Report

of the

Tomato Genetics Cooperative

Number 50 - August 2000

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

Foreword

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

Membership currently stands at approximately 200 from 30 countries. Requests for membership (US$15 plus $5 shipping if international) should be sent to Theresa Fulton, 252 Emerson Hall, Cornell University, Ithaca, NY 14853-1901.

Cover photo taken by Esther van der Knaap, Cornell University. *Lycopersicon esculentum* cv. Prince Borghese (LA0089)

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From the editor

Welcome to the 50th Anniversary Issue of the Tomato Genetics Cooperative Report! Subscriptions have remained at the same level in recent years, suggesting that interest in receiving information and updates is still high. Submissions, however, have been decreasing, and so I would like to remind everyone that in order to disperse information we must have information to disperse! Remember, putting out information in the TGC Report in no way inhibits you from publishing it later in a peer-reviewed journal. It is, however, a way to disseminate information to your colleagues, therefore generating helpful feedback and possibly opening the door to rewarding collaborations. Submissions can be very brief, and can be submitted at any time throughout the year. So please be thinking about articles you could contribute to our next Report.

Deadline for submissions for the next report is June 1, 2001. Submissions received after this date will be accepted but not guaranteed publication in the current issue. As always, articles should be as concise as possible, 2 pages recommended. Submissions (preferably in Microsoft Word) should be sent to the managing editor as Macintosh or compatible diskettes (with an included hard copy), emailed as attachments (preferable), or uploaded by FTP.

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

http://genome.cornell.edu/tgc

Managing Editor:
Theresa M. Fulton
Plant Breeding Dept.
Cornell University
252 Emerson Hall
Ithaca, NY 14853-1901
Email: tf12@cornell.edu

Associate Editors:
Steve Tanksley, Cornell University, Ithaca, NY USA
Roger Chetelat, TGRC, UC Davis, Davis, CA USA
Dani Zamir, Hebrew University, Rehovot, Israel
Mathilde Causse, INRA, Montfavet Cedex, France

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

Announcement: Tomato Disease Workshop

The 16th Annual Tomato Disease Workshop will be held **November 30 – December 1, 2000 at the Westin Great Southern Hotel, Columbus, OH**. This meeting traditionally focuses on emerging and long-standing tomato disease problems, and a wide range of management strategies, including disease resistance and cultural, chemical and biological options. The Workshop is open to representatives from industry, academia and the farming community, students and other research, teaching and Extension professionals. A call for offered papers and/or posters will be made in July.

For information regarding this Workshop, please contact Sally Miller, Department of Plant Pathology, The Ohio State University, OARDC, 1680 Madison Avenue, Wooster, OH 44691 USA

phone: 330-263-3678
fax 330-263-3838
email miller.769@osu.edu

Announcement from Seminis Vegetable Seeds:

Tomato Breeders Round Table Meeting

Seminis has agreed to host the next TBRT meeting. We have chosen the week of **March 12-16, 2001 in Antigua, Guatemala**. For Guatemalans and international travelers, Antigua is a popular destination with views of an active volcano, beautiful Spanish colonial architecture, world class restaurants, language schools, and plenty of indigenous arts and crafts to bring home.

Guatemala is a fascinating country, with many interesting archeological sites, colorful Mayan villages, rainforests, Caribbean and Pacific beaches, mountains and lakes. With the meeting held during the week, you will have ample time during the preceding and following weekends for adventure. We should have an interesting meeting. The next announcement with registration material will come out in September.

We have booked the Hotel Santo Domingo, a restored 16th century monastery. The hotel has 90 rooms for $65 to $80 per night, which we will fill on a first come, first served basis. We will try to accommodate extra reservations in other similarly priced hotels in the area.

The tentative schedule is Monday, March 12 - welcome reception in the evening, Tuesday and Wednesday – meetings, including a Latin America session, a geminivirus session, and traditional reports. Wednesday evening - banquet at hotel. Thursday - field trip to visit the Seminis station in Salama. The Salama station is one of our major facilities for production of small lots of warm season vegetables such as tomatoes, peppers, and melons. Salama is a four-hour drive from Antigua. We are looking at several options for the tour, and will be asking for your choices with the next announcement. As part of the tour, we would like to offer scientists the opportunity to have their geminivirus resistant/tolerant tomato breeding lines or varieties challenged against the local geminivirus strains. We ask anyone who would like to see their material planted in a non-insecticide field trial to send us up to three entries by September 2000. Generally we see very nice symptoms in the Salama area by March. Please send at least 100 seeds of each entry. DO NOT SEND ANY LINES, WHICH YOU EXPECT TO BE “SECURE.” We do not want to have act as the germ plasm police.

We are still in the planning stages of the meeting, so if anyone has any major conflicts with the dates, please let us know immediately. (April 2-6 is Holy Week so that is not an option.) If anyone you know does not receive an announcement and would like to, please tell them to send us their address. Our mailing list is incomplete, and for many people we only have a name, no address.

Contact person:

Dr. Catherine Thome
Seminis Vegetable Seeds
500 Lucy Brown Lane
San Juan Bautista, CA 95045 USA
email: cathy.thome@svseeds.com

Jumping tomato gene "*gs*"

Avdeyev, Y.I. and Kigashpaeva, O.P.

Russian Scientific Institute of Irrigative Vegetable and Melon Growing

The gene "*gs*" determines green stripes in the epidermis of unripe fruit and golden stripes in ripe fruit. It is located on chromosome 7 in position 5, in the same location as the *pst* gene, which controlls the persistance of the style on the fruit, resulting in beak (Mutschler et al. 1987). The gene "*gs*" is accepted as being recessive, but on the fruits of gs/+ genotype pale green stripes are visible, especially on the lower fruits shaded by leaves.

Using the variety Tigerella as background, we selected several samples with round and plum-like fruit shapes, including such types as Crupny Avuri, in which the *pst* gene is not expressed (photo 1). After 10-12 years of using *gs*-selection we noted that some plants in the original lines, not hybridized with *gs*-forms, had developed obvious stripes. In 1996, among lines of the parental variety Bachtemir 2, we discovered one line in which some plants formed all *gs*-fruits or all normal fruits; on other plants *gs*-fruits were only on one main or lateral stems; on a third group of plants such fruits were only on 1-2 or more clusters, or only on 1-2 or more fruits. In addition, fruits with green stripes at 1/2 or 1/4 of the surface and only with 1-4 or more stripes were found (photo 2). Some plants were with very clear stripes on the fruit, similar to those of genotype *gs/gs*, but on other plants the stripes were pale, comparable to plants of genotype *gs*/+. From plants of this line we gathered seed for screening the next generations.

Analysis of the next and the following generation showed that all plants kept the genotype of the initial Bachtemir 2 variety (genes *d*, *u*, *j-2*; round fruit, 100 g, etc.) but segregation of the *gs* character was also present, as described above. The *gs* character demonstrated nonstability. In the generation of one plant (No. 4/10) a *gs*-character disappeared. The individual plant selection did not result in fixing the *gs* character in 100% of the plants in the succeeding generations (Table 1). Similar results were observed in one line of the variety Astrakchanky as well.

Combining the data of 1996-1999, we fixed the occurrences of the appearance of single plants of bright *gs/gs* phenotype in the varieties Richansky (*sp*, *U*, *j-2*; long fruit, 80g), Moriana (*sp*, *u*, *j-2*; oval fruit, 70g), Astrakhansky (*d*, *U*, *j*+; round fruit, 120g, h=80cm) and in some other varieties reproduced on our selection plots. In the years 1998-1999 we discovered 2 plants of phenotype *gs/gs* in the variety Novichok on a seed plot of more than 80 ha. In the previous period of more than 15 years such plants had not been noted.

The unique aspect of the discovered plants with striped fruits was the retention of a set of common traits from the initial parent, the lack of segregation of other traits, and the appearance of the *gs/gs* phenotype. All this contradicts the supposition of the hybrid origin of the described plants, in which case *gs/*+ (pale stripe) phenotypes (F1), or segregating groups of different phenotypes (F2) should be seen.

These phenomena, the nonstability of appearance of *gs*-phenotypes on the same plant and among different plants, and cases of the transference of the *gs/gs* phenotype into other varieties may be explained by the participation in these processes by mobile genetic elements (MGE). The authors suggest that in these described cases the tomato gene *gs* was included in one or more vectors of the transposon type, which belong to the MGE class. It is known that these elements can

initiate mutations and suppress gene expression, in those genes into which they are inserted (Ayala and Kiger, 1987). In our case the supposed vector(s) could be inserted into the different tomato varieties, causing suppression of the *gs*+ gene and expression of the joining *gs* gene. The transferring of the supposed MGE vector into plant cells could be occurring, for example, through pests, wounding of tissue, by some type of infection, etc. Different forms of MGE are described in maize and in *D. melanogaster* (Alihanian et al., 1985).

The occurrence of "walking" of the "green stripes" trait in plant fruits and "jumping" into other varieties evidently are not limited to only one described gene, which is highly visible. Our observations show similar occurrences in the properties of fruit form and color of skin. The authors suggest that in the selection material, which for a long time have been used for linear selections of permanent genetically distinct forms, an accumulation and increase of concentration of genetic variables such as transposon vectors (MGE) occurs. The latter being inserted near an individual gene can "pull it out" from one genotype and transfer it to other genotypes by similar infection.

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Alihanian S, Akifiev A, Chernin L. (1985) Common Genetics p.326 (Russian)
Ayala F, Kiger J. (1987) Jr Modern Genetics, Devis 2: 365 (Russian)
Mutschler M, Tanksley SD, Rick C. (1987) Linkage maps of the tomato. TGC Report 37: 5-34.

Table 1. Segregation of offspring in the Bachtemir-2 tomato line.

No. selected	1997	1998	
plant in the line	Fruit taken for seed	Total plants	Plants with *gs* fruit
3	100% *gs* fruits on one lateral stem	39	25
4	100% *gs*+ fruit on the central stem	12	11
6	Only 1 *gs* fruit out of 4 in one cluster	37	17
7	Only 2 *gs* fruit - 1 each from 2 clusters	36	28
	1998	1999	
4/8	Only 1 *gs* fruit on the plant	4	1
4/10	Only 1 *gs* fruit on the plant	8	0
9/13	Only 1 cluster with all *gs* fruit	7	1
5/1	100% *gs*+ fruit on the plant	12	2
5/2	100% *gs* fruit only on 1 cluster	15	7
5/3	100% *gs* fruit on the plant	12	5

Photo 1. Tomato variety Kzupny Avuzi (Large Avuzi)

Photo 2. Different variants of green-striped fruits in one line of Bachtemir 2.

Cotyledon tops bifurcation

Avdeyev, Y.I.

Russian Scientific Research institute of Irrigative Vegetable and Melon Growing

In one tomato line of the variety Bachtemir we found a mutation expressed as a bifurcation of the cotyledon tops by a central vein. The degree of cut in the bifurcation varied from faint to 0.3-0.5 cm in length. The property is recessive. The ratio of normal plants to mutants in the F2 was 19:6 and 47:14, showing a monohybrid inheritance (X^2 = 0.013, X^2 = 0.136).

The described gene is best identified after the appearance of cotyledons. It has no negative influence on other production-related traits.

For this discovered gene determining cotyledon tops bifurcation, the symbol *ctb* is proposed.

A Genetic Linkage Map of Eggplant

Doganlar, S., Frary, A., Daunay, M.C., Lester, R.N., and Tanksley, S.D.

Cornell University, Plant Breeding Department, Ithaca, NY, USA

A genetic linkage map is being constructed for eggplant using an interspecific F2 population from a cross between cultivated eggplant *Solanum melongena* cv. Rima and its wild relative *S. linneanum* MM195. Rima bears large, oblong, purple fruit whereas *S. linneanum* has small, round, green fruit. The mapping population consists of 58 F2 individuals which have been scored for several qualitative and quantitative traits including fruit size and shape characteristics. The final map will consist of RFLP markers that are single copy in tomato, thereby allowing comparative mapping between the two Solanaceous species. Examples of gene conservation in eggplant and tomato include regions on chromosome 10 of tomato that contain the anthocyanin gainer (*ag*) and uniform shoulder (*u*) genes (Figure 1). In addition, a marker (CT16) linked to *u* in tomato is strongly associated with the presence of stripes on eggplant fruit. The availability of a complete genetic linkage map for eggplant that can be easily compared to tomato will allow us to use the tremendous wealth of knowledge from tomato genetics to characterize the genome of its relative, eggplant.

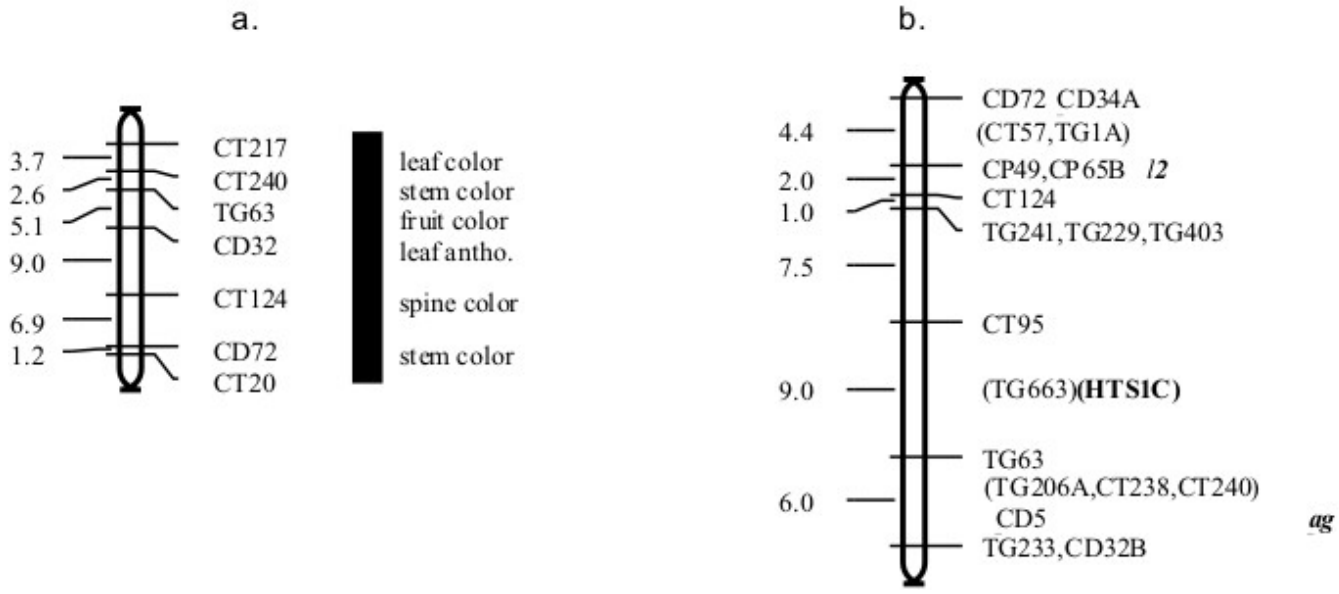

Figure 1. Comparative map of the bottom of chromosome 10 of tomato and eggplant.
a) eggplant map, b) tomato map. Mapping indicated that this region of the chromosome is inverted in eggplant relative to tomato.

Screening of wild accessions resistant to gray mold (*Botrytis cinerea* Pers.) in *Lycopersicon*

Egashira, H., Kuwashima, A., and Imanishi, S.

Faculty of Agriculture, Yamagata University, Tsuruoka 997-8555, Japan

Tomato gray mold (*Botrytis cinerea* Pers.) is a common disease worldwide, and often causes serious production loss by infecting leaves, stems, flowers and fruits. Presently, no resistant cultivars are available and there are very few reports about resistant materials in tomato cultivars and wild accessions (Urbasch 1986, Chetelat and Stamova, Eucarpia Tomato 97, unpubl.). To find new breeding materials for gray mold resistance, assessment for resistance of the leaflet and stem in six tomato cultivars, 44 wild tomato accessions and a *Solanum lycopersicoides* accession were performed.

Leaflets of the sixth compound leaf from the shoot apex, and 5 cm-stem-segments were used for the leaflet and stem bioassays. Conidial suspension with a density of 1×10^6 conidia / ml was inoculated onto the center of a leaflet using a bunch of sewing needles and onto the cut surface of a stem segment. Inoculated leaflets and stem-segments were incubated at 20°C under humid and 16-h photoperiod conditions for three days. The total numbers of leaflets and stem-segments inoculated were five to twenty and seven to nine per accession, respectively. Data were analyzed using GLM procedure and its REGWQ (Ryan-Einot-Gabriel-Welsch) option of SAS®.

Although no correlation was observed ($r=-0.127^{ns}$) between resistance of the leaflet and the stem, *L. peruvianum* LA2745, *L. hirsutum* LA2314 and *L. pimpinellifolium* LA1246 showed high resistance both in the leaflet and in the stem. Particularly, in the leaflets of LA2745, no lesion was observed even more than two weeks after the conidia inoculation. LA2745 is thought to be a promising material for breeding gray-mold resistant cultivars.

Literature cited:

Urbasch I. 1986. Resistenz verschiedener Kultur- und Wildtomatenpflanzen (*Lycopersicon* spp.) gegenuber *Botrytis cinerea* Pers. J. Phytopathology. 116: 344-351.

