

2007
Tomato Breeders Roundtable
The Pennsylvania State University
University Park, Pennsylvania USA



November 4-7, 2007
Nittany Lion Inn, 200 West Park Avenue
State College, Pennsylvania USA

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Tomato Breeders Roundtable (TBRT)
November 4-7, 2007
The Pennsylvania State University
University Park, Pennsylvania

Sunday, November 4

- 5:00 PM – 7:00 PM** **Registration** (Alumni Fireside Lounge)
- 6:30 PM – 8:30 PM** **Welcome Reception** (Alumni Fireside Lounge)

Monday, November 5

- 7:30 AM – 8:30 AM** **Registration** (Atrium)
- 8:30 AM – 5:00 PM** **Presentations** (Ballroom C)
- 8:30 AM – 8:50 AM** **Welcome**
Majid Foolad, Organizer, 2007 TBRT
Bruce McPheron, Director, PA Agric. Exp. Station, Associate Dean of Research,
College of Agricultural Sciences, Penn State University
Rich Marini, Head, Dept. of Horticulture, Penn State University
- 8:50 AM – 9:10 AM** **A Look Back at the Tomato Breeders Roundtable**
John W. Scott
University of Florida, GCREC, Wimauma, FL

Biotechnology/Molecular Markers and MAS

Mikel Stevens, Moderator

- 9:10 AM – 9:30 AM** **Update on the international tomato sequencing project**
Joyce Van Eck
Boyce Thomson Institute, Ithaca NY
- 9:30 AM – 9:50 AM** **Translating genome sequence resources into applied outcomes in the Solanaceae: The vision of SolCap**
David Francis^{1*}, *David Douches*², *Walter De Jong*³, *Shanna Moore*³, *Allen Van Deynze*⁴, *C. Robin Buell*², *Esther van der Knaap*¹, *Matthew Robbins*¹, and *Sung-Chur Sim*¹
¹ The Ohio State University/OARDC, Wooster, OH 44691;
² Michigan State University, East Lansing, MI 48824
³ Cornell University, Ithaca, NY 14853
⁴ University of California, Davis, CA, 95616
- 9:50 AM – 10:10 AM** **EST, COSII, and arbitrary markers give similar estimates of nucleotide diversity in cultivated tomato (*S. lycopersicum*)**
Joanne A. Labate^{1*}, *Larry D. Robertson*¹, *Susan M. Sheffer*¹, *Warren F. Lamboy*¹, *Feinan Wu*², *Steve D. Tanksley*², and *Angela M. Baldo*¹
¹ USDA-ARS Plant Genetic Resources Unit, Geneva, NY
² Cornell University, Ithaca, NY
- 10:10 AM – 10:40 AM** **Coffee Break** (Atrium)

Biotechnology/Molecular Markers and MAS (continued.....)

Mikel Stevens, Moderator

10:40 AM – 11:00 AM Marker assisted breeding for tomato begomovirus resistance

Yuanfu Ji and John W. Scott*
University of Florida, GCREC, Wimauma, FL

11:00 AM – 11:20 AM Identification of markers linked to Sw-7 a new *tomato spotted wilt virus* resistance gene, derived from *S. chilense*

Mikel R. Stevens^{1}, David L. Price¹, Frederic D. Memmott¹, John W. Scott², and Steve Olson³*

¹Brigham Young University, Provo, UT

²University of Florida, GCREC, Wimauma, FL

³University of Florida, NFREC, Quincy, FL

Bacterial Resistance

James Brusca, Moderator

11:20 AM – 11:40 AM Genetics of resistance to bacterial spot

Matthew D. Robbins^{1}, Sung-Chur Sim¹, Wencai Yang¹, Melanie L. Lewis Ivey, Sally A. Miller¹ John W. Scott², Jeff Jones³ and David M. Francis¹*

¹ The Ohio State University, OARDC, Wooster, OH

² University of Florida, GCRE, Bradenton, FL

³ University of Florida, Gainesville, FL

11:40 AM – 12:00 PM Resistance to race 1 of *Pseudomonas syringae* pv. *tomato*

Liliana Stamova
California Tomato Research Institute, Davis, CA

12:00 PM – 1:00 PM Lunch Break (Ballrooms D & E)

Lunch will be provided.

1:00 PM – 1:20 PM Genetic studies of resistance to bacterial spot race T4 in tomato

Samuel Hutton and John W. Scott*
University of Florida, GCREC, Wimauma, FL

Fungal Resistance

Ray Volin, Moderator

1:20 PM – 1:40 PM Innovations in grape tomato breeding

Randy Gardner
North Carolina State University, Fletcher, NC

1:40 PM – 2:00 PM Progress toward fine mapping of *Ph5*, a new late blight resistance gene in tomato

Heather Merk, Hamid Ashrafi, Matthew Kinkade and Majid R. Foolad*
The Pennsylvania State University, University Park, PA

Fungal Resistance (continued.....)

Ray Volin, Moderator

2:00 PM – 2:20 PM Mapping of early blight resistance QTLs in a RIL population of tomato

*Hamid Ashrafi**, *Guoyang Lin* and *Majid R. Foolad*
The Pennsylvania State University, University Park, PA

2:20 PM – 2:30 PM Development of Fresh market and processing tomatoes at Penn State

*Majid R. Foolad**, *Guoyang Lin* and *Heather Merk*
The Pennsylvania State University, University Park, PA

2:30 PM – 3:00 PM Coffee Break (Atrium)

Viral and Insect Resistance

Martha Mutschler, Moderator

3:00 PM – 3:20 PM Inheritance of tomato spotted wilt virus resistance derived from *Solanum chilense* accession LA1938

John W. Scott^{1*}, *Steve M. Olson*² and *Mikel L. Stevens*³

¹ University of Florida, GCREC, Wimauma, FL

² University of Florida, NFREC, Quincy, FL

³ Brigham Young University, Provo, UT

3:20 PM – 3:40 PM Pest resistance derived from *S. pimpinellifolium* accession TO-937

*Juan M. Alba*¹, *María J. Rodríguez-López*¹, *María Salinas*², *Juan Capel*², *Rafael Lozano*², *Jesús Cuartero*¹, and *Rafael Fernández-Muñoz*^{1*}

¹ Estación Experimental La Mayora – CSIC, Málaga, Spain

² Universidad de Almería, Almería, Spain

3:40 PM – 4:00 PM Modulating acylsugar level and type, and its effects on whitefly control

Martha Mutschler^{1*}, *Ricardo Lobato-Ortiz*¹, *Darlene DeJong*¹, *Stephen Southwick*¹ and *Dave Schuster*²

¹ Cornell University, Ithaca, NY

² University of Florida, GCREC, Wimauma, FL

Area Reports

Larry Robertson, Moderator

4:00 PM – 5:00 PM

Florida and Southeastern U.S.: *David Linde*, BHN Seed
Northeast US, Midwest US and Canada: *David Francis*, Ohio State U.
California and Mexico Fresh Market: *Douglas Heath*, Seminis
California Processing: *Michael Kuehn*, Harris-Moran
Europe: *Ruud Verhoef*; Rijk ZwaanBreding B.V.
Middle East and North Africa: *Amit Shiftan*; Zeraim Gedera LTD
Southeast and South Asia: *Henk Jan Pascha*; East-West Seed Group

7:00 PM – 10:00 PM Tomato Crop Germplasm Committee Meeting

David Francis, Chair
(Ballroom D)

Tuesday, November 6

8:15 AM – 5:00 PM **Tours** (Transported by maxi-vans)

