

Community News



The EU-SOL proposal was recently funded. Congratulations to all involved! Below is the proposal summary.

EU-SOL

Provided by: Willem Stiekema

High Quality Solanaceous Crops for Consumers, Processors and Producers by Exploration of Natural Biodiversity

Strategic objectives addressed by EU-SOL:

1. To extract the under-exploited natural biodiversity present in Solanaceae to improve consumer-driven and environmentally-directed quality of tomato fruits and potato tubers.
2. To map, isolate and characterise genes responsible for quality traits and to dissect the molecular mechanisms underlying these trait by application of state-of-the-art knowledge and innovative technologies.
3. To assemble these genes within new elite genotypes to boost our knowledge and provide a blueprint for novel high quality varieties to be developed by EU breeding companies.
4. To coordinate and integrate breeding research for quality traits, to provide training in innovative technologies, to disseminate the results and to transfer knowledge and technologies to industry.
5. To participate in the international tomato genome sequencing initiative that will tie European Solanaceae research and innovation into the full global activities in this area. This is of pivotal importance for Europe.
6. To create a model for how world-wide scientific collaboration can lead to innovative research that can set the road map on how to improve global food security related to a wide variety of other crop plants.

EU-SOL is a network of plant scientists from universities, research institutes and industry within the EU, its partner countries Bulgaria, Israel and USA and INCO countries Westbank, Morocco, Argentina, Brazil and South-Africa. EU-SOL focuses on the development of high quality and healthy tomato and potato varieties with improved consumer-, processor- and producer-directed traits. The consortium brings together expertise across a wide variety of disciplines across the EU - from taxonomy to molecular biology to consumer integration. Quality and wholesomeness of food and food products are two issues addressed prominently by society especially in relation to obesity (and atherosclerosis), the most important cause of cardiovascular disease, age-related diseases, such as cancer and diabetes and to the increasing preference of consumers for 'regional' and 'niche' food specialties. Additionally producers are challenged by constraints in plant architecture and development such as fruit set and tuberisation.

The **strategic objectives** of EU-SOL are to understand the factors that affect consumer-driven and environmentally-directed quality of the two most important vegetable products in the EU, tomato fruits and potato tubers, both belonging to the Solanaceae. To this end, EU-SOL will attempt to dissect the genetic and molecular components that control these quality traits by applying state-of-the-art knowledge and technologies. EU-SOL particularly focuses on mapping, isolation and characterization of genes responsible for traits important for consumers and processors (health, nutrition, flavour, fragrance, soluble solids, texture, colour, shelf-life, starch, chipping quality) as well as for producers (plant architecture, fruit set and tuberisation) and the mechanisms underlying these traits (control of gene activity, regulatory networks). Important goals are to understand the factors that affect tomato and potato architecture and fruit and tuber composition, to acquire knowledge of carbon and nitrogen acquisition, partitioning and allocation during fruit and tuber development, and to identify the key genes involved. Assembly of these genes within new genotypes will boost our knowledge of the factors that control quality and provide a blueprint for novel high quality varieties to be developed by EU breeding companies using efficient and rational breeding strategies based on marker-assisted breeding and genetic engineering that exclusively use natural plant genes.

Tomato Sequencing Updates

Chromosomes 1, 10, 11 (US)

BAC end sequences: New batches of sequence have arrived from the US sequencing partner, SeqWright, Inc. The current counts of reads are: 152,818 Tomato HindIII BAC Library, 101,371 Tomato Mbol BAC Library, and, a new library has been started last month, EcoRI, which already has a read total of 46,463. In all cases, the acceptable rate was close to 85%. All BAC ends can be searched, blasted, and downloaded on SGN (<http://sgn.cornell.edu/>). The total number of reads now amounts to 300,652, out of a budgeted total of 400,000.

Full BAC sequences: Korea was the first project to submit full BAC sequences to SGN. The data can be downloaded from the SGN ftp site (ftp://ftp.sgn.cornell.edu/tomato_genome/bacs/chr02/). We are working on an interactive display of the BACs based on GBrowse that should be available by the end of the summer. China, the Netherlands, Japan and Italy will soon submit a number of BACs for chromosome 3, 6, 8 and 12.

As for FISH, the images in the two figures below illustrate results of recent FISH experiments using two tomato BACs that were believed to contain sequences located on Chromosome 12. The figures show fluorescence (left panels) and phase-contrast (right panels) images of tomato SC spreads. In Figure 1, the white arrow indicates a unique locus of FITC fluorescence representing hybridization of BAC 026C13 very near the telomeric end of the short arm of Chromosome 12 (identified by the black arrow in the right-hand panel). Figure 2 shows the result of a similar FISH experiment with BAC 107D15, which produced many sites of FITC fluorescence throughout the pericentromeric heterochromatin of all twelve of the chromosomes. To determine whether BAC 107D15 contains any single-copy sequences that will hybridize to a unique site on Chromosome 12, it will be necessary to repeat the experiment using CISS hybridization with tomato Cot100 DNA.

