Report

of the

Tomato Genetics Cooperative Number 53 – September 2003

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Foreword

The Tomato Genetics Cooperative, initiated in 1951, is a group of researchers who share an interest in tomato genetics, and who have organized informally for the purpose of exchanging information, germplasm, and genetic stocks. The Report of the Tomato Genetics Cooperative is published annually and contains reports of work in progress by members, announcements and updates on linkage maps and materials available. The research reports include work on diverse topics such as new traits or mutants isolated, new cultivars or germplasm developed, interspecific transfer of traits, studies of gene function or control or tissue culture. Relevant work on other Solanaceous species is encouraged as well.

Paid memberships currently stand at approximately 150 from 28 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, Gulf Coast Research and Education Center, 5007 60th Street East, Bradenton, FL 34203, USA, jwsc@ifas.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, wire transfers or credit cards.

Cover photo provided by Carl Jones and Roger Chetelat (photo by Jones and Rick): Leaflets of obscuravenosa (*obv*), a leaf vein mutation located on chromosome 5L. Left to right: *L. pennellii* IL 5-3 (*obv*), 5-4 (+), and 5-5 (*obv*). This and other mutants can be seen on the Tomato Genetics Resource Center website http://tgrc.ucdavis.edu/

- J.W. Scott

Table of Contents

From the editor

Greetings to the TGC membership from your not-so-new editor. We have some experience now and getting this issue out has been easier for Gail Somodi (who does most the work) and me than was the last issue. I invite you to submit your recent research results for volume 54 (2004). TGC Reports are only as good as the information they contain. Again I remind you to submit a report if you are naming a new gene so we can get it approved and on the official tomato gene list. We hope to get a new linkage map published in next year's volume as there has not been such a list in the TGC since 1987.

One of our goals is to get all back volumes of the Reports of the Tomato Genetics Cooperative on our website http://gcrec.ifas.ufl.edu/tgc and in a keyword searchable format. Many issues are now available on line, some are searchable by keyword and some are not. Volume 52 from last year is now on line. It will be our policy to put volumes on line one year after they are published. During the year check the website for updates. We are open to any suggestions from you as to how we can improve.

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First International Symposium on Tomato Disease

This meeting will take place from June 21-24, 2004 in Orlando, Florida at the Grosvenor Resort at Walt Disney World**.** To find out more about the conference and receive meeting announcements see the website:

http://plantdoctor.ifas.ufl.edu/istd.html

Announcement: USDA Funding for Tomato Germplasm Evaluation

Funding will again be available from the USDA, ARS in FY 2004 for evaluation of tomato germplasm. Evaluation funding will be used on germplasm maintained in or destined for the National Plant Germplasm System (NPGS). Relevant NPGS germplasm includes the tomato collection maintained by USDA's Plant Genetic Resources Unit in Geneva, New York and the collection at the University of California, C.M. Rick Tomato Genetics Resource Center, Davis, California. Proposal guidelines are noted below.

All proposals will be evaluated on the need for evaluation data, national and/or regional interest in the problem, scientific soundness and feasibility of the proposal, the likelihood of success, germplasm to be screened, and the likelihood that data will be entered into NPGS databases and freely shared with the user community. The GRIN web site *http://www.ars-grin.gov/npgs/cgclist.html* hosts an updated list of tomato germplasm evaluation priorities. Proposals will be reviewed by the Tomato Crop Germplasm Committee (CGC) and applicable ad hoc reviewers and ranked in priority order for funding. All proposals and CGC prioritization are forwarded to USDA for a final decision on funding. Multiple year projects

are welcomed, but funding must be applied for each year and is subject to a progress review. Please note that in recent years, requested budgets have been capped in the range of $16,000-$18,000.

STANDARD EVALUATION PROPOSAL FORMAT FOR THE NPGS

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 (no overhead charges are permitted).

V. Personnel:
   a. What type of personnel will be used to 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).

The crop curator will enter evaluation data obtained into NPGS databases. Funding for data entry should be considered when developing proposals. Evaluation proposals covering several descriptors, such as several diseases, should give the cost and time frame for each descriptor along with the combined cost. Funding may only be available to cover one of the projects.

Submission deadline: Proposals must be submitted electronically as Word documents. Please submit electronic files of your proposals by October 15, 2003 to Dr. Martha Mutschler at: mam13@cornell.edu

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Inheritance of the force of fruit putting out (separation) from pedicel

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For study of the inheritance of the force of fruit putting out were taken contrastive parents - Vkusny-j, U, o (green back on the fruit base, plumy-type fruit form) and Volganin-j, u, O (without green back, round fruit). Both parents have jointless pedicels (gene j) that gives possibility to determine the force of fruit putting out once from plant with dynamometer having the special fixing seizure for fruit.

In P_1-P_2-F_1 from 9 to 20 plants, and in F_2 - 92 plants were evaluated. Every plant was estimated by 10 fruits and average forces of putting out for all individual plants were calculated. After that all variability of plants by force of fruit putting out (P_1-P_2-F_1-F_2) we divided by 10 classes and determined the frequency distribution for the parents and F_1-F_2 hybrids.

The parents were differed by borders of varying of trait. Their average data of force differed almost in 2 times (0.84 and 1.56 kg) (Table 1). In F_1 hybrid the intermediate inheritance of trait was observed.

Comparing of borders of varying of the trait of parents and hybrids we determined the number of F_2 plants with weak force of putting out (P_1-type) and the number of rest plants. The number of plants with weak force, similar to P_1, was 16 and its relation to the rest plants 16:76. This segregation corresponds to monogenic 23:69 under $0.10>P>0.05$; $X^2=2.84$. In accordance with rules of genetic nomenclature the symbol fpo for monogene of weak force of fruit putting out it is proposed. Its allelic gene, determining more force of putting out in the Volganin j variety, may be designated as fpo-1. Analogical monogenes of force of fruit putting out from plant in the cucumber crop were earlier already revealed (Avdeyev Y.I., 1994).

In our experiments with tomato some traits of every F_2 plant were described. The study showed that there is not visible difference by force of putting out between F_2-plants with u-gene and plants with U-gene (1.39 kg against 1.31 kg; difference 1.06 times), but considerable difference between F_2 plants distinguished by fruit form is manifested. Plants with plumy-type form of fruits had strength of putting out 1.33 times less than the rest group of plants (1.07 against 1.42 kg). Similarly, considerable difference between such groups of plants in the study of F_2 (VM-93 x Slivovidny Shtambovy) was seen (1.49 times).

The comparing of the average forces of fruit putting out in groups of F_2-plants, differed by genotypes, showed differences 1.08 (d^+-plants : d-plants), 1.01 (u : U) and 1.07 (j-2 : j^+) times.

From experiments we made conclusion, that the main gene, controlling the weak force of fruit putting out from pedicel, is connected with gene "o" - plumy-type (ovate) form fruit. Small genes with forces of influence on trait 3,5-7 times less than the main genes (fpo, fpo-1) are connected with genes d, j-2 and "u" (in some varieties) and may be with others. They cause of some level of transgression of the trait in F_2-plants.

The genetic analysis of the crossing over between genes fpo (fpo-1) and o (O) was carried out. The frequency of recombination with usual method was calculated

(Orlova,1991).The segregation in the F_2 on plants with plumy-type form fruits and rest plants is 22:70, that corresponds to monogenic inheritance: 0.90>P>0.75, X^2=0.06. This fact gives basis for the analysis of the dihybrid segregation data AB:Ab:aB:ab, which in our experiment was 62:8:14:8. Such segregation did not correspond to theoretical independence – 51.75:17.25:17.25:5.75, because X^2=8.57 ($X^2_{theor.}$=7.81). The frequency of genes recombination r=30.5±3.9%.

According to known data gene o (ovate) is located on chromosome 2, position 55 (Rick et al., 1987). In the segregation F_2 (Volganin, d x Mh. Florida, d^+) the gene fpo had not manifested coupling with the gene d (chrom. 2, position 70). It means that gene fpo there is on the other side of gene "o" on chromosome 2, or in the position 25, near with gene "mgh" (marginal necrotic). Gene fpo may be used in the breeding of varieties suited for combine harvesting.

Table 1.

Inheritance of the force of fruit putting out in hybrid combination Vkusny-j x Volganin-j

Sample	Number of plants	The force of fruit putting out			Relation of number plants with weak force of putting out to rest plants in F_2
		average	min	Max	
Vkusny-j (P_1)	10	0.84±0.046	0.57	1.08	-
Volganin-j (P_2)	20	1.56±0.067	1.13	2.20	-
F_1 (P_1 x P_2)	9	1.08±0.089	0.74	1.43	-
F_2 (P_1 x P_2)	92	1.38±0.096	0.48	2.48	16:76
F_2 plants with different fruit form					
Plumy-type (ovate)	22	1.07±0.097	0.53	2.09	8:14
Rest group	70	1.47±0.098	0.48	2.48	8:62

Literature cited:

1. Avdeyev Y.I. Genetic analysis of stems and fruits traits of the *Cucumis sativus* L. J. Cytology and genetics, No. 5, 1994, p.34-46 (in Russian).
2. Orlova N.N. Genetic analysis. B. 1991, Moscow, p.317 (in Russian).
3. Rick C. Mutschler, M. Tanksley S. Linkage maps of the tomato. TGC Report, 37, 1987, pp. 5-34.

Mutation of fruit diameter

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In 1997 in the tomato variety Malinovka, forming plumy-type form (ovate) fruits 5-5.5 cm in length and 3.0-3.5 cm in diameter, we found one plant ($1:10^5$) with fruits, the length of which is equal to initial variety, but diameter decreased in 1.5-1.7 times. The mutant trait was inherited. The hybrid F_1 (mutant x Malinovka) had intermediate fruit diameter. In F_2 we found monohybrid segregation; 9 (small diameter) : (31 large diameter), X^2=0.133; 0.75>P>0.50. We also observed 1.3-1.5 times diminishing of fruit diameter in the spontaneous mutant of Bahtemir variety (frequency $1:8 \times 10^3$).

In 2002 year the spontaneous mutation of considerable decreasing of fruit diameter in the variety Transnovinka (sp, o, j-2, u) was found. The fruit diameter of the mutant was 2 times smaller than in Transnovinka variety (2.2 cm against 4.5 cm) (Figure 1). The length of fruit was not changed. The mutation was named "small diameter". It is known, that plumy form (ovate) of fruit is inherited as recessive monogene, named by symbol "o" and localized in the chromosome 2, position 55 (Rick et. al., 1987). Gene of round fruit (0) is its dominant allele (Kirillova et al., 1990).

Figure 1. Transnovinka variety on top, mutant fruit on bottom.

On the basis of the above-mentioned facts it is supposed existence two alleles of gene "o" and that both alleles of fruit form represent a cluster of two connected different monogenes, one of which is controlling length, and other width of fruit. Mutation of each of them leads to genetic change of fruit form. The existence of many alleles of both genes in

tomato genotypes may result in vast polymorphism of fruit forms. Besides the fruit form may be also conditioned by other nuclear genes, increasing the polymorphism of the trait.

In the tomato collection studied we observed varieties with fruit diameter from 2 to 12 cm in height and from 1.5 to 14 cm in width.

In connection with facts of the mutation of fruit diameter we propose to introduce together with described genes o-O, the registration genes of diameter by width (dfw - diameter of fruit width) and diameter by height (diameter of fruit height). The described gene of small diameter in the mutant of Transnovinka variety we propose to mark as dfw (d ~ 2.2 cm) and its allele in initial variety of Transnovinka as dfw-1 (d .~ 4.5 cm).

Literature cited:

1. Rick C., Mutschler M., Tanksley S. Linkage maps of the tomato. TGC Report, No. 37, 1987, pp. 5-34.
2. Kirillova G., Lukianenko A. Genetics of tomato. B. Genetics of cultural crops. Leningrad, 1990, pp. 164-206 (in Russian).

Heat tolerance and bacterial wilt resistance of tomato genotypes in the humid tropics of Kerala.

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The warm humid tropical climate characterized by high day and night temperature and rainfall leading to high humidity makes it extremely difficult to grow the large fruited fresh market tomatoes in Kerala. This coupled with high soil acidity causes the bacterial wilt incited by *Ralstonia solanacearum* resulting in complete devastation of the crop. Hence, to identify tomato genotypes suitable for the humid tropics of Kerala, a study was taken up at the Department of Olericulture, College of Agriculture, Vellayani, Thiruvananthapuram, Kerala. The experimental site is located at 8.5º N latitude and an altitude of 29.0 m above MSL.

Forty two genotypes collected from different sources (Table 1) were evaluated in a randomized block design with two replications during June to September (South West monsoon period). The mean day and night temperature for the crop period was 29.4º C and 23.8º C. The rainfall received was 652.9 mm spread over 66 days. The land selected for the experiment was a bacterial wilt sick plot wherein a solanaceous crop was cultivated previously.

Observations on fruit set, pollen sterility, yield and bacterial wilt were recorded. The fruit set percentage ranged from 17.57 in LE 11 to 70.57 in LE 46. The lowest percentage of pollen sterility was noticed in LE 30 (2.31) whereas the line LE 36 recorded the maximum (71.25). The highest yielder LE 34 (1967.5 g / plant) recorded high fruit set (65.83%) and low pollen sterility (3.66%). High temperature often results in low fruit set due to pollen sterility, stigma elongation and low pollen germination (Rudich, *et al*., 1977; Weaver and Timm, 1989).

The correlation studies revealed significant correlation between fruit set and yield (0.5153) whereas the correlation of pollen sterility with fruit set and yield was negative, though not significant (- 0.1394 and - 0.1922). Wessel-Beaver and Scott (1992) reported strong positive correlation between fruit set and yield. As high fruit set ability is controlled by dominant genes (Hanson *et. al*, 2002), the lines with high fruit set *viz*. LE 46, LE 38 and LE 34 may be of use in further breeding to obtain a high yielding variety.

The results of the observations on bacterial wilt incidence under field conditions revealed that 20 accessions were resistant whereas, four accessions showed 100 per cent bacterial wilt. Screening under artificial epiphytotic condition is essential to confirm the resistance of these 20 accessions.

The highest yield was recorded by LE 34 followed by LE 1 and LE 22. They were also resistant to bacterial wilt. They possessed high fruit set ability and pollen viability and can be considered as the high temperature tolerant accessions suitable for the humid tropics.

References

Hanson, P. M., Chen, J. T. and Kuo, G. 2002. Gene action and heritability of high temperature fruit set in tomato line CL 5915. *HortScience*, **37**: 172- 175.

Rudich, J., Zanski, E. and Regev, Y. 1977. Genotypic variation for sensitivity to high temperature in tomato: pollination and fruit set. *Bot. Gaz*. **138**: 448- 452.

Weaver, M. L. and Timm, H. 1989. Screening tomato for high temperature tolerance through pollen viability tests. *HortScience*, **24**: 493- 495.

Wessel- Beaver, L. and Scott, J. W. 1992. Genetic variability of fruit set, fruit weight and yield in tomato population in two high temperature environments. *J. Amer. Soc. Hort. Sci.* **117**: 867- 870.

Table 1.Heat tolerance and bacterial wilt incidence of tomato genotypes

Accession No.	Genotype	Source	Fruit set (%)	Pollen sterility (%)	Yield / plant (g)	Bacterial wilt (%)
LE 1	Xiang Fan Quei-1	Changsha, Hunan, China	47.60	18.23	1774.78	0
LE 2	Neptune	Univ. Florida, Bradenton	53.08	3.42	1130.79	15.70
LE 4	Solar Set	Univ. Florida, Bradenton	61.91	6.59	1606.07	14.25
LE 5	Fla 7156	Univ. Florida, Bradenton	44.77	9.10	992.11	95.00
LE 6	Fla 7171	Univ. Florida, Bradenton	36.16	6.31	1066.28	85.71
LE 8	Pant T 3	Pantnagar, India	33.44	18.91	1681.00	17.15
LE 10	Sakthi	KAU, India	65.14	10.40	1208.57	0
LE 11	Heinz 1370	USA	17.57	2.81	1245.05	45.36
LE 12	Ronco	Hybrid , India	49.67	47.19	1116.35	17.15
LE 13	Sele	Hybrid , India	40.71	14.29	1503.96	4.25
LE 14	Tolstoi	Hybrid , India	63.99	17.33	1537.01	4.25
LE 15	Benito	Hybrid , India	42.37	20.00	1365.12	12.15
LE 16	Needhari	Hybrid , India	64.16	8.23	1539.75	4.25
LE 17	Yogi	Hybrid , India	44.23	17.33	1583.75	58.55
LE 18	Century 12	Hybrid , India	39.78	34.29	1268.09	29.28
LE 20	Co 1	TNAU, India	50.20	3.27	1086.50	66.05
LE 21	Co 3	TNAU, India	54.26	7.26	1628.90	61.45
LE 22	Mukthi	KAU, India	61.71	12.56	1770.87	0
LE 24	LE 615	KAU, India	27.32	6.35	419.85	0
LE 25	LE 560	KAU, India	47.51	21.30	1474.99	0
LE 26	LE 558	KAU, India	28.56	22.40	594.15	64.28
LE 27	LE 571	KAU, India	60.95	16.60	1227.14	45.21
LE 28	LE 578	KAU, India	23.48	17.73	800.00	8.30
LE 29	LE 584	KAU, India	42.93	2.55	1182.37	0
LE 30	LE 556	KAU, India	44.21	2.31	1218.52	17.15
LE 31	LE 568	KAU, India	51.03	5.88	1105.00	0
LE 32	LE 14	KAU, India	45.53	14.22	950.85	0
LE 33	LE 4	KAU, India	42.43	34.62	1056.00	0
LE 34	LE 16	KAU, India	65.83	3.66	1967.50	0
LE 35	LE 43	KAU, India	46.41	27.55	1406.54	0
LE 36	LE 65	KAU, India	25.58	71.25	1420.00	28.57
LE 37	CLN 2001 C	AVRDC, Taiwan	44.12	27.40	626.85	0
LE 38	CLN 2026 C	AVRDC, Taiwan	69.91	10.26	1531.66	0
LE 39	CLN 2026 D	AVRDC, Taiwan	62.33	34.96	1731.66	0
LE 40	CLN 2026 E	AVRDC, Taiwan	45.41	23.95	1471.54	0
LE 42	CLN 1466 P	AVRDC, Taiwan	64.31	46.92	1358.00	0
LE 43	CLN 1466 S	AVRDC, Taiwan	54.21	9.38	926.28	0
LE 44	CLN 1621 E	AVRDC, Taiwan	42.75	39.30	1032.82	0
LE 45	CLN 1621 F	AVRDC, Taiwan	52.75	36.97	1323.83	0
LE 46	CLN 1621 N	AVRDC, Taiwan	70.57	14.16	961.73	0
LE 47	Pusa Sheetal	IARI, New Delhi	38.49	13.64	682.00	83.50
LE 48	Pusa Gaurav	IARI, New Delhi	45.96	18.87	1095.55	86.43

Improved maintenance of the tomato-like *Solanum* spp. by grafting

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We have struggled over the years to reproduce the tomato-like *Solanum* species in our collection. *S. juglandifolium* is difficult because some accessions refuse to flower under our greenhouse conditions, even during short-day regimes which induce other sensitive species. Its close cousin *S. ochranthum* flowers somewhat more readily, but only after growing so tall that it becomes difficult to handle. Finally, the xerophyte *S. sitiens* is hypersensitive to soil-borne fungal pathogens, usually brought on by over watering or transplant stress. As a result, many plants succumb before seed can be harvested, resulting in inadvertent selection and loss of genetic diversity in subsequent generations. Our repeated attempts to ameliorate this problem by careful watering, applications of fungicides, or use of specialized soil mixes have met with limited success.

