



**Identification of a pollen factor involved in unilateral incompatibility.**

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**Developing TILLING for tomato.**

Junda Jiang, Roger Chetelat, Allen Van Deynze and Luca Comai, Dept. of Plant Sciences and Genome Center, University of California, Davis. [trchetelat@ucdavis.edu](mailto:trchetelat@ucdavis.edu) ...Page 7

**Phenotypic and molecular variation in 44 vintage tomato varieties.**

J.A. Labate<sup>1,\*</sup>, D.R. Panthee<sup>2</sup>, M. McGrath<sup>3</sup>, D.M. Francis<sup>4</sup>, A. Breksa<sup>5</sup>, and L.D. Robertson<sup>1</sup>, <sup>1</sup>USDA-ARS, Plant Genetic Resources Unit, Geneva, NY 14456, <sup>2</sup>Dept. of Horticultural Science, North Carolina State University, Mountain Horticultural Crops Research and Extension Center, Mills River, NC 28759, <sup>3</sup>Dept. of Plant Pathology and Plant-Microbe Biology, Cornell University, Long Island Horticultural Research & Extension Center, Riverhead, NY 11901, <sup>4</sup>Dept. of Horticulture and Crop Science, The Ohio State University, Ohio Agricultural Research and Development Center, Wooster,

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**Acylsugar QTL and their impacts on Acylsugar characteristics and whitefly response.**

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**Issues and strategy for modifying interspecific introgressions in tomato: *Solanum pennellii* Chromosome 3.**

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**Breeding tomato for pigments.**

Dilip R. Panthee and Penelope Perkins-Veazie, Dept. of Horticultural Science, North Carolina State University. [dilip\\_panthee@ncsu.edu](mailto:dilip_panthee@ncsu.edu) ...Page 11

**Identification of trichomes, loci and chemical compounds derived from *Solanum habrochaites* accession LA1777 that are associated with resistance to the sweetpotato whitefly, *Bemisia tabaci* in tomato, *S. lycopersicum*.**

Mohamed T. Rakha<sup>1,2</sup>, Jay W. Scott<sup>2</sup>, Samuel F. Hutton<sup>2</sup> and Hugh Smith<sup>2</sup>

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**Fresh market tomato breeding: visions or folly.**

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**Fine mapping of the *Tomato Yellow Leaf Curl Virus* resistance gene *Ty-2* on Chromosome 11 of tomato**

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## Identification of a pollen factor involved in unilateral incompatibility

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Cultivated tomato can be crossed with nearly all of its wild relatives, but many crosses succeed only if the cultivar is used as female. In these cases, the reciprocal crosses are blocked by unilateral incompatibility (UI), a prezygotic reproductive barrier that prevents fertilization by foreign (interspecific) pollen through the inhibition of pollen tube growth. UI occurs most often when the female is a self-incompatible species and the male is self-compatible (the 'SI x SC rule'). Pistils of *Solanum lycopersicoides* (SI) reject pollen of cultivated tomato (SC) in the upper style, whereas on pistils of *S. lycopersicum* x *S. lycopersicoides* hybrids, rejection occurs lower in the style, indicating a weakened UI. On allotriploid hybrids (i.e. two tomato and one *S. lycopersicoides* genomes), two pollen factors introgressed from *S. pennellii* are sufficient for full compatibility: *ui1.1* on chromosome 1, and *ui6.1* on chromosome 6. The *ui6.1* factor was mapped to a ~20 kb interval containing a pollen-expressed *Cullin1* (*Cull1*) gene with similarity to SI factors from *Petunia*. Cultivated tomato and related red or orange-fruited species (all SC) exhibit the same loss of function mutation in this gene, whereas the green-fruited species (mostly SI) contain a functional allele. Transgenic tomato plants expressing the *S. pennellii* *Cull1* gene are compatible on pistils of the allotriploids, but only if they also contain *ui1.1*. The latter factor has been mapped to a ~20 Mb region containing the *S*-locus. A large number of potentially SI-related genes were identified in this region, from which several are being studied as possible candidates for *ui1.1*. Potential applications of this research to tomato breeding will be discussed.

### **Genetics and breeding of LB resistance and high fruit lycopene content.**

Majid R. Foolad, Heather L. Merk, Matthew P. Kinkade, Hamid Ashrafi and Matthew T. Sullenberger, Dept. of Horticulture and The Inter-college Graduate Degree Programs in Genetics and Plant Biology, The Pennsylvania State University, University Park, PA 16802.