Figure 1

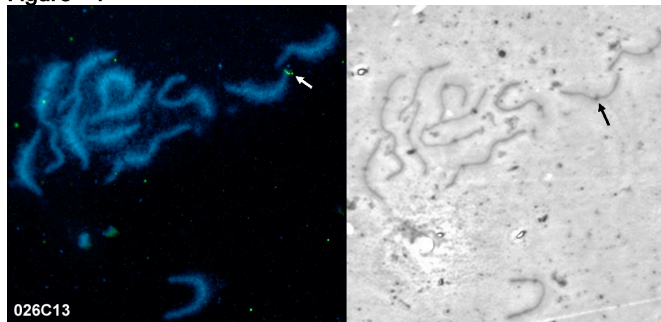
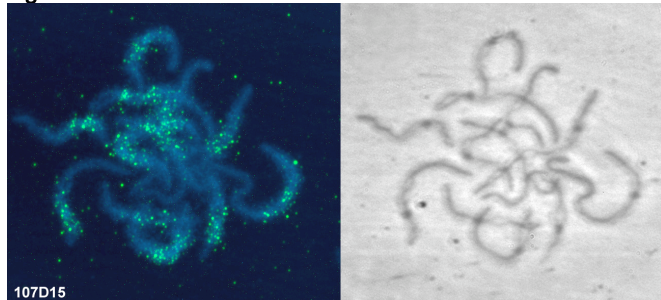


Figure 2



Chromosome 2 (Korea)

Since our last update two months ago, we have sequenced 5 additional BAC clones, and 13 clones are in progress. We have a total of 35 seed BAC clones for chromosome 2. The newly sequenced BAC clones are as follows: LE_HBa177F12 (marker; T1554), LE_HBa172G12 (T1480), LE_HBa064B17 (CT24), LE_HBa164H08 (T1535), LE_HBa194L19 (T1096).

In addition, 13 BAC extensions from 17 previously sequenced BAC clones were applied using FPC and BAC end sequences, and confirmation is being done by PCR and FISH. Lastly, the annotation (Phase I) of 22 BAC clone sequences was completed.

Chromosome 3 (China)

Update pending

Chromosome 4 (UK)

Further to receiving the LE_HBa and SL_Mbol libraries we have recently obtained the SL_EcoRI library (72,264 clones). The libraries are now all in place for us to isolate single colonies for sequencing purposes. *In silico* analysis of the Tomato FPC database is being conducted. We have made use of the seed BACs and contigs identified from Cornell's overgo probe analysis. All contigs containing a chromosome 4-assigned marker have been through an initial round of assessment to confirm contig construction and examine marker information. Nascent contigs have been merged where possible on the basis of fingerprint data. At present we have 58 contigs potentially assigned to chromosome 4.

To date, 5 LE_HBa clones have been selected for sequencing from the FPC database. These BACs are from two contigs in different regions of the chromosome and once sequenced will provide information regarding overlap sizes between neighbouring clones and hence assist with future tilepath detection. PCR/fingerprint verification of single colony isolates of these initial sequence BACs is underway. The next aim is to reduce the current contig number so that larger, more efficient tilepaths can be selected across the contigs with minimal overlaps between successive clones. To accomplish this, *in silico* analysis of the FPC database will continue and further BAC end sequence information will be incorporated into our database as it is generated.

Chromosome 5 (India)

Two tomato BAC libraries (HindIII and Mbol) and a set of seed BAC clones for chromosome 5 were obtained. Seed BACs were replicated and distributed to three centres (i.e., University of Delhi South Campus, Indian Agricultural Research Institute and National Centre for Plant Genome Research) participating in the Indian Initiative on Tomato Genome Sequencing. As per standard guidelines, seed BACs for five marker positions have been selected for verification and sequencing.

Chromosome 6 (The Netherlands)

To date, 52 BACs have been mapped on chromosome 6 using AFLP markers and also some available RFLP markers. After FISH analyses, 36 BACs were found suitable for sequencing. The remaining BACs are either still in the FISH-pipeline, or were found to be derived from heterochromatic regions on chromosome 6 or from different chromosomes. Of the 36 selected BACs, 16 BACs have been completed to Phase 1 and an additional 16 BACs are currently in the sequencing pipeline.

