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THE SOL NEWSLETTER

IN THIS ISSUE.....

Community News

SolCAP: Translating *Solanaceae* Sequence Diversity and Trait Variation into Applied Outcomes through Integrative Research, Education, and Extension

by David Douches

(Source: Kelly Zarka SolCAP)

Co-Directors: David S. Douches, C. Robin Buell, David M. Francis, Allen Van Deynze, Walter S. De Jong, Lukas Mueller, Alexandra Stone. Project Assistant: Kelly A. Zarka

The USDA-CSREES National Research Initiative (NRI) awarded a Coordinated Agricultural Project (CAP) for the improvement of *Solanaceae* crops, which began in October 2008 and will continue through September 2012, if awarded a renewal in 2009. The project is called the *Solanaceae* Coordinated Agricultural Project (SolCAP; see http://solcap.msu.edu) and it focuses on the two most important vegetable crops in the *Solanaceae*: potato and tomato. The project vision is to move translational genomics beyond commodity boundaries toward an emphasis on taxonomic groups and DNA sequence homology, leveraging knowledge and resources across species. Sequencing efforts in *Solanaceae* have lead to extensive expressed EST resources and genome sequence is emerging for both potato and tomato. Ultimately, understanding variation at the DNA sequence level is useful in crop improvement only to the extent that it helps us understand and/or predict phenotypic variation for agriculturally important traits.

The primary research objective of the SolCAP project is to provide the infrastructure to link allelic variation in genes to valuable traits in cultivated germplasm of potato and tomato. Focusing on elite breeding material will increase the probability that these solanaceous crops will benefit from genotype-based selection. Discovery of new polymorphisms for elite North American tomato and potato breeding populations is based on both *de-novo* sequencing and bioinformatic investigation of existing data sets. Normalized libraries for sequencing have been constructed from multiple tissues including leaves, tubers, flowers and callus for potato. For tomato, they are being constructed from three stages of fruit development, callus, leaves, roots, and flowers. To maximize SNP discovery, we have optimized bioinformatic pipelines to identify putative SNPs (eSNPs) within existing tomato and potato Expressed Sequence Tag (EST) data sets and emerging genome sequence. Pipelines have been developed to assemble Sanger-derived ESTs on a single accession basis and then to identify high confidence eSNPs between genomic and EST contigs as well as between EST contigs of different accessions. We are also developing bioinformatic pipelines to identify eSNPs between genomic or Sanger-derived EST contigs and short read transcript data such as those being generated in this project. To link these bioinformatic predictions with experimental data, we are validating these predicted SNPs to benchmark our pipeline. Illumina genotyping chips are planned for 1536 and 7600 loci for tomato and potato, respectively, beginning in 2009. We will develop a database of integrated and mapped markers and genotypes for at least 480 accessions for each crop by the end of 2009 and then in an effort to increase breeder engagement with genomics, we will provide opportunities to genotype up to 16 populations and validate marker linkages to major QTL among the research community.

The extension and education components of SolCAP will integrate training in genomics and plant breeding with curriculum aimed at students and existing breeders seeking to make better use of sequence data for crop improvement. This year SolCAP will host workshops at both the Tomato Breeders Round Table meeting on June 28 - July 1, 2009 in Sacramento, CA and at the

Potato Association of America (PAA) 93rd Annual Meeting, August 9 - 13, 2009 in Fredericton, New Brunswick, Canada. A survey was conducted among the potato and tomato communities to help target the content for the workshops. These surveys will continue to be conducted throughout the life of the SolCAP project to assist in bringing useful and informative content to future workshops.

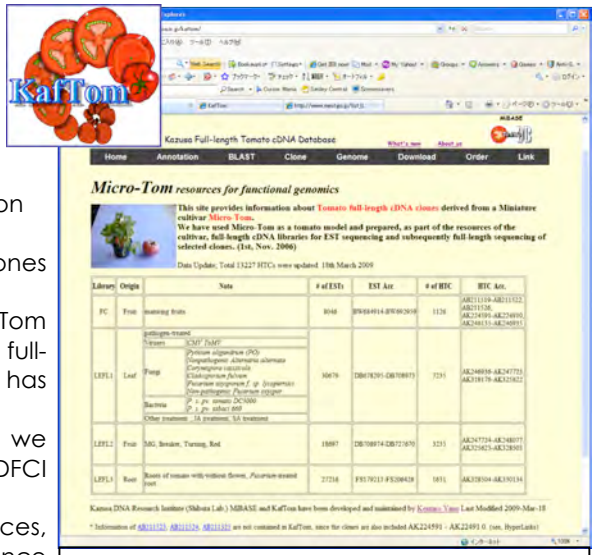
SolCAP also plans on creating integrated, breeder-focused resources for genotypic and phenotypic analysis by leveraging existing databases and resources at SOL Genomics Network (SGN) located on-line at http://sgn.cornell.edu/index.pl. We plan on creating integrated genomic and phenotypic databases, the breeders toolbox, that serves the entire Solanaceae breeding and genetics community through SGN.