8:15 AM **Depart from front door of Nittany Lion Inn**

Stop 1: 8:30 AM – 9:30 AM: **PSU Mushroom Research Center**

Hosts: *Daniel Royse*, Professor of Plant Pathology
John Pechcia, Supervisor, PSU MTFD/MRC

Group 1 (A-K): Visit Unit 1 (MRC) first and then Unit 2 (MTDF)
Group 2 (L-Z): Visit Unit 2 (MTDF) first and then Unit 1 (MRC)

Stop 2: 9:45 AM – 10:30 AM: **PSU Air Quality Learning and Demonstration Center**
(ice-cream break)

Host: *Dennis Decoteau*, Prof. of Horticulture and Plant Ecosystem Health

Stop 3: 10:45 AM – 12:00 PM: **PSU Life Sciences and Food Sciences Buildings**

Hosts: *Mark Guiltinan*, Professor of Plant Molecular Biology
Luke LaBorde, Assoc. Professor of Food Science

Group 1 (A-K): Visit Cacao GH and LSB first and then Creamery and FSB
Group 2 (L-Z): Visit Creamery and FSB first and then Cacao GH and LSB

12:00 Depart from behind Horticulture greenhouses

Stop 4: 12:30 PM – 2:00 PM: **PA Department of Agriculture/ Livestock Evaluation Center**
Rock Springs, PA

Lunch: 12:30 PM – 1:30 PM

Tour of PDA-LEC: 1:30 PM – 2:00 PM (Hosts: *Glen Eberly* and *Jessica Bisko*)

Stop 5: 2:15 PM – 3:15 PM **PSU Agricultural Experiment Station**
Rock Springs, PA

2:15 PM – 2:45 PM: Hort Farm (*Bob Oberheim*, Manager)

2:45 PM – 3:15 PM: PSU Center for Plasticulture's High Tunnel Research and Education
Facility (*Mike Orzolek*, Professor of Horticulture)

Stop 6: 3:30 PM – 4:30 PM **AccuWeather, Inc.**

Host: *Tom Loebig*, Program Director
(soft-drink break)

4:30 PM **Depart from AccuWeather**

5:00 PM **Return to Nittany Lion Inn**

5:00 PM – 7:00 PM **Free Time**

7:00 PM – 9:00 PM **Dinner Banquet** (Ballroom C)
Speaker: *Randy Gardner*

Wednesday, November 7

7:45 AM – 8:15 AM **Registration** (Atrium)

8:15 AM – 12:00 PM **Presentations** (Ballroom C)

Fruit Nutritional-Quality and Ripening

David Francis, Moderator

8:15 AM – 8:40 AM **Genetic regulation of tomato fruit ripening and nutritional quality**

Jim Giovannoni

USDA-ARS and Boyce Thompson Institute for Plant Research, Ithaca, NY

8:40 AM – 9:00 AM **Tomato *high pigment* mutants and their central role in enhancing fruit pigmentation and functional quality**

Ilan Levin, Yaakov Tadmor, Michal Oren-Shamir, Moshe Reuveni, Ayala Meir, Rinat Ovadia, Maya Sapir, Igor Kolotilin, Dalia Evenor, Sahadia Nahon, Haviva Shlomo, Lea Chen, and Amir Bootbool*

Institute of Plant Sciences, The Volcani Center, Bet Dagan, Israel

9:00 AM – 9:20 AM **Breeding Tomatoes for Increased Flavonoid Content**

Peter Boches and James Myers*

The Oregon State University, Corvallis, OR

9:20 AM – 9:40 AM **Progress toward the validation and isolation of novel genetic factors controlling lycopene content in a *S. pimpinellifolium* × *S. lycopersicum* RIL population**

Matthew Kinkade, Hamid Ashrafi and Majid R. Foolad*

The Pennsylvania State University, University Park, PA

9:40 AM – 10:00 AM **Breeding for Human Health and Nutrition**

David M. Francis¹, Audrey Darrigues¹, Susana De Jesus¹, Steven Schwartz², Luis Rodriguez-Saona²*

¹ The Ohio State University, OARDC, Wooster, OH

² Food Science and Technology, Columbus, OH

10:00 AM – 10:30 AM **Coffee Break** (Atrium)

Germplasm and Genetic Variation

Joanne Labate, Moderator

10:30 AM – 10:50 AM **Genetic variation among tomato landraces**

Angela M. Baldo, Warren F. Lamboy, Larry D. Robertson, Susan M. Sheffer and Joanne A. Labate*

USDA-ARS Plant Genetic Resources Unit, Geneva, NY

10:50 AM – 11:10 AM **Evaluation of greenhouse, field and heirloom tomato varieties in hydroponic greenhouse production**

Barbara E. Liedl and Jeremy M. Sisson*

West Virginia State University, Institute WV

Tomato Germplasm and Committee Reports

11:10 AM – 11:20 AM Plant Introduction Center

Larry D. Robertson

USDA-ARS Plant Genetic Resources Unit, Geneva, NY

11:20 AM – 11:30 AM Tomato Crop Germplasm

David M. Francis

The Ohio State University, OARDC, Wooster, OH

11:30 AM – 11:40 AM Tomato Genetic Cooperatives

John W. Scott

University of Florida, GCREC, Wimauma, FL

Business Meeting

11:40 AM – 12:00 PM Next Meeting Location and Date

Majid R. Foolad

The Pennsylvania State University, University Park, PA

Adjourn. Have a safe trip back home.

Tomato Breeders Roundtable

November 4-7, 2007

Program Abstracts

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A Look Back at the Tomato Breeders Roundtable

John W. Scott

University of Florida, IFAS, Gulf Coast Research & Education Center, 14625 CR 672, Wimauma, FL 33598

The Tomato Breeders Roundtable (TBRT) has been the premier meeting in North America of public and industry scientists interested in tomato improvement and it attracts researchers from around the world. The impetus for the TBRT started with a group of tomato researchers primarily interested in sharing information useful to the tomato canning industry in the Midwest. Early meetings were rather informal and associated with field days in Ohio and Indiana. The first mention of the Tomato Breeders Round Table was made for a meeting in Illinois in 1957. Thus, this year marks the 50th Anniversary of the TBRT! Meetings were held annually until 1981 and since then has been meeting about every 1 ½ years. The meeting name used to have both words Round and Table until 1988 when Roundtable was adopted. Many early meetings were held in Chicago during February at the La Salle Hotel. Meetings then began to be held at various locations including warmer climates where field plots could be examined. Most meetings have been in the United States with one in Canada, two in Mexico, and one in Guatemala. The TBRT met 6 times with the Tomato Quality Workgroup and one time with the Tomato Disease Workshop. Early meetings were methods related and much informal discussion occurred. The forum facilitated much germplasm exchange which was very useful to the breeding programs and grower clientele alike. Over the years the meetings have become more formal but still maintain the spirit of the original meetings where there is more discussion than at many types of meetings. Panel discussions have been an integral component for many meetings. The meetings still have area reports to allow participants to be aware of the latest issues in various growing regions. These reports now include some from around the world from international participants. The Tomato Crop Germplasm Committee meets in conjunction with the TBRT and a summary report is given to the group. Reports from the USDA germplasm program, the Tomato Genetics Resource Center, and the Tomato Genetics Cooperative (TGC) are typically presented. Discussion of the early years including some of the participants and accomplishments will be made and contrasted with present day issues. A paper describing the TBRT history is in the 2007 TGC and this will be updated on the TGC website <http://tgc.ifas.ufl.edu/> with the help of TBRT group who will be solicited for their input.