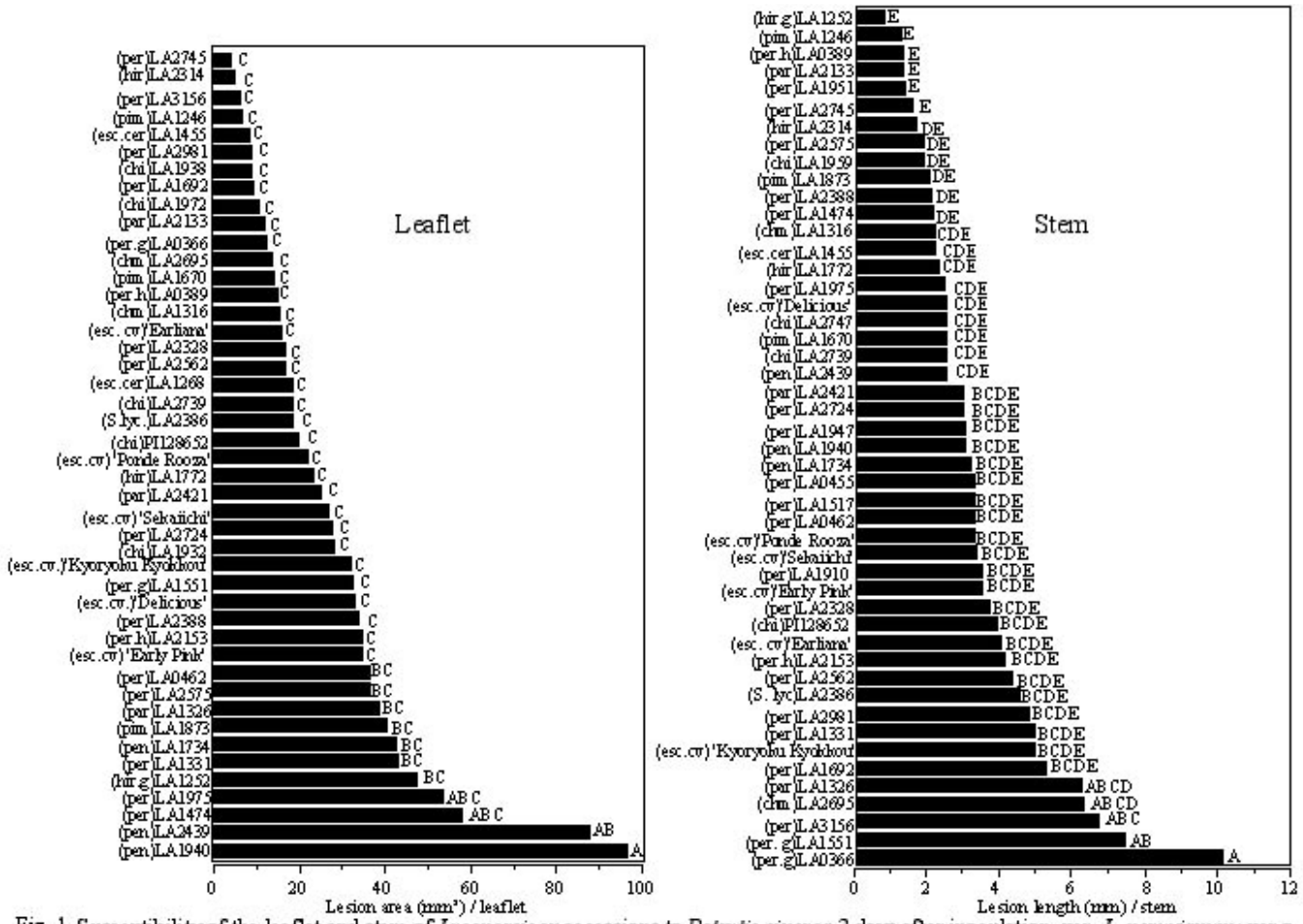

Fig. 1. Susceptibility of the leaflet and stem of *Lycopersicon* accessions to *Botrytis cinerea* 3 days after inoculation. per, *L. peruvianum;* per.g, *L. peruvianum* f. *glandulosum;* per. h, *L. peruvianum* var. *humifusum;* chi, *L. chilense;* hir, *L. hirsutum;* hir.g, *L. hirsutum* f. *glabratum;* pim, *L. pimpinellifolium;* esc.cv, *L. esculentum* cv.; esc.cer, *L. esculentum* var. *cerasiforme;* par, *L. parviflorum;* chm, *L. chmielewskii,* pen, *L. pennellii*; S. lyc, *Solanum lycopersicoides.* Same letters next to the graph bars show that difference of values between accessions are not significant at 5% level according to REGWQ multiple comparison procedure.

‘Ohio OX52’ Hybrid Processing Tomato

Francis, D.M. and Berry, S.Z.

Ohio Agricultural Research and Development Center, Horticulture and Crop Science, 1680 Madison Ave., Wooster, OH 44691 USA

‘Ohio OX52’ is an early-season processing tomato (*Lycopersicon esculentum* Mill.) hybrid adapted to high population transplant culture, machine harvest, and bulk handling under humid growing environments. It is suited for the production of peeled, whole-canned, and diced tomato products.

Origin: ‘Ohio OX52’ is the F1 hybrid resulting from the cross of the inbred line O87160 and Ohio 7814 (Berry et al. 1983). The line O87160 is an F6 selection from the cross of Ohio breeding lines B2905-1 and B2634-1; B2905-1 was derived from the cross ‘Ohio 7870’ X ‘K1483-3’. B2634-1 was derived from the cross Heinz 2653 and Heinz 722. O87160 is derived from the same F_3 as O88119 (Berry et al., 1995)

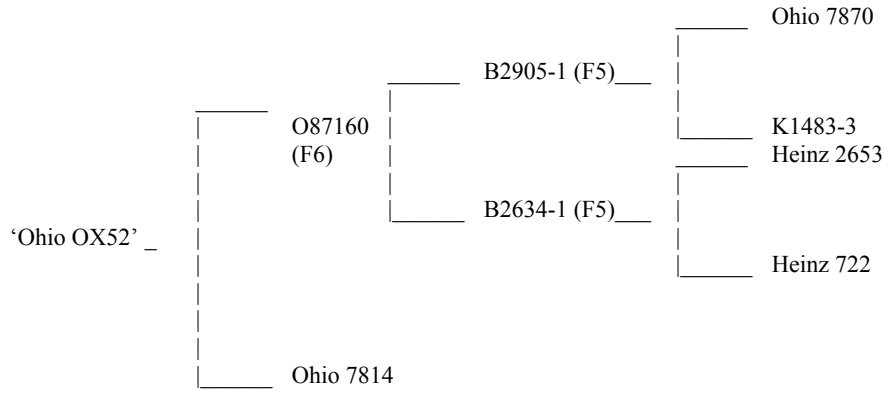

Fig. 1. Pedigree of ‘Ohio OX52’

Description: ‘Ohio OX52’ vines are medium in size, semi-prostrate, and determinate (sp). Foliage cover is adequate for ensuring good fruit quality and at maturity the vines cover the row area uniformly. The average maturity from transplant to harvest of ‘Ohio OX52’ is 97.1 days over four years of field testing, and is comparable in maturity to the early season standard, ‘Ohio 7983’ (Berry et al. 1992).

The average machine harvest yield of ‘Ohio OX52’ was 33.2 T/A over four years of testing (Table 1), outperforming the major early season varieties ‘Ohio OX 88’ and ‘Ohio 7983’ (though differences were not always significant). Yields of ‘Ohio OX52’ were comparable to the main-season variety ‘Ohio OX38’ and somewhat less than the major main-season variety Peto 696.

Fruit of ‘Ohio OX52’ average 2.1 oz with two to three locules. The shape is ovate. Fruit have a small stem scar and core, are uniform ripening (u), and are attached by a jointless pedicel (j2). The color and uniformity of color (expressed as a color difference) for fruit from ‘Ohio OX52’ are comparable to other varieties of the same maturity and superior to the main-season varieties OX38 and Peto 696 (Table 2).

Table 1. Four Year yield data for commercial varieties, checks, and potential varieties. Rank by maturity

Variety	Mat	T/A	T/A SDEV	Rel-1	SD Rel-1	Rel-2	SD Rel-2
O 7983	96.2	27.63	4.54	-2.84	4.13	-4.61	3.52
OX 88	96.9	31.64	5.79	1.41	3.84	-0.23	4.41
OX 52	97.1	33.21	8.10	2.74	7.71	0.96	7.63
TR 12	98.2	34.98	3.81	3.28	1.5	2.3	2.63
OX 38	101.2	32.66	3.83	2.2	3.89	0.42	4.66
PS 696	101.8	34.72	8.42	4.75	6.96	2.98	6.16
H 9423	102.7	37.77	6.98	7.23	5.09	4.78	3.33
O 8245	103.7	32.72	6.92	2.52	5.51	0.72	4.34

Rel-1: Relative to the yield of the trial
Rel-2: Relative to the yield of the trial checks (O 7983, PS696, H 9423, O 8245).

Table 2. Objective color measurements and color difference (dif) measurements from three years with three locations per year.

Genotype	N	L	a	b	Chroma	Hue	Ldif	adif	bdif	Cdif	Hdif
O7983	18	40.9	25.8	24.4	36.0	43.7	3.9	3.3	3.1	2.7	5.7
OX52	17	41.1	25.9	24.7	36.4	44.0	4.0	3.7	2.9	2.6	6.2
TR12	18	39.8	26.7	24.3	36.4	42.5	3.2	2.8	2.5	2.5	4.2
O8245	18	43.1	26.0	25.9	37.6	45.4	5.4	5.2	3.8	3.1	8.5
PS696	18	42.1	26.4	25.7	37.5	44.7	4.1	3.8	3.0	2.6	6.2
LSD (0.05)		1.3	1.0	0.8	0.6	1.9	0.5	0.7	0.3	0.2	1.3

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Berry, S.Z. K.L. Weise, and W.A. Gould. 1992. "Ohio 7983" Processing Tomato. Hortscience 27: 939.

Berry, S. Z., T.S. Aldrich, K.L. Wiese, and W.D. Bash. 1995. 'Ohio OX38" Hybrid Processing Tomato. Hortscience 30:159.

The possible involvement of phenolic substances in heat shock response of tomato pollen

Georgieva, I.D., Kruleva, M., Danailov, Zh., Kraptchev, B.

Institute of Genetics, Bulgarian Academy of Sciences, Sofia 1113, Bulgaria

Exposure to high temperature is one of the environmental stresses that limit plant productivity and survival. Poor fruit set after high temperature treatment is not well understood in terms of the importance of these effects on male and female reproductive tissues. It was reported that high day temperatures increase floral sterility associated with decreased pollen viability at anthesis (Ziska and Manaldo, 1996). High temperature shock disturbs the polarity in the microspory (Tanaka, 1993). Temperature stress applied to pollen leads to destruction of long lived mRNA and thus affects the ability of pollen grains to incite protein synthesis needed for germination. (Ciampoluni et al.,1991) The effect of high temperature on pollen have been studied in connection with the synthesis of heat shock proteins as well (Maskarenhas, Crone, 1996). Our previous investigation on the enzyme activities in tomato pollen after heat shock showed that pollen metabolism is strongly affected by high temperature (Georgieva et al., 1998). A large body of evidence points that secondary metabolites are implicated in stress responses of plant as well (Edreva, 1996). This study covers a heat stress response of mature tomato pollen connected with changes of phenolic substances in pollen grains of plantes subjected to high temperatures during the anthesis.

Two parental lines, tolerant (T) and susceptible (S), and their F1 hybrid (with intermediate thermotolerance), characterized previously by differences in temperature tolerance at sporophytic level (Georgieva et al. 1998) were used as experimental material. The plants were grown in the field until anthesis. Then they were transferred to temperature chamber at 42/28 C (day/night) and photoperiod 16/18 hours (day/night) for 48 hours. Pollen from untreated plants was used as a control.

Cytochemical reactions were applied to demonstrate different classes of phenolic compounds Total phenolics were tested using 2-3 min staining with 0.5% toluidine blue O in acetate buffer at pH 4.4 followed by washing in the buffer solution (Feder, O'Brein, 1968) Flavonoids were determined by their fluorescence after 5 min incubation in 5% ethanolic A13C13 solution and observation into a drop of tap water (Wollenweber et al. 1992). The fluorescence of flavonols was observed after staining with 0.5% solution of ethylflavognost in absolute alcohol (Hauserman and Waltz, 1962). Condensed tannings were detected with 2% vanillin in concentrated HCl (Lees et al., 1993). Polyphenols were localized by means of notroso reaction (Mace, 1963). Lignin was stained with phloroglucinol-HCl reaction (Gahan, 1984). Pollen viability was assessed on the basis of the fluorochromatic (FCR) test (Heslop-Harrisson et al., 1984).

The results clearly show that the exposure of tomato plants to heat stress during the stage of pollen shed had significant effect on pollen viability and phenolic content of pollen grains. The high temperature stress was associated with decrease of pollen viability which was strongly expressed in the S line. The hybrid showed intermediary values. The heat treatment brought about a rise in the percentage of pollen grains with positive cytochemical reaction for total phenolic compounds, flavonoids, flavonols and condensed tannins. This increase in the case of total phenolics and condensed tannins was more prominent in the T line, whereas in the case of flavonoids and flavonols it was better expressed in the S line. In the pollen of the hybrid the flavonols exhibited a significant increase. (Fig. 1) The cytochemical reaction for polyphenols in the pollen grains of treated and untreated plants was negative. A slightly positive reaction for lignin was observed in the exine of the pollen grains, but the lignin content was not affected by the heat treatment.

In general, the pollen of the three tomato genotypes under study showed similar responses to the high temperature concerning the increase of phenolic content in pollen grains. Under stress conditions plants mount a broad range of defense mechanisms including the rapid and transient generation of reactive oxygen species (Bolwell, Vojtaszek, 1977). This oxidative burst has been suggested to be a trigger of stress responses in plants (Low and Merida 1996). To avoid oxygen mediated toxicity the scavenging of reactive oxygen species by some phenolics, especially flavonoids, is critical as they may act as endogenous antioxidants because of their radical scavenging ability (Castellucio et al., 1995, Yamasaki, 1997). It is well documented that heat stress results in the production of both superoxide anions and hydrogen peroxide indicating that the heat treated plants underwent an oxidative burst (Vallerian-Bindschedler et al., 1998). In addition, heat treatment of plants is associated with the accumulation of phenolic compounds in their leaves (Ferraris et al., 1987). It can be accepted that the observed increase of the percentage of pollen grains containing phenolic compounds is a response reaction of tomato pollen to the heat stress. However, the enhancement of the different classes of phenolic compounds in tomato pollen after heat stress did not correlate with the thermotolerance of the sporophyte uniformly.

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Figure 1, next page

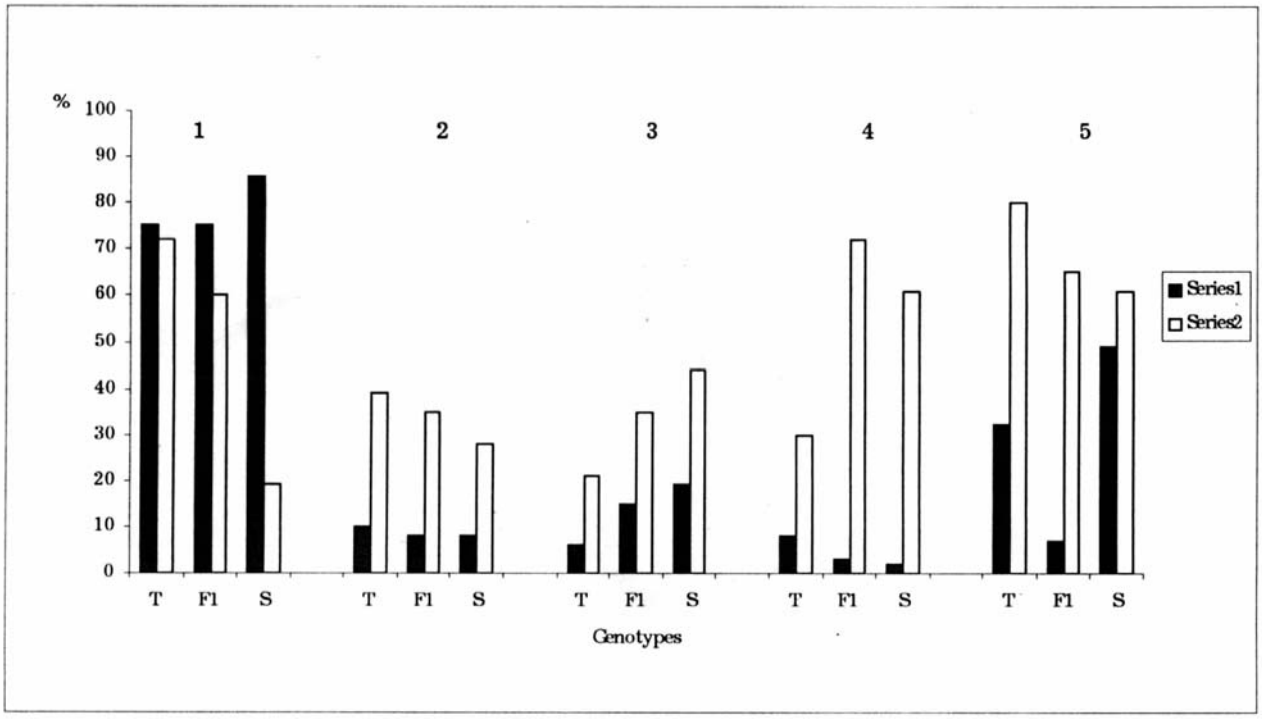

Figure 1. Changes of viability and phenolics in tomato pollen subjected to heat stress, expressed as the percentage of pollen grains with positive cytochemical reaction.
Series 1 - Control. Series 2 - t^o
1 - Pollen variability; 2 - Total phenolics; 3 - Flavonoids; 4 - Flavonols; 5 - Condensed tannins

Use of a single probe CP58 for simultaneous selection of resistance genes to potato virus Y (PVY), PVA and cyst nematode (GCN) in the tuber-bearing *Solanum*

Hamalainen[1], J.H., Valkonen[1], J.P.T., Pineda[2], O., Slack[2], S., Gebhardt[3], C., and Watanabe[4], K.N.