SolCAP led an eXtension.org workshop for plant translational genomics CAPs at the 2009 Plant and Animal Genome meetings in San Diego, CA. We reached a consensus to name, create, and initiate a Plant Breeding and Genomics Community of Practice (PBGCoP) and are in the process of submitting an application to eXtension to formalize the CoP. The purpose of the CoP is to develop information for practicing breeders, their staff, and allied professionals in order to improve the use of emerging sequence data in applied programs. To foster interaction across plant translational genomics CAPs we have invited other projects into the CoP, created a Plant Breeding and Genomics workspace to leverage Web 2.0 interactive functions, and we are developing content for publication to eXtension.org. The USDA Extension Service is developing eXtension.org as a major communication link from the Land Grant University system to the public.

The *Solanaceae* breeding and genetics community is welcome to visit our SolCAP website on-line at http://solcap.msu.edu/.

Tomato Full-length cDNA Update

Provided by Koh Aoki
Kazusa DNA Research Institute



KaFTom top page and new logo

We updated the information of Micro-Tom full-length cDNA sequences on March 19th, 2009.

(1) Information on 13,227 full-length sequences is now available. cDNA clones (84,638 clones) are also available.
(2) Sequences and annotations are provided through our database KaFTom (http://www.pgb.kazusa.or.jp/kaftom/). KaFTom is now specialized to full-length cDNA information. The information on 5'-end sequences has moved to MiBASE (http://www.kazusa.or.jp/jsol/microtom/).
(3) In addition to similarity-search results against TAIR, RAP-DB, and nr, we added similarity-search results against UniProt, SGN unigenes, and DFCI tomato gene index.
(4) We also added the results of similarity search against SGN BAC sequences, including an alignment of a full-length sequence versus BAC sequence and exon/intron prediction.

For questions and comments on the database, please contact Kentaro Yano (Meiji University) kyano@isc.meiji.ac.jp. For questions and comments on the full-length cDNA clones, please contact Koh Aoki (Kazusa DNA Research Institute) kaoki@kazusa.or.jp.

This work was based on a collaboration between Kazusa DNA Research Institute and the Yano lab in Meiji University. This work was supported by the Genome Program of the National BioResource Project tomato (NBRP tomato), MEXT, Japan http://tomato.nbrp.jp/indexEn.html.

We look forward to your visit to KaFTom website and clone requests.

3rd National Plant Breeding Workshop

Contributed by Shelley H. Jansky

The 3rd National Plant Breeding Workshop (sponsored by SCC-080, the Plant Breeding Coordinating Committee) will be held on August 3 - 5, 2009, in Madison, Wisconsin. The Plant Breeding Coordinating Committee serves as a forum regarding issues and opportunities of national and global importance to the public and private sectors of the U.S. national plant breeding effort.

The workshop has three goals: 1) to carry out discussions on strategies to shape the future of plant breeding, 2) to expose participants to state of the art plant breeding research through invited speakers, and 3) to encourage the exchange of knowledge through poster presentations by participants. Confirmed speakers for the meeting include Mike Cassler (optimizing experiment design), Jim Bradeen (tertiary gene pool of potato), Charlie Brummer (sustainability issues in agriculture), Paul Gepts (bean domestication), Jim Holland (association mapping), and Jeff Doyle (soybean genomics).

All plant breeders are encouraged to attend - student and professional, public sector and industry, U.S. and abroad. An optional tour of public and private breeding facilities is also planned (meeting registration: $235 until July 24; on-site $300). For more information contact Shelley Jansky shjansky@wisc.edu or register online at: http://www.peopleware.net/2723/index.cfm?siteID=358&eventDisp=0-43-01. Or see the meeting web page at http://cuke.hort.ncsu.edu/gpb/meetings/pbccmeeting2009.html.

Fifth EPSO Conference

by Isabelle Caugant

The next EPSO Conference 'Plants for Life' will take place from April 18 - 22, 2010 in Lapland, Finland.

