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SOL Newsletter

Contents of this Issue

Community News

SOL 2009, The 6th Solanaceae Genome Workshop

An announcement was made during SOL 2008 in Germany that the 6th Solanaceae Genome Workshop will be held in New Delhi, India from November 8 – 13, 2009. The organizers will announce the venue and additional details at a later date.

Here are a few urls for websites with information about New Delhi and sites of interest in the area:

http://en.wikipedia.org/wiki/New_Delhi
http://en.wikipedia.org/wiki/Taj_Mahal
http://en.wikipedia.org/wiki/Lotus_Temple

Taj Mahal

Bahai Lotus Temple

The Interspecific Reproductive Barriers in Tomato Research Group

Contributed by Paul Covey

The Interspecific Reproductive Barriers in Tomato research group (IRBT) is currently comprised of six laboratories from across the US whose specialties range from cytogenetics to quantitative genetics to molecular biology. They include: Patricia Bedinger and Steve Stack, Colorado State Univ., Jocelyn Rose, Cornell, Esther Van der Knaap, Ohio State Univ./OARDC, Roger Chetelat, Univ. of California Davis, and Bruce McClure, Univ. of Missouri. The aims of the group are to elucidate the underlying factors that contribute to Unilateral Incongruity (UI) within the tomato clade of the genus *Solanum* and to provide the scientific community with tools to enhance the understanding of reproductive biology.

IRBT is pleased to announce the release of pre-publication data of a style and pollen iTRAQ proteomics meta-endeavor, as well as a publicly accessible broad-spectrum mutagenesis tool called FISH Cassette for Mutagenesis (pFCM100). Information on both these projects can be found at http://irbtomato.org under 'Data and Tools'. Visitors to the site can also find protocols and a guided tour of tomato reproduction.

Proteomics from Pollen and Unpollinated Styles of *Solanum spp.*: A major goal of IRBT is to identify the molecular components involved in prezygotic barriers to interspecies reproduction. iTRAQ analysis is a powerful proteomics method that allows us to identify peptides that may be hydrophobic, low in abundance, or post-translationally modified. It utilizes specific signature labeling of up to four separate peptide samples in a single run. Because four samples can be analyzed together we can use the levels of relative quantification in each sample to identify putative candidate proteins involved in interspecific reproductive barriers. We have analyzed peptides of unpollinated styles and pollen from four different tomato accessions LA0407, LA1777 (SC and SI S*olanum habrochaites*), LA0716 (SC *S. pennellii*), and cultivar M82 (SC *S. lycopersicum*).

These accessions have long been used as sources of agronomic traits for introduction into domesticated species and for genetic studies. For example, well-characterized isogenic lines from both parental accessions of LA1777 and LA0716 have been widely used for QTL mapping and trait domestication. The domestic tomato, *S. lycopersicum*, lacks SRNase based gametophytic self-incompatibility and accepts pollen from the other three wild accessions. However, its pollen is rejected by *S. habrochaties* and *S. pennellii*. LA1777 and LA0716 pistils reject M82 pollen rapidly, whereas LA0407 pistils reject M82 pollen more slowly.

Multiple peptides were found in all samples. Uniquely identified peptides represent close to 37% of the total peptide spectra (769 from pollen and 493 from Mature Unpollinated Styles). SGN-unigene numbers and *GO* terms can be used to search the available *.xls* data file and all raw spectral data is listed as *.wiff* files on the website http://irbtomato.org.

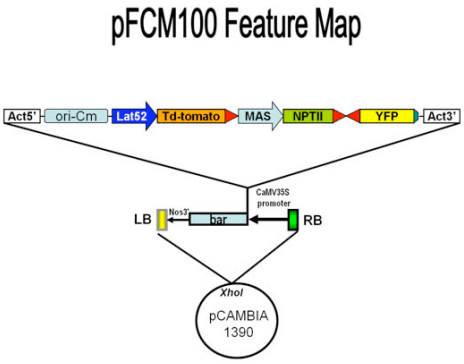
IRBT will also do parallel 454 sequencing of pollen and mature unpollinated styles from M82 and LA0716. Once complete, this will increase the number of tissue specific genes in gene banks and allow the identification of hundreds of genes from wild tomato species that are not presently represented. This will also strengthen the results of our iTRAQ analysis. Check out http://irbtomato.org for project updates.

FISH Cassette for Mutagenesis (pFCM100): We have completed the assembly of a versatile insertional mutagenesis tool (pFCM100) (Fig. 1) and are in the process of making available M82 lines that carry the transgene on each arm of the 12 tomato chromosomes. This transgene can be tracked in transgenic plants, using FISH (**F**luorescent ***In Situ*** **H**ybridization) technology. The three main objectives of this tool are to:

1) Identify genes involved in tomato reproductive biology (in particular, inter-specific reproductive barriers) by following the segregation distortion of a dominant marker, Kan^r.

2) Use a pollen-expressed fluorescent protein to follow transgene segregation and visualize pollen tube growth in styles.
3) Make the tomato genome more accessible to the tomato community by providing a highly efficient global insertional mutagenesis approach.

Figure 1: pFCM100



We brought together several useful features from different sources such as pJasm13 (Gidoni et al., Plant Mol Biol **51:** 83-98 2003) to construct a T-DNA cassette containing a Ds element. The power of insertional mutagenesis is enhanced in pFCM100 by combining T-DNA and transposon tools with a gene trap (a promoter-less YFP gene). The FISH cassette has kanamycin resistance (NPTII) driven by the MAS promoter as the plant transformation marker. After the excision of the Ds element, Basta resistance (bar gene) comes under the regulation of the 35S promoter to select for transposition events. Ac lines are available in multiple tomato cultivars, such as VF36, VFNT Cherry, Moneymaker and Microtom. The pollen-genotyping cassette consists of an enhanced fluorescent protein, Td-Tomato, under the control of a pollen-specific promoter, LAT52, which allows tracking transgene segregation and visualization of growing pollen tubes. We have also incorporated a plasmid rescue cassette (ori-cm) to clone flanking plant genomic DNA in *E. coli* using convenient restriction enzyme sites and selecting transformants on chloramphenicol.

We foresee the utility of pFCM100 in tomato and other plant species, as well. Interested labs may contact *IRBT* on the web (http://irbtomato.org) or send an e-mail to Subbaiah Chalivendra (schalive@lamar.colostate.edu).

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La Tomatina

Ever since 1945, La Tomatina or the Tomato Festival has been held in Buñol, Spain on the last Saturday of August. Basