2006
Tomato Breeders
Round Table
& Tomato Quality Workshop

May 7-11, 2006
Tampa, Florida USA

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Tomato Breeders Round Table
& Tomato Quality Workshop
May 7-11, 2006
Tampa, Florida USA

Sunday, May 7

5:00 PM - 7:00PM **Registration**

6:30 PM - 8:00PM **Welcome Reception – Atrium Waterfall Area**

Tomato Quality Workshop – Salon F

Monday, May 8

7:30 AM - 8:30 AM **Registration**

8:30 AM - 8:45 AM **Welcome**
Dr. Douglas Archer, Associate Dean of Research,
IFAS University of Florida
Mr. Reggie Brown, Manager, Florida Tomato Committee

8:45 AM - 9:45 AM **Panel Discussion: What is tomato quality?**
Millard Quillian, Taylor & Fulton, Inc., Palmetto, FL (Grower and Packinghouse)
Jay Bennett, Category Manager, Albertson's Inc. (Retailer)

9:45 AM - 10:15 AM **Premium quality program for fresh-market tomatoes: From ripening to enhancing harvest efficiency.**
Steven A. Sargent, Horticultural Sciences Department, University of Florida

10:15 AM - 10:45 AM **Coffee Break**

10:45 AM - 11:15 AM **Diallel analysis of resistance to bacterial soft rot infection of tomatoes by stem scar water uptake and the effects of time between harvest and dump tank immersion on water uptake.**
Sarah Smith*, Jay W. Scott and Jerry A. Bartz, GCREC, University of Florida

11:15 AM - 11:45 AM **Understanding the contributions and interactions of sugars, acids and aroma volatiles to overall tomato flavor.**
Elizabeth A. Baldwin, USDA-ARS, US Citrus and Subtropical Laboratory, Winter Haven, FL

* Denotes speaker

11:45 AM - 12:00 PM **Discussion**

12:00 PM - 1:30 PM **Lunch – Atrium**

1:30 PM - 2:00 PM **Molecular approaches to tomato flavor analysis.**
Denise Tieman and Harry J. Klee*, Horticultural Sciences Department, University of Florida

2:00 PM - 2:30 PM **Shelf-life limiting quality factors in fresh-cut (sliced) tomatoes: Anti-ethylene treatment and maturity & variety selection to ensure quality retention.**
Jeff Brecht, Horticultural Sciences Department, University of Florida

2:30 PM - 3:00 PM **'Flora-Lee': a field tomato for the premium tomato market.**
Jay W. Scott*, GCREC, University of Florida, and Elizabeth Baldwin, USDA-ARS, US Citrus and Subtropical Laboratory, Winter Haven, FL

3:00 PM - 3:45 PM **Panel Discussion: Processing tomato quality.**
Rich Ozminkowski, Heinz N.A., Ag. Research, Stockton, CA
Dawn Adams, Campbell Research, Davis, CA
Steve Schroder, Nunhems USA, Acampo, CA

3:45 PM - 4:15 PM **General Discussion on Future Directions of Tomato Quality Research**

Tuesday May 9 Tour

8:30 AM Depart hotel

Stop 1: 9:00 AM -10:15 AM Artesian Farms: Tomato Variety Trial and commercial tomato harvesting. See trial maps and descriptions on page

Stop 2: 10:45 AM -12:30 PM Gulf Coast Research & Education Center: TYLCV and ToMoV trial and lunch. See trial maps and descriptions on page

Stop 3: 1:00 PM-3:00 PM West Coast Tomato, Palmetto: Tomato packing (v. modern packing line), ethylene treatment and shipping.

Stop 4: 3:30 PM-4:30 PM DiMare Fresh Tampa: Tomato repacking for foodservice, consumer & specialty tomato packaging.

5:00 PM Return to hotel

5:30 - 7:00 PM **Happy Hour – Atrium Area**

7:00 - 9:00 PM **Banquet – Salon F**

Tomato Breeders Roundtable – Salon E
Wednesday May 10

Biotechnology/Markers
Mikel Stevens, Moderator

8:00 AM - 8:30 AM **The international tomato sequencing project and related *Solanaceae* initiatives.**
Joyce Van Eck, Boyce Thompson Institute, Ithaca, NY

8:30 AM - 9:00 AM **The SolCAP Initiative: Translating plant genome sequence data into applied outcomes.**
David Francis, The Ohio State University, Wooster, OH

9:00 AM - 9:20 AM **Polymorphism among EST-based markers in tomato.**
A.M. Baldo*, L. Robertson, S.M. Sheffer, J.A. Labate, USDA, Geneva, Cornell University

9:20 AM - 9:40 AM **Genetic variability in tomato.**
N.I. Bocharnikova, Yu. V. Chesnokov, All Russian Research Institute of Vegetable Breeding and Seed Production. Moscow reg., Odinstove dis, p/o Lesnoi gorodok, Russia N.I. Vavilov All-Russian Research Institute of Plant Industry (VIR)

9:40 AM - 10:10 AM **Coffee Break**

Insect Resistance in Tomato
David Schuster, Moderator

10:10 AM - 10:30 AM **The evaluation of insect resistance in the core collection of *Lycopersicon hirsutum* Dunal and inheritance of resistance to leafminer (*Liriomyza sativae* Blandchard).**
Zhimin Wang, Chai Min, Jiang Ligang, Qiu Jiyan* and John C. Snyder Institute of Plant & Environment protection, Beijing Academy of Agricultural and Forestry Science, Beijing, 100089, China

10:30 AM - 10:50 AM **Spider mite resistance and trichome secretions in *Lycopersicon hirsutum* LA2329 and hybrids with *L. esculentum***
John Snyder* and Chai Min, Department of Horticulture, University of Kentucky and Beijing Vegetable Research Center, Beijing

10:50 am - 11:10 am **The evaluation of the *Lycopersicon pennellii* core collection for pest resistance.**
Chai Min*, Yu Shuancang, Jiang Ligang, Tang Xiaowei,
Qiu Jiyan and John Snyder, Beijing Vegetable Research Center, Beijing Academy of Agriculture and Forestry Sciences, Beijing, 100089, China

11:10 AM - 11:40 AM **Rapid generation and characterization of tomato lines with acylsugar mediated broad spectrum insect resistance.**
Martha Mutchler and Ricardo Lobato-Ortiz, Cornell University

11:40 AM - 12:00 PM Identification of silverleaf whitefly resistance loci in *L. hirsutum* accession LA 1777.
Aliya Momotaz*, Jay W. Scott and David J. Schuster, GCREC, University of Florida

12:00 PM - 1:30 PM Lunch – Atrium

Area Reports
Tito Alacantra Moderator

1:30 PM - 2:30 PM
Florida and Southeast U.S - Lisa Cook, Syngenta, Naples, FL
Northeast US, Midwest US, and Canada - David Francis, The Ohio State University, Wooster, OH
California and Mexico Fresh Market - Doug Heath, Seminis, Woodland, CA
California Processing - Mike Kuehn, Harris Moran, Winters, CA
Europe and Middle East - Amit Shiftan, Zeraim Gedera, Gedera, Israel
Australia - Des McGrath, BPI Australia, Gaton, Queensland, Australia
China – Chai Min, Beijing Vegetable Research Center, Beijing, China

Tomato Disease Resistance
Ray Volin-Moderator

2:30 PM - 2:50 PM New late blight resistance genes in tomato.
Majid Foolad, Penn State University

2:50 PM - 3:10 PM Resistance to California isolates of *Pseudomonas syringae* pv. tomato race 1.
Liliana Stamova, California Tomato Research Institute, Davis CA

3:10 PM - 3:40 PM Coffee Break

3:40 PM - 4:00 PM Mapping quantitative resistance loci to bacterial wilt in tomato line Hawaii 7996.
Jaw-Fen Wang, E.B. Graham, A. Kilian, C. Ballatero, A. Cameille, P. Besse, T.X. Jaunet, V. Dittapongpitch, N. Hidayati, S.M. Huang, T.H.H. Truong, P.M. Hanson,* and R.C. de la Peña, Asian Vegetable Research and Development Center, Tainan Taiwan

4:00 PM - 4:20 PM Breeding tomatoes for resistance to begomoviruses and *Ralstonia solanacearum* for Central America.
Luis Mejia, Douglas P. Maxwell*, Henryk Czosnek, and Favi Vidavski. San Carlos University, University of Wisconsin, The Hebrew University