The program is now available online and looks once again very attractive as it addresses many of the challenges faced by the plant science community. As usual during EPSO Conferences, plant scientists and policy-makers from Europe and around the world will present and discuss cutting-edge science, plant science policy and societal issues. Several sessions will be of specific interest for scientists working on *Solanaceae* species.

The science policy session will provide an overview of the current policy issues at both European and international levels. During the science and society session, the panel discussion will focus on food security and safety. Speakers and members of the audience will discuss how to provide safe and healthy food to a growing world population without compromising economic sustainability and environmental preservation.

As for the scientific sessions, they will cover the latest scientific results and challenges to achieve sustainability and quality, and to strengthen ecosystem functioning. The sessions on sustainability will include presentations on crop genomes to understand the basis of sustainable traits, with a focus on comparative genomics, as well as talks on novel breeding tools and strategies. The sessions on plant quality will explore the latest research achievements on plant architecture, photosynthesis for solar fuels, biotechnology and genomics of trees, plant-made pharmaceuticals, and plant nutritional value. The sessions on ecosystem functioning will provide insights on how to improve plant health, how climate change impacts plant production, and how landscape genomics, population genetics and conservation research can contribute to maintaining and restoring biodiversity.

The registration will open on September 1, 2009. A reduced registration fee applies to EPSO personal members.

The conference is organized by Karin Metzlaff, EPSO Executive Director, and the local conference organizer is Kirsi-Marja Oksman-Caldentey, Head of Medical Biotechnology Department at VTT Technical Research Centre.

Please send an email to Katrien Molders [Katrien.Molders@epsomail.org], EPSO Conference Officer, if you wish to receive updates about the conference.

The EPSO team is looking forward to seeing you in Lapland.

Conference website: www.epsoweb.org/catalog/conf2010.htm
Conference program: www.epsoweb.org/catalog/conf2010/5CF_Programme.pdf

Solanaceae Highlight Article

Georg Bitter's Bitter Tomatoes: An Evasive Group of Invasive Weeds

Contributed by John Samuels

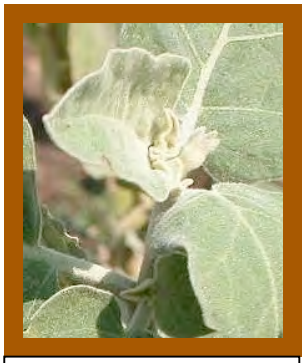


Figure 1. Detail of hoary covering of hairs typical of bitter tomatoes (photo: S. Heinrichs, OIRED, Virginia Tech, USA).

Hairy, prickly, and tricky

Since their description in the early twentieth century, the group of spiny solanums known in Africa as the bitter tomatoes has caused great taxonomic bewilderment. These plants were last examined in detail by the aptly named Georg Bitter, working in Germany (Bitter, 1923). They include *Solanum incanum* L. (the "hoary" bitter tomato), *S.campylacanthum* A. Rich. (the "curvy-spined" bitter tomato) and several others. Of these species, *S. incanum* is the best known and, on this basis, the various species are collectively referred to as *S. incanum sensu lato* (Samuels, 1996). In turn, they are classified as part of Bitter's series *Incaniformia*, named for their dense covering of hairs (Fig. 1).

As with many other spiny solanums, the inherently variable nature of the bitter tomatoes has caused many difficulties with identification. As a consequence, they have often been confused with several cultivated species, including *S. melongena* L. (the brinjal eggplant) and *S. aethiopicum* L. (the scarlet eggplant). However, many years since they were first studied by Bitter we now have a much better understanding of their taxonomic relationship with allied crop species.

Successful, weedy and pretty

The various species are to be found across much of eastern and southern Africa, and parts of western Africa and western Asia. Typically, they are ruderal shrubs and may successfully colonize roadsides or recently disturbed land.

They may become invasive weeds, sometimes appearing in cultivated fields, spreading by suckers. Most species reach around 1.5 meters in height and often have a covering of dense prickles and wavy-edged, hairy leaves (Fig. 2). Several attractive, violet flowers are borne in small groups and are a favorite of pollinating bees (Fig. 3).

Figure 2. *S. incanum* from Ethiopia, showing leaf and armature characteristics (photo: Radboud University Botanical and Experimental Garden, Netherlands).