Each of these challenges can be overcome by grafting the nightshades onto a tomato rootstock. Rick (TGC 37:62) used *L. esculentum* cv. VF36 as a graft rootstock to promote flowering in *S. juglandifolium*. However, during the time it takes to reproduce this species (up to ~ 2 years), rootstocks would eventually lose vigor or die altogether due to attack by Phytophthora root rot and other diseases. We therefore tested the interspecific hybrid F_1 *L. esculentum* cv VF36 x *L. pennellii* LA0716 as a potential graft rootstock. This genotype has several advantages for grafting applications. First, the hybrid is amazingly vigorous in its vegetative growth, as anyone who has had the misfortune to include it in a field trial can attest (a single plant will quickly overwhelm rows on either side). Secondly, the *L. pennellii* parent contributes dominant resistances to multiple races of Fusarium wilt. As a result, roots of the hybrid are either resistant to or can 'outgrow' our common soil-borne diseases, and plants can be maintained indefinitely in pot culture. Thirdly, the hybrid has wide graft compatibility, not only with the *Solanum* spp. in question, but also with more distantly related Solanaceous crops, such as eggplant (*S. melongena*) and pepper (*Capsicum* spp.). Finally, *L. pennellii* and its hybrid with tomato are daylength insensitive, and flower continuously throughout the year, with relatively few leaves between successive inflorescences (sympodial index = 2 in *L. pennellii*). Although the hybrid has an annoying tendency to sprout adventitious shoots, these are easily distinguished from scion branches and pruned off.

Standard cleft type grafts were made when the rootstock was at the ~4-5 true leaf stage, using stems of roughly the same diameter, from each of the three *Solanum* spp. Graft unions were wrapped with Nescofilm, and scion branches were pruned to several axillary buds, then enclosed in a Ziploc plastic bag for 10-14 days. Only a small proportion (<10%) of grafts failed on the first attempt, generally due to a poor match in stem diameter/age, or Botrytis infection. Both graft partners recovered readily from wounding, with shoots of the *Solanum* spp. becoming woody and strong, and growing vigorously. For *S. juglandifolium* (LA2120 and LA2788) and *S. ochranthum* (LA2166 and LA2682), grafts were made starting

in early spring, and by July, nearly 100% of plants (4-34 per accession) were flowering. Plants remained more compact and easy to train than ungrafted shoots, continued to flower throughout the year, and set abundant fruit upon cross pollination. Grafts of *S. sitiens* (LA4105, and LA4110 - LA4114) were made with equal success at various times of the year, and plants flowered prolifically within 1-2 months. Grafted *S. sitiens* plants were free of the usual root rots, vascular wilts, and other diseases, and produced mature fruit and seed without interference. In light of its positive aspects for grafting, as well as other potential uses, we now maintain seed of the rootstock genotype (LA4135 = VF36 x LA0716) for distribution to interested researchers.

Chromosome location of tomato ESTs related to carbon metabolism

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In order to screen for putative candidate genes linked to sugar/acid metabolism content in tomato fruit, we selected 48 EST clones in the TIGR tomato EST database (http://www.tigr.org/tdb/tgi/lgi/). These clones were located on the tomato map using the population of introgression lines (ILs) having one segment of *L. pennellii* (LA716) in a *L. esculentum* (M82) background (Eshed and Zamir, 1995). The 75 ILs allow the genome to be segmented into 107 bins (Pan et al, 2000; http://www.sgn.cornell.edu/). The IL population was connected to the high-density map of tomato (Tanksley et al, 1992) by probing all the ILs with the RFLP markers from the framework F2 map (Pan et al, 2000). The ESTs were mapped by RFLP after screening for polymorphism using four restriction enzymes (EcoRI, EcoRV, Hind III, and XbaI). Genomic DNA extraction, digestion, and hybridization were as described in Saliba-Colombani et al (2000). A few ESTs were also mapped in an intraspecific population (Saliba-Colombani et al, 2000) and their location in the IL map was deduced from the common RFLP markers.

All fourty eight ESTs involved in carbon metabolism were mapped (Table 1). They represented enzymes involved in Calvin cycle, glycolysis, TCA cycle, sugar and starch metabolism, transport and a few other functions. They revealed 57 loci. Their involvement as candidate genes for QTLs related to carbon metabolism remains to be studied.

References

Eshed Y, Zamir D (1995) An introgression line population of *Lycopersicon pennellii* in the cultivated tomato enables the identification and fine mapping of yield-associated QTLs. Genetics 141: 1147-1162

Pan Q, Liu Y-S, Budai-Hadrian O, Sela M, Carmel-Goren L, Zamir D, Fluhr R. (2000) Comparative genetics of nucleotide binding site-leucine rich repeat resistance gene homologues in the genomes of two dicotyledons: tomato and Arabidopsis. Genetics 155: 309-322

Saliba-Colombani V, Causse M, Gervais L, Philouze J (2000) Efficiency of AFLP, RAPD and RFLP markers for the construction of an intraspecific map of the tomato genome. Genome 43: 29-40

Tanksley SD, Ganal MW, Prince JP, de Vicente MC, Bonierbale MW, Broun P, Fulton TM, Giovannoni JJ, Grandillo S, Martin GB, Messeguer R, Miller JC, Miller L, Paterson AH, Pinedo O, Roder MS, Wing RA, Wu W, Young ND (1992) High density molecular linkage maps of the tomato and potato genomes. Genetics 132: 1141-1160

Table 1: Chromosomal segments containing the EST.

The most likely function is indicated together with the library of origin, the species showing the highest percentage of homology, the clone, EST and TC numbers. The bin location corresponds to the chromosome number followed by a letter corresponding to the chromosome segment. When the location was obtained on the first subset of 50 ILs, it is indicated by (50), and sometimes, two successive bins are proposed; the ESTs mapped in the intraspecific map are indicated in the bin location by CL.

	Gene Code	Function	Library of origin	Homology : species and % DNA Id	Unigene TC	EST	Clone	Bin location
	Calvin cycle, photorespiration (chloroplast)							
1	**Tpi**	triose P isomerase chp	Pseudo. res.	87% S. ole.	TC116802	254452	cLER6C10	1-H (50)
2	**Pgk**	Phosphoglycerate kinase chp	tomato shoot	98% S. tub.	TC123837	241836	cLEB3N22	7-H
3	**Fbpa (1)**	Fructose biphosphate aldolase chp	Pseudo. res.	96.5% N. pan.	TC115763	255130	cLER9O11	1-H (50)
4	**Fbpa (2)**	Fructose biphosphate aldolase chp	tomato shoot	91.6% N. pan.	TC123871	242757	cLEB8C17	3-E (50)
5	**Fbpa (3)**	Fructose biphosphate aldolase chp	tomato shoot	95.2% N. pan.	TC123875	242661	cLEB8K5	2-B
6	**G3pdh**	Glyceraldehyde 3P dehydrogenase chp	Pseudomonas susceptible	91.8% N. tab	TC123860	259181	cLES4J22	3-D, 4-C
	Glycolysis, oxidative pentose phosphate pathway (cytosol)							
7	**G3pdh (2)**	Gly3P dehydrogenase	Pseudomonas susceptible	99% S. tub.	TC115908	248485	cLES1O9	11-B
8	**Ppc3 (2)**	PEPC LePPC3	tomato ovary	88.7% A. th.	TC127922	249198	cLED24K5	5-A
9	**Ppck**	PEP carboxykinase	tomato ovary	99% L. esc.	AI486825	245147	cLED11I21	8-E
10	**Hk2 (2)**	Hexokinase LeHK2	tomato ovary	99.4% L. esc.	TC119716	245474	cLED9E12	6-D
11	**Eno**	Ethylene-responsive enolase	tomato ovary	100% L. esc.	TC123931	244947	cLED9L20	9-C, 10-F
12	**Fk (1)**	Fructokinase	tomato ovary	80% A. th.	AI487966	246288	cLED19J22	4-I
13	**Fk (2)**	Fructokinase	tomato ovary	100% L. esc.	TC116377	249263	cLED24E14	6-E, 5-A
14	**Pfpa**	6 phosphofructokinase, PFP alpha subunit	tomato ovary	90.3% S.tub	TC124642	243736	cLED7O17	12-G
15	**Pfpb**	6 phosphofructokinase, PFP beta subunit	tomato ovary	99% S. tub.	TC116691	249287	cLED24M16	2-G (CL)
16	**Pgi**	G6P isomerase cyt	tomato shoot	85.2% C. gra.	TC115933	242354	cLEB8K2	12-D
17	**Tpi**	triose P isomerase cyt	Pseudomonas susceptible	91.6% P. hyb.	TC116205	258698	cLES3M17	4-C
	Sugars and starch metabolism (cytosol, apoplast)							
18	**Stp**	starch phosphorylase	tomato ovary	98.6% S. tub.	TC118244	244550	cLED5N5	3-D, 3-E
19	**Inv5**	Invertase Le LIN5	tomato ovary	99.3% L. esc.	TC125260	248779	cLED21P10	9-D (CL)
20	**Udpg**	UDPG pyrophosphorylase	tomato ovary	99.4% S. tub.	TC124052	243067	cLED3C19	11-C
21	**Urt**	UDPG pyrophosphorylase	Pseudo. res.	99.4% S. tub.	TC124052	256075	cLER13N22	11-C (50)
22	**Inhi**	Invertase inhibitor	tomato ovary	98.8% L. esc.	TC117406	249221	cLED24I21	12-H
23	**Pgm**	phosphoglucomutase	Pseudo. res.	96.2% S. tub.	TC123362	249326 / 249339	cLER1G13	3-B
	TCA cycle (mitochondria)							
24	**Aco**	cytosolic aconitase	tomato ovary	93.0% N. tab.	TC116361	244107	cLED4K20	7-E
25	**Idh**	cytosolic Isocitrate dehydrogenase NADP	tomato ovary	86% H. sap.	AI487357	245679	cLED13C18	2-A (CL)
26	**Mdh**	malate dehydrogenase mitochondrial	tomato shoot	87.5% C. vul.	TC116427	242126 / 242132	cLEB3L13	1-I (CL)
27	**Me**	malic enzyme NADP cytosolic	Pseudo. res.	99% L. esc.	TC124237	248835 / 248819	cLES1A11	5-E
28	**Cis**	citrate synthase mitochondrial	Pseudomonas susceptible	97.6% S. tub.	TC117430	262252	cLES15O17	1-D (50)
29	**Sdh**	succinate dehydrogenase (ubiquinone)	tomato ovary	89% A. th.	TC116576	248781	cLED21P12	2-L

Transport								
30	**VatpB**	vacuolar ATPase, B subunit	tomato ovary	97.5% A. th.	TC98991	244301	cLED3H2	10-B
31	**VatpB**	vacuolar ATPase, B subunit	tomato ovary	97.9% N. tab.	TC116119	244235	cLED4D21	1-H, 10-B
32	**VatpE (1)**	vacuolar ATPase, E subunit	tomato ovary	88.7% L. esc.	TC124795	245076	cLED11F7	8-G
33	**VatpE (2)**	vacuolar ATPase, E subunit	tomato ovary	99.6% L. esc.	TC118357	245600	cLED11M13	8-A
34	**Vatp**	vacuolar ATPase		91% A.th.	TC124856		cLED23F24	4-B, 6-C
35	**Sut**	Sucrose carrier	tomato ovary	99.1% L. esc.	TC116887	243704	cLED7H11	11-C
36	**Hxt (2)**	Hexose transporter HT2	Pseudo. res.	100% L. esc.	TC117292	253148	cLER1D7	2-A, 2-I (CL)
37	**Hxt (3)**	Hexose transporter	Pseudo. res.	52.3% A. th.	TC117137	248869	cLER1M15	1-G (50)
38	**Hxt (4)**	Hexose transporter	Pseudo. res.	72.4% R. com.	AI774617	255717	cLER12J12	3-D
39	**Hxt (5)**	Hexose transporter HT1	Pseudo. res.	100% L. esc.	TC130952	257786	cLER19B17	8-GH (50)
40	**Hxt (6)**	Putative hexose transporter	Pseudo. res.	78.2% B. vul.	TC121028	258258	cLER20L10	1-I
41	**Hxt (7)**	Hexose transporter like protein	Pseudomonas susceptible	69,2% A.th.	TC131345	258464	cLES2O22	2-B
42	**Hxt (8)**	Putative hexose transporter ST3	Pseudomonas susceptible	99 % L.esc.	TC117919	258465	cLES2O24	9-G
43	**pTom75**	pTOM75 (RAMP Ripening Associated Membrane Protein)	Pseudo. res.	100% L. esc.	TC124034	253417	cLER2G6	8-G
44	**PPcyt**	cytosolic pyrophosphatase	tomato ovary	83% O.sat.	TC104308	245190	cLED7P14	2-I
Miscellaneous								
45	**Hdec**	Histidine decarboxylase	tomato ovary	75.7% L. esc.	TC124717	243128	cLED3A23	8-D
46	**Thio (1)**	Acetoacetyl coA thiolase	tomato ovary	84% A.th.	TC117209	243932	cLED6J18	5-D, 7-A, 7-D
47	**Thio (2)**	3-ketoacyl-CoA thiolase	tomato ovary	88% A. th.	TC115961	243859	cLED7E24	9-J
48	**Lpt**	Lipid transfer protein precursor	tomato ovary	68.1% N. tab.	TC125406	246579	cLED22K5	10-B

A method for DNA extraction from leaves in a 96-well format

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We describe here a microtiter-based method for rapid DNA isolation that was developed for tomato from leaf tissue that can be used directly as a genomic template for polymerase chain reaction (PCR). This method is useful for large-scale genotyping performed in marker-assisted selection programs, the screening of transgenic plants by PCR amplification and for fine mapping in large segregating populations. This latter application is necessary for high resolution mapping of Mendelian genes or quantitative trait loci (QTL) in projects aimed at map based cloning. Although several protocols are available for small DNA extraction (1, 2, 3), the 96-well format described here can enhance the productivity to hundreds of samples a day at reduced cost. The method was developed for mapping experiments in tomato but is also shown to be efficient for other crops, such as potato and melon. A single leaf disc is obtained from each individual plant using a single-hole paper punch that is placed in a 96-flat-well microtiter plate. The leaf samples can be kept in a -80°C freezer for extended periods and the final DNA product is sufficient for at least 10 PCRs. The entire procedure is performed in a 96-well microtiter plate, using a multichannel pipet, a swinging-bucket centrifuge (Eppendorf; 5810) and a 96-plate thermocycler (MJ PTC 225).