Update on the International Tomato Sequencing Project

Joyce Van Eck^{1}, Jim Giovannoni^{1,2}, Lukas Mueller³, Steve Tanksley³, Steve Stack⁴*

¹ The Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, NY 14853, USA

² Department of Agriculture-Agricultural Research Service, Plant, Soil, and Nutrition Lab, Cornell University, Ithaca, NY 14853, USA

³ Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853, USA

⁴ Department of Biology, Colorado State University, Fort Collins, CO 80523, USA

The International Tomato Genome Sequencing Project is a consortium of research groups representing ten different countries committed to sequencing the gene-rich euchromatin for all twelve chromosomes, which accounts for roughly 25% of the DNA and approximately 90% of the estimated 35,000 genes. We are following a BAC-by-BAC sequencing strategy that allowed assignment of chromosomes to each participating group, often based on their interest in particular mapped loci. To date, Korea, the UK, and the Netherlands have sequenced more than 30% of the euchromatin in chromosomes 2, 4, and 6, respectively. In addition, the euchromatin of the short arm of chromosome 6 is almost completely sequenced with the exception of two gaps that will be filled by the end of 2007. The US team continues to develop resources and provide support infrastructure for the consortium. The most recent resource made available by the US team is a fosmid library of small inserts with an average size of 40 kb, which will play an important role in filling gaps along the minimum tiling path of each chromosome. To date, end sequences have been generated for 1,152 fosmid clones, and this preliminary sequence data has already been proven useful for closing a gap on chromosome 4. The repository for all data generated through this consortium is the SOL Genomics Network (SGN; www.sgn.cornell.edu). SGN continually upgrades the database with new tools for end sequence queries and repeat sequence identification, in addition to developing preliminary sequence annotation pipelines and visualization tools. We are particularly interested in feedback from genome sequence users regarding the types of tools and information that might be developed within SGN.

Translating Genome Sequence Resources into Applied Outcomes in the Solanaceae: The Vision of SolCap.

David Francis^{1*}, David Douches², Walter De Jong³, Shanna Moore³, Allen Van Deynze⁴, C. Robin Buell², Esther van der Knaap¹, Matthew Robbins¹, and Sung-Chur Sim¹.

¹ The Ohio State University/OARDC, Wooster, OH 44691

² Michigan State University, East Lansing, MI 48824

³ Cornell University, Ithaca, NY 14853

⁴ University of California, Davis, CA, 95616

Data from expressed sequence tags and from whole-genome sequencing has opened opportunities for plant breeding application in the Solanaceae. These sequence resources are also driving agricultural research toward a perspective that emphasizes taxonomic groups and DNA sequence homology rather than traditional commodity boundaries. The long-term objective of the Solanaceae Coordinated Agricultural Project (SolCAP) is to provide infrastructure to link allelic variation in genes for valuable traits in the three most important vegetable crops in the Solanaceae: potato, tomato and pepper. Leveraging resources between commodities has resulted in tools to manipulate phytonutrient biosynthesis pathways affecting potato tuber and tomato fruit nutritional quality. Strategies to develop Single Nucleotide Polymorphisms (SNPs) as molecular markers for whole-genome analysis include analysis of polymorphisms in EST databases, hybridization to oligonucleotide arrays to detect single feature polymorphisms (SFPs), and *de novo* sequencing using ultra-high throughput techniques. In our work with tomato, application of SNPs has emphasized genotyping of 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). By extending sequence resources horizontally to encompass both accessions of wild relatives and populations of elite varieties, a greater understanding of how variation in DNA sequence affects variation in phenotype is expected.

EST, COSII, and Arbitrary Markers Give Similar Estimates of Nucleotide Diversity in Cultivated Tomato (*S. lycopersicum*)

Joanne A. Labate^{1*}, *Larry D. Robertson*¹, *Susan M. Sheffer*¹, *Warren F. Lamboy*¹, *Feinan Wu*², *Steve D. Tanksley*², and *Angela M. Baldo*¹

¹ USDA-ARS Plant Genetic Resources Unit, 630 W. North Street, Geneva, NY 14456, USA

² Dept. of Plant Breeding & Genetics, Cornell Univ., Ithaca, NY 14853, USA

Because cultivated tomato (*Solanum lycopersicum*) is low in genetic diversity, public, verified single nucleotide polymorphisms (SNP) markers within the species are in demand. To promote marker development we resequenced fragments of 51 genes in a diverse set of 31 tomato lines. Three classes of markers were sampled: i) 26 expressed-sequence tag (EST), ii) 14 Conserved Ortholog Set II (COSII) or unigene, and iii) 11 published genes, 10 of which are related to fruit quality. The latter two types contained mostly noncoding DNA. Totals of 156 SNPs and 35 indels were found in 24 kb. The distributions of nucleotide diversity estimates among marker types were not significantly different from each other. These data demonstrate that public EST databases and noncoding regions are a valuable source of unbiased SNP markers in tomato.

Marker Assisted Breeding for Tomato Begomovirus Resistance

Yuanfu Ji and Jay W. Scott*

Gulf Coast Research and Education Center, University of Florida, 14625 CR 672, Wimauma, FL 33598

Another begomovirus resistance gene *Ty-3* was recently mapped to a marker interval of 7 cM on the long arm of chromosome 6, ~15 cM apart from the partially dominant gene *Ty-1*. Recently, we identified 30 recombinants from a population of 717 F₂ progeny. Linkage analysis delimits the *Ty-3* gene to a shorter marker interval from cLEG-31-P16 to PG9 (~5 cM). Homozygous sub-recombinant inbred lines (subRILs) have been identified from these recombinants and advanced breeding lines genotyped in the previous seasons. Disease severity indexes (DSI) for the subRILs infected with begomovirus supported the map position of the *Ty-3* gene. In addition, the DSI also indicated *Ty-1* was absent in *Solanum chilense* accession LA2779-derived lines, although they carry an introgression spanning both *Ty-1* and *Ty-3* regions. Evaluation of begomovirus resistance among the subRILs in replicated trails will validate the *Ty-3* gene position on the linkage map and allow construction of a high-resolution map. Most resistant breeding lines and commercial hybrids originating from other tomato wild species including *S. habrochaites*, *S. peruvianum*, and *S. pimpinellifolium* carried alien introgressions spanning the *Ty-3* region, suggesting that these wild species most likely also contain begomovirus resistance alleles at the *Ty-3* locus. In addition, a higher resolution map of another major begomovirus resistance gene *Ty-2* has also been constructed, which delimits the *Ty-2* gene to a much smaller interval. A fourth potential resistance gene on a different region on chromosome 6 was also explored using numerous approaches. Begomovirus genes could be pyramided into elite breeding lines and hybrids with the assistance of molecular markers to maximize utilization of existing genes and provide improved durable resistance.