Deadly nightshade with traditional benefits

The unripe fruits are highly astringent and have probably been used for thousands of years for tanning hides; this may have contributed to the spread of *S. incanum* from north-east Africa to the Middle East and perhaps further eastwards towards Indo-China (Lester & Hasan, 1991). As with other nightshades, they have a disagreeable, bitter taste and are poisonous when still green, with domestic ruminants being the most common victims.

Ripe fruits resemble small, yellow tomatoes (Fig.4) and have many uses in traditional medicine across much of Africa and western Asia. These range from the treatment of skin infections, fevers and epilepsy, to curing sexual infections and even snake bites! The leaves are used in several ways including poultices for dermatitis and as tobacco for the treatment of asthma.

Figure 3. *S. campylacanthum* from Zimbabwe showing typical flowers.

Weeds with value

High levels of steroidal alkaloids are found in all parts of *S. incanum* and its allies, and considerable interest in the potential for commercial steroid production has been generated (e.g. Eltayeb et al, 1997). Certain of these phytochemicals also appear to have useful anti-tumour properties (Kuo et al, 2000).

S. incanum is believed to be the wild ancestor of the brinjal eggplant, *S. melongena* (Lester & Hasan, 1991; Samuels, 1996) and, along with its close relatives, has been the subject of extensive plant breeding, taxonomic and genomic research. *S. melongena* is one of the most economically important crops in Asia, but is subject to frequent pest damage and microbial and fungal attack. Much research has therefore been devoted to genetic improvement relating to pest resistance.

Technology confirms our suspicions...finally

Our taxonomic understanding of the bitter tomato group and its relatives has developed alongside the increasingly sophisticated technology that has become available with time. Thus, around 30 years ago, we had to rely on comparative morphology and interfertility studies (e.g. Pearce, 1975). Nowadays, we have complex DNA techniques at our disposal, e.g. RFLP (Frary et al, 2003), AFLP (Furini & Wunder, 2004) and RAPD (Singh et al, 2006) analyses. In general, earlier findings have been confirmed by subsequent studies using more complex, up-to-date technology.

At the time of Georg Bitter, 86 years ago, the bitter tomatoes were believed to be an assemblage of over 25 species. This taxonomically evasive group of invasive weeds is now much better understood. As our knowledge and understanding of these plants have broadened, so has our species concept, and it now seems likely that they are a group of no more than just a handful of good species.

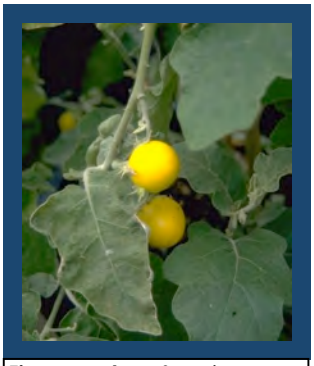


Figure 4. *S. incanum* showing ripening fruits (photo: Radboud University Botanical and Experimental Garden, Netherlands).

Contact information: John Samuels, Cornwall, UK, john.samuels@virgin.net

References

Bitter G. 1923. *Solana Africana* Part IV. *Repertorium Novarum Specierum Regni Vegetabilis.* **16**: 1-320.

Eltayeb EA, Al-Ansari AS, Roddick JG. 1997. Changes in the steroidal alkaloid solasodine during development of *Solanum nigrum* and *Solanum incanum*. *Phytochemistry* **46** (3): 489-494.

Frary A, Doganlar S, Daunay M-C, Tanksley SD. 2003. QTL analysis of morphological traits in eggplant and implications for conservation of gene function during evolution of solanaceous crops. *Theoretical and Applied Genetics* **107** (2): 359-370.

Furini F, Wunder J. 2004. Analysis of eggplant (*Solanum melongena*)-related germplasm: morphological and AFLP data contribute to phylogenetic interpretations and germplasm utilization. *Theoretical and Applied Genetics* **108**: 197-208.

Kuo K-W, Hsu S-H, Li Y-P, Lin W-L, Liu L-F, Chang L-C, Lin C-C, Lin C-N, Sheu H-M. 2000. Anticancer activity evaluation of the *Solanum* glycoalkaloid solamargine: triggering apoptosis in human hepatoma cells. *Biochemical Pharmacology* **60** (12): 1865-1873.

Lester RN, Hasan SMZ. 1991. Origin and domestication of the brinjal eggplant, *Solanum melongena* from *S. incanum* in Africa and Asia. In: Hawkes JG, Lester RN, Nee M, Estrada N, eds. *Solanaceae III: Taxonomy, Chemistry, Evolution.* Kew: Royal Botanic Gardens, Kew, 369-387.