4:20 PM - 4:40 PM Pile up of resistant genes to *TYLCV* found in wild tomato species to produce resistant cultivars.
Favi Vidavski, The Hebrew University, Moshe Lapidot, The Volcani Center and Henryk Czosnek, The Hebrew University

4:40 PM - 5:00 PM **Development of breeder friendly markers for begomovirus resistance genes derived from L. chilense.**
Yuanfu Ji* and Jay W. Scott, University of Florida

7:00 PM - 10:00 PM **Tomato Crop Germplasm Committee Meeting – Cypress Room**
David Francis, Chair

Thursday May 11 – Salon F

Tomato Disease Resistance (continued)
Ray Volin-Moderator

8:00 AM - 8:20 AM **Screening accessions for resistance to pepino mosaic virus resistance**.
Kai-Shu Ling* and Jay W. Scott, USDA Charleston, SC

8:20 AM - 8:40 AM **Current status of resistance to tospoviruses in tomato.**
Mikel R. Stevens*, Jay W. Scott, Bradley D. Geary, John J. Cho, Luis F. Gordillo, Frederic D. Memmott, and JoLynn J. Stevens, Brigham Young University

Botanical Issues and Breeding for Horticultural Attributes
Majid Foolad, Moderator

8:40 AM - 9:20 AM **Nomenclature for wild and cultivated tomatoes.**
Iris Peralta, National University of Cuyo and IADIZA-CONICET Mendoza, Argentina

9:20 AM - 9:40 AM **Tomato fruit firmness attributes in hybrids from crosses between *Solanum lycopersicum* and *S. lycopersicum* x *S. galapagense* derived parental genotypes.**
John R. Stommel, Vegetable Laboratory, USDA, ARS, Beltsville, MD

9:40 AM – 10:00 AM **Tomato production in China and breeding program in BVRC**
Chai Min, Beijing Vegetable Research Center, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China

10:00 AM - 10:30 AM **Coffee Break**

10:30 AM - 10:50 AM **The structure of tomato breeding programs: Progress towards association mapping of horticultural traits.**
David Francis, The Ohio State University, Wooster, OH

10:50 AM - 11:10 AM **Biological values of tomato fruit growing in greenhouses with and without soils.**
S.I. Ignatova, All Russian Research Institute for Vegetable Crops, SSAF Ilynichna 141018 Moscow region, Russia

Tomato Germplasm and Committee Reports

11:10 AM - 11:20AM Plant Introduction Center
Larry Robertson, USDA, Geneva, NY

11:20 AM - 11:30AM Tomato Crop Germplasm
David Francis, The Ohio State University, Wooster, OH

11:30 AM - 11:40 AM Tomato Genetics Cooperative
Jay W. Scott, University of Florida

Business Meeting

11:40AM – 12:00 PM Next meeting location and date
Jay W. Scott, University of Florida

Adjourn.

Tomato Breeders Round Table

May 7-11, 2006

Program Abstracts

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Premium quality program for fresh-market tomatoes: From ripening to enhancing harvest efficiency

Steven A. Sargent
Horticultural Sciences Department, University of Florida/IFAS
PO Box 110690, Gainesville FL 32611
(Email:sasa@ufl.edu)

Since the early 1990's we have been developing harvest and postharvest handling information handling to assist tomato growers in shipping tomatoes with high consumer acceptance. The goal of this Premium-Quality Tomato Program has been to refine established handling procedures and evaluate new technologies for growers to be more competitive in domestic and world markets with tomatoes that have consistently high flavor and quality. This program has focused on four areas:

1. Minimizing mechanical injury during harvest and handling operations
2. Using ethylene treatment to sort green-harvested tomatoes with the best flavor
3. Employing proper storage temperature throughout shipping and marketing
4. Evaluating harvest aids to improve harvest efficiency

Using extensive trained taste panel, it was determined that tomatoes harvested at mature-green stage with minimal internal bruising can be ripened with excellent flavor being equivalent in quality to tomatoes picked at pink stage or later. Currently, we are evaluating continuous harvest aids that show promise for reducing picking costs and permitting in-field presorting.

Diallel analysis of resistance to bacterial soft rot infection of tomatoes by stem scar water uptake and the effects of time between harvest and dump tank immersion on water uptake.

Sarah M. Smith, Jay W. Scott and Jerry A. Bartz
University of Florida, GCREC, 14625 County Road 672, Wimauma, FL
(Email: smith04@ufl.edu)

Tomato (*Lycopersicon esculentum* Mill.) fruit can absorb water into and through stem scar tissues during certain postharvest handling steps. The tissue water congestion leads to excessive postharvest development of bacterial soft rot, caused by *Erwinia carotovora*, and certain other bacterial hazards. Previously, fruits of certain cultivars were found to differ in the tendency to take up water during a simulation of packinghouse handling procedures. Studies were conducted to determine if the interval between harvest and exposure to water affected uptake and to estimate if this fruit characteristic was inherited. For the first experiment, 'Florida 47' and 'Sebring' were grown in a completely randomized block design with three blocks and 10 plants per block. At 0, 6, 12 or 24 h after harvest, mature green fruit were weighed, submerged in water for 2 min and then reweighed to determine water uptake. During the submergence, air pressure was applied such that the fruit were exposed to water head equivalent to 1.3 meters. For the second experiment, six inbred parents of tomato were intercrossed to develop a complete diallel to determine the inheritance of fruit water uptake tendencies. The parents and hybrids were grown in a completely randomized block design with three blocks and 10 plants per block. Fruit of 'Sebring' absorbed significantly less water than 'Florida 47', confirming results of previous studies. The amount of water absorbed by both cultivars was significantly greater at 0 as compared with 6, 12 or 24 hours after harvest. Fruit of 'Florida 47' tested at 6, 12 or 24 h after harvest absorbed similar amounts of water. By contrast, the 6 h 'Sebring' fruit absorbed less water than those tested at 12 h after harvest. In the diallel analysis, both the general combining ability (GCA) and specific combining ability (SCA) were significant with GCA having a higher level of significance than SCA. The water uptake tendency of the progeny was reduced if the low uptake parent was used as a female, suggesting a cytoplasmic inheritance pattern. Parents were significantly different for five hybrids, and three of these reciprocal hybrids with a low water infiltration female parent had significantly less water uptake than their reciprocals. The other two hybrids where the reciprocals were not significantly different had a parent in common possibly indicating some genotypes may not respond cytoplasmically.

Understanding the contributions and interactions of sugars, acids and aroma volatiles to overall tomato flavor.

Elizabeth Baldwin, Kevin Goodner and Anne Plotto
USDA-ARS Citrus & Subtropical Products Laboratory, 500 Ave S N.W.,
Winter Haven, FL 33881
(Email: ebaldwin@citrus.usda.gov)

The contribution and interaction of sugars, acids and volatiles to tomato (*Lycoperscon esculentum* Mill.) flavor is little understood. Coarsely chopped deodorized tomato puree was spiked with different levels of individual food grade volatiles, reported to contribute to tomato flavor, as well as two levels of fructose/glucose and citric/malic solutions and presented to a trained descriptive panel for flavor analysis. Fresh tomato homogenate was also analyzed by gas chromatography/olfactometry (GCO) and an aromagram generated. Based on descriptors resulting from the aromagram, past panel rating of these individual aroma compounds, volatiles were then grouped based on similarities of descriptors into “green”, “earthy” and “fruity” mixtures, again added to bland homogenate at different levels and presented to a trained panel. Six to eight panelists rated 5 aroma, 8 taste, and 3 after-taste descriptors on a 15 cm unstructured line scale and data are an average of two panels. The “green” mix enhanced overall and green aromas while decreasing perception of tropical taste. The “earthy” mix enhanced perception of vine and earthy aromas, and sweet taste, while negatively impacting sour and ripe tomato taste. The “fruity” mix enhanced overall, sweet tomato, and tropical aromas as well as sweet, tropical and fruity tastes. This mix also negatively impacted perception of green and musty aromas as well as sour taste. The sugar/acid ratio of tomato puree was found to correlate with perception of taste descriptors sweet (+), sour (-), bitter (-) ($P \leq 0.05$), and citrus (-) ($P \leq 0.15$) for most volatiles tested. When sugars were added (Brix =19) then perception of overall (-), floral (-) and musty (+) aromas were impacted. Perception of floral aroma was also less when acids were added (Brix= 4.88). Correlations were also found for the sugar/acid ratio with overall aftertaste (-) when the puree was spiked with furanol, *trans*-2-hexenal, geranylacetone, or acetaldehyde; fruity (+) with beta-ionone and linalool; and tropical (+) with *cis*-3-hexenal and geranylacetone ($P \leq 0.15$). The study suggests that increasing taste factors, like sweetness, results in decreased perception of tomato aroma in general, and affects how aroma compounds influence sensory descriptors.

