.g. *Solanum tuberosum*), where the plant was found (e.g. *Solanum peruvianum*) or are sometimes used to honor particular people (e.g. *Solanum neorickii*).

How are plants named? *Species plantarum*, written by the Swedish botanist and Doctor Carl Linnaeus and published in 1753, is considered the starting point for scientific nomenclature of plants. The International Code of Botanical Nomenclature (ICBN, McNeill et al., 2006; revised and updated every 6 years at International Botanical Congresses, the most recent held in Vienna in 2005) provides a framework to properly name species and other taxonomic ranks, as well as a set of rules to determine the priority of plant names when competing names refer to the same organism. In cultivated plants, new forms or cultivars have been generated by domestication and artificial selection. The application of the ICBN to cultivated taxa could produce complex scientific names of limited utility to either taxonomists or plant breeders. For that reason a different set of nomenclatural rules can be used for cultivated plants, laid out in the International Code of Nomenclature for Cultivated Plants (ICNCP, Brickell et al., 2004).

The names of wild tomatoes

In a taxonomic treatment of tomatoes and their wild relatives it is important to study the diversity and distribution of the species as well as their natural history. Species delimitation is a synthetic interpretation of our knowledge of a group (Spooner et al., 2003), and what constitutes a species is a hypothesis that changes over time as more information becomes available.

Wild tomatoes are native of western South America, distributed from Ecuador to northern Chile, and with two endemic species in the Galápagos Islands (Darwin et al., 2003; Peralta and Spooner, 2005). They grow in variety of habitats, from near sea level to over 3,300 m in elevation, in arid coastal lowlands and adjacent lomas where the Pacific winds drop scarce rainfall and humidity; in isolated valleys in the high Andes, and in deserts like the severe Atacama Desert in northern Chile. Andean topography, diverse ecological habitats, and different climates have all contributed to wild tomato diversity.

We have recently completed an in-depth study of tomatoes and their wild relatives, with the aim to provide new species definitions, revised and updated the nomenclature and to synthesize

knowledge about these plants. We have treated tomatoes in the large genus *Solanum*, rather than as the segregate genus *Lycopersicon*, based on a weight of evidence coming largely, but not exclusively, from studies of DNA sequences. In the past decade, several molecular phylogenetic studies of the Solanaceae have unambiguously showed tomatoes to be deeply nested within *Solanum* (Spooner et al., 1993; Bohs and Olmstead, 1997, 1999; Olmstead and Palmer, 1997; Olmstead and al., 1999; Peralta and Spooner, 2001; Bohs, 2005; Spooner et al., 2005). We propose a phylogenetic classification philosophy that simply states the hypothesis that tomatoes may have more "predictivity" under *Solanum*, and also apply a Linnaean nomenclatural system (hierarchical) to provide the valid names of wild species under *Solanum* and their equivalents in *Lycopersicon* for ease of comparison to the literature (Table 1).

Based on morphological characters, phylogenetic relationships, and geographic distribution, we proposed the segregation of four species within the highly polymorphic green-fruited species *S. peruvianum* sensu lato (sensu lato refers to a broad concept of a species): *S. arcanum*, *S. huaylasense*, *S. peruvianum*, and *S. corneliomulleri*. The first two have been described as new species (Peralta et al., 2005) from Perú, while the latter two had already been named by Linnaeus (1753) and MacBride (1962) respectively. We recognize yet another new yellow- to orange-fruited species, *S. galapagense*, segregated from *S. cheesmaniae*; both are endemic to the Galápagos Islands (Darwin et al., 2003; Knapp and Darwin, in press). In total, we recognize 13 species of wild tomatoes, including the cultivated tomato (*Solanum lycopersicum*) and its weedy escaped forms that are distributed worldwide (Table 1). This is an increase from the nine species of tomatoes traditionally recognized (Rick et al., 1990). We are treating these 13 species, in addition to four closely related species (*S. juglandifolium*, *S. lycopersicoides*, *S. ochranthum*, *S. sitiens*), in the taxonomic series *Systematic Botany Monographs* (Peralta et al., in press).

Cultivated tomatoes and the history of their scientific naming

Tomatoes were introduced into Europe from the Americas and became known to botanists about the middle of the sixteenth century, thus the scientific naming of tomatoes, including wild species, is linked to concepts of diversity in *Solanum lycopersicum*, the cultivated species. Pietro Andrea Matthioli (1544) described tomatoes for the first time with the common name "Pomi d'oro" (Golden Apples) in the first edition (written in Italian) of his 'Commentary' upon the work of the 1st century Greek botanist Dioscorides of Anazarbos. In the Latin edition, Matthioli (1554) referred to tomatoes as "Mala aurea" (the Latin equivalent of Golden Apple). Matthioli greatly enriched the tomato description with Italian traditional knowledge and uses of plants previously not known in Europe, and many editions of Matthioli's work were translated in different languages throughout Europe (Watson, 1989). Other early herbalists referred to the tomato as "mala peruviana" or "pommi del Peru" (Peruvian Apples), "pomi d'oro", "mala aurea", "poma aurea", pomme d'Amour, "pomum amoris" or often used polynomial names like *Poma amoris fructu luteo* or *Poma amoris fructu rubro*. Some of these common names like "pomum amoris" were also used for eggplants (*S. melongena*) and "mala peruviana" was used for a species of another solanaceous genus, *Datura* (Jimson weed or thorn apple). Different names in different languages were used to name tomatoes in the time before standardized scientific naming. Pre-Linnaean botanists usually used polynomial, or phrase, names, consisting of several words describing the plant itself and distinguishing it from all others. They did not employ today's genus and species concepts, but did seek to name plants in a way that reflected their affinities. Interestingly, early botanists recognized the close relationship of tomatoes with the genus *Solanum*, and commonly referred to them as *S. pomiferum* (Luckwill, 1943). Tournefort (1694) was the first to name cultivated tomatoes as *Lycopersicon* ("wolf peach" in Greek). Tournefort placed

forms with large multilocular fruits in the set of plants he called *Lycopersicon*, but kept the plants with bilocular fruits as *Solanum*. Linnaeus (1753) began to consistently use Latin binomials in *Species Plantarum*, as polynomials were becoming too complicated and difficult to memorize. He classified tomatoes in the genus *Solanum* and described *S. lycopersicum* (the cultivated tomato) and *S. peruvianum*. The very next year Miller (1754) followed Tournefort (1694) and formally described the genus *Lycopersicon*. Miller did not approve of Linnaeus's binomial system, and he continued to use polynomial phrase names for all plants until 1768 (Miller, 1768). Miller's circumscription of the genus *Lycopersicon* also included potatoes as "*Lycopersicon radice tuberosa, esculentum*" supported by the argument that "This Plant was always ranged in the Genus of *Solanum*, or Nightshade, and is now brought under that Title by *Dr. Linnaeus*; but as *Lycopersicon* has now been established as a distinct Genus, on account of the Fruit being divided into several Cells, by intermediate Partitions, and as the Fruit of this Plant [the potato] exactly agrees with the Characters of the other species of this Genus, I have inserted it here."

Later, Miller (1768) began to use Linnaeus' binomial system and published descriptions under *Lycopersicon* for several species, among them were *L. esculentum*, *L. peruvianum*, *L. pimpinellifolium* and *L. tuberosum* (potatoes). In the posthumously published edition of *The gardener's and botanist's dictionary* (Miller, 1807) the editor, Thomas Martyn, followed Linnaeus and merged *Lycopersicon* back into *Solanum*. Following Miller's early work, a number of classical and modern authors recognized tomatoes under *Lycopersicon*, but other taxonomists included tomatoes in *Solanum*.

Today, based on evidence from phylogenetic studies using DNA sequences and more in-depth studies of plant morphology and distribution, there is general acceptance of the treatment of tomatoes in the genus *Solanum* by both taxonomists and breeders alike. For example, the use of *Solanum* names has gained wide acceptance by the breeding and genomics community such as the Solanaceae Genomics Network (SGN) and the International SOL Project (<http://www.sgn.cornell.edu/>). These names in *Solanum* are being incorporated in germplasm bank databases as in the C.M. Rick Tomato Genetic Resources Center (<http://tgrc.ucdavis.edu/>).

In conclusion, the generic status of tomatoes has been in flux since the eighteenth century, reflecting two main and often competing goals in taxonomy, that of 1) predictive natural classifications (treatment in *Solanum*) and 2) the maintenance of nomenclatural stability (treatment in *Lycopersicon*). The economic importance of tomatoes has stimulated discussion within the scientific community of taxonomists and breeders about the relative value of classifications that emphasize predictivity versus stability (Peralta and Spooner, 2000; Spooner et al., 2003).

Hypotheses of cultivated tomato domestication

Tomatoes were domesticated in America and two competing hypotheses have been advanced for the original place of domestication. Alfonse De Candolle (1886) used linguistic evidence like the names "mala peruviana" or "Pommi del Peru" (Peruvian apples) to suggest a Peruvian origin. He also considered the cherry tomato 'cerasiforme' types as the ancestor of the crop that spread worldwide, but recent genetic investigations have shown that the plants known as 'cerasiforme' are a mixture of wild and cultivated tomatoes rather than being "ancestral" to the cultivars (Nesbitt and Tanksley, 2002).

The Mexican hypothesis was advanced by Jenkins (1948), who also used linguistic evidence, but it is not clear that the plant cited as "tomati" from Mexico referred to the true tomatoes or a native *Physalis* species ("tomate" or "tomatillo" is the common name in Mexico for *Physalis philadelphica*, the husk tomato, while "jitomate" refers to cultivars with large fruits of *Solanum lycopersicum*). Jenkins (1948) agreed with DeCandolle (1886) that *S. lycopersicum* from South America was the progenitor

of the European domesticated cultivars, but disagreed with the place of domestication in Peru. We consider the question of the original site of domestication of cultivated tomato to be unsolved (Peralta and Spooner, in press).

Nomenclature of cultivated tomato

Regardless of where tomatoes were first domesticated, human beings have created a huge array of morphologically different cultivars and forms from the single species *S. lycopersicum* using traditional techniques of plant breeding. Some taxonomists (e.g. Brezhnev, 1958) have attempted to treat this diversity using the ICBN, and have created an enormously complex and almost unworkable nomenclature for wild and cultivated species that is neither predictive nor stable.

For tomato cultivars, we support a taxonomy under the Code of Nomenclature for Cultivated Plants (ICNCP; Brickell et al., 2004), which provides a framework more appropriate to name the great diversity of cultivated tomatoes, all members of the single biological species *S. lycopersicum*, generated by breeding. This taxonomy has yet to be developed on a global scale, but would be useful to standardize the naming and exchange of the wide variety of tomato cultivars in use today.

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TABLE 1. Species list for tomatoes and their wild relatives (with equivalents in the previously recognized genus *Lycopersicon*, now part of a monophyletic *Solanum*), and with their fruit color and breeding system.

Name in Peralta et al. in press	<i>Lycopersicon</i> equivalent	Fruit color	Breeding system ¹
<i>Solanum lycopersicoides</i> Dunal	<i>Lycopersicon lycopersicoides</i> (Dunal in DC.) A. Child ex J.M.H. Shaw	Green-yellow when maturing, black when ripe	SI, allogamous
<i>Solanum sitiens</i> I.M. Johnst.	<i>Lycopersicon sitiens</i> (I.M. Johnst.) J.M.H. Shaw	Green-yellow when maturing, black when ripe	SI, allogamous
<i>Solanum juglandifolium</i> Dunal	<i>Lycopersicon ochranthum</i> (Dunal) J.M.H. Shaw	Green to yellow-green	SI, allogamous
<i>Solanum ochranthum</i> Dunal	<i>Lycopersicon juglandifolium</i> (Dunal) J.M.H. Shaw	Green to yellow-green	SI, allogamous
<i>Solanum pennellii</i> Correll	<i>Lycopersicon pennellii</i> (Correll) D'Arcy	Green	Usually SI, some SC in S of species range
<i>Solanum habrochaites</i> S. Knapp and D.M. Spooner	<i>Lycopersicon hirsutum</i> Dunal	Green with darker green stripes	Typically SI, 1-2 collections SC, but with later inbreeding depression
<i>Solanum chilense</i> (Dunal) Reiche	<i>Lycopersicon chilense</i> Dunal	Green to whitish green with purple stripes	SI, allogamous
<i>Solanum huaylasense</i> Peralta and S. Knapp	Part of <i>Lycopersicon peruvianum</i> (L.) Miller	Typically green with dark green stripes	Typically SI, allogamous,
<i>Solanum peruvianum</i> L.	<i>Lycopersicon peruvianum</i> (L.) Miller	Typically green to greenish-white, sometimes flushed with purple	Typically SI, allogamous,
<i>Solanum corneliomuelleri</i> J.F. Macbr. (1 geographic race: Misti nr. Arequipa)	Part of <i>Lycopersicon peruvianum</i> (L.) Miller; also known as <i>L. glandulosum</i> C.F. Müll.	Typically green with dark green or purple stripes, sometimes flushed with purple	Typically SI, allogamous,
<i>Solanum arcanum</i> Peralta (4 geographic races: 'humifusum', lomas, Marañon, Chotano-Yamaluc)	Part of <i>Lycopersicon peruvianum</i> (L.) Miller	Typically green with dark green stripes	Typically SI, allogamous, rare pop SC, autogamous, facultative allogamous

<i>Solanum chmeilewskii</i> (C.M. Rick, Kesicki, Fobes and M. Holle) D.M. Spooner, G.J. Anderson and R.K. Jansen	<i>Lycopersicon chmeilewskii</i> C.M. Rick, Kesicki, Fobes and M. Holle	Typically green with dark green stripes	SC, facultative allogamous
<i>Solanum neorickii</i> D.M. Spooner, G.J. Anderson and R.K. Jansen	<i>Lycopersicon parviflorum</i> C.M. Rick, Kesicki, Fobes and M. Holle	Typically green with dark green stripes	SC, highly autogamous
<i>Solanum</i> <i>pimpinellifolium</i> L.	<i>Lycopersicon</i> <i>pimpinellifolium</i> (L.) Miller	Red	SC, autogamous, facultative allogamous
<i>Solanum lycopersicum</i> L.	<i>Lycopersicon esculentum</i> Miller	Red	SC, autogamous, facultative allogamous
<i>Solanum cheesmaniae</i> (L. Riley) Fosberg	<i>Lycopersicon cheesmaniae</i> L. Riley	Yellow, orange	SC, exclusively autogamous
<i>Solanum galapagense</i> S.C. Darwin and Peralta	Part of <i>Lycopersicon</i> <i>cheesmaniae</i> L. Riley	Yellow, orange	SC, exclusively autogamous

¹SI = Self-incompatible; SC = Self-compatible.

Figure 1 (cover illustration). The woodcut of “*Poma aurea*” or “Goldapffel” (*Solanum lycopersicum*) from Matthioli (1586), a German edition edited not by Matthioli, but by the German herbalist Joachim Camerarius. This copy has been hand-colored, but the flowers were left unpainted, presumably because their color was not known. Reproduced with permission of the Natural History Museum Botany Library.

Recent Wild Species Collections from Chile

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Our *ex situ* collections of the four wild tomato spp. native to Chile – *L. chilense*, *L. peruvianum*, *S. sitiens* and *S. lycopersicoides* – were vastly improved by several collecting expeditions made in the 1980's (Rick and Holle 1989). However, even with the newly acquired accessions, there were still significant gaps in the geographic representation of each species.

To address these deficiencies, two expeditions to northern Chile (Regions I and II) were sponsored by the USDA Plant Exchange Office in 2001 and 2005. In addition to the authors, the participants were Elaine Graham (UC-Davis) and Pedro León (INIA, Chile) on the first trip, Carl Jones (UC-Davis) on the second, and Luis Faúndez (Univ. de Chile) on both trips. The primary goal of the 2001 expedition was to obtain additional populations of *S. sitiens* and *S. lycopersicoides*, species that at the time were represented by only a handful of accessions each. The objectives of the 2005 jaunt focused on collecting new populations of *L. chilense* from the arid coast ranges. Our combined observations from both trips regarding the ecology and distribution of each species, and characteristics of selected accessions, are summarized below.

L. chilense – 2004/2005 was a dry year along the coast of Chile, and few actively growing populations were found in this region. One notable exception was a population from Quebrada los Zanjones (LA4339), located about 15 Km further south and in a different drainage system than previous collections near Taltal. The Zanjones population represents the southern limit of the distribution of *L. chilense*. In the opposite direction, we collected a population from Estación Puquío (LA4324), located near the border with Peru, and the northernmost accession ever collected from Chile. Previously known only from an herbarium specimen made in the 1950's, the Estación Puquío population grows in an extremely arid, desolate, and inaccessible region. Several other new accessions (LA4117, LA4329, LA4330, LA4332) were collected in the Andes near Calama and San Pedro de Atacama, an area from which few collections had been previously made. These new accessions link the populations to the southeast – a distinctive race once recognized as a separate species (*L. atacamense*) – with those to the northwest and the center of the distribution. Interestingly, the population from below Paso Jama (LA4117) grows at up to nearly 3,600m elevation, extremely high, possibly the highest, for any *Lycopersicon* species. Considering its lower latitude, which is over 12 degrees further from the equator than the high altitude *L. hirsutum*'s for instance, this *L. chilense* accession would likely be a good source of cold tolerance.

L. peruvianum – We collected two populations (LA4317 and LA4325) growing in agricultural fields near the coast. At both locations, but especially the first, large 'metapopulations' extended from sea level up to mid elevations in the river valleys. As expected for large populations of an obligate outcrosser, we noted abundant morphological variation between plants, hinting at a relatively high level of genetic diversity in this material. We also made new collections from the upper Río Lluta and Río Camarones drainages (LA4318 and LA4328). The latter population, of which we could find only one plant with fruit, was morphologically distinct from our existing accessions of *L. peruvianum*, but unfortunately could not be regenerated at Davis. Another high elevation population was collected at Camiña (LA4125) which is the southern limit of this species' distribution. This population proved to be

entirely self-compatible (Graham et al. 2003), a situation similar to that of *L. hirsutum* and *L. pennellii*, both of which are mostly SI but include Sc races on their southern geographic margins.