Protocol

- Collect a single leaf disc per plant using a single-hole paper punch. Put each disc at the bottom of a well (flat-bottom microtiter plate).
- Add 100 μl of grinding buffer (using a multichannel pipet).
- Grind the leaves gently with a seed crusher (HyPure HSC-200) using a rubber mallet (HyPure SCM-100).
- Incubate at 60°C for 20 min.
- While in incubation, take a new 96-well microtiter plate (with a round bottom). Put 100 μl of cold storage buffer.
- Transfer 50 μl from the leaf extract to the plate with storage buffer, mix by pipetting and put at -20°C for 20 min (this stage can last longer in order to group successive plates before centrifugation).
- Spin in a swinging-bucket centrifuge– 4000 rpm for 15 min.
- Discard supernatant and dry the plate upside down on a paper towel.
- Add 50 μl of TE and put in 60°C for 20 min.
- Take 5 μl for a 30-μl PCR in a 96-well microtiter plate. Perform PCR according to primer specifications.
- Add 3 μl loading dye to the wells and load 15 μl of the reaction on a 1.5% agarose gel. Using Owl D3-14 horizontal system (150 ml gel and four combs of 50 wells), it is possible to score the genotypes of 2 microtiter plates (192 samples). Loading can be performed using the multichannel pipet and it is suggested to do so before the gel is carefully submerged in the electrophoresis buffer.

Solutions:

- Grinding buffer: A mix of extraction buffer, nuclei lysis buffer and 5% sarcosyl in a 10:10:4 volume ratio.
-
- Extraction buffer (1 liter):

64 g	Sorbitol
12 g	Trizma base
1.7 g	EDTA

  Bring to pH 7.5 using concentrated HCl, keep at 4°C.
  Before use add 3.8 g of sodium bisulfite.

- Nuclei lysis buffer (1 liter):

20 g	CTAB
200 ml	1 M Tris pH 7.5
200 ml	0.25 M EDTA

  Mix all of the above. After CTAB dissolves completely, add 400 ml of 5M NaCl.
  Bring to pH 7.5 using concentrated HCl

- 5% Sarcosyl (1 liter): 50 g N-Lauroylsarcosine
-
- Storage buffer (1 liter):

800 ml	95% Ethanol
100 ml	2 M Sodium Acetate

  Bring to pH 7.0 using concentrated 5 M NaOH.

- TE; Tris EDTA buffer (100 ml)

1 ml	1 M Tris pH 8.0
40 μl	0.25 M EDTA

  Bring to pH 8.0 using 5 M NaOH.

Figure 1 demonstrates the segregation of 192 tomato plants for the PCR marker 91SP6. The plants were sown in 16 x 8 (columns x rows) trays and leaf disks from the seedlings were placed in the 96 microtiter plate for DNA isolation. All plants were sampled, extracted and genotyped on the same day. The genotype of the plants was verified using a conventional RFLP analysis with the PCR product. The time spent on extracting the DNA from 384 leaf samples (four plates) was only 2 h, for one person. This technique enables the genotyping of a large population in a short time to identify rare genetic events.

References

1. Deragon, J.M. and Landry, B.S. (1992) *PCR Methods Appl.* 3, 175-180.
2. Geuna, F., Hartings, H. and Scienza, A. (2000) *Anal. Biochem.* 278, 228-230.
3. Wang, H., Qi, M. and Cutler, A.J. (1993) *Nucleic Acids Res.* 21, 4153-4154.

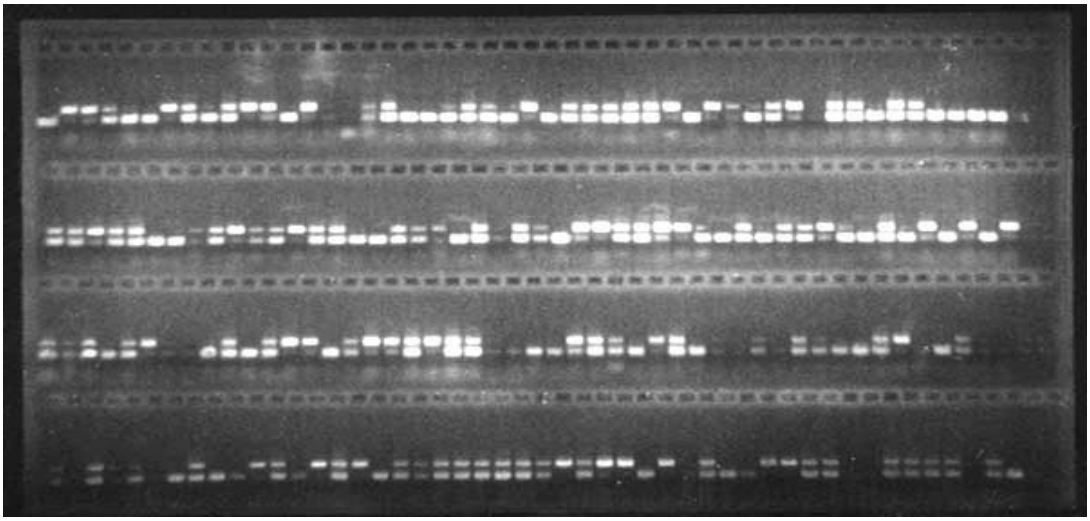

Figure 1. Segregation of 192 F_2 plants for the PCR marker 91SP6. Leaf disks of the seedlings were placed into 96-well microtiter plates and DNA was isolated according to the method described here. The DNA was used in a PCR and the products were loaded to a 1.5% agarose gel. The gel was run at 80 V for 45 min and then stained in 10 mg/ml ethidium bromide.

A self-compatible population of *Lycopersicon peruvianum* collected from N. Chile

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Lycopersicon peruvianum accession LA4125 was collected in 2001 on a TGRC-led trip to Northern Chile. It was found growing along a roadside in the valley of the Rio Camina, near the town of Camina, in the Tarapaca region (19°18'22" S, 69° 25'14" W, 2510 masl). This drainage represents the southernmost limit of the distribution of *L. peruvianum*, as far as we can tell. While growing plants for seed increase in the greenhouse at UC Davis in 2002-03 we observed fruit set without manual cross pollination, suggesting that it might be a self-compatible (Sc) strain. The nature of its mating system was investigated further by performing controlled self pollinations and recording fruit set. Of the 10 plants tested, all set fruit after manual self pollinations (Table 1). Selfed fruit harvested from three plants showed normal seed set (40-60 seeds/fruit). In addition, growth of pollen tubes was observed following self-pollination of three flowers from each of 10 plants using the aniline fluorescence method of Martin (1959). In all flowers we observed pollen tubes reaching the bottom of the style and the ovaries, consistent with a Sc reaction (Table 1). In contrast, flowers from known self-incompatible (SI) accessions of *L. peruvianum* or *L. chilense* showed the normal arrest of pollen tube growth in the upper half of the style following self pollination.

Inflorescences of LA4125 are unbranched, with enlarged bracts and curved anthers, all traits seen in SI *L. peruvianum*. Several morphological features of the Camina *peruvianum* differ from typical SI accessions, and are suggestive of self-pollination in the wild. First, overall leaf size is reduced, mostly due to a shorter rachis, with little apparent reduction in leaflet size or number of leaflets per leaf. Plants also have a more diminutive stature than outcrossing forms. Secondly, flowers are somewhat smaller, with less pronounced coloration of the corolla, and a moderate degree of stigma exsertion (average 1.5 mm). Finally, plants are morphologically uniform, and showed complete homozygosity at 11 isozyme loci (*6pgdh-1*, *-2*, *-3*, *Aco-1*, *-2*, *Got-2*, *-3*, *Idh-1*, *Pgi-1*, *Pgm-1*, and *Prx-2*).

Nearly all accessions of *L. peruvianum* examined to date are SI. Of the ca. 180 active collections maintained at our Center only one accession (LA2157) is fully self compatible (Rick 1986). The latter was collected at Tunel Chotano in Dept. Cajamarca, a location which is close to the northern boundary of this species' native distribution. LA2157 has all the hallmarks of a naturally self-compatible race, including small flowers with little or no stigma exsertion, heavy fruit set, and diminutive stature. Other accessions have been reported to segregate for Sc vs. SI, possibly as a result of artificial inbreeding. These include LA1708 and LA2172 from Cajamarca (R. Robinson, pers. comm.), and LA1278 from Dept. Lima (J. M. Guerra-Sanz, pers. comm.). Regarding the latter accession, we observed partial fruit set after selfing on only a minority of the plants tested (3 of 15). Examination of pollen tube growth revealed a nearly complete SI response. Based on our observations of pollen tube growth, fruit set, morphology, and marker homozygosity, LA4125 appears to have a

facultative mating system similar to LA2157. The geographic distribution of these two populations with respect to the rest of *L. peruvianum* is analogous to the situation in *L. hirsutum* and *L. pennellii*. All are predominantly SI, with Sc biotypes occurring at the northern or southern margins (Rick et al, 1979, Rick and Tanksley 1981).

An interesting aspect of the Camina Sc population is the nature of its unilateral incompatibility reaction. In the case of *L. peruvianum* LA2157 and *L. pennellii* LA716, the Sc biotype hybridizes successfully as the male parent with an SI accession and the progeny exhibit the same level of self-compatibility as the parent (Hardon 1967, Rick 1986). When LA4125 is crossed as the male parent with an SI *L. peruvianum* accession the cross fails, although the reciprocal cross is fully compatible (Table 2). Like LA716, styles of LA4125 reject pollen of fully self-compatible (SC) *L. esculentum*. These observations suggest that expression of self-compatibility in LA4125 is fundamentally different from that manifested by LA716. The former appears to carry a lack of function mutation for pollen phenotype, whereas the latter expresses a self-fertility allele that is functional on styles with SI activity. For a discussion of symbols used to describe compatibility reactions (SI, Sc, SC, and UI) and evolutionary theory see Lewis and Crowe (1958).

Literature Cited

Hardon, JJ. 1967. Unilateral incompatibility between *Solanum pennellii* and *Lycopersicon esculentum*. Genetics 57:795-808.

Lewis, D and Crowe, LK. 1958. Unilateral incompatibility in flowering plants. Heredity 12:233-256.

Martin, FW. 1959. Staining and observing pollen tubes in the style by means of fluorescence. Stain Technology 34:125-128.

Rick, CM. 1986. Reproductive isolation in the *Lycopersicon peruvianum* complex. In: D'Arcy WG (ed) Biology and Systematics of the *Solanaceae*. Columbia University Press, New York, pp 477-495.

Rick CM, Fobes JF, and Tanksley SD. 1979. Evolution of mating systems in *Lycopersicon hirsutum* as deduced from genetic variation in electrophoretic and morphological characters. Plant Sys Evol 132:279-298.

Rick CM, and Tanksley SD. 1981. Genetic variation in *Solanum pennellii*: Comparisons with two other sympatric species. Plant Sys Evol 139:11-45.

Table 1. Results of controlled self pollinations of individual plants from LA4125 (TGRC pedigree 02L7141). Phenotype describes the self compatible reaction when pollen tubes were observed throughout the style and in the ovaries.

02L7141 Plant ID	# Styles stained	Pollen tube observed	Phenotype	# Flowers selfed for fruit	# Fruit set
-2	2	in ovaries	Sc	7	2
-4	3	in ovaries	Sc	3	3
-5	3	in ovaries	Sc	5	4
-7	3	in ovaries	Sc	5	1
-10	2	in ovaries	Sc	14	13
-11	4	in ovaries	Sc	9	8
-12	3	in ovaries	Sc	8	4
-14	3	in ovaries	Sc	1	1
-15	3	in ovaries	Sc	9	8
-54	3	in ovaries	Sc	4	4

Table 2. Results of cross pollinations involving LA4125. Mating system describes the species (peruv=*L. peruvianum*, chil=*L. chilense*, penn=*L. pennellii*, and esc=*L. esculenum*) and the self compatibility reaction. Phenotype describes a compatible cross [C] where pollen tubes were observed throughout the style and in the ovaries or unilaterally incompatible [UI] where pollen tubes showed a definitive arrest in the upper 1/3 of the style.

Female	Accession	Mating system	Male	Accession	Mating system	# Styles stained	Pollen tube observed	Phenotype
02L7141	LA4125	peruv Sc	00L3290	LA1947	peruv SI	3	in ovaries	C
00L3290	LA1947	peruv SI	02L7141	LA4125	peruv Sc	3	arrested in upper 1/3 of style	UI
02L7141	LA4125	peruv Sc	02L7185	LA4118	chil SI	3	in ovaries	C
02L7185	LA4118	chil SI	02L7141	LA4125	peruv Sc	2	arrested in upper 1/3 of style	C
00L3290	LA1947	peruv SI	03L8066	LA716	penn Sc	3	in ovaries	C
02L7141	LA4125	peruv Sc	03L8066	LA716	penn Sc	3	in ovaries	C
03L8066	LA716	penn Sc	02L7141	LA4125	peruv Sc	3	bottom of the style	C?
03L8065	LA3475	esc SC	02L7141	LA4125	peruv Sc	2	in ovaries	C
02L7141	LA4125	peruv Sc	03L8065	LA3475	esc SC	3	arrested in upper 1/3 of style	UI

Effect of TYLCV infection on fruit yield of tolerant greenhouse tomato cultivars

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Introduction

The purpose of this study was to evaluate the effect of *Tomato Yellow Leaf Curl Virus* (TYLCV-Is) infection on fruit yield in commercial and experimental cultivars that are resistant or tolerant to this virus. Since the virus is present in the resistant plants (Cohen and Antignus, 1994) we prefer to use the term tolerance instead of resistance. Although the amount of the virus in tolerant plants is significantly less than in susceptible ones the yield in infected tolerant plants is affected. In this study we compared six cultivars with different levels of tolerance to the standard susceptible cultivar.

Material and Methods

Cultivars:
Anastasia (Bruinsma) High level of tolerance. (Ana.)
Boloudo (Petoseed) High level of tolerance. (Bol.)
916- Amareto (Zeraim) - Low level of tolerance for TYLCV-Is. This cultivar was tested in the TBRT- Guatemala and had good tolerance to the Central American virus isolates (no symptoms in field trial in the Seminis experimental station in Guatemala).
922- Tovi-Green (Zeraim) -Medium level of tolerance.
932 - Tovi-Can (Zeraim) -High level of tolerance.
957-(Zeraim) -Medium level of tolerance – Based on TY1 gene.
144-Daniela (Hazera)-Susceptible control.

Seedlings were obtained from a commercial nursery (Speedling) 25 days after sowing. Ten plants of each cultivar were inoculated by caging the seedlings for 4 days before planting with viruliferous whiteflies in an insect proof greenhouse. Another 10 plants of each cultivar were kept until planting in the nursery, protected from whiteflies. All the seedlings were treated with Confidor before transplanting. The infected and the protected plants were planted on September 15 in a commercial insect proof greenhouse and grown under standard conditions. All red fruits were harvested five times during the growing season, from the end of January to the beginning of May.

Results

Four weeks after planting TYLCV symptoms were detected in all of the infected susceptible control plants. The less tolerant cultivar 916 had clear but milder symptoms of the disease, which were visible throughout the season. The medium tolerant cultivars 922 and 957 showed very mild symptoms during the early stage of growth. The symptoms became very

difficult to detect later on. At harvest stage the plants of 922 and 957 were fully recovered, i.e. symptomless. The other cultivars: Anastasia, Boloudo and 932-Tovi-Can were symptomless throughout the trial.

In all the tested cultivars, the infected plants had smaller fruits and lower yield compared to the non-infected controls, regardless of the presence of TYLCV symptoms in the leaves (Figure 1). There seems to be some relation between the level of tolerance and the decrease in fruit weight (Figure 2). In the symptomless cultivars: Fruit size decreased by 6-10% only, while in the less tolerant cultivars 916 and 922 the fruit size decreased by 36% and 16%, respectively. Fruit size of the susceptible control decreased from 140 g to 80 g i.e. 42%, with fruit of non-marketable quality.

Percent yield loss is given in Figure 3. In the highly tolerant – symptomless cultivars, the yield loss varies from 17% (932-Tovi-Can), up to 36% (Boloudo). The yield loss of the medium tolerant cultivars 922 and 957 was about 25% and that of the susceptible control 144 (Daniela) reached 72%.

Conclusions

1. Infection of TYLC virus causes damage to tolerant cultivars, in terms of yield and fruit weight.
2. Mild symptoms of the virus, visible during early growth, are not an indication for increased loss of yield when compared to symptomless tolerant cultivars.

Literature cited

Cohen, S., Antignus, Y. 1994. Tomato yellow leaf curl virus, a whitefly-borne Geminivirus of tomatoes. Adv. Dis. Vector Res. 10: 259-288

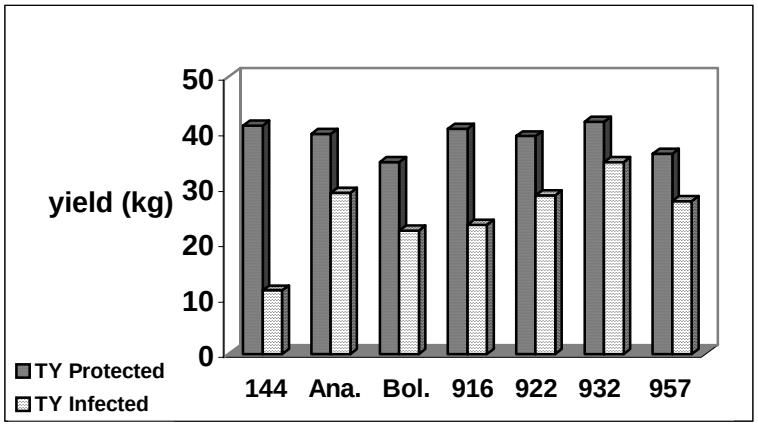

Figure 1. Yield of 10 plants of protected and of TYLCV infected tomato cultivars.