1. Swedish Univ. Agr. Sci., Uppsala, Sweden; 2. Mendel Biotechnology, 21375 Cabot Blvd.,Hayward, CA, 94546, USA; 3. Max-Planck Inst.-Koln, Germany; 4. Fac. Biosci., Kinki Univ., Japan

Potato virus Y(PVY) is the major viral pathogen of potato in most temperate areas in the world, e.g. Northern Europe, North Eastern region of USA and Canada, and Hokkaido, Japan. Potential yield loss could be 70% or even higher. PVA is also a causal agent for the viral disease commonly occurring in temperate zones. Cultivars with resistance to PVY and PVA have promise as a persistent and cost-effective means of control augmented by a strict seed certification system.

Potato golden cyst nematode (GCN, *Globodera rostochiensis*), pathotype Ro1 occurs in the same regions as PVY, and also causes serious damage to potato production.

Extreme resistances (ER) are available against both PVY and GCN, and hypersensitive resistance is available against PVA. The ERs to PVY are available from several cultivated and wild relative species: *S. tubersum ssp. andigena* (*Ryadg*), *S. stoloniferum* (*Rysto*), *S. chacoense* (*Rychc*) and putative resistance loci were reported on *S. brevidens* and *S. phureja*. *Ryadg* and *Rysto* are single dominant genes. The ER genes to GCN are also available from a couple of sources: the major source is *H1* gene from *S. tubersum ssp. andigena*. The HR gene against PVA is also located on Chrom XI of potato (Hamalainen et al. 2000) with the same region as *Ryadg.*

To facilitate potato breeding for the resistances, molecular markers have been employed on these traits. *Ryadg* is located on Chromosome XI at the proximal end, closely linked with RFLP markers such as *TG508, GP125, CD17,* and *CT168*. *CP58(A)* on Chrom XI was successful in distinguishing *Ryadg* (R) and S genotypes in 96% out of 200 cultivars and breeding lines from the Americas and Europe.

H1 gene is located at Chromosome V linked to *TG403, TG 69* and *CD78*. *CP58(B)* on Chrom V was efficiently used to identify *H1*(R) and S potato genotypes with 98% chance in 200 cultivars from Americas and Europe (Pineda *et al.* 1993). Japanese cultivars with pedigree derived from Dansyaku (Irish Cobbler) and May Queen (White Rose) could not be separated with the marker.

Ryadg and *H1* should be incorporated into the same cultivar. If one probe/marker could provide both information instead of using separate probes or makers, it would be a more informative and efficient way of marker assisted selection (MAS).

CP58 is a RFLP probe generated at Max Plank-Koln, Germany, which identifies multiple loci, one on Chromosome V (*CP58 B*) and another on Chromosome XI (*CP58A*). Thus, the probe CP58 could be simultaneously used for selecting *Ryadg* and *H1* in one lab selection process. Using 200 cultivars from Europe, Japan and the Americas and 100 of 2x and 4x lines from various origins including wild species, the probe CP58 was employed in MAS for the two traits. The cultivars with *Ryadg* and *H1* genetic background have been selected with 90% probability and other cultivars/ breeding lines with different resistance origins were not effectively selected. Resistance to PVA can also be distinguished using the *CP58(A)* locus which is linked with *Ryadg*, too. Overall, the probe CP58 is useful for primary selection of the three resistance traits with these specific origins.

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Differential response of resistant lines derived from the *L. pimpinellifolium* accession L3708 and *L. hirsutum* accession LA 1033 against different isolates of *Phytophthora infestans* in detached leaf lab assays

Kim, M.J., Mutschler, M.A.

Dept. of Plant Breeding, Cornell University, Ithaca, NY 14853

The disease late blight (caused by the pathogen *Phytophthora infestans*) is an increasingly significant problem to processing tomato production. Transfer of resistance into processing tomato lines could materially reduce reliance on chemical sprays for control of this disease. We are working with two potential sources of Late Blight resistance, *L. hirsutum* accession LA 1033 and the *L. pimpinellifolium* accession L3708. The first source is the *L. hirsutum* accession LA 1033-2, a sub-selection of LA 1033 created by Dr. R. Gardner, N.C. These sources are reported to hold up to challenges by late blight in a number of locations. In North Carolina, these sources of resistance have held up under conditions in which Hawaii 7998 source and the Ph2 gene fail (Gardner, per. comm.). Dr R. Gardner had provided us with a series of cuttings of BC1F2 plants, each of which was derived from the cross (and subsequent backcross) of one of the resistance sources with the fresh market line NC215-E, a VFF early blight tolerant elite fresh market line. These plants were used in further backcrosses to processing tomato parents to transfer the resistance to processing lines fixed for resistance. These lines were tested in lab assays using a series of isolates of the pathogen to determine if either of the sources of resistances is limited in utility by race specificity.

Greenhouse grown plants were tested in the laboratory by detached leaflet droplet tests that were modified from those reported by Mizubuti and Fry (1998). In the detached leaflet droplet test method, tomato leaflets from the 3-4th leaf from the tip were placed abaxial surface down on water agar plates. Care was taken to choose flat leaflets. Each leaflet was inoculated with two 20μl drops of 30,000 sporangia/ml. (When 10,000, 20,000, 30,000 and 40,000/ml concentrations was pre-tested on susceptible plants, escape did not occur using the 30,000 and 40,000/ml concentrations). The plates were incubated upside down at 18°C and 16hr light for 7-8 days. Sporangia count was followed after incubation. Leaflets were placed into 5ml of preservation solution (2.5ml of d $H_2O$and 2.5ml of 0.04M $CuSO_4^-$ 0.2M Sodium acetate- acetic Acid at pH 5.4) followed by 10 sec. Mixing using a Vortex. Leaflets were removed from vials and used to measure leaf area using an area meter. The detached leaflet droplet test is effective for classifying plants as highly resistant versus moderately resistant plants versus susceptible.

Several isolates of *Phytophthora infestans* provided by Dr. W. Fry were used in laboratory screens:

US-7: a metalaxyl resistant race of A2 mating type that is widespread in the U.S. US-7 was used for field screening in N.Y. summer of 1998.

US-8: a potato isolate which can cause milder disease on tomato

US 11: metalaxyl resistant race of A1 mating type. US-11 was described in 1994. It has been a problem in CA in the 1998 season. US-11 was used for lab assays of detached leaves from N.Y. greenhouse grown plants in 1998.

US-17: metalaxyl resistant race of A1 mating type. It is very virulent on tomato. US-17 was found in four states (Florida, Alabama, New York and New Jersey) in 1996. ((Fry and Goodwin

1997)) DNA analysis and GPI tests indicate that US17 may have been derived from US-6 or US-8. US-17 was used for lab assays of detached leaves from N.Y. field and greenhouse grown plants in 1998.

DR4B: isolate recently collected in the Dominican Republic. This isolate is very virulent on tomato and is of the A1 mating type

Table 1. Response of resistant and control lines against different isolates of *Phytophthora infestans* in detached leaf laboratory assays.

Isolate	Pik Rite	VFT Vendor	New Yorker *Ph-1*	WV63 *Ph--2*	*L. pimp* L3708 derived	*L. hirsutum* LA1033-2 derived
US-7	S	S	S	S	R	R*
US-8	S	R	M	M	R	R
US-11	S	S	S	M	R	R
US-17	S	S	S	M*	R	R*
DR4B	N.A.	S	S	S	R	NA

S: susceptible, M: moderately resistant, R: highly resistant
M* variable between susceptible and moderately resistant
R* variable between resistant and moderately resistant
NA data not available

Table 1 gives a summation of multiple tests of these isolates on control and resistant tomato lines. The susceptible control, Pik-Rite, uniformly showed strong susceptible reactions, indicating that the screens were reliable. In the droplet assay using susceptible leaflets, hyphae overrun the leaf surface causing a fuzzy appearance, and high numbers of sporangia are produced within 4 to 5 days after inoculation, even though leaf tissues remain green.

It was a surprise that Vendor is resistant to the potato stain, US-8. However, Vendor reputedly has the Cf-9 gene, which a recent report indicated produces a protein that detects the INF1 protein of *Phytophthora infestans* (Kamoun, Honee et al. 1999). Neither the Ph-1 nor the Ph-2 sources had strong resistance to any of the isolates used in our lab assay. This is in agreement with tests by other groups.

The breeding lines with the L3708- derived resistance were remarkable in that they were uniformly and fully resistant to all isolates of the pathogen tested. We intend to test with additional highly virulent isolates from diverse locations. However, at this point we cannot identify an isolate that will overcome this source of resistance. Leaflets from lines carrying resistance from *L. pimpinellifolium* L3708show small black lesions by 3 to 4 days. This spot can expand somewhat thereafter, but little fuzziness is observed, and sporangia counts per leaflet are reduced 100 fold compared to those of the susceptible controls.

The lines derived from *L. hirsutum* LA 1033-2 do not have as strong a resistance as that derived from *L pimpinellifolium* L3708. Leaflets from lines carrying resistance from *L. hirsutum* LA 1033-2 showed reactions that are similar in appearance and timing to those from lines derived from *L pimpinellifolium* L3708 except that a yellowish region surrounds the black lesions produced. It is unclear at this point whether the two types of resistance are related, or if there would be any benefit in combining sources of resistance.

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A Tomato Sequence-tagged Connector (STC) Database

Lee, S., Mao, L., Main, D., Wood, T., Wing, R.A.

Clemson University Genomics Institute, 100 Jordan Hall, Clemson, SC 29631 USA

In an effort to develop a tomato STC database for genome sequencing, we are sequencing the ends of BAC clones from a 15x genome equivalent *L. esculentum* BAC library (Budiman, 2000). To date, we have generated 4,990 tomato STCs with 4,310 of them (86.4%) having an average sequence length of 372.4 high quality bases. All STCs were searched against SwissProt using FASTX (Pearson, 1988) and against all plant sequences downloaded from GenBank, using FASTA (Pearson, 1988).

With a cutoff expectation (E) value of <10-5, 1,756 sequences (35.19%) were found to show homology with known sequences. As shown in Fig.1, about 40% of the 1,756 STCs share sequence similarity to defined gene-related sequences. Various retrotransposons comprise another 40% of all the STCs having a match with GenBank, suggesting that retrotransposons are a major component of the tomato genome. STCs homologous to non-LTR retrotransposons were also found and reported here for the first time in the tomato genome according to our GenBank search results. STCs similar to repetitive elements constitute 13% of these sequences. The remaining STCs (6%), which we labeled miscellaneous DNA, were homologous with GenBank sequences that are poorly annotated or constitute non-genomic DNA, such as chloroplast and mitochondrial DNA.

Retrotransposon polyproteins, i.e. T17459 (GenBank acc. no., gypsy-like, tomato), Lere1 (copia-like, tomato, Mao et al. unpublished) and CAA73798.1 (GenBank acc. no., non-LTR, Beta vulgaris), were used as queries to search against all the tomato STCs sequences using FASTA and TFASTA (Pearson, 1988). A total of 304 STCs were obtained, of which 195 were homologous to gypsy-like retrotransposons, while the numbers of STCs that were homologous to copia-like and non-LTR retrotransposons were 92 and 17, respectively. It is interesting that the ratio of tomato STCs homologous to each type of retrotransposons are similar to that shown in rice (Fig.2), i.e. gypsy-like retrotransposons make up more than half of the total STCs homologous to retrotransposons (Mao, 2000).

As sequencing has progressed, the number of STCs that have no homology to GenBank sequences has decreased from 70% in our previous study of 1205 STCs (Budiman, 2000) to 64%. We expect that this number will continue to decrease, although slowly due to the expected large number of retrotransposon sequences in the tomato genome.

The 4,990 tomato BAC ends and the results of the FASTX and FASTA searches are accessible at (http://www.genome.clemson.edu/~dorrie).

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Fig.1. The major groups of STCs in 1,756 tomato STCs.

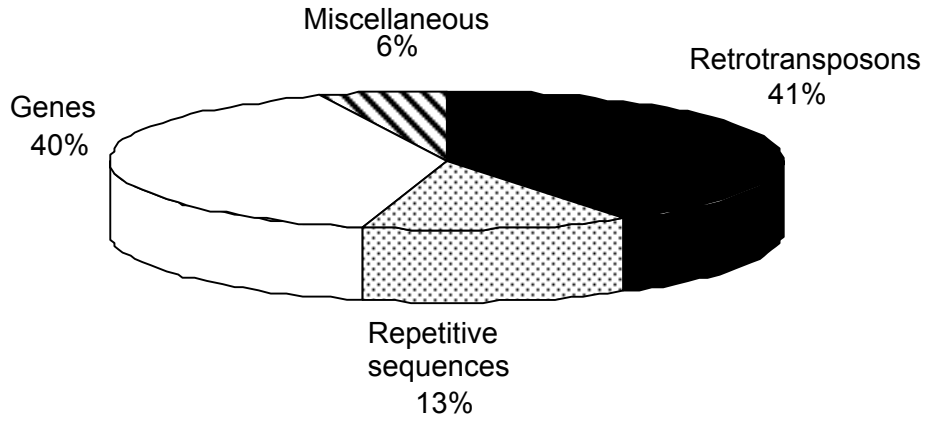
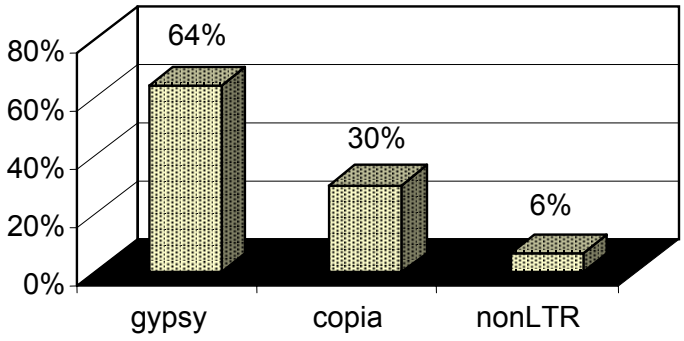


Fig. 2. Retrotransposons composition in tomato STCs. The results were obtained by searching the tomato STC database using FASTA and TFASTA with representative retrotransposon sequences as queries as described in the text.



Resistance to *Oidium lycopersicum* : allelism test between *Lycopersicon hirsutum* G1.1560 and *L. hirsutum* PI247087

Moretti, A. and Caranta, C.

INRA, Genetics and Breeding of Fruits and Vegetable, Dom. St Maurice, BP94, 84143 Montfavet cedex, France.
E-mail : Carole.Caranta@avignon.inra.fr

Resistance to powdery mildew (*Oidium lycopersicum*) in *Lycopersicon hirsutum* G1.1560 was shown to be controlled by an incompletely-dominant gene, *Ol-1*, mapped on chromosome 6 in the vicinity of the resistance genes *Mi*/*Meu-1*, *Cf-2*/*Cf-5* (van der Beek *et al.* 1994).

Among the accessions of wild species frequently used at INRA, a very high level of resistance to *O. lycopersicum* was identified in *L. hirsutum* PI247087. The intermediate levels of resistance observed during the introgression of PI247087 resistance into elite tomato lines attested to the oligo- or polygenic nature of this resistance. Moreover, fruits from all the plants with the higher level of resistance were yellow. An allelism test between these plants and a tomato line homozygous for the *r* gene (yellow flesh) was performed and revealed a linkage between *r* and resistance to *O. lycopersicum* (Laterrot & Moretti, unpublished data).

To determine whether a part of PI247087 resistance to *O. lycopersicum* is due to the gene *Ol-1*, an allelism test was performed between PI247087 and *L. hirsutum* G1.1560.

Resistance of *L. esculentum* Momor, *L. hirsutum* PI247087 and G1.1560, the F1 hybrids (Momor X PI247087) and (PI247087 X G1.1560) and the F2 progeny (PI247087 X G1.1560) to *O. lycopersicum* was evaluated during two independent tests. Plants were inoculated three weeks after sowing by spraying with a suspension of 10^4 conidia ml^{-1}. Inoculum was prepared from freshly sporulating leaves of heavily diseased tomato plants. After inoculation, plantlets were transferred into growth chamber with 100% relative humidity, 24°C day/18°Cnight and 12 hours light. Disease was evaluated 18 days after inoculation according to the following index : 0=no visible sporulation (healthy plants), 1=very few powdery mildew spots surrounded by a necrosis (stopped sporulation), 2=moderate number of spots (moderate sporulation), 3=very high number of spots (strong sporulation). Plants classified 0 or 1 were considered resistant and plants classified 2 or 3, susceptible.