S. sitiens – Our recent collections of *S. sitiens* nearly triple the number of accessions of this species maintained by the TGRC, and greatly expand the geographic range preserved *ex situ*. A population found near Mina La Escondida (LA4105) is located over 100 Km to the south of any other known *S. sitiens* populations, and is morphologically distinctive. Another interesting accession was collected from Cerro Quimal (LA4331), located further to the east than any other known population of this species. It survives close to a mountaintop bordering the Salar de Atacama, in an extremely arid environment, and probably subject to periodic frosts. Tests of soil samples taken at several *S. sitiens* collection sites indicated high levels of salinity – up to 500 meq/L Na⁺ at Estación Cere (LA4113) – which suggests this species could also be a source of salt tolerance for tomato improvement. Like the existing accessions of *S. sitiens*, the new populations are all SI.

S. lycopersicoides – We collected two small populations (LA4320 and LA4326) at 1200 - 1400m elevation, lower than any previously known population of this species, which generally prefers high elevations (up to nearly 3,800m). Additional accessions (LA4123 and LA4126) were collected from the Río Camiña drainage, near the location of an earlier collection (LA2951) noteworthy for producing hybrids with cultivated tomato that are unusually fertile, a feature that facilitates introgression (Canady et al. 2005). In addition, we collected the first accessions of this species from the Río Camarones canyon (LA4130, LA4131). The physical barriers – arid ridges and coastal plain, distance, etc. – that separate neighboring river valleys in this part of Chile likely result in reproductive isolation and genetic differentiation of local populations. This underscores the importance of a thorough geographic sampling for conservation of these species *ex situ*.

Our two expeditions afforded an opportunity to observe ecological preferences and evaluate changes in the status of individual populations from one visit to the next. By far the most widespread in Chile, populations of *L. chilense* were generally robust and healthy. Nonetheless, some populations have been impacted by human activities, such as road construction and heavy grazing, which in some cases precluded viable seed collections. Grazing is a serious concern with *S. lycopersicoides*, a relatively rare plant to begin with, whose preferences for more mesic, high elevation sites places it in prime territory for herds of goats, sheep, llamas and alpacas. This situation is exacerbated by low seed production, a long fruit ripening phase, and lack of fruit abscission, all of which increase vulnerability to herbivory. Populations of *S. sitiens* appear to avoid this threat thanks to the lack of vegetation in its hyperarid habitat. On the other hand, many populations grow in the vicinity of active mines. The Mina Escondida population, for instance, is threatened by construction of a nearby pipeline. In light of these concerns, we recently filed petitions to add *S. lycopersicoides* and *S. sitiens* to the IUCN red list of endangered species in Chile.

Detailed passport information on each accession can be obtained at our website, <http://tgrc.ucdavis.edu>. After multiplication of seed at Davis, samples will be provided, upon request, to interested researchers (check website for current availability).

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Obtaining tomato form with higher lycopene content in fruits after seed treatment with diagnostic imaging element Tc-99m

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Introduction

For induction of genetic variability in many crops including tomato, specialists often combine the mutagenesis with *in vitro* techniques (Jain, 1998; Emmanuel and Levy, 2002). Results obtained by utilization of chemical and physical mutagens in tomato include changed growth habit (*sp*), inflorescence (*s*) and other characters, with positive effects on plant productivity, higher pigment content in the fruits, disease resistance, etc. (Nabisan et al., 1992; Rodeva, 2003; Mukandama et al., 2003). Some of these changed forms are successfully included in tomato breeding programs.

The radionuclides are still not widely used in mutation breeding. Nell and Onasch (1989) have observed cytological changes in somatic cells and intercellular spaces as well as structural disturbances of cell membranes in young soybean plants after treatment with Tc-99m. We didn't find data in the literature about the mutagenic effect of the diagnostic imaging elements of Tc-99m in tomato.

The goal of this experiment was to study some of the altered characteristics in plants of two seed generations of tomato obtained after seed treatment with Tc-99m.

Material and methods

The experiments were carried out in 2003-2005. The plants of M₂ /200/ and M₃ /50/ generations of tomato form N1276-13, were obtained as a result of a 24-hour treatment of seeds from line N120 with Tc-99m (as Na⁺TcO⁴⁻ with average specific concentration 35 MBq/ml) and *in vitro* germination, then grown in the field. Control plants were grown after treating the seeds of the same line in modified Krebs solution /C1/ and non-treated seeds germinated *in vitro* /C2/. Thirty plants were in each of the controls. Data recorded included: productivity/plant, fruit weight and index. In 20% of the plants in each of the studied generations and also in the controls, dry matter content (⁰brix), total pigments and lycopene were analyzed in the fruits (Manuelyan, in Kalloo, 1991) .

Results and discussion

In year 2003, tomato plant N1276-13 was selected with higher pigment content in the fruits compared to all other studied plants obtained after seed treatment with Tc-99m. The data in Table 1 proves that the plants in M₂ and M₃ generation of N1276-13 are distinguished by some characteristic compared with control plants of the original line N120. The observed differences in the plants are significant especially regarding total pigments and lycopene content which was confirmed by the statistical analysis. The values of these characteristics are higher in the plants of the experimental tomato compared to the control plants. The recorded lower values in year 2005 probably are due to unfavorable weather conditions – wide temperature fluctuations and high humidity because of daily rain. Although the pigment content in the fruits of plants N1276-13 (M₃) was lower than in the previous year, it was again two times higher than that of the control plants. The statistical analysis shows lower coefficients of variability for these two characteristics in year 2005, probably due to the selection process in M₂.

There were no statistically significant differences established for any other studied characteristics in tomato plants with the exception of fruit index. The fruit index showed that the fruit shape in tomato plants of N1276-13 is more elongated (1,23 and 1,24 respectively) compared to the oval fruit shape of the control plants (from 1,10 to 1,16).

As a result of this experiment and treating the seeds with radionuclide Tc-99m it was possible to obtain a change in tomato form with a characteristic of interest for breeders. We suppose that Tc-99m influences the mechanism that controls carotenoid biosynthesis in tomato fruits. Much of what has been learned about the carotenoid pathway in the last decade has come from the selection and analysis of mutants, primarily of *Arabidopsis* and tomato (Francis and Cunningham, 2002). High resolution mapping of QTLs in such forms is important for finding the differences in carotenoid content and may lead to the identification of gene(s) that influence carotenoid accumulation.

Table 1. Comparison of morphological and biochemical characteristics of tomato plants of N1276-13 and control plants

Genotype	Productivity per plant g	Fruit index	Fruit weight g	Dry matter content %	Total pigments mg%			Lycopene mg%		
					mean	sd	CV%	mean	sd	CV%
2004										
M ₂	3500ns	1,23a ^z	65,3b	5,7ns	13,41a	2,77	20,63	11,27a	3,14	27,86
C1	3700ns	1,10b	76,0a	5,5ns	6,19b	0,25	3,96	4,84b	0,48	9,91
C2	3600ns	1,11b	78,7a	5,3ns	6,94b	0,22	3,22	5,10b	0,58	11,24
2005										
M ₃	3300ns	1,24a	76,3ns	5,0ns	9,00a	0,87	9,62	5,59a	0,79	14,20
C1	3400ns	1,16b	75,0ns	5,0ns	4,57b	0,13	3,07	3,27b	0,31	9,67
C2	3250ns	1,11b	73,5ns	5,2ms	4,25b	0,08	1,97	2,91b	0,19	6,87

^z Means in column for each year not followed by same letter are significantly different by Duncan's Multiple Range Test at P≤0.05.; ns – not significant

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Ty-2, a gene on chromosome 11 conditioning geminivirus resistance in tomato

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Whitefly-transmitted geminiviruses drastically reduce tomato yields and increase production costs throughout the tropics and subtropics as well as southern temperate regions. Losses due to geminivirus infection became a major production problem in Southeast Asia and Taiwan by the mid-1990's and the disease is currently spreading in China as far north as the Yangtze River (T-C Wang, personal communication). Resistance is the cheapest and most effective means of control. Almost all geminivirus resistance genes were introgressed into tomato from wild species. *Ty-1*, the first reported geminivirus resistance gene, originated from *S. chilense* accession LA1969 and was mapped to the top of chromosome 6 (Zamir et al., 1994). H24 is a tomato line bred in India (Kaloo and Banerjee, 1990) with geminivirus resistance derived from a *S. habrochaites* accession called B6013. H24 has demonstrated high levels of resistance to monopartite geminiviruses which prevail in south India and Taiwan (Hanson et al., 2000), Japan, and north Vietnam, and has been used as a source of resistance by AVRDC and other breeding programs. Banerjee and Kaloo (1987) reported that two genes acting epistatically conditioned resistance in H24 although our mapping study found a single wild introgression of over 14 cM on the bottom of chromosome 11 between TG393 and TG36 associated with resistance (Hanson et al., 2000).

RFLP probing of resistant lines developed at AVRDC derived from crosses with H24 revealed that some lines carry the entire introgression on the bottom of chromosome 11 while other lines contained a smaller introgression with the region from TG26 to TG393 replaced with *S. lycopersicum* DNA. We conducted a study in 2001 to compare the resistance of lines with the entire introgression and lines with the shorter introgression. Entries included thirteen F₆ lines from three AVRDC double crosses (Table 1). Cross codes and parents were as follows: CLN2114= (CL5915-93D4 x H24) x (PT4671A x CRA84-58-1); CLN2116= (CL5915-93D4 x H24) x (UC204A x CRA84-58-1); CLN2131= (CL5915-93D4 x CRA84-58-1) x (PT4664 x H24). H24 was the only source of geminivirus resistance in these crosses. F₆ entries and checks were evaluated for reaction to Tomato leaf curl Taiwan virus (ToLCTWV) and probed with RFLP markers TG393, TG26, and TG36 to determine the presence or absence of *S. habrochaites* DNA. Each plot included five plants. Entries were replicated five times and arranged in a RCBD. Fifteen-day-old seedlings of entries were exposed to viruliferous whiteflies maintained in a plastic house and scored for disease incidence and severity at two, four, and six weeks after exposure.

Almost 100% of plants of the susceptible check CL5915 and the two entries homozygous for *S. lycopersicum* alleles at the three regions developed severe stunting, yellowing and curling by two weeks after whitefly exposure. The three entries possessing the full *S. habrochaites* introgression and the four entries containing the shorter introgression around TG36 were almost completely free of virus symptoms until conclusion of the experiment. Our results indicate that no geminivirus resistance genes are located on that portion of the *S. habrochaites* introgression from TG26 to TG393 and resistance was associated with presence of wild alleles at TG36. Fine-mapping of geminivirus resistance in this region is ongoing at AVRDC.

The mapping paper of Hanson et al. (2000) did not propose a name for the geminivirus resistance on chromosome 11 because of the possibility that such a large wild DNA fragment might harbor several resistance loci. However, the gene has already been referred to as 'Ty-2' informally and in several literature citations (Grube et al., 2000; Giordano et al., 2005). In order to avoid confusion we propose the name 'Ty-2' for the geminivirus resistance gene on chromosome 11 located around TG36.

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Table 1. RFLP genotype and geminivirus reactions of F₆ lines derived from crosses with H24, AVRDC, 2000.

Entry	RFLP ¹			Incidence (weeks after exposure)		
	TG393	TG26	TG36	2	4	6
CLN2131-5M-1	LL	LL	LL	100	100	100
CLN2131-5M-22	LL	LL	LL	100	100	100
CLN2114-2-17	HH	HH	HH	0	0	0
CLN2114-1-9	HH	HH	HH	0	0	0
CLN2116-39-4	HH	HH	HH	0	0	0
CLN2116-25-8	LL	LL	HH	4	4	4
CLN2116-25-22	LL	LL	HH	0	0	0
CLN2116-11-12	LL	LL	HH	0	0	0
CLN2131-4M-15	LL	LL	HH	0	0	0
CLN2114-23-14	LL	LH	HH	0	0	0
CLN2114-23-21	LH	LH	HH	0	0	0
CLN2114-16-5	HH	LH	HH	0	0	0
CLN2131-4M-11	LL	LL	LH	16	16	16
CL5915 (S ck)	LL	LL	LL	96	100	100
H24 (R ck)	HH	HH	HH	0	0	0
LSD (0.05)	-	-	-	7	6	5

¹ LL=homozygous for *S. lycopersicum* alleles at that locus; HH=homozygous for *S. habrochaites* alleles; LH=heterozygous. TG36, TG26, and TG393 are RFLP markers mapped to the bottom of chromosome 11.

² n=25 plants per entry with 5 plants per plot and 5 replications

Changes in light scattering properties of healthy and infected by *Xanthomonas vesicatoria* tomato leaves as indicator for the initial stage of the development of bacterial spot disease.

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Bacterial spot of tomato caused by *Xanthomonas vesicatoria* has become a very important disease of tomato in Bulgaria. In our country, the population of *X. vesicatoria* belongs to T (consisting of races T1 and T3) and PT pathotypes (Bogatzevska and Sotirova, 1992; Bogatzevska and Sotirova, 2001-2002).

X. vesicatoria penetrates by wounds or by stomata openings. It was established that the number of stomata on leaf surface and the time for stomata opening correlated to the number of leaf spots during development of the infection (Ramos and Volin 1987). After penetration water-soaked lesions are formed on the leaves, which later become necrotic.

The changes in photosynthesis induced by plant pathogens are characterized with a complex nature (Tesci et al., 1996). The development of leaf symptoms changes leaf anatomy and is related to the appearance of spatio-temporal heterogeneity in photosynthetic responses to different bio-stresses (Berger et al., 2005). The application of chlorophyll fluorescence imaging techniques revealed that inhibition of photosynthetic electron transport was restricted to the direct vicinity of the infection site, which was surrounded by a circle of increased photosynthetic activity. The photosynthesis of the remaining leaf was not affected at this stage. The availability of necrotic zones on leaf surface and spatio-temporal heterogeneity make studies on photosynthetic responses to bio-stress difficult.

The aim of this investigation was to examine the effect of *X. vesicatoria* leaf infection on far red light (FR) induced photo-oxidation of the first electron donor of Photosystem I (PSI), P700, immediately after penetration of the pathogen before formation of water-soaked lesions and necrotic spots. The changes in leaf absorbance were used as an indicator for bacteria induced alterations in tomato leaves.

Tomato plants susceptible to *X. vesicatoria* at the 5-6 true leaf phase were vacuum infiltrated with a bacterial suspension obtained from a 36h culture at a concentration of 10^8 cfu/ml of strain 42 of race T1 and strain 56 of T3 (Bogatzevska and Sotirova, 1992). The redox state of P700 was investigated *in vivo* with a dual wavelength (810/860 nm) unit (Walz ED 700DW-E) attached to a PAM101E main control unit (Klughamer and Schreiber, 1998) of a PAM fluorometer (Walz, Effeltrich, Germany, model PAM 101-103). P700 was oxidized by irradiation with FR (13.4 Wm^{-2}) provided by a photodiode (FR-102, Walz, Effeltrich, Germany) that was controlled by the PAM 102 unit.

The investigation of leaf absorbance in the FR region (ΔA_{830}) excited by FR light ($>715 \text{ nm}$) reflects P700 oxidation because PSII is not activated by FR light and linear electron transport in thylakoid membranes of chloroplasts was not induced. Water infiltration of non-inoculated tomato leaves showed a great increase in ΔA_{830} signal (Fig. 1A). Leaf infiltration caused mechanically induced changes in leaf anatomy that influences global absorption properties of a leaf. Light scattering in leaves is largely determined by the intercellular air spaces (Evans et al. 2004). Scattering is determined by changes in refractive index between air and cells. Water infiltration of the leaves leads to changes in the mesophyll tissue that induces a decrease in light scattering and thence an increase in probability for light capture by P700, i.e. increased FR leaf absorption. The inoculation with *X. vesicatoria* caused a significant decrease in ΔA_{830} . The entrance of bacteria in

intercellular spaces and the subsequent increase in bacterial concentration enhanced light scattering and therefore decreased leaf absorption (Fig. 1B and C). This effect was further expressed after inoculation with race T3 of *X. vesicatoria* (Fig. 1B and C). All these changes are immediately observed after inoculation. When above-mentioned infiltration-induced changes disappear, the differences between leaf absorbance between non-inoculated and inoculated leaf are thereafter not observed (data not shown).

On the basis of these results, it could be concluded that changes in PSI photochemical activity as evaluated by changes in FR induced P700 oxidation are not a direct effect of bacteria on PSI activity. Decreased leaf absorbance in infiltrated *X. vesicatoria* tomato leaves caused enhanced light scattering and hence a decrease in A830. We suggest that efficiency for penetration of *X. vesicatoria* in intercellular spaces is the reason for decreased A830.

