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Editor: Joyce Van Eck

SOL Newsletter

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Community News

There is still time to register……..

The 5th Solanaceae Genome Workshop will be held in Cologne, Germany from October 12 – 16, 2008. The preliminary program includes sessions on the following topics: Genome Sequencing & Bioinformatics, Abiotic Interactions, Biotic Interactions, Plant Development, Biodiversity and Evolution, and Applied Omics. There will also be satellite sessions for tomato, potato, pepper, tobacco, and coffee. In addition to the scientific program, there are a number of social activities planned, which include tours of the Cologne Cathedral, the Chocolate Museum, Max-Planck-Institute for Plant Breeding Research, and several other sites of interest. For additional information, visit the website at http://www.sol2008.org.

Hairy Vetch Mulch Activates Genes for Phytonutrients in Tomatoes

Adapted from a USDA-ARS press release written by Don Comis

Hairy vetch

Hairy vetch mulch activates some of the same metabolic pathways and genes in regular tomato plants as are activated in biotech tomatoes by the insertion of the *ySAMdc* gene, which makes tomato plants more vigorous, tasty and nutritious.

In collaborative work with Purdue University's Avtar Handa and the Italian National Research Agency's Annalaura Segre, the Agricultural Research Service's (ARS) Autar K. Mattoo made this finding after growing transgenic and non-transgenic tomato lines in both black plastic and hairy vetch mulch. Mattoo is a plant physiologist with the ARS Sustainable Agricultural Systems Laboratory at Beltsville, MD.

The transformed gene creates higher levels of polyamines, organic nitrogen compounds that make tomato plants more vigorous, tasty, and nutritious.

Findings indicate that polyamines might act as signaling molecules and steer metabolic pathways so fruits produce more phytonutrients.

Mattoo found that tomatoes reacted to the extra polyamines produced by the new gene the same way as to the yet-to-be-determined compounds/signals from hairy vetch. He saw significant buildup of amino acids and choline, an essential micronutrient for brain development, as well as other nutrients/antioxidants in both transgenic and non-transgenic plants grown in hairy vetch.

The study's results testify to the power of organic legume cover crops or mulches like hairy vetch. And, when transgenic tomatoes engineered to accumulate polyamines in the fruit are planted in hairy vetch, there is a synergy that causes these fruits to have even more nutrients than the non-transgenic fruits.

These findings were published in The Journal of Experimental Botany (see the Announcements section of this newsletter for details on the reference).

ARS is the U.S. Department of Agriculture's chief scientific research agency.

Contact Autar K. Mattoo at the USDA-ARS Sustainable Agricultural Systems Laboratory, 10300 Baltimore Avenue, Bldg. 001 BARC-WEST, Beltsville, MD 20705-2350; phone: (301) 504-6622, fax (301) 504-6491, e-mail autar.mattoo@ars.usda.gov.

Potato Web Sites

Thought I would share some fun and interesting web sites for potato-related information that people have shared with me.

The Potato Museum Blog: Potato Heads Talking:
http://foodmuseum.typepad.com/potato_museum_blog

Mr. Potato Head: http://en.wikipedia.org/wiki/Mr._Potato_Head

The Potato Joke Book: http://jaybooks.com

Potato Recipes: http://bigspud.com/

Potato Movie: http://www.youtube.com/watch?v=6uLUVI3Y0q0

Mr. and Mrs. Potato Head

Taxonomy of Wild Tomatoes and their Relatives (*Solanum* sect. *Lycopersicoides*, sect. *Juglandifolia*, sect. *Lycopersicon*; *Solanaceae*)