Molecular approaches to tomato flavor analysis.

Denise Tieman and Harry Klee
Horticultural Sciences, University of Florida, PO Box 110690, Gainesville, FL 32611
(Email: hjklee@ufl.edu)

Flavor in tomato consists of the combined contributions of sugars, acids and a set of approximately 15 volatile compounds. We have focused our efforts on identification of genes that contribute to synthesis of the volatiles. These compounds are a chemically diverse, being derived from multiple amino acids, lipids and carotenoids. While the identities of the volatiles has been known for many years, the pathways for their synthesis have for the most part not been defined. Using genomics, metabolomics and targeted approaches, we have identified genes encoding steps in synthesis of several flavor volatiles. In particular, we have identified the rate-limiting step in the pathway for synthesis of 2-phenylacetaldehyde and 2-phenylethanol. We have also identified the enzyme responsible for synthesis of the apocarotenoid volatiles b-ionone, pseudoionone and geranylacetone. Employing transgenes, we have engineered plants for altered volatile content and can now examine the functions of these flavor and fragrance *in vivo*. By identifying these genes, we can in the future engineer precise alterations in subsets of the important flavor volatiles. Further, the genes should be valuable tools for marker assisted breeding in quality improvement programs.

Shelf-life limiting quality factors in fresh-cut (sliced) tomatoes: Anti-ethylene treatment and maturity & variety selection to ensure quality retention.

Jeffrey K. Brecht
Horticultural Sciences Department, University of Florida, PO Box 110690, Gainesville, FL 32611-0690
(Email: jkb@ifas.ufl.edu)

A major limitation in marketing fresh-cut tomato products is watersoaking of the fruit tissue and, in extreme cases, juice leakage. This problem renders fresh-cut tomato slices and dices unmarketable, and the accumulation of juice in the bottom of containers can promote obnoxious fermentative volatile formation and microbial proliferation. In order to slow deterioration and reduce microbial growth, fresh-cut tomato products are necessarily stored at 2-5 ?C, which is normally considered to be a chilling temperature for tomatoes, but it appears that watersoaking is caused by wounding, not chilling injury. When the relationship between storage temperature, fruit developmental stage, initial tissue firmness and tissue watersoaking development was investigated, we found that watersoaking is much worse in slices prepared and/or held at temperatures higher than 5 ?C. Watersoaking development in fresh-cut tomato slices became more rapid as initial fruit ripeness advanced from the breaker to red stage, and 1-MCP (1 µL L^{-1}) was more effective in reducing watersoaking in slices from light red stage than red stage fruit. Slices from fruit of the same ripeness stage (i.e., color), from either the same or different varieties, that had higher initial firmness values also developed less watersoaking and responded better to 1-MCP treatment. Our results support the idea that watersoaking development in fresh-cut tomato slices during storage at 5 ?C is an ethylene-mediated symptom of senescence. However, tomato varieties with firmer texture at advanced ripeness stage, or cultural and postharvest practices that result in firmer light-red-to-red fruit would be most useful for marketing fresh-cut tomato products.

‘Flora-Lee’: A field tomato for the premium tomato market.

Jay W. Scott[1] and Elizabeth Baldwin[2]
[1]Gulf Coast Research & Education Center, University of Florida,
14625 CR 672, Wimauma, FL 33598
[2]USDA-ARS Citrus & Subtropical Products Laboratory, 600 Ave. S N.W.,
Winter Haven, FL 33881
(Email: jwsc@ufl.edu)

Over the last 10 years much of the supermarket tomato trade has shifted from field grown tomatoes to greenhouse grown tomatoes. The tomatoes on the vine (TOV) or hydroponic tomatoes with calyx attached grown in greenhouses have attained considerable shelf space and are often sold for significantly higher prices than are field tomatoes. The reason for this is a perceived improvement in fruit quality or freshness often due to appearance of the product. There has also been an increase in specialty tomatoes on the shelves that are sometimes field grown. An example would be the grape tomatoes that are popular because of their sweet flavor. Florida tomatoes and other field grown tomatoes are primarily bought by the food service industry. ‘Flora-Lee’, tested as Fla. 8153, is being considered for a release in the near future as a cultivar for growers of field tomatoes to regain an increased share of the supermarket trade. This is a crimson (*og*^{c}) hybrid with approximately 25% more lycopene than standard cultivars. Thus, it can be sold as a more healthful tomato. The interior color is a deeper red than standard tomatoes making for an attractive fruit likely to be popular with consumers. ‘Flora-Lee’ has been tested in six sensory panels over six seasons, and has been rated in the most preferred group every time. Furthermore, in five of the six panels it was significantly preferred ($P>0.1$) over commercial cultivars like ‘Florida 47’. It has twice been compared to store bought TOV cultivars and three times been compared store bought tomatoes of the cultivar sold as “Ugly Ripe”, and in each case was significantly preferred. The strength of ‘Flora-Lee’ from a flavor standpoint is that it tastes good under a range of environmental conditions. This should provide tomatoes that are consistently high quality and, therefore can be branded to attract repeat customers. Flavor ranges from good but mild to excellent with a “clean tomato” balance of sweetness and acidity. To avoid immature harvest, it will be recommended that ‘Flora-Lee’ be picked at the breaker stage or beyond. Numerous trials on University and grower farms indicate ‘Flora-Lee’ reliably sets firm, marketable fruit on a medium sized but strong vine. Fruit size has a range from 5 x 6 to 6 x 7 but with less 5 x 6 fruit than cultivars typically grown in Florida. The cultivar does get some graywall, which may reduce marketable yields under some conditions. ‘Flora-Lee’ has a jointed pedicel. It is resistant to Fusarium wilt races 1, 2, and 3, Verticillium wilt race 1, and gray leafspot. Implications as to the myriad of factors that may affect the impact of this release will be discussed.

The international tomato sequencing project and related *Solanaceae* initiatives.

Joyce Van Eck[1], Steve Tanksley[2], Jim Giovannoni[1,3], Lukas Mueller[2], and Steve Stack[4]

[1]The Boyce Thompson Institute for Plant Research,
Cornell University, Ithaca, NY 14853
[2]Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853
[3]U.S. Department of Agriculture-Agricultural Research Service, Plant, Soil, and Nutrition Lab, Cornell University, Ithaca, NY 14853
[4]Department of Biology, Colorado State University, Fort Collins, CO 80523
(Email: jv27@cornell.edu)

Sequencing the tomato genome is the foundation for a large and ambitious international project – the International *Solanaceae* Genomics Project. The intention is to produce a high quality, ordered sequence, which can be used to facilitate research not only in tomato, but also serve as a guide in future sequencing of other *Solanaceae* genomes through comparative maps. An international consortium comprised of ten countries is sequencing the gene-rich euchromatin regions of the twelve chromosomes. The US team is sequencing three chromosomes (1, 10, 11), and the remaining nine are each being sequenced by an international partner. The chromosomes are divided into manageable sections known as BACs (Bacterial Artificial Chromosomes), which are sequenced separately. The starting point for sequencing the genome is approximately 1500 "seed" BAC clones individually anchored to a high density genetic map based on a *Solanum lycopersicum* x *S. pennellii* F2 population. Sequencing is following a BAC-by-BAC basis, and each sequenced anchor BAC serves as a seed from which to radiate out into the minimum tiling path. We are particularly interested in BACs that are located as close as possible to telomeres and at euchromatin/heterochromatin borders. To steer sequencing activities into the euchromatin and away from the heterochromatin, Fluorescence In Situ Hybridization (FISH) is being utilized for BAC localization. The repository for all information and data generated is the SOL Genomics Network (www.sgn.cornell.edu). Additional *Solanaceae* initiatives have formed recently including EU-SOL, SOL-ANDINO, and Lat-SOL.

The SolCAP Initiative: Translating plant genome sequence data into applied outcomes.