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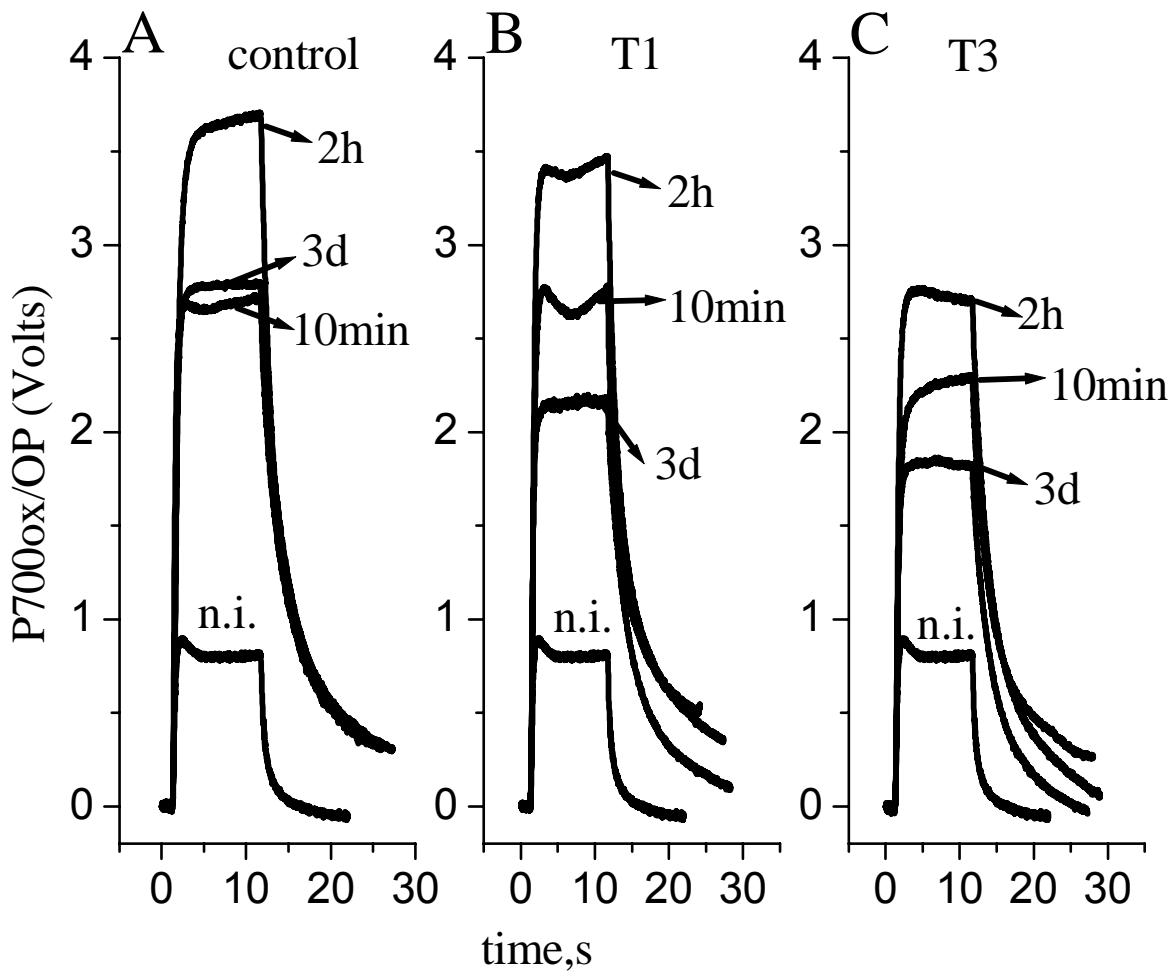


Figure caption:

Figure 1. The onset of photo-oxidation of P700 by far-red light and the subsequent re-reduction of P700+ (decay signal) on cessation of illumination. Far-red light (13.4 W m^{-2}) was turned on at time zero and off after 10 s FR illumination. Each trace is the average for 8 separate leaf discs. Leaf discs were infiltrated with water (non-inoculated leaves, n.i.) and inoculated with bacteria and measured after different periods after inoculation. OP = output signal in volts.

Ty-3, a begomovirus resistance locus linked to Ty-1 on chromosome 6 of tomato

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Whitefly-transmitted begomoviruses, such as tomato yellow leaf curl virus (TYLCV) and tomato mottle virus (ToMoV), cause great losses to tomato production in the United States and other tropical and subtropical regions in the world (Polston and Anderson, 1997). To date, no resistance has been found in the *Solanum lycopersicum* germplasm although some tomato varieties have been reported to be less susceptible than others during severe epidemics (Hassan et al., 1991, Laterrot, 1993). However, resistance to TYLCV has been found in numerous tomato wild species, including *S. pimpinellifolium*, *S. peruvianum*, *S. chilense*, *S. habrochaites*, and *S. cheesmaniae* (Pico et al., 1996). *S. chilense* accession LA1969 showed the highest level of resistance among the 23 accessions representing 5 tomato species based on symptom expression and virus detection criteria (Zakay et al., 1991). A partially dominant major gene, *Ty-1*, which contributed most of the resistance to TYLCV in LA1969, was mapped closely to the RFLP marker TG97 on chromosome 6 (Zamir et al., 1994). Another gene locus responsible for resistance to TYLCV in the tomato line 'H24' derived from *S. habrochaites* was localized to the long arm of chromosome 11 delimited by RFLP markers TG393 and TG36 (Hanson et al., 2000). This locus was further delimited to a smaller interval (P. Hanson, personal communication), and formally named as *Ty-2* (Hanson et al., 2006).

S. chilense accessions LA1932, LA2779 and LA1938 also showed high levels of resistance to begomoviruses (Scott and Schuster, 1991, Scott et al., 1996) and have been useful sources of resistance in the tomato breeding program in Florida and elsewhere in the world (Mejía et al., 2005, Scott, 2001). Inheritance studies and QTL mapping analysis using RAPD markers revealed three regions on chromosome 6 contributing to resistance to both TYLCV and ToMoV in these accessions (Agrama and Scott, 2006, Griffiths, 1998). The first region encompass the *Ty-1* region, while the other two regions flank either side of the self-pruning (*sp*) and potato leaf (*c*) loci. The RAPD markers mapped to these resistance regions were used to screen more advanced resistant breeding lines in search for tightly linked markers, which were then converted to sequence characterized amplified region (SCAR) markers (Ji and Scott, 2005a, b).

These SCAR markers, as well as other PCR-based markers on chromosome 6 obtained from public domains or designed from public sequences, were used in the present study to localize the introgression in the advanced breeding lines derived from LA2779, which were resistant to both TYLCV and ToMoV. A large introgressed segment was found in these lines, which spans markers from C2_At2g39690 at 5.3 cM in Tomato-EXPEN 2000 map (Fulton et al., 2002; <http://sgn.cornell.com>) to T0834 (32 cM) (Figure 1). Using an F₂ population of susceptible *S. lycopersicum* × a resistant advanced breeding line having this introgression, we mapped a partially dominant gene, that we hereby designate *Ty-3*, to the marker interval between cLEG-31-P16 (20 cM) and T1079 (27 cM) on the long arm of chromosome 6. This gene has a dominance-to-additive effect ratio of 0.47 for resistance to TYLCV, suggesting a nearly equal contribution to the variance in TYLCV resistance from additive and dominance effects. Additionally, ~65% of the variance in TYLCV resistance in the F₂ progeny can be explained from this gene locus, suggesting this gene had a major effect on the resistance. Besides TYLCV resistance, *Ty-3* might also contribute resistance to ToMoV, but to a lesser degree, although the possibility of a different gene locus in the same region accounting for ToMoV resistance cannot be ruled out. QTL analysis of F₂ progeny from the same cross, but

inoculated with ToMoV, revealed that ~41% of the variance in ToMoV resistance in the progeny could be explained by this gene locus, which had a dominance-to-additive ratio of 0.35. No recombinants were found between TG590 (22 cM) and T1079, which prevented a fine-scale mapping of the *Ty-3* gene using this LA2779-derived F₂ population.

Besides the *Ty-3* gene, introgression in the advanced breeding lines derived from LA2779 also span the *Ty-1* region near the *Mi* gene, suggesting possible coexistence and linkage of resistance alleles at both *Ty-1* and *Ty-3* loci in these lines. The large introgression in these breeding lines was further confirmed from sequence alignments at numerous marker loci, including markers located in both *Ty-1* and *Ty-3* regions (Maxwell et al., 2006). At the REX-1 locus, which is tightly linked to the *Ty-1* gene (Milo, 2001), the sequence of a LA2779-derived advanced breeding line (Gc9) was identical to that of TY52, a TYLCV-resistance line that is homozygous for *Ty-1* gene (Maxwell et al., 2006, Zamir et al., 1994). The presence of both *Ty-1* and *Ty-3* genes in a single genotype most likely offers the highest resistance to TYLCV, which might be the case for some of the present commercial hybrids in the market (Ji and Scott, unpublished data).

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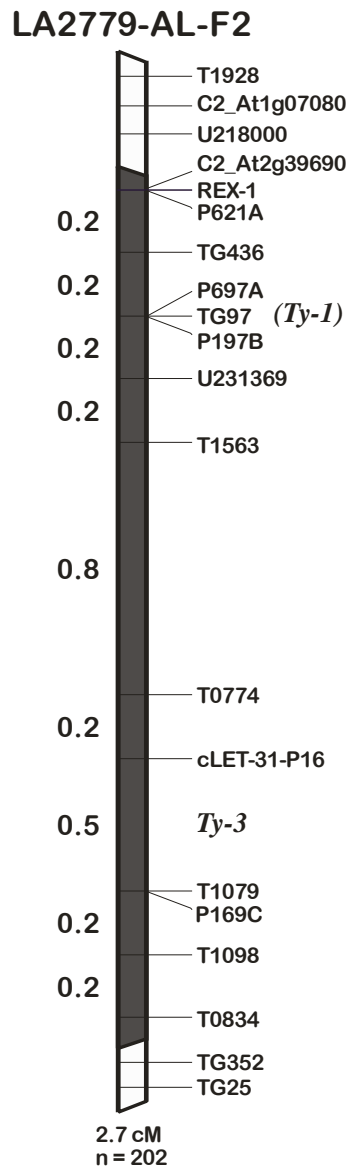


Figure 1. Linkage of the *Ty-3* locus to the *Ty-1* locus on chromosome 6 of tomato. Linkage maps were constructed from F₂ populations of susceptible *Solanum lycopersicum* × resistant LA2779-derived advanced breeding line. All the markers are PCR-based, including SCAR markers (P621A, P197B, P697A, and P169C) converted from RAPD markers, and CAPS markers taken from either the public domain or designed from the public sequences except T1098 and T0834, which are kindly provided by C. T. Martin and D. P. Maxwell. Shaded regions represented introgression from *S. chilense*. The markers in non-introgression regions are not drawn to scale.

A new reporter construct to monitor IAA dynamics during tomato development

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Studying the function of plant growth regulators (PGRs) has historically been hindered by the difficulty of detecting their very low concentrations at the tissue level. Recently, new solutions were offered by the introduction of improved instruments of analysis, of immunological methods, and of tissue-specific PGR genetic engineering. In parallel, plant transformation has offered new tools to detect hormone distribution in plant organs and tissues by using constructs where reporter genes are driven by PGR-inducible promoters.

The plant growth hormone auxin (typified by indoleacetic acid, IAA) affects several primary cellular processes and is responsible of lateral organ patterning, differentiation and elongation. In addition, IAA mediates apical dominance, stimulates the differentiation of vascular tissue, induces root initiation and lateral root development, mediates the tropistic responses, and finally exerts various effects on leaf and fruit abscission and fruit set, development and ripening. Therefore, the characterization of mutants, whose phenotype is putatively determined by altered IAA levels or perception may shed light on the role played by this PGR in different aspects of plant developmental biology. In this perspective, the tomato is a favoured experimental species, because a plethora of more or less characterized monogenic mutants have been described to date, that cover all aspects of plant growth and development (<http://tgrc.ucdavis.edu/>; <http://zamir.sgn.cornell.edu/mutants/>).

A number of constructs suitable to report IAA kinetics in plant tissues have been proposed using natural (*GH3* gene promoter from soybean, Hagen et al., 1991; *PS-IAA4/5* gene promoter from pea, Ballas et al., 1995) as well as synthetic (*DR5* promoter, Ulmasov et al. 1997) auxin-response elements fused to reporter proteins (e.g. GUS and GFP). All these constructs have been useful to detect IAA dynamics in higher and even lower plants, although their efficiency and sensitivity was variable depending on the species and the tissue assayed (Oono et al., 1998; Brierfreund et al., 2003; Aloni et al., 2006).

In this study, we used the IAA-inducible promoter of the *Agrobacterium tumefaciens* gene 5 (Koncz and Shell, 1986; Körber et al., 1991) to construct a tomato transgenic line expressing the β -glucuronidase (*GUS*) reporter in an IAA-dependent manner. A 1060 bp-long 5' fragment upstream to the gene 5 start transcription codon (*p5*) was amplified from the *pGV0153* plasmid (Koncz and Shell, 1986) and ligated to the *GUS* coding sequence. The *p5::GUS* fusion product was cloned in *E. coli*, transferred to *A. tumefaciens* and used to transform tomato (cv. Chico III) cotyledons as described (Caccia et al., 1999). PCR-positive primary transformants were assayed for GUS staining in root tips and a plant with good expression was selected for further experiments. Inspection of its progeny revealed that genetic transformation targeted a single insertion site and allowed to select a plant homozygous for the reporter gene (assessed by further progeny testing).

To demonstrate the IAA-sensitivity of the construct, we treated two-weeks old seedlings by deepening them overnight in solutions containing different IAA concentrations and carried out the GUS assay the day after. As shown in Fig. 1B-E, root apices showed GUS staining around the tip (quiescent centre and columella root cap initials) with an intensity that increased with IAA concentration in the treatment up to a maximum reached at 10^{-5} M (Fig. 1D). This behaviour

corresponded to the range of functionality obtained with other IAA-responsive reporter constructs (Oono et al., 1998; Aloni et al., 2006).

Another site of IAA accumulation in the root was the region of initiation (Fig. 1F) and emergence (Fig. 1G) of lateral roots. In leaflets (Fig. 1H), as in sepals (Fig. 1I) and petals (Fig. 1J), IAA was detected in the vascular tissue, although with different, distinctive patterns. In the mature anther, the reporter gene was expressed in the region corresponding to the pollen sacs (Fig. 1K), whereas in the ovary only the basal vascular bundles possessed clear IAA accumulation (Fig. 1L). Accordingly to its connective function towards all the floral whorls, a strong signal was observed throughout the receptacle vascular tissues (Fig. 1M).

The *p5::GUS* Chico III line has been crossed with several tomato mutants with primary defects in cotyledon (*pct*), stem (*ls*, *mon*, *oli*, *pro*, *sd*), leaf (*cb*, *Cu*, *marm*, *Me*, *tf*), flower (*an*, *ex*, *ps-2*, *sl-2*, *uf*), and fruit (*f*, *pat*, *pat-2*) development. The F₂ populations, segregating the mutations together with the *p5::GUS* construct, will be used to study IAA dynamic in the mentioned phenotypes, thus allowing a deeper understanding of its role in plant growth and development.

Acknowledgements

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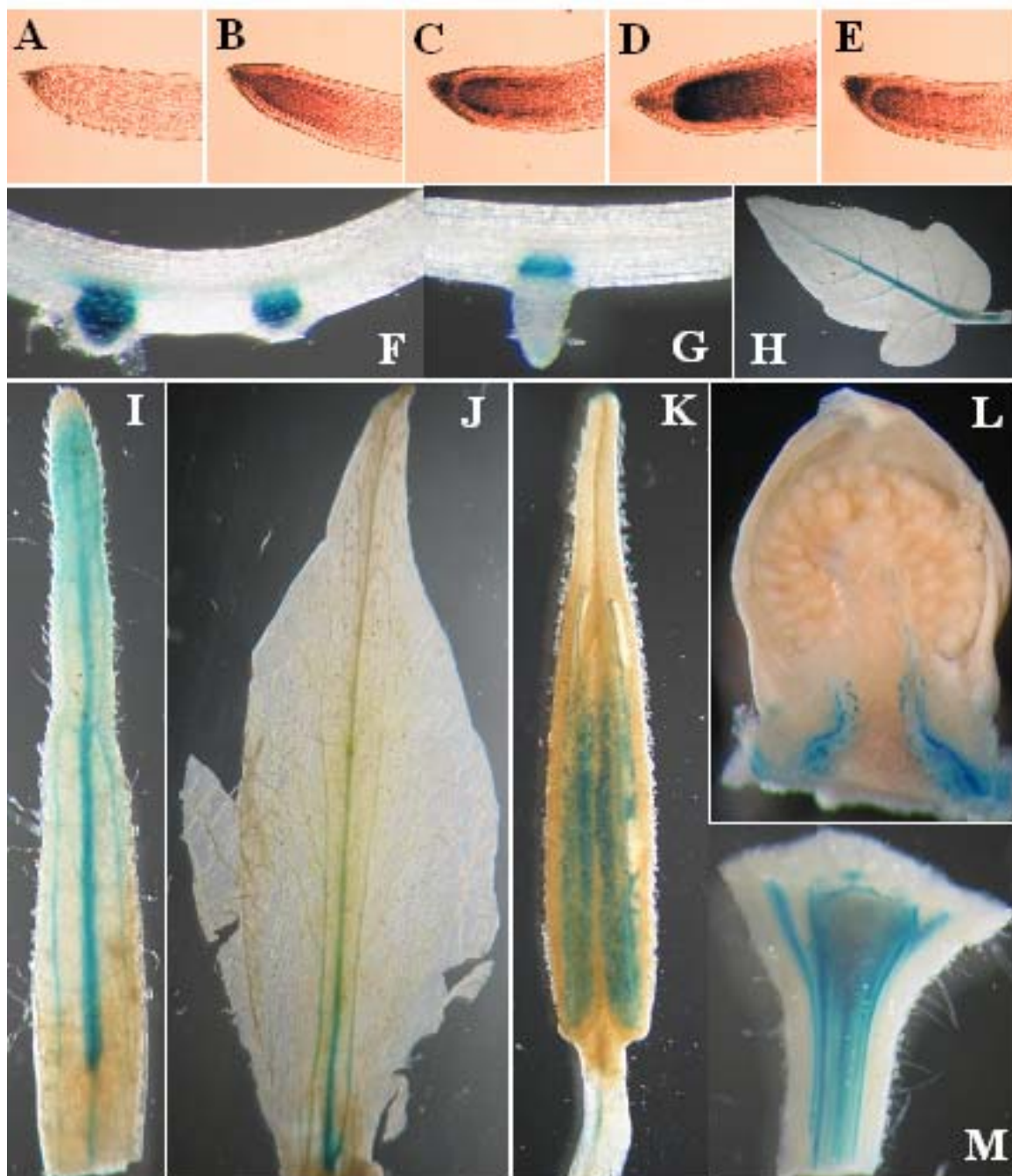


Figure 1. Histochemical analysis of GUS activity in the root apex of a control, untransformed plant (A) and in several organs of Chico III plants transgenic for the *p5::GUS* reporter construct (B-M). Bright field microscope images of root apices from Chico III *p5::GUS* plants treated with 0 (B), 10^{-7} (C), 10^{-5} (D) and 10^{-3} (E) M IAA. Stereomicroscope images of the region of initiation (F) and emergence (G) of lateral roots, of a young leaflet (H), and of a sepal (I), a petal (J), a stamen (K), a ovary (L), and a receptacle (M) dissected from a flower at anthesis.

Reciprocal grafting of 61 randomly selected morphological tomato mutants reveal no evidence for systemically transmitted phenotypic alterations.