Results are presented in Table 1. All plants could be classified unambiguously. *L. esculentum* Momor was completely susceptible with most of the plants with a high number of “sporulation spots”. *L. hirsutum* PI247087 and G1.1560 were resistant with most of the plants without sporulation. A small number (3/15) of the F1 (Momor X PI247087) showed some sporulation. The same observation was made by van der Beek et al. (1994) on the F1 hybrid between G1.1560 and a susceptible *L. esculentum* line. On the contrary, all the F1 between the two *L. hirsutum* were resistant. Among the 247 F2 (PI247087 X G1.1560) evaluated, 219 presented no symptoms and 28 a stopped sporulation. The observed segregation suggests that *Ol-1* is probably involved in PI247087 resistance to *Oidium lycopersicum*.

Literature cited:

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Table 1. Results of the allelism test between *L. hirsutum* PI247087 and *L. hirsutum* G1.1560 for resistance to *Oidium lycopersicum*.

Disease Index	**Number of plants**				**Total**
	0	**1**	**2**	**3**	
L. esc. Momor	0	0	5	14	19
L. hirs. PI247087	16	6	0	0	22
L. hirs. G1.1560	15	6	0	0	21
F1 (Momor X PI247087)	4	8	3	0	15
F1 (PI247087 X G1.1560)	10	9	0	0	19
F2 (PI247087 X G1.1560)	219	28	0	0	247

Lycopersicon chilense-derived bridge lines for introgressing *L. peruv*ianum traits into the esculentum genome

Picó, B., Herraiz, J., and Nuez, F.

Department of Biotecnology (Genetics). Universidad Politécnica de Valencia E-46022. Valencia, Spain. E-mail: fnuez@btc.upv.es

Lycopersicon peruvianum is a highly polymorphic species not cross-compatible with the cultivated tomato, *L. esculentum* (Taylor, 1986). The successful of embryo and ovule culture techniques in interspecific crosses, using *L. peruvianum* as male parent, highly depends on the accession employed (Gradziel and Robison, 1991). One method to overcome this crossability barriers involves the construction of "bridging genotypes" readily crossable with both *L. esculentum* and a considerable set of *L. peruvianum* accessions.

Taylor and Al-Kummer (1982) constructed complex hybrids between *L. esculentum* and *L. peruvianum* which showed strong sexual compatibility with *L.esculentum* and *L.chilense*, but a weaker degree of compatibility with one specific race of *L.peruvianum*. Rick (1983) identified two *peruvianum* "Marañon" accessions, LA 1708 and LA 2172, which set 0.2 seed/fruit in crosses with *L.esculentum*. By using the hybrid between *L. esculentum* and the cross-compatible *L.peruvianum* PE-23, Ayuso *et al*. (1987) obtained seeds in crosses with other incompatible *L. peruvianum* lines, and the hybrid could be crossed with *L.esculentum* (0.1-0.3 seed/fruit). Poysa (1990) developed bridging genotypes derived from *L.esculentum* x *L.peruvianum* to facilitate gene transfer. However, these lines did not provide an easy method to routinely transfer genes from *L.peruvianum* in later studies, and had to be used in combination with seed-rescue culture (Veremis and Roberts, 1996).

The use of wild species other than *peruvianum* in bridging lines was attempted by Sotirova and Vulkova-Atchkova (1988), who used one *L.esculentum x L.chilense* hybrid as a bridge, and successfully crossed it to one accession of *L.peruvianum var humifusum*.

We obtained interspecific hybrids *L.esculentum* x *L.chilense* LA 1932 (0.6 viable seeds/fruit) in a program aimed to breeding tomato wtih resistance to Tomato Yellow Leaf Curl Virus. These hybrids could also be easily backcrossed to tomato (26 viable seeds/fruit). This low degree of incompatibility to tomato led us to test genotypes derived from this line as bridges in transferring *L.peruvianum* traits to tomato.

From all previous studies it appears that an ideal bridging genotype will be predominantly composed of wild genome (50-87.5%). Therefore, using the interspecific hybrid F1 1932, we obtained the first backcross to the wild parent (BC1´-*chilense*), with 75% of the *chilense* genome. The bridging capacity of this line was studied in comparison with that of the "Marañon" races (LA 1708 and LA 2172), and with that of a first backcross to *peruvianum* (BC1´-*peruvianum*), with 75% of *peruvianum* genome, derived from the accession *L. peruvianum* PI-143679, crossable to tomato *via* embryo culture.

The crossability of these genotypes, as male or female parents, with *L.esculentum* and three highly incompatible *L.peruvianum* accessions was evaluated by scoring the number of viable seeds set in mature fruits of each cross. The "Marañon" races could be crossed to tomato only as male parents (Table 1). The reciprocal cross failed due to unilateral incompatibility. Only aborted seeds were found when using these accessions in crosses with the other three *L.peruvianum* accessions, both as male or female parents.

The BC1´- *peruvianum* line failed to set viable seeds when crossed to tomato as male or female parent (Table 1), but plants could be recovered with the aid of immature embryo culture in one cross direction. More relaxed crossability barriers occurred in crosses with the three *L.peruvianum* accessions as male parents, and more than 20 seeds per fruit could be recovered.

In conclusion, these three potential bridge lines (the two “Marañon” races and the BC1´-*peruvianum*) do not appear to provide an effective mean for overcoming crossability barriers within the *Lycopersicon* genus, and only could be used in combination with embryo rescue techniques. These results do not support Poysa's (1990) suggestion that the ideal bridge lines should be composed of 75% *L. peruvianum* genome.

The BC1´-*chilense* line exhibited unilateral incompatibility in crosses to tomato as female parent (Table 1), but it set at least 0.4 viable seed/fruit when crossed to tomato as male parent. Viable seeds per fruit ranged from 3.5 to 28 in crosses with the 3 *L.peruvianum* accessions.

This line has the same percentage of wild genome as BC1´-*peruvianum*, but its crossability to *L. esculentum* is significantly higher, probably due to the lower degree of incompatibility to the accession *L.chilense* LA 1932 to *L.esculentum* when compared with most *L.peruvianum* accessions. This behavior, along with the good level of success of BC1´-*chilense* in crosses with accessions highly incompatible to tomato, such as *L. peruvianum* PI-126944 and *L. peruvianum* PI-126935 (both resistant to TSWV and TYLCV), makes this line appropriate as a bridge to introgress these and other *peruvianum* traits into the *esculentum* genome.

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Table 1, next page

TABLE 1. Number of viable seeds per fruit in crosses of 4 potential bridging lines with *L.esculentum* and 3 accessions of *L.peruvianum.*

Bridging line	**L. esculentum**	**L. peruvianum**		
		PI-126944	**PI-126935**	**PI-143679**
L .peruvianum 2172	0.28/UI *	AS/AS	AS/AS	AS/AS
L. peruvianum 1708	0.2/UI	AS/AS	AS/AS	AS/AS
BC1´-*peruvianum*	AE/UI	UI/33	UI/29	UI/21.6
BC1´-*chilense*	0.4/UI	UI/5	UI/3.5	UI/28

*First and second data refers to crosses in which the bridge line has been employed as male or female parent in the cross respectively.

IU: Unilateral Incompatibility: incompatibility mechanisms only act in one cross- direction.
AS: Fruit set occurred, but aborted seeds were found in mature fruits.
AE: Fruit set occurred, and aborted seeds were found in mature fruits. However, plants could be obtained by in vitro embryo-rescue from immature fruits.

Sources of high soluble solid and vitamin C content from *Lycopersicon pimpinellifolium* are interesting in breeding for internal quality of fresh market tomato

Roselló, S., Galiana-Balaguer, L. and Nuez, F.

Biotechnology Dept. Universidad Politécnica de Valencia (UPV). Cno. Vera, 14; 46022 Valencia. Spain

Currently, improvement for internal quality (nutritive and organoleptic) is one of the main breeding objectives for fresh market tomato. Flavour and nutritive value are complex characteristics because they are conditioned by the content of many chemical compounds of tomato fruits. The precise analytical determination of each of these compounds could become a very laborious task. However, a preliminary screening trial can be performed to determine, by quick analyses, the main groups of compounds responsible for internal quality in tomato. It would permit the preselection interesting accessions and it would greatly reduce the number of detailed subsequent characterizations with more precise techniques. Screening *L. pimpinellifolium* germplasm for soluble solids content (SSC), titratable acidity and vitamin C content is the objective of this work.

Twenty accessions of *L. pimpinellifolium* collected in Ecuador and Peru by the Vegetable Genetics Breeding Group (Politechnic University of Valencia) were tested (Table 1). Three experimental breeding lines of tomato (FLA7060, NEMA-R and NE-1), two Spanish varieties of processing tomato (GEVORA and GUADAJIRA) and one commercial hybrid (CAMBRIA, Seminis Vegetable Seeds, Almería, Spain) were used as controls. Plants were cultivated in the greenhouse during spring. Fruits were collected at the completely mature stage. SSC was determined with a refractometer (ATAGO-N1 Tokyo, Japan) and the results are reported as ºBrix at 20 ºC. Vitamin C content and titratable acidity were determined immediately after blending and made from aliquots of the homogenized sample. Vitamin C content was titrated with 2,6 dichloroindo-phenol. Total acidity was titrated with 0.1 N NaOH and phenoftalein (AOAC, 1990).

Screened accessions have shown a wide range of variation for SSC and vitamin C (Table 1). The range of variation for titratable acidity was smaller. The most interesting accessions were UPV-17039, UPV-16978, UPV-16984, UPV-16982 and UPV-16985 because their SSC was twice the value of the controls and sometimes more. The ratio SSC/Titratable acidity seems to suggest that the taste of UPV-17039, UPV-16984 and UPV-16985 is slightly sweeter than that of the controls, while UPV-16978 and UPV-16982 have approximately the same taste as the controls. On the other hand, UPV-16985 is very interesting as a source for high vitamin C content, since it exceeds 3.5 times the content of the best control (CAMBRIA). UPV-16984 is also an interesting source for high vitamin C, as it surpasses more than 2 times the vitamin C content of CAMBRIA.

These results point out that some of the screened *L. pimpinellifolium* accessions could be very interesting to increase both flavour and vitamin C content of tomato. SSC values found (maximum at 13.6º Brix) are much greater than previously determined in this species (9.2º Brix) (Lambeth *et al.*, 1966). Furthermore, they are greater than the 10º Brix found in *L. chmielewskii* (Rick, 1974) and in *L. cheesmanii* race *typicum* (Hewitt and Garvey, 1987). However, although values of SSC detected are a bit lower than those of *L. cheesmanii* race *minor* (15º Brix)(Hewitt and Garvey, 1987) *L. pimpinellifolium* is a better source for beginning a breeding program because it is the species phyletically nearest to *L. esculentum* and it permits quicker recovery of agronomic traits.

Table 1 : Results for every line/accession (mean ± standard error)

LINE OR ACCESSION	SPECIES	SSC (ºBRIX)	TITRATABLE ACIDITY (g citric cid/ 100g)	SSC/ TITRATABLE ACIDITY RATIO	VITAMIN C (mg/100g)
UPV-17039	*L. pimpinellifolium*	13,60±0,78	0,69±0,06	19,64±2,04	23,52±0,56
UPV-16978	*L. pimpinellifolium*	10,70±0,15	0,96±0,01	11,19±0,18	31,36±0,35
UPV-16984	*L. pimpinellifolium*	10,67±1,03	0,60±0,01	17,80±1,74	43,49±0,91
UPV-16982	*L. pimpinellifolium*	10,20±0,10	1,02±0,01	9,95±0,14	35,79±0,26
UPV-16985	*L. pimpinellifolium*	9,95±0,03	0,44±0,07	22,51±3,37	76,00±7,39
UPV-16986	*L. pimpinellifolium*	8,95±0,05	0,66±0,05	13,53±1,03	29,80±0,14
UPV-17047	*L. pimpinellifolium*	8,60±0,15	0,92±0,12	9,38±1,24	27,19±0,25
UPV-16949	*L. pimpinellifolium*	8,55±0,05	0,90±0,02	9,52±0,17	8,68±1,11
UPV-18262	*L. pimpinellifolium*	8,25±0,59	0,65±0,01	12,61±0,91	51,46±0,15
UPV-16904	*L. pimpinellifolium*	8,00±0,10	0,99±0,11	8,12±0,91	52,72±0,38
UPV-16976	*L. pimpinellifolium*	7,90±0,09	0,88±0,22	8,98±2,25	40,00±0,33
UPV-16964	*L. pimpinellifolium*	7,60±0,43	0,74±0,10	10,31±1,52	6,61±0,43
UPV-14344	*L. pimpinellifolium*	7,55±0,10	0,53±0,01	14,22±0,35	19,95±2,20
UPV-17044	*L. pimpinellifolium*	7,30±0,17	1,12±0,11	6,54±0,66	31,17±0,23
UPV-16981	*L. pimpinellifolium*	6,90±0,72	0,79±0,05	8,77±1,06	30,47±1,39
UPV-16951	*L. pimpinellifolium*	6,53±0,05	0,76±0,15	8,54±1,70	14,23±2,02
UPV-16965	*L. pimpinellifolium*	6,40±0,32	1,02±0,13	6,27±0,86	16,37±0,72
UPV-16962	*L. pimpinellifolium*	6,20±0,26	0,62±0,08	9,97±1,35	7,68±0,29
UPV-16966	*L. pimpinellifolium*	5,40±1,10	0,51±0,20	10,66±4,65	12,33±0,33
UPV-16957	*L. pimpinellifolium*	4,73±0,57	0,33±0,14	14,35±6,33	3,43±0,29
CAMBRIA	*L. esculentum*	5,87±0,06	0,57±0,01	10,33±0,24	21,96±0,01
FLA7060	*L. esculentum*	5,40±0,03	0,42±0,01	12,85±0,18	20,70±1,03
Gevora	*L. esculentum*	5,23±0,12	0,61±0,08	8,57±1,10	17,15±0,37
NE-1	*L. esculentum*	5,3±0,09	0,79±0,03	6,74±0,25	16,24±0,76
Nema-R	*L. esculentum*	5,5±0,10	0,67±0,03	8,25±0,40	15,40±0,06
Guadajira	*L. esculentum*	5,1±0,06	0,32±0,05	15,75±2,58	18,32±1,00

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Increased efficiency of interspecific hybrids by embryo rescue in crosses between *L.esculentum* and *L. peruvianum*

Sánchez-Donaire[1], A., Encina[2], C.L., Cuartero[2], J., Guerra-Sanz[1], J.M.

1) C.I.F.H. Almería.- P.O. Box 91, EL EJIDO (Almería.-Spain)
2) La Mayora, CSIC. Algarrobo-Costa.-Malaga.-Spain
e-mail: jmguerra@arrakis.es

Procedures for hybridization between domestic tomato varieties and *L. peruvianum* have to be improved to make easier use of the great diversity of genes belonging to *peruviamun* complex. Although procedures to avoid incompatibility barriers have been described, mainly using *in vitro* culture of the embryos and ovules (Imanishi, 1991; LanZhuang & Adachi, 1991; Imanishi *et al.*, 1996; Doganlar *et al.*, 1997; Sacks *et al.*, 1998), the number of hybrid plants obtained have been always low. Therefore the objective of the present work was to improve the methodology to get a high number of hybrid plants by embryo rescue following crosses between *L. esculentum* and *L. peruvianum*.

Two accessions of *L. peruvianum* (LA 1278 and LA 98) from TGRC (Dr. R. Chetelat, Univ. Of California, Davis, USA), and two varieties of *L. esculentum* (Muchamiel and Moneymaker) from "La Mayora" (Dr. J. Cuartero) were used. Plants from those genotypes have been grown under greenhouse conditions and kept until flowering and harvesting under optimal nutritional conditions.

Manual crosses have been carried out using *L peruvianum* as pollen donor and *L. esculentum* as pollen receptor. Pollen from each genotype was collected by breaking and mixing at least ten mature anther cones in a Petri dish. The flower of the female partner was emasculated just before anthesis. Pollination was made by rubbing the pollen obtained on the surface of the stigma of the emasculated flower.

At least four fruits of each cross were harvested between 30 to 45 days after pollination. The fruits were surface-sterilized by 10 minutes immersion in 97% ethanol, left to dry out inside the flow bench and dissected under sterile conditions. Embryos were selected, only those cultures that were bigger, green (the majority appeared white) and with plump appearance were chosen for culture. A superficial cut was done with the scalpel on the embryo coat in the zone of the cotyledons and passed immediately into Petri dishes containing OMS medium (Finer, 1987): MS (Murashige & Skoog, 1962) mineral salts and Gamborg's F5 vitamins (Gamborg *et al.,* 1968), 30 g/l sucrose, 8 g/l Bacto-agar and pH adjusted to 5,7 before sterilizing by autoclave at 121ºC.