David Francis[1], David Douches[2], and Walter DeJong[3]

[1]Department of Horticulture and Crop Science, The Ohio State University, 1680 Madison Ave. Wooster, OH 44691; [2]Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI 48824; [3]Department of Plant Breeding & Genetics, Cornell University Ithaca, NY 14853

The USDA/NRI Coordinated Agricultural Project (CAP) program offers a template for organization of researchers for application of genomic resources in order to maximize the benefit of translational research. The *Solanaceae* Coordinated Agricultural Project (SolCAP) is an effort to organize an inclusive community of public and private researchers to develop a shared vision and plan to facilitate translation of basic discoveries and technology for crop improvement. A theme that has emerged during the course of planning activities is that translational research involving genome sequence information may require that we think about agricultural research from the point of view of taxonomic groups and DNA sequence homology rather than traditional commodity boundaries. To maximize the use of resources, a research community must be willing to work beyond traditional commodity divisions. The *Solanaceae* offer an opportunity to transcend commodity boundaries, but there is a need to balance goals that are generalized for several commodities while providing sufficient resources to accomplish specific goals with impact. Our intention is to focus the SolCAP on both fresh and processed germplasm for potato, pepper and tomato.

A roadmap for the SolCAP is emerging. Standard germplasm panels for potato, pepper and tomato are being developed that represent a balance between relevant breeding lines and populations for mapping of traits. The germplasm will be grouped according to specific market classes and will include a broad genetic-base to survey allelic diversity. Including germplasm that represents either important varieties or advanced lines of value to the breeding community will be stressed. To provide a taxonomic perspective, a set of species and accessions will be sampled representing all major clades, ploidies, and breeding systems. Lastly, structured mapping populations will also be included. A subset of the panel will be used for deep-sequencing of genes and promoters related to carbohydrate and sugar metabolism due to the importance of these traits in both processing quality and flavor. Genotyping platforms based on size polymorphisms (SSR and InDel) and Single Nucleotide Polymorphisms (SNPs) will be standardized and used to develop a database for the entire germplasm panel. Phenotyping platforms will facilitate data collection for the germplasm panels while providing breeders a low-cost means of collecting quantitative data related to key traits. Adopting standardized genotyping platforms, developing user-friendly tools for analysis, and linking this information to phenotypes will help translate genome sequence information and increase access to the breeding community. At the same time such approaches will help elucidate the genes and gene systems under selection during domestication and breeding.

Polymorphism among EST-based markers in tomato.

A.M. Baldo, L. Robertson, S.M. Sheffer, and J.A. Labate
USDA Geneva, Cornell University

Cultivated tomato (*Lycopersicon esculentum* Mill.) has a narrow genetic base. This is in part due to population genetic processes such as founder events, genetic bottlenecks, and natural and artificial selection during domestication. We characterize the nucleotide polymorphism in 26 EST-based markers, including Single Nucleotide Polymorphisms (SNPs) and Insertions/Deletions (Indels). Five of these markers are hypothesized to be cryptic wild species alleles (introgressions) within *L. esculentum*. These gene fragments were also resequenced in a diverse panel of 30 Plant Genetic Resources Unit (PGRU) tomato accessions, line TA496, and *Lycopersicon peruvianum* accession G 32591. The majority of sampled tomato accessions represented the primary center of diversity (Peru, Chile, and Ecuador), and countries contiguous with the primary center. Original collections were made between 1932 and 1976. These data will enhance our understanding of EST-based markers and the nature of genetic variation within cultivated tomato.

Genetic variability in tomato.

Bocharnikova N.I., Chesnokov Yu.V.
All Russian Research Institute of Vegetable Breeding and Seed Production, 134080 Moscow reg., Odintsov dis, p/o Lesnoi gorodok, Russia N.I. Vavilov All-Russian Research Institute of Plant Industry (VIR)

With the discovery of the phenomenon of genetic transformation, it became possible to transfer certain characters from one organism to another via exogenous DNA. Pollination with exogenous DNA-treated pollen has resulted in the appearance of plants with unusual character combinations which are of interest to the breeder. Use of exogenous DNA in interspecific crosses has broadened the range spectrum of genetic variability resulting in the occurrence in the population of KmR transformants-recombinants with unusual combinations of agronomic characters. This provides a means for speeding up the breeding process.

The evaluation of insect resistance in the core collection of *Lycopersicon hirsutum* Dunal and inheritance of resistance to leafminer (*Liriomyza sativae* Blandchard).

Zhimin Wang[1], Chai Min[2], Jiang Ligang[2], Qiu Jiyan[3] and John Snyder[4]
[1]School of Agriculture and Biology, Shanghai Jiaotong University, Shanghai, 201101, China
[2]Beijing Vegetable Research Center, Beijing Academy of Agriculture and Forestry Sciences, Beijing, 100089, China
[3]Institute of Plant & Environment protection, Beijing Academy of Agricultural and Forestry Science, Beijing, 100089, China
[4]Dept. of Horticulture, University of Kentucky, Lexington, KY 40546 USA
(Email: chaimin@nercv.com)

The evaluation of the *Lycopersicon hirsutum* Dunal core collection for insect resistance took place at the Beijing Vegetable Research Center during 2001 and 2002. In the open field, most accessions were resistant to aphids. In the greenhouse, most accessions were resistant or immune to leafminer (*Liriomyza sativae* Blandchard). LA2329 was used in the study of inheritance of resistance to leafminer because of its high resistance to aphids, leafminers, ToMV as well as its vigorous growth under our conditions. Inheritance of resistance to leafminer was analyzed by crossing LA2329 with a highly susceptible cultivated tomato variety, Zaofen 2, as female and subsequently backcrossing Zaofen 2 × F_1. Results from artificial infestation with adult leafminer on P_1, P_2, F_1 and BC_1 indicated that the resistance is controlled by a single dominant gene. To our knowledge, this is the first report of resistance to leafminer in *Lycopersicon* that is conferred by a single dominant gene. The resistance gene will provide an invaluable source to breeding of tomato resistance to leafminer, and hopefully will be introduced into cultivated tomato through marker-assisted selection which will lead to a sustainable, economical and efficient way to control leafminer in tomato production.

Spidermite resistance and trichome secretions in *Lycopersicon hirsutum* LA2329 and hybrids with *L. esculentum.*

John Snyder[1] and Chai Min[2]
[1]Dept. of Horticulture, University of Kentucky, Lexington, KY 40546
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Spidermite resistance and its causal mechanisms were evaluated in *Lycopersicon hirsutum* LA2329 and hybrids with *L. esculentum*, Zaofen 2. In whole leaf bioassays, LA2329 was highly resistant, as were F1 hybrids. Resistance in F2 hybrids appeared to segregate in a 3:1 fashion, with resistant plants at the higher frequency. In the F3 generation, two families segregated (4:1 and 7:1, resistant:susceptible) and another F3 family did not segregate (0:9). Based on the results of whole leaf tests, resistance is likely dominant and controlled by one or a few genes. In thumbtack bioassays, Zaofen 2 is not repellent and LA2329 is highly repellent. A few F2 individuals had highly repellent leaflets. In the F2, abaxial type VI trichome density ranged from 6 to 13/mm², and adaxial density ranged from 7 to 25/mm². Abaxial type IV density ranged from 0 to 59/mm² and adaxial density, from 0 to 29 per mm². Separation of trichome secretions by reverse phase thin layer chromatography indicated that some components of the secretions are more repellent than others. Predominant components of the LA2329 trichome secretions are oxygenated derivatives of sesquiterpenes. Additional characterization of the trichome secretions is underway.

The evaluation of the *Lycopersicon pennellii* core collection for pest resistance.

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Aphid and spider mite resistance were studied in 16 accessions of the core collection of *L. pennellii,* a wild relative of the cultivated tomato. In open field experiments, 10 accessions set fruit, and the seeds were saved only from 8 accessions. All 16 accessions were resistant to aphids in open field. Two of the accessions were immune to aphids, and 14 accessions were highly resistant. Resistance to spider mites was evaluated by infestation with the mites from the edible amaranth (*Amaranthus mangostanus* L.) in lab. The results showed that 15 accessions were resistant to spider mite, but LA1920 was highly susceptible. Of the 15 resistant accessions, one was immune, 12 were highly resistant, and 2 were resistant.

Rapid generation and characterization of tomato lines with acylsugar mediated broad spectrum insect resistance.