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The availability of a large collection of isogenic mutants (Menda et al., 2004) and the ease of grafting (Sachs, 1949) prompted us to estimate the extent of association between long range signaling pathways and development (Lucas and Lee 2004). Thus, 61 monogenic tomato mutants with distinct alterations in a range of morphological syndromes and inheritance modes were randomly selected (Table 1). These mutants were top-grafted on their isogenic wild type (M82) rootstock, and when possible were also used as rootstock in a reciprocal graft. Moreover, Y grafts were employed as well, where shoots of both rootstocks and scions are allowed to develop. This way, transmission of potential donor signals from roots or from shoots could be examined. Wild type M82 plants were homo-grafted as a negative control and mutants previously reported to display graft transmissible phenotypic alterations served as positive ones. These included: 1) The recessive iron uptake mutants *fer* and *chloronerva* (Brown et al., 1971; Ling et al., 1996) 2) The recessive abscisic acid deficient *flacca* mutant (Tal, 1967) 3) The dominant tomato mutant *Mouse ears* (*Me*; LA3552) (Kim et al., 2001; Figure 1). As reported previously, the *chloronerva*, *fer* and *flacca* mutants were completely restored upon grafting on wild type rootstock. On the other hand *Me* as well as the other 61 reciprocally grafted mutants did not show obvious transmissible changes of form either as rootstocks or as scions (Table 1). However, visible changes such as reduced internode elongation in growth-retarded mutant scions (e0329m1 and e4572m1) or shortening of internodes in wild-type scions grafted onto growth-retarded mutant rootstocks (e0329m1 and n2087m1), were recorded. We attribute these changes to the physiological consequences of grafts between plants with very different vigor. Six independent reciprocal grafting experiments involving *Me* rootstock and various wild type genotypes (including the yellow-leaves *Xanthophylllic* mutation (*Xa*) LA3579) and totaling 65 independent plants failed to show any transmissible phenotype when grown under high and low light intensities in a growth chamber (16h constant daylight of 20 $\mu\text{mol s}^{-1} \text{m}^{-2}$ and 200 $\mu\text{mol s}^{-1} \text{m}^{-2}$, 30°C during day, 20°C during night). The lack of transmissible phenotypic alterations in grafts involving wide range of mutants, as well as *Me*, indicates that long-distance movement of signal molecules may have a role in determining plant shape and form only for very specific processes or conditions. This conclusion is consistent with the wide range of applications of grafting in agriculture such as eggplant on tomato, watermelon on pumpkin, loquat on pears etc; in all of these cases each component of the graft unit maintains its morphological autonomy.

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Table 1. The phenotype and description of the mutants used in the experiment can be viewed at (<http://zamir.sgn.cornell.edu/mutants/>; Menda et al., 2004). Two weeks old seedlings of 61 recessive (r), and dominant (D) mutants were reciprocally grafted. Y-grafts were performed following apex removal of 10 days old rootstock seedlings, which conditioned the growth of two new axillary shoots. On the same day of apex removal the scion plants were sown. Two weeks later the scions were grafted onto one of the axillary shoots leaving the plant with one shoot of the rootstock and one grafted shoot. Recessive mutants were Y-grafted only as scions, and dominant ones were Y-grafted reciprocally. Forty-eight genotypes were grafted using both Y and reciprocal top grafting, five were tested only as scions in Y-grafts, five dominant mutants were only Y-grafted reciprocally, and seven mutants were only top grafted reciprocally. Two to three plants from each combination were transplanted into pots in a glasshouse 14 days after grafting. The grafted plants of each mutant were placed next to non- or homo-grafted controls. All plants were examined separately by two people + Grafting combinations where recipient shoots adopted the donor phenotype. +* Grafting combination with altered phenotype associated with growth retardation/enhancement depending on rootstock vigor. ND Not Determined - grafting combination not performed.

Genotype	Mode of inheritance	Y-graft	Single-graft	Phenotype
M82	r	-	-	Wild-type
<i>Me</i>	D	-	-	Enhanced leaf complexity
<i>flacca</i>	r	+	+	Wilty. ABA deficiency
<i>fer</i>	r	+	ND	Iron-deficiency
<i>chloronerva</i>	r	+	ND	Iron-deficiency
e0087m1	r	-	-	Anthocyanin gainer
e2126m1	r	-	-	Yellow young leaf turning green, white flower
e1415m1	r	-	-	Yellow leaves
e4781m1	r	-	-	Late flowering
e0902m1	r	ND	-	Round leaves & flowers; all organs are shortened
e0251m1	r	-	-	Round leaves & flowers; all organs are shortened
e1976m1	r	-	-	Goblet. Aborted growth
n2087m1	r	+*	+*	Curling leaves. kanadi-like
e1239m1	r	-	-	Ultra determinate
e0557m1	r	-	-	sp enhancer
e0042m1	D	-	-	Duplicator
e1952m2	r	-	-	Mouse - ear like leaves; deformed flower
e3852m1	r	-	-	Crawling elephant
e0067m1	D	-	-	<i>Lanceolate</i> - long simple leaves
e3628m1	D	-	-	<i>Lanceolate</i> - long simple leaves
e4249m1	r	ND	-	Mouse-ear like; partial sterility
e0652m1	r	ND	-	Double feathered leaves; small plant
e0150m1	r	ND	-	Narrow leaves; elongated fruit

n0741m1	r	-	-	<i>entire</i>
e1247m1	r	-	-	Small plant; curling leaves
e2102m2	r	-	-	Complex thick leaf
e2217m1	r	-	-	Hair absent; rigorous; mouse-ear like leaves
e2707m1	r	-	-	Narrow leaves; bushy; weak wiry filamentous flower
e3463m1	r	ND	-	Clausula-like leaves
e3833m1	r	-	-	Potato leaf; non-organized inflorescence
e4274m1	r	-	-	Double feathered leaves. pts-like
e4583m2	r	-	-	Simple leaves
e4387m1	r	-	-	Small plant; reduced leaf complexity; narrow petals
n5257m1	D	-	ND	Leaves turning upside down
n7062m1	D	-	ND	Small plant; curly leaves
e0873m1	r	-	ND	<i>wiry</i>
e1756m1	r	-	ND	Dead-wiry
e1383m1	r	-	ND	<i>wiry-9</i>
e1043m1	r	-	ND	<i>wiry-3</i>
n0307m1	r	-	ND	New wiry
e0329m1	r	+*	+*	dpy
e0846m1	D	-	-	Small plant & fruit
e3167m1	D	-	-	Small plant
e3495m1	D	-	-	Small plant; late ripe fruit
e1258m1	D	-	-	Dwarf
e4572m1	r	+*	+*	dpy
Genotype	Mode of inheritance	Y-graft	Single-graft	Phenotype
e0434m1	r	-	-	<i>wiry-4</i>
e4714m1	r	-	-	<i>wiry-1</i>
n5286m1	D	-	ND	Light colored leaves; thin stems
n6029m1	D	-	ND	Small plant; yellow-purple leaves
n7102m1	D	-	ND	Partial sterility
e4537m1	r	-	-	<i>sft</i>
n2326m1	r	-	-	Fasciated fruit; rosette flower
e4489m1	r	-	-	Fasciated fruit; rosette flower
e1476m1	r	-	-	Small fruit; no pedicel; pb-like
e1906m1	r	-	-	Small fruits; remain green; turn brown inside
e0423m2	r	-	-	Pepper fruit; light-colored variegated leaf
e0070m1	r	-	-	Small fruit; wilted; stamen-less
e0089m1	r	-	-	Yellow virescence; yellow fruit
e0530m1	r	-	-	Ripening inhibitor; bushy-cabbage leaves
n3122m1	r	-	-	Ripening inhibitor
e1329m1	r	ND	-	Inhibited growth; disease response
e0086m1	r	-	-	Disease response
e1142m2	r	-	-	Disease response - ragy plant habit
e1165m1	r	ND	-	Disease response; small purple leaves; partial sterility
n4144m1	r	-	-	Disease response; small burnt leaves

**Figure 1**

fer mutant on the day of grafting onto wild-type M82 rootstock (left). Recovery of the scion is visible 3-4 days after grafting (right).

Y-graft of M82 scion on *Me* mutant rootstock. No phenotypic changes are visible in either the wild-type scion or the mutant rootstock.

Resistance to bacterial spot race T4 and breeding for durable, broad-spectrum resistance to other races.

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Four races of the bacterial spot pathogen in tomato have been isolated under field conditions (Jones et al., 2005) with some evidence that there might be a fifth race based on a lack of hypersensitivity to the *avrXv4* gene in a strain that mutated from race T3 (Minsavage et al., 2003). In Florida race T3 largely replaced race T1 and the former was antagonistic to the latter (Jones et al., 1998). However, race T4 has been isolated in several locations in Florida since 1999 and it is evident that the best protection will be provided by varieties with resistance to races T3 and T4. In 2002, breeding line Fla. 8233 was the only line out of nearly 300 lines being bred for T3 resistance with homozygous resistance to a mixed infection of races T3 and T4. A breeding project was then started using this line as a source of resistance to both T3 and T4. Previously we have found sources of resistance to races T1, T2, and T3 (see Scott et al., 2003). Resistance to T4 has been identified in breeding lines Fla. 8233, as mentioned, and Fla. 8326 (Scott, 2004). The former likely derived the T4 resistance from PI 114490 while the latter appeared to have T4 resistance from *S. piminellifolium* accession PI 126932. Observations over several seasons have verified that these breeding lines have resistance, but also that their resistance is only partial under high disease pressure. Thus, we have been searching for other resistance sources and need to verify that the accessions mentioned above do in fact have T4 resistance. This is a main objective of this report. The broad goal of our resistance program is to identify bacterial spot resistance genes, determine their effects on all the tomato races, and to breed tomato varieties with broad-spectrum resistance that will not break down to races of the pathogen that may mutate in the future. So far, this pathogen has mutated at least 4 races in the absence of monocultures of resistant varieties. Herein, we present some data on some genotypes that appear to have some broad spectrum resistance.

In 2005 16 genotypes including a susceptible control were grown in a completely randomized design with three blocks and five plant plots at Citra, Florida (Table 1). The breeding lines were selected based on either previous performance under T4 infection and the accessions were included based on their presence in pedigrees of resistant breeding lines or on their resistance to other races of the pathogen. The plants were inoculated with race T4 and each plot was rated for disease severity using the Horsfall-Barratt (1945) scale. Data are also presented for eight breeding lines and five control genotypes that were inoculated for races T1 and T2 in Ohio and T4 in Florida at various locations and seasons (Table 2).

PI 114490 and PI 128216-T2 had less disease than did the susceptible control Horizon (Table 1). The other four PI's did not have significantly less disease than did Horizon. This included PI 126932 which was expected to be resistant based on the resistance in Fla. 8326 which has this PI (and not Hawaii 7981) in it's pedigree as a T3 resistance source. PI 126932 was also susceptible at

Balm in 2005 (data not shown). Later in the season at Balm PI 126932 did not have bacterial spot lesions in the top of the plant and it is possible that this accession may have a mechanism that does not prevent an initial infection under conditions which favor the disease, but does prevent the secondary spread of the disease. Fla. 8326 and a related breeding line with this PI in their pedigrees did show resistance in the Citra trial (Table 1). This suggests resistance came from PI 126932 unless there is a mistake in the pollen originally used in these crosses. Two of the resistant breeding lines had PI 128216-T2 in their pedigree and thus it appears that resistance has been derived from this source. Furthermore, Fla. 8517 was highly resistant to T4 at Citra (another experiment) and Balm (Table 2). Fla. 8517 has PI 128216-T2 in it as well as PI 114490 and may have resistance gene(s) from both sources. However, Fla. 8517 did not look as resistant later in the season at Balm and more recently in Fletcher, NC. Further studies with this line are underway. The other breeding line with resistance has Richter's Wild, a small cherry tomato, in its pedigree. This line was sent to us by Randy Gardner at North Carolina State University where he is working with it for its resistance to late blight. Unfortunately Richter's Wild was not in this test but did show bacterial spot race T4 resistance at our old research center in 2003.

Forty breeding lines were tested for T1 and T2 resistance in Ohio and in several Florida locations for T4 resistance; those with the best broad spectrum resistance are in Table 2. This includes Fla. 8233 and Fla. 8326 that have already been mentioned above. Two of the lines derived from Fla. 8233 (Fla. 7776 and Fla. 8044 A lines) show a fair level of broad spectrum resistance (Table 2) and improved horticultural type. Many of the lines derived from Fla. 8233 have not had good resistance. This may relate to low disease pressure when the F₂ selections were made in 2003. The most severe disease pressure was in the summer 2005 at Balm and higher disease ratings resulted in this germplasm (Table 2). The data indicate that there is potential to develop broad spectrum resistance. A gene from PI 114490 has shown resistance to races T2, T3, and T4 (Yang et al., 2005). Other genes with effects on multiple races may be identified in the future. However, it would be desirable to develop higher levels of resistance. This may require combining genes from different sources. Sam Hutton is studying the inheritance of T4 resistance from several of the sources mentioned and will be attempting to find molecular markers linked to the resistance genes. From this work it is hoped that breeding can be expedited with marker assisted selection and that testing can be done to verify which genes have broad-spectrum effects. Use of such genes may finally provide commercially acceptable varieties with durable bacterial spot resistance.

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- Yang, W., S.A. Miller, J.W. Scott, J.B. Jones, and D.M. Francis. 2005. Mining tomato genome sequence databases for molecular markers: Application to bacterial resistance and marker assisted selection. *Acta Horticulturae* 695:241-249.

Table 1. Bacterial spot race T4 disease severity for tomato (*S. lycopersicum*) and *S. pimpinellifolium* genotypes at Citra, Florida Fall 2005.

Genotype	Disease severity ^z	Resistance sources in pedigree
(Fla. 7655 × RW) F ₅	6.7 a ^y	Hawaii 7998 and Richter's Wild
PI 126932-1-2 ^x	6.0 ab	
PT 195002	5.7 a-c	
Fla. 7335	5.3 bc	Hawaii 7998
Horizon	5.3 bc	Susceptible control
PI 155372-S1	5.0 b-d	
(Fla. 8022 × RW) F ₅	5.0 b-d	Richter's Wild
PI 126428	4.7 c-e	
Fla. 8326	4.0 de	PI 126932 and Hawaii 7998
PI 128216-T2 ^x	4.0 de	
PI 114490	3.7 ef	
(050624-SBK) F ₇	3.7 ef	PI 128216, Hawaii 7981 and Hawaii 7998
(Fla. 7987 × Fla. 7981) F ₆	3.7 ef	PI 126932, Hawaii 7998
(050542-SBK) F ₇	3.7 ef	PI 128216 and Hawaii 7998
Fla. 8233	3.7 ef	PI 114490, Hawaii 7981 and Hawaii 7998
(Fla. 7776 × RW) F ₄	2.7 f	Richter's Wild

^z Horsfall-Barrett (1945) scale, lower numbers indicate less disease.

^y Mean separation in column by Duncan's multiple range test at P<0.50.

^x *S. pimpinellifolium* accession.

Table 2. Bacterial spot races T1, T2, and T4 disease severity ratings^z for selected tomato lines in 2005.

Genotype ^y	Location and race					
	Fremont Ohio T1	Wooster Ohio T2	Homestead Winter T4	Balm Summer T4	Citra T4	Balm Fall T4
Fla. 8233	2.5	4.0	3	4.5	4	4
Fla. 8286	3.5	3	2	6	5	(5.5) ^x
Fla. 8326	4.5	4.5	3	5	4	4.5
(Fla. 7776 × Fla. 8233) F ₄ A	3	2.5	3	5	4	5
(Fla. 7776 × Fla. 8233) F ₄ B	5	4.5	3	7	4.5	---
(Fla. 8044 × Fla. 8233) F ₄ A	4.5	5	2	6.5	6	4.5
(Fla. 8044 × Fla. 8233) F ₄ B	3.5	4.5	2	7	5.5	6
Fla. 8517	---	---	---	---	3	3
PI 114490	2	2	1	3.5	4.5	2.5
Hawaii 7998	5	7	4	7	6	6
Hawaii 7981	7	6	5	7	6	6.5
C-28	4.5	5.5	4	7	5.2	5
Susceptible controls ^w	6.5	6.0	5	7	5.2	7

^z Horsfall-Barratt (1945) Scale. Lower numbers indicate less disease.

^y See Table 1 for resistance sources in Fla. 8233 and Fla. 8326. Fla. 8286 has same sources as Fla. 8233; Fla.8517 has PI 128216, PI 114490, and Hawaii 7998 in it. Hawaii 7998 is T1 resistant, Hawaii 7981 is T3 resistant.

^x Parenthesis indicates data is from a sister line.

^w 'Solar Fire' in Fremont, Wooster, and Balm Summer; Fla. 7771 in Balm Fall; 'Horizon' at Citra; and 'Sanibel' at Homestead.

Revised List of Miscellaneous Stocks

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This list of approx. 1,560 miscellaneous genetic stocks is a revision of the previous one issued in TGC 53 (2003). Extinct, obsolete, or faulty accessions have been dropped. New accessions that have been added to the list include a group of 'provisional mutants' originating from various sources. These are mostly morphological traits detected in M2's and later generations from mutagenesis populations. Most are probably monogenic characters, with a few containing multiple mutant loci per line. Also, several new and useful linkage tester stocks, each containing two or more morphological markers on a single chromosome, have been acquired. The new tester stocks represent chromosomes 1, 7, 10 and 11.

We attempt to maintain all listed accessions in adequate seed supply for distribution. However, some stocks, such as certain multiple marker combinations, aneuploids, or prebreds, are weak and require special cultural care; consequently, seed supplies may at times be too low to permit distribution.

Names and phenotypic classes of individual mutations are given in the last Monogenic Stock List (TGC 55); other pertinent data are presented in previous TGC Reports, as cited below. More detailed information on these stocks are available at our website (<http://tgrc.ucdavis.edu>), including genotype, phenotype, origin, and recommendations for growth and reproduction.

see also:

Wild Species Stocks (1,131 accessions total) are listed in TGC 54 (2004)

Monogenic Stocks (994 accessions total) are listed in TGC 55 (2005)

Types of Stocks on this List

- | | |
|-------------------------------------|--|
| 1. Cultivars and Landraces | 4. Cytogenetic Stocks |
| 1.1. Modern and Vintage Cultivars | 4.1. Translocations |
| 1.2. Latin American Cultivars | 4.2. Trisomics |
| 2. Prebred Lines | 4.3. Autotetraploids |
| 2.1. Introgression Lines | 5. Cytoplasmic Variants |
| 2.2. Backcross Recombinant Inbreds | 6. Genetic Marker Combinations |
| 2.3. Alien Substitution Lines | 6.1. Chromosome Marker Stocks |
| 2.4. Monosomic Alien Addition Lines | 6.2. Linkage Screening Testers |
| 2.5. Other Prebred Lines | 6.3. Miscellaneous Marker Combinations |
| 3. Stress Tolerant Stocks | 7. Provisional mutants |

1. CULTIVARS AND LANDRACES

1.1. Modern and Vintage Cultivars (198)

We maintain the following set of cultivars, inbreds, and breeding lines for various purposes, mainly as isogenic (or nearly isogenic) stocks for specific mutants, standards for genetic comparison, sources of disease resistances, or other purposes. Marglobe is considered the standard for tomato gene (mutant) nomenclature. Most lines have been maintained by selfing for many generations.