Identification of Markers Linked to Sw-7 a New *Tomato Spotted Wilt Virus* Resistance Gene, Derived from *S. chilense*

Mikel R. Stevens^{1*}, *David L. Price*¹, *Frederic D. Memmott*¹, *John W. Scott*², and *Steve M. Olson*³

¹ Brigham Young University, Department of Plant and Animal Sciences, 287 Widstoe Bldg. Box 25183, Provo, UT 84602-5183

² University of Florida, IFAS, Gulf Coast Research & Education Center, 14625 CR 672, Wimauma, FL 33598

³ University of Florida, IFAS, North Florida Research & Education Center, 30 Research Road, Quincy, FL 32351

Several *Tomato spotted wilt virus* (TSWV) resistance genes have been identified (*Sw*₁^a, *Sw*₁^b, *sw*₂, *sw*₃, *sw*₄, *Sw-6*, and *Sw-5*); however, *Sw-5* is the only gene that has been broadly utilized in tomato breeding because of its durability to multiple tospoviruses (Boiteux and Giordano, 1992; Stevens et al, 1992, Stevens, unreported data). Although rare, there have been new TSWV isolates identified that overcome *Sw-5* (Latham. and Jones, 1998; McMichael et al. 2002). Tospovirus resistance from *Solanum chilense* has been identified by Stevens et al. (1994) and introgression from this species has demonstrated to be useful under field conditions (Canady et al., 2001). This germplasm has demonstrated resistance to isolates that overcome *Sw-5* (Stevens, unreported data). Recently we concluded that this resistance was conferred by a single dominant gene not linked to *Sw-5* (Scott, Olson, and Stevens, unpublished data). This gene is tentatively being referred to as *Sw-7*. Thirty-seven sister lines putatively containing *Sw-7* (developed from F₂ and BC₁ plants suggesting TSWV resistance) have been used to identify molecular markers. After an initial screening of six *Sw-7* segregating lines using over 256 AFLP primer combinations we identified 16 combinations which revealed 30 candidate markers suggesting linkage to *Sw-7*. These 30 putative *Sw-7* markers have been examined on our carefully screened 37 F₂ and BC₁ lines along with the seven field selected Florida lines. One strong candidate AFLP marker has been identified (~200bp) in both the 37 greenhouse selected lines and the seven Florida field selected lines. This candidate marker is currently being prepared to be cloned and sequenced. We are hoping to use this marker to identify where in the tomato genome *Sw-7* is located. Additionally, analysis with this marker is currently being conducted on a much larger TSWV resistant population derived from the same germplasm.

Literature Cited

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Genetics of Resistance to Bacterial Spot

*Matthew D. Robbins*¹, *Sung-Chur Sim*¹, *Wencai Yang*¹, *Melanie L. Lewis Ivey*², *Sally A. Miller*², *Jay W. Scott*³, *Jeff Jones*⁴ and *David M. Francis*¹

¹ Horticulture and Crop Science, The Ohio State University, OARDC, 1680 Madison Ave., Wooster, OH 44691

² Plant Pathology, The Ohio State University, OARDC, 1680 Madison Ave., Wooster, OH 44691

³ University of Florida, GCRE, 5007 60th Street East, Bradenton, FL 34203

⁴ Department of Plant Pathology, University of Florida, 2515 Fifield Hall; P. O. Box 110680, Gainesville, FL 32611.

Bacterial spot is an economically important disease of tomato (*Solanum lycopersicum* L.) that is caused by as many as four species of *Xanthomonas*. Resistance has been identified in several accessions and breeding lines which are closely related to the cultivated tomato. These include resistance from Hawaii breeding lines 7998 and 7981, which may trace to introgressions from *S. pimpinellifolium*; resistance from *S. lycopersicum* var. *cerasiforme* accession PI 114490; and resistance from *S. pimpinellifolium* accessions such as PI 128216. We will review progress in developing genetic markers to facilitate simultaneous genetic dissection and breeding for resistance in crosses to close relatives of the cultivated tomato. Quantitative resistance to race T1 was identified from Hawaii 7998 by using marker-trait association analysis in intraspecific crosses. A single locus on chromosome 5, *Rx3*, explained 41% of the phenotypic variation for resistance in replicated field trials. Marker-assisted selection was utilized to combine *Rx3* in coupling phase with *Pto*, a single, dominant gene that confers resistance to bacterial speck race 0 (caused by *Pseudomonas syringae* pv. *tomato*). Resistance to both spot and speck was successfully combined and verified in field trials. Accession PI 114490 appears to resist multiple races of bacterial spot. We utilized single marker-trait analysis in an Inbred Backcross (IBC) population derived from PI 114490, FL 7600, and OH 9242 to identify a locus on chromosome 11 that explained 16.6%, 13.7%, 56.5%, and 29.4% of the variation for resistance to races T1, T2, T3, and T4, respectively. Both PI 114490 and FL 7600 alleles contributed to resistance relative to the OH 9242 allele. The PI 114490 allele conferred the highest level of resistance to T2 strains while the FL 7600 allele was most effective against T1 strains. A PI 114490 allele on chromosome 1 was associated with resistance to T2, T3 and T4 strains, explaining up to 11% of the variation. Resistance to T2 strains from QTL on chromosomes 1, 3, and 11 were confirmed in subsequent crosses. To characterize resistance to race T3 from PI 128216 (*S. pimpinellifolium*), we developed an IBC population from a cross to the *S. lycopersicum* breeding line OH 88119. Marker-trait analysis indicates that two major loci from PI 128216 contribute to a T3 mediated HR response following greenhouse inoculation. We are seeking to verify these results in subsequent crosses. Our results indicate progress in simultaneous introgression, selection, and genetic characterization using inbred backcross population designs. At the same time, there remains a need to develop population structures that allows us to pyramid resistance while retaining desirable field characteristics.

Resistance to Race 1 of *Pseudomonas syringae* pv. *tomato*

Liliana Stamova

California Tomato Research Institute, Davis, CA

Pseudomonas syringae pv. *tomato*, the causal agent of bacterial speck disease on tomato inflicts serious problems in many tomato production areas throughout the world. There are limited options to control the disease. As the cultural practices are not always effective, the use of resistant cultivars is the best managing strategy. For a long time race 0 of the pathogen has been successfully controlled by *Pto1* gene introgressed in some tomato cultivars. A race, detected in 1986 in Canada and designated race 1 broke the resistance of gene *Pto1*. There has been published some information about resistance to race 1 found in some wild species. Unfortunately for the present there are no tomato cultivars with resistance to race 1 available to tomato growers. In 2006 we screened 60 cultivated types tomato lines for resistance to California isolate A9 of race 1. Lines that have been uniformly resistant to European isolates were not among the best after challenging them with A9 isolate. High level of resistance was found in several cultivated type tomato lines coming from crosses with different wild species. Resistant lines and plants from segregating populations were saved for selection. In 2007 a second screening was carried out. All genetic materials selected as resistant to A9 isolate were inoculated separately with six California isolates. The evaluation of resistance was made based on scale of 1 to 5. Plants with scores 4 (41 – 60 bacterial lesions/plant) and 5 (more than 60 lesions/ plant) were considered susceptible. Disease severity index (DSI) was calculated. DSI of the best resistant lines varied according to the isolate – for line Rioli it ranged from 1.10 (isolate A9) to 1.66 (isolate 7) and for line Stella - from 1.5 to 1.63 respectively. At the same time the susceptible controls Glamour (susceptible to race 0 and race 1) and ONT 7710 (*Pto1*) (resistant to race 0 and susceptible to race 1) had DSI of 5.00 and 4.90 respectively. Along with the screening for resistance a genetic test was carried out aiming to define the mode of inheritance and number of genes controlling resistance to race 1. The responses of the following lines and generations to inoculation with isolate A9 were evaluated: Rioli, Stella, Glamour, F1's and F2's. The level of resistance of F1 generations was a little lower compared with the level of the resistant lines. The results of the investigation lead to the following conclusion: high level of resistance to California isolates of P.s.t. race 1 was found in cultivated type tomato lines coming from crosses with different wild species. The data from the genetic test suggest the dominance of a major factor for resistance to race 1 in the investigated lines.