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The wild tomato *Solanum pennellii (formerly Lycopersicon pennellii*) is resistant to a broad spectrum of tomato pests due to the presence of acylsugars, which deter pests, reducing their feeding and/or oviposition. The initial transfer of acylsugar production to tomato produced 97FL, a line producing moderately high levels of acylsucroses, and demonstrable pest resistance. 97FL possesses 9 *S. pennellii* introgressions, representing 27% of its nuclear genomes. Using this information, we created a series of hybrids demonstrating that acylsugar level can be modulated through manipulation of the subset of introgressions that are present in the heterozygous vs. homozygous state. Selected acylsugar producing hybrids also showed sharply reduced infection by a greenhouse whitefly transmitted virus.

97FL is not directly useful horticulturally, since negative horticultural characteristics were also carried by the larger *S. pennellii* introgressions. A series of PCR based markers were created to allow efficient screening of segregating populations for modifications of introgressions through recombination. The integration of the direct acylsugar assay and the molecular markers allowed the rapid creation of acylsugar lines possessing fewer and/or smaller introgressions, accompanied by improvements in horticultural type. Work in 2002/2003 resulted in the second generation of 5 acylsugar lines, with 4 to 9 introgressions for 77 to 90% of their genomes derived from tomato. Work in 2004/2005 resulted in the third generation of 21 acylsugar lines with 4 to 8 introgressions for 85 to 90% of their genomes derived from tomato. 2006 trials of these lines and their hybrids in tomato in Florida and/or NY should determine the best hybrids for advanced testing. I am currently building a consortium to facilitate performing multisite trials of insect control using acylsugar hybrids.

Acylsugar producing hybrids would be of use to reduce crop loss or damage directly caused by insect pests when used alone. Additionally, the addition of acylsugar mediated pest resistance in hybrids transgenic for Bt could provide greater breadth or levels of control and reduce the likelihood of creating Bt resistant insects. Acylsugar producing hybrids might also be of use to reduce crop loss or damage indirectly caused by insect pests that vector virus. The likelihood that acylsugar hybrids significantly reduce viral disease depends on the biology of the virus, its vector, and characteristics of the transmission of the virus. For some pathogens, the strongest use of the system might be in hybrids also possessing virus resistance. The dual vector/virus protection could reduce the challenge to the virus resistance mechanism, strengthening disease control and perhaps extending the useful life of the virus resistance.

Identification of *Bemisia argentifolii* resistance loci in *L*ycopersicon *hirsutum* accession LA1777.

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Silverleaf whitefly, *Bemisia argentifolii* Bellows & Perring [formerly strain B of the sweetpotato whitefly, *B. tabaci* (Genn.)], is a destructive pest of tomato throughout the warmer growing regions of the world. It's feeding habit, begomovirus vectoring, and ability to overcome insecticides make it a serious problem to crop producers. Resistant cultivars would be an economical and environmentally sound way of managing *B*. *argentifolii* in tomato production, but no resistant cultivars are currently available. The objective of this study was to locate silverleaf whitefly resistance loci from *L. hirsutum*. Ninety-four recombinant inbred lines (RIL) derived from tomato crossed with *Lycopersicon hirsutum* LA1777 showed no silverleaf whitefly resistance. Thus, an interspecific F_2 population of 171 plants was assayed for resistance based on egg counts and type IV trichome counts after inoculation with 10 female whiteflies in clip cages for 24h. From this study 11 resistant and 10 susceptible plants were selected for testing with molecular markers to find polymorphisms between the two groups. Over 400 molecular markers that span the tomato genome at 10cM intervals have been tested. So far, markers in 5 regions on 4 different chromosomes appear clearly associated with resistance and markers in 4 other regions might be associated with resistance. Crosses have been made between RILs to combine the target resistance regions in plants that will be bioassayed to determine if resistance is obtained.

New late blight resistance genes in tomato.

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Late blight (LB), caused by Oomycete *Phytophthora infestans*, occurs throughout tomato and potato growing regions of N. America and elsewhere in the world. This disease is best known as being responsible for the Irish potato famine in the 1840's, when over one million people died and 1.5 million emigrated. Recently, late blight is re-emerging and becoming a major disease of both tomato and potato. In 2004, for example, LB was confirmed in at least 26 PA counties, which totally destroyed some commercial organic plantings and many home garden tomatoes. The disease can occur every year, but the intensity of the disease and races of the pathogen found can vary with years and conditions. LB normally occurs under wet and cool conditions. It can infect all above ground parts of the tomato plant, causing leaf and stem necrosis, fruit rot, and eventual plant death. The success of *P. infestans* as a pathogen owes to its effective life cycles both in asexual and sexual stages. While asexual spores (zoospores) are air-borne and need live plants for survival, sexual spores (oospores) can survive in the soil for long time and under harsh conditions. Currently, no LB-resistant cultivar of tomato is available and the disease control measures include preventive cultural practices and heavy use of protectant and systemic fungicides. Although fungicide applications can be effective in certain conditions, they have many drawbacks. Furthermore, the recent occurrence in the U.S. of both mating types (*A1* and *A2*), which are necessary for sexual propagation, is alarming as they can result in the production of oospores and emergence of new races, which might be fungicide resistant. Thus, there is a pressing need to develop tomato cultivars with durable LB resistance. In tomato, 3 major LB resistance genes have been identified and mapped, *Ph-1* (chr. 7), *Ph-2* (chr. 10) and *Ph-3* (chr. 9). While *Ph-1* has been overcome by new races and *Ph-2* provides only partial resistance to several isolates and fails in response to aggressive ones, *Ph-3* exhibits strong resistance. However, new *P. infestans* isolates have emerged which overcome *Ph-3*. It is imperative to explore new resistance genes or QTLs and pyramid them to attain durable resistance. At Penn State, our germplasm screening has resulted in identification of several new sources of resistance. In recent studies, we have attempted to identify and locate resistance genes in two *L. pimpinellifolium* accessions. Screening of an interspecific RI population has resulted in the identification and mapping of a new major resistance gene on chromosome 2. Mapping in F_2/F_3 populations of another *L. esculentum* ? *L. pimpinellifolium* cross is underway. Presently we are incorporating LB resistance genes into our previously-developed early-blight-resistant breeding lines. The nature of the newly identified LB-resistant resources and genes and the current status of our breeding program will be presented.

Resistance to California isolates of *Pseudomonas syringae* pv. *tomato* race 1.

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Bacterial speck on tomatoes, caused by *Pseudomonas syringae* pv. *tomato* (Pst) has become both widespread and economically important. Race 0 of the pathogen has been successfully controlled by the gene *Pto*-1, derived from *L. pimpinellifolium*. In 1986 Lawton and MacNeil reported the appearance of a new race, race 1. In the search for resistance to race 1, a lot of wild tomatoes have been screened. Stockinger and Walling found gene *Pto*-4 in *L. hirsutum* var. *glabratum* that was incompletely dominant and inherited in a complex fashion. In previous investigations carried out in Bulgaria several advanced tomato lines having different wild species in their pedigree were found resistant to race 1. As there is no information whether the California Pst isolates are the same or differ from Bulgarian race 1 isolates, we found it necessary to screen some Bulgarian breeding lines with California isolates. Sixty lines were inoculated with isolate A9 obtained from UC Davis. The inoculum was applied onto upper and lower surface of the leaves with an electric sprayer. For three days the inoculated plants were kept under 95% humidity. Ten days after the inoculation the plants were scored according to the following scale: 1=plants with 0 to 10 bacterial spots, 2= plants with 11 - 20 spots, 3= plants with 21 - 40 spots, 4= plants with 41-60 spots and 5= plants with more than 60 spots. Plants with ratings 4 and 5 were considered susceptible. Dark brown lesions surrounded by large chlorotic haloes characterized the susceptible response of Chico III and ONT 7710 (*Pto*-1), with Disease Severity Indexes (DSI) 4.70 and 4.80 respectively. The lines RIOLI (DSI=1.10), Denali-64 (DSI=1.15) and Stella-4 (DSI=1.20) showed very high level of resistance. No lesions appeared on the inoculated leaves on most of the RIOLI plants and a few plants showed small number small-sized lesions without large chlorotic haloes. Fifteen lines showed also high level of resistance having most of the plants rated 1, a few with rating 2 and only one plant with rating 3. Several lines, that were uniformly resistant to race 1 in Bulgaria showed segregation after inoculation with isolate A9, having different ratios of resistant and susceptible plants. The differences in responses of these lines could be explained by differences in the nature of the strains, variations in strain virulence and the environmental conditions. Genotypic diversity of resistant and susceptible responses was also observed. The size of the necrotic lesions, the presence and the size of the haloes varied from line to line. Stockinger and Walling notice that "*Lycopersicon* ssp. might utilize different strategy to combat Pst infection..." The data of the test indicate the existance in the investigated tomato lines of a type of high level of resistance to California isolates of Pst race 1. The resistance of the best line RIOLI, a cultivated type tomato, can answer the popular demand from seed companies being of value in their breeding programs for resistance to Pst race 1.