Accession	Cultivar
LA0818	A-1
LA0516	Ace
LA2838A	Ailsa Craig
LA2529	Alcobaca
LA2463	Allround
LA1995	Angela
LA3244	Antimold-B
LA3527	Apex 1000
LA0657	Beaverlodge
LA2973	Big Rainbow
LA2972	Big Yellow Red Ctr.
LA4347	B-L-35
LA1499	Break O'Day
LA0198	Cal 255
LA2414	Cal Ace
LA1439	Calmart
LA3316	Campbell 24
LA3317	Campbell 28
LA3228	Canary Export
LA2374	Caro Red
LA2400	Castlemart
LA3121	Chico Grande
LA4285	CLN2264F
LA4286	CLN2264G
LA3213	Columbian
LA0533	Condine Red
LA0817	CP-2
LA3247	Craigella
LA1162	Cuba Plum
LA1219	Dwarf San Marzano
LA0313	Dwarf Stone
LA3245	E.S.1
LA4024	E-6203
LA3238	Earliana
LA2006	Earlinorth
LA0266	Earlipak
LA3010	Earlipak
LA0517	Early Santa Clara
LA2711	Edkawi
LA3800	Fargo Self-pruning
LA3024	Fireball
LA3840	FLA 7060
LA3242	Flora-Dade
LA4026	Florida 7481
LA4025	Florida 7547

Accession	Cultivar
LA3030	Gardener
LA2969	Georgia Streak
LA2802	Globonnie
LA4011	GT
LA3231	Gulf State Market
LA0314	Hardin Miniature
LA3202	Hawaii 7997
LA3856	Hawaii 7998
LA4345	Heinz 1706-BG
LA0806	High Crimson
LA3237	Homestead 24
LA3320	Hotset
LA3144	Hunt 100
LA2805	Indehiscent Currant
LA3201	IRB 301
LA1089	John Baer
LA1131	Kallio's Alaskan Dwarf
LA0025	King Humbert #1
LA3240	Kokomo
LA3526	L04012
LA0505	Laketa
LA3203	Large Plum
LA3118	Laurica
LA0791	Long John
LA0534	Lukullus
LA3475	M-82
LA3120	Malintka 101
LA3007	Manapal
LA2451	Manapal
LA0502	Marglobe
LA1504	Marmande
LA0278	Marzano Grande
LA3151	Mecline
LA0011	Michigan State Forcing
LA3911	Micro-Tom
LA2825	Mobaci
LA2824	Moboglan
LA3152	Moboline
LA2821	Mobox
LA2830	Mocimor
LA3471	Mogeor
LA2828	Momor
LA2829	Momor Verte
LA2818	Monalbo
LA2706	Money maker

Accession	Cultivar
LA2819	Monita
LA2713	Montfavet 167
LA2714	Montfavet 168
LA2827	Moperou
LA2822	Mossol
LA2820	Motabo
LA2826	Motaci
LA2823	Motelle
LA3472	Movione
LA2661	Nagcarlang
LA3845	NC EBR-5
LA3846	NC EBR-6
LA3847	NC HS-1
LA3625	NC265-1 (93)-3-3
LA3802	New Hampshire Victor
LA2009	New Yorker
LA3321	Ohio 7663
LA1088	Ohio Globe A
LA2447	Ontario 717
LA2449	Ontario 7517
LA2396	Ontario 7710
LA2448	Ontario 7818
LA2970	Orange, Red Ctr.
LA2376	Pan American
LA0012	Pearson
LA0020	Pennheart
LA3528	Peto 95-43
LA3243	Platense
LA3312	Platense
LA3125	Pomodorini Napolitan
LA2715	Porphyre
LA3820	Potentate
LA3903	Primabel
LA0089	Prince Borghese
LA3233	Pritchard
LA3229	Prospero
LA2446	Purdue 135
LA2377	Purple Calabash
LA2378	Purple Smudge
LA0337	Red Cherry
LA0276	Red Top VF
LA3129	Rehovot 13
LA2356	Rey de Los Tempanos
LA0535	Rheinlands Ruhm
LA3343	Rio Grande

Accession	Cultivar
LA3145	Rockingham
LA0503	Roumanian Sweet
LA3214	Rowpac
LA2088	Royal Red Cherry
LA3215	Roza
LA1090	Rutgers
LA2662	Saladette
LA3216	Saladmaster
LA3008	San Marzano
LA0180	San Marzano (autodiploid)
2-297	San Marzano (autodiploid)
LA1021	Santa Cruz
LA2413	Severianin
LA2912	Short Red Cherry
LA3234	Sioux
LA3221	Slender Pear
LA3632	Start 24
LA0030	Stemless Pennorange
LA2443	Stirling Castle
LA1091	Stokesdale
LA1506	Stone
LA0164	Sutton's Best of All
LA2399	T-5
LA2590	T-9
LA0154	Tiny Tim
LA1714	UC-134
LA3130	UC-204C
LA1706	UC-82
LA2937	UC-MR20
LA2938	UC-N28
LA2939	UC-T338
LA2940	UC-TR44
LA2941	UC-TR51
LA0021	Uniform Globe
LA2445	V-121
LA0745	V-9 Red Top
LA3246	Vagabond
LA3905	Vantage
LA3122	Vendor
LA2911	Vendor (Tm-2 ^a)
LA2968	Vendor (Tm-2a)
LA2971	Verna Orange
LA2444	Vetomold K10
LA0744	VF-11
LA1023	VF-13L

Accession	Cultivar
LA1507	VF-145 21-4
LA0816	VF-145 22-8
LA1222	VF145 78-79
LA0742	VF-34
LA0490	VF-36
LA0743	VF-6
LA2086	VFN Hi Sugar
LA0815	VFN-14
LA1022	VFN-8

Accession	Cultivar
LA1221	VFNT Cherry
LA3630	Vrbikanske nizke
LA3465	Walter
LA0279	Webb Special
LA2464A	White Beauty
2-473	Yellow Cherry
LA2804	Yellow Currant
LA2357	Yellow Peach
LA3148	Zemer Kau

1.2. Latin American Cultivars (226)

This collection of Latin-American cultivars has been assembled from various sources but principally from our collecting trips, often at local markets. With a few exceptions they are indigenous in the sense that they are not recently introduced lines. Many of them are extinct in the source region, having been replaced by modern cultivars.

Accessions	Location
Bolivia	
LA0172	Santa Cruz
LA2699	Coroica
LA2871	Chamaca
LA2873	Lote Pablo Luna #2
LA2874	Playa Ancha
Brazil	
LA1021	Santa Cruz
Chile	
LA0466	Hacienda Rosario
LA0467	Lluta Valley
LA0468	Iquique
Colombia	
LA0356 - LA0358	Buenaventura
LA1539	Cali to Popayan
Costa Rica	
LA1215	
LA3453A - LA3453D	Turrialba
Cuba	
LA1162	
Ecuador	
LA0126	Quito mercado
LA0292	Santa Cruz
LA0408 - LA0410	Guayaquil
LA0415	Daular
LA0416	Puna
LA0423	Wreck Bay: Cristobal
LA1224	Puyo
LA1238	Viche
LA1239 - LA1241	Esmeraldas
LA1244	Coop Carmela
LA1249	Loja
LA1250	Loja

Accessions	Location
LA1251	Loja
LA2094	El Naranjo
LA2132	Chuchumbetza
LA2381 - LA2384	Malacatos
LA3126	Malacatos
LA3624	Santa Rosa
El Salvador	
LA1210	San Salvador
LA1211	San Salvador
Guatemala	
LA1460	Antigua
Honduras	
LA0147	Tegucigalpa mercado
LA0148	Tegucigalpa mercado
Mexico	
LA0146	Mexico City mercado
LA1218	Vera Cruz
LA1459	Huachinango
LA1462	Merida
LA1544	Xol Laguna
LA1564	Culiacan
LA1565	Val. nacionale
LA1566	Val. nacionale
LA1567	Sinaloa
LA1568	Yucatan
LA1702	Sinaloa
LA1703	Rio Tamesi
LA1704	Rio Tamesi
LA1994	
LA2083	Guaco, Culiacan
LA2084	Comala, Culiacan
Nicaragua	
LA1212	

Accessions	Location
LA1213	
Panama	
LA1216	
LA1217	
Peru	
LA1570	Cerro Azul
LA0113	Hacienda Calera
LA0116	Chiclayo mercado
LA0117	Piura mercado
LA0125D	Trujillo mercado
LA0131H	Arequipa mercado
LA0134C	Ayacucho mercado
LA0393 - LA0396	Chiclayo
LA0401 - LA0405	Piura
LA0457	Tacna mercado
LA0472	Tacna
LA0473	Calana
LA0477	Chincha
LA0478	Chincha
LA0721	Chiclayo
LA1313	Convento de Sivia
LA1315	Ayna
LA1390	La Molina
LA1397	Iquitos
LA1398	Iquitos
LA1650	Fundo Bogotalla
LA1655	Tarapoto
LA1669	Jahuay
LA1698	Kradolfer Chacra
LA1701	Trujillo
LA1976A	Calana

Accessions	Location
LA1976B	Calana
LA1976C	Calana
LA1988	Iquitos
LA2207 - LA2212	Bajo Naranjillo
LA2213 - LA2220	Nueva Cajamarca
LA2221 - LA2235	Moyobamba mercado
LA2237 - LA2244	La Habana
LA2245 - LA2253	Soritor
LA2254 - LA2257	Puerto Moyobamba
LA2258	Fundo Conovista
LA2259A-2259D	Moyobamba mercado
LA2260 - LA2264	La Huarpia
LA2265 - LA2268	Casaria de Pacaisapa
LA2269 - LA2276	Km 57 from Tarapoto
LA2278 - LA2282	Tabalosas
LA2283 - LA2307	Tarapoto mercado
LA2309 - LA2311	Punto Santa Cruz
LA2316	Sargento
LA2622	Mangual Pucallpa
LA2623	Pucalepillo Pucallpa
LA2676	San Juan del Oro
LA2841	Chinuna
LA2842	Santa Rita
LA2843	Moyobamba mercado
LA2844	Shanhao
LA2845	Moyobamba mercado
LA3222 - LA3226	San Isidro mercado
LA3646	Puente Tincoj

2. PREBRED STOCKS

2.1. Introgression Lines (ILs)

2.1.1. *L. pennellii* ILs (76)

The following group of introgression lines (ILs) was developed by Eshed & Zamir (Euphytica 79:175-179, 1994; TGC 49:26-30). Each IL (except IL8-1) is homozygous for a single introgression from *L. pennellii* (LA0716) in the background of *L. esculentum* cv. M-82 (LA3475). The entire *L. pennellii* genome is thereby represented by overlapping introgressions in a group of 50 lines. An additional 26 sublimes provide increased mapping resolution in some regions. The IL # indicates the *L. pennellii* chromosome and introgressed segment number in each.

Access.	Line
LA4028	IL1-1
LA4029	IL1-1-2
LA4030	IL1-1-3
LA4031	IL1-2
LA4032	IL1-3
LA4033	IL1-4
LA4034	IL1-4-18

Access.	Line
LA4035	IL2-1
LA4036	IL2-1-1
LAA4037	IL2-2
LA4038	IL2-3
LA4039	IL2-4
LA4040	IL2-5
LA4041	IL2-6

Access.	Line
LA4042	IL2-6-5
LA4043	IL3-1
LA4044	IL3-2
LA3488	IL3-3
LA4046	IL3-4
LA4047	IL3-5
LA4048	IL4-1

Access.	Line
LA4049	IL4-1-1
LA4050	IL4-2
LA4051	IL4-3
LA4052	IL4-3-2
LA4053	IL4-4
LA4054	IL5-1
LA4055	IL5-2
LA4056	IL5-3
LA4057	IL5-4
LA4058	IL5-5
LA4059	IL6-1
LA4060	IL6-2
LA4061	IL6-2-2
LA4062	IL6-3
LA4063	IL6-4
LA4064	IL7-1
LA4065	IL7-2
LA4066	IL7-3
LA4067	IL7-4

Access.	Line
LA4068	IL7-4-1
LA4069	IL7-5
LA4070	IL7-5-5
LA4071	IL8-1
LA4072	IL8-1-1
LA4073	IL8-1-5
LA4074	IL8-2
LA4075	IL8-2-1
LA4076	IL8-3
LA4077	IL8-3-1
LA4078	IL9-1
LA4079	IL9-1-2
LA4080	IL9-1-3
LA4081	IL9-2
LA4082	IL9-2-5
LA4083	IL9-2-6
LA4084	IL9-3
LA4085	IL9-3-1
LA4086	IL9-3-2

Access.	Line
LA4087	IL10-1
LA4088	IL10-1-1
LA4089	IL10-2
LA4090	IL10-2-2
LA4091	IL10-3
LA4092	IL11-1
LA4093	IL11-2
LA4094	IL11-3
LA4095	IL11-4
LA4096	IL11-4-1
LA4097	IL12-1
LA4098	IL12-1-1
LA4099	IL12-2
LA4100	IL12-3
LA4101	IL12-3-1
LA4102	IL12-4
LA4103	IL12-4-1

2.1.2. *L. hirsutum* ILs (98)

The following group of introgression lines represent the genome of *L. hirsutum* (LA1777) in the background of *L. esculentum* cv. E-6203 (LA4024) via homozygous chromosome segments (Monforte & Tanksley, Genome 43:803-813; 2000). The first 57 lines (LA3913 - LA3969) represent approximately 85% of the donor genome, while the remaining 41 lines (LA3970 - LA4010) contain different introgressions, mostly derivatives of the first group. Unlike the *L. pennellii* ILs above, each *L. hirsutum* line may contain more than one introgression, representing one to several chromosomes, as indicated below.

Access.	Line	Chr.
LA3913	TA1258	1
LA3914	TA523	1
LA3915	TA1229	1
LA3916	TA1223	1
LA3917	TA1535	1
LA3918	TA1127	1
LA3919	TA1128	1
LA3920	TA1536	1
LA3921	TA1105	2
LA3922	TA1266	2
LA3923	TA1537	2
LA3924	TA1538	2
LA3925	TA1111	3
LA3926	TA1276	3
LA3927	TA1277	3
LA3928	TA1540	3
LA3929	TA1541	3
LA3930	TA1133	4
LA3931	TA1280	4
LA3932	TA1562	4

Access.	Line	Chr.
LA3933	TA1542	4
LA3934	TA1459	4
LA3935	TA517	4
LA3936	TA1475	4
LA3937	TA1473	4
LA3938	TA1287	5
LA3939	TA1293	5
LA3940	TA1112	5
LA3941	TA1543	5
LA3942	TA1117	5
LA3943	TA1544	5
LA3944	TA1539	6
LA3945	TA1545	6
LA3946	TA1546	6
LA3947	TA1559	6
LA3948	TA1303	7
LA3949	TA1304	7
LA3950	TA1547	7
LA3951	TA1312	7
LA3952	TA1315	8

Access.	Line	Chr.
LA3953	TA1316	8
LA3954	TA1548	8
LA3955	TA1320	8
LA3956	TA1324	9
LA3957	TA1325	9
LA3958	TA1330	9
LA3959	TA1331	9
LA3960	TA1550	10
LA3961	TA1551	10
LA3962	TA1552	10
LA3963	TA1337	10
LA3964	TA1339	10
LA3965	TA1555	11
LA3966	TA1554	11
LA3967	TA1342	11
LA3968	TA1350	12
LA3969	TA1121	12
LA3970	TA1219	1
LA3971	TA1218	2
LA3972	TA1173	2

Access.	Line	Chr.	Access.	Line	Chr.	Access.	Line	Chr.
LA3975	TA1629	3	LA3989	TA1319	8	LA4001	TA1644	1, 7, 12
LA3976	TA1138	4	LA3990	TA1560	8	LA4002	TA1645	1, 8, 12
LA3977	TA1467	4	LA3991	TA1326	9	LA4003	TA1648	2, 11
LA3978	TA1468	4	LA3993	TA1549	10	LA4004	TA1649	2, 3, 6
LA3979	TA1630	4	LA3994	TA1635	10	LA4005	TA1652	3, 5
LA3980	TA1290	5	LA3995	TA1553	11	LA4006	TA1654	4, 10, 11
LA3981	TA1116	5	LA3996	TA1120	11	LA4007	TA1655	4, 12
LA3983	TA1631	5	LA3997	TA1563	1, 10	LA4008	TA1656	5, 6, 9
LA3984	TA1632	5	LA3998	TA1637	1, 11, 12	LA4009	TA1564	5, 7, 10
LA3985	TA1306	7	LA3999	TA1638	1, 12	LA4010	TA1561	8, 12
LA3986	TA1309	7	LA4000	TA1557	1, 4			
LA3988	TA1318	8						

2.1.3. *S. lycopersicoides* IL (99)

The following group of ILs have been bred from *S. lycopersicoides* into the background of *L. esculentum* cv. VF36. These lines represent ~96% of the donor genome and are described in the following publications: Canady et al., 2005, Genome 48: 685-697; Rick et al. 1988 Theor. Appl. Genet. 76: 647-655. While some lines are available in the homozygous condition, many others are associated with sterility and must be maintained via heterozygotes. Marker analysis is required to identify heterozygous progeny. Seed of some lines may be limited or temporarily unavailable.