Petri dishes containing embryos were incubated in a growth chamber at 23 ºC +/- 0,5 ºC , 16/8 hours day/night and around 10000 lux provided by fluorescent lamps (White-light type). After three weeks, they were subcultured into a second culture medium which consisted of MS complete medium (Murashige & Skoog, 1962), with 30 g/l sucrose, 8 g/l Bacto-agar and pH adjusted to 5,7. The plantlets were kept in the same medium until roots appeared. Those rooted plantlets were transplanted to pots containing artificial substrate (mixture 50:50 of vermiculite and pit) and 'hardened' under a plastic tunnel with high humidity for two weeks. During that time they were fertilized with MS mineral solution. After that period, the plants were moved to a normal greenhouse.

The number of cultured embryos which have developed into plantlets has been analyzed by one-way analysis of variance (Table 1). Only those which resulted in a

complete plant at the end of the experiment were considered viable embryos. The results are summarized in the next table.

Table 1. Viable embryos obtained in four crosses between *L. esculentum* x *L. peruvianum*

CROSS	VIABLE OVULES (% AVERAGE)	TOTAL PLANTLETS (AVERAGE)
Moneymaker X LA 98	0a	0
Muchamiel X LA 98	15,99911054b	28
Moneymaker X LA 1278	11,42857143b	9
Muchamiel X La 1278	26,19838617b	23

Means followed by a different letter are different with p> 0.95.

Moneymaker as the maternal parent gave significantly less viable embryos than Muchamiel. The influence of the maternal genotype on the percentage of viable embryos has also been noted by Sacks *et al.* (1998), however, the number of plants recovered in their experiment was much lower than in our case, perhaps because they did their pollination with a bulked mixture of four *L. peruvianum* accessions. A viability so high as in our case (25% of viability and 5-28 plants obtained), has only been registered before in the work of Lan Zhuang & Adachi (1996), but they used a different culture medium and their rescue technique was more complex than ours.

The increase of the embryo viability obtained in our case could be attributed to the conjunction of the following factors:

a) Abundant pollination in each cross.

b) Moderately aggressive disinfectant procedure in comparison with procedures described by (Imanishi (1991), Chen & Adachi (1996), Imanishi *et al.* (1996), where at least two desinfection steps with bleach were used**.**

c) Induction medium (OMS medium) with a higher concentration of vitamins than other commonly used media (Imanishi, 1991; Chen & Adachi, 1996; Imanishi *et al.*, 1996; Doganlar *et al.*, 1997; Sacks *et al.*, 1998).

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Influence of *in vitro* cultivation on meiotic recombination

Soloviev, A.A., Kirukhova, O.B., Ash, O.A.

Department of Genetics, Moscow K.A.Timiryazev Agricultural Academy, Moscow, 127550, Russia

Meiotic recombination is a very important process for generating genetic diversity. Many factors influence meiotic recombination. We started to study the influence of transformation on meiotic recombination. The first step was the organization of a model experiment with tomato cultivation *in vitro*. We used tomato F1 hybrids between the cultivar Marglobe and morphological marker forms – Mo 304 (marker gene -*bip*), Mo393 (*c, m-2*), Mo 504 (*Wo, d, aw, bk, o, p, s*) and Mo 938 (*wv, aw, d*). Analysis of regenerants did not show morphological anomalies of the cultivated *in vitro* hybrid plants. The cultivated plants did not show anomalies in meiosis either.

An investigation of meiotic recombination by product ratio for all F2 phenotypes showed a change of recombination frequency by *Wo-d, Wo aw, aw-d* and *c-m-2* loci. Three families of hybrid 6 had increased recombination frequency by *aw-d* loci in comparison to the control plants.

Inheritance of resistance to race 1 of *Pseudomonas syringae pv. tomato* in line LCHG 177

Sotirova, V [1]., Bogatsevska, N[2]. and Vulkova, Zl[1]

[1]Institute of Genetics, BAS, 1113 Sofia, Bulgaria
[2] Institute of Plant Protection, 2230 Kostinbrod, Bulgaria

Bacterial speck, caused by Pseudomonas syringae pv. tomato (Pst), is a widespread disease in various areas of the world (Pitblado and Kerr, 1980; Goode and Sasser, 1980; Bogatsevska, 1980; Gitaitis et al., 1992). The investigation into the race status of Pst isolates was reported by Lawton and MacNeil (1986), Bogatsevska et al. (1989), Buonario et al. (1996). There are two known races of Pst – race 0 and race 1. Resistance to Pst is genetically well characterized in the Canadian lines ONT 7710, ONT 7611 and ONT 782. According to Pitblado and Kerr (1980) resistance in these lines was controlled by one dominant gene designated as Pto (Kerr, 1982). The gene is localized on chromosome 5 at position 30 (Pitblado and MacNeil, 1984).

The line LCHG 177 was developed from a BC2 of (*L. esculentum* – *L. chilense* LA 456 – *L. peruvianum* PI 127829) x *L. hirsutum* f. *glabratum* LA 407 accompanied by selection of resistant plants to race 1 of Pst. The material discussed presents the following: 1). To determine the mode of inheritance to race 1 of Pst found in the line LCHG 177. 2). Test of allelism for gene in line LCHG 177 and gene Pto responsible for resistance to bacterial speck in Canadian line ONT 7710.

A study of F1 progenies of crosses Ideal x LCHG 177 and Ace x LCHG 177 indicated that the resistance is dominant. F2 segregating progenies consisted of resistant and susceptible plants in approximately a 3:1 ratio indicating a single dominant gene for resistance. A segregation ratio of one resistant to one susceptible plant in BC1 of the susceptible parent confirm the hypothesis that resistance to race 1 of Pst in line LCHG 177 is controlled by a single dominant gene (Table1)

Table 1. Segregation of resistance to race 1 of Pseudomonas syringae pv. tomato in LCHG 177

Progenies	Segregation				$\chi 2$	P>
	Observed		Expected			
	R	S	R	S		
Ideal	0	17				
Ace	0	25				
LCHG 177	22	0				
F1 Ideal x LCHG 177	31	0				
F1 Ace x LCHG 177	28	0				
F2 Ideal x LCHG 177	269	93	271.5	90.5	0.092	0.50>P>0.80
F2 Ace x LCHG 177	164	66	172.5	57.5	1.674	0.05>P>0.20
BC1 (IdealxLCHG177)xIdeal	27	36	31.5	31.5	1.284	0.20>P>0.50
BC1 (AcexLCHG177)xAce	38	45	41.5	41.5	0.59	0.20>P>0.50

R - resistant; S - susceptible

The allelism study between Canadian line ONT 7710 and line LCHG 177 showed that in the F1 all plants were susceptible. The F2 population segregated. Eighty six plants from a total of 320 tested plants were

susceptible. This fact indicates that the gene of resistance in line LCHG 177 is not allelic to gene Pto in ONT 7710 (Table 2).

Table 2. Test of allelism in line ONT 7710 and line LCHG 177

Crosses	Progenies	Segregation		χ^2	P>
		R	S		
ONT 7710 x LCHG 177	F1	32	0		
ONT 7710 x LCHG 177	F2	234	86	0.075	0.50>P>0.80

R - resistant, S – Susceptible

We believe that the presence of a novel gene could be responsible for the resistance to race 1 of Pst. Further studies are required to clarify the nature and the expression of this novel gene in line LCHG 177.

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Chiasmata frequency and distribution depending on the age in *L. pimpinellifolium*

Strelnikova S. R.

Department of Genetics,Moscow K.A. Timiryazev Agricultural Academy, Moscow, 127550, Russia

The research carried out in recent decades caused a revision of certain theses of the chiasmotype theory. In particular, the series of investigations demonstrated the absence of the terminalization phenomenon and, thus, considerably enlarged the value of the chiasma analysis. This means that the chiasma frequency observed in the late first prophase reflects the frequency of recombination, and the distribution of chiasmata over the length of a chromosome corresponds to the distribution of cross-over exchanges (Vysotskaya, 1995).

On the other hand, the frequency of recombination obtained with use of the traditional hybridological analysis is affected by many factors, such as violations at the post-meiotical stages of development, differing viability and ability to compete of gametes and zygotes, and also of different genotypes at the further stages of the ontogenesis, effect of the abscission of a part of reproductive organs on the structure of segregating progeny, *etc.* For the objective evaluation of the influence of a given factor on the recombination process, cytological methods must also be employed; in particular, the most simple and considerably informative technique for this purpose is counting of the chiasmata number.

There are numerous investigations performed on the effect of age on recombination. For example, Griffing and Langridge (1963) in tomato, with the use of *hl* and *a* markers located at a distance of 20 centimorgans from each other, showed appreciable decay of the crossing-over frequency with the increasing of the ordinal number of cluster. Further research demonstrated that this relation is not very strong and does not hold for every section of chromosome (Zhuchenko, Korol, 1985). All cited experiments do not reflect the events taking place in the cell but concern only a small segment of a particular chromosome. In order to gain a deeper comprehension of the causes of recombination variation we performed an analogous experiment using the chiasmata frequency as a criterion of recombination.

For the investigation, the plants of *Lycopersicon pimpinellifolium* (collection of IEG, No. 176) were taken. The flower-buds for the analysis were taken from the main stalk, from the middle part of cluster. The fixated buds were stained with acetocarmine. The pressed temporary preparations of the maternal cells of pollen (MCP) were made in chloral hydrate by the modified procedure (Turkov *et al.*, 1988). The analysis of the preparations was performed at the magnification: 100× at the objective, 2.5× at the ocular. The chiasmata count was carried out for the MCP that had 12 pairs of chromosomes per cell in the same plane. We counted the total quantity of chiasmata in a cell, and also the particular quantity of the distal and interstitial chiasmata. The number of chiasmata located at the bivalent formed by the second chromosome and their situation over the bivalent was accounted for as well. The pairwise comparison between the variants by Student's criterion was performed.

The results obtained are as follows:

1. Flower-buds taken from different clusters do not differ in the number of chiasmata per cell. The frequency of distal chiasmata also holds at the same level though at the same time the frequencies of interstitial chiasmata in the cells occasionally have significant divergences (see Table 1). No regularity in relation to the ordinal number of a cluster was seen. The number of chiasmata per bivalent fluctuated from 1 to 3. In the chiasmata analysis the strict bivalent

conjugation and the absence of uni- and polyvalents were observed. The frequency of the distal chiasmata by five or more times exceeds the frequency of interstitial ones.

2. The analogous investigations concerning the second, well discernible pair of chromosomes were performed. In respect to this a substantial difference in the chiasmata frequency was observed between the second cluster and the others. At the 2nd cluster, the chiasmata frequency (2nd chr.) is the least of all and amounts to 1.29 ± 0.073. Likewise, the distal chiasmata frequency is significantly lower at the 2nd cluster. The frequency of interstitial chiasmata at the 2nd pair of chromosomes does not differ with the growth of number of cluster, and every time exceeds the frequency of distal ones. In addition, interstitial chiasmata at the second pair accounts for 1/3 of the total number of interstitial chromosomes in a cell, *i.e.* per 12_{II}. This shows that particular chromosomes may have individual peculiarities in their chiasmata distribution.

3. We also compared chiasmata frequencies between *L. pimpinellifolium* plants of the 1st and 2nd years of life. For the purpose of purity of experiment, the bud fixations were performed simultaneously. Eventually, significant differences between the plants were not obtained either in the amount and distribution of the total chiasmata or at the bivalent formed by the 2nd chromosome.

From the above-stated results one can conclude the following statements. The total chiasmata frequency remains unperturbed during the entire period of vegetation. The distribution of chiasmata over locations at a bivalent, both totally and particularly at the 2nd pair of chromosomes, does not demonstrate any explicit dependence on age. The changes in the frequencies of distal and interstitial chiasmata most likely should be ascribed to external factors.

All the above-mentioned facts show the necessity of the use of cytological analysis, along with hybridological, for the purpose of more profound penetration into the specifics of the formation of recombinational variability.

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Table 1. Variation of chiasmata frequency in *L. pimpinellifolium* depending on the age.

No. of plant, No. of cluster	Total chiasmata frequency (over 12_{II})			Chiasmata frequency at the 2nd pair of chrom.		
	general	distal	interstitial	general	distal	interstitial
Plant No. 1						
30.06.99 2nd cluster	20,04 ± 0,22	17,42 ± 0,27	2,63 ± 0,13	1,29 ± 0,073	0,42 ± 0,078	0,89 ± 0,046
08.07.99 5th cluster	20,08 ± 0,26	16,92 ± 0,29	3,17 ± 0,14	1,63 ± 0,10	0,79 ± 0,12	0,83 ± 0,078
16.07.99 7th cluster	19,88 ± 0,29	17,18 ± 0,28	2,77 ± 0,18	1,62 ± 0,085	0,79 ± 0,092	0,82 ± 0,066
28.07.99 10th cluster	19,87 ± 0,14	17,05 ± 0,18	2,82 ± 0,10	1,49 ± 0,062	0,67 ± 0,062	0,82 ± 0,047
Plant No. 2						
26.06.99	19,96 ± 0,36	16,56 ± 0,40	3,44 ± 0,17	1,63 ± 0,095	0,85 ± 0,070	0,78 ± 0,082
Plant No. 3 at the 2nd year of life						
26.06.99.	19,92 ± 0,25	16,14 ± 0,3	3,78 ± 0,17	1,62 ± 0,081	0,89 ± 0,093	0,73 ± 0,074

Reduction of fruit growth results in lower incidence of blossom-end rot in tomato

van der Knaap, E. and Tanksley, S.D.

Departments of Plant Breeding and Plant Biology
Cornell University, Ithaca NY, 14853

Blossom-end rot (BER) in tomato is associated with a localized calcium deficiency in the distal portion (blossom end) of the fruit. BER is induced by poor watering conditions; either too much or too little water. However, BER is not the result of a single factor, but from the interaction of several conditions such as light, temperature, relative humidity and nutrient status, with the genotype (Ho et al., 1993; Mutsumi and Taikichi, 1995a,b,c).

During the course of an unrelated experiment, measurements of individual fruits of TA491 (Sun 1642) were taken at regular intervals from the time of pollination to ripe fruit. We found that fruits that were to develop BER grew faster following pollination, than fruits that were not developing BER (Figure 1). Furthermore, fruits of plants treated with Bonzi (growth retardant; inhibitor of GA biosynthesis) developed less BER than fruits of non-treated plants (14% vs 81%; Table 1). However, Bonzi treatment resulted in reduced fruit set compared to non-treated plants (70% vs 98%; Table 1). The results suggest that reduced fruit growth in TA491 may prevent BER. At this time, it is unclear whether reduced fruit growth is accomplished directly by changes in environmental conditions (temperature, nutrient status or relative humidity) and/or indirectly by poor seed set. Poor seed set may be the consequence of reduced levels of GA.

Table 1. Incidence of BER and fruit set in Bonzi-treated vs non-treated TA491 fruit.

	incidence of BER	fruit set
Bonzi treatment	2 out of 14	14 out of 20
No treatment	44 out of 53	53 out of 54

Literature cited:

Ho, L.C., Belda, R., Brown, M., Andrews, J., Adams, P. (1993) J of Exp Botany 44, 509-518.
Mutsumi, W., and Taikichi, T. (1995a) Environmental Control in Biology 33, 7-14.
Mutsumi, W., and Taikichi, T. (1995b) Environmental Control in Biology 33, 15-21.
Mutsumi, W., and Taikichi, T. (1995c) Environmental Control in Biology 33, 49-57.

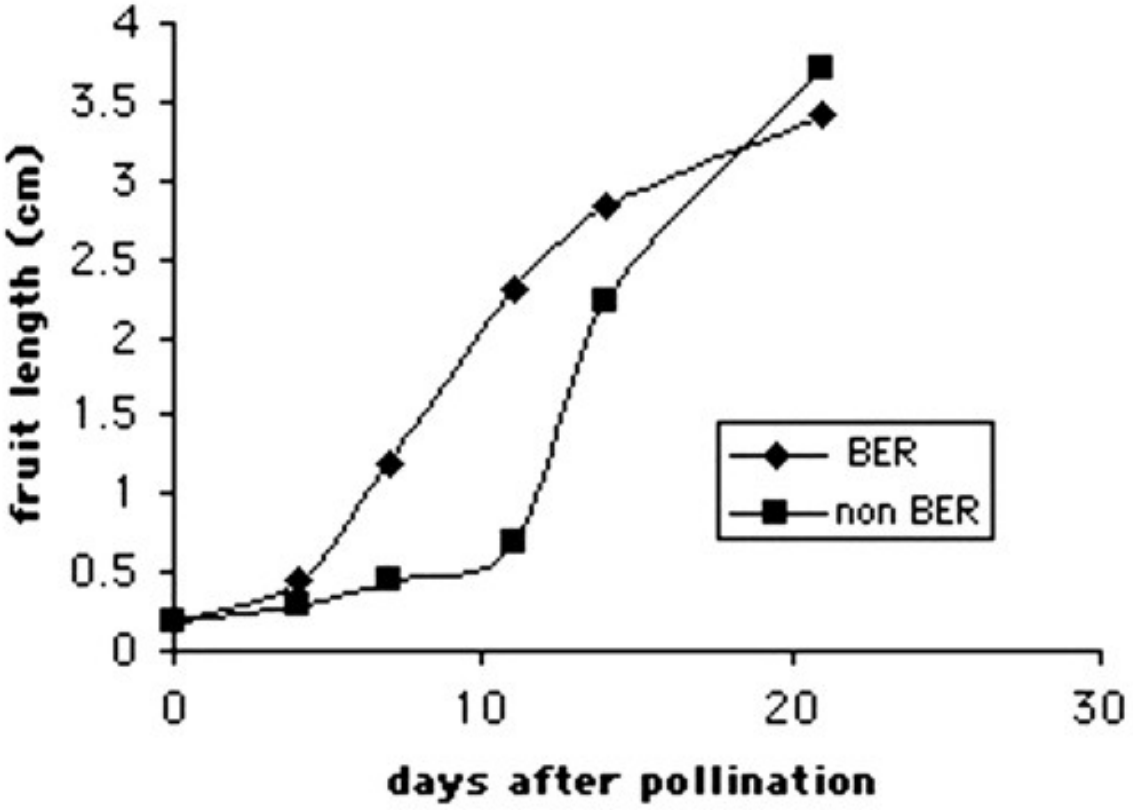

Figure 1. Fruit growth of greenhouse grown TA491 following pollination. Significant differences in fruit length of fruits that were to develop BER or not, were observed at 7 and 11 days after pollination ($p < 0.005$). For BER fruit, N=44; for non-BER fruit, N=8.