Screening of approximately 300 accessions of the tomato wild species *Solanum pimpinellifolium* for various agriculturally important traits, including fruit quality, early blight resistance, and tolerance to various abiotic stresses, resulted in the identification of 70 accessions with numerous desirable characteristics. Subsequently the core collection of 70 *S. pimpinellifolium* accessions was screened for late blight (LB; caused by *Phytophthora infestans*) resistance under different conditions, including field, high tunnel, greenhouse and growth chamber (using detached leaflets). There were high correlations between screenings under different conditions. Several accessions of *S. pimpinellifolium* were identified with strong resistance to different isolates of *P. infestans*. One accession was chosen for genetic characterization of LB resistance, including inheritance studies and genetic mapping. Using parent-offspring correlation analysis, heritability of LB resistance was estimated to be 0.86, indicating that this resistance was highly heritable and could be transferred to the cultivated tomato via phenotypic selection. Using a selective genotyping approach (a.k.a. trait-based marker analysis) two genomic locations on tomato chromosomes 1 and 10 were associated with LB resistance in this accession. Research is currently underway to fine map the two LB resistance genes. Simultaneously, this resistance and the LB resistance conferred by two previously known genes (*Ph-2* and *Ph-3*) are being incorporated into Penn State fresh-market and processing tomato breeding lines.

Screening of the *S. pimpinellifolium* accessions for various fruit quality characteristics resulted in the identification of one accession with exceptional fruit lycopene (LYC) content. This accession was used for extensive genetic and breeding research for fruit LYC content. Several QTLs for fruit LYC content were identified in different filial and backcross populations. Two major QTLs on chromosomes 12 (*lyc12*) and 7 (*lyc7*) have been fine mapped. For example, *lyc12* has been mapped to within 1-2 cM, and NILs containing this QTL have been developed and verified. Simultaneously, the high LYC trait has been incorporated into Penn State breeding germplasm and fresh market (cherry, grape, plum and large round) and processing tomato breeding lines with exceptional fruit LYC content have been developed. Several breeding lines with high fruit LYC content and other desirable horticultural characteristics are available for commercial evaluation.

### **Quality is color, and color is lycopene, or not...**

David Francis, The Ohio State University, Ohio Agricultural Research and Development Center, Dept. of Horticulture and Crop Sciences.

Quality is defined by the market, however the market is not always willing to pay for the traits of expressed interest. Arguably, in some cases, quality has been replaced by industry standards and grades that may no longer track well with what we perceive as consumer or market preferences. This situation makes setting objective breeding goals difficult. This dilemma is particularly troubling as genetic and genome sciences continue to drive practical plant breeders toward objective measures of traits on a large scale. Fruit appearance is in part derived from pigments, carotenoids, which are of interest for dietary and human health. However, pigment composition is not directly valued in contract and pricing structures for tomato. In contrast, both absolute color and color uniformity are valued in contracts for processing tomatoes and in USDA product grades. Color and color uniformity represent traits that return value to both growers and processors and are therefore worth targeting in processing tomato breeding efforts. From the perspective of human health and nutrition, assessing quality may be much more ambiguous than is commonly understood. In this presentation at the TBRT, I will use color and carotenoid content to explore issues of how plant breeders can place value on traits, increase our capacity for objective phenotyping, and develop indices of net merit.

## **Present status of begomovirus resistance breeding efforts at University of Florida.**

S. F. Hutton and J. W. Scott, IFAS, University of Florida, Gulf Coast Research & Education Center, 14625 CR 672, Wimauma, Florida, 33598