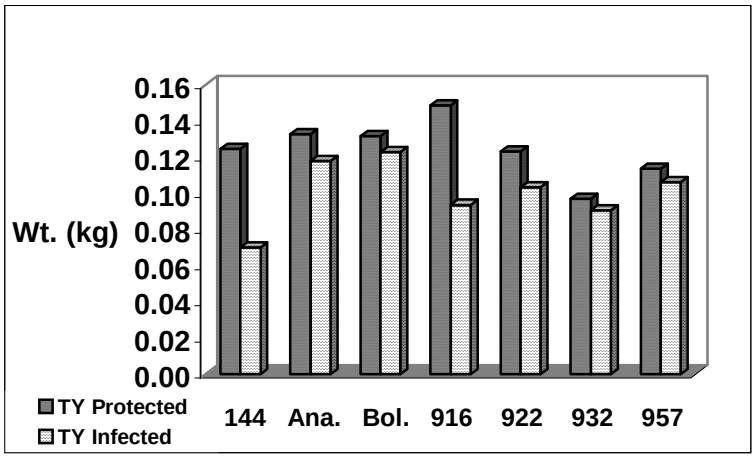

Figure 2. Fruit weight of TYLCV infected and of protected tomato cultivars.

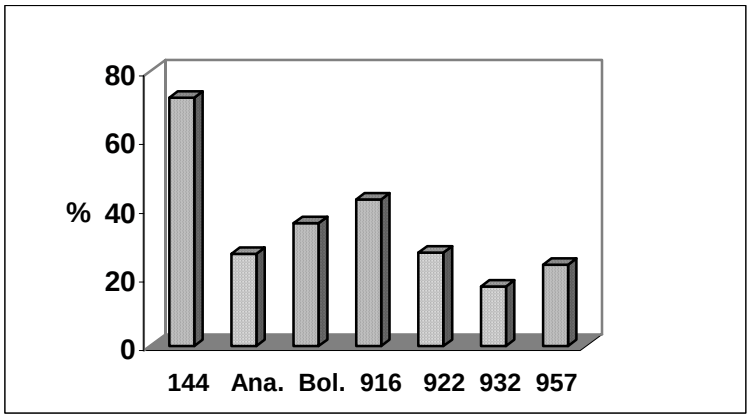

Figure 3. Yield loss (%) in TYLCV infected tomato plants.

Characterization of North American heirloom tomatoes

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The interest in heirloom or traditional varieties of tomato is increasing, notably for specialty markets and for organic agriculture (Nuez, 1995). North America is home to an important array of heirloom varieties of tomato. Some of them were introduced by European inmigrants, while others are the result of the selection by growers, gardeners and local plant breeders interested in developing tomatoes with improved taste but also with distinctive traits, like unusual shapes and colors (Male, 1999). Many of these varieties are named after its breeder or somebody to be honored, or make reference to its place or country of origin, and/or to a particular attribute (on many occasions exaggerated), like the color.

In this work, 59 heirloom tomatoes from North America were grown in Valencia, Spain, under greenhouse conditions and were characterized by four fruit attributes (mean fruit weight, predominant color of ripe fruit, shape and ribbing) using IPGRI descriptors (1996). With these data, the tomato varieties have been classified into groups (Table 1).

In general, low variation was found within each variety, probably as a consequence of the high degree of homozygosis and purity of these materials. On the contrary, a high degree of variation among varieties was found for the traits studied and, consequently, several different morphotypes could be distinguished (Table 1).

Although mean fruit weight ranged between 5 g (‘Moira’) and 265 g (‘Orange Strawberry’), most varieties were considered as small-medium sized (<100 g). Regarding fruit predominant color, most varieties were red-colored, although other colors, like yellow, orange, pink, green, as well as intermediate colors, were also present (Table 1). In most varieties, ripe fruit color was uniform, though variegated (e.g. ‘Green Zebra’) or bicolor (e.g. ‘Regina´s Bicolor’) varieties were also found. In addition, variation among varieties was found within each state of the color descriptor. Thus, within “red” varieties we observed from pale red (e.g. ‘Mankin Plum’) to dark red (e.g. those with the adjective “black”) varieties. The same was found in the “yellow” group: from pale colored (e.g. ‘Ivory Egg’ or ‘White Queen’) to golden yellow (e.g. ‘Yellow Pear’) varieties. Such variation within the same state of the color descriptor suggests the use of methods that allow an objective description of colors, like the “CIE L*, a*, b color space”. This would give more precise information on the color of each variety.

The most usual fruit shapes were flattened and rounded, though several elongated, heart-shaped, squared and pyriform varieties were also found (Table 1). As for fruit color, variation within a particular descriptor state was found.

Approximately, one fourth of the varieties had intermediate-strong ribbing (Table 1), which could even result in fruits that looked as if they were malformed, like in ‘Purple Calabash’. The other varieties showed weak or no ribbing. In general, little variation was found for the degree of ribbing among fruits from the same variety. However, some varieties like ‘Buckbee´s New 50 Day’ or ‘Mikado’ yielded fruits ranging from no ribbed to strongly ribbed. In these varieties, the stronger ribbing was found in fruits originated from fasciated flowers.

We also found an association of fruit size with fruit shape and ribbing. Thus, the higher the mean fruit weight of a variety, the higher proportion of flattened vs. round fruits. In the same way, the frequency of intermediate-strong ribbing (2-3) was higher in big-sized varieties than in small-sized ones. Because of that, there are no varieties with ribbed fruits and mean fruit weight lower than 30 g. In the same way, “yellow” varieties were usually small-fruited (<55 g). In addition, several varieties yielded pseudofruits, suggesting they are adapted to short growing seasons with cold periods.

Although we found a high degree of variation for the fruit traits we studied, several of them (in particular fruit color) show a mono or oligogenic control. Therefore, despite the variation observed, the genetic bottleneck that this species suffered in the process of introduction from Europe to North America (Rick, 1978) suggests that, despite their unquestionable value, the genetic base of North American heirloom varieties might be narrow.

Literature cited

IPGRI 1996. Descriptors for tomato (*Lycopersicon* spp.). International Plant Genetic Resources Institute, Rome.

Male, C.J. 1999. 100 heirloom tomatoes for the American garden. Workman Publishing Company, New York.

Nuez, F. 1995. Desarrollo de nuevos cultivares, pp.625-669. In: F. Nuez (ed.). El cultivo del tomate. Mundi-Prensa, Madrid.

Rick, C.M. 1978. The tomato. Scientific American 239:76-87.

Table 1. Fruit traits of 59 heirloom tomato varieties from North America. Fruit shape and color for each variety are included between brackets. Fruit shape is coded with a letter (F=flattened, R=rounded, H=heart-shaped, E=elongated, S=squared, and P=pyriform) and fruit ribbing with a number (0=no ribbing, 1=weak, 2=intermediate and 3=strong).

Fruit weight	Predominant skin color	Variety (shape/ribbing)
≤ 30 g	Yellow	Dr. Carolyn Ivory Cherry (R/0), Esther Hess Yellow Cherry (R/0-1), Garden Peach (F/1), Green Gage (F-S/0), Hssaio Hungshih (S/0), Yellow Pear (P/0)
	Orange	Aunt Ruby´s German Cherry (R/0)
	Red	American Beauty (R-H/1), Aunt Ruby´s German Black (H/0-1), Black Plum (E-S/0), Grape (R/0), Moira (R/1), Robin Dwarf (R/0)
31-55 g	Yellow	Banana (E/1), Green Zebra (F/1), Old Ivory Egg (E/1), Livingston´s Golden Queen (R/2)
	Orange	Orange Banana (F/2)
	Red	Black Pearl (R-H/0), Cardinal (F/1), Doublerich (F-R/1), Eva´s Purple Ball (F/1), Livingston´s Globe (R/1), Livingston´s Magnus (F-R/0-1), Maule´s Earliest of All (F/3), Maule´s Success (F/1), Paragon (F/1), Oli Rose de St Dominique (E/0), Optimus (F/1)
	Red-Pink	Purple Calabash (F/3)
56-100 g	Yellow	White Queen (F/2)
	Orange	Livingston´s Favorite (R/0)
	Orange-Red	Burpee's Matchless (F/1), Early Large Red (F/1), Maria Agustina (H-E/0-1), Mikado (F/1-3), Regina´s Bicolor (F/2)
	Red	Berkshire Oxheart (F/1), Berkshire Polish (F/1), Buckbee´s New 50 Day (F/0-3), Ed´s Fat Plum (F-R/1), Enormous (F/1), Livingston´s Marvelous (F-R/1), Northampton Italian Plum (E/1), Pruden´s Purple (F/2), Purple Brandy (F/2)
	Pink	June Pink (F-R/1)
101-170 g	Green	Aunt´s Ruby German Green (F/2)
	GreenYellow	Greeny Smith (F-R/2)
	Orange	Limmony (F/2)
	Red	Black Aisberg (F/1), Black from Tula (F/3), Carbon (F/1), Lutescent (F/1), Mankin Plum (E-S/0)
	Pink-Red	Newton Italian Plum (H/1)
> 170 g	Orange	Orange Strawberry (F-H/2)
	Red	Black Prince (F/3), Cuban Black (F/3)

An AFLP Marker-Based Linkage Map of *Solanum chacoense* Bitter Chromosome 1

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Introduction

Solanum chacoense Bitter, the Chaco potato, is a wild species related to the cultivated potato, *S. tuberosum* L. *Solanum chacoense* is diploid, tuberous, and self-incompatible, and is indigenous to northern Argentina and the surrounding areas. The species is of interest to plant breeders because some individuals produce leptine glycoalkaloids, which are believed to be factors in the resistance of *S. chacoense* to the Colorado potato beetle (CPB; *Leptinotarsa decemlineata* Say) (Kuhn and Löw, 1961). The leptines are a unique class of glycoalkaloids whose production and accumulation is foliar-specific (Kuhn and Löw, 1961; Sinden et al., 1986b). Since resistance-conferring glycoalkaloids are toxic to humans and accumulate in tubers, foliar-specific leptines offer an attractive opportunity to develop useful CPB host-resistance in *S. tuberosum,* and perhaps in related species.

In reciprocal F_1 crosses and backcrosses between high-leptine producing *S. chacoense* genotypes and nil-leptine genotypes, leptine content exhibited discrete distributions in most families with high and low classes of leptine-producing individuals, suggestive of genetic control by a single recessive gene. However, a number of families produced from crosses of high x low leptine-producers and low x low leptine-producers exhibited continuous distributions for leptine content, suggesting the presence of additional genetic factors that affect the inheritance of leptine glycoalkaloids in these *S. chacoense* populations (Ronning et al., 1998).

A RAPD marker, UBC370-1500, was identified in selected reciprocal F_1 families as being tightly linked to nil/low leptine content (Ronning et al., 1999). RAPD marker UBC370-1500 was mapped to chromosome 1 of potato and tomato (Ronning et al., 1999), near the site of a major QTL for solanidine accumulation in *S. tuberosum* x *S. berthaultii* (Yencho et al., 1998), suggesting that this region on chromosome 1 may be important in glycoalkaloid production. In this paper, we report results contributing to the construction of a marker-based linkage map of *S. chacoense* chromosome 1 using primarily AFLPs, plus a number of RAPD markers. The marker UBC370-1500 was used as an “anchor” to coordinate linkage data from five related F_1 families, derived from crosses between high x low and high x high leptine-producing lines that originated from three different *S. chacoense* accessions, in the construction of an integrated linkage map for this chromosome. The results presented are intended for further use by programs active in glycoalkaloids and marker-based research in Solanaceous species.

Materials and Methods

Plant Material: The five *S. chacoense* families utilized for map construction have been previously described (Ronning et al., 1998, 1999). Lines 55-1 and 55-3 are sibling selections from PI 320387 and produce high and nil leptine as a percentage of total foliar glycoalkaloids, respectively. Line 8380-1 is a sibling selection from PI 458310 and produces high levels of leptine (Sinden et al., 1986; Sanford et al., 1997). Reciprocal crosses were made between 55-1 and 55-3 to produce two segregating F_1 families, 9501 (55-3 x 55-1, 94 individuals) and 9502 (55-1 x 55-3, 65 individuals). Reciprocal crosses were also made between 55-3 and 8380-1 (family 55-3 x 8380-1, 29 individuals; family 8380-1 x 55-3, 31 individuals). The fifth mapping population was derived from a cross between the two high leptine-producing genotypes 55-1 and 8380-1 (family 55-1 x 8380-1, 20 individuals).

PCR analysis: AFLP reactions were carried out with the AFLP Analysis System I kit (Gibco BRL) using the manufacturer's protocol, but omitting the labeling reactions. Twelve primer pair combinations that produced numerous polymorphic markers were selected for screening of progeny. Markers amplified by respective primer combinations were designated as follows: M1E6, M-CAA/E-ACT; M1E7, M-CAA/E-AGC; M2E3, M-CAC/E-ACA; M2E4, M-CAC/E-ACC; M3E3, M-CAG/E-ACA; M3E4, M-CAG/E-ACC; M3E8, M-CAG/E-AGG; M4E1, M-CAT/E-AAC; M5E4, M-CTA/E-ACC; M6E4, M-CTC/E-ACC; M6E5, M-CTC/E-ACG; and M6E7, M-CTC/E-AGC (M, *Mse*-I +3 primer; E, *Eco*-RI +3 primer). Following selective amplification, AFLP products were separated via electrophoresis using 5% denaturing polyacrylamide gels and visualized using the Silver Stain System (Promega, Madison WI). RAPD reactions were performed as previously described (Ronning et al. 1999). Individual loci were named according to the primer(s) used to generate the fragment followed by its size in base pairs. Markers that deviated strongly from expected chi-square ratios ($p<0.001$) were omitted from subsequent mapping analysis.

Map analysis: Map construction was conducted using JoinMap version 2.0 (Stam and Van Ooijen, 1996). Since the parents are cross-pollinating and heterozygous, segregation types and ratios varied between loci within each F_1 population. Therefore, the JoinMap population code "CP" (Cross Pollinator), which allows for the simultaneous analysis of different segregation types, was used. Marker linkage groups were determined for each family, analyzing only those markers that were nonsignificant by chi-square test for fit to expected ratios ($p>0.5$). Modified LOD thresholds of 7.0, 7.0, 3.0, 3.5, and 3.0 based on the chi-square test for independence of segregation were utilized for grouping markers into linkage groups for families 9501, 9502, 55-1x8380-1, 8380-1 x 55-3, and 55-3 x 8380-1, respectively. Estimates of recombination frequencies were calculated and the pairwise recombination estimates, together with their modified LOD scores, were used to order markers within each linkage group. The LOD threshold for map construction was 0.1 and the recombination threshold 0.49. Markers were included in a linkage group if they exhibited linkage to other markers with less than 5, 10 or 20% recombination with corresponding LOD values for linkage greater than 10, 5, and 1, respectively (Haanstra et al. 1999). Maps generated from the 55-1x8380-1 cross and the two reciprocal crosses, 9501 / 9502 and 55-3 x 8380-1 / 8380-1 x 55-3, were subsequently combined using JoinMap 2.0. A recombination threshold of 0.49 and Kosambi's mapping function were utilized for calculating map distances. The modified LOD threshold value for the integrated map was set at 0.1 (Haanstra et al., 1999).

Results and Discussion

A total of 201, 218, 258, 253, and 244 polymorphic AFLP and RAPD markers were scored in families 9501, 9502, 55-3 x 8380-1, 8380-1 x 55-3, and 55-1 x 8380-1, respectively. These markers were primarily AFLP loci, but also included an average of 38 RAPD loci in each of the five families. An average of 17 polymorphic loci (range 9-33) were scored for each AFLP primer pair. An average of 39 AFLP loci were monomorphic across all individuals in each family. One to nine (mean 3.6) polymorphic RAPD loci were scored for each RAPD primer in these families. Unambiguous mapped markers in families 9501, 9502, 8380-1 x 55-3, 55-3 x 8380-1, and 55-1 x 8380-1 totaled 158, 141, 180, 185, and 118, respectively. The integrated map for chromosome 1, derived from merging linkage groups from 9501/9502, 55-3 x 8380-1/8380-1 x 55-3, and 55-1 x 8380-1 populations, focused on markers exhibiting linkage with chromosome 1 marker UBC370-1500 and allied linkage groups. This map contained six RAPD markers and 45 AFLP markers and spanned 77.9 centimorgans (Figure 1). Markers exhibiting identical segregation are evident at twelve different map locations, with each locus containing two to four markers.

Dense clustering of *Eco*RI + *Mse*I AFLP markers occurred in linkage groups of all *S. chacoense* populations. Haanstra et al. (1999) observed clustering of *Eco*RI + *Mse*I AFLP markers, but not *Pst*I + *Mse*I AFLP markers, in centromeric regions on all chromosomes of a map constructed from a cross of *Lycopersicon esculentum* x *L. pennellii* and suggested that the clustering of markers was due to a suppression of recombination in the heterochromatic regions near the centromeres, rather than to a non-random distribution of markers on the chromosomes. Using 6 AFLP primer combinations and a mapping population generated from a cross of non-inbred potato parents, Van Eck et al. (1995) found that AFLP markers were generally randomly distributed, but also observed clustering of *Eco*RI + *Mse*I-based markers.