The results of the BAC-end approach to radiate out of the seed BACs are very encouraging. Using the latest data set from SGN, which contains approximately 220,000 BAC ends both from the HindIII and Mbol libraries; we identified multiple flanking BACs for 13 out of 16 seed BACs. Currently, these flanking BACs are fingerprinted to identify the minimal overlapping ones. Sequencing two such BACs confirmed their predicted minimal overlap with the corresponding seed BACs as predicted by AFLP fingerprinting.

Chromosome 7 (France)

Recently, the group received seed BACs for chromosome 7. The HindIII and Mbol libraries were requested.

Chromosome 8 (Japan)

Update pending

Chromosome 9 (Spain)

The group recently received seed BACs for chromosome 9.

Chromosome 12 (Italy)

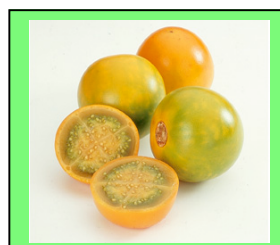
In the two months since our last update, our work has been dedicated to the following activities: assembly of sequences from two BACs produced from the shotgun library, extension of the tile path around these BACs, and selection of new candidate seed BACs on both arms of chromosome 12. The full sequences of two BACs are ready to be submitted to Phase II or III on the SGN register. However, the BAC ends of one clone, located both by IL and FISH (Steve Stack's lab) on chromosome 12, did not match with the one reported on the SGN database. Considering that other mismatches were found between our data and the SGN data, we are now selecting new seed BACs according to very strict parameters to avoid any sequence uncertainties or contaminated clones. Using these parameters, we have recently picked three BACs from a new plate verified at Cornell University. They were sent to the CRIBI sequence service along with 20 candidate seed BACs that are being analyzed.

TOWARDS THE DEVELOPMENT OF A BASIC GENOMICS PLATFORM FOR EXOTIC FRUIT SOLANACEAE

Contributed by: Stella Luz Barrero

Exotic fruit Solanaceae, such as naranjilla or lulo (*Solanum quitoense*), tamarillo or tree tomato (*Solanum betaceum*), and Cape Gooseberry or uchuva (*Physalis peruviana*) have great potential to become premium products for Colombian local and export markets with a high economic return to the farmers. They represent excellent sources of vitamins, minerals, proteins, and carbohydrates. These Andean species constitute alternative crops in growing areas of illicit crops, and at the same time their cultivation can help conservation and regeneration of Andean ecosystems.

Despite an increasing market value for these exotic fruit, the major constraint for adoption by local farmers is the lack of technological support associated with a shortage of breeding materials. In Colombia, the only improved materials that have been developed are a lulo known as "Lulo La Selva" that is resistant to *Meloidogyne incognita*, and some breeding lines of the tree tomato that are resistant to *Colletotrichum gloeosporioides* (Bernal et al., 1998; Heiser and Anderson, 1999; Lobo et al., 2000). A broad genetic base is needed to develop these exotic fruit Solanaceae into high-yielding, sustainable crops. In this regard, the Colombian Corporation for Agricultural Research (CORPOICA) maintains the largest collections of these exotic species and their wild relatives, for which there is partial phenotypic characterization and knowledge about the genotypic variation. A profound understanding of the genetic basis of diversity is needed to guide



Lulo fruit
(*Solanum quitoense*)



Tree tomato fruit
(*Solanum betaceum*)

the sustainable use of this exotic germplasm to meet the needs of our society. CORPOICA is proposing to develop a basic genomic platform for these exotic fruit Solanaceae (i.e. EST databases, comparative maps, among others), so that improvement of these species can benefit from the overall genetic information and genomic tools generated by the International Solanaceae Genome Project (SOL).

Bernal, J., Lobo, M., and Londoño, M. 1998. Documento de presentación del material "Lulo La Selva" (Rionegro: Corpoica), pp. 77.

Heiser, C. and G. Anderson. 1999. "New" solanums. p. 379-384. In: J. Janick (ed.), Perspectives on new crops and new uses. ASHS Press, Alexandria, VA.

Lobo, M; Medina, C, Cardona, M. 2000. Resistencia de campo a la antracnosis de los frutos (*colletotrichum gloeosporioides*) en tomate de árbol (*Cyphomandra (Solanum) betacea (betaceum)* Cav. Sendt.) Rev. Fac. Nat. Agr. Medellín. Vol.53, No.2. p. 1129-1142.



Cape gooseberry
(*Physalis peruviana*)

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What's New on SGN?