Breeding for resistance to tomato yellow leaf curl virus (TYLCV) has been a major focus of the University of Florida tomato breeding program since 1990. Sources of resistance in the program have included *Solanum chilense* accessions LA 1932, LA 1938 and LA 2779, as well as the cultivar Tyking. The *S. chilense*-derived *Ty-3* and *Ty-4* alleles were both identified at UF, and *Ty-3* has proven to be an important element of the program's TYLCV-resistance breeding efforts. We recently determined that resistance derived from 'Tyking' is recessive and co-segregates with the *Ty-5*-linked marker, *SINAC1*. A survey was conducted in Spring 2011 to determine the underlying genetics of resistance in the program's most advanced breeding lines. Results indicated that *Ty-4* has so far played only a minor role in the program, and the primary contributors to resistance are *Ty-3*, "*Ty-5*", and an unmapped resistance locus, that herein will be tentatively called *Ty-6*. Towards mapping of the "*Ty-6*" locus, a population was phenotyped in Spring 2011, and genotyping is presently underway at SolCAP. Additionally, evaluations in the survey for non-viral disease severity indicated that the *Ty-3* introgression is associated with greater susceptibility to some foliar diseases (eg. *Xanthomonas*, *Alternaria*). Material has been developed which has an approximately 0.2 cM *Ty-3* introgression. Preliminary data from Spring 2011 indicated that this material does not have the foliar problems, and present breeding strategies aim to incorporate this minimal introgression into more than 40 of the program's most advanced parent materials via a MAS backcrossing strategy. Resistance alleles *Ty-2*, *Ty-4*, and "*Ty-5*" are also being backcrossed into these parental lines using the same approach.

## **Developing TILLING for tomato**

Junda Jiang, Roger Chetelat, Allen Van Deynze and Luca Comai

Dept. of Plant Sciences and Genome Center, University of California, Davis

TILLING (Targeting Induced Local Lesions IN Genomes) is a reverse genetics technique that uses traditional chemical mutagenesis methods to create libraries of mutagenized individuals that are later subjected to high-throughput DNA screens for the discovery of mutations. To develop TILLING resources for tomato, we have concentrated on optimizing material and methods for mutagenesis. We have developed methods for mutagenesis of pollen using UV and gamma ray irradiation. The treated genomes were characterized by Illumina sequencing. The mutation level in the genomes of the pilot populations treated with an optimized dose of UV (180 mJol/cm<sup>2</sup>) was low, whereas deletions were easily found after gamma irradiation of pollen at the dose of 150 Gy. To induce point mutations, we compared the responses of four tomato varieties (Heinz 1706, M82, VFNT Cherry, and E6203) to two mutagens, EMS (40, 60, 80, 100, 120 and 140 mM) and MNU (5, 10, 15, and 20 mM). VFNT Cherry was the most tolerant to both mutagens and was selected for development of the TILLING populations, based on the assumption that a tolerant genotype can be exposed to higher mutagen doses, which should yield more mutations. We produced a population by sequential application of 140mM EMS to single-seed generations resulting in 4,000 families at M2M3 stage. The mutation rate of this twice-mutagenized population was tested on 11 genes with Illumina sequencing and found to be unexpectedly low (1 mutation/Mb or less). Therefore, we selected Heinz 1706, a line more sensitive to both EMS and MNU, for production of a new TILLING population. To date, we have developed 1,300 M2 families of H1706 treated with 100 mM EMS and 4,400 M1 individuals treated with 5 mM MNU. The frequency of phenotypic variants in this M2 population is distinctly higher than in VFNT Cherry. We have developed efficient methods to detect mutation in individual plants using reduced genomic complexity. The mutation rate is being tested. The prospects and plans for a TILLING service to the community will be described.

### **Phenotypic and molecular variation in 44 vintage tomato varieties.**

J.A. Labate<sup>1</sup>, D.R. Panthee<sup>2</sup>, M. McGrath<sup>3</sup>, D.M. Francis<sup>4</sup>, A. Breksa<sup>5</sup>, and L.D. Robertson<sup>1</sup>, <sup>1</sup>USDA-ARS, Plant Genetic Resources Unit, Geneva, NY 14456,

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An important goal of tomato breeding is to develop varieties that will provide high quality product for fresh consumption. Traits such as lycopene, total soluble solids (TSS), vitamin C and titratable acids (TA) are major components of fruit flavor and quality. Although several-thousand genotypes are available from the Plant Genetic Resources Unit (PGRU) for potential exploitation of such traits, they have not been previously assessed in replicated field trials. To take steps to address this problem, 44 vintage tomato varieties of diverse origins were acquired and evaluated in a total of four environments (NC, NY, OH in 2009 and OH in 2010). Descriptive summaries and quantitative genetic analyses of the four traits will be presented. Significant differences among the genotypes indicated that certain lines may be of interest to use as parents in tomato breeding programs aiming to improve fruit quality, whereas significant GxE interactions indicated that the performance of the varieties may be location specific. Molecular genetic markers showed that this set of vintage varieties was only slightly less diverse than two geodiversity panels. Cluster analysis using markers was inconclusive with the exception of a separate clade consisting of two cherry tomato varieties. Seed is being increased for all varieties not previously held by PGRU and they will be added to the germplasm repository for distribution to breeders and researchers upon request.