The RAPD marker UBC370-1500, previously mapped to the top of chromosome 1 of potato and tomato and shown to be linked to nil leptine production in the 9501/9502 populations of *S. chacoense* (Ronning et al., 1999), has similarity over the 3' end to a region on *Arabidopsis thaliana* chromosome 1 (BAC F3F20.1; annotated as callose synthase). This region may be a key site for determination of solanidine in *Solanum* spp., solanidine or solasodine in *S. tuberosum* x *S. berthaultii* progeny (Yencho et al. 1998), and for accumulation of solanidine or leptinidine in *S. chacoense* (Ronning et al. 1999). Marker UBC370-1500 exhibited linkage to a number of AFLP and RAPD markers in linkage group 1 marker frameworks for 55-3x8380-1/8380-1x55-3 and 9501/9502 populations. This marker was also detected in the high-leptine genotype 8380-1. As a result, we would expect no correlation between presence of the marker and leptine content in the 55-3x8380-1/8380-1x55-3 and 55-1x8380-1 families. These results, together with previous genetic studies involving crosses with 8380-1 (Ronning et al., 1998), suggest that additional genetic factors likely influence the inheritance and expression of leptine glycoalkaloids in *S. chacoense*. The markers mapped here provide an opportunity for additional fine mapping of this region on chromosome 1 and investigation of glycoalkaloid inheritance.

Literature Cited

Haanstra, JPW, C Wye, H Verbakel, F Meijer-Dekens, P van den Berg, P Odinot, AW van Heusden, S Tanksley, P Lindhout, and J Peleman. 1999. An integrated high-density RFLP-AFLP map of tomato based on two *Lycopersicon esculentum* x *L. pennellii* F_2 populations. Theor Appl Genet 99:254-271.

Kuhn R and I Löw. 1961. Zur konstitution der leptine. Chem Ber 94:1088-1095.

Ronning, CM, LL Sanford, RS Kobayashi, and SP Kowalski. 1998. Foliar leptine production in segregating F_1, inter-F_1, and backcross families of *Solanum chacoense* Bitter. Amer J Potato Res 75:137-143.

Ronning, CM, JR Stommel, SP Kowalski, LL Sanford, RS Kobayashi, and O Pineada. 1999. Identification of molecular markers associated with leptine production in a population of *Solanum chacoense* Bitter. Theor Appl Genet 98:39-46.

Sanford, LL, RS Kobayashi, KL Deahl, and SL Sinden. 1997. Diploid and tetraploid *Solanum chacoense* genotypes that synthesize leptine glycoalkaloids and deter feeding by Colorado potato beetle. Amer Potato J 74:15-21.

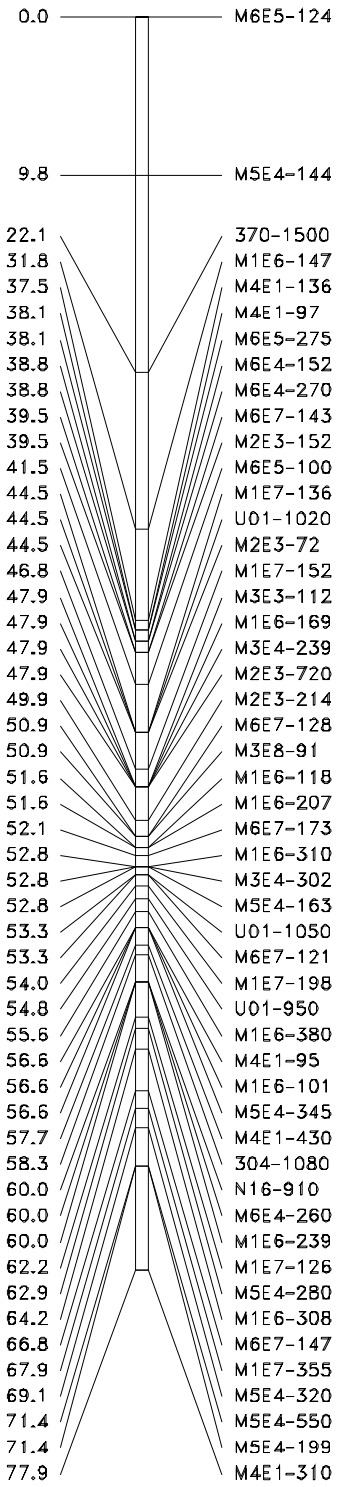
Sinden, SL, LL Sanford, and KL Deahl. 1986. Segregation of leptine glycoalkaloids in *Solanum chacoense* Bitter. J Agric Food Chem 34:372-377.

Stam, P and JW Van Ooijen. 1996. JoinMap version 2.0: software for the calculation of genetic linkage maps. CPRO-DLO, Wageningen.

Van Eck, HJ, J Rouppe van der Voort, J Draaistra, P Van Zandvoort, E Van Enckevort, B Segers, J Peleman, E Jacobsen, J Helder, and J Bakker. 1995. The inheritance and chromosomal localization of AFLP markers in a non-inbred potato offspring. Mol Breed 1:397-410.

Yencho, GC, SP Kowalski, RS Kobayashi, SL Sinden, and KL Deahl. 1998. QTL mapping of *Solanum* steroid alkaloids in interspecific potato crosses: quantitative variation and biosynthesis pathways. Theor Appl Genet 97:563-574.

Figure 1. Linkage group framework generated from *S. chacoense* mapping populations (9501/9502, 55-3x8380-1/8380-1x55-3, and 55-1x8380-1) for chromosome 1. Cumulative distances in centimorgans (left) and markers (right) are shown.



Development of a large fruited tomato with a high level of resistance to bacterial wilt (*Ralstonia solanacearum*).

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Bacterial wilt is a serious disease problem in many humid, tropical growing areas around the world. Unfortunately breeding for resistance has been difficult for a number of reasons including different races, complex resistances, and environmental effects on disease expression that have limited the development of artificial seedling screening techniques. There have also been reports of associations of resistance with small fruit size (Acosta et al., 1964) although other researchers did not find such an association (Danesh et al., 1994; Monma and Sakata, 1993). Some of the most widely adapted sources of resistance have been a series of lines from Hawaii, bred by Dr. J.C. Gilbert in the 1960's and 1970's. In our breeding program we use mainly Hawaii 7997 as a source of resistance, but we have had great difficulty developing large-fruited types with resistance comparable to Hawaii 7997. Our bacterial wilt resistant release 'Neptune', tested as Fla. 7421, had medium-large fruit but its resistance was less than that of Hawaii 7997 and not as broadly adapted (Scott et al., 1995; Wang et al., 1998). Numerous selections over the years with large fruit size turned out to have less resistance than that of Hawaii 7997.

Attempts were made to break the apparent linkage of a hypothetical fruit size gene with a bacterial wilt resistance gene by crossing breeding lines with medium-large fruit and intermediate resistance back to Hawaii 7997 in 1996 and then re-selecting resultant F_2 progeny for resistance and larger fruit. Eight breeding lines were originally crossed with Hawaii 7997. From this original crossing a F_5 line was selected that had a high level of resistance, but only a moderate fruit size increase over Hawaii 7997. A selection from this line was crossed to Fla. 7834, a large-fruited breeding line and progeny from the F_2 and further generations were screened for bacterial wilt resistance and fruit size. This time a large fruited F_2 was selected and screening and selection continued until the F_6 generation. In the F_6, two selections were made and designated Fla. 8109 and Fla. 8109B.

In Summer 2002 these two lines and nine others were grown in a completely randomized block design with 3 blocks and 10 plants per plot. Three days before transplanting to the field, the plants 30 days past the cotyledon stage were inoculated with the pathogen in Todd® planter flats. Each plant received 5 mL of a suspension containing 10^7 cfu/mL of the bacteria. Twenty-two days after the inoculation the plants in the field were scored for disease symptoms that included death, stunting, wilting, and/or chlorosis leading to browning of foliage. Plants were checked later in the season but there was no further disease development. In Spring 2003 Fla. 8109, Fla. 8109B, Neptune, Horizon, and Sanibel were grown in a completely randomized design with two replications and 4 to 6 plants per plot. Fruit reaching the breaker or beyond stage were harvested three times at weekly intervals. For each plot, fruit were counted and weighed in order to obtain yield and fruit size information.

The bacterial wilt incidence for the tomato inbreds is in Table 1. Both Fla. 8109 and Fla. 8109B had percentages of healthy plants that were not significantly different than that of Hawaii 7997 but significantly greater than that of susceptible Florida MH-1 and bacterial wilt tolerant Neptune. Fla. 8109 had significantly greater resistance than the bacterial wilt tolerant Caravel variety from Guadeloupe. Fla. 7997 is an experimental variety meant to be an improvement over Neptune and it had significantly greater resistance in this experiment. The other inbreds are small fruited. They all had good resistance in this experiment (Table 1) and in previous testing. Fla. 8109 and Fla. 8109B do not have heat-tolerance so the test for fruit size was conducted in the spring. This experiment did demonstrate the large fruit size of these two sister lines as they were statistically similar to Sanibel, a large fruited commercial tomato grown in Florida (Table 2). Fla. 8109 and Fla. 8109B were larger fruited than Horizon and Neptune. Yield of the lines was less than the other three varieties but this was not unexpected because they still need some breeding work.

Collectively the data support the contention that Fla. 8109 and Fla. 8109B have a good level of bacterial wilt resistance and large fruit. They need to be tested further in Florida and elsewhere to determine their potential in other regions of the world where bacterial wilt is a problem. If a repulsion linkage between a bacterial wilt resistance gene and a gene enhancing fruit size has been broken then the new coupling linkage should make Fla. 8109 an especially attractive resistance source to work with for those interested in developing large fruited varieties. Selecting for bacterial wilt resistance with this material should carry a tendency for larger fruit.

Literature Cited

Acosta, J.C., Gilbert, J.C., and V.L. Quinon. 1964. Heritability of bacterial wilt resistance in tomato. American Society for Horticultural Science. 84:455-462.

Danesh, D. Aarons, S., McGill, G.E., and N. Young. 1994. Genetic dissection of oligogenic resistance to bacterial wilt in tomato. Mol. Plant-Microbe Interactions 7:464-471.

Monma, S. and Y. Sakata. 1993. Inheritance of resistance to bacterial wilt in tomato. In: Bacterial Wilt, Proceedings of an international conference held at Kaohsiung, Taiwan. ACIAR Proceedings No. 45, 381 pp.

Scott, J.W., Jones, J.B., Somodi, G.C., Chellemi, D.O., and S.M. Olson. 1995. ‘Neptune’, a heat-tolerant, bacterial-wilt-tolerant tomato. HortScience 30:641-642.

Wang, J-F., Hanson, P.M., and Barnes, J.A. 1998. Worldwide evaluation of an international set of resistance sources to bacterial wilt in tomato. Pages 269-275. In: Bacterial Wilt Disease: Molecular and Ecological Aspects. Prior, P., Allen, C. and Elphinstone, J. eds. Springer-Verlag, Berlin.

Table 1. Bacterial wilt incidence for tomato inbreds 22 days after inoculation at Bradenton, Florida in Summer 2002.

Inbred	Healthy plants (%)[z]
E306	96.7 a[y]
E305	93.3 ab
Hawaii 7997	90.0 ab
Fla. 7997	89.7 ab
E304	83.3 abc
Fla. 8109	82.3 abc
E307	76.7 bc
Fla. 8109B	75.3 bc
Caravel	58.7 cd
Neptune	34.3 d
Florida MH1[x]	33.3 d

[z]Rated 22 days after inoculation
[y]Mean separation performed on data transformed to $\sqrt{}$ arcsine by Duncan's Multiple Range Test at $P \leq 0.05$
[x]Susceptible control

Table 2. Yield and fruit size for bacterial wilt resistant and standard tomato varieties at Bradenton, Florida in Spring 2003.

Genotype	Yield per Plant (kg)	Fruit Size (g)
Fla. 8109	4.17 b[z]	225 a
Fla. 8109B	3.90 b	212 a
Sanibel	7.93 a	194 ab
Horizon	7.57 a	162 bc
Neptune	7.36 a	133 c

[z]Mean separation in columns by Duncan's Multiple Range Test at $P \leq 0.05$.

Screening bacterial wilt resistant tomatoes for shade tolerance

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The cultivable area in Kerala is dominated by perennial plantation crops leaving very little space for vegetables. Identification of shade tolerant genotypes deserve priority to utilize the available interspaces, especially of coconut (Sreelathakumary and Rajamony, 2002). Bacterial wilt caused by *Ralstonia solanacearum* is another handicap in tomato cultivation in Kerala accounting for even 100 per cent crop loss (Bose and Rajan, 2000). The present study was conducted to identify shade tolerant genotypes in a bacterial wilt resistant background. The experiment was laid out at College of Agriculture, Vellayani using 10 bacterial wilt resistant tomato genotypes under different shade levels (0%, 25% and 50%). Black high density polyethylene net fabricated for 25 and 50% shade was used for the study. The net was spread at a height of 2.5 m from ground level and supported on GI pipes. The presence of bacterial wilt was confirmed by planting a susceptible line Fla 7156 as check.

A perusal of the results clearly indicated significant variation among genotypes and shade levels for yield per plant. LE 45 recorded maximum yield under all shade levels with 1523.5 g, 1670.37 g and 643.68 g respectively in open, 25% and 50% shade (Table 1). Similar results were reported in tomato under 15% shade by Smith *et al*. (1984). There was significant variation in number of fruits per plant also among genotypes and shade levels. It is observed that mild shade of 25% did not affect the fruits per plant while 50% shade reduced it considerably in the present study which agrees with the findings of Yamashiti and Hayashi (1994). The highest fruit set of the top yielder LE 45 under all shade levels shows its ability to perform well under the stress of shade.

The genotypes were scored under all shade levels for the incidence of important pests and diseases on a 0 – 5 scale depending on the severity of infection. The low incidence of spotted wilt virus (TSWV) observed under shade may be due to the reduced activity of thrips, the vector for the virus transmission. Among the genotypes, LE 34 recorded the least incidence whereas the maximum incidence was in LE 1. Similarly, the fruit borer (*Helicoverpa armigera*) and serpentine leaf miner (*Liriomyza trifolii*) incidence was also significantly low under shade. The genotype least affected by leaf miner was LE 2 and fruit borer was LE 42. The study confirmed the bacterial wilt tolerance in all the breeding lines selected even under shade whereas the susceptible check Fla 7156 completely succumbed to the disease irrespective of the shade level. Though none of the genotypes was found completely resistant to pests and diseases, the incidence was comparatively low under shade suggesting the scope for production of healthy plants by providing mild shade of 25%. Moreover, the tomato yield under 25% shade was on par with the yield in open. Hence in Kerala, where the majority of the land is occupied by perennials especially coconut, the interspaces with approximately 25% shade can be effectively utilized for growing tomato.

Literature Cited

Bose, S.C.S and Rajan, S. 2000. Peroxidase isozyme as marker for bacterial wilt resistance in tomato (*Lycopersicon esculentum* Mill.). *Veg. Sci*., **27**: 136-141.

Smith, I.E., Savage M.J. and Mills. P. 1984. Shading effect on greenhouse tomatoes and cucumbers. *Acta Hort*. **148**: 491-500.

Sreelathakumary, I and Rajamony, L. 2002. Variability, heritability and correlation studies in chilli (*Capsicum* spp.) under shade. *Indian J. Hort*., **59**: 77-83.

Yamashiti, F and Hayashi, G. 1994. Studies on year round production of tomato in water culture method for prevention of fruit cracking during high temperature periods. *Res. Bull. Aichi. Ken. Agri. Res. Center*. **26**: 157-162.