Pearce KG. 1975. *Solanum melongena* L. and Related Species. Ph.D. Thesis, University of Birmingham, U.K.

Samuels BJ. 1996. *Solanum incanum sensu lato* (Solanaceae): Taxonomy, Phylogeny and Distribution. Ph.D Thesis, University of Birmingham, U.K.

Singh AK, Singh M, Singh AK, Singh R, Kumar S, Kalloo G. 2006. Genetic diversity within the genus *Solanum* (Solanaceae) as revealed by RAPD markers. *Current Science* **90** (5): 711-716.

Company Profile

by Myrna Q. Sevilla

Fresh market tomato specialists at BHNSeed develop hybrid tomato seed for the global fresh-market tomato industry. BHN varieties are known for their high yield, excellent fruit quality, and resistance characteristics. BHN tomato seed is processed and tested in Florida and marketed worldwide through seed distributors.

The BHNSeed tomato breeding program began in 1980 in Naples/Bonita Springs, Florida to improve yield, quality, and disease resistance for its parent company, Gargiulo, Inc., which is the largest fresh market tomato shipper in the U.S. The program has expanded to include varieties adapted to different climates of the world. In its current location in Immokalee, Florida, BHNSeed has over 50+ acres of greenhouse space and arable land devoted to tomato research.

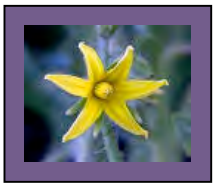
BHNSeed ventured into the international seed trade in the late 1980s and domestic seed sales in 1998. Today, BHNSeed is a seed market leader in various countries while continuing to expand in new markets.

BHNSeed's success is based on an extensive and focused breeding program with breeding stations located in Florida, California, Mexico, Chile, and Brazil. While superior hybrids are developed by intense selection in different environments with classical plant breeding techniques, molecular markers and molecular biology techniques are also utilized extensively. Field trials of new experimental hybrids are conducted by distributors domestically and internationally under different climate, cultural, and soil conditions. The most adapted hybrids are selected for trial and potential sales in their respective area.

BHNSeed offers both greenhouse and outdoor hybrids adapted to arid and humid climate conditions. The range of fruit type include globe, roma, and cherry with determinate or indeterminate growth habit. The varieties possess resistance/tolerance to several economically important fungal, bacterial, nematode, and viral diseases. BHNSeed was the first company to release a variety with resistance to tomato spotted wilt virus in 2004.

Research Director, Dr. Jim Augustine, is mindful of the future and the ever-changing needs of the volatile tomato industry. To this end BHNSeed recently joined a newly created venture called Ninsar Agrosciences along with two other international seed companies to meet current and future market needs through sustainable state-of-the- art plant biotechnology innovations.

To find out more about BHNSeed and Ninsar Agrosciences, please visit: www.bhnseed.com and www.ninsar.com.



Tomato Sequencing Updates

Chromosomes 1, 10 (US)

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

The US team is happy to announce that they have received funding from the National Science Foundation Plant Genome Research Program sufficient to complete sequencing of the euchromatin of chromosomes 1 and 10, contribute to the whole genome shotgun sequencing effort, create a new tomato physical map, maintain and expand the SGN database and provide resources to support the efforts of the broader international sequencing consortium which has and continues to do the bulk of tomato genome sequencing. We are very pleased and fortunate to welcome the world-renowned genome sequencing group of Dr. Bruce Roe at the University of Oklahoma (http://www.genome.ou.edu/) to our team. We look forward to rapidly expanding our efforts and contributions to the international effort.

The Stack lab at Colorado State University has now localized a total of 168 tomato BAC clones on tomato pachytene synaptonemal complex spreads using fluorescence in situ hybridization. They are distributed among the chromosomes as follows: 1 – 31; 2 – 16; 3 – 13; 4 – 16; 5 – 10; 6– 9; 7 – 13; 8 – 4; 9 – 18; 10 – 20; 11 – 13; 12 – 5. Four of these BAC clones are newly localized since our last report and are all on the long arm of chr2. The newly localized clones are: Le_HBa0064B17, Le_HBa0072B02, Le_HBa0257H21, SL_MboI0055O24.

Chromosome 2 (Korea)

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

To extend chr2 contigs, size and close the gaps, we have been focusing on finding new clones by two approaches.