## **Acylsugar QTL and their impacts on acylsugar characteristics and whitefly response.**

Brian Leckie, Darlene DeJong, and Martha Mutschler, Dept. of Plant Breeding and Genetics, Cornell University

Part of the Cornell tomato breeding program is focused on the development of acylsugar-mediated insect resistant tomato lines. The current benchmark acylsugar breeding line, CU071026, contains 4 *Solanum pennellii* LA716 introgressions on chromosomes 2, 3, 7, and 10, and produces modest levels of acylsucroses (~15  $\mu\text{mol/g}$  dry leaf tissue) with a fatty acid profile predominated by i-C5, n-C12, and i-C4 fatty acids. This benchmark line has been demonstrated to significantly reduce incidence of both thrips and whiteflies in field studies. To identify additional regions of *S. pennellii* to raise acylsugar level or modify acylsugar chemotype, a BC<sub>1</sub>F<sub>1</sub> population was produced by crossing the F<sub>1</sub> 071026 x *S. pennellii* LA716 with CU071026 as the recurrent parent. This BC<sub>1</sub>F<sub>1</sub> population was genotyped with 94 PCR markers positioned in the segregating regions of the nuclear genome and was phenotyped for levels of acylsugar production, the sugar moiety produced, and the fatty acid profile. Data was analyzed by QTLNetwork 2.1 for the detection of QTL and epistatic interactions. This study identified QTL for total acylsugar level, acylsucrose production, acylglucose production, and/or for modifying the fatty acid profile. Additionally, epistatic interactions between QTL were found to control levels of total acylsugar production and to determine both the sugar moieties and fatty acid profiles of the acylsugars produced. To confirm the major total acylsugar QTL identified in this study on chromosome 6, two independently derived sets of related acylsugar tomato lines either containing or lacking the region of this QTL were tested in two field cages infested with silverleaf whitefly, *Bemisia argentifolii*. All acylsugar lines evaluated in this test were observed to have significantly lower incidence of whitefly when compared to the tomato control. Additionally, lines with the chromosome 6 total acylsugar QTL produced significantly more total acylsugar, had significantly higher densities of type IV glandular trichomes, and significantly lower incidence of whiteflies than comparable acylsugar lines lacking the chromosome 6 QTL. The other QTL identified in this study are currently undergoing confirmation by multiple strategies, including testing of BC<sub>1</sub>F<sub>2</sub> populations and crossing *S. pennellii* introgression lines with breeding lines.

### **Issues and strategy for modifying interspecific introgressions in tomato: *Solanum pennellii* Chromosome 3**

Martha A. Mutschler and Darlene DeJong, Dept of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853

Genes to improve plant type, fruit type, or provide disease resistance have been introgressed from wild species into cultivated tomato. Transfer of an introgression containing the desired gene from a wild species to tomato can also have undesirable impacts on horticultural qualities if the introgression carries negative traits as well as the gene controlling the desired trait (linkage drag). Modifying an introgression can be challenging if the introgression includes features or genes that impede progress.

The Cornell breeding program produced a series of lines that possess acylsugar mediated resistance to multiple pest species by introducing introgressions from *S. pennellii* into tomato. The current benchmark acylsugar line, CU071026, has 4 introgressions on chromosomes 2, 3, 7, and 10, together accounting for *ca.* 10% of the plants nuclear genome. The chromosome 3 introgression CU071026 is by far the largest introgression, at *ca.* 77.5 cM, over 50% of chromosome 3, and *ca.* 64% of the *S. pennellii* DNA in 071026. Prior work indicated that in addition to a major acylsugar QTL, the large chromosome 3 introgression included QTL within this region for yellow fruit, later maturity, reduced fruit size, and had regions subject to strong segregation distortion. Therefore it is necessary to modify the chromosome 3 introgression to eliminate unnecessary regions associated with these negative traits while retaining the necessary acylsugar QTL.