Acc.	Line	Chr.s	Acc.	Line	Chr.s	Acc.	Line	Chr.s
LA3344	<i>Mdh-1</i>	3	LA4238	LS5-1	2	LA4266	SL-8A	8
LA3345	<i>Dia-3</i>	9	LA4239	LS41-20	2	LA4267	LS16-10	8
LA3668	<i>Abg</i>	10	LA4240	LS1-13	3	LA4268	LS14-7	9
LA3866	LS1-1	1	LA4241	LS40-2	3	LA4269	LS12-2	9
LA3867	LS11-9	1	LA4242	LS14-8	3	LA4270	LS10-6	9
LA3869	LS42-4	2	LA4243	LS1-3	3	LA4271	LS49-5	9
LA3870	LS38-10	2	LA4244	LS10-9	4	LA4272	LS41-11	9
LA3871	LS41-3	2	LA4245	LS10-11A	4	LA4273	LS12-8	10
LA3874	LS20-9	3	LA4246	LS49-8B	4	LA4274	LS4-14	10
LA3875	LS24-14	4, 12	LA4247	LS12-9	4	LA4275	SL-10	10
LA3876	LS29-1	8	LA4248	LS11-6	5	LA4276	LS12-12	10
LA3878	LS24-6	5	LA4249	LS9-1	5	LA4277	LS24-11	11
LA3879	LS1-5	5, 11	LA4250	LS49-8C	5	LA4278	LS3-2	11
LA3882	LS43-14	2, 6	LA4251	LS49-3	5	LA4279	LS19-11	11
LA3883	LS48-6	7, 11	LA4252	LS32-11	5	LA4280	LS1-5	11, 5
LA3886	LS48-5	7	LA4253	LS11-11B	6	LA4281	LS13-13	12
LA3889	LS41-13	8	LA4254	LS32-14	6	LA4282	LS45-7	12
LA3892	LS48-2	11	LA4255	LS38-5	6	LA4283	LS8-9	12
LA3893	LS16-6	5, 12	LA4256	LS9-22	6	LA4284	LS9-13	12
LA3906	<i>Wa, DI</i>	8	LA4257	LS46-3	7			
LA4230	LS15-2H	1	LA4258	LS19-7	7	LA4293	LS5-8	1
LA4231	LS15-2B	1	LA4259	LS32-4	7	LA4294	LS15-2AD	1
LA4232	LS11-11A	1	LA4260	SL-7F	7	LA4295	LS15-2A	1
LA4233	LS20-9	1	LA4261	LS8-11	7	LA4296	LS15-2AA	1
LA4234	LS21-2	1	LA4262	LS20-16	8	LA4297	LS15- 2AAA	1
LA4235	LS10-2	1	LA4263	LS46-6A	8			
LA4236	LS49-8A	2	LA4264	LS9-26A	8	LA4298	LS15-2BA	1
LA4237	LS40-8	2	LA4265	LS9-26B	8	LA4299	LS4-9	5

Acc.	Line	Chr.s	Acc.	Line	Chr.s	Acc.	Line	Chr.s
LA4300	LS9-7B	5, 6	LA4306	LS46-6	8	LA4312	LS45-7C	12
LA4301	SL-7A	7	LA4307	SL-8	8	LA4313	LS8-12A	12
LA4302	SL-7C	7	LA4308	LS32-10	9	LA4314	LS12-9B	4, 10
LA4303	SL-7D	7	LA4309	LS10-6D	9	LA4315	SL-7	7
LA4304	LS8-11A	7	LA4310	LS19-10A	11			
LA4305	LS9-26C	7, 8	LA4311	LS14-2	12			

2.2. Backcross Recombinant Inbreds (99).

The following group of backcross recombinant inbred lines originated from the cross *L. esculentum* × *L. pimpinellifolium* (Doganlar et al. Genome 45: 1189-1202, 2002). The result of 2 BC's and at least 6 generations of inbreeding via single seed descent, the lines are highly homozygous (residual heterozygosity ~3%). The population has been genotyped at 127 marker loci, and the corresponding maps, map files, and QTL data are available from the Solanaceae Genome Network (www.sgn.cornell.edu). This set of 99 lines has been selected for optimum mapping resolution using the MapPop software, and provide a permanent, high resolution mapping population.

LA4139 through LA4229	BC-RIs
LA4024	<i>L. esculentum</i> parent (E-6203)
LA1589	<i>L. pimpinellifolium</i> parent

2.3. Alien Substitution Lines (7)

In the course of his study of segregation and recombination in *L. esculentum* × *L. pennellii* hybrids, Rick (Genetics 26:753-768, 1969; Biol. Zbl. 91:209-220, 1971) progressively backcrossed certain chromosomes of *L. pennellii* LA0716 into *L. esculentum*. Selected heterozygotes of later generations were selfed and subsequent progenies free of *esculentum* markers were selected as the substitution lines. The chromosome 6 substitution (LA3142) was further selected with RFLP markers to eliminate residual heterozygosity (Weide et al., Genetics 135:1175-1186, 1993). The mutant loci used to select each substitution are indicated.

LA	Chrom.	Marker Loci
2091	1	<i>au, dgt, inv, scf</i>
1639	2	<i>Me, aw, m, d</i>
1640	3	<i>sy, bls, sf</i>
3469	4	<i>clau, ful, ra, e, su³</i>

LA	Chrom.	Marker Loci
3142	6	<i>yv, ndw, m-2, c</i>
1642	8	<i>l, bu, dl, al</i>
1643	11	<i>j, hl, a</i>

2.4. Monosomic Alien Addition Lines (10)

In the following group of monosomic additions (MA), each line contains a single extra chromosome from *S. lycopersicoides* LA1964 added to the *L. esculentum* genome (Chetelat et al., Genome 41:40-50, 1998). Intactness of the *S. lycopersicoides* chromosomes in these stocks has been tested with a limited number of markers, hence some may be recombinant. For example, our stock of MA-8 lacks *S. lycopersicoides* markers distal to TG330 on the long arm. Furthermore, we were unable to maintain MA-1 and MA-6, both of which are now extinct.

Like other types of trisomics, progeny of the monosomic additions include both diploids and trisomics, the proportion of which varies between each chromosome group. Identification of monosomic additions in each generation is facilitated by their phenotypic resemblance to the corresponding primary trisomic. Therefore, the guidelines of Rick (TGC 37:60-61, 1987) for identifying trisomics in the seedling stage are useful for selecting monosomic additions as well. To further simplify this process, we have backcrossed some

of the monosomic additions into the background of multiple marker stocks for the corresponding chromosomes. In this configuration, diploids are more easily distinguished from trisomics by the expression of recessive mutant alleles in the former, and dominant wild type in the latter. For example, in our stock of MA-2, the 2n progeny would have the phenotype *wv-aa-d*, whereas 2n+1 plants would be wild type at these marker loci (as well showing the expected trisomic syndrome). In addition, some monosomic additions carry dominant morphological markers that can be used to distinguish them from 2n progeny. The marker genotypes of 2n+1 vs 2n progeny are listed below for each chromosome.

LA	Chrom.	2n+1	2n
3454	MA-2	+--+	<i>wv-aa-d</i>
3455	MA-3	+--+	<i>sy-bls-sf</i>
3456	MA-4	+	+
3457	MA-5	+	<i>obv</i>
3459	MA-7	<i>Bco-+-+</i>	<i>+var-not</i>

LA	Chrom.	2n+1	2n
3460	MA-8	<i>Wa</i>	+
3461	MA-9	+	+
3462	MA-10	<i>Abg-+-+--+</i>	<i>+u-t-nd-ag</i>
3463	MA-11	+	+
3464	MA-12	+	+

2.5. Other Prebreds (13). This group of prebreds contain selected morphological traits bred into cultivated tomato from related wild species. Some traits may be simply inherited, others likely involve multiple genetic loci. Also included are two interspecific hybrids useful for various purposes.

2.5.1. High soluble solids derivatives of *L. chmielewskii*. Bred from LA1028 into the background of VF145-7879 (Rick, 1974, Hilgardia 42:493-510).

LA1500
LA1501
LA1502
LA1503
LA1563.

2.5.2. Monogenic and provisional mutants from *L. cheesmanii* (Rick, Econ. Bot. 21: 171-184, 1967).

LA1015 *h*, 'cps' (compressed fruit = reduced L/W ratio)
LA1016 *dps*, 'yg' (yellow green leaves)
LA1017 *ptb*, 'Ppc' (pachypericarp = thick-walled fruit)
LA1018 *ptb*, *u^G*, *Od*, *h*, dark buds (anthocyanin in bud calyces), bitter fruit
LA1019 'Ppc', thick calyx, firm fruit

2.5.3. Exserted stigmas from *L. pimpinellifolium*. Bred from LA1585 (Rick TGC 33:13-14, 1983):

LA2380

2.5.4. Interspecific hybrids.

LA3857 *L. esculentum* cv. VF36 × *S. lycopersicoides* LA2951, relatively male-fertile F₁ hybrid (clonally propagated).
LA4135 *L. esculentum* cv. VF36 × *L. pennellii* LA0716; useful as a rootstock for maintenance of *S. sitiens*, *S. juglandifolium*, and *S. ochranthum*.

3. STRESS TOLERANT STOCKS (50+)

We receive many requests for stocks with tolerances to environmental stresses (abiotic or biotic). Therefore, we chose this group of mostly wild species accessions based

on our observations of plants in their native habitats and/or reports in the literature. If TGC members know of other accessions which should be added to this group, we would be grateful for the information and seed samples to accession in the TGRC.

3.1. Drought tolerance

- L. pennellii* (general feature): LA0716, and others
L. chilense (esp. coastal sites): LA1958, LA1959, LA1972, and others
S. sitiens (general feature): LA1974, LA2876, LA4105, and others

3.2. Flooding tolerance

- L. esculentum* var. *cerasiforme* (wet tropics): LA1421, and others
S. juglandifolium, *S. ochranthum* (probably a general feature): LA2120, LA2682

3.3. High temperature tolerance

- L. esculentum* cv.s Nagcarlang (LA2661), Saladette (LA2662), Malintka-101 (LA3120), Hotset (LA3320)

3.4. Chilling tolerance

- L. hirsutum* (from high altitudes): LA1363, LA1393, LA1777, LA1778
L. chilense (from high altitudes): LA1969, LA1971, LA4117A
S. lycopersicoides (from high altitudes): LA1964, LA2408, LA2781

3.5. Aluminum tolerance

- L. esculentum* var. *cerasiforme* LA2710 (suspected)

3.6. Salinity and/or alkalinity tolerance

- L. cheesmanii* (from littoral habitats): LA1401, LA1508, LA3124, LA3909
L. chilense: LA1930, LA1932, LA1958, LA2747, LA2748, LA2880, LA2931
L. esculentum cv. Edkawi LA2711
L. esculentum var. *cerasiforme*: LA1310, LA2079 - LA2081, LA4133
L. pennellii: LA0716, LA1809, LA1926, LA1940, LA2656
L. peruvianum: LA0462, LA1278, LA2744
L. pimpinellifolium LA1579

3.7. Arthropod resistance

- L. hirsutum*, esp. *f. glabratum*: LA0407 and many others
L. pennellii: LA0716, and others

4. CYTOGENETIC STOCKS

4.1. Translocations (37)

The following group of translocation stocks have been assembled from the collections of their originators - D.W. Barton, C.D. Clayberg, B.S. Gill, G.R. Stringham, B. Snoad, and G. Khush. As far as we know, they are all homozygous for the indicated structural changes. They are described by Gill *et al.* (TGC 23: 17-18; TGC 24:10-12). Accessions with an asterisk comprise the tester set.

Accession	Chrom.s
*LA1115	T9-12
*LA1119	T3-8
*LA1120	T6-12
LA1876	T1-2

Accession	Chrom.s
LA1885	T5-7
LA1898	T2-10a
LA1899	T6-11
LA1903	T4-7

Accession	Chrom.s
LA1049	T1-9
LA1116	T1-11
LA1117	T5-7

Accession	Chrom.s
LA1118	T7-11
LA1121	T4-9
LA1122	T2-9
LA1123	T2-9
LA1124	T3-9
LA1125	T5-7
LA1126	T7-9
LA1127	T3-5
LA1129	T3-9

Accession	Chrom.s
LA1877	T2-4
LA1878	T2-7
LA1879	T2-9
LA1880	T2-11
LA1881	T2-12
LA1882	T12-3 or -8
LA1883	T3-7
LA1884	2 IV T3-8,9-12
LA1886	T12-3 or 8

Accession	Chrom.s
LA1892	2 IV T9-12, ?-?
LA1894	T2-9a
LA1895	T2-9b
LA1896	T1-12
LA1897	T7-11?
LA1902	T2- ?
LA1904	T2-9d
LA1905	T1-3 or 8
LA1906	T2-10b

4.2. Trisomics (35)

The following series of trisomics contain various kinds of extra chromosomes. Since the extras are transmitted irregularly, each stock necessarily produce a majority of diploid progeny, the remainder aneuploid. Primary trisomics yield mostly $2n$ and $2n+1$, and rarely tetrasomics ($2n+2$). Telotrisomics yield telos and an occasional rare tetratelosomic. Secondary, tertiary, and compensating trisomics transmit other trisomic types as expected. Because transmission is irregular and reproduction of stocks requires much labor, our stocks are limited. In requesting our aneuploids, researchers are asked to keep these points in mind. To assist in the identification of primary trisomics at the seedling stage, the key features of each have been summarized by Rick (TGC 37:60-61, 1987). Additional $2n+1$ stocks are listed under Monosomic Alien Additions.

Accession	Genotype
Primary trisomics	
delta-10	Triplo-1
delta-06	Triplo-2
delta-08	Triplo-3
delta-02	Triplo-4
delta-04	Triplo-5
delta-12	Triplo-6
delta-07	Triplo-7
delta-03	Triplo-8
delta-05	Triplo-9
delta-01	Triplo-10
delta-40	Triplo-11
delta-09	Triplo-12
Telo-trisomics	
delta-14	$2n + 3S$
delta-17	$2n + 3L$
delta-21	$2n + 4L$
delta-20	$2n + 7L$
delta-19	$2n + 8L$
delta-35	$2n + 10S$

Accession	Genotype
Secondary trisomics	
delta-44	$2n + 2S \cdot 2S$
delta-43	$2n + 5L \cdot 5L$
delta-36	$2n + 7S \cdot 7S$
delta-26	$2n + 9S \cdot 9S$
delta-31	$2n + 9L \cdot 9L$
delta-28	$2n + 10L \cdot 10L$
delta-41	$2n + 11L \cdot 11L$
delta-29	$2n + 12L \cdot 12L$
Tertiary trisomics	
delta-18	$2n + 2L \cdot 10L$
delta-16	$2n + 4L \cdot 10L$
delta-39	$2n + 5L \cdot 7S$
delta-15	$2n + 7S \cdot 11L$
delta-25	$2n + 9L \cdot 12L$
delta-23	$2n + 1L \cdot 11L$
Compensating trisomics	
delta-32	$2n - 3S \cdot 3L + 3S + 3L \cdot 3L$
delta-33	$2n - 3S \cdot 3L + 3S \cdot 3S + 3L \cdot 3L$
delta-34	$2n - 7S \cdot 7L + 7S \cdot 7S + 7L \cdot 7L$

4.3. Autotetraploids (17)

We are currently maintaining only the following group of tetraploids. Whereas we formerly stocked many more lines, their rapid deterioration, low seed yields, and lack of demand required that we prune them to a smaller group of more frequently used genotypes. All are *L. esculentum* unless otherwise noted, and arose from either induced or spontaneous chromosome doubling.

Accession	Genotype
2-095	cv. San Marzano
2-483	cv. Red Cherry
LA0457	cv. from Tacna mercado
LA0794	<i>ag, t^v</i>
LA1917	<i>L. chilense</i>
LA2335	<i>L. pimpinellifolium</i>
LA2337	cv. Stokesdale
LA2339	cv. Pearson
LA2340	<i>L. pimpinellifolium</i>
LA2342	cv. Danmark

Accession	Genotype
LA2343	cv. Waltham Fog
LA2581	<i>L. peruvianum</i>
LA2582	<i>L. peruvianum</i> var. <i>humifusum</i>
LA2583	<i>L. chilense</i>
LA2585	<i>L. pimpinellifolium</i>
LA2587	<i>L. esculentum</i> var. <i>cerasiforme</i>
LA3255	cv. Ailsa Craig

5. CYTOPLASMIC VARIANTS (3)

The following three lines are cytoplasmically-inherited chlorotic variants maintained by the TGRC and included in the miscellaneous group for want of better classification. They were induced by mutagens and are inherited in strictly maternal fashion. They are not transmitted by pollen but in reciprocal crosses -- no matter what male parents we have used -- the progeny are 100% variant.

LA1092	Uniform yellow, induced by fast neutrons in hybrid background (G.S. Khush)
LA1438	Light green, induced by X-rays in cv. Moneymaker (K. Kerkerk)
LA2979	Cyto-variegated, in cv. Glamour (R.W. Robinson)

6. GENETIC MARKER COMBINATIONS**6.1. Chromosome Marker Stocks (182)**

This group consists of stocks in each of which has been assembled a series of marker genes for a single chromosome. In a few cases markers on other chromosomes are also present (listed in parentheses). Some of the more useful stocks have been combined with male steriles in order to make them useful for large scale test crossing. These stocks are listed below according to chromosome, and within each chromosome group by accession number. Asterisks indicate the preferred marker combination for each chromosome (i.e. that which provides the best map coverage).