Genetic Studies of Resistance to Bacterial Spot Race T4 in Tomato

Samuel Hutton and Jay Scott*

Gulf Coast Research and Education Center, University of Florida, 14625 CR 672, Wimauma, FL 33598
USA

Resistance to bacterial spot of tomato, race T4 (*Xanthomonas perforans*), in three advanced breeding lines was characterized. Populations were developed for generation means analysis (GMA) with Fla. 8326, Fla. 8233, and Fla. 8517. GMA of Fla. 8326 (resistance derived from PI 126932) in the fall of 2005 indicated resistance is additive and controlled by one gene, with a moderate to high heritability. When the experiment was repeated in the spring of 2006, additive, dominant and epistatic effects were all significant. GMA of Fla. 8233 (resistance derived from PI 114490) in the spring of 2007 indicated resistance is controlled by additive, dominant and epistatic effects. Generation means analyses were repeated in the summer of 2007 on each of these breeding lines, and performed on Fla. 8517 (resistance derived from PI 114490 and/or PI 128216). Resistant and susceptible F₂ plants were selected from each of the three populations to identify markers linked to resistance by bulk segregant analysis (BSA). The F₂ and F₃ progeny of these selections were evaluated to confirm the resistance or susceptibility prior to including them in the BSA. Approximately 300 PCR-based markers, located near areas of the genome where resistance genes to various bacterial diseases have previously been identified, were screened for polymorphisms between the three PIs and susceptible breeding lines. The polymorphic markers were used to screen for introgressions of PI germplasm into each of the resistant breeding lines. BSA will be used to determine which of these introgressed areas are linked to resistance. The possibility to enhance resistance by combining resistance genes from the three sources will be discussed.

Innovations in Grape Tomato Breeding

Randy Gardner

Department of Horticultural Science, North Carolina State Univ., 455 Research Drive, Fletcher, NC 28742

Grape tomato breeding in the North Carolina fresh market tomato breeding program is focused on developing hybrids with superior fruit quality, multiple disease resistance, and improved plant growth habit. Breeding materials have originated primarily from various cherry, large fruited and plum tomato backgrounds within the program. The first lines were developed by crossing compact growth habit brachytic (*br* gene) cherry tomato lines with 'Santa' to obtain high sugar and desired fruit shape followed by selfing and backcrossing to NC breeding lines to obtain other desired traits. Recently the hybrid 'Smarty' and three inbred lines (NC 1 grape, NC 2 grape, and NC 3 grape) were released from the breeding program. 'Smarty' is a compact indeterminate hybrid homozygous for *br* and heterozygous for the *rin* gene. Additional breeding has led to the incorporation of the crimson gene (*og*) into brachytic, indeterminate lines of normal ripening, *rin*, and *nor* types. Disease resistances being incorporated into grape tomato backgrounds include the *Sw-5* gene for TSWV resistance, the *I-3* gene for fusarium wilt race 3 resistance, early blight resistance, and the *Ph-2* and *Ph-3* genes combined for late blight resistance. Selection has also been made for tolerance to bacterial spot. The male sterile, green stem linked marker combination *ms-10*, *aa* has been incorporated into several grape tomato breeding lines to facilitate F₁ hybrid seed production. A few of the male sterile lines are capable of setting seedless fruit of high quality. The primary limitation for potential use of male-sterile plants for commercial seedless grape tomato production has been smaller fruit size than the seeded fruit, which limits yield. Breeding is underway in an effort to greatly increase the number of fruit per cluster as a means to increase yield. In addition to fresh use, the seedless fruit have potential for being used as a dried product.

Progress Toward Fine Mapping of *Ph5*, a New Late Blight Resistance Gene in Tomato

Heather Merk*, Hamid Ashrafi, Matthew Kinkade and Majid R. Foolad

Department of Horticulture and the Intercollege Graduate Degree Programs in Genetics and Plant Biology, The Pennsylvania State University, University Park, PA

Late blight (LB), caused by the oomycete *Phytophthora infestans*, can devastate tomato and potato crops within days, rendering their economically important products useless. Responsible for the Irish potato famine, LB re-emerged as an important plant disease in the 1970s, with annual control costing billions. Current LB control methods include cultural practices and the heavy use of fungicides. Although three LB resistance genes have been reported in tomato (*Ph-1*, *Ph-2*, *Ph-3*), new, aggressive isolates have overcome all three resistance genes, necessitating the search for new and durable sources of LB resistance. Through extensive germplasm screening with 7 *P. infestans* isolates in the field, high tunnel, greenhouse and growth chamber, we have identified several highly resistant accessions of the wild tomato species *Solanum pimpinellifolium*. One accession, PSLP153, was selected for further study. An F₂ mapping population was developed from a cross between NCEBR-2 (*S. lycopersicum*, susceptible parent) and PSLP153. Using a selective genotyping approach and F₂ and F₃ populations, a new late blight resistance gene, *Ph-5*, was mapped to the long arm of chromosome 1. Near isogenic lines (NILs) are being developed to fine map *Ph-5*. To develop the NILs, a series of backcrosses is being made using NCEBR-2 as the recurrent parent. Currently, an F₄BC₂ population is being developed. Extensive foreground and background marker assisted selection (MAS) will be conducted in this and further backcross generations. It is anticipated that by a combination of phenotypic selection for LB resistance and MAS for *Ph-5*, NILs will be generated by the BC₄ generation. Once NILs and subNILs are developed, *Ph-5* will be fine-mapped using the substitution mapping approach.

Mapping of Early Blight Resistance QTLs in a RIL Population of Tomato

Hamid Ashrafi*, Guoyang Lin and Majid R. Foolad

Department of Horticulture and the Intercollege Graduate Degree Program in Genetics, The Pennsylvania State University, University Park, PA

Early blight (EB), caused by *Alternaria solani* and *A. tomatophila*, is one of the most common and destructive diseases of the cultivated tomato (*Solanum lycopersicum*) in areas of heavy dew, frequent rainfall, and high relative humidity. In the U.S. the disease can be very severe in the Midwestern, eastern and northeastern regions. EB is associated with physiological maturity of the plant; older, senescing leaves are more susceptible than young, immature leaves, and a heavy fruit set enhances the disease. No genetic source with strong resistance to EB is known in the cultivated species. At present, sanitation, long crop rotation, and routine application of fungicides are the most common disease control measures. Sources of genetic resistance to EB were previously identified within the green-fruited species *Solanum habrochaites* (formerly *Lycopersicon hirsutum*) and several breeding lines with measurable level of resistance were developed at the NC State Tomato Breeding Program (RG Gardner). The NC lines can tolerate an extended fungicide spray interval, however, they are a bit late maturing. We have identified sources of EB resistance within the red-fruited species *S. pimpinellifolium*. While we have used these accessions in our traditional breeding program at Penn State to develop high-yielding, early-maturing tomatoes with improved EB resistance, we also have identified and mapped resistance QTLs in different *S. lycopersicum* × *S. pimpinellifolium* populations to facilitate marker-assisted breeding. Here we report on development and use of a new RIL population (n = 172 lines) for mapping EB resistance QTLs. A genetic linkage map of the population was developed with ~275 molecular markers, which was used to identify QTLs based on a 4-year field study (F₇ - F₁₀). Five QTLs were identified with individual phenotypic effects ranging from 6.0% to 26%, of which three QTLs on chromosomes 5, 6 and 9 were consistent across 3-4 years/ generations. Co-localizations of QTLs with candidate ESTs such as *Mi-1*, ethylene response factor-5, lipoxygenase B were observed.