By: Iris E. Peralta, David M. Spooner, and Sandra Knapp

Systematic Botany Monographs, Vol 84

The American Society of Plant Taxonomists

Abstract. *Solanum* section *Lycopersicon* (Solanaceae) includes the cultivated tomato (*S. lycopersicum*) and 12 additional wild relatives, endemic to western South America from Ecuador to northern Bolivia and Chile, and with two endemic species in the Galápagos Islands; weedy escaped forms of *S. lycopersicum* are distributed worldwide. Two species in *Solanum* section *Juglandifolia*, distributed in Colombia, Ecuador, and Peru, are sister to section *Lycopersicon*, and two species of *Solanum* section *Lycopersicoides*, distributed in southern Peru and northern Chile, are sister to sections *Lycopersicon* and *Juglandifolia*. The delimitation and relationships of wild tomatoes have differed widely depending upon whether morphological or biological species concepts are considered more important. Our monograph summarizes recent morphological and molecular studies of section *Lycopersicon*, section *Juglandifolia*, and section *Lycopersicoides*, and utilizes data from herbarium specimens and observations of germplasm accessions of all species grown in gardens. We recognize four species from the previously polymorphic *S. peruvianum* sensu lato: *S. arcanum, S. corneliomulleri, S. huaylasense*, and *S. peruvianum* sensu stricto, and recognize section *Lycopersicoides* at sectional level for the first time. Full descriptions and synonymies (including designations of lectotypes), illustrations, distribution maps, and an extensive list of localities are provided for all of tomato and outgroup species.

For ordering information, go to: http://herbarium.lsa.umich.edu/SBMweb/index.html

XVIth EUCARPIA Meeting/Working Group Tomato

Provided by Sjaak van Heusden
Chair of the Organizing Committee

EUCARPIA/Working Group Tomato Participants

A Eucarpia Meeting of the Working Group Tomato is organized every three to five years. The XVI edition was successfully organized in Wageningen, The Netherlands, from May 12 – 15, 2008. A total of 120 scientists attended the meeting; forty-five from the Netherlands and the others mainly from Europe, but also some from the USA and India. Not only do people like tomatoes, but also so do viruses (old and new ones), bacteria, fungi and insects, and what to do about that was the main issue in several of the meeting sessions. In other sessions, the emphasis was on breeding tomatoes in the era of genomics with special attention to metabolomics. Health promoting components in tomato and other vegetables were discussed and it is clear now that it is healthier to eat a tomato instead of a candy bar. Many other claims are more difficult to prove. The meeting showed, according to Dr. Henrik Czosneck, that a tomato is much more than a vegetable with all kinds of colors and chemicals, it has monetary value, a piece of polymorphic DNA, stock shares, and is a potential gold mine with a nutritional spreadsheet; in a nutshell a focus to make people happy with their lives. The social program with

visits to modern greenhouses and the Rotterdam Harbor was topped off with a dinner and party to celebrate the official opening of the new complex of De Ruiter Seeds. A digital version of the abstract book can be obtained by sending an e-mail to Sjaak van Heusden (sjaak.vanheusden@wur.nl).

Tomato Sequencing Updates

Chromosomes 1, 10 (US)

Contact: Joyce Van Eck (jv27@cornell.edu)

In total, the Stack laboratory has made 106 unique localizations of BACs to tomato chromosomes. The locations of these BACs are illustrated on a pachytene chromosome idiogram and described in terms of their location as a percentage of chromosome arms on SGN (http://www.sgn.cornell.edu/cview/map.pl?map_id=13). This total number represents nineteen BACs on chromosome 1 (USA), five on chromosome 2 (Korea), eleven on chromosome 3 (China), fifteen on chromosome 4 (UK), nine on chromosome 5, seven on chromosome 6 (The Netherlands), ten on chromosome 7 (France), four on chromosome 8 (Japan), eleven on chromosome 9 (Spain), two on chromosome 10 (USA), nine on chromosome 11 (China), and four on chromosome 12 (Italy). Within this group are BACs that can be used as markers for all tomato chromosome arms.

Lukas Mueller and the SGN group have completed their move to The Boyce Thompson Institute (BTI; www.bti.cornell.edu). The move was a relatively easy one with minimal impact on the SGN group and the SGN site because of the physical proximity of BTI on the Cornell campus.