Dihaploid production as a result of interspecific hybridization in genus *Lycopersicon*

Vulkova Z.[1], Stoeva - Popova P.[2]*, and Atanassov A.[2]

[1] Institute of Genetics, 1113 Sofia, Bulgaria
[2] Institute of Genetic Engineering, 2232 Kostinbrod -2, Bulgaria

* Department of Biology, Winthrop University, Rock Hill, SC

L. peruvianum is reproductively isolated from other species of the genus *Lycopersicon* (Rick 1963; 1979). This reproductive isolation barrier can be easily overcome if the hybridization is carried out between diploid plants of *L. peruvianum* and colchicine induced autotetraploid plants from another *Lycopersicon* species (Vulkova-Achkova and Stoeva 1978). As a result sequidiploids are produced that are highly sterile but can be used as bridge hybrids for the introgression of genes from *L. peruvianum*.

In our experiments sesquidiploid F1 hybrid plants produced from the cross between *L. hirsutum typicum* (2n 48) X *L. peruvianum* (2n 24) were used. Explants from *in vitro* propagated sesquidiploid F1 plants were cultivated on solid MS (Murashige and Skoog 1962) medium supplemented with 30 g/l sucrose, 2 mg/l TDZ, 0.5 mg/l IAA and 1 mg/l GA. After 20 -25 days on this induction medium callus with shoot primordia were produced on the cultivated explants. The formed structures were transferred for further development on MS medium with 30 g/l sucrose and reduced amounts of TDZ – 0.5 mg/l, IAA – 0.1 mg/l, and GA – 0.5 mg/l. On this medium shoots developed. The regenerated shoots were rooted on hormone free MS medium.

The produced R1 plants were transferred to soil and grown in pots in the greenhouse. According to their morphological characteristics the regenerants (R1) were classified in two groups. The first group comprised of 10 plants with indistinguishable *L. peruvianum* phenotype. In the second group 13 plants with intermediate habitus were classified. The meiotic and mitotic divisions as well as pollen stainability were studied in all R1 plants produced. To study mitosis, root tips were treated with α- brom naphtalene and fixed in acetic acid and 96% ethyl alcohol (1:3 w/w). Schiff's reagent was used to stain the mitotic chromosomes in squash preparation. Meiosis was studied in squash preparations of acetocarmine (4%) stained anthers. Pollen stainability was investigated with 1% acetocarmine.

All plants from the first group had 24 chromosomes. It is known that the mean value of the index for the longest chromosome of *L. peruvianum* is 0.53, while for *L. hirsutum* it is 0.78 (Upadhya and Majid 1964). We established that the mean value of the index for the longest chromosome in this group of plants was in the range characteristic for *L. peruvianum* - about 0.57. The meiotic division was normal, and the stainability of pollen was 94 – 100 %. The outcrossing of R1 plants from this group proved that they were fertile, with normal fruit and seed set. All R2 plants produced from these seeds were with the *L. peruvianum* phenotype. The results from the morphological and cytological analysis give us the ground to consider the plants from group one as dihaploid *L. peruvianum* plants produced by regeneration from cells in which the chromosomes of *L. hirsutum f. typicum* were eliminated, while the chromosomes of *L. peruvianum* were doubled.

The study of metaphase plates in the plants of group two showed that they all were aneuploids with chromosome number ranging from 26 to 34. These results corroborate with a pattern of chromosome elimination that takes place during regeneration of plants from the triploid somatic

tissue (2n 36) of the cross *L. hirsutum f. typicum* (2n 48) X *L. peruvianum* (2n 24). The meiotic division was abnormal as expected with aneuploids. The stainability of the pollen was between 28 to 72 %.

The obtained results show that chromosome elimination takes place during in vitro plant regeneration from somatic triploid tissue of the sesquidiploid *L. hirsutum f. typicum* (2n 48) X *L. peruvianum* (2n 24). In 10 (30%) of the produced regenerants the 2n (24) chromosomes of *L. hirsutum f. typicum* were eliminated while the n (12) chromosomes of *L. peruvianum* were doubled and dihaplid *L. peruvianum* plants were produced. Further studies are in progress to apply this approach for the production of dihaploids from other species of genus *Lycopersicon.*

Literature cited:

1. Murashige T., Skoog. 1962. Physiol. Plant. 15, 73-79.
2. Rick C. 1963. Evolution 17, 216-232.
3. Rick C. 1979. In: Hawkes J., Lester R., Skelding A. (ed.) The Biology and Taxonomy of the *Solanaceae*. Acad. Press London, pp. 667-677.
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Effects of segments of *chromosome 1* and *3* from *L. hirsutum* (LA1777) on anther and style length in *L. esculentum* background

Weiner, J.L., Bernatzky, R.

Department of Plant and Soil Sciences, University of Massachusetts, Amherst, MA 01003

The major locus controlling self-incompatibility (*S*-locus) is located on the short arm of chromosome 1. We have introgressed chromosome 1 segments from self-incompatible *L. hirsutum* (LA1777) into *L. esculentum* cv Vendor by marker-assisted selection to study the effects on self-fertility in cultivated tomato. Although the *S*-locus alone is not sufficient to establish self-incompatibility in *L. esculentum* (Bernatzky et al. 1995), we have used these partial substitution lines to screen for other chromosome segments that, in combination with the *S*-locus, reduce self-fertility. We have identified a region of chromosome 3 that greatly reduces self-fertility in the presence of the *S*-locus in greenhouse grown late generation backcross material (unpublished).

We have also examined this material for effects on flower morphology, specifically stigma exsertion. We measured anther length and style and stigma length on two BC7 plants containing a chromosome 1 segment bearing the *S*-locus of *L. hirsutum* from RFLP markers CT197 to CT231 (approximately 36 cM) and a chromosome 3 segment from CT118B to *Rbcs2* (approximately 8 cM). We also measured flowers of the original parents, cv Vendor and an individual of *L. hirsutum* (LA1777). The average of 12 measurements of cv Vendor, LA1777, and 12 each of the two BC7 individuals (data combined) was as follows:

Genotype	Style and Stigma	Anther
Vendor	7.33 $\pm$ 0.44	9.55 $\pm$ 0.25
BC7	7.98 $\pm$ 0.34	9.97 $\pm$ 0.80
LA1777	10.29 $\pm$ 0.58	9.58 $\pm$ 0.32

Both anther (α = 0.05) and style and stigma (α = 0.001) lengths differ significantly for all three genotypes. However, the stigmas of cv Vendor and the BC7 individuals are well contained within the anther cone. This data suggests that, at least in the heterozygous condition, these chromosome 1 and 3 segments from LA1777 do not cause stigma exsertion in the cv Vendor background.

Literature cited:

Bernatzky, R., R.H. Glaven and B.A. Rivers. 1995. *S*-related protein can be recombined with self-compatibility in interspecific derivatives of *Lycopersicon*. Biochemical Genetics 33:215-225.

TGRC STOCK LIST

Roger T. Chetelat, Charles M. Rick
Tomato Genetics Resource Center
Department of Vegetable Crops
University of California
Davis, CA 95616, USA

chetelat@vegmail.ucdavis.edu
rick@vegmail.ucdavis.edu
tgrc@vegmail.ucdavis.edu
fax: (530) 752-9659
http://tgrc.ucdavis.edu

Wild Species Stocks (1,106 accessions total) are listed in TGC 48 (1998)
Monogenic Stocks (978 accessions total) are listed in TGC 49 (1999)

REVISED LIST OF MISCELLANEOUS STOCKS

This list of ca. 1,262 miscellaneous genetic stocks is a revision of the previous one issued in TGC 47 (1997). Extinct, obsolete, or faulty accessions have been dropped and new accessions have been added. Noteworthy new items on this list include a series of *L. hirsutum* introgression lines (developed by A. Monforte and S.D. Tanksley), a group of *S. lycopersicoides* monosomic alien addition lines in *L. esculentum* (R.T. Chetelat), new marker gene combinations (M. Koornneef, H. Laterrot, J. Maxon Smith, C.M. Rick) and additional cultivars (R. Gardner, J. Scott).

We attempt to maintain all listed accessions in adequate 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, issued in TGC 49; other pertinent data are presented in previous TGC Reports, as cited below. Additional information concerning the origin of these accessions, recommendations for growing and reproducing them, and other aspects of these stocks will be gladly furnished on request. Previous stock lists and information such as phenotypic descriptions, collection notes, images of mutants, etc., can be obtained from our website (http://tgrc.ucdavis.edu).

Accession Categories

I. Chromosome Marker Stocks
II. Linkage Screening Testers
III. Miscellaneous Marker Combinations
IV. Translocations
V. Autotetraploids
VI. Trisomics
VII. Modern and Vintage Cultivars
VIII. Latin American Cultivars
IX. Stress Tolerant Stocks
X. Monosomic Alien Addition Lines
XI. Alien Substitution Lines
XII. Introgression Lines
XIII. Other Prebred Stocks
XIV. Cytoplasmic Variants

I. Chromosome Marker Stocks (185)

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). We have combined some of the more useful groups 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. The preferred (usually most complete) marker combination for each chromosome is indicated in bold.

Chromosome 1

LA 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}, scf, 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, in*
3302 *imb, in*
3303 *imb, inv*
3304 *au, Lpg*
3305 *imb, Lpg*
3306 *in, inv*
3307 *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

LA 0157 *p, d, m*
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

LA 0644 *r, wf*
2379 *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

LA 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*)
0911 *clau, afl, ful*
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}*
0991 *ful, e, 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

LA 0512 *mc, tf, wt, obv*
1188 *frg, tf*
3850 *af, tf*

Chromosome 6

LA 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, vf, c*
1527 *d-2, c*
3805 *m-2, gib-1*
3806 *yv, Mi, og, sp, c*
3807 *tl, yv, c*

Chromosome 7

LA 0788 *La/+, deb*
0882 *La/+, deb*
0923 *ig, La/+*
0924 *not, La/+*
1083 *ig, flc*
1103 *var, not*
1104 *deb, not*
1172 *La/+, lg-5*

Chromosome 8

LA 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*
1179 *l, bu, dl, al* (*ms-31*)
1191 *spa, ae*

1442 *dl, glg, marm*
1666 ***l, bu, dl, ae***
3906 *Wa, dl*^{s}

Chromosome 9

LA 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

LA 0158 *Xa/+, u, t*
0341 *h, ag* (*ms-2*)
0642 *u, h, l-2* (*al, d, h, j, wt*)
0643 *u, l-2*
0649 *t*^{v}*, ag*
0794 *t*^{v}*, ag* (4x)
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*
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, nd, ag, Xa*
2506 *ag, h, l-2, oli, t*^{v}
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

LA 0291 *hl, a* (*ms-2*)
0729 *neg, a*
0730 *a, pro*
0761 *a, hl, j*
0803 *hl, a, pro* (*ms-2*)
0881 *neg, hl, a*
0925 *j, hl, a, f*
1102 *a, hl, tab*
1113 *j, hl, a, f* (*ms-31*)
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

LA 1111 *fd, alb*
1171 *$yg\text{-}2^{aud}$, fd*
1177 *alb, mua*

II. Linkage Screening Testers (16)

As explained previously (TGC 22:24), we have endeavored to synthesize a set of linkage testers, each of which has two pairs of strategically situated markers on two different chromosomes. They are intended primarily for screening new, unmapped markers. The next group of chromosomal markers 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. Numbers of the respective chromosomes are indicated in parentheses. The mutant *scf* is bracketed in stocks in which it was inadvertently lost in the course of segregation and selection.

LA 0780 *yv, c* (6)*; h, ag* (10)
0781 *ful, e* (4)*; neg, a* (11)
0784 *ful, e* (4)*; hl, a* (11)
0982 *clau, e* (4)*; hl, a* (11)
0983 *l, dl* (8)*; ah, marm* (9)
1164 *var, not* (7)*; ah, marm* (9)
1166 *clau, su^{3}* (4)*; icn, ag* (10)
1182 *sy, sf* (3)*; alb, mua* (12)

1183 *clau, ra* (4)*; icn, ag* (10)
1189 *pds, c* (6)
1431 *au^{tl}, scf, dgt* (1)
1441 *coa, c* (6)*; hl, a* (11)
1443 (*scf*)*, dgt* (1)*; l, al* (8)
1444 *wv, d* (2)*; af, tf* (5)
1491 (*scf*)*, dgt* (1)*; spa, ae* (8)
1665 (*scf*)*, dgt* (1)*; l, ae* (8)

III. Miscellaneous Marker Combinations (372)

We have acquired and synthesized, in addition to the above categories, a group of 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 include the same combinations or because they are more useful as markers of several chromosomes.

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*
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*
0298	*Xa, Wo, dv, tf*
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* (exserted)*, a, c, y*
0638	*ht, d, r*
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*
0775	*tf, h, au, +/d*
0779	*clau, rv*
0783	*Wo^{m}, d, au, tf*
0796	*vms, Hrt, lg-5*
0801	*atv, slx*

LA	Genotype
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*
0996	*um, ig*
0997	*um, not*
1018	*h, Od, ptb*
1072	*sy, sf, um*
1079	*c, ves-2*
1105	*con, cur*
1106	*fsc, ah*
1163	*wv, d, tf*
1170	*cn, con*
1219	*d, u*
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*

LA	Genotype
2369	*p, Tm-1*
2370	*wf, n, gs*
2371	*d, wf, wt, c, f*
2372	*sp, fl*
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*
2491	*stu, mc, c, gs, dl, u, h, j*
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*
2523	*r, mc, c, pdw, u, h, f*
2524	*af, sd*
2526	*dp, sp, u*
2527	*l allele, sp, u*
2528	*ti, y, wf, sf, f*
2531A	*pyl, Tm-2^{a}*
2531B	*pyl, Ve, Tm-2^{a}*
2531C	*pl, pyl, Tm-2^{a}*
2595	*br, d, dm, wt, al, h, j, f*
2596	*y, d, wf, at, m-2, c, sp, u, a, yg-2*
2597	*y, r, wf, mc, m-2, c, gs, gf, marm*, *h*
2598	*y, wf, at, m-2, c, sp, u, a, yg-2, gs*
2599	*y, wf, at, m-2, c, gf, h, a, yg-2*
2600	*y, wf, at, m-2, c, sp, u, a, yg-2*
2601	*y, e, mc, gs, gf, u, t* (dk purple)
2602	*scf, dp, r, wf, m-2, c, gs, marm, u*, *hp*
2603	*scf, dp, r, wf, c, gs, marm, u, hp*
2605	*scf, dp, r, wf, c, gs, marm, a, hp*
2606	*lg, pe, Nr-2, tmf, cjf, jl, j-2*
2607	*lg, pe, tnf, cjf, wf, c, gs, marm, h, j*
2608	*lg, pe, tnf, d, r, c, gf, marm, h,* (green

LA	Genotype
	stem)
2609	*lg, pe, tnf, d, r, c, gf, marm, h, (al?)*
2611	*lg, pe, wf, m-2, c, gs, gf, marm, h, hp*
2612	*d, at, m-2, c, sp, gs, u, a, yg-2*
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*

The following group of accessions (LA3248-3838) are NILs in cv. Ailsa Craig (LA2838A).

LA	Genotype
3248	bls, u
3249	a, c, (long style)
3250	t, u
3251	Del, y
3252	Del, t
3253	r, y
3254	a, c, l, Ve, (long style)
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-22, u
3265	bls, Tm-1, Tm-2, nv
3266	bls, Cf-/?, u
3267	Cf-?, 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-22
3274	ah, Tm-2, nv, u, (lethal)
3275	ah, Gp, Tm-22
3276	Tm-1, u, Ve
3278	bls, l, u, Ve

LA	Genotype
3279	at, Del
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	ogc, u
3315	sp, pst, u, j-2, up, (virescent), 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
3378	o, u
3379	bls, 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
3388	gs, ug
3389	Nr, y
3390	Nr, ug
3391	gf, hp
3392	hp, Nr
3393	r, t
3394	at, ug
3395	gs, hp, y
3396	at, u, y

LA	Genotype
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-? (Potentate)
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

LA	Genotype
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-22, 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	dx, 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

LA	Genotype
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
3708	Nr, 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
3761	ls, u
3771	hp, ogc
3810	hp, t
3811	gf, r
3812	bls, Tm, Tm-2, nv
3815	Del, t, ug
3821	dil, pum, u
3822	cor, de, sp, u
3823	pum, sp, u
3826	mon, u
3827	dil, cor, sp, u
3830	ep, ogc, u
3831	gf, gs, r, y

IV. 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. Special thanks are due to Dr. Gill and his colleagues for their efforts in assembling and increasing this collection. Accessions with an asterisk comprise the tester set.