Work prior to 2011 delineated the impact of some of the subregions within the chromosome 3 introgression, facilitating a plan for stepwise reduction of this introgression, eliminating undesirable subregions while maintaining subregions with necessary QTL. As a result of the stepwise plan, a series of lines were created in which the chromosome 3 introgression was ultimately broken into 6 subregions, three of which were eliminated and three maintained. In all lines created the uppermost region (*ca.* 9 cM) and a central region (*ca.* 17 cM) were first eliminated. This central region removed included what appears to be a paracentric inversion and also contained the *S. pennellii* *r* gene for yellow fruit, therefore its elimination resulted in production of red fruit. Additional steps eliminated variable sized portions of the lowest part of the introgression. This subregion contained the small fruit QTL shown by prior publications to be in the central region on chromosome 3, since in some lines the fruit size nearly doubled (averaging *ca.* 200+ g).

Considering the different lines obtained, elimination of 3 subregions removed 54 to 64% of the *S. pennellii* DNA of the chromosome 3 introgression. The best lines obtained after elimination of 3 subregions produce similar levels of acylsugars as the parental acylsugar line 071026, so elimination of their 3 subregions did not negatively impact acylsugar production.

### **Breeding tomato for pigments**

Dilip R. Panthee and Penelope Perkins-Veazie, Dept. of Horticultural Science, North Carolina State University

Tomato (*Solanum lycopersicum* L.) is one of the major vegetables consumed daily throughout the world. Consumers' preferences for external features such as color and size drive purchases. In addition, consumers have become much more aware of traits such as flavor and phytonutrient properties and this has led to the incorporation of phytonutrient improvement into tomato breeding programs. Lycopene, the pigment imparting red color in tomato, has been widely studied for its antioxidant properties. Lycopene has been reported to delay or prevent chronic diseases such as cancer, diabetes, and cardiovascular disease. A number of non-red tomato cultivars are available including green, yellow, orange, striped, and purple types. Phytonutrient composition in these tomatoes is of interest for flavonoids, pro-lycopene, and xanthophylls. We used 10 breeding lines with different colors to develop hybrids in diallel combinations (excluding reciprocals) to investigate the gene action for color and lycopene levels. Fruits of the hybrids under greenhouse and field conditions were evaluated for colors and lycopene. General and specific combining ability for different colors and lycopene were determined, and a subjective rating for overall taste in different hybrids is reported. This study may help us to identify the best combination for colors, lycopene and taste.

**Identification of trichomes, loci and chemical compounds derived from *Solanum habrochaites* accession LA1777 that are associated with resistance to the sweetpotato whitefly, *Bemisia tabaci* in tomato, *S. lycopersicum*.**

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The sweetpotato whitefly (SPWF), *Bemisia tabaci* (Genn.) is a major tomato pest, causing serious losses by vectoring begomoviruses or by inducing irregular ripening. *Solanum habrochaites* accession LA1777 has been reported to be highly resistant to SPWF. Approximately 2400 F<sub>3</sub>BC<sub>2</sub>F<sub>2</sub> plants derived from LA1777 were genotyped using four putative resistance loci previously identified on chromosomes 9, 10 and 11. The same plants along with controls were bioassayed for adult SPFW per leaf in choice experiments conducted in growth chambers. On the basis of high or low numbers of SPFW 500 plants were selected and these plants were re-evaluated using the choice assay prior to subjection to a no-choice bioassay using SPFW in clip cages. Based on results of the no-choice assay, plants were partitioned into five groups; complete resistance, high resistance, moderate resistance, low resistance and susceptibility. A clear picture did not emerge from genotyping work since no genotype was uniformly resistant, and analysis of distal flanking markers indicated crossovers were absent; apparently at least one unidentified locus is important for resistance. Of 135 plants selected by the choice assay for low numbers of SPFW, no-choice results confirmed that 60 were highly resistant and 7 were completely resistant. Overall, the choice bioassay had significant positive and negative correlations with the no-choice measurements of egg number and adult mortality, respectively. Type IV trichomes and globular shaped type VI trichomes were evaluated using a subjective scale, and both had highly significant correlations with resistance. Chemicals associated with resistance were identified using gas chromatography-mass spectrometry (GC/MS). The most important compounds for resistance were the sesquiterpenes gemacrene B, alpha-zingiberene and beta-farnesene, both singly and in synergistic combinations with each other or with other sesquiterpene compounds.