First, additional BAC candidates were pooled and sequenced using 454 without IL-map validation. As a result, 12.3 Mb sequence was obtained from a pool of ninety-six fosmids and seventy-three BACs. Although many of them are redundant, we expect that the sequences will serve as a bridge for searching extension clones, which is underway.

Second, we found chr2 contigs showed high gene colinearity with the grape genome. After comparing gene content and gene order of neighboring tomato contigs in the grape genome, candidate genes of the gap region for searching tomato BACs or fosmid clones were selected. For example, the region of 46-63 cM of Tomato-EXPEN 2000 was the biggest gap of chr2 where we had difficulty finding marker-anchored BACs and extension clones. The region showed colinearity of genes with chr10 of the grape genome. We found approximately 150 genes and an additional four BACs as "seeds" by BES-BLAST using tomato unigenes. In addition, the syntenic block analysis aided in determining the gap size and contig order.

To date, 181 BAC clones (20,202,853 bp) whose positions were confirmed on chr2 have been sequenced. 167 BAC clones are completed as HTGS phase 3 and fourteen clones are completed as HTGS phase 1. Combining massive sequencing of candidate clones and synteny based cloneselection may help us to find additional clones for extending and filling the existing gaps.

Chromosome 3 (China)

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

Our effort is currently focused on sequencing eighty BACs, which were confirmed to be on chr3 by introgression line (IL) mapping. To date, forty-six BAC clones (4735.33-kb) were completed as HTGS phase 3 and the remaining were completed as HTGS phase 2 and HTGS phase 1. As for the finished BACs at stages I and II, the average length is 6586.45 and 107.97 kb. The success rate of the sequencing reaction is more than 90% and the average length of reads is about 1,000 bp. The reads coverage rate for each BAC is more than 10 fold. All the BACs assembled well. At the same time, we initiated an effort to sequence 100 BACs (all were confirmed by IL mapping) using the next-generation sequencing platform the Illumina Genome Analyzer after making a label to each BAC. Forty BAC clones have been extracted and the paired-end libraries are being constructed.

Chromosome 4 (UK)

Contact: Gerard Bishop and R. Lopez-Cobollo (g.bishop@imperial.ac.uk, r.lopez-cobollo@imperial.ac.uk*)*

Currently, we are focusing on identifying new BACs by screening the 3D BAC superpools. We have also been carrying out analysis of our Gbrowse based Golden Path (AGP based) viewer in order to identify extension BACs.

Missing markers: most recent analysis of the databases indicate that on chr4 there are a total of 141 markers existing for which the corresponding BACs have not been identified. Twenty-two of these markers are currently being screened in the 3D superpools and we have isolated four new BACs to be sent for sequencing (SLMboI0090M22, LE_HBa0091M11, LE_HBa0054E15 and LE_MboI0048I03).

Extension BACs: we have used the J-SOL SBM database to find contigs that allow us to identify better homology between BAC end sequences/fosmid end sequences and chr4 sequence. We have identified six BACs and three fosmids (SL_MboI0105G02, SL_MboI0069J23, LE_HBa0051E04, LE_HBa0102P20, LE_HBa0063F20, SL_EcoRI0041M09, SL_FOS0279J18, SL_FOS0162E05, SL_FOS0010B17) as candidate extenders. These BACs are under verification prior to sending for sequencing.

BACs from others: we have received information from the Korean team that certain BACs are on chr4. These BACs are being isolated and verified prior to sending for sequencing. We have confirmed by IL mapping that two BACs on chr0 should be moved to chr4: C00HBa0198A03 (from chr2), C00HBa0103J09 (from chr4).

Next Generation Sequencing: we will also be providing use of our SOLID 3 machine in sequencing the 10 Kb mate pair library.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have confirmed positions of ninety-five BACs on chr5, an increment of ten BACs since the last report. Sequencing is in progress on all these BACs, out of which forty-eight BACs are in phase III, twenty BACs are in phase II and eighteen BACs are in phase I. The remaining nine 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, PCR screening on the 3-D DNA pools of HindIII and MboI BAC libraries, the fosmid end sequences and SBM (selected BAC mixture) shotgun data. In addition, new nucleation points are also being identified by developing CAPS markers for the 200 BACs assigned to India for mapping purposes.

Chromosome 6 (The Netherlands)

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

Update pending.

Chromosome 7 (France)

Contact: Murielle Philippot (murielle.philippot@ensat.fr)

Update pending.