LA 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
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
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

V. Autotetraploids (15)

We are currently maintaining only the following group of tetraploids. Whereas we formerly stocked many more lines, the rapid deterioration, low seed yields, and lack of demand required that we prune them to a smaller group of more frequently used lines. Additional autotetraploids appear in the wild species stock list (TGC 48) and below under Latin American Cultivars.

	2-095	cv. San Marzano
	2-483	cv. Red Cherry
LA	0793	*a, c, d, l, r, y*
	0794	*ag, t*^{v}
	2335	*L. pimpinellifolium*
	2336	*r* in *L. pimpinellifolium*
	2337	cv. Stokesdale
	2338	cv. Break O'Day
	2339	cv. Pearson
	2340	*L. pimpinellifolium*
	2341	*L. pimpinellifolium*
	2342	cv. Danmark
	2343	cv. Waltham Fog
	3131	cv. UC82B
	3255	cv. Ailsa Craig

VI. Trisomics (31)

The following series includes 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, rarely tetrasomics. 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 Alien Additions.

Primary:	∆10	Triplo-1
	∆06	Triplo-2
	∆08	Triplo-3
	∆02	Triplo-4
	∆04	Triplo-5
	∆12	Triplo-6
	∆07	Triplo-7
	∆03	Triplo-8
	∆05	Triplo-9
	∆01	Triplo-10
	∆40	Triplo-11
	∆09	Triplo-12

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
	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
	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

VII. Modern and Vintage Cultivars (193)

We maintain the following set of cultivars 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. The autodiploid stock of San Marzano originated by spontaneous chromosome doubling from a haploid. Other lines have been maintained by selfing for many generations.

LA	Variety
0818	A-1
0516	Ace
2838A	Ailsa Craig
2463	Allround
3143	Anahu
1995	Angela
3244	Antimold-B
3527	Apex 1000
0657	Beaverlodge (Chanasyk's early)
1499	Break O'Day
2414	Cal Ace
1439	Calmart

LA	Variety
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
3238	Earliana
2006	Earlinorth
0266	Earlipak
0517	Early Santa Clara
2711	Edkawi
3245	E.S. 1
3800	Fargo
3801	Farthest North
3024	Fireball
3242	Floridade
3030	Gardner
2802	Globonnie
4011	GT
3231	Gulf State Market
0314	Hardin Miniature
3857	Hawaii 7998
0806	High Crimson
3110	Hires Rootstock
3237	Homestead 24
3320	Hotset
3144	Hunt 100
1089	John Baer
1131	Kallio's Alaskan Dwarf
0025	King Humbert #1
3240	Kokomo
0505	Laketa
3203	Large Plum
3118	Laurica
3146	Libohova
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

LA	Variety
3911	Micro-Tom
2825	Mobaci
2824	Moboglan
3152	Moboline
2821	Mobox
2830	Mocimor
3471	Mogeor
2828	Momor
2829	Momor verte
2818	Monalbo
2706	Moneymaker
2713	Montfavet 167
2714	Montfavet 168
2819	Monita
2827	Moperou
2822	Mossol
2820	Motabo
2826	Motaci
2823	Motelle
3472	Movione
3466	Murrieta
2661	Nagcarlang
3845	NC EBR-5
3846	NC EBR-6
3847	NC HS-1
3802	New Hampshire Victor
2009	New Yorker
1088	Ohio Globe A
3321	Ohio 7663
2447	Ontario 717
2449	Ontario 7517
2396	Ontario 7710
2448	Ontario 7818
2969	Oxheart variant: Georgia Streak
2970	Oxheart variant: Or- Red Center
2971	Oxheart variant: Verna Orange
2972	Oxheart variant: Big Yell. Red Ctr
2973	Oxheart variant: Big Rainbow
2376	Pan American
0012	Pearson
0020	Pennheart
3528	Peto 95-43
3312	Platense
3125	Pomodorini Napolitani
2715	Porphyre
3820	Potentate
3236	Prairiana
3903	Primabel
0089	Prince Borghese
3233	Pritchard
3229	Prospero
2446	Purdue 135

LA	Variety
2377	Purple Calabash
2378	Purple Smudge
0337	Red Cherry
0276	Red Top
3129	Rehovot 13
2356	Rey de los Tempranos *Sw-1*
0535	Rheinlands Ruhm
3343	Rio Grande
3145	Rockingham
3214	Rowpac
0503	Roumanian Sweet
2088	Royal Red
3215	Roza
1090	Rutgers
2662	Saladette
3216	Saladmaster
3008	San Marzano
0180	San Marzano (autodiploid)
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
1706	UC82
3772	UC82B
2898	UC82C
3773	UC82L
1714	UC134
3526	UC134-61D
3130	UC204C
2937	UC-MR20
2938	UC-N28
2939	UC-T338
2940	UC-TR44
2941	UC-TR51
0021	Uniform Globe
3246	Vagabond
3905	Vantage
3122	Vendor
3029	Vendor (*Tm-2^a, I, Ve*)

LA	Variety
2444	Vetomold K10
2806	Vis Grise
2445	V121
0745	V-9 Red Top
0743	VF-6
0744	VF-11
1023	VF-13L
0742	VF-34
0490	VF-36
0816	VF-145 22-8
1222	VF-145 78-79
1507	VF-145 21-4
1022	VFN-8
0815	VFN-14
2086	VFN Hi Sugar
1221	VFNT Cherry
2705	VFNT Cherry (*sp*)
0279	Webb Special
3204	VFT-36
3465	Walter
2464	White Beauty
2-473	Yellow Cherry
2804	Yellow Currant
2357	Yellow Peach
3148	Zemer Kau

VIII. Latin American Cultivars (194)

This collection of Latin-American cultivars has been assembled from various sources but principally from our collecting trips. 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.

ARGENTINA

LA 3243 cv. Platense

BOLIVIA

LA 0172 Santa Cruz
2699 Coroica
2871 Chamaca (Yungas)
2873 Lote Pablo Luna (Yungas)
2874 Playa Ancha (Yungas)

BRAZIL
- LA 1021 Santa Cruz

CHILE
- LA 0466 Hda. Rosario (Azapa)
- 0467 Lluta
- 0468 Iquique

COLOMBIA
- LA 0356 Buenaventura
- 0357 Buenaventura
- 0358 Buenaventura
- 0359 Buenaventura

COSTA RICA
- LA 1215 (no location)
- 3453 Turrialba

CUBA
- LA 1162 (no location)

ECUADOR
- LA 0126 Quito
- 0408 Guayaquil
- 0409 Guayaquil
- 0410 Guayaquil
- 0415 Daular
- 0416 Puna
- 0423 Wreck Bay (Galapagos)
- 1224 Puyo (3 items)
- 1238 Viche
- 1239 Esmeraldas
- 1240 Esmeraldas
- 1241 Esmeraldas
- 1244 Carmela (Guayas)
- 1249 Loja
- 1250 Loja
- 1251 Loja
- 2094 El Naranjo
- 2381-2384 Malacatos

GUATEMALA
- LA 1460 Antigua

HONDURAS
- LA 0147 Tegucigalpa
- LA 0148 Tegucigalpa

NICARAGUA
- LA 1213 (no location)

MEXICO

LA	0146	Mexico City
	1218	Vera Cruz
	1457	Tehuacan
	1459	Huachinango
	1462	Yucatan
	1544	Laguna
	1564	Sinaloa
	1565	Oaxaca
	1566	Oaxaca
	1567	Oaxaca
	1568	Yucatan
	1702	Sinaloa
	1703	Sinaloa
	1994	unknown
	2083	Guaco, Culiacan
	2084	Comala, Culiacan

PANAMA

LA	1216	(no location)

PERU

LA	0113	Hda. Calera (La Libertad)
	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
	0457	Tacna (4x)
	0472	unknown
	0473	Calana (Tacna)
	0477	Chincha
	0478	Chincha
	0721	Chiclayo
	1313	Convento de Sivia (Cuzco)
	1315	Ayna
	1390	La Molina (Lima)
	1397	Iquitos
	1398	Iquitos
	1650	La Bogotalla-Ingenio
	1654	Tarapoto
	1655	Tarapoto
	1669	Jahuay (Ica)
	1698	Chancay
	1976	Calana

1988 Mercado Central
2207-2212 Naranjillo
2213-2220 Nueva Cajamarca
2221-2235, 2259 Moyobamba mercado
2237-2244 Habana
2245-2253 Soritor
2254-2256 Pto. Moyobamba
2257 Hotel Albricias
2258 Yautalo
2260-2264 La Huarpia
2265-2268 Pacaisapa
2269-2276 km 57
2278-2282 Tabalosas
2283-2307 Tarapoto Mercado
2309-2311 Pto. St. Cruz
2316 Sargento
2622 Margual
2623 Pucalepillo
2676 San Juan Del Oro
2841 Chinuna (Amazonas)
2842 Sta. Rita (San Martin)
2843 Moyobamba
2844 Shanhoa
2845 Moyobamba mercado
3221-3226 San Isidro mercado (Lima)

IX. Stress Tolerant Stocks (40)

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.

1. Drought tolerance
   L. pennellii (general feature) LA0716, others
   L. chilense (coastal habitats) LA1958, 1959, 1972
   S. sitiens (general feature) LA1974, 2876, others

2. Flooding tolerance
   L. esculentum var. *cerasiforme* (wet tropical habitats): LA1421
   S. juglandifolium, *S. ochranthum* (probably a general feature)

3. High temperature tolerance
   L. esculentum cv.s Nagcarlang (LA2661), Saladette (LA2662), Malintka-101 (LA3120), Hotset (LA3320)

4. Chilling tolerance

L. hirsutum (from high altitudes) LA1363, 1393, 1777
L. chilense (from high altitudes) LA1969, 1971
S. lycopersicoides (possibly a general feature) LA1964, 2408

5. Aluminum tolerance (suspected): *L. esc*. var. *cerasiforme* LA2710

6. Salinity - alkalinity tolerance

L. cheesmanii (from littoral habitat): LA1401
L. pennellii: LA0716, 2656, 1926, 1809, 1940
L. peruvianum: LA0462, 1278, 2744
L. chilense: LA2748, 2931, 2880, 1930, 1932, 2747, 1958
L. esculentum var. *cerasiforme*: LA1310
L. esculentum cv. Edkawi LA2711
L. pimpinellifolium LA1579

7. Arthropod resistance

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

X. Monosomic Alien Addition Lines (10)

The following group of monosomic alien addition lines each contain a single extra chromosome from *S. lycopersicoides* LA1964 added to the *L. esculentum* genome (Chetelat et al., Genome 41:40-50, 1998). MAAL-1 and MAAL-6 are not listed due to our inability to maintain them via seed. Transmission rate of the extra chromosome differs greatly between individual MAALs, however the phenotype of each MAAL tends to resemble that of the corresponding primary trisomic, hence the recommendations of Rick (TGC 37:60-61, 1987) for identifying trisomics at the seedling stage are helpful for selecting 2n+1 progeny of the MAALs as well. Intactness of the *S. lycopersicoides* chromosomes in these stocks has been tested with only a limited number of markers, hence some may be recombinant.

LA	3454	MAAL-2
	3455	MAAL-3
	3456	MAAL-4
	3457	MAAL-5
	3459	MAAL-7
LA	3460	MAAL-8
	3461	MAAL-9
	3462	MAAL-10
	3463	MAAL-11
	3464	MAAL-12

XI. Alien Substitution Lines

In the course of our study of segregation and recombination in *L. esculentum* x *L. pennellii* hybrids, we progressively backcrossed certain chromosomes of *L. pennellii* LA0716 into *L. esculentum* (see Genetics 26:753-768; Biol. Zbl. 91:209-220). Selected heterozygotes of later generations were selfed and subsequent progenies free of *esculentum* markers were selected as the substitution lines.

LA	2091	Chromosome 1
	1639	2

	1640		3
	3469		4
LA	3142	Chromosome	6
	1642		8
	1643		11

XII. Introgression Lines

1. *L. pennellii* Introgression Lines.

The following group of introgression lines was developed by Eshed & Zamir (Euphytica 79:175-179, 1994; see additional information in TGC 49:26-30). Each line is homozygous for a single introgression (i.e. segmental substitution) from *L. pennellii* LA0716 in the background of *L. esculentum* cv. M-82; the entire *L. pennellii* genome is represented by overlapping introgressions in this set of 50 lines. The IL # indicates the *L. pennellii* chromosome and introgressed segment number in each.

LA	Line
3475	M-82
3476	IL1-1
3477	IL1-2
3778	IL1-3
3479	IL1-4
3480	IL2-1
3481	IL2-2
3482	IL2-3
3483	IL2-4
3484	IL2-5
3485	IL2-6
3486	IL3-1
3487	IL3-2
3488	IL3-3
3489	IL3-4
3490	IL3-5
3491	IL4-1
3492	IL4-2
3493	IL4-3
3494	IL4-4
3495	IL5-1
3496	IL5-2
3497	IL5-3
3498	IL5-4
3499	IL5-5
3500	IL6-1
3501	IL6-2
3502	IL6-3
3503	IL6-4
3504	IL7-1
3505	IL7-2
3506	IL7-3
3507	IL7-4
3508	IL7-5
3509	IL8-1
3510	IL8-2

LA	Line
3511	IL8-3
3512	IL9-1
3513	IL9-2
3514	IL9-3
3515	IL10-1
3516	IL10-2
3517	IL10-3
3518	IL11-1
3519	IL11-2
3520	IL11-3
3521	IL11-4
3522	IL12-1
3523	IL12-2
3524	IL12-3
3525	IL12-4

2. *L. hirsutum* introgression lines

The following group of introgression lines representing the genome of *L. hirsutum* LA1777 were developed by Monforte & Tanksley (Genome in press; 2000). The first 57 lines (LA3913-LA3969) represent approximately 85% of the donor genome via homozygous overlapping introgressions, while the remaining 41 lines (LA3970-LA4010) contain different recombinant segments, 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
3920	TA1536	1
3921	TA1105	2
3922	TA1266	2
3923	TA1537	2
3924	TA1538	2
3925	TA1111	3
3926	TA1276	3
3927	TA1277	3
3928	TA1540	3-8
3929	TA1541	3-8
3930	TA1133	4
3931	TA1280	4
3932	TA1562	4
3933	TA1542	4
3934	TA1459	4
3935	TA517	4
3936	TA1475	4

LA	Line	Chrom.s
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
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
3986	TA1309	3-7

LA	Line	Chrom.s
3987	TA1633	7
3988	TA1318	8
3989	TA1319	8
3990	TA1560	8
3991	TA1326	9
3992	TA1634	1-10-11-12
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

XIII. Other Prebreds

1. High soluble solids - derivatives of *L. chmielewskii* LA1028 (see Hilgardia 42:493-510).
LA1500, 1501, 1502, 1503, and 1563.