Chromosome 2 (Korea)

Contact: Sunghwan Jo (shjo@kribb.re.kr)

As of today, 171 BAC clones (18,991,304 bp) have been completed as HTGS phase 3. Four additional BACs are currently in the sequencing pipeline. Of this figure, 14,447,062 bp are unique. We generated thirty contigs that constitute 12,846,116 bp and eleven singletons that constitute 1,600,946 bp. The longest contig constitutes 1,143 kb long and contains fourteen BACs. Gaps between contigs might be short in that most gaps are 1 - 3cM apart on the Tomato-EXPEN 2000 map. To fill out the chromosome gaps, we are screening three libraries by overgo hybridization with contig ends where no candidates for extending have been found by BES BLAST. Dani Zamir provided several BACs, which allowed us new seed points in a large space of chr 2.

Chromosome 3 (China)

Contact: Chuanyou Li (cyli@genetics.ac.cn)

Update pending.

Chromosome 4 (UK)

Contact: Karen McLaren (kb1@sanger.ac.uk) or Helen Beasley (hr1@sanger.ac.uk)

13,270,272 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr 4 as of July 1, 2008. Of this figure, 12,643,692 bp are unique. The sequence has been produced from 125 BACS originating from the LE_HBa, SL_MboI, and SL_EcoRI libraries. We currently finish all BACS to HTGS phase 3 and 96 BACs that correspond to 9,483,205 bp of sequence have been deposited in the public databases at EMBL/GenBank/DDBJ as phase 3. All other chr 4 BACs with EMBL/GenBank/DDBJ accessions are currently active in our sequencing pipeline at HTGS phases 0 to 2.

Additional chr4 verification for a number of BACs selected for our sequencing pipeline is ongoing and being investigated using the IL mapping technique.

The progress of chr 4 can be viewed through the development of the TPF and AGP files that we upload to SGN. The TPF indicates the

expected relative positions of the BACs along the chromosome and the AGP provides assembly information of the finished sequences.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have been able to confirm the positions of seventy-three BACs on chr 5. Sequencing is in progress on all these BACs, out of which thirty-nine BACs are in phase III, twenty-one BACs are in phase II and ten BACs are in phase I. The remaining three BACs are in the early phase of sequencing or library preparation. A search is on to find new extension BACs by performing overgo hybridizations on the filters available for the three tomato libraries and PCR screening on the 3-D DNA pools obtained from France. In addition, new nucleation points are also being identified by development of CAPS markers for the 200 BACs assigned to India for mapping purposes. We have been able to map nearly 40% of the BACs from a sub-set of 120 BACs so far.

Chromosome 6 (The Netherlands)

Contact: Sander Peters (sander.peters@wur.nl)

Update pending.

Chromosome 7 (France)

Contact: Mondher Bouzayen (bouzayen@ensat.fr)

To date, 149 BACs have been selected and validated on chr 7 distributed in eighty-seven seed BACs and sixty-two overlapping BACs. Seventy-four BACs have been sequenced to phase 2 or 3 and seventy-five are in phase 0 or 1. In total, 15.6 Mb of sequence were generated of which 13.6 Mb are non-redundant (49% of the total estimated euchromatin of chr 7). Overall, we submitted 100 BAC sequences to Genbank and SGN. The BACs are organized in thirty-four contigs on chr 7. Our largest contig contains thirteen BAC members and covers 1137kb. This mega-contig is situated in the distal portion of the long arm of chr 7 and includes the Tomato-EXPEN 2000 genetic markers from cM 80 to 110.

In terms of new resources generated to support the tomato genome sequencing project, our group built in collaboration with the CNRGV (INRA Toulouse) 3D-DNA pools from the HindIII and MboI libraries. These resources have proven to be very efficient and screening these 3D pools allowed the selection of twenty new seed BACs using the Tomato-EXPEN 2000 genetic marker sequences. The screening is now performed using the EST markers recently released by Kazusa DNA Research Institute. It is important to mention that many other partners of the consortium are now using these resources since we have sent them upon request to Spain, Italy, USA, India, UK and Israel. We also started to use intensively the fosmid library and the fosmid end sequences.