Mapping quantitative resistance loci to bacterial wilt in tomato line Hawaii 7996.

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Bacterial wilt caused by *Ralstonia solanacearum* is a devastating disease of tomato production in warm and humid regions worldwide. Symptom development is highly affected by environment, including pathogen strain, temperature, and soil properties. Therefore DNA markers linked to resistance alleles would be very valuable in breeding resistant varieties. A population consisting of 188 recombinant inbred lines was developed from the cross of resistant Hawaii 7996 with susceptible West Virginia 700. The mapping population and checks were evaluated for disease reaction against local pathogen strains in a total of 13 field or greenhouse trials conducted in India, Indonesia, the Philippines, Taiwan, Thailand, and Réunion. All strains in trials were race 1, biovars 3 or 4, except Réunion where a strain of race 3, biovar 2 isolated from potato was used. Disease incidence (percent wilted plants) of the resistant and susceptible parents ranged from 0 to 24%, and 80 to 100%, respectively, while mean incidence for the mapping population was 21 to 83%. Final disease incidence data after arcsine square root transformation were employed for mapping resistance. Identification of polymorphic markers was a challenge and 338 polymorphic diversity array (DArT) and simple sequence repeat (SSR) molecular markers were identified and mapped. A linkage map of 132 evenly distributed markers was generated and used for QTL analysis. Results of composite interval mapping identified ten QTLs significantly associated with variation in resistance in 11 trials although four were considered important. A major QTL mapped on chromosome 3 between TG564 and K4a showed a significant effect in six trials and accounted for 10.6 to 53.2% of the phenotypic variation. A second QTL mapped on the bottom of chromosome 4 was important in eight trials and accounted for 6.9 to 18.0% of the phenotypic variation. Two QTLs were found on chromosome 6 confirming results from previous studies. Fine-mapping of important QTLs is ongoing and studies to evaluate interactions among QTL are planned.

Overview of USAID MERC/CDR programs on breeding tomatoes for resistance to begomoviruses for the Middle East and Guatemala.

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Begomoviruses, whitefly-transmitted geminiviruses, are a major constraint for tomato production in many parts of the world. The Middle East (MERC) project involves scientists from Egypt, Israel, Jordan, Lebanon, Morocco, Palestinian National Authority, Tunisia, and USA, and the Guatemalan (CDR) project involves scientists from Guatemala, Israel, AVRDC, and USA. Begomoviruses identified in the Middle Eastern countries were TYLCV, TYLCV-mild, and TYLCSV. Seven begomoviruses were identified in Guatemala. For each country, the focus has been on breeding of begomovirus-resistant tomatoes for the most common local market, e.g. determinate, round fruits for Egypt and Jordan, indeterminate, round fruits for Morocco, determinate, roma-type fruits for Tunisia and Guatemala, and a large, specialty tomato for Lebanon. Local lines or commercial hybrids were used as parental lines and crosses were made with begomovirus-resistant lines having introgressions from *S. habrochaites* (Hebrew University of Jerusalem), *S. peruvianum* (Volcani Center), and *S. chilense* (University of Florida). In field trials in Guatemala, the virus pressure was severe and growth conditions are marginal. Crosses of begomovirus resistant parents were made with susceptible lines. For the *habrochaites* resistance, there was a dominant component, whereas the resistance from *peruvianum* and *chilense* were recessive. F1 populations from crosses of lines with *habrochaites* resistance with lines having resistance from another species exhibited the highest level of resistance. GenTropic Seeds S. A. was formed in Guatemala to produce and market the hybrids. Marker-assisted selection efforts developed new PCR-based methods for the *Mi-I* locus and the *I2* locus. Two anti-viral strategies are being evaluated and transformation protocols have been standardized among several laboratories. It is expected that each country will develop local ways to market the derived hybrids from this publicly supported breeding effort.

Pile up of resistant genes to Begomoviruses found in wild tomato species to produce resistant cultivars.

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Begomoviruses, Whitefly-transmitted geminiviruses are currently the main biotic constraint to Tomato production in the Middle-East and many other countries in the tropical and subtropical regions. Tomato production is limited by the endemic presence of the Begomoviruses, Whitefly-transmitted geminiviruses. This virus is transmitted by an insect, the whitefly Bemisia tabaci. In Israel, much of the tomato production has been transferred to greenhouses covered with insect-proof nets. Multiple applications of insecticides, sometimes daily, in attempt to control the insect vector have failed to eradicate the virus. The most efficient way to increase tomato production is the introduction of resistant cultivars.

Breeding programs aimed at producing tomato cultivars resistant to TYLCV and to other Begomoviruses, have started in the late 1960s and have expanded since. These programs are based on the introduction of resistance or tolerance found in some accessions of wild tomatoes species into the domesticated tomato *Lycopersicon esculentum*. Depending on the plant source, resistance was reported to be controlled by one to five genes, either recessive or partly dominant. A Begomoviruses, Whitefly-transmitted geminiviruses Resistant gene where introduced from different sources by different breeders at different location: *L. chilense* (Israel, Florida), *L. peruvianum* (Israel), *L. pimpinellifolium* (INRA*), L. hirsutum* (Israel, AVRDC,).
Pyramiding the chromosomal regions associated with resistance in the lines from different origins might broaden the resistance against a wider range of Begomoviruses or improve the degree of resistance or tolerance.

TYLCV resistant line derived from different resistance sources and a susceptible line were crossed in all combinations without reciprocal. Parents and F1 progenies were evaluated in open field after controlled inoculation with viruliferous whiteflies. The objective of this study was to learn the combining abilities of the different sources of resistance.

Development of breeder friendly markers for begomovirus resistance genes derived from *Lycopersicon chilense*

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Resistance to begomoviruses including bipartite tomato mottle virus (ToMoV) and monopartite tomato yellow leaf curl virus (TYLCV) has been introgressed to tomato (*Lycopersicon esculentum*) from *L. chilense* accessions LA1932, LA2779, and LA1938. Previous research demonstrated that three regions on chromosome 6 were associated with the resistance using randomly amplified polymorphic DNA (RAPD) markers. It appeared that two of the three regions were needed in a line to provide a high level of resistance. In various seasons, 19-38% of the F_2 progenies of susceptible × resistant lines were highly resistant to TYLCV or ToMoV, suggesting a major gene locus was involved in the resistance. This locus was mapped to chromosome 6 near TG118 and several other conserved ortholog set markers using a F_2 population of *L. esculentum* × LA2779-derived resistance breeding line (021108). This is a region with a cluster of resistance genes, including the major TYLCV-tolerance gene (*Ty-1)* derived from *L. chilense* accession LA1969. The introgressed segment in line 021108 spans across markers GP79 and TG118, a 3.2cM interval in the present linkage map. In contrast, an introgressed segment in this region for LA1932-derived resistance lines was much shorter, and only a few CAPS markers showed polymorphisms for this introgression. No recombination was observed among these markers in 320 F_2 progenies of *L. esculentum* × LA1932-derived resistant line. These CAPS markers displayed a significant association with disease severity using ANOVA analysis. The CAPS markers developed in the present study can be used in the marker-assisted selection for resistance to both TYLCV and ToMoV.