Chromosome 8 (Japan)

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

As of May 20, 2009, 185 BAC clones (106% of initial target) have been completed as Phase 3 that produced a non-redundant length of 18,121,370 bp, and an additional ten BAC clones are in the sequencing pipeline.

We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached to 4.2 million files generating 2.3 Gb of total length. These shotgun sequences have been assembled into 217,257 contigs covering approximately 670 Mbp regions of the genome.

Chromosome 9 (Spain)

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

To date, ninety-four clones have been sequenced corresponding to 9.2 Mbp or 52% of the initial goal. We are currently identifying extension BACs from the sequencing information for chr9 that will lead to the identification of new BACs. These BACs will be verified and validated using the ILs, and then retrieved, purified and sequenced following a pooled BAC-454 sequencing strategy.

Together with other partners we are moving to a whole genome sequencing (WGS) strategy that is aimed to produce a first draft of the tomato genome sequence by the end of the year. This will include from our side the contribution in constructing a mate-paired 4-5 kb library for SOLiD sequencing that will be done by our sequencing partner Sistemas Genómicos with a sequence of up to 15X.

Chromosome 11 (China)

Contact: Zhonghua Zhang (zhangzh.ivf@caas.net.cn) or Sanwen Huang (huangsanwen@caas.net.cn)

Update pending.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolanao@unina.it)

To date eighty-nine chr12 BACs are in various stages of the sequencing process. Of these, twenty-one are in HTGS1, fifteen are in HTGS2 and twenty-six are in HTGS3 and have been submitted to GenBank/SGN. All the BACs underwent genetic mapping through IL to confirm their positions on chr12. In parallel, we performed a search for new markers to increase the number of seed points and we identified forty-five candidates mapping on chr12. PCR screening on the 3-D DNA pools of the HindIII and MboI BAC libraries developed at INRA-CNRGV resulted in BAC hits for seventeen of those that are currently being validated prior to sequencing. Moreover, we are continuing with IL mapping of those BACs that have been completely sequenced and then found not to map on the correct chromosome (chr0 BACs). To date eighteen out of ninety BACs have already been mapped on various chromosomes and the data was uploaded on SGN.

In collaboration with the de Jong lab at Wageningen, we are performing FISH analysis of all our seed BACs to create a genetic-cytogenetic map of chr12 in order to visually identify the presence of gaps. To date, we mapped fifty-one BACs, including four putatively localizing close to the telomeres. Of those, six did not actually map on chr12 and it was the same for three of the telomeric ones. The data will be uploaded on SGN shortly.

As part of the Next Generation Sequencing Initiative, we provided nuclear genomic DNA for the preparation of random shotgun and paired end libraries; the DNA has been QC-ed and proven to be of good quality (contamination with only 4,3 % chloroplast DNA). A first GS FLX Titanium run test performed here provided 550,000 reads (almost 200 million bases) that passed the quality filters, which is on the average for a good quality run and a good number of reads. Sequence analysis of these reads is currently underway.

Announcements

Publications

Journal Articles

Barchi L, Lefebvre V, Sage-Palloix AM, Lanteri S, Palloix A (2009) QTL analysis of plant development and fruit traits in pepper and performance of selective phenotyping. Theoretical and Applied Genetics 118:1157–1171.

Chen S, Gollop N, Heuer B (2009) Proteomic analysis of salt-stressed tomato (*Solanum lycopersicum*) seedlings: effect of genotype and exogenous application of glycinebetaine. Journal of Experimental Botany 60: 2005–2019.

D'Introno A, Paradiso A, Scoditti E, D'Amico L, De Paolis A, Carluccio MA, Nicoletti I, DeGara L, Santino A, Giovinazzo G (2009) Antioxidant and anti-inflammatory properties of tomato fruits synthesizing different amounts of stilbenes. Plant Biotechnology Journal 7:422–429.

Mueller L, et al. (2009) A snapshot of the emerging tomato genome sequence. Plant Genome 2:78–92.

Pajerowska-Mukhtar K, Stich B, Achenbach U, Ballvora A, Lübeck J, Strahwald J, Tacke E, Hofferbert H-R, Ilarionova E, Bellin D, Walkemeier B, Basekow R, Kersten B, Gebhardt C (2009) Single nucleotide polymorphisms in the *allene oxide synthase 2* gene are associated with field resistance to late blight in populations of tetraploid potato cultivars. Genetics 181:1115-1127.