Chromosome 8 (Japan)

Contact: Shusei Sato (ssato@kazusa.or.jp)

As of July 14, 2008, 140 BAC clones have been completed as Phase 3 that produced a non-redundant length of 13,827,446 bp, and an additional twenty-nine BAC clones are in the sequencing pipeline.

We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached 2.6 million files generating 1.8 Gb of total length. These shotgun sequences have been assembled into 193,330 contigs covering approximately 470 Mbp regions of the genome. In order to increase the genome regions covered by the SBM assembly, we have started sequencing the second set of the BAC mixture from this month.

Chromosome 9 (Spain)

Contact: Antonio Granell (agranell@ibmcp.upv.es)

We have completed sixty-six BACs, of which fifty-seven can be obtained from SGN and the remaining nine will be available as soon as we get access numbers from GenBank. Out of those sixty-six BACs, thirty-four are seed BACs and thirty-two are extension clones.

Currently, we have fourteen clones in progress, including three fosmids. In addition, we have eleven clones in the verification step, nine of which are fosmids. This means that the fosmid clones are currently our best bet for extending especially from the dead ends

generated and that up to now had found no extension BAC clones. Despite the smaller size generated and that up to now we have found none of the fosmid clones as compared to BAC clones, we decided to include them in those cases where no BAC was possible with the hope that they will serve as bridges to identify BACs further extending from these fosmids. When we have the sequence from these fosmids we will see the usefulness of including fosmids in the sequencing of dead ends.

We are currently verifying seventeen seed BACs: twelve derived from the Syngenta FPC and five from the BAC mapping in the IL population conducted by Italy. Syngenta BACs will be against the ILs for chr 9 location. Our previous experience with Syngenta markers is that when they failed to map in chr 9 using polymorphism detection in the ILs, FISH finally found them in other chromosomes. That is when polymorphism detection in the ILs failed and most likely the BAC corresponds to another chromosome.

We are also identifying BACs corresponding to new chr 9 markers (Kazusa) by doing a PCR screen of the different BAC pools obtained either from Kazusa or CNRGV.

Finally, we are completing the finishing of all sequenced BACs to have them in HTGS2 2 and 3, closing gaps and putting contigs in order. For this, the unigene database recently published has been very useful at least for ordering contigs. We plan to submit this update in finishing in the next few weeks.

Chromosome 11 (China)

Contact: Zhonghua Zhang (zhangzhonghua.cass@gmail.com) or Sanwen Huang (huangsanwen@cass.net.cn)

Update pending.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

Currently, eighty-six BAC clones belonging to chr 12 are in various steps of the sequencing process. Of these, nineteen are in HTGS3, eleven are in HTGS2 and twenty-one HTGS2 have been submitted to GenBank/SGN. Three BACs were shown by genetic (IL mapping) and cytogenetic (FISH) methodologies actually to not map on chr 12 and one more BAC was shown to be chimeric. They were thus annotated and uploaded as C00 on the SGN website. All the sequenced seed BACs have been sent for FISH to the de Jong lab in Wageningen to build a genetic-cytogenetic comparison map. De novo mapping data for fifty-six BACs using the IL strategy have been uploaded on SGN.

Using this strategy it was also possible to verify that ten BACs out of thirty-three previously mapped on chr 12 by Syngenta were shown to map on other chromosomes. Moreover, we began to use 454 technologies for sequencing BAC clones. Out of twenty-four BAC clones processed, three were already sequenced using ABI-Sanger sequencing technology. Comparing the results of all gene-containing regions, they were covered efficiently and at high quality with 454 sequencing, whereas repetitive sequences were more problematic with 454 sequencing than with ABI-Sanger sequencing. Preliminary analysis of nine BACs provided evidence of high coverage of the BAC clones with 454 sequencing, resulting in almost complete assembly of all genic sequences at HTGS2 stage. To obtain highly advanced working draft sequences for the BACs, we are developing a strategy to assemble large parts of the BAC sequences by combining comparative genomics, detailed repeat analysis and use of reads from 454 sequencing.

What's New on SGN?

SGN has recently spearheaded a new approach by developing community annotation tools to expand the curational capacity for the *Solanaceae*. These tools effectively allow some curation to be performed by qualified researchers from the community thereby complementing in-house curation efforts, and resulting in more detailed and up-to-date annotations.

All community annotations are credited to the submitters, who also have full edit privileges. Currently, the SGN database has more than fifty 'locus editors' in charge of 112 loci, and more than 300 community-submitted annotations, descriptors, sequences, publications, images, gene-gene and gene-phenotype associations.

To start annotating your favorite genes and phenotypes you will need an SGN submitter account, which can be obtained by contacting SGN (http://www.sgn.cornell.edu/tools/contact.pl). Alternatively, you can find your gene (http://www.sgn.cornell.edu/search/direct_search.pl?search=loci) and while on the gene page, click on the 'Request editor privileges' link. Shortly after, you will receive an approval email from SGN.

Read more about our on-line annotation tools at http://www.sgn.cornell.edu/phenome.

Large-scale data can be submitted directly to SGN by contacting sgn-feedback@sgn.cornell.edu, and we will guide you on how to organize your data in files ready for online publishing.

While community-based annotation is not the major resource for maintaining the database, it provides very valuable and high quality information directly from authors and experts in their field. It creates an interactive social network for the research community to share biological knowledge.

Announcements

Publications

Neelam A, Cassol T, Mehta RA, Abdul-Baki AA, Sobolev AP, Goyal RK, Abbott J, Segre AL, Handa AK, Mattoo AK. 2008. A field-grown transgenic tomato line expressing higher levels of polyamines reveals legume cover crop mulch-specific perturbations in fruit phenotype at the levels of metabolite profiles, gene expression, and agronomic characteristics. J Exp Bot 59(9):2337-2346.

Rairdan GJ, Collier SM, Sacco MA, Baldwin TT, Boettrich T, Moffett P. 2008. The coiled-coil and nucleotide binding domains of the Potato Rx disease resistance protein function in pathogen recognition and signaling. Plant Cell 20(3):739-751.

EU SOL Newsletter, Number 2, May 2008
http://www.eu-sol.net/public/news/newsletters/EU%20SOL%20Newsletter%2002.pdf

A Passion for Tomatoes
http://www.smithsonianmag.com/science-nature/passion-for-tomatoes.html

Conferences

Plant and Animal Genome XVII Conference
January 10 - 14, 2009
Town & Country Convention Center
San Diego, California
http://www.intl-pag.org

Patates Fournou: Roasted Lemon Garlic Potatoes
In Greek: πατάτες φούρνου, pronounced pah-TAH-tes FOOR-

http://greekfood.about.com/od/greeksidedishes/r/patatesfournou.htm

Simpler or more complex variations of this recipe are served in homes all over Greece.

Prep Time: 20 minutes
Cook Time: 1 hour, 30 minutes
Yield: 5-6 servings

5 large potatoes (baking size)
3/4 cup of olive oil
2 1/2 cups of water
juice of 1 lemon
2-3 cloves of garlic, minced
3/4 teaspoon of dried Greek oregano (rigani)
2 teaspoons of salt
freshly ground pepper
juice of 1/2 orange

Preheat oven to 480°F (250°C).

Peel the potatoes, cut in half lengthwise, and in half lengthwise again, into quarters. Rinse well and shake to remove excess water. Spread the potatoes out in an 11 X 14 inch (or equivalent) roasting pan. Toss the potatoes with the salt, pepper, oregano, garlic and olive oil (using hands works best), and sprinkle with lemon juice. Add the water to the pan (do not pour over the potatoes). Put on lowest rack in the oven, and roast at 480°F (250°C) until the water boils. Then reduce heat to 355°F (180°C) and cook for 1 hour. Drizzle the orange juice over the potatoes, and continue to cook another 30 minutes or until potatoes are soft and toasty looking.

Note: If you cut the potatoes into smaller pieces, reduce cooking time. Check at 1 hour for doneness.