Screening Tomato Germplasm for Resistance to Pepino Mosaic Virus

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Pepino mosaic virus (PepMV), a *Potexvirus*, is an emerging disease of tomato. The disease has caused major concerns in the greenhouse tomato production in Europe and North America. PepMV is a seed-borne but likely not a seed-transmitted virus on tomato. However with mechanical inoculation, the virus can be easily transmitted to seedlings from contaminated seed extract, thus making tomato seed a potential initial virus inoculum for PepMV. Characterization of PepMV isolates indicates the presence of various strains. Although most of European isolates are similar, US isolates are more diverse in genome sequence. The objective of this study was to evaluate tomato (*lycopersicum esculentum*) germplasm core collections for resistance to PepMV US isolates. A total of 99 accessions were evaluated. These included 18 *L. chilense*, 21 *L. esculutum*, 27 *L. hirsutum*, and 33 *L. peruvianum*. Preliminary results showed that all plants in the accessions corresponding to *L. esculentum* were systemically infected by PepMV with severe symptoms. Although all accessions of *L. chilense*, *L. hirsutum* and *L. peruvianum* were infected with PepMV, a small portion of individual plants did not express visible signs of virus infection. Further analyses with ELISA, however, showed that all plants of *L. chilense* and *L. peruvianum* accessions had high virus titer regardless of the symptom expression. On the other hand, virus titer was significantly lower in the symptomless plants from several plants in two *L. hirsutum* accessions, especially on the top portion of the plants. A second test is underway with additional seedlings germinated from the selected resistant PI accessions to confirm this initial observation.

Current Status of Resistance to Tospoviruses in Tomato

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For a number of years *Sw-5* (derived from *L. peruvianum*) has provided acceptable control of TSWV (Tomato spotted wilt virus). Recently, *Sw-5* has been overcome by virulent TSWV isolates in areas such as Spain and Italy. We completed a study where a total of 16,335 *L. peruvianum* plants, from 285 accessions, were screened with either the TSWV6 (a TSWV isolate from Hawaii which overcomes *Sw-5*) and/or An_{wa}-1 (an isolate from Australia that partially overcomes *Sw-5*). Of the 285 accessions screened for TSWV resistance 172 (60%) were tested with both isolates (6,683 and 5,516 *L. peruvianum* plants with TSWV6 and An_{wa}-1 respectively). There were 39 (~23%) of these 172 accessions which did not indicate resistance to either isolate, although, specific accessions responded differently to the two isolates. Of the 172 accessions tested with both isolates there were 23 (~13%) indicating resistance to An_{wa}-1 but not to TSWV6 and 31 of 172 accessions (~18%) with plants with a resistance response to TSWV6 and not to An_{wa}-1.

Attempts to introgress TSWV6 resistance from *L. peruvianum* (PI 128660) have provided unacceptable results in the advanced interspecific BC generations, although, the initial F_1 between the *L. peruvianum* and *L. esculentum* was essentially as resistant as the *L. peruvianum* parent. Field tests of the BC populations are not significantly different to TSWV than *Sw-5*$^+$/*Sw-5*$^+$ lines; however, *Sw-5* based tomato lines were significantly more resistant to the disease. Nevertheless a *L. chilense* (LA 1938) derived TSWV resistance line did demonstrate acceptable levels of resistance in the same field trials. In these studies it was evident that this new source was highly resistant to TSWV in Hawaii, Florida/Georgia, and South Africa. Additionally, greenhouse screening trials have clearly demonstrated that the *L. chilense* source of TSWV resistance is resistant to TSWV6. Subsequent studies suggest that this resistance is controlled by a dominant, "probable" single gene. If future data demonstrate this to be the situation we suggest the name of this gene be "*Sw-7*." Presently, the *L. chilense* based germplasm is being tested in Australia under field conditions which have tospoviruses overcoming *Sw-5* and are not the TSWV species. Furthermore, this germplasm is being tested for tospovirus resistance in Thailand, Taiwan and plans are underway to test it in Italy.

Nomenclature for wild and cultivated tomatoes

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Tomatoes were introduced into Europe from the Americas and became known to botanists about the middle of the sixteenth century. Matthioli described tomatoes for the first time in 1544 using the Italian common name "Pomi d'oro". During the late sixteenth and early seventeenth century botanists recognized the close relationships of tomatoes with the genus *Solanum* and commonly referred to them as "*Solanum pomiferum*" or apple-bearing nightshade. Tournefort (1694) was the first to consider tomatoes at the generic level using the Greek term *Lycopersicon*. In *Species Plantarum*, Linnaeus (1753) was the first to consistently use binominal nomenclature; he classified tomatoes in the genus *Solanum* and described *S. lycopersicum* and *S. peruvianum*. Miller (1754), however, included tomatoes in *Lycopersicon*, criterion that numerous classical and modern authors have followed. Taxonomy has two main and often competing goals, the maintenance of nomenclatural stability (treatment in *Lycopersicon*) and the predictivity of natural classifications (treatment in *Solanum*). More recently, the treatment of tomatoes in *Solanum*, and indeed as a monophyletic sister group to potatoes, has been supported by several morphological and molecular data. Based on these evidences, tomatoes may be more "predictively" classified in *Solanum* section *Lycopersicon*, which includes the cultivated tomato, *Solanum lycopersicum* and 12 additional wild relatives, endemic to western South America from Ecuador to northern Chile, and with two endemic species in the Galápagos Islands. The delimitation and relationships of tomato species, as well as nomenclature issues will be discussed.

Tomato fruit firmness attributes in hybrids from crosses between *Solanum lycopersicum* and *S. lycopersicum* x *S. galapagense* derived parental genotypes.

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Despite inferior phenotypes, wild species of tomato contain loci that may substantially increase tomato fruit quality. Introgression of novel alleles from wild germplasm has been demonstrated to enhance fruit quality attributes such as soluble solids, color, viscosity, yield, and earliness. Fruit firmness is a key quality component of tomatoes produced for fresh-market and processing applications. Utilizing progeny from a six-parent diallel, fruit firmness was evaluated using compression and puncture tests. Four of the parental genotypes with fruit firmness scores that ranged from firm to soft were derived from intraspecific *Solanum lycopersicum* (*Lycopersicon esculentum*) crosses. Two additional firm-fruited genotypes were developed from an interspecific cross between *S. galapagense* (*L. esculentum* f. *minor*) and breeding lines with no know introgressions of the wild species. Location effects and relationships between fruit compression and puncture tests and fruit fresh weight and dry matter in the 36 hybrid lines and their parental genotypes are discussed. The development of an inbred backcross population derived from a cross between parental genotypes with divergent fruit firmness attributes, together with increased availability of molecular markers that are informative in interspecific as well as intraspecific *S. lycopersicum* crosses, provides new opportunities to identify individual loci associated with fruit firmness attributes and evaluate intra-locus and inter-locus interactions that contribute to improved fruit quality.

Tomato production in China and breeding program in BVRC.

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Tomato is one of the main vegetables in China. According to the FAO, the harvested area in 2005 was 1,305,053 hectares, about 29% of the world tomato area. Total production was 31.6 million tons (Mt), about 26% of world tomato production. Cultivated area for processed tomato was about 87,000 hectares, and the total production of processed tomato was 6.5 Mt. 90% of processed products were exported. Cherry tomato was about 3%~4% of the total cultivated area. Tomato consumption per capita is more than 20 kg. Almost all of the tomato consumption is fresh tomato according to the food or cuisine habits of Chinese. Pink varieties are mainly grown for fresh market; 70% of the fresh tomato market consists of pink varieties.

A tomato breeding program has been carried out at BVRC for more than 30 years, since the early of 1970's. Generally speaking, the breeding objectives are resistance, high yield and high quality. However, specific objectives have changed over time. The varieties released by BVRC have been mainly for fresh market. The first generation of tomato varieties released by BVRC consisted of large fruited, pink types with resistance to TMV. Varieties released in recent years have resistance to four different diseases, which are TMV, leaf mould, fusarium wilt and nematode. The types of varieties released have also been expanded to include cherry tomatoes, among others. The *rin* gene has been transferred into parental lines of the pink fruit type in order to improve shelf life and shipping. The technique of marker assisted selection is being adopted. Interesting progress on pest resistance has been made by evaluation and genetic improvement with wild tomato germplasm.

The structure of tomato breeding programs: Progress towards association mapping of horticultural traits.