SGN has recently added two new pepper maps, kindly submitted by Dr. Arnon Ben Chaim. These are inter-specific SSR-based maps from F2 populations of *C. frutescens* x *C. annuum* (FA03) and *C. annuum* x *C. chinense* (AC99). This was a collaboration between Cornell University, USA, Alcorn State University, USA, Seoul University, South Korea, Agricultural Biotechnology Center, Hungary, DNA Landmarks, KeyGene, Seminis, Sunseeds, and Syngenta. The work was supported in part by USDA IFARS Plant Genome Award No. 2001-52100-11347. The maps are available at: http://sgn.cornell.edu/cgi-bin/mapviewer/mapTop.pl?map_id=10 and http://sgn.cornell.edu/cgi-bin/mapviewer/mapTop.pl?map_id=11.

A new tomato map is available: Tomato-EXPIMP 2005, *S. lycopersicum* TA209 x *S. pimpinellifolium* LA1589, 2005, kindly provided by Dr. Jiping Liu, Cornell University. http://sgn.cornell.edu/cgi-bin/mapviewer/mapTop.pl?map_id=12

In addition, a new potato unigene build is available, comprising 134,365 ESTs, 18,564 contigs, 12,508 singlets for a total of 31,072 unigenes, incorporating almost 50,000 new EST sequences from the Canadian Potato Genome Project (<http://www.genomecanada.ca/>) kindly provided by Dr. Barry Flinn.

There will be a new, featured lab posted on SGN this month (<http://www.sgn.cornell.edu/community/feature/200504.html>). It will be a profile of the Coffee Biotechnology Lab at the Agronomic Institute in Campinas, Brazil.

Conference and Workshop Announcements

2nd Solanaceae Genome Workshop September 25 - 29, 2005 *Hotel Continental Terme - Ischia - Italy*

As of July 5th, more than 300 people have registered. Approximately 180 abstracts have been submitted of which more than 80 were submitted for evaluation as oral presentations. The website for information related to the meeting is <http://www.solanaceae2005.org>.

The VIth World Petunia Days Conference - 2005

Provided by: Tim Robbins

This conference will be held from September 15th-17th 2005 at the University of Nottingham, UK. Although aimed primarily at the petunia research community (<http://www.petuniaplatform.net/>), we welcome the participation of researchers working in related areas in other species of the Solanaceae. There are usually major contingents from the Free University of Amsterdam and the University of Nijmegen but many delegates travel from further afield including the US and Japan. The talks at the last meeting covered topics as diverse as floral scent, shoot apical meristems and mycorrhizal symbiosis. Following the traditions of previous World Petunia Days, the format will be to allow as many oral presentations as possible including those from graduate students.

Further details are available at the conference website that can also be accessed from the Petunia Platform website. The meeting could be conveniently combined with the 2nd Solanaceae genome meeting in Italy for those traveling from outside Europe.



The registration form, details of abstract submission and travel and accommodation information are available on the meeting website. Please note the registration deadline is **31st July 2005**. Please address any conference queries to either myself (tim.robbs@nottingham.ac.uk +44 (0) 115 951 6329) or the conference secretariat (sonoko.mitsui-angwin@nottingham.ac.uk +44 (0) 115 951 6332). We hope that some of the wider Solanaceae community will be able to attend this meeting.

Conference Website

<http://www.nottingham.ac.uk/pvu/petunia.html>



European Plant Science Organization Conferences, Workshops, and Publications

Provided by: Katrien Molders

3rd EPSO Conference: "Plant Dynamics: from molecules to eco-systems"
28 May - 1 June 2006, Visegrad, Hungary
Info at www.epsoweb.org/catalog/conf2006.htm

EPSO Workshop: "Environmental plant biology; adaptation of plants to Biotic and abiotic stress"
21 November - 22 November 2005, Amsterdam, The Netherlands
Info at www.epsoweb.org/Catalog/epsoweb%20workshops/amsterdam.htm

(Continued on page 6)

EPSO Workshop: "Molecular Farming"

3 - 4 October 2005, Aachen, Germany

Info at www.epsoweb.org/Catalog/epso%20workshops/aachen.htm

Launch of the Stakeholders Proposal for a Strategic Research Agenda of The European Technology Platform
"Plants for the Future"

5 July 2005, Strasbourg, France

Info at www.epsoweb.org/Catalog/TP/TP%20launch_stakeholder_proposal.htm

ESPO Publication:

European Plant Science: a field of opportunities

An EPSO Publication in The Journal of Experimental Botany, July 2005

JXB 2005 56(417):1699-1709

Information and link to full text at

www.epsoweb.org/commun/ESPO_plantscience_JEXB.htm