ABSTRACT
The oomycete *Phytophthora infestans* causes late blight disease on potato (*Solanum tuberosum*). Field resistance to late blight is a complex trait controlled by genetic and environmental factors. When cultivated under long day conditions in temperate climates, potato field resistance to late blight is correlated with late plant maturity, an undesirable characteristic. We aim at the identification of genes and their natural variants, which control field resistance to late blight not compromised by late maturity. An association study was conducted in a population of tetraploid potato individuals that were phenotyped in replicated field trials for resistance to late blight and plant maturity. The individuals were genotyped for single nucleotide polymorphisms (SNPs) at candidate loci and for microsatellites to analyze population structure. For association analysis a mixed model was used, taking into account population structure, kinship, allele substitution and interaction effects of the marker alleles at a locus with four allele doses. Nine SNPs were associated with maturity corrected resistance ($P < 0.001$), which collectively explained 50% of the genetic variance of this trait. The major association with resistance to late blight was found at the *StAOS2* locus encoding allene oxide synthase 2. StAOS2 is a key enzyme in the biosynthesis of jasmonates, plant hormones that function in defense signaling.

Peters SA, Datema E, Szinay D, van Staveren MJ, Schijlen EGWM, van Haarst JC, Hesselink T, Abma-Henkens MHC, Bai Y, de Jong H, Stiekema WJ, Klein Lankhorst RM, van Ham RCHJ (2009) Solanum lycopersicum cv. Heinz 1706 chromosome 6: distribution and abundance of genes and retrotransposable elements. The Plant Journal 58:857-869.

Xiao H, Radovich C, Welty N, Hsu J, Li D, Meulia T, van der Knaap E (2009) Integration of tomato reproductive developmental landmarks and expression profiles, and the effect of *SUN* on fruit shape. BMC Plant Biology 9:49 doi:10.1186/1471-2229-9-49.

Website Resources

Breeders Toolbox

Check out the new information that has been added to the Breeders Toolbox (http://www.sgn.cornell.edu/breeders/). Feedback on the toolbox is welcome and can be sent to Joyce Van Eck (jv27@cornell.edu).

Conferences

42nd Tomato Breeders Roundtable
June 28 - July 1, 2009
Embassy Suites, Sacramento, CA
www.cevs.ucdavis.edu/confreg/index.cfm?confid=421

93rd Annual Meeting of The Potato Association of America
August 9 - 13, 2009
Delta Fredericton Hotel
Fredericton, New Brunswick, Canada
Conference website: www.paa2009.org
Contact person: Loretta Mikitzel (loretta.mikitzel@gnb.ca)

SOL 2009, The 6th Solanaceae Genome Workshop
November 8 – 13, 2009
New Delhi, India
www.sol2009.org

Solanaceae Recipes

Zesty Chicken Enchiladas

From the magazine Real Simple, May, 2009

Ingredients:

1 tablespoon canola oil
1 pound tomatillos (papery husks removed), chopped
1 onion, chopped
1 poblano pepper, seeded and chopped
2 glove garlic, chopped
¾ teaspoon cumin
Salt and black pepper
1 cup heavy cream
1 2 to 2½ pound roasted chicken, meat shredded
1 14.5 ounce can diced tomatoes, drained
1¼ cups grated Monterey Jack cheese (5 ounces)
8 6-inch corn tortillas
Salsa (see recipe below)

Preparation:

1. Heat oven to 400°F. Heat the oil in a large skillet over medium-high heat. Add the tomatillos, onion, poblano, garlic, cumin, and ½ teaspoon salt. Cook, stirring occasionally, until the vegetables are tender, 10 – 12 minutes. Transfer to a food processor, add the cream, and puree.
2. In a large bowl, combine the shredded, cooked chicken, tomatoes, 1 cup of the cheese, ½ cup of the tomatillo sauce, and ½ teaspoon each salt and pepper.
3. Warm the tortillas according to the package directions. Spread 1 cup of the remaining sauce in a 9-by-13-inch baking dish. Roll the chicken mixture in the tortillas and place them in the dish, seam-side down.
4. Top with the remaining sauce and cheese. Bake until beginning to brown, 10 – 15 minutes. Serve warm with salsa.

Simple Salsa

www.marthastewart.com

1 3/4 cups diced tomato (about 1 large tomato)
1/4 cup diced white onion (about half of an onion)
1 finely chopped fresh jalapeno chile (seeded, if you like, for a milder salsa)
1 teaspoon coarse salt

Stir ingredients together. Refrigerate for 1 hour before serving to let the flavors develop.