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The inefficient integration of molecular discovery with plant improvement has become more pronounced as vast amounts of information become available through genome sequencing initiatives. To more effectively leverage sequence data, and the proven power of plant breeding we are developing Single Nucleotide Polymorphisms (SNPs) as molecular markers for application in cultivated tomato (*S. lycopersicum*). At the same time we are exploring and validating statistical methods for genetic analysis in complex populations to facilitate simultaneous QTL mapping and breeding. Implementing SNP-based marker technology has the potential to dramatically alter approaches to both gene discovery and genetic characterization. Our strategies for marker discovery include analysis of polymorphisms in EST databases, *de novo* sequencing across introns, and hybridization to a custom oligonucleotide array to detect single feature polymorphisms (SFPs). We are developing a panel of molecular markers for application within domesticated germplasm (http://www.tomatomap.net). These markers have been used to genotype a core collection (n = 99) of *S. lycopersicum* varieties representing heirloom (19), fresh market (23), and processing germplasm (39). Greenhouse varieties (3), land races (5) and wild species accessions from *S. lycopersicum* var *cerasiformae*, *S. pimpinellifolium*, *S. pennellii*, and *S. habrochaites* are also included in the core collection. A variety of indexes and clustering procedures were used to analyze population structure within the cultivated germplasm. These analyses reveal sub-populations consistent with market class differentiation (P = 0.0001) and adaptation to arid or humid growing environments (P = 0.003). Eigenvectors from PCA were used to identify markers and genes that are most informative for differentiating germplasm. These analysis can be performed in a hierarchical fashion, an approach which may elucidate the evolutionary history of individual genes. In addition the markers have been applied to the rational design of hybrids and to association mapping of disease resistance. For mapping in breeding populations derived from as many as eleven parents, we adapted statistical models used for association mapping by incorporating pedigree information into both the models and marker scoring. The application of general linear model and mixed model approaches that incorporate structure due to individual crosses and inheritance by descent of markers based on pedigrees has great potential for simultaneous breeding and genetic analysis.

Biological values of tomato fruit growing up greenhouses with and without soils

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Fresh tomato consumption has been redusing during few years. It is related espessialy to tomato which are transported from far places. The reason is their poor tasted caracteristics.Fresh tomato grown on soils in greenhouses and named organic are more popular in the market, but there are in insuffisient quantaty. Thats why many farmers have begun to grow tomato on artifisial growing mediums using high techology. So the aim of our investigation was to compare the biochemical and tasted parameters of tomato grown up with and without soils.

The results show that the hybrid fruit obtained from artifisial grounds have less dry substanses 5,35 % vs. 5,96 % and soluble dry substanses (Brix) 4,2 % vs. 4,6 % respectively. The same situation we can see in total sugars - 0,5 % less in rock wool and in vitamine C - 4-10 mg% less in groduns. The best result show the Hybrids from Firm ILYNICHNA Bolero 7,05% dry substanses on soil vs. 5.56 % without soil , Brix 3,8% vs.2,8%, vitamine C 21,16 mg% - 14,27mg% relatively. The high quantaty of vitamine C was in hybrids Vasilievna – 22,46mg%, Magistral 21,33 mg% ,these parametres without soil were 16,1-16,4 mg% and 14,0-16,4 mg% respectively.

So the hybrid geneticaly depending capacity to accumulate and to save the high biochemical paramrters under different conditions allow to select hybrids with valuable tasted and biochamical qualities.

Tomato Variety Lists

Maps for Artesian and Gulf Coast Research Trials

Tomato Variety Trials

Artesian Farms, Ruskin, FL

Field No.	pedigree	Seed source	description
G1	HA3811	Hazera Seeds	Roma; resist: TSW
G2	HA3811	Hazera Seeds	Roma; resist: TSW
G3	UGR-60304	United Genetics Seeds Co.	
G4	Sweet, Sweet	Daniel S. Jacoby	Determinate, very sweet
G5	Super Giant	Daniel S. Jacoby	Tall, sweet, large fruit
G6	Huge Super Deluxe	Daniel S. Jacoby	Similar to above, smaller
G7	Hybrid	Daniel S. Jacoby	Tall, giant fruit
G8	VT-60774	Zeraim Gedera Ltd.	Semi Determinate round
G9	VT-60780	Zeraim Gedera Ltd.	Semi Determinate round
G10	FLA 7964	Zeraim Gedera Ltd.	Semi Determinate round
G11	S-65037	Zeraim Gedera Ltd.	Semi Determinate round
G12	VT-62901	Zeraim Gedera Ltd.	Indeterminate round
G13	VT-62903 (Tovi Star)	Zeraim Gedera Ltd.	Indeterminate round
G14	VT-62910	Zeraim Gedera Ltd.	Indeterminate round
G15	Biltmore	Seminis Vegetable Seeds, Inc.	
G16	Florida 91	Seminis Vegetable Seeds, Inc.	
G17	Florida 47R	Seminis Vegetable Seeds, Inc.	
G18	Quincy	Seminis Vegetable Seeds, Inc.	Resist: TSWV
G19	Phoenix	Seminis Vegetable Seeds, Inc.	
G20	Crown Jewel	Seminis Vegetable Seeds, Inc.	Resist: FCRR
G21	H2105	H.J. Heinz Co.	Roma for fresh market
G22	H9605	H.J. Heinz Co.	Roma for fresh market
G23	FG04-478	D. Francis- Ohio State U	Color & partial resist to bac. spot
G24	FG04-479	D. Francis- Ohio State U	Color & partial resist to bac. spot
G25	FG04-472	D. Francis- Ohio State U	Speck race 0 & part resist bac spot
G26	FG02-107	D. Francis- Ohio State U	Speck race 0 & part resist bac spot
G27	FG01-160	D. Francis- Ohio State U	Field Storage
G28	HMX5826	Harris Moran	
G29	Fla. 8516	University of Florida	Spotted wilt R-*L. chilense* derived
G30	Fla. 8153	University of Florida	Flora-Lee, og^c
G31	Solar Fire	University of Florida	Heat tolerant, Fusarium race 1,2,3 R
G32	Fla. 8365	University of Florida	Heat tolerant
G33	Fla. 8414	University of Florida	Fusarium crown rot R

Seed sown 1/13/06, Greenhouse transplant 1/30, Field transplant 3/7

2006 TBRT TYLCV and ToMoV Trials

GCREC- Wimauma, FL

Field No.	Field No.	Pedigree	Seed Source	Comments
TO1	TY1	HA-3813	Hazera	
TO2	TY2	HA-3074	Hazera	
TO3	TY3	HA-3371	Hazera	
TO4	TY4	HA-3075	Hazera	
TO5	TY5	UGR-54904	United Genetics	
TO6	TY6	UGR-64804	United Genetics	
TO7	TY7	UG-55884	United Genetics	
TO8	TY8	UG-55885	United Genetics	
TO9	TY9	UGR-54704	United Genetics	
TO10	TY10	Charai	Western Seed	
TO11	TY11	WS-830305017	Western Seed	
TO12	TY12	H8804	Heinz	
TO13	TY13	H9205	Heinz	
TO14	TY14	H9881	Heinz	
TO15	TY15	Tygress	Seminis	
TO16	TY16	Fla. 8502	054524-Y2	LA 2779 R
TO17	TY17	Fla. 8503B	054527-Y7	LA2779 R
TO18	TY18	Fla. 8504	054573-Y6	LA 1938/Tyking
TO19	TY19	Fla. 8472B	054656-Y12	LA1938/Tyking
TO20	TY20	Fla. 8302	054670-Y8	LA 2779 R
TO21	TY21	Fla. 8501B	054495-13	LA 2779 R
TO22	TY22	Fla. 8469B	054607-3	LA1938/Tyking
TOHOR	TYHOR	Horizon	SP 99 BK	
TOHOR	TYHOR	Horizon	SP 99 BK	

2006 TBRT TYLCV and ToMoV Trials Map

LAND 37

ROW 1		ROW 2		ROW 3	
TY HOR	13	TO HOR	13	TY8	13
TY1	13	TO1	13	TY9	13
TY2	13	TO2	13	TY10	13
TY3	13	TO3	13	TY11	13
TY4	13	TO4	13	TY12	13
TY5	13	TO5	13	TY13	13
TY6	13	TO6	13	TY14	13
TY7	13	TO7	13	TY15	13

LAND 38

ROW 1		ROW 2		ROW 3	
TO8	13	TY16	13	TO16	13
TO9	13	TY17	13	TO17	13
TO10	13	TY18	13	TO18	13
TO11	13	TY19	13	TO19	13
TO12	13	TY20	13	TO20	13
TO13	13	TY HOR	13	TO HOR	13
TO14	13	TY21	13	TO21	13
TO15	13	TY22	13	TO22	13

Seed sown 2/10/06, Greenhouse transplant 2/24, Inoculated 3/9-3/30 (21 days), Field transplant 3/31