Development of Fresh Market and Processing Tomatoes at Penn State

Majid R. Foolad*, Guoyang Lin and Heather Merk

Department of Horticulture and the Intercollege Graduate Degree Program in Genetics, The Pennsylvania State University, University Park, PA

The Penn State Tomato Genetics and Breeding Program has developed improved germplasm for producing fresh-market and processing tomato breeding lines and cultivars, mainly suitable for production in the northeast. Of particular interest has been development of short-season and mid-season tomatoes with high yield, good fruit quality (e.g. high lycopene) and disease resistance (e.g. resistance to early blight and late blight). Genes for desirable traits have been introgressed, mainly from the red-fruited wild species *Solanum pimpinellifolium*. In the fresh market tomato background, we have developed new inbred lines of plum (Roma type), cherry and grape tomatoes. Inbred lines of large and medium size round tomatoes are in the pipeline. We have developed a series of experimental hybrids from crosses among our inbred lines as well as with a few inbred lines from the NC State Tomato Breeding Program. These hybrids were evaluated in the field during summer 2007 and a subset will be showcased for industry review in summer 2008. Most of our current fresh market inbred lines and hybrids are high yielding tomatoes with exceptional fruit lycopene content and good foliage and fruit disease resistance. We expect that we will have available inbred lines of processing tomato background within a few years. Many of our recent efforts have focused on incorporating late blight (LB) resistance genes into our germplasm. Progress is being made in incorporating *Ph-2* and *Ph-3* into our fresh market and processing tomatoes. Simultaneously we are incorporating *Ph-5*, a new LB resistance gene discovered at Penn State, into our genetic materials. A goal is to pyramid *Ph-2*, *Ph-3* and *Ph-5* in our breeding lines and hybrids.

Inheritance of Tomato Spotted Wilt Virus Resistance Derived from *Solanum chilense* Accession LA1938

John W. Scott^{1*}, *Steve M. Olson*² and *Mikel L. Stevens*³

¹ Gulf Coast Research and Education Center, University of Florida, 14625 CR 672, Wimauma, FL 33598 USA

² North Florida Research & Education Center, University of Florida, 30 Research Road, Quincy, FL 32351 USA

³ Department of Plant and Animal Sciences, Brigham Young University, 287 Widstoe Bldg. Box 25183, Provo, UT 84602 USA

Previously we reported that resistance to tomato spotted wilt virus (TSWV) from Fla. 8516, a breeding line derived from LA1938, was conferred by one or two dominant genes (Rept. Tomato Genetics Coop. 2005). Fla. 8516 was backcrossed into 21 recurrent parents including Fla. 8124D which has the *Sw-5* gene. In Spring 2006 F₁s were advanced to the F₂ and 106 selections were made for horticultural performance without TSWV disease pressure in Fall 2006. These 106 F₃ selections plus resistant and susceptible controls, Fla. 8516 and Fla. 8153 respectively, were planted in a completely randomized block design with 3 blocks and 10 plant plots at the North Florida Research & Education Center in Quincy in Spring 2007. Late in the season incidence of TSWV was evaluated from a natural TSWV infection by a virus strain controlled by the *Sw-5* gene. Disease incidence for Fla. 8153 was 76.6% and for Fla. 8516 was 3.4% (1/29). Conservatively, there were 20 or 18.9% of the F₃ lines rated as resistant based on an incidence of 0 or 1 infected plants. There were 27 resistant lines (25.5% of F₃s) if lines with 2 infected plants (<8% incidence) are considered. There were 26 lines that were susceptible based on >50% disease incidence. There were 35 lines rated as clearly segregating but incidence was variable and thus 20 lines had segregation ratios that were more difficult to delineate. Nevertheless, the data clearly indicate that resistance was conferred by a single dominant gene as opposed to two dominant genes where only 6.25% of the lines would be expected to breed true for resistance. We will name this gene *Sw-7*. Four lines were from the cross with *Sw-5* resistance and none were rated as resistant indicating that *Sw-7* is not allelic or linked to *Sw-5*. Breeding implications will be discussed.

Pest Resistance Derived from *S. pimpinellifolium* Accession TO-937

Juan M. Alba¹, María J. Rodríguez-López¹, María Salinas², Juan Capel², Rafael Lozano², Jesús Cuartero¹, and Rafael Fernández-Muñoz^{1*}

¹ Departamento de Mejora Vegetal, Estación Experimental La Mayora – CSIC, E-29750 Algarrobo-Costa, Málaga, Spain

² Departamento de Biología Aplicada – Genética, Universidad de Almería, Ctra. Sacramento s/n, E-04120 Almería, Spain

Pest resistance based on trichome secretions has been extensively studied in green-fruited wild tomato species such as *S. habrochaites*, *S. habrochaites* f. *glabratum*, and *S. pennellii*. In 2000 we reported TO-937 as an accession from *S. pimpinellifolium*, much closer to the cultivated tomato, that was highly resistant to the twospotted spider mite (*Tetranychus urticae* Koch). Based on evaluation of F₂ and BC₁ generations from an interspecific cross with susceptible *S. lycopersicum* cv. MoneyMaker, we showed in 2003 that resistance of TO-937 seemed to have a relatively simple control and that it was probably due to presence of type IV glandular trichomes. Herein we report our advances since then. One hundred and sixty four recombinant inbred lines (RIL) derived from the cross cv. MoneyMaker x TO-937 were obtained. Intermediate generations while obtaining the RILs were repeatedly evaluated for resistance by infestation in greenhouse and repellence thumbtack laboratory bioassays, which served for searching of linked markers. After a bulked segregant analysis in those intermediate generations, a few markers from chromosome 2 seemed to be associated with resistance. That was confirmed after obtaining the RILs, evaluating them in the greenhouse and the construction of a low-density molecular map. A single QTL for resistance to *T. urticae* was located in chromosome 2 long-arm in the proximity of *ovate* and *fw2.2* loci. We sought assistance from chemists who helped to know that TO-937 epicuticular secretions were rich in acylsugars, specifically acylsucroses. Segregation for spider mite resistance in the greenhouse, leaf trichomes densities, and acylsucrose contents was evaluated in the RIL population. Also, laboratory bioassays of mite mortality, repellence, and oviposition were performed in the population. Wide segregation was observed for all traits. Multiple regression analysis revealed that acylsucrose content was the most important variable to explain both greenhouse and laboratory resistance to *T. urticae*. Genetic correlations and high heritability values pointed to that successful selection for acylsucrose production / resistance was feasible. Recently we analyzed trichome exudates of parents and RILs by thin layer chromatography. Seven different bands were present on TLC plates of TO-937 nonpolar extracts and only one on those of cv. MoneyMaker. Multiple regression analysis of segregation in the RIL population showed that three of the TO-937 bands could statistically explain resistance to the spider mite and one of those bands explained alone 54% of variance of resistance. From the beginning of our studies with spider mite resistance, we aimed to obtain a resistant line nearly isogenic to cv. MoneyMaker. We started a recurrent backcross selection scheme by selecting for high type IV trichome density and acylsucrose production and currently we have already reached BC₆ lines with leaf type IV trichome densities and acylsucrose contents similar to those of the donor parent that at the same time recovered most of recurrent parent traits, particularly fruit size and shape. From segregation for type IV trichomes in BC₃, a couple of sister lines contrasting deeply for that trait were obtained. Together with the parents and the F₁, the sister lines were studied for resistance to the whitefly *Bemisia tabaci* Genn. (biotype Q) in both free-choice and non-choice greenhouse experiments. Type IV trichome-bearing genotypes exhibited resistance to the whitefly in terms of reduced oviposition and egg hatching, almost impeded larval stages development, and moderate adult infestation. Interestingly, tomato yellow leaf curl disease natural incidence was reduced in TO-937 and the whitefly resistant BC₃ line. Currently we are studying by controlled whitefly inoculations whether or not presence of *S. pimpinellifolium* type IV trichomes and associated resistance to *B. tabaci* in the advanced backcross resistant line result in reduced transmissibility of TYLCV. We also aim to combine this source of resistance with known genes for geminivirus resistance.