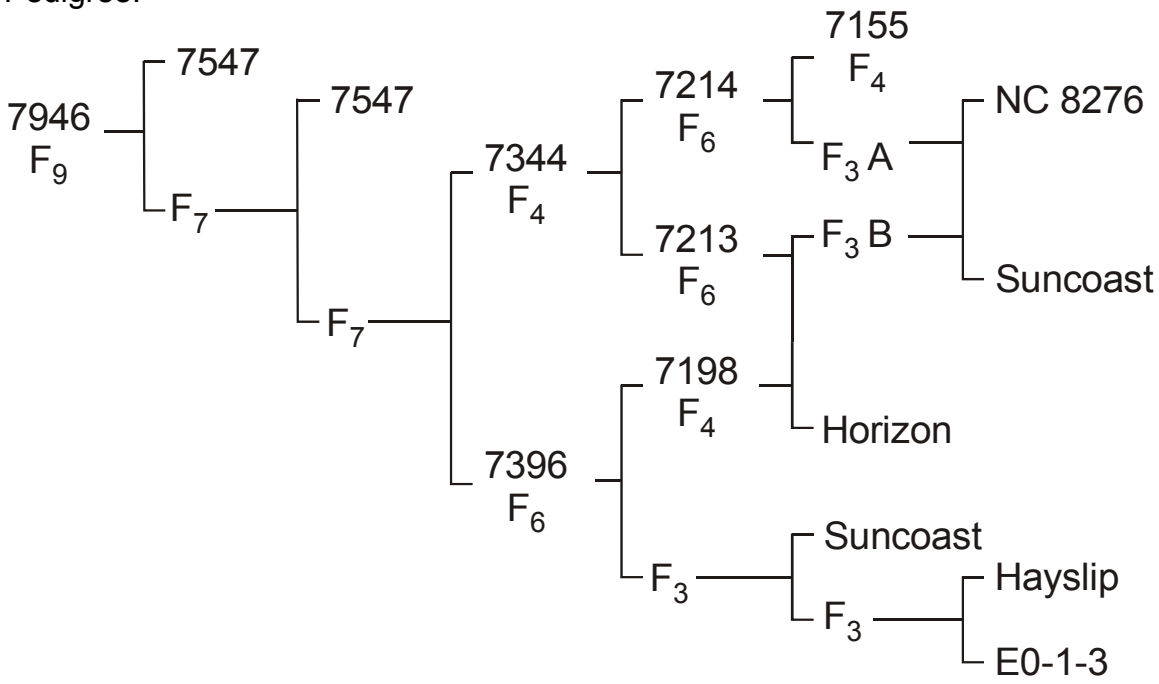
Table 1. Yield and pests and disease incidence of tomato genotypes under shade

Treatment	Genotype & source	Shade (%)	Fruits/ plant	Yield/ plant (g)	Reaction to the stress due to		
					TSWV	ASLM	TFB
LE 1	Xiang Fan Qui- 1, China	0	8.75	512.15	3.58	1.42	0.92
		25	10.75	559.51	2.58	1.33	0.52
		50	3.50	192.90	1.50	1.00	0.08
LE 2	Neptune, Florida	0	6.25	607.47	2.42	1.50	0.83
		25	7.50	649.89	1.67	1.08	0.58
		50	1.33	118.60	0.92	0.75	0.08
LE 22	Mukthi, Kerala	0	34.17	1114.29	2.83	1.42	1.58
		25	33.83	1130.33	1.92	1.08	1.33
		50	13.67	390.86	1.33	1.00	0.83
LE 34	ARS 16, Mannuthy, Kerala	0	33.83	1312.34	1.33	2.75	1.25
		25	36.23	1288.67	0.92	1.83	0.83
		50	14.25	495.56	0.58	1.58	0.17
LE 38	CLN 2026 C AVRDC,Taiwan	0	10.08	604.26	2.25	1.67	1.17
		25	9.50	545.92	1.50	1.58	1.25
		50	3.67	225.50	0.83	1.42	0.58
LE 39	CLN 2026 D AVRDC,Taiwan	0	12.67	776.38	2.08	2.58	1.42
		25	14.08	776.36	1.08	2.17	1.17
		50	4.33	263.20	0.75	2.08	0.42
LE40	CLN 2026 E AVRDC,Taiwan	0	29.25	1142.47	1.92	1.75	1.00
		25	27.92	1031.55	1.5	1.67	0.75
		50	9.92	401.71	0.67	1.33	0.50
LE 42	CLN 1466 P AVRDC,Taiwan	0	8.92	621.92	1.83	1.33	0.67
		25	8.94	609.56	1.75	1.25	0.33
		50	2.86	226.43	1.00	0.92	0.08
LE 44	CLN 1621 E AVRDC,Taiwan	0	23.58	1104.84	1.50	3.17	1.25
		25	21.33	993.80	1.25	3.00	1.00
		50	7.83	373.53	0.50	2.58	0.33
LE 45	CLN 1621 F AVRDC,Taiwan	0	38.17	1523.51	1.67	3.33	1.08
		25	37.67	1670.37	1.08	2.67	0.83
		50	16.00	643.68	0.75	2.17	0.17

TSWV-Tomato spotted wilt virus
ASLM- American serpentine leaf miner
TFB- Tomato fruit borer

Scott, J.W. 2003. Fla. 7946 tomato breeding line resistant to *Fusarium oxysporum* f.sp. *lycopersici* races 1, 2, and 3. Hortscience 38: (in press)

Pedigree:



Characteristics:

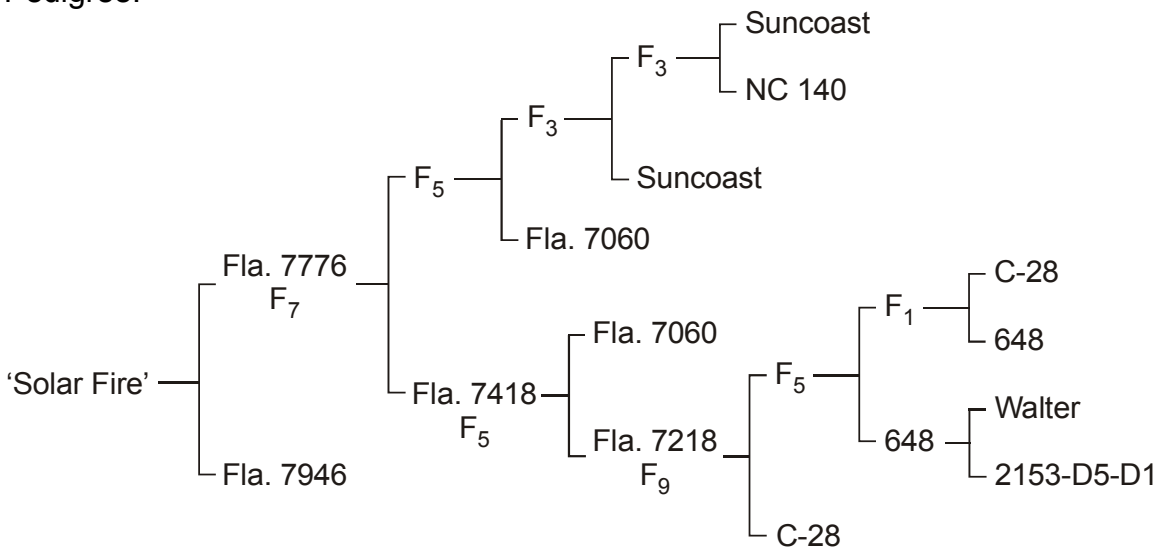
Fruit: Flat round shape, light green shoulder, medium-large fruit (175 g), firm, deep red internal color (og^c), good crack and check resistance.

Plant: *sp, I, I-2, I-3, Ve, Sm*, medium vine

Utility and maturity: Mid-season fresh market breeding line for use in making hybrids and breeding for resistance to Fusarium wilt race 3 and/or high lycopene tomatoes.

Scott, J.W., S.M. Olson, H.H. Bryan, J.A. Bartz, D.N. Maynard, and P.J. Stofella. 2003. 'Solar Fire' hybrid tomato. HortScience 39: (to be submitted)

Pedigree:



Characteristics:

Fruit: Large, flat round shape, smooth, firm, light-green shoulders, good crack and check resistance

Plant: *sp, I, I-2, I-3/+, Ve, Sm,* moderate resistance to soft rot, medium vine

Utility and maturity: Fresh market hybrid with heat-tolerant fruit setting (>32ºC day/>21ºC night) and resistance to Fusarium wilt race 3, early under high temperatures, early to mid-season under cooler temperatures.

Revised List of Miscellaneous Stocks

Chetelat, R. T., and J. P. Petersen

C.M. Rick Tomato Genetics Resource Center, Dept. of Vegetable Crops, University of California, Davis, CA 95616

This list of 1,535 miscellaneous genetic stocks is a revision of the previous one issued in TGC 50 (2000). The current list has been reformatted to group related types of stocks and to make it easier to find the more popular items. Extinct, obsolete, or faulty accessions have been dropped. New accessions that have been added to the list include a second set of *L. pennellii* introgression lines (ILs) in the 'M-82' background, among which are a number of sublines that provide increased mapping resolution. Similar ILs that represent a portion of the *S. lycopersicoides* genome in 'VF-36' are also listed. A set of backcross recombinant inbred lines (BC-RIs) derived from *L. esculentum* x *L. pimpinellifolium* offer a permanent, high resolution mapping population for tomato. Finally, two types of interspecific hybrids that are useful for reproduction and introgression of the *Solanum* spp. have been added to our list of prebreds.

We attempt to maintain all listed accessions in adequate seed supply for distribution. However, some stocks, such as certain multigenic 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 52); 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 51 (2001)
Monogenic Stocks (994 accessions total) are listed in TGC 52 (2002)

Accession Categories

1. CULTIVARS AND LANDRACES

1.1. Modern and Vintage Cultivars (201)

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, and additional purposes. Marglobe is maintained as the standard for tomato genetics nomenclature. Most lines have been maintained by selfing for many generations.

LA	Cultivar
0818	A-1
0516	Ace
2838A	Ailsa Craig
2463	Allround
3143	Anahu
1995	Angela
3244	Antimold-B
3527	Apex 1000
0657	Beaverlodge (Chanasyk Early)
1499	Break O'Day
2414	Cal Ace
1439	Calmart
3316	Campbell 24
3317	Campbell 28
3228	Canary Export
2374	Caro Red
2400	Castlemart
3121	Chico Grande
3213	Columbian
0533	Condine Red
0817	CP-2
3247	Craigella
1162	Cuba Plum
1219	Dwarf San Marzano
0313	Dwarf Stone
3245	E.S. 1
4024	E-6203
3238	Earliana
2006	Earlinorth
0266	Earlipak
0517	Early Santa Clara
2711	Edkawi
3800	Fargo self pruning
3801	Farthest North
3024	Fireball
3840	Florida 7060
4026	Florida 7481
4025	Florida 7547
3242	Flori-Dade
3030	Gardner
2802	Globonnie
4011	GT
3231	Gulf State Market
0314	Hardin Miniature
3202	Hawaii 7997
3857	Hawaii 7998
0806	High Crimson

LA	Cultivar
3110	Hires Rootstock
3237	Homestead 24
3320	Hotset
3144	Hunt 100
2805	Indehiscent Currant
1089	John Baer
1131	Kallio’s Alaskan Dwarf
0025	King Humbert #1
3240	Kokomo
0505	Laketa
3203	Large Plum
3118	Laurica
3146	Libohova
0791	Long John
3232	Long Red
0534	Lukullus
3475	M-82
3120	Malintka-101
2451	Manapal
0502	Marglobe
1504	Marmande
0278	Marzano Grande
3151	Mecline
0011	Michigan State Forcing
3911	Micro-Tom
2825	Mobaci
2824	Moboglan
3152	Moboline
2821	Mobox
2830	Mocimor
3471	Mogeor
2828	Momor
2829	Momor verte
2818	Monalbo
2706	Moneymaker
2819	Monita
2713	Montfavet 167
2714	Montfavet 168
2827	Moperou
2822	Mossol
2820	Motabo
2826	Motaci
2823	Motelle
3472	Movione
3466	Murrieta
2661	Nagcarlang
3625	NC 265-1(93)-3-3

LA	Cultivar
3845	NC EBR-5
3846	NC EBR-6
3847	NC HS-1
3802	New Hampshire Victor
2009	New Yorker
3321	Ohio 7663
1088	Ohio Globe A
2447	Ontario 717
2449	Ontario 7517
2396	Ontario 7710
2448	Ontario 7818
2973	Oxheart variant: Big Rainbow
2972	Oxheart variant: Big Yell. Red Ctr
2969	Oxheart variant: Georgia Streak
2970	Oxheart variant: Or- Red Center
2971	Oxheart variant: Verna Orange
2376	Pan American
0012	Pearson
0020	Pennheart
3528	Peto 95-43
3243	Platense
3125	Pomodorini Napolitani
2715	Porphyre
3820	Potentate
3236	Prairiana
3903	Primabel
0089	Prince Borghese
3233	Pritchard
3229	Prospero
2446	Purdue 135
2377	Purple Calabash
2378	Purple Smudge
0337	Red Cherry
0276	Red Top
3129	Rehovot 13
2356	Rey de los Tempranos
0535	Rheinlands Ruhm
3343	Rio Grande
3145	Rockingham
0503	Roumanian Sweet
3214	Rowpac
2088	Royal Red
3215	Roza
1090	Rutgers
2662	Saladette
3216	Saladmaster
3008	San Marzano

LA	Cultivar
0180	San Marzano (doubled haploid)
3147	Saniollas
1021	Santa Cruz
2413	Severianin
2912	Short Red Cherry
3234	Sioux
3221	Slender Pear
3632	Start 24
0030	Stemless Pennorange
2443	Stirling Castle
1091	Stokesdale
1506	Stone
0164	Sutton's Best of All
2399	T5
2590	T9
3230	Targinnie Red
0154	Tiny Tim
2803	Tropic
1714	UC134
3526	UC134-61D
3130	UC204C
1706	UC82
3772	UC82B
2898	UC82C
3773	UC82L
2937	UC-MR20
2938	UC-N28
2939	UC-T338
2940	UC-TR44
2941	UC-TR51
0021	Uniform Globe
2445	V121
0745	V-9 Red Top
3246	Vagabond
3905	Vantage
3122	Vendor
3029	Vendor (*Tm-2*^{a}*, I, Ve*)
2444	Vetomold K10
0744	VF-11
1023	VF-13L
1507	VF-145 21-4
0816	VF-145 22-8
1222	VF-145 78-79
0742	VF-34
0490	VF-36
0743	VF-6
2086	VFN Hi Sugar

LA	Cultivar
0815	VFN-14
1022	VFN-8
1221	VFNT Cherry
3204	VFT-36
2806	Vis Grise
3630	Vrbikanske nizke
3465	Walter

LA	Cultivar
0279	Webb Special
2464A	White Beauty
2-473	Yellow Cherry
2804	Yellow Currant
2357	Yellow Peach
3148	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.

LA	Location
BOLIVIA	
0172	Santa Cruz
2699	Coroica
2871	Chamaca (Yungas)
2873	Lote Pablo Luna (Yungas)
2874	Playa Ancha (Yungas)
BRAZIL	
1021	Santa Cruz
CHILE	
0466	Hda. Rosario (Azapa)
0467	Lluta
0468	Iquique
COLOMBIA	
0356	Buenaventura
0357	Buenaventura
0358	Buenaventura
0359	Buenaventura
COSTA RICA	
1215	(unknown)
3453A-D	Turrialba
CUBA	
1162	(unknown)
ECUADOR	
0126	Quito
0408	Guayaquil
0409	Guayaquil
0410	Guayaquil
0415	Daular
0416	Puna

LA	Location
0423	Wreck Bay (Galapagos)
1224	Puyo (Napo)
1238	Viche (Esmeraldas)
1239	Esmeraldas
1240	Esmeraldas
1241	Esmeraldas
1244	Carmela (Guayas)
1249	Loja
1250	Loja
1251	Loja
2094	El Naranjo
2132	Chuchumbetza (Zamora-Chinchipe)
2381-2384	Malacatos (Loja)
3624	Santa Rosa (Napo)
EL SALVADOR	
1210, 1211	San Salvador
GUATEMALA	
1460	Antigua
HONDURAS	
0147	Tegucigalpa
0148	Tegucigalpa
MEXICO	
0146	Mexico City
1218	Vera Cruz
1457	Tehuacan
1459	Huachinango
1462	Merida
1544	Xol Laguna
1564	Culiacan

LA	Location
1565	Oaxaca
1566	Oaxaca
1567	Sinaloa
1568	Yucatan
1702	Sinaloa
1703	Tamaulipas
1704	Tamaulipas
1705	Sinaloa
1994	(unknown)
2083	Culiacan
2084	Culiacan
NICARAGUA	
1213	(unknown)
PANAMA	
1216	(unknown)
PERU	
0113	Hda. Calera (La Libertad)
0116	Chiclayo
0117	Piura
0125	Trujillo
0131	Arequipa
0134	Ayacucho
0393	Chiclayo
0394	Chiclayo
0395	Chiclayo
0396	Chiclayo
0401	Piura
0402	Piura
0403	Piura
0404	Piura
0405	Piura
0472	(unknown)
0473	Calana (Tacna)
0477	Chincha
0478	Chincha
0721	Chiclayo

LA	Location
1313	Convento de Sivia (Cusco)
1315	Ayna
1390	La Molina (Lima)
1397	Iquitos
1398	Iquitos
1650	Fundo Bogotalla (Ica)
1654	Tarapoto
1655	Tarapoto
1669	Jahuay (Ica)
1698	Chancay
1701	Trujillo
1976	Calana (Tacna)
1988	Iquitos
2207-2212	Naranjillo (San Martin)
2213-2220	Nueva Cajamarca
2221-2235	Moyobamba (San Martin)
2237-2244	Habana (San Martin)
2245-2253	Soritor (San Martin)
2254-2259	Moyobamba (San Martin)
2260-2264	La Huarpia (San Martin)
2265-2268	Pacaisapa (San Martin)
2269-2276	Tarapoto (San Martin)
2278-2282	Tabalosas (San Martin)
2283-2311	Tarapoto (San Martin)
2316	Sargento (Amazonas)
2622	Margual (Loreto)
2623	Pucalepillo (Loreto)
2676	San Juan Del Oro (Puno)
2841	Chinuna (Amazonas)
2842	Sta. Rita (San Martin)
2843	Moyobamba (San Martin)
2844	Shanhoa (San Martin)
2845	Moyobamba (San Martin)
3221-3226	San Isidro (Lima)
3646	Puente Tincoj (Cusco)

2. PREBRED STOCKS

2.1. Introgression Lines

2.1.1. *L. pennellii* Introgression Lines (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 sublines provide increased mapping

resolution in some regions. The IL # indicates the *L. pennellii* chromosome and introgressed segment number in each.