Access.	Genotype
Chromosome 1	
LA0910	<i>per, inv</i>
LA0984	<i>scf, inv</i>
LA0985	<i>inv, per</i>
LA1003	<i>scf, inv, per</i>
LA1082	<i>era, um</i>
LA1107	<i>inv, co</i>
LA1108	<i>inv, dgt</i>
LA1169	<i>scf, dgt</i>
LA1173	<i>gas, co</i>
LA1184	<i>au^{tl}, dgt</i>

Access.	Genotype
LA1185	<i>au^{tl}, scf, inv</i>
LA1186	<i>au^{tl}, scf, inv, dgt</i>
LA1431	<i>au^{tl}, dgt</i>
LA1490	<i>au^{tl}, co, inv, dgt</i>
LA1492	<i>ms-32, bs</i>
LA1529*	<i>au^{tl}, co, scf, inv, dgt</i>
LA2354	<i>br, y (p, l)</i>
LA3209	<i>imb, irr, y</i>
LA3301	<i>fla, comⁱⁿ</i>
LA3302	<i>imb, comⁱⁿ</i>

Access.	Genotype
LA3303	<i>imb, inv</i>
LA3305	<i>imb, Lpg</i>
LA3306	<i>comⁱⁿ, inv</i>
LA3307	<i>comⁱⁿ, Lpg</i>
LA3346	<i>au, bs</i>
LA3347	<i>au, ms-32</i>
LA3348	<i>au, com</i>
LA3349	<i>au, imb</i>
LA3350	<i>au, br</i>
LA3351	<i>imb, Lpg/+</i>
LA3352	<i>imb, au, Lpg/+?</i>

Access.	Genotype
Chromosome 2	
LA0271	<i>aw, O</i>
LA0286	<i>d, m</i>
LA0310	<i>Wo^m, d</i>
LA0330	<i>bk, o, p, d, s (r, y)</i>
LA0342	<i>Wo^m, d (ms-17)</i>
LA0514	<i>aw, Wo^m, d</i>
LA0639	<i>Me, aw, d</i>
LA0650	<i>aw, d</i>
LA0715	<i>Wo^m, Me, aw, d</i>
LA0732	<i>suf, d</i>
LA0733	<i>Wo^m, d, ms-10</i>
LA0754	<i>aw, p, d, m, o</i>
LA0777	<i>dil, d</i>
LA0789	<i>Me, aw, d, m</i>
LA0790	<i>wv, Me, aw, d</i>
LA0986	<i>s, bk, Wo^m, o, aw, p, d</i>
LA1525	<i>aa, d</i>
LA1526	<i>are, wv, d</i>
LA1699	<i>Wo^m, bip</i>
LA1700*	<i>wv, aa, d</i>
LA3132	<i>Prx-2¹, ms-10, aa</i>
Chromosome 3	
LA0644	<i>r, wf</i>
LA0782	<i>sy, sf</i>
LA0877	<i>pau, r</i>
LA0880	<i>sf, div</i>
LA0987	<i>pli, con</i>
LA0988	<i>ru, sf</i>
LA1070	<i>ru, sf, cur</i>
LA1071	<i>sy, bls, sf</i>
LA1101	<i>cn, sy, sf</i>
LA1175	<i>bls, aut</i>
LA1430*	<i>sy, Ln, bls, sf</i>
Chromosome 4	
LA0774	<i>ful, e</i>
LA0885	<i>ful, e, su³</i>
LA0886	<i>ful, ra, e</i>
LA0888	<i>ful, ven, e</i>
LA0889	<i>ra, su³</i>
LA0890	<i>ra, ven</i>
LA0902	<i>ful, ra², e (ms-31)</i>
LA0915	<i>clau, ful</i>
LA0916	<i>clau, ra, su³</i>
LA0917*	<i>clau, ful, ra, e, su³</i>
LA0920	<i>ful, ra, e, su³</i>
LA0989	<i>afI, ful</i>
LA0990	<i>cm, ful, e, su³</i>
LA0992	<i>clau, ra, su³ (com)</i>
LA0993	<i>ra, si</i>
LA0994	<i>cm, ver</i>

Access.	Genotype
LA1073	<i>clau, afl</i>
LA1074	<i>clau, ver</i>
LA1075	<i>ver, e, su³</i>
LA1536	<i>clau, su³, ra; icn</i>
Chromosome 5	
LA0512	<i>mc, tf, wt, obv</i>
LA1188	<i>frg, tf</i>
LA3850*	<i>af, tf, obv</i>
Chromosome 6	
LA0336	<i>c, sp (a, y)</i>
LA0640	<i>yv, c</i>
LA0651	<i>m-2, c</i>
LA0773	<i>yv, m-2, c</i>
LA0802	<i>yv, m-2, c (ms-2)</i>
LA0879	<i>tl, yv</i>
LA1178	<i>yv, coa, c</i>
LA1189*	<i>pds, c</i>
LA1190	<i>pds, yv</i>
LA1489	<i>yv, ves-2, c</i>
LA1527	<i>d-2, c</i>
LA3805	<i>m-2, gib-1</i>
LA3806	<i>yv, Mi, B^{og}, sp, c</i>
LA3807	<i>tl, yv, c</i>
Chromosome 7	
LA0788	<i>La/+, deb</i>
LA0882	<i>La/+, deb, adp</i>
LA0923	<i>ig, La/+</i>
LA0924	<i>La/+, not</i>
LA1083	<i>ig, flc</i>
LA1103*	<i>var, not</i>
LA1104	<i>deb, not</i>
LA1172	<i>La/+, lg-5</i>
Chromosome 8	
LA0513	<i>l, bu, dl</i>
LA0712	<i>l, bu, dl; ms-2</i>
LA0776	<i>l, va^{virg}</i>
LA0897	<i>l, bu, dl, al</i>
LA0922	<i>bu, dl, spa</i>
LA0998	<i>l, bu, dl, Pn/+</i>
LA0999	<i>tp, dl</i>
LA1012	<i>dl, l</i>
LA1191	<i>spa, ae</i>
LA1442	<i>dl, glg, marm</i>
LA1666*	<i>l, bu, dl, ae</i>
Chromosome 9	
LA0883	<i>pum, ah</i>
LA0884	<i>wd, marm</i>
LA1000	<i>nv, ah</i>
LA1001	<i>pum, ah, marm</i>
LA1100	<i>ah, pla, marm</i>
LA1112	<i>marm, lut</i>
LA1176	<i>Crk, ah, marm</i>

Access.	Genotype
LA3353*	<i>ah, marm, pct</i>
LA3841	<i>Tm-2^a, Frl, nv, TM</i>
Chromosome 10	
LA0158	<i>Xa/+, u, t (y)</i>
LA0339	<i>ag, u</i>
LA0341	<i>h, ag (ms-2)</i>
LA0643	<i>u, l-2</i>
LA0649	<i>t^v, ag</i>
LA0711	<i>t^v, ag (ms-2)</i>
LA1002	<i>h, u, l-2, t, ag (pe, lg)</i>
LA1085	<i>h, res</i>
LA1086	<i>h, ten</i>
LA1110	<i>icn, ag</i>
LA1192	<i>hy, ag</i>
LA1487	<i>icn, t^v</i>
LA2493	<i>Xa-2, hy, h, ag</i>
LA2495	<i>Xa-2, h, ten, ag, al</i>
LA2496	<i>Xa-2, h, l-2, t</i>
LA2497	<i>hy, u, icn, h, ag</i>
LA2498	<i>u, Xa-3, h</i>
LA2499	<i>u, nor, t</i>
LA2500	<i>u, icn, h</i>
LA2501	<i>u, icn, h, ag</i>
LA2502	<i>u, h, auv, l-2, t^v</i>
LA2503	<i>u, h, l-2, t^v, ag</i>
LA2504*	<i>u, h, t, nd, ag</i>
LA2505	<i>u, l-2, t, ag, Xa</i>
LA2506	<i>ag, h, l-2, oli, t^v</i>
LA2507	<i>h, t, nd, ag</i>
LA2508	<i>h, t, ag, Xa</i>
LA2509	<i>oli, l-2, t^v, ag (wf)</i>
LA2591	<i>Xa-2, h, ag</i>
LA2592	<i>u, h, t, nd, ag</i>
LA2593	<i>u, auv, ag</i>
LA4341	<i>h, hy, u</i>
Chromosome 11	
LA0259	<i>hl, a</i>
LA0291	<i>hl, a (ms-2)</i>
LA0729	<i>neg, a</i>
LA0730	<i>a, pro</i>
LA0761	<i>a, hl, j</i>
LA0798	<i>a, hl, j (ms-2)</i>
LA0803	<i>hl, a, pro (ms-2)</i>
LA0881	<i>neg, hl, a</i>
LA0925*	<i>j, hl, a, f</i>
LA1102	<i>a, hl, tab</i>
LA1109	<i>j, hl, mnt</i>
LA1488	<i>neg, ini</i>
LA1786	<i>j, f, a, bi (c)</i>
LA2352	<i>j, f (p, c)</i>
LA2364	<i>j, a, f (y, wt, c, l, u)</i>
LA2489	<i>neg^{ne-2}, a</i>

Access.	Genotype	Access.	Genotype	Access.	Genotype
LA4290	<i>a, bks</i>	LA4344	<i>a, mon</i>	LA1171	<i>yg-2^{aud}, fd</i>
LA4291	<i>a, bks²</i>	Chromosome 12		LA1177*	<i>alb, mua</i>
LA4292	<i>j-2, up, wv-3</i>	LA1111	<i>fd, alb</i>		

6.2. Linkage Screening Testers (13)

The following set of linkage testers each combines two pairs of strategically situated markers on two different chromosomes (see TGC 22: 24). They are intended primarily for assigning new, unmapped markers to a chromosome. The more complete chromosome marker combinations (list 6.1 above) should be used for subsequent testing to delimit loci more accurately. Whereas six of these stocks should pretty well cover the tomato genome, we list below the entire series of the current available testers because alternative stocks differ in their usefulness, depending upon the phenotype of the new mutant to be located. The chromosomal location of each pair of markers is indicated in parentheses.

Access.	Genotype	Access.	Genotype
LA0780	<i>yv, c</i> (chr 6); <i>h, ag</i> (chr 10)	LA1182	<i>sy, sf</i> (chr 3); <i>alb, mua</i> (chr 12)
LA0781	<i>ful, e</i> (chr 4); <i>neg, a</i> (chr 11)	LA1441	<i>coa, c</i> (chr 6); <i>hl, a</i> (chr 11)
LA0784	<i>ful, e</i> (chr 4); <i>hl, a</i> (chr 11)	LA1443	<i>scf, dgt</i> (chr 1); <i>l, al</i> (chr 8)
LA0982	<i>clau, e</i> (chr 4); <i>hl, a</i> (chr 11)	LA1444	<i>wv, d</i> (chr 2); <i>af, tf</i> (chr 5)
LA0983	<i>l, dl</i> (chr 8); <i>ah, marm</i> (chr 9)	LA1491	<i>scf, dgt</i> (chr 1); <i>spa, ae</i> (chr 8)
LA1164	<i>var, not</i> (chr 7); <i>ah, marm</i> (chr 9)	1665	<i>scf, dgt</i> (chr 1); <i>l, ae</i> (chr 8)
LA1166	<i>clau, su³</i> (chr 4); <i>icn, ag</i> (chr 10)		

6.3. Miscellaneous Marker Combinations (288)

The following list groups stocks in which various mutant genes have been combined for various purposes. A few of these items include linked genes, but are classified here because other linkage testers provide the same combinations or because they are more useful as markers of several chromosomes. Some multiple marker combinations that are of limited usefulness, difficult to maintain, and/or redundant with other genotypes, have been dropped from the current list.

Access.	Genotype	Access.	Genotype	Access.	Genotype
LA0013	<i>a, c, d, l, r, y</i>	LA0499	<i>Od, sn, at, cm/+</i>	LA0913	<i>ful, su³, ht</i>
LA0014	<i>al, d, dm, f, j, wt, h</i>	LA0508	<i>gf, d, c, a, r, y</i>	LA0914	<i>com, ful</i>
LA0052	<i>j, wt, br</i>	LA0638	<i>ht, d, r</i>	LA0991	<i>ful, e, com</i>
LA0085	<i>Wo, d, h</i>	LA0648	<i>rv, e, Wo, wf, j, h</i>	LA0995	<i>deb, um</i>
LA0137	<i>dl, wd, gq</i>	LA0719	<i>Jau, clau</i>	LA0996	<i>um, ig</i>
LA0154	<i>u, d, sp, h</i>	LA0727	<i>wv, d, c, r</i>	LA1018	<i>h, Od, ptb</i>
LA0157	<i>d, m, p, r, y</i>	LA0728	<i>a, lut</i>	LA1038	<i>e, ht, su</i>
LA0158	<i>t, u, Xa, y</i>	LA0759	<i>lg, vi, pe, t</i>	LA1072	<i>sy, sf, um</i>
LA0159	<i>a, e, mc, t, u, y, wf</i>	LA0760	<i>lg, vi</i>	LA1078	<i>ria, ves-2</i>
LA0169	<i>ps, wf, wt</i>	LA0770	<i>clau, pa</i>	LA1079	<i>c, ves-2</i>
LA0189	<i>bl, cl-2</i>	LA0775	<i>tf, h, au, +/-d</i>	LA1105	<i>con, cur</i>
LA0190	<i>wf, br, bk</i>	LA0801	<i>atv, slx</i>	LA1106	<i>fsc, ah</i>
LA0215	<i>at, y, u</i>	LA0875	<i>hp, u, sp</i>	LA1163	<i>wv, d, tf</i>
LA0281	<i>e, t, u</i>	LA0876	<i>hp, sp</i>	LA1170	<i>cn, con</i>
LA0296	<i>br, bk, wf</i>	LA0895	<i>tp, sp, u, Hr</i>	LA1219	<i>d, u</i>
LA0297	<i>tf, ug, Nr</i>	LA0907	<i>lut, pr</i>	LA1663	<i>Ln, Wo^m</i>
LA0299	<i>ag, rv</i>	LA0908	<i>per, var</i>	LA1664	<i>hp, lp</i>
LA0345	<i>ch, j-2</i>	LA0909	<i>con, sf</i>	LA1783	<i>ad, sp</i>
LA0497	<i>ch, j-2, sf</i>	LA0912	<i>ht, su³</i>	LA1787	<i>Bk-2, en</i>

Access.	Genotype
LA1789	<i>sf^{cs}, a</i>
LA1796	<i>Rs, d, h</i>
LA1804	<i>sr, sp, u</i>
LA1805	<i>sr, y</i>
LA1806	<i>ti, y, wf, al, j</i>
LA2349	<i>p, d, r, wt, j, f</i>
LA2350	<i>y, ne, p, c, sp, a</i>
LA2351	<i>c, l, u, h</i>
LA2353	<i>y, wt, n</i>
LA2355	<i>sp, ug</i>
LA2360	<i>e, wt, l, u</i>
LA2363	<i>y, Wo, wt, c, t, j</i>
LA2369	<i>p, Tm-1</i>
LA2370	<i>wf, n, gs</i>
LA2372	<i>sp, fl</i>
LA2441	<i>d, m-2, mc, rvt, t, u</i>
LA2452	<i>B, f, gf, y</i>
LA2453	<i>Gr, u</i>
LA2454	<i>neg^{ne-2}, u</i>
LA2457	<i>u, so</i>
LA2458	<i>Pto, sp, u</i>
LA2461	<i>sp, stu, u</i>
LA2464	<i>aer-2, r, upg, y</i>
LA2465	<i>sp, u, v-2</i>
LA2466	<i>d, t, v-3</i>
LA2467	<i>pe, u, vi</i>
LA2473	<i>alb, c, gra, sft</i>
LA2477	<i>vo, cjf, wf, sp, l, u, h</i>
LA2478	<i>ae^{atr}, r, gs, h</i>
LA2486	<i>inc, pds, sp, u, t</i>
LA2490	<i>pdw, mc, pst, dl</i>
LA2492	<i>ti, wf, e, mc, u, a</i>
LA2524	<i>af, sd</i>
LA2526	<i>dp, sp, u</i>
LA2527	<i>l allele, sp, u</i>
LA2595	<i>br, d, dm, wt, al, h, j, f</i>
LA2597	<i>y, r, wf, mc, m-2, c, gs, gf, marm, h</i>
LA2797	<i>bu, j</i>
LA3128	<i>Ln, t, up</i>
LA3212	<i>tmf, d, sp, u</i>
LA3217	<i>glg, Pts</i>
LA3250	<i>t, u</i>
LA3251	<i>Del, y</i>
LA3252	<i>Del, t</i>
LA3254	<i>a, c, l, Ve</i>
LA3256	<i>at, t</i>
LA3257	<i>gf, gs, r</i>
LA3258	<i>u, Ve</i>
LA3261	<i>Del, gs</i>
LA3262	<i>Del, ug</i>
LA3267	<i>Cf-4, u</i>

Access.	Genotype
LA3268	<i>Tm-2, nv, u</i>
LA3269	<i>Tm-1, u</i>
LA3271	<i>Cf-?, Tm-1, u</i>
LA3273	<i>Gp, Tm-2²</i>
LA3274	<i>ah, Tm-2, nv, u</i>
LA3275	<i>ah, Gp, Tm-2²</i>
LA3276	<i>Tm-1, u, Ve</i>
LA3279	<i>at, Del</i>
LA3284	<i>at, gf</i>
LA3286	<i>r, ug, y</i>
LA3287	<i>hp, r, ug</i>
LA3288	<i>hp, ug, y</i>
LA3289	<i>gf, r, y</i>
LA3290	<i>gf, hp, y</i>
LA3291	<i>at, hp, t</i>
LA3292	<i>Tm-2, u</i>
LA3294	<i>bl, d, u</i>
LA3297	<i>Tm-1, Tm-2, nv</i>
LA3299	<i>ep, u</i>
LA3311	<i>og^c, u</i>
LA3315	<i>sp, pst, u, j-2, up, vo</i>
LA3362	<i>gs, t</i>
LA3363	<i>at, gs</i>
LA3364	<i>gs, u</i>
LA3365	<i>gf, gs</i>
LA3366	<i>t, y</i>
LA3367	<i>hp, t</i>
LA3368	<i>hp, y</i>
LA3369	<i>at, y</i>
LA3370	<i>at, hp</i>
LA3371	<i>hp, u</i>
LA3372	<i>gs, y</i>
LA3373	<i>at, u</i>
LA3374	<i>u, y</i>
LA3375	<i>gs, r</i>
LA3376	<i>Del, hp</i>
LA3381	<i>r, y</i>
LA3382	<i>r, u</i>
LA3383	<i>gs, hp</i>
LA3384	<i>gf, y</i>
LA3385	<i>gs, Nr</i>
LA3386	<i>gf, t</i>
LA3387	<i>Nr, t</i>
LA3389	<i>Nr, y</i>
LA3390	<i>Nr, ug</i>
LA3391	<i>gf, hp</i>
LA3393	<i>r, t</i>
LA3394	<i>at, ug</i>
LA3395	<i>gs, hp, y</i>
LA3396	<i>at, u, y</i>
LA3397	<i>gs, t, y</i>
LA3398	<i>gs, hp, t</i>