**Fresh market tomato breeding: visions or folly.**

J. W. Scott, IFAS, University of Florida, Gulf Coast Research & Education Center, 14625 CR 672, Wimauma, Florida, 33598.

I have been involved in fresh market tomato breeding for over 35 years and have seen many changes and a lot of exciting developments. However, in this presentation I will provide some insights that are meant to provide food for thought as to what it is that tomato breeders in general do. My major theme is that we are all pawns in our industry and are basically told what to do with little thought as to if it makes any sense in the long run. The people who call the shots are generally business people and lawyers who may not always have good ideas. Is true creativity encouraged, recognized or tolerated in either the public or private sector? In my opinion the answer is “No”, at least not before the fact. One reason for this is that creative ideas often don’t meet with market success. Paradigm-shifts in breeding do occur occasionally, but I maintain that this is despite administrative or big business mindsets, not because of them. I will illustrate with the development of shrunken-2 sweet corn, small watermelons, and parthenocarpic pickling cucumbers before presenting information on what is happening with the Tasti-Lee™ tomato variety. Once I’ve irritated everyone in some way or another (not really my goal), information will be presented on a few of our current breeding efforts including preliminary work on graywall resistance and the genetic control of non-blighting foliage.

## **Fine mapping of the *Tomato Yellow Leaf Curl Virus* Resistance Gene *Ty-2* on Chromosome 11 of Tomato**

Xiaohui Yang<sup>1,2</sup>, Jay Scott<sup>1</sup>, Sam Hutton<sup>1</sup>, and Yongchen Du<sup>2</sup>

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Tomato yellow leaf curl virus (TYLCV) is a *Begomovirus* of the family Geminiviradae, transmitted by adult silverleaf whiteflies and has caused serious losses to tomato production in tropical and subtropical regions of the world. In recent years, breeding programs have been based mainly on the transfer of resistance genes from wild tomato species into the cultivated tomato. *Ty-2* is a single dominant gene that originated from *Solanum habrochaites* f. *glabratum* accession 'B6013' and was previously mapped to a 19 cM region on the long arm of chromosome 11, delimited by molecular markers TG36 and TG393. Additional mapping localized the *Ty-2* gene to a marker interval of 8.0 cM between TG36 and TG26 and then in 2007, the *Ty-2* gene was further delimited to a 6.5 cM interval between C2\_At1g07960 and T0302. In this research, approximately 11,500 plants were genotyped with flanking markers C2\_At1g07960 and T0302 and approximately 160 recombination events were identified between these molecular markers. Lines homozygous for the recombinations were inoculated with whiteflies viruliferous for TYLCV for two weeks, and transplanted to the field or greenhouse to evaluate disease severity. In addition, recombinants were genotyped with additional molecular markers developed from the tomato public genomic sequence within the ~6.5 cM target region. Results further delimited the *Ty-2* gene to a region between molecular markers C2\_At1g07960 and Ty2M1, an interval of approximately 260,000 bases on a single scaffold of the tomato assembly. No recombination events occurred in an interval of about 82,165bp, which indicated the existence of suppression. To identify candidate genes we plan to generate sequence data for the resistant genotype specific to the *Ty-2* region by enrichment technology and a Next-Generation Sequencing (NGS) method. This will be compared to the susceptible sequence already available.

## Discussion Topics

### *Gemini Virus Resistance Worldwide*

Discussion will center around the deployment of Gemini virus resistance genes worldwide.

- Which genes are being used against which GVs; Ty1, Ty2, Ty3, Ty4, Ty5, other new genes.
- How effective are these genes in the homozygous/heterozygous state and /or in combinations.
- Are there noticeable differences in resistance between the different alleles at the major loci, ie Ty1 from LA 1969 vs LA2779, Ty3-Ty3A-Ty3B.
- Which markers are being used effectively to locate the major genes. Has there been any recombination which renders these markers ineffective.
- Are new, more effective genes in the pipeline from new or old sources of resistance.
- Is there any evidence that the GVs are developing resistance to any of the available genes.
- Do we still see linkage-drag effects.
- Does GV resistance give any protection against irregular ripening.
- Is there any evidence that other viruses such as TIC, TOC, Torrado render current GV resistance genes ineffective.

### *Using DNA Markers in a Real World Tomato Breeding Program*

- How effective are markers in current breeding programs.
- Dealing with problems such as preferential amplification, fragment weight differences, background effects, base-pair effects, phantom bands.
- Dealing with marker-trait recombination.
- Cost saving methods - bulking, sampling.
- Use of seed versus plant tissue.
- Will SNPs solve all marker problems.