LA	Line
4028	IL1-1
4029	IL1-1-2
4030	IL1-1-3
4031	IL1-2
4032	IL1-3
4033	IL1-4
4034	IL1-4-18
4035	IL2-1
4036	IL2-1-1
4037	IL2-2
4038	IL2-3
4039	IL2-4
4040	IL2-5
4041	IL2-6
4042	IL2-6-5
4043	IL3-1
4044	IL3-2
4045	IL3-3
4046	IL3-4
4047	IL3-5
4048	IL4-1
4049	IL4-1-1
4050	IL4-2
4051	IL4-3
4052	IL4-3-2
4053	IL4-4

LA	Line
4054	IL5-1
4055	IL5-2
4056	IL5-3
4057	IL5-4
4058	IL5-5
4059	IL6-1
4060	IL6-2
4061	IL6-2-2
4062	IL6-3
4063	IL6-4
4064	IL7-1
4065	IL7-2
4066	IL7-3
4067	IL7-4
4068	IL7-4-1
4069	IL7-5
4070	IL7-5-5
4071	IL8-1
4072	IL8-1-1
4073	IL8-1-5
4074	IL8-2
4075	IL8-2-1
4076	IL8-3
4077	IL8-3-1
4078	IL9-1
4079	IL9-1-2

LA	Line
4080	IL9-1-3
4081	IL9-2
4082	IL9-2-5
4083	IL9-2-6
4084	IL9-3
4085	IL9-3-1
4086	IL9-3-2
4087	IL10-1
4088	IL10-1-1
4089	IL10-2
4090	IL10-2-2
4091	IL10-3
4092	IL11-1
4093	IL11-2
4094	IL11-3
4095	IL11-4
4096	IL11-4-1
4097	IL12-1
4098	IL12-1-1
4099	IL12-2
4100	IL12-3
4101	IL12-3-1
4102	IL12-4
4103	IL12-4-1

2.1.2. *L. hirsutum* introgression lines (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.

LA	Line	Chrom.s
3913	TA1258	1
3914	TA523	1
3915	TA1229	1
3916	TA1223	1
3917	TA1536	1-2-12
3918	TA1127	1
3919	TA1128	1

LA	Line	Chrom.s
3920	TA1536	1
3921	TA1105	2
3922	TA1266	2
3923	TA1537	2
3924	TA1538	2
3925	TA1111	3
3926	TA1276	3

LA	Line	Chrom.s
3927	TA1277	3
3928	TA1540	3-8
3929	TA1541	3-8
3930	TA1133	4
3931	TA1280	4
3932	TA1562	4
3933	TA1542	4

LA	Line	Chrom.s
3934	TA1459	4
3935	TA517	4
3936	TA1475	4
3937	TA1473	4
3938	TA1287	5
3939	TA1293	5
3940	TA1112	5
3941	TA1543	5
3942	TA1117	5-8
3943	TA1544	5
3944	TA1539	6
3945	TA1545	6-10
3946	TA1546	6
3947	TA1559	6
3948	TA1303	7
3949	TA1304	7
3950	TA1547	7
3951	TA1312	7
3952	TA1315	8
3953	TA1316	8
3954	TA1548	8-10
3955	TA1320	8
3956	TA1324	9
3957	TA1325	9
3958	TA1330	9-11
3959	TA1331	4-9-11

LA	Line	Chrom.s
3960	TA1550	9-10-12
3961	TA1551	10
3962	TA1552	10-12
3963	TA1337	10
3964	TA1339	10
3965	TA1555	2-11
3966	TA1554	10-11-12
3967	TA1342	11
3968	TA1350	12
3969	TA1121	12
3970	TA1219	1
3971	TA1218	2
3972	TA1173	2
3973	TA1627	2
3974	TA1628	2
3975	TA1629	3
3976	TA1138	4
3977	TA1467	4
3978	TA1468	4
3979	TA1630	4
3980	TA1290	5
3981	TA1116	5
3982	TA1293	5
3983	TA1631	5
3984	TA1632	5
3985	TA1306	2-7

LA	Line	Chrom.s
3986	TA1309	3-7
3987	TA1633	7
3988	TA1318	8
3989	TA1319	8
3990	TA1560	8
3991	TA1326	9
3992	TA1634	1-10-11-
3993	TA1549	1-10-11
3994	TA1635	10
3995	TA1553	1-11-12
3996	TA1120	3-11
3997	TA1563	1-10
3998	TA1637	1-11-12
3999	TA1638	1-12
4000	TA1557	1-4
4001	TA1644	1-7-12
4002	TA1645	1-8-12
4003	TA1648	2-11
4004	TA1649	2-3-6
4005	TA1652	3-5
4006	TA1654	4-10-11
4007	TA1655	4-12
4008	TA1656	5-6-9
4009	TA1564	5-7-10
4010	TA1561	8-12

2.1.3. *S. lycopersicoides* introgression lines (80)

The following group of ILs have been bred from *S. lycopersicoides* (LA2951) into the background of *L. esculentum* cv. VF36 (LA0490). These 80 lines represent ~95% of the donor genome (Canady & Chetelat unpublished; Chetelat & Meglic, Theor. Appl. Genet. 100: 232-241, 2000). While some lines are available in the homozygous condition, many others are associated with sterility and must be maintained via heterozygotes. As a result, available seed quantities may be limited in some cases.

LA	Line	Chrom.
3866	LS1-1	1
3867	LS11-9	1
3869	LS42-4	2
3870	LS38-10	2
3871	LS41-3	2
3873	LS14-6	2
3874	LS20-9	3
3875	LS24-14	4, 12
3876	LS29-1	8
3877	LS42-2	4
3878	LS24-6	5

LA	Line	Chrom.
3879	LS1-5	5, 11
3881	LS4-17	6
3882	LS43-14	2, 6
3883	LS48-6	7, 11
3884	LS9-7	5, 7
3885	LS46-1	7
3886	LS48-5	7
3890	LS16-15	9
3892	LS48-2	11
3893	LS16-6	5, 12
3894	LS8-10	12

LA	Line	Chrom.
3895	LS9-21	12
4230	LS15-2H	1
4231	LS15-2B	1
4232	LS11-11A	1
4233	LS20-9	1, 3
4234	LS21-2	1, 11
4235	LS10-2	1
4236	LS49-8A	2
4237	LS40-8	2
4238	LS5-1	2
4239	LS41-20	2

LA	Line	Chrom.
4241	LS40-2	3
4242	LS14-8	3
4243	LS1-3	3
4244	LS10-9	4
4245	LS10-11A	4
4246	LS49-8B	4
4247	LS12-9	4
4248	LS11-6	5
4249	LS9-1	5
4250	LS49-8C	5
4251	LS49-3	5
4252	LS32-11	5
4253	LS11-11B	6
4254	LS32-14	6
4255	LS38-5	6

LA	Line	Chrom.
4256	LS9-22	6
4257	LS46-3	7
4258	LS19-7	7
4259	LS32-4	7
4260	SL-7F	7
4261	LS8-11	7
4262	20-16	6, 8
4263	LS46-6A	3, 8
4264	LS9-26A	8
4265	LS9-26B	8
4266	SL-8A	8
4267	LS16-10	8
4268	LS14-7	9
4269	LS12-2	9
4270	LS10-6A	9

LA	Line	Chrom.
4271	LS49-5	9
4272	LS41-11	9
4273	LS12-8	10
4274	LS4-14	10
4275	SL-10	10
4276	LS12-12	4, 10
4277	LS24-11	11
4278	LS3-2	9, 11
4279	LS19-11	11
4280	LS1-5	11
4281	LS13-13	12
4282	LS45-7	12
4283	LS8-9	12
4284	LS9-13	12

2.2. Alien Substitution Lines (7)

In the course of his study of segregation and recombination in *L. esculentum* x *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	*au, dgt, inv, scf*
1639	2	*Me, aw, m, d*
1640	3	*sy, bls, sf*
3469	4	*clau, ful, ra, e, su*^{3}

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

2.3. Backcross Recombinant Inbreds (99).

The following group of backcross recombinant inbred lines originated from the cross *L. esculentum* x *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 – LA4229 BC-RIs
LA4024 *L. esculentum* parent (E-6203)
LA1589 *L. pimpinellifolium* parent

2.4. Monosomic 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	+-+-+	*wv-aa-d*
3455	MA-3	+-+-+	*sy-bls-sf*
3456	MA-4	+	+
3457	MA-5	+	*obv*
3459	MA-7	*Bco*-+-+	+-*var-not*
3460	MA-8	*Wa*	+

LA	Chrom.	2n+1	2n
3461	MA-9	+	+
3462	MA-10	*Abg*-+-+-+- +	+-*u-t-nd-ag*
3463	MA-11	+	+
3464	MA-12	+	+

2.5. Other Prebreds (13)

2.5.1. High soluble solids - derivatives of *L. chmielewskii* LA1028 (Rick, Hilgardia 42:493-510, 1974).

LA1500 – LA1503, and LA1563.

2.5.2. Misc. traits – monogenic and provisional mutants derived 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 stigma - derivative of *L. pimpinellifolium* LA1585 (Rick TGC 33:13-14, 1983): LA2380.

2.5.4. Interspecific hybrids. We maintain the following hybrids for various purposes:

LA3857	F_1 *L. esculentum* cv. VF36 x *S. lycopersicoides* LA2951 (relatively male-fertile clone for introgression)
LA4135	F_1 *L. esculentum* cv. VF36 x *L. pennellii* LA0716 (used as a graft rootstock for reproducing *S. ochranthum*, *S. juglandifolium*, and *S. sitiens*)

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 (coastal habitats): LA1958, LA1959, LA1972, and others
S. sitiens (general feature): LA1974, LA2876, LA4105, and others

3.2. Flooding tolerance

L. esculentum var. *cerasiforme* (wet tropical habitats): 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
L. chilense (from high altitudes): LA1969 , LA1971, LA4117A
S. lycopersicoides (from high altitudes): LA1964, LA2408, LA2781

3.5. Aluminum tolerance

L. esc. var. *cerasiforme* LA2710 (suspected)

3.6. Salinity - alkalinity tolerance

L. cheesmanii (from littoral habitat): 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, and B. Snoad. As far as we know, they are all homozygous for the indicated structural changes. They are listed in the order presented by Gill *et al*. (TGC 24:10-12). This list is followed by a few items in our collections originated by G.S. Khush. Accessions with an asterisk comprise the tester set.

LA	Chrom.s
1876*	T1-2
1877	T2-4
1878	T2-7
1879	T2-9
1880	T2-11
1881	T2-12
1882	T12-3 or -8
1883	T3-7
1884	2 0 4
1885*	T5-7
1886	T12-3 or -8
1892	2 0 4 (T9-12)+?
1894	T2-9a

LA	Chrom.s
1895	T2-9b
1896	T1-12
1897	T7 or 11-?
1898*	T2-10
1899*	T6-11
1902	T2 or -7
1903*	T4-7
1904	T2-9d
1905	T1-3 or -8
1906	T2-10
1049	T5-9 (*af* stock)
1115*	T9-12
1116	T1-11

LA	Chrom.s
1117	T5-7
1118	T7-11
1119*	T3-8
1120*	T6-12
1121	T4-9
1122	T2-9
1123	T2-9
1124	T3-9
1125	T5-7
1126	T7-9
1127	T3-5
1129	T3-9

4.2. Trisomics (31)

The following series of trisomics contain various kinds of extra chromosomes. Since the extras are transmitted irregularly, each stock necessarily consists of a majority of diploids, the remainder aneuploid. Primary trisomics yield primaries (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, correspondents should 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 below under Monosomic Additions (sect. 2.4 above).

Delta	Genotype
Primary	
Δ10	Triplo-1
Δ06	Triplo-2
Δ08	Triplo-3
Δ02	Triplo-4
Δ04	Triplo-5
Δ12	Triplo-6
Δ07	Triplo-7
Δ03	Triplo-8
Δ05	Triplo-9
Δ01	Triplo-10
Δ40	Triplo-11
Δ09	Triplo-12

Delta	Genotype
Telo-	
Δ14	2n + 3S
Δ17	2n + 3L
Δ21	2n + 4L
Δ20	2n + 7L
Δ19	2n + 8L
Δ35	2n + 10S
Secondary	
Δ44	2n + 2S·2S
Δ43	2n + 5L·5L
Δ36	2n + 7S·7S
Δ26	2n + 9S·9S

Delta	Genotype
Δ30	2n + 9L·9L
Δ28	2n + 10L·10L
Δ41	2n + 11L·11L
Δ29	2n + 12L·12L
Tertiary	
Δ18	2n + 2L·10L
Δ16	2n + 4L·10L
Δ39	2n + 5L·7S

Delta	Genotype
Δ15	2n + 7S·11L
Δ25	2n + 9L·12L
Δ23	2n + 1L·11L
Compensating	
Δ32	2n - 3S·3L + 3S + 3L·3L
Δ33	2n - 3S·3L + 3S·3S + 3L·3L
Δ34	2n - 7S·7L + 7S·7S + 7L·7L

4.3. Autotetraploids (20)

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
LA0793	*a, c, d, l, r, y*
LA0794	*ag, t^v*
LA1917	*L. chilense*
LA2335	*L. pimpinellifolium*
LA2337	cv. Stokesdale
LA2338	cv. Break O'Day
LA2339	cv. Pearson
LA2340	*L. pimpinellifolium*

Accession	Genotype
LA2342	cv. Danmark
LA2343	cv. Waltham Fog
LA2581	*L. peruvianum*
LA2582	*L. peruvianum* var. *humifusum*
LA2583	*L. chilense*
LA2585	*L. pimpinellifolium*
LA2587	*L. esculentum* var. *cerasiforme*
LA3131	cv. UC82B
LA3255	cv. Ailsa Craig

5. CYTOPLASMIC VARIANTS (3)

The following three lines are cytoplasmically-inherited chlorotic variants maintained in the TGRC collections 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-found by G.S. Khush in hybrid background
LA1438	Light green induced by X-rays-found by K. Verkerk in cv. Moneymaker
LA2979	Cyto-variegated in cv. Glamour (contributed by R.W. Robinson)

6. GENETIC MARKER COMBINATIONS

6.1. Chromosome Marker Stocks (194)

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).

LA	Genotype
Chromosome 1	
0910	*per, inv*
0984	*scf, inv*
0985	*inv, per*
1003	*scf, inv, per*
1082	*era, um*
1107	*inv, co*
1108	*inv, dgt*
1169	*scf, dgt*
1173	*gas, co*
1184	*au^{tl}, dgt*
1185	*au^{tl}, scf, inv*
1186	*au^{tl}, scf, inv, dgt*
1431	*au^{tl}, dgt*
1490	*au^{tl}, co, inv, dgt*
1492	*ms-32, bs*
1529*	*au^{tl}, co, scf, inv, dgt*
2354	*br, y* (*p, l*)
3209	*imb, irr, y*
3301	*fla, com^{in}*
3302	*imb, com^{in}*
3303	*imb, inv*
3304	*au, Lpg*
3305	*imb, Lpg*
3306	*com^{in}, inv*
3307	*com^{in}, Lpg*
3346	*au, bs*
3347	*au, ms-32*
3348	*au, com* (*Tm-2^{a}*)
3349	*au, imb* (*Tm-2^{a}*)
3350	*au, br*
3351	*imb, Lpg/+*
3352	*imb, au, Lpg/+*
Chromosome 2	
0157	*p, d, m* (*r, y*)
0271	*aw, O*
0286	*d, m*
0310	*Wo^{m}, d*
0330	*bk, o, p, d, s* (*r, y*)
0342	*Wo^{m}, d* (*ms-17*)
0514	*aw, Wo^{m}, d*
0639	*Me, aw, d*
0650	*aw, d*
0715	*Wo^{m}, Me, aw, d*
0732	*suf, d*
0733	*Wo^{m}, d, ms-10*
0754	*aw, p, d, m, o*
0777	*dil, d*
0789	*Me, aw, d, m*
0790	*wv, Me, aw, d*
0986	*s, bk, Wo^{m}, o, aw, p, d*
1525	*aa, d*
1526	*are, wv, d*
1699	*Wo^{m}, bip*
1700*	*wv, aa, d*
2366	*bk, d* (*ds, j, nc, pox*)
3132	*Prx-2^{1}, ms-10, aa*
Chromosome 3	
0644	*r, wf*
0782	*sy, sf*
0877	*pau, r*
0880	*sf, div*
0987	*pli, con*
0988	*ru, sf*
1070	*ru, sf, cur*
1071	*sy, bls, sf*
1101	*cn, sy, sf*
1175	*bls, aut*
1180	*sy, bls, sf* (*ms-31*)
1430*	*sy, Ln, bls, sf*
Chromosome 4	
0774	*ful, e*
0885	*ful, e, su^{3}*
0886	*ful, ra, e*
0888	*ful, ven, e*
0889	*ra, su^{3}*
0890	*ra, ven*
0902	*ful, ra^{2}, e* (*ms-31*)
0915	*clau, ful*
0916	*clau, ra, su^{3}*
0917*	*clau, ful, ra, e, su^{3}*
0920	*ful, ra, e, su^{3}*
0989	*afl, ful*
0990	*cm, ful, e, su^{3}*
0992	*clau, ra, su^{3}* (*com*)
0993	*ra, si*
0994	*cm, ver*
1073	*clau, afl*
1074	*clau, ver*
1075	*ver, e, su^{3}*
1536	*clau, su^{3}, ra; icn*
Chromosome 5	
0512	*mc, tf, wt, obv*
1188	*frg, tf*
3850*	*af, tf, obv*
Chromosome 6	
0336	*c, sp* (*a, y*)
0640	*yv, c*
0651	*m-2, c*
0773	*yv, m-2, c*
0802	*yv, m-2, c* (*ms-2*)
0879	*tl, yv*
1114	*m-2, ms-33, yv, c*
1178	*yv, coa, c*
1189*	*pds, c*
1190	*pds, yv*
1489	*yv, ves-2, c*
1527	*d-2, c*
3805	*m-2, gib-1*
3806	*yv, Mi, og, sp, c*
3807	*tl, yv, c*
Chromosome 7	
0788	*La/+, deb*
0882	*La/+, deb, adp*
0923	*ig, La/+*
1083	*ig, flc*
1103*	*var, not*