Access.	Genotype
LA3399	<i>at, gs, hp</i>
LA3400	<i>at, hp, u</i>
LA3401	<i>at, gs, y</i>
LA3402	<i>hp, t, u</i>
LA3403	<i>gf, gs, u</i>
LA3404	<i>hp, u, y</i>
LA3405	<i>gs, hp, u</i>
LA3406	<i>at, hp, y</i>
LA3407	<i>gs, u, y</i>
LA3408	<i>t, u, y</i>
LA3409	<i>gs, t, u</i>
LA3410	<i>at, gs, u</i>
LA3411	<i>gs, r, u</i>
LA3412	<i>gf, gs, hp, u</i>
LA3413	<i>at, gf</i>
LA3414	<i>t, ug</i>
LA3415	<i>ug, y</i>
LA3416	<i>hp, ug</i>
LA3417	<i>r, ug</i>
LA3418	<i>gf, gs, ug</i>
LA3419	<i>at, gf, gs</i>
LA3420	<i>gf, ug</i>
LA3421	<i>Nr, u</i>
LA3422	<i>at, gs, ug</i>
LA3423	<i>gf, gs, hp, u, y</i>
LA3424	<i>gs, hp, u, y</i>
LA3425	<i>gf, gs, hp, t, u</i>
LA3426	<i>gs, hp, t, u</i>
LA3427	<i>gf, gs, t, u</i>
LA3428	<i>l, u, Ve</i>
LA3429	<i>Del, gs, hp</i>
LA3432	<i>Tm-1, Tm-2, nv, u</i>
LA3433	<i>ah, Tm-2, nv, u</i>
LA3437	<i>at, Nr</i>
LA3442	<i>de, dil, u</i>
LA3443	<i>cor, de, u</i>
LA3444	<i>cor, dil, u</i>
LA3445	<i>cor, pum, u</i>
LA3446	<i>cor, sp, u</i>
LA3447	<i>dil, sp, u</i>
LA3448	<i>in, u</i>
LA3449	<i>d, sp, u</i>
LA3450	<i>bls, sp, u</i>
LA3451	<i>bl, sp, u</i>
LA3540	<i>l, u</i>
LA3541	<i>gs, r, ug</i>
LA3542	<i>u, ug</i>
LA3543	<i>bls, o, u</i>
LA3545	<i>Del, u, y</i>
LA3546	<i>bls, Cf-?, u</i>
LA3547	<i>ah, u</i>
LA3548	<i>pum, u</i>

Access.	Genotype
LA3549	<i>bls, Gp, Tm-2², u</i>
LA3557	<i>Del, gf</i>
LA3558	<i>gf, Nr</i>
LA3559	<i>Del, gs, y</i>
LA3561	<i>gf, gs, hp, Nr, u</i>
LA3562	<i>gf, gs, u, y</i>
LA3563	<i>sp, u</i>
LA3585	<i>gf, u, ug</i>
LA3586	<i>t, u, ug</i>
LA3587	<i>r, u, ug</i>
LA3589	<i>u, ug, y</i>
LA3590	<i>Nr, gs, y</i>
LA3591	<i>Nr, u, y</i>
LA3593	<i>hp, u, ug</i>
LA3594	<i>gs, hp, u, ug</i>
LA3595	<i>gf, hp, ug</i>
LA3596	<i>hp, t, ug</i>
LA3597	<i>at, hp, ug</i>
LA3598	<i>r, t, ug</i>
LA3599	<i>at, t, ug</i>
LA3600	<i>t, ug, y</i>
LA3601	<i>gf, r, t</i>
LA3603	<i>at, gf, y</i>
LA3604	<i>hp, r, t</i>
LA3605	<i>at, ug, y</i>
LA3606	<i>r, t, y</i>
LA3607	<i>gs, hp, Nr</i>
LA3608	<i>hp, Nr, t</i>
LA3609	<i>hp, Nr, y</i>
LA3615	<i>d[*], u</i>
LA3675	<i>hp, Nr, u</i>
LA3676	<i>gf, hp, t</i>
LA3677	<i>gf, hp, r</i>
LA3678	<i>Nr, u, ug</i>
LA3679	<i>gs, Nr, ug</i>
LA3680	<i>Nr, t, u</i>
LA3682	<i>gs, t, ug</i>
LA3683	<i>gs, ug, y</i>
LA3684	<i>Nr, t, y</i>
LA3686	<i>gs, Nr, t</i>
LA3688	<i>gf, gs, hp</i>
LA3689	<i>gs, hp, r</i>
LA3691	<i>r, u, y</i>
LA3692	<i>at, r, y</i>
LA3693	<i>g, t, u</i>
LA3694	<i>Del, gs, u</i>
LA3695	<i>Del, hp, t</i>
LA3697	<i>gs, r, t</i>
LA3698	<i>gs, r, y</i>
LA3699	<i>gf, u, y</i>
LA3700	<i>at, gf, u</i>
LA3701	<i>at, t, u</i>

Access.	Genotype
LA3702	<i>gf, gs, y</i>
LA3703	<i>gf, hp, u</i>
LA3704	<i>at, gf, hp</i>
LA3706	<i>at, gs, t</i>
LA3706	<i>Del, t, y</i>
LA3709	<i>Del, gf, gs, hp, u</i>
LA3741	<i>pum, u</i>
LA3742	<i>de, u</i>
LA3743	<i>cor, u</i>
LA3744	<i>sph, u</i>
LA3745	<i>bl, u</i>
LA3771	<i>hp, B^c</i>
LA3810	<i>hp, t</i>
LA3811	<i>gf, r</i>
LA3812	<i>bls, Tm, Tm-2, nv</i>
LA3815	<i>Del, t, ug</i>
LA3821	<i>dil, pum, u</i>
LA3823	<i>pum, sp, u</i>
LA3826	<i>mon, u</i>
LA3827	<i>dil, cor, sp, u</i>
LA3830	<i>ep, B^c, u</i>
LA3831	<i>gf, gs, r, y</i>
LA4136	<i>Rg-1, r</i>
LA4342	<i>oli, u, y</i>
LA4343	<i>gq, h</i>
LA4348	<i>yg-2, c^{int}</i>

7. Provisional mutants (107).

The following group of provisional mutants are listed here, rather than with the monogenic stocks because they have not been fully characterized. For some, a monogenic segregation has not been verified, for others complementation tests were either not performed or did not detect allelism with existing mutants of similar phenotype. Most of these lines resulted from mutagenesis experiments, the remainder occurring spontaneously. Genetic background is indicated, if known. More information on these stocks is available at our website.

Access.	Traits	Phenotype	Background
2-293	Snout	Fruits distorted, always snouted.	S. Marzano
2-305	Broad	Leaves broader and more divided than Pearson, internodes shortened; fruits elongate.	Pearson
2-473	Yellow fruit, pale corolla	Spontaneous mutant	Red Cherry
2-493	Purple tipped leaves, puny	Miniature plant, reduced fruit set, parthenocarpic fruit.	Peto 795
2-575	Poxed fruit	Pox marks in radial lines, in ripe fruit = yellow or necrotic.	PI 260395
2-585	Balloon	Short internodes, leaves dark green, acuminate, extremely plicate and veins prominent; leaves broad and wavy, highly divided; flowers small, poorly opened; mostly parthenocarpic fruit.	CP-2
2-621	Turbinate	Flowers semiturbinate, corolla wavy, anthers semi-dialytic.	VFN-8
2-625	Prolific leaves	Leaves highly modified and proliferated, dark green.	VFN-8
2-629	Me-oid	Plant rank, most branches do not terminate, yet have sp gene; leaves ext. reduced with long terminal segment, laterals short and strongly recurved.	VFN-8
2-633	Hooded flowers	Corolla funneliform as a result of corolla segments being joining distally more than normal.	breeding line
2-643	Yellow green	Whole plant yellow green, moderate vigor, good fruit set. Similar to fy and yt genes.	VF36
3-003	yv-oid	Yellow green cots, very chlorotic leaves, later chlorosis is general, strong anthocyanin. In field, entirely normal.	VF36
3-055	Round cotyledons and leaves	Chlorotic interveinal regions, normal vigor, short round cots.	VF36
3-073	Abnormal flowers	Calyx and corolla segments enlarged; stamens deformed, dialytic and petaloid; pistil fasciated, distorted.	VF36
3-077	Dwarf	Slow, dwarf, broad recurved leaves, heavy stems, short internodes. Leaves dark green, strongly recurved at tips of all segments, not rugose. As brittle as hl.	VF36
3-082	Dwarf	Short stocky dwarf, recurved leaves. Leaves not rugose or stiff, but strongly recurved. Good expression at seedling stage.	VF36
3-083	Yellow virescent	Bright yellow virescent, paler later.	VF36
3-084	Yellow green	Leaves overall yellow green, becoming speckled green.	VF36
3-088	Light green, dark veins	Light green, miniature stature.	VF36
3-097	Yellow green	Yellow green, narrow leaves, entire margins.	VF36
3-098	Slow chlorotic	Slow chlorotic, yellow green leaves, not fully divided (clavate).	VF36
3-101	tl mimic	Probably an allele of tl, complete response to thiamine application.	VF36
3-106	Strong anthocyanin	Strong anthocyanin under leaf, slow slender and erect.	VF36
3-107	Bright yellow virescent	Bright yellow virescent leaves.	VF36
3-112	Crippled	Leaf rugose, rough, variegated dark green / grey green; older leaves deformed.	VF36

Access.	Traits	Phenotype	Background
3-115	rv-oid	Overall light green leaves with dark veins; stunted, narrow segments.	VF36
3-118	Rugose recurved leaves	Leaves rugose, recurved; plant dwarfish, 2/3 size.	VF36
3-127	Bright yellow	Overall bright yellow, plant 2/3 size.	VF36
3-241-1	Yellow, anthocyanin	Overall yellow, anthocyanin on stem.	VF36
3-243	Long narrow	Long narrow twisted leaves, anthocyanin on stem. Entire, narrow segments, suggesting triplo-3., flowers with elongate parts.	VF36
3-303	Slow, narrow leaves	Very slow,(1/10), yellow green virescent, leaves narrow and acute, deep dark veins	Moneymaker
3-305	La-mimic	Identical with La in all respects, except leaves more subdivided.	Moneymaker
3-307	Broad, grey green	Seedling dwarf, cotyledons and leaves broad, light grey green leaves very convex, deep veined. Mature plant normal size, leaves reduced, slightly chlorotic interveinally, bullate, few fruits set.	Moneymaker
3-309	Bunchy growth, mitten leaves	Seedling dwarf, (1/3 size) short internodes, leaves abbreviated, mitten shaped. Same phenotype in mature plant.	Moneymaker
3-311	Slow, rugose	Seedling extremely slow (1/20), leaves with fewer segments, very rugose, dark green.	Moneymaker
3-315	Glossy dwarf	Extreme dwarf (1/10 size), dark glossy green, like d^x.	Moneymaker
3-317	ra-oid	2/3 size, leaves rounded, convex, recurved, resembles rava. Flowers tiny, hooded, set few fruit.	Moneymaker
3-319	Striated, divided	1/3 size, cotyledons and leaves variably striated, leaves short, convex, recurved, well divided and variably deformed, leaves dark green, variably bullate, twisted and deformed flowers, very few fruit set.	Moneymaker
3-321	Narrow, dissected	Cotyledons narrow, small elliptical; leaves narrow, deeply serrated, surface irregular, turning grey-green, small flowers, scattered fruit set.	Moneymaker
3-323	Spirally coiled	1/3 size, cotyledons ext. narrow, leaves spirally coiled and large; plant gets all wrapped up in itself, leaves very dark green, rugose and dentate.	Moneymaker
3-325	Short, yv	Dwarf, short internodes (1/3), leaves and cotyledons broad, leaves slightly paler with deep veins. Mature plant (GH only): very short compact, yv like, extreme distinct.	Moneymaker
3-329	Bronzing	Dwarf (1/5 size), cotyledons and leaves large, leaves broad and convex, later bronzing interveinally, flowers tiny.	Moneymaker
3-331	Serrated leaves	Leaves extremely narrow, deeply serrated like acl. Mature plant 1/3 size, tiny dark green plicate leaves, dainty appearance, flowers hooded.	Moneymaker
3-335	Gold dust virescent	1/3 size, bright yellow virescent (gold dust), Narrow acute leaves with deep veins	Moneymaker
3-337	Glossy dwarf	Leaves short, smooth and glossy, compact (1/20 size) plant, delayed flowering.	Moneymaker
3-341	Dwarf	Dwarf stature (1/2 size), very short internodes, concave leaves, deep veins, interveinal chlorosis, leaf segments small and few, flowers small.	Moneymaker
3-403	Fimbriate leaves	Two plants with fimbriate leaves, like nv (from Epstein 516)	VF36
3-404	Speckled white	Fine white marginal speckling, nearly normal size.	VF36
3-405	Streaked virescent	2\3 size, streaked cotelydons, strong yellow green virescence.	VF36
3-406	Streaked variegated	Large size, streaked and variegated, extremely irregular, like "crippled"	VF36
3-408	bu mimic	Early seedlings show bunch habit with extremely short internodes, almost rosette like; exceeds bu in compactness	VF36
3-411	Blue green; bushy roots	1/4 size, dark blue green, streaked anthocyanin of leaf undersides; bushy roots, dense growth of solely twisted lateral roots	VF36
3-423	ra-oid	Slender seedling with grey-green colour and recurved leaves. Slow (1/3 normal). Prominent silky hairs of type ra syndrome, like 3-318	VF36
3-424	Extreme dwarf	Extreme dwarf with type d syndrome; intermediate between dd and d:x in stature	VF36

Access.	Traits	Phenotype	Background
3-434	d ^{cr} like	Dwarf like allele of d:cr, except leaves are more obtuse, broader, and more ruffled	VF36
3-436	Overall yellow	Uniformly overall yellow like au and var.	VF36
3-441	Singed hairs	Nearly normal size, also hairless with less suppressed hairs above cotyledons, like singed	VF36
3-601	clau mimic	Resembles clausa, but F1 allele test shows not allelic.	VFNT Ch
3-612	wiry mimic	Resembles wiry, strong expression.	VFNT Ch
3-613	La mimic	Segregates as a dominant La mimic in M2. Also segregates for a dgt-like mutant.	VFNT Ch
3-614	pds-oid	Short, stocky, 1/4 size, light green, not much like pds.	VFNT Ch
3-617	Dwarf	Dwarf like, not allelic with d, linked to bip but not Wo.	VFNT Ch
3-618	mimic of a	Reduced anthocyanins.	VFNT Ch
3-619	wiry mimic		VFNT Ch
3-621	d mimic	Typical d syndrome, though more extreme, but not allelic with d.	VFNT Ch
3-622	d mimic	Typical d syndrome, but not allelic with d.	VFNT Ch
3-624B	Yellow virescent		VFNT Ch
LA0506	Triplo-8 mimic	Triplo-8 mimic, ex. 2-72. Maybe dominant deficiency transmitted through egg, not pollen.	S. Marzano
LA0652	calycine poked	Spotting is pox. Calycine trait is allele of ch. Both spotting and calycine appear as dominants.	
LA0739	ag mimic	allele of ag?	
LA0765	Acute leaves	Acute leaves.	
LA0791	Long John	Originated from crosses among pear types. Elongate fruit shape segregates about 120 long : 48 + in F2's with wild type.	
LA0801	Pseudopolyploid		
LA0870	frizzled virescent		
LA0871	Calico		
LA1012	Mottled, chlorotic petiole	Also segregates for dl, l.	
LA1060	spl-oid	Derived from hg x (sy sf) F2; bright yellow interveinal areas, leaves strongly rolled and reduced especially at growing point.	
LA1065	Miniature	Derived from pic x (ag h, c yv) F2. Phenotype like rmt, leaves reduced and strongly plicate, 1/3 size plant.	
LA1066	Speckled	Speckled mutant derived from lutea, small darker colored seedling, tiny lighter colored specklings, closely resembles pun, probably allelic.	
LA1095	fy-oid	Low grade yg chlorophyll deficiency, uniform over plant; expr. stronger in field.	Rutgers
LA1098	Multiple inflor.	Proliferated and elongate inflorescence, in sp line.	
LA1144	ful mimic	Uniform strong yg, like ful.	Earlipak 7
LA1148	Light green	Light yellow green, normal vigor, poor expression in seedling.	VF145 7879
LA1149	Xanthoid	Bright yellow, stronger at growing point, segregates 2 normal, 1 Xanthoid, 1 chlorotic lethal.	
LA1154	pale virescent, twisted leaves	Pale virescent, twisted leaves; strongly chlorotic growing point, green at first, turning pale, almost whitish; extremely slow (1/10+ normal); twisted and distorted cotyledons.	
LA1160	Fused cotyledons	Cotyledons fused along the proximal part of the margins, net effect suggesting cot's of morning glory.	
LA1193	Yellow-sectored	Extremely stunted and sterile in field.	
LA1201	rv-oid		
LA1202	Dirty orange cherry		

Access.	Traits	Phenotype	Background
LA1436	Withered cotyledons	Withered cotyledons, slow (1/3 size), compact seedling, strong yellow virescent, older leaves are strongly yellow green.	
LA1494	Adventitious roots		
LA1532	rv-oid	Clearly defined, useful seedling marker.	VF145-7879
LA1533	Purple stem	Incompletely dominant, Early seedlings not well distinguished, later moderately intense purpling, especially on leaf veins on undersides.	
LA1707	Short stature	Not true dwarf phenotype; good vigor and distinct in seedling stage.	VF145-7879
LA2018	Anthocyanin deficient	No anthocyanin at any stage.	Niagara
LA2019	Virescent tangerine mimic	Homozygous for phenotype exactly like t ^v . Jointless, very firm fruit, determinate canning type vine, vigorous.	
LA2020	Dark green foliage	Dark green foliage; fruit 10-12 locules, catfaced, yellow skin and red flesh.	
LA2021	Variegated yellow	Very slow and stunted; variegated yellow in large patches over most of the older foliage. Seedling: bright yellow green, the yellow spots turning to white.	
LA2358	Marginal leaf chlorosis		
LA2375	Lc- reduced locule	May not be monogenic, possibly pleiotropic effect of pear shape (ovate gene).	
LA2806	Incomplete anthocyanin mutant	Grey green hypocotyl, similar to ai and pai, but darker. Spontaneous mutant.	Vis
LA2817	Ig mimic	Ig mutant, possibly allelic	
LA2897	Virescent gold top		
LA2899	Wrinkled fruit		
LA3851	Virescent		R.Ruhm

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