2. Misc. traits – monogenic and provisional mutants derived from *L. cheesmanii* (Econ. Bot. 21: 171-184):

LA	1015	*h*, 'cps' (compressed fruit = reduced L/W ratio)
	1016	*dps,* 'yg' (yellow green leaves)
	1017	*ptb*, 'Ppc' (pachypericarp = thick-walled fruit)
	1018	*ptb, u^G, Od, h,* dark buds (anthocyanin in bud calyces), bitter fruit
	1019	'Ppc', thick calyx, firm fruit

3. Exserted stigma - derivative of *L. pimpinellifolium* LA1585 (see TGC 33:13-14): LA2380.

XIV Cytoplasmic Variants

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
1438	Light green induced by X-rays-found by K. Verkerk in cv. Moneymaker
2979	Cyto-variegated in cv. Glamour (contributed by R.W. Robinson)

Membership List

Aarden, Harriette, Western Seed Semillas S.A., Apdo Correos 22, 35240 - Carrizal - Ingenio, Las Palmas de Gran Canaria, Spain, wse@lix.intercom.es
Acquisitions Dept, North Carolina State University, DH Hill Library, P. O. Box 7111, Raleigh, NC, 27695-7111, USA
Adams, Dawn, Campbell R&D, 28065 County Road 104, Davis, CA, 95616, USA
Alvarez-Luna, Eduardo, AGROMOD, S.A. DE C.V., 9051-C Siempre Viva Rd, Suite 051-21, San Diego, CA, 92173-3628, alvrz@tsi.com.mx
Anand, N., Namdhari Seeds, Bidadi-562 109, Bangalore, INDIA
Angell, Frederick, Asgrow Seed Company, 500 Lucy Brown Lane, San Juan Bautista, CA, 95045, USA
Arora, R.S., "Century Seeds, Pvt.Ltd.", BA-22 Phase II, Industrial Area Mangolpuri, Delhi-110034, INDIA, hybrids@bol.net.in
Augustine, Jim, BHN Research, 16750 Bonita Beach Rd., Bonita Springs, FL, 34135, USA
Avdeyev, Y.I., Flat 69, Botweena Street 10, Astrakhan, 414052, RUSSIA
Ayuso, Ma Cruz, Petoseed Iberica, Carretera de Malaga 34, 04710 Santa Maria del Aguila, Almeria, SPAIN
Baker, Barbara, USDA-ARS-PGEC, 800 Buchanan St., Albany, CA, 94710, USA
Bar, Moshe, Zeraim Gedera Co. Ltd., Post Box 103, Gedera, 70750, Israel
Barker, Susan, University of Western Australia, Dept of Plant Sciences, Nedlands, W.Australia 6907, AUSTRALIA
Beck Bunn, Teresa, PetoSeed , Research Center, 37437 State Highway 16, Woodland, CA, 95695, USA, teresa.beck.bunn@svseeds.com
Bergamini, Leopoldo, ESASEM SPA., Via San Biagio 25, 37052 Casaleone Vr, ITALY, LBergamini@esasem.com
Bernatzky, Robert, Univ. of Massachusetts, Dept of Plant and Soil Science, French Hall, Amherst, MA, 01003-2910, USA, rb@pssci.umass.edu
Bessey, Paul, 2602 E. Arroyo Chico, Tucson, AZ, 85716, USA
Bieche, Bernard, AMITOM, 27, avenue de l'Arrousaire, BP 235, 84010 Avignon Cedex 1, FRANCE, tomato@tomate.org
Bistra, Atanassova, Inst. Gen. & Plant Breeding, Sofia 1113, BULGARIA, anbilid@cserv.mgu.bg
Bowler, Chris, Stazione Zooligica, Molecular Plant Biology, Villa Communale, I 80121 Napoli, ITALY, chris@alpha.szn.it
Briggs, Carroll, Shamrock Seed, P.O. Box 1318, San Juan Bautista, CA, 95045-1318, USA, cbriggs@shamrockseed.com
Burdick, Allan, 3000 Woodkirk Drive, Columbia, MO, 65203, USA
Caranta, Carole, INRA, Genetics & Breeding of Fruits&Veget., Dom.St Maurice, BP94, 84143 Montfavet Cedex, FRANCE, Carole.Caranta@avignon.inra.fr
Carrijo, Iedo Valentim, Caixa Postal 1260, 32920-000 - Igarape, M.G., BRAZIL
Castagnoli, Franca, S.A.I.S. seed, Ravennate 214, Postbox 154, 47023, Cesena, ITALY, f_casta@libero.it
Causse, Mathilde, Station d'Amelioration des Plantes Maraicheres, BP94, 84143 Montfavet, Cedex, FRANCE
Chen, Fang Chin, AVRDC, Information and Documentation, PO Box 42, Shanhua, Tainan, Taiwan 741, Republic of China
Chetelat, Roger, Univ. Calif., Dept. Veg Crops, One Shields Ave., Davis, CA, 95616, USA
Chiasson, L.P., 36 Greenwold Dr, Antigonish NS, B2G 2H8, CANADA
Colten, Romano St. 18a, Tel-Aviv 69018, ISRAEL
Creech, Roy, MS State University, Department of Agronomy, MS, 39762, USA
Crill, Pat, 308 Manatee Dr., Ruskin, FL, 33570-5629, USA
Cuartero, Jesus, C.S.I.C., Estacion Exp. La Mayora, 29750 Algarrobo-Costa (Malaga), SPAIN
de Saravia, Elsa, Sarmiento 674, 7 piso depto 139, 4.400 SALTA, ARGENTINA, gilardon@unsa.edu.ar

Della Vecchia, Paulo, Agroflora, Caixa Postal 427, Braganca Paulista - SP, 12.900-000, BRAZIL
Dhaliwal, M.S., Department of Vegetable Crops, P.A.U. Ludhiana 141004, PANJAB, INDIA
Dick, Jim, 23264 Mull Rd, RR 4, Chatham, ONT N7M 5J4, CANADA, jimdick@netrover.com
Doganlar, Sami, Cornell University, Plant Breeding Dept., 252 Emerson Hall, Ithaca, NY, 14853, USA, sd21@cornell.edu
Earle, Elizabeth, Cornell University, Plant Breeding Dept., 252 Emerson Hall, Ithaca, NY, 14853, USA
Ecker, Ron, Hazera (1939) Ltd. Research Dept., Mivhor Farm, Sde Gat 79354, ISRAEL
Egashira, Hiroaki, Yamagata University 1-23, Faculty of Agriculture, Wakaba-machi, Tsuruoka city 997-8799, JAPAN
Farkas, Joseph, Seminis Hungaria Ltd., H-1238 Budapest, Majori ut, HUNGARY
Fernandez-Munoz, Rafael, CSIC Estacion Exp. La Mayora, 29750 Algarrabo-Costa (Malaga), SPAIN, rfern@eelm.csic.es
Ganal, Martin, Inst. for Plant Genetics & Crop Plants, (IPK), Correnssstr. 3, D-06466 Gatersleben, GERMANY, ganal@IPK-Gatersleben.de
Garvey, T.Casey, Hunt Foods Company, 1111 E. Covell Blvd., Davis, CA, 95616-1209, USA, 75154.204@compuserve.com
Gautier, Graines, B.P.1, 13630 Eyragues, FRANCE, gautier.graines@wanadoo.fr
George, B. F., H.J. Heinz Co., P. O. Box 57, Stockton, CA, 95201, USA, BGeorge@husa.com
Gidoni, David, The Volcani Center, Dept. of Plant Genetics, PO Box 6, Bet-Dagan 50250, ISRAEL
Grierson, Don, University of Nottingham, Sutton Bonington Campus, Loughborough LE12 5RD, Leicestershire, UK, Donald.Grierson@nottingham.ac.uk
Hagan, William, 17493 Oak Canyon Place, Castro Valley, CA, 94546, USA
Han, Sang Joo, Novartis Seeds Co. Ltd., 8th Fl.,SunAm Bldg., #114, Nonhyun-dong, Kangnam-ku, Seoul 135-010, KOREA, sangjoo2.han@seeds.novartis.com
Hanson, Peter, AVRDC, PO Box 42, Shanhua, Tainan, Taiwan 741, Republic of China, hansp@netra.avrdc.org.tw
Hassan, Ahmed Abdel-Moneim, Cairo University, Dept. of Horticulture, Giza, EGYPT
Hayashi, Masako Yaguchi, Asahi Industries, Biol.Engineering Lab, 222 Watarase, Kamikawa, Kodama-gun, Saitama-ken 367-0394, JAPAN, m.hayashi@asahi-kg.co.jp
Hein, Mich, Scripps Research Foundation, 10666 N. Torrey Pines Rd., La Jolla, CA, 92037, USA
Himmel, Phyllis, Seminis Vegetable Seeds, 37437 State Highway 16, Woodland, CA, 95695, USA
Hoa, Vu Dinh, Hanoi Agricultural University, Dept.Plant Breeding and Genetics, Gialam, Hanoi, VIETNAM
Holle, Miguel, Calle 2 No. 183, Urb El Rancho - Miraflores, Lima 18, PERU
Hoogstraten, Jaap, Royal Sluis France, Mas de Rouzel, Chemin des Canaux B.P. 7049, 30911 Nimes Cedex, FRANCE
Ignatova, Svetlana, Moscow E-215, Box 15, 105215, RUSSIA, tter@sonnet.ru
Imanishi, Shigeru, Yamagata University, Bioresource Engineering, 1-23, Wakaba-cho,Tsuruoka, Yamagata, JAPAN
Ito, Kimio, Vegetable Breeding Lab, Hokkaido National Agric. Expt. Stat., Hitsujigaoka, Sapporo, 062-8555, JAPAN
Jacoby, Daniel, 3055 Kirkup Lane PO Box 1560, Mattituck, NY, 11952, USA
Kedar, N., Hebrew Univ of Jerusalem, Faculty of Agriculture, P. O. Box 12, Rehovot 76-100, ISRAEL
Khush, Gurdev, IRRI, P. O. Box 933, Manila, PHILLIPINES
Kim, Byung-Dong, Seoul National University, Department of Horticulture, College of Agriculture and Life Sciences, SUWON 441-744, KOREA
Kim, Ji-kwang, Puyo Tomato Expt. Station, 325-48 Nohwari, Gyuammyeon, Puyo 323-810, KOREA, goldkr@kornet.net
Kopliovitch, Ehud, Hazera Genetics, Mivhor, M.P. Lachish Darom, 79354 ISRAEL
Lapidot, Moshe, The Volcani Center, P.O.Box 6, Bet Dagan, 50250, ISRAEL, lapidotm@netvision.net.il
Lineberger, Dan, Texas A&M Univ., Dept. Horticultural Sciences, College Station, TX, 77843-2133, USA
Lundin, Marianne, Svalof Weibull AB, Cereal Breeding Dept., S-268 81 Svalov, SWEDEN

Maluf, Wilson Roberto, Universidade Federal de Lavras, Dept. de Agricultura, Caixa Postal 37, 37200-000 Lavras-MG-, BRAZIL, wrmaluf@esal.ufla.br
Martin, Gregory, Cornell University, Plant Pathology, 323 Boyce Thompson, Ithaca, NY, 14853, USA, gbm7@cornell.edu
McCarthy, William, Seminis Vegetable Seeds, PO Box 249, Felda, FL, 33930, USA, Bill.Mccarthy@svseeds.com
McGlasson, W. B., Univ of Western Sydney, Hawkesbury Bourke St., Richmond NSW 2754, AUSTRALIA, B.McGlasson@uws.edu.au
McGrath, D. J., Horticulture Research Station, P. O. Box 538, Bowen, Queensland 4805, AUSTRALIA
Min, Chai, PO Box 2443, Beijing 100089, PEOPLES REPUBLIC of CHINA
Miranda, Baldwin, 1519 Ivygate Lane, Naples, FL, 34105, USA, ronnamira@aol.com
Mochizuki, Tasuya, Nationa Research Inst. of Vegetables, Ornamental Plants & Tea, 1823 Mii-machi, Kurume, Fukuoka 839-0851, JAPAN, tmochi@nivot-krm.affrc.go.jp
Murao, Kazunori, Sakata Seed Co., Kimitsu Station, 358 Uchikoshi, Sodegaura,Chiba, 299-0217, JAPAN
Mutschler, Martha, Dept. Plant Breeding & Biometry, 410 Bradfield Hall, Ithaca, NY, 14853-1901, USA, mam13@cornell.edu
Myers, James, Oregon State University, Vegetable Breeding and Genetics, Dept of Horticulture,4017 ALS, Corvallis, OR, 97331-7304, USA, myersja@bcc.orst.edu
Nei, Mirella, Univ. Bologna, Dept.of Agronomy, Via Filippo Re 6-8, 40126 Bologna, ITALY
Nuez, Fernando, Universidad Politecnica, Departamento de Biotecnologia, Camino de Vera 14, 46022 - Valencia, SPAIN
Ozminkowski, Richard, Heinz North America, Sr.Plant Breeder, P.O.Box 57, Stockton, CA, 95201, USA, rich.ozminkowski@husa.com
Palomares, Gloria, Universidad Politecnica de Valencia, Departmento de Biotecnologia, Camino de Vera, s/n, E-46022 Valencia, SPAIN, gpaloma@btc.upv.es
Pape, Greg, 1181 Trieste Dr., Hollister, CA, 95023, USA
Paredes, Maria Ines, EE La Consulta-INTA, Biblioteca, Casilla de Correo 8, (5567)La Consulta-Mendoza, ARGENTINA
Peng-fi, Li, Veg. Breeding Division, Horticulture Department, South China Agric. College, Guangzhou, PEOPLES REPUBLIC OF CHINA
Peters, Susan, Sunseeds, 7087 E. Peltier Rd., Acampo, CA, 95220, USA, speters%Sunseeds@mcimail.com
Piccinino, Lisa, Novartis Seeds, Inc., 10290 Greenway Road, Naples, FL, 34114, USA, lisa.piccinino@seeds.novartis.com
Poysa, Vaino, Agriculture Canada, Research Station, Harrow, Ontario N0R 1G0, CANADA
Rabinowitch, Haim, Hebrew Univ of Jerusalem, The Dean's Office, P.O.Box 12, Rehovot 76100, ISRAEL, rabin@agri.huji.ac.il
Reeves, Alvin, 1331 Houlton Rd., Westfield, ME, 04787, USA
Reynaerts, Arlette, Plant Genetic Systems, J Plateaustraat 22, 9000 Gent, BELGIUM
Rick, Charley, University of California, Department of Veg. Crops, Davis, CA, 95616, USA
Rivara, Charles, CA Tomato Research Inst., 18650 East Lone Tree Rd., Escalon, CA, 95320-9759, USA, chuck@tomatonet.org
Sasaki, Seiko, Plant Breeding Station of Kaneko Seeds, 50-12, Furuichi-machi 1-chome, Maebashi City, Gunma 371, JAPAN
Sayama, Haruki, Nippon Del Monte Corp., 3748 Shimizu-Cho, Numata,Gumma 378, JAPAN, hs3@ma3.justnet.ne.jp
Shimizu, Yoshitomi, Nagano Tomato Co. Ltd., Crop Breeding, 223 Yoshikawa Murai-Machi, Matsumoto, Nagano, JAPAN
Shintaku, Yurie, Shimizu, Suginami-ku, Tokyo 113, JAPAN
Soloviev, Alexander, Dept. of Genetics, K. Timiryazev's Agricultural Academy, Timiryazevskaya ul., 49, 127550 Moscow, RUSSIA

Soressi, Gian Piero, Univ. Degli Studi Della Tuscia, Agrobiologia E Agrochimica, Via S. Camillo de Lellis, 01100 Viterbo, ITALY
Spooner, David, University of Wisconsin, Dept of Horticulture, 1575 Linden Drive, Madison, WI, 53706, USA
St. Clair, Dina, Dept. Veg Crops, University of California, Davis, CA, 95616, USA
Stack, Stephen, Colorado State University, Department of Biology, Fort Collins, CO, 80523-1878, USA
Stamova, Liliana, 300 Solano Park Circle, 13F, Davis, CA, 95616, USA, wasyst@calweb.com
Stamova, Boryana, 300 Solano Park Circle, 13F, Davis, CA, 95616, USA, bsstamova@ucdavis.edu
Stein, Ira, Campbell Research & Development, 28605 County Rd 104, Davis, CA, 95616, USA, IraStein@compuserve.com
Stevens, Mikel, Brigham Young Univ., 275 Widtsoe Bldg, PO. Box25183, Provo, UT, 84602, USA, mikel_stevens@byu.edu
Stoeva-Popova, Pravda, Winthrop University, Dept. of Biology, 701 W. Oakland Rd., Rock Hill, SC, 29733, USA, jrpopov@cetlink.net
Stommel, John, USDA-ARS, Beltsville Ag. Res. Ctr., Beltsville, MD, 20705, USA, jstommel@asrr.arsusda.gov
Summers, William, Iowa State University, Department of Horticulture, Horticulture Building, Ames, IA, 50011-1100, USA
Tanksley, Steven, 252 Emerson Hall, Ithaca, NY, 14853-1901, USA
Tarry, Jerry, Orsetti Seed Co.Inc, 2301 Technology Parkway, Hollister, CA, 95024-2350, USA, JTARRY@prodigy.net
Thomas, Paul, 4 Juniper Court, Woodland, CA, 95695, USA
Thome, Catherine, Asgrow Veg. Seeds, 500 Lucy Brown Lane, San Juan Bautista, CA, 95045, USA
Vakalounakis, Demetrios, NAGREF, Plant Protection Institute, PO Box 1802, 711 10 Heraklio, Crete, GREECE, vakalounakis@nefeli.imbb.forth.gr
Vick, Halley, Applied Genetics, 238 Peckham Rd., Watsonville, CA, 95076, USA, vhalley@aol.com
von Wettstein-Knowles, Penny, Copenhagen University, Molecular Biology Institute, Oester Farimagsgade 2A, DK-1353 Copenhagen K, DENMARK, knowles@biobase.dk
Vulkova, Zlatka, Institute of Genetics, Sofia 1113, BULGARIA
Watanabe, Kazuo, Kinki University, Dept. BiotechnologicalScience, 930 Nishi-Mitani, Uchita, Wakayama, 649-6493, JAPAN, watanabe@bio.waka.kindai.ac.jp
Williamson, Valerie, University of California, Dept of Nematology, One Shields Ave., Davis, CA, 95616, USA, vmwilliamson@ucdavis.edu
Wing, Rod, Clemson University, Director, Inst. of Genomics, 100 Jordan Hall, Clemson, SC, 29634-5708, USA, rwing@clemson.edu
Young, Harold, Route 4,Box 237B, Greenville, FL, 32331-9802, USA, hwyoung@digitalexp.com
Zamir, Dani, Hebrew Univ of Jerusalem, Dept of Field Crops, P.O.B. 12 Rehovot, ISRAEL
Zischke, Jeff, Sakata Seed America, 105 Boronda Rd, Salinas, CA, 93907, USA

Libraries, Institutions, etc.

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