Modulating Acylsugar Level and Type, and its Effects on Whitefly Control

Martha Mutschler^{1*}, Ricardo Lobato-Ortiz¹, Darlene DeJong¹, Stephen Southwick¹ and Dave Schuster²

¹ Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY

² University of Florida, Gulf Coast Research & Education Center, University of Florida, Wimauma, FL

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, but very poor horticultural type. 97FL possesses 8 *S. pennellii* introgressions, representing 27% of its nuclear genomes. The combination of PCR based markers and selection for acylsugar production allowed creation of a series of second and third generation acylsugar lines with reduced numbers or sizes of introgressions. Significant differences in the levels of acylsugars were found among these acylsugar lines in greenhouse and field studies. All of the later generation acylsugar lines had acylsugar levels that were lower than that of 97FL. The density of acylsugar-producing type IV trichomes showed considerably less variation among the lines tested than did acylsugar levels, and did not account for differences in acylsugar level among lines. The types of acylsugar produced by the lines are very similar, and are largely restricted to acylsucroses, rather than the acylglucoses of the original source of acylsugar production, *Solanum pennellii* LA716. The cooperative 2006 and 2007 Florida field trials demonstrated the affect of different acylsugar levels on the degree of silverleaf whitefly (SLW) control. The lowest levels of SLW infestation, across developmental stages, were on 97FL, the line with the highest acylsugar level. The only evidence of SLW on 97FL in 2007 was the presence of less than one egg per sample. Infestation levels across stages were also significantly reduced for the new lines with the higher acylsugar levels. In these lines, some levels of SLW were present at all stages, but the levels of infestation were so low that they were not significantly different from that of 97FL. Increasing SWF counts are seen as acylsugar levels drop further in other lines. Acylsugar levels comparable or higher than that of 97FL lines should provide the most reliable control of SLW control. Further testing of the acylsugar lines in other locations, against a variety of insect pests, should identify the levels of acylsugars that would best control the desired spectrum of important tomato pests. Additional breeding is focused on raising acylsugar level, moderating acylsugar type, and further improving horticultural type with decreased introgression size.

Genetic Regulation of Tomato Fruit Ripening and Nutritional Quality

James Giovannoni

USDA-ARS and Boyce Thompson Institute for Plant Research, Ithaca, NY USA

Research in the laboratory focuses on understanding key regulatory genes which influence overall-ripening control but also with an interest in those contributing more directly to nutritional attributes. Carotenoids are important plant-derived contributors to human health and nutrition. While the majority of genes involved in carotenoid synthesis and metabolism have been identified, genetic mechanisms underlying regulation of the pathway leading to specific carotenoid profiles of plant tissues remains largely unknown. Ripening tomato fruit accumulate large amounts of carotenoids (especially lycopene and beta-carotene) over a short period of time. This fact combined with rapidly expanding genomics resources for tomato makes this an excellent model system for investigating carotenoid pathway control. Our group is employing a combination of metabolic profiling and genomics approaches to understand the regulation of carotenoid flux during fruit ripening. Specifically, we have identified key ripening genes that regulate numerous ripening pathways including those involved in carotenoid metabolism. We are also examining single-gene carotenoid mutants to assess the regulation of carotenoid genes in response to alterations in metabolite levels. Preliminary results indicate that key steps in the carotenoid pathway are regulated during ripening but that many genes in the pathway are responsive to feedback regulation. Genomics approaches have lead to a number of interesting candidate genes and at least one that appears to have more specific effects on carotenoid levels of ripening fruits when assayed in transgenic plants.

Tomato *high pigment* Mutants and their Central Role in Enhancing Fruit Pigmentation and Functional Quality

Ilan Levin*, Yaakov Tadmor, Michal Oren-Shamir, Moshe Reuveni, Ayala Meir, Rinat Ovadia, Maya Sapir, Igor Kolotilin, Dalia Evenor, Sahadia Nahon, Haviva Shlomo, Lea Chen, and Amir Bootbol

Institute of Plant Sciences, the Volcani Center, P.O.Box 6, Bet Dagan, Israel 50250

Phenotypes of the tomato (*S. lycopersicum*) *high pigment* (*hp*) mutants are caused by lesions in genes encoding DEETIOLATED1 (*hp-2*, *hp-2^j*, *hp-2^{dg}*) and UV-DAMAGED DNA BINDING PROTEIN 1 (*hp-1*, *hp-1^w*), proteins that regulate of light-signaling. Homozygous *hp* plants display a plethora of developmental and metabolic phenotypes in comparison to their normal isogenic counterparts, but they are best known for their increased levels of fruit carotenoids, primarily lycopene. Moreover, recent studies generalize earlier ones showing that fruits harvested from *hp* mutant plants are also characterized by significantly higher levels of other plastid-accumulating phytonutrients, such as: vitamins C and E. Further, these fruits are also enriched with certain flavonoid compounds, also known for their functional, or health-promoting, value. Commutatively, these results highlight a strong link between light-signaling and over-production of fruit phytonutrients. Results recently obtained show that *hp* mutants, in combination with other mutant genes, can enhance fruit pigmentation and functional quality in a more-than-additive manner. We have recently demonstrated this interaction with ANTHOCYANIN FRUIT (*AFT*, formerly *AF*) mutants. *AFT* mutant plants were originally characterized as sharing excess anthocyanins, functional flavonoid metabolites, in fruits and vegetative tissues. We have recently found that: **(1)** *AFT* fruits are characterized by significantly higher levels of the flavonols quercetin and kaempferol, in addition to anthocyanins; and **(2)** Double homozygous *AFT/AFT hp-1/hp-1* plants display a more-than additive effect of on the production of the anthocyanins delphinidin, petunidin and malvidin and the flavonols quercetin and kaempferol in fruits. This effect was strongly manifested by ~24-fold average increase in fruit anthocyanin content in the double mutants in comparison to the cumulative levels of their parental lines, thus enhancing their functional and pigmentation qualities. These results are in agreement with an additional study showing a strong interaction between *AFT* and both *hp-1^w* and *hp-2^j* and between each of the latter two mutations and the recessive *atroviolacium* (*atv*) mutation. Mutant *HP* genes share adverse pleiotropic effects, such as slow germination and seedling growth, seedling mortality, inferior leaf coverage, brittle stems, low yield, reduced total acidity and soluble solids content, high sensitivity to various pathogens and premature defoliation, which have prohibited widespread commercial use of these genes. However, their central role in enhancing fruit pigmentation and functional quality, demonstrated herein, justifies extended breeding efforts to reduce these negative effects. Such efforts have already led to the development of several “lycopene rich” tomato cultivars carrying *hp* mutations that are being successfully used in production.

Breeding Tomatoes for Increased Flavonoid Content

Peter Boches* and Jim Myers

Department of Horticulture, Oregon State University, Corvallis, OR

One of the major goals of the tomato breeding program at Oregon State is the development of tomato cultivars with increased levels of polyphenolics (including flavonoids and anthocyanins) for their health benefits and novelty. Current projects related to this goal include: (1) development of a high anthocyanin cherry tomato cultivar, (2) screening a *S. lycopersicum* var. *cerasiforme* tomato core collection for high total phenolics, (3) combining the high pigment *hp2^{dg}* allele with the anthocyanin fruit genes *Aft* and *atv*, (4) combining the dihydroflavonol reductase null mutant *aw* with *Aft* and *atv* to create a high flavonoid tomato, and (5) sequencing of the *An2* locus (the putative tomato homolog of the maize transcription factor *C1*) in anthocyanin fruit mutants such as *Aft* and 'Purple Smudge'. Recent progress in these areas will be discussed using results from Folin-Ciocalteu assays, pH differential tests, HPLC, and DNA sequencing.