LA	Genotype
1104	*deb, not*
1172	*La/+, lg-5*
Chromosome 8	
0513	*l, bu, dl*
0712	*l, bu, dl; ms-2*
0776	*l, va^{virg}*
0897	*l, bu, dl, al*
0922	*bu, dl, spa*
0998	*l, bu, dl, Pn/+*
0999	*tp, dl*
1012	*dl, l*
1191	*spa, ae*
1442	*dl, glg, marm*
1666*	*l, bu, dl, ae*
3906	*Wa, dl^{s}*
Chromosome 9	
0883	*pum, ah*
0884	*wd, marm*
1000	*nv, ah*
1001	*pum, ah, marm*
1100	*ah, pla, marm*
1112	*marm, lut*
1176	*Crk, ah, marm*
3353*	*ah, marm, pct*
3841	*Tm-2^{a}, Frl, nv,* (*Tm*)
Chromosome 10	
0158	*Xa/+, u, t* (*y*)

LA	Genotype
0339	*ag, u*
0341	*h, ag* (*ms-2*)
0642	*u, h, l-2* (*al, d, j, wt*)
0643	*u, l-2*
0649	*t^{v}, ag*
0711	*t^{v}, ag* (*ms-2*)
1002	*h, u, l-2, t, ag* (*pe, lg*)
1085	*h, res*
1086	*h, ten*
1110	*icn, ag*
1192	*hy, ag*
1487	*icn, t^{v}*
2493	*Xa-2, hy, h, ag*
2494	*Xa-2, l-2, h, t, u*
2495	*Xa-2, h, ten, ag, al*
2496	*Xa-2, h, l-2, t*
2497	*hy, u, icn, h, ag*
2498	*u, Xa-3, h*
2499	*u, nor, t*
2500	*u, icn, h*
2501	*u, icn, h, ag*
2502	*u, h, auv, l-2, t^{v}*
2503	*u, h, l-2, t^{v}, ag*
2504*	*u, h, t, nd, ag*
2505	*u, l-2, t, ag, Xa*
2506	*ag, h, l-2, oli, t^{v}*

LA	Genotype
2507	*h, t, nd, ag*
2508	*h, t, ag, Xa*
2509	*oli, l-2, t^{v}, ag* (*wf*)
2591	*Xa-2, h, ag*
2592	*u, h, t, nd, ag*
2593	*u, auv, ag*
Chromosome 11	
0259	*hl, a*
0291	*hl, a* (*ms-2*)
0729	*neg, a*
0730	*a, pro*
0761	*a, hl, j*
0798	*a, hl, j* (*ms-2*)
0803	*hl, a, pro* (*ms-2*)
0881	*neg, hl, a*
0925*	*j, hl, a, f*
1102	*a, hl, tab*
1488	*neg, ini*
1786	*j, f, a, bi* (*c*)
2352	*j, f* (*p, c*)
2364	*j, a, f* (*y, wt, c, l, u*)
2489	*neg^{ne-2}, a*
Chromosome 12	
1111	*fd, alb*
1171	*yg-2^{aud}, fd*
1177*	*alb, mua*

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.

LA	Genotype
0780	*yv, c* (chr 6)*; h, ag* (chr 10)
0781	*ful, e* (chr 4)*; neg, a* (chr 11)
0784	*ful, e* (chr 4)*; hl, a* (chr 11)
0982	*clau, e* (chr 4)*; hl, a* (chr 11)
0983	*l, dl* (chr 8)*; ah, marm* (chr 9)
1164	*var, not* (chr 7)*; ah, marm* (chr 9)
1166	*clau, su^{3}* (chr 4)*; icn, ag* (chr 10)

LA	Genotype
1182	*sy, sf* (chr 3)*; alb, mua* (chr 12)
1441	*coa, c* (chr 6)*; hl, a* (chr 11)
1443	*scf, dgt* (chr 1)*; l, al* (chr 8)
1444	*wv, d* (chr 2)*; af, tf* (chr 5)
1491	*scf, dgt* (chr 1)*; spa, ae* (chr 8)
1665	*scf, dgt* (chr 1)*; l, ae* (chr 8)

6.3. Miscellaneous Marker Combinations (377)

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.

LA	Genotype
0013	*a, c, d, l, r, y*
0014	*al, d, dm, f, j, wt, h*
0052	*j, wt, br*
0085	*Wo, d, h*
0137	*dl, wd, gq*
0154	*u, d, sp, h*
0157	*d, m, p, r, y*
0158	*t, u, Xa, y*
0159	*a, e, mc, t, u, y, wf*
0169	*ps, wf, wt*
0189	*bl, cl-2*
0190	*wf, br, bk*
0215	*at, y, u*
0281	*e, t, u*
0296	*br, bk, wf*
0297	*tf, ug, Nr*
0299	*ag, rv*
0302	*ag, dv, h, sp*
0312	*cm, vms, u, f*
0345	*ch, j-2*
0497	*ch, j-2, sf*
0499	*Od, sn, at, cm/+*
0508	*gf, d, c, a, r, y*
0511	*ps, a, c, y*
0638	*ht, d, r*
0642	*al, d, h, j, l-2, u, wt*
0648	*rv, e, Wo, wf, j, h*
0719	*Jau, clau*
0727	*wv, d, c, r*
0728	*a, lut*
0741	*sy, d, u*
0759	*lg, vi, pe, t*
0760	*lg, vi*
0770	*clau, pa*
0775	*tf, h, au, +/d*
0779	*clau, rv*
0796	*vms, Hrt, lg-5*
0801	*atv, slx*
0805	*a, c, l, sp*
0875	*hp, u, sp*
0876	*hp, sp*
0895	*tp, sp, u, Hr*
0907	*lut, pr*
0908	*per, var*
0909	*con, sf*
0912	*ht, su^3*
0913	*ful, su^3, ht*
0914	*com, ful*
0991	*ful, e, com*
0995	*deb, um*
0996	*um, ig*
0997	*um, not*
1018	*h, Od, ptb*
1038	*e, ht, su*
1072	*sy, sf, um*
1078	*ria, ves-2*
1079	*c, ves-2*
1105	*con, cur*
1106	*fsc, ah*
1163	*wv, d, tf*
1170	*cn, con*
1493	*ms-32, au*
1663	*Ln, Wo^m*
1664	*hp, lp*
1783	*ad, sp*
1784	*ae^{afr}, h, gs, sp*
1786	*bi, f, a, j, c*
1787	*Bk-2, en*
1789	*sl^{cs}, a*
1791	*Gp, Tm-2^a*
1796	*Rs, d, h*
1797	*Rs, d, wf, gf, h*
1798	*Rs, wf, h, a*
1804	*sr, sp, u*
1805	*sr, y*
1806	*ti, y, wf, al, j*
1807	*ti, a, e, u, h, mc, wf*
1808	*ti, c, mc*
2348	*l, x*
2349	*p, d, r, wt, j, f*
2350	*y, ne, p, c, sp, a*
2351	*c, l, u, h*
2352	*p, c, j, f*
2353	*y, wt, n*
2354	*br, y, p, l*
2355	*sp, ug*
2359	*y, Wo, r, c*
2360	*e, wt, l, u*
2363	*y, Wo, wt, c, t, j*
2364	*y, wt, c, l, u, j, a, f*
2365	*wf, r, sp, wd*
2366	*bk, d, ds, j, nc, pox*
2367	*y, m, t, f*
2368	*r, wt, mc, c, l, j*
2369	*p, Tm-1*
2370	*wf, n, gs*
2371	*d, wf, wt, c, f*
2372	*sp, fl*
2441	*d, m-2, mc, rvt, t, u*
2452	*B, f, gf, y*
2453	*Gr, u*
2454	*neg^{ne-2}, u*
2457	*u, so*
2458	*Pto, sp, u*
2461	*sp, stu, u*
2464A	*aer-2, r, upg, y*
2465	*sp, u, v-2*
2466	*d, t, v-3*
2467	*pe, u, vi*
2473	*alb, c, gra, sft*
2474	*d, gq, pst, ug, y*

LA	Genotype
2475	*ug, inc, tf, gs, al, Nr, h, hp*
2477	*vo, cjf, wf, sp, l, u, h*
2478	*ae^{afr}, r, gs, h*
2479	*ck, s, p, d*
2480	*ck, o, aw, p, m, d*
2481	*fn, in, bls, mc, gs*
2482	*fu, r, wf, mc, c, gs, u, h, hp*
2483	*fu, wf, mc, pdw, gs, u, hp*
2485	*inc, y, d, r, wf, mc, c, gs, l, gf, h, a*
2486	*inc, pds, sp, u, t*
2487	*c^{int}, sp, u, t*
2488	*mon, y, r, h, a, alb*
2490	*pdw, mc, pst, dl*
2492	*ti, wf, e, mc, u, a*
2510	*inc, d, r, wf, mc, gs, gf, h, a*
2512	*y, lg, pe, r, wf, m-2, c, gs, gf, marm, h, hp*
2513	*y, d, r, mc, gf, c, marm, gs, h, a, wf*
2514	*y, d, at, mc, m-2, c, sp, gs, u, yg-2*
2515	*y, r, wf, m-2, c, sp, gs, gf, u, a, yg-2*
2516	*r, wf, c, u, h, j, rvt, lg, pe, tmf, cjf, vo*
2517	*rvt, r, wf, m-2, c, gs, gf, marm, h, hp*
2518	*dp, m-2, c, gs, gf, h*
2520	*r, wf, mc, m-2, c, gs, 1, marm, h, hp*
2521	*r, clau, m-2, c, gs, gf, marm, u, h, a*
2522	*r, mc, m-2, c, gf, marm, u, h, f, hp*
2524	*af, sd*
2526	*dp, sp, u*
2527	*l allele, sp, u*
2528	*ti, y, wf, sf, f*
2595	*br, d, dm, wt, al, h, j, f*

LA	Genotype
2597	*y, r, wf, mc, m-2, c, gs, gf, marm, h*
2601	*y, e, mc, gs, gf, u, t*
2796	*lg, pe, vi*
2797	*bu, j*
2798	*f, h, ri*
2799	*f, h, j, l, wt*
2800	*hl, l*
3128	*Ln, t, up*
3208	*y, rot, d, c, l*
3210	*y, lg, pe, r, l, gf, h, a, (c/+)*
3211	*lg, pe, tmf, cjf, y, d, r, c, h*
3212	*tmf, d, sp, u*
3217	*glg, Pts*
3248	*bls, u*
3249	*a, c*
3250	*t, u*
3251	*Del, y*
3252	*Del, t*
3253	*r, y*
3254	*a, c, l, Ve*
3256	*at, t*
3257	*gf, gs, r*
3258	*u, Ve*
3259	*bls, u, Ve*
3260	*bls, l, u*
3261	*Del, gs*
3262	*Del, ug*
3264	*Tm-2^{2}, u*
3265	*bls, Tm-1, Tm-2, nv*
3266	*bls, Cf-4, u*
3267	*Cf-4, u*
3268	*Tm-2, nv, u*
3269	*Tm-1, u*
3270	*bls, Tm-2, nv, u*
3271	*Cf-?, Tm-1, u*
3272	*bls, Cf-?, u*
3273	*Gp, Tm-2^{2}*
3274	*ah, Tm-2, nv, u*
3275	*ah, Gp, Tm-2^{2}*
3276	*Tm-1, u, Ve*
3278	*bls, l, u, Ve*
3279	*at, Del*

LA	Genotype
3284	*at, gf*
3285	*gf, ug, y*
3286	*r, ug, y*
3287	*hp, r, ug*
3288	*hp, ug, y*
3289	*gf, r, y*
3290	*gf, hp, y*
3291	*at, hp, t*
3292	*Tm-2, u*
3294	*bl, d, u*
3297	*Tm-1, Tm-2, nv*
3298	*ep, sp, u*
3299	*ep, u*
3311	*og^{c}, u*
3315	*sp, pst, u, j-2, up, vo*
3362	*gs, t*
3363	*at, gs*
3364	*gs, u*
3365	*gf, gs*
3366	*t, y*
3367	*hp, t*
3368	*hp, y*
3369	*at, y*
3370	*at, hp*
3371	*hp, u*
3372	*gs, y*
3373	*at, u*
3374	*u, y*
3375	*gs, r*
3376	*Del, hp*
3379	*o*
3380	*gf, u*
3381	*r, y*
3382	*r, u*
3383	*gs, hp*
3384	*gf, y*
3385	*gs, Nr*
3386	*gf, t*
3387	*Nr, t*
3389	*Nr, y*
3390	*Nr, ug*
3391	*gf, hp*
3392	*hp, Nr*
3393	*r, t*
3394	*at, ug*
3395	*gs, hp, y*

LA	Genotype
3396	*at, u, y*
3397	*gs, t, y*
3398	*gs, hp ,t*
3399	*at, gs, hp*
3400	*at, hp, u*
3401	*at, gs, y*
3402	*hp, t, u*
3403	*gf, gs, u*
3404	*hp, u, y*
3405	*gs, hp, u*
3406	*at, hp, y*
3407	*gs, u, y*
3408	*t, u, y*
3409	*gs, t, u*
3410	*at, gs, u*
3411	*gs, r, u*
3412	*gf, gs, hp, u*
3413	*at, gf*
3414	*t, ug*
3415	*ug, y*
3416	*hp, ug*
3417	*r, ug*
3418	*gf, gs, ug*
3419	*at, gf, gs*
3420	*gf, ug*
3421	*Nr, u*
3422	*at, gs, ug*
3423	*gf, gs, hp, u, y*
3424	*gs, hp, u, y*
3425	*gf, gs, hp, t, u*
3426	*gs, hp, t, u*
3427	*gf, gs, t, u*
3428	*l, u, Ve*
3429	*Del, gs, hp*
3431	*bls, Cf-?*
3432	*Tm-1, Tm-2, nv, u*
3433	*ah, Tm-2, nv, u*
3434	*bls, Tm-1, u, Ve*
3435	*al, u*
3436	*Tm-1, Tm-2, nv, u, Ve*
3437	*at, Nr*
3438	*Del, hp, y*
3441	*dil, u*
3442	*de, dil, u*
3443	*cor, de, u*
3444	*cor, dil, u*
3445	*cor, pum, u*
3446	*cor, sp, u*
3447	*dil, sp, u*
3448	*in, u*
3449	*d, sp, u*
3450	*bls, sp, u*
3451	*bl, sp, u*
3540	*l, u*
3541	*gs, r, ug*
3542	*u, ug*
3543	*bls, o, u*
3545	*Del, u, y*
3546	*bls, Cf-?, u*
3547	*ah, u*
3548	*pum, u*
3549	*bls, Gp, Tm-2^2, u*
3557	*Del, gf*
3558	*gf, Nr*
3559	*Del, gs, y*
3561	*gf, gs, hp, Nr, u*
3562	*gf, gs, u, y*
3563	*sp, u*
3585	*gf, u, ug*
3586	*t, u, ug*
3587	*r, u, ug*
3588	*at, u, ug*
3589	*u, ug, y*
3590	*Nr, gs, y*
3591	*Nr, u, y*
3592	*gf, t, ug*
3593	*hp, u, ug*
3594	*gs, hp , ug*
3595	*gf, hp, ug*
3596	*hp, t, ug*
3597	*at, hp, ug*
3598	*r, t, ug*
3599	*at, t, ug*
3600	*t, ug, y*
3601	*gf, r, t*
3602	*at, gf, t*
3603	*at, gf, y*
3604	*hp, r, t*
3605	*at, ug, y*
3606	*r, t, y*
3607	*gs, hp, Nr*
3608	*hp, Nr, t*
3609	*hp, Nr, y*
3615	*d^x, u*
3675	*hp, Nr, u*
3676	*gf, hp, t*
3677	*gf, hp, r*
3678	*Nr, u, ug*
3679	*gs, Nr, ug*
3680	*Nr, t, u*
3681	*Nr, ug,* y
3682	*gs, t, ug*
3683	*gs, ug, y*
3684	*Nr, t, y*
3685	*gf, t, y*
3686	*gs, Nr, t*
3687	*gs, Nr, u*
3688	*gf, gs, hp*
3689	*gs, hp, r*
3690	*r, t, u*
3691	*r, u, y*
3692	*at, r, y*
3693	*g, t, u*
3694	*Del, gs, u*
3695	*Del, hp, t*
3696	*gf, gs, r*
3697	*gs, r, t*
3698	*gs, r, y*
3699	*gf, u, y*
3700	*at, gf, u*
3701	*at, t, u*
3702	*gf, gs, y*
3703	*gf, hp , u*
3704	*at, gf, hp*
3705	*gf, gs, t*
3706	*at, gs, t*
3706A	*Del, t, y*
3707	*at, gs, r*
3709	*Del, gf, gs, hp, u*
3741	*pum, u*
3742	*de, u*
3743	*cor, u*
3744	*sph, u*
3745	*bl, u*
3755	*lz-2, sp, u*
3771	*hp, B^c*
3810	*hp, t*
3811	*gf, r*
3812	*bls, Tm, Tm-2, nv*
3815	*Del, t, ug*

LA	Genotype
3821	*dil, pum, u*
3823	*pum, sp, u*
3826	*mon, u*
3827	*dil, cor, sp, u*
3830	*ep, B^c, u*
3831	*gf, gs, r, y*
4136	*Rg-1, r*

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