Progress Toward Validation and Isolation of Novel Genetic Factors Controlling Lycopene Content in a *S. pimpinellifolium* × *S. lycopersicum* RIL Population

Matthew P. Kinkade, Hamid Ashrafi, and Majid R. Foolad*

The Intercollegiate Graduate Degree Programs in Plant Biology and Genetics, and the Department of Horticulture, The Pennsylvania State University, University Park, PA 16802

Numerous epidemiological and intervention studies have indicated that dietary intake of lycopene-rich food may result in a decreased incidence of certain cancers. Fresh tomatoes and tomato-based products are the leading sources of dietary lycopene, a major tomato carotenoid and a potent natural antioxidant. As such, the identification of genetic factors which regulate high fruit lycopene content is imperative. To facilitate this endeavor, identification of genetic sources of high fruit lycopene content, genetic factors controlling lycopene content, lycopene assays that are rapid, accurate, high-throughput and low-cost, and production of robust, reliable phenotypic data are all essential. Here we report a genetic analysis of fruit lycopene content in a genetically mapped RIL population developed from a cross between a *Solanum pimpinellifolium* accession, with exceptionally high fruit lycopene content, and a *S. lycopersicum* breeding line. The RIL population was grown under field conditions in four years (F₇ – F₁₀) and fruit lycopene was analyzed using HPLC, spectrophotometric and colorimetric assays. Using the data obtained from each lycopene assay and using simple, composite and multiple interval mapping analyses, we have identified new major QTLs which affect lycopene content in this population. These QTLs do not correspond to known map positions of carotenoid biosynthetic genes. In order to study the QTLs further, we have initiated a marker-assisted backcross program to develop near-isogenic lines (NILs) in the cultivated tomato genetic background for two of the QTLs. We will discuss our QTL analyses, our rapid and accurate spectrophotometric method of lycopene measurement and the status of NIL development.

Breeding Tomatoes for Human Health and Nutrition

David M. Francis^{1*}, Audrey Darrigues¹, Susana De Jesus¹, Steven Schwartz², Luis Rodriguez-Saona²

¹ Horticulture and Crop Science, The Ohio State University, OARDC, 1680 Madison Ave., Wooster, OH 44691

² Food Science and Technology, 2015 Fyffe Rd., Columbus, OH 43210

Correlative evidence suggests that enhanced consumption of carotenoids may decrease the risk of certain cancers. The lack of knowledge concerning how carotenoid structure and concentration affect uptake and biological activity in the human body limits the use of tomato products as functional foods (foods designed to provide a specific and beneficial physiological effect on health). Numerous tools exist for genetic and phenotypic selection in order to develop tomato lines and varieties with altered carotenoid content. In order to develop genetic resources to test the physiological effects of dietary carotenoids in the food matrix, we used molecular-marker-assisted selection, Attenuated Total Reflectance Infrared (ATR-IR) spectroscopy, and classical selection to combine genes that affect both the biochemical synthesis of carotenoids and the structure of the chromoplast. As expected from past work, increased content of lycopene is often accompanied by a decrease in beta-carotene. When genes that affect chromoplast development (e.g., *dg* and *gf*) or genes that affect fruit ripening (*rin* and *alc*) are combined with genes that affect the conversion of cis-lycopene (*t* and *t'*) to lycopene, zeta-carotene content is enhanced. Genetic resources developed from these studies have been used to verify the increased adsorption of cis-lycopene relative to trans-lycopene in human trials. Despite increased awareness and interest in dietary carotenoids, pigment composition is not yet directly valued in contract and pricing structures for tomato. In contrast, color and color uniformity are given value in contracts and in USDA product grades for processing tomatoes. Poor color uniformity is due to disorders that alter the ripening process resulting in internal white tissue and yellow or green sectors. Scanned images of tomato fruits were analyzed for internal fruit color with both the Tomato Analyzer Software ([Brewer et al., Plant Physiology, 2006, 141, 15-25](#)) and a colorimeter. We showed high correlations ($r^2 > 0.96$) and linearity of L^* , a^* , b^* values obtained from scanned images and the colorimeter. The proportion of total phenotypic variance attributed to genotype for color and color uniformity measured from images was significantly improved relative to the colorimeter. Principle components analysis of color data from segregating populations revealed that color uniformity contributes high positive and negative loadings to PCA1, confirming the importance of color uniformity to variance in populations. In addition, fruit affected by color disorders have reduced lycopene and beta-carotene content. Varieties with improved color uniformity therefore have potential to return value to growers, processors and consumers.

Genetic Variation Among Tomato Landraces

Angela M Baldo^{1,2*}, Warren F Lamboy¹, Larry D Robertson^{1,2}, Susan M Sheffer¹, Joanne A Labate^{1,2}

¹ USDA-ARS Plant Genetic Resources Unit, Geneva, NY

² Department of Horticultural Sciences, Cornell University, Geneva, NY

Cultivated tomato (*Solanum lycopersicum* L.) is known to have a narrow genetic base. COSII, EST-based, and several loci related to fruit quality traits were resequenced in a diverse panel of 30 Plant Genetic Resources Unit (PGRU) tomato accessions and line TA496. The majority of sampled tomato accessions represented the primary center of diversity (Peru, Chile, and Ecuador), and countries contiguous with the primary center. These were the same accessions studied by Villand et. al. (1998) using RAPDS. Original collections were made between 1932 and 1976. Evidence of historical introgression and the population-level distribution of genetic variation reveal relationships between tomato landraces. There is the most genetic diversity among the samples collected in the primary center of domestication and the least from secondary centers of domestication. The single cherry tomato in the study did not appear particularly divergent relative to the other samples from the primary center of domestication.

Evaluation of Greenhouse, Field and Heirloom Tomato Varieties in Hydroponic Greenhouse Production

Barbara E. Liedl and Jeremy M. Sisson*

West Virginia State University, Gus R. Douglass Institute, Agricultural and Environmental Research Station, Institute, WV 25112-1000

The greenhouse tomato industry in North America accounts for 37% of fresh tomato sales compared to 10% in 1999. This rapid growth in supply has led to declining prices, which challenges growers to be profitable. Controlling disease and insects can often be eliminated with good management practices and variety choice. However, greenhouse growers struggle more than field growers to control pests and diseases during their crop's long-term production in an enclosed environment. Thus, developing greenhouse varieties with pest and disease resistance would support the US greenhouse tomato industry. The first step in initiating our greenhouse tomato breeding program was to evaluate existing cultivars and germplasm. In this study, indeterminate heirloom varieties, resistant field germplasm and greenhouse hybrids were grown using commercial hydroponic production standards. Fruit were harvested and graded using USDA standards. Field varieties produced a greater percentage of large or extra large fruit and the heaviest fruit; however, they produced so few fruit, it would not be profitable to use these in greenhouse production. Greenhouse lines produced fruit earlier and higher number of large or extra large fruit. However, average fruit weight for the greenhouse lines was less than 200 g and the brix readings were in the bottom half of the lines studied. Thus, greenhouse growers require lines developed specifically for greenhouse production, but with some of the traits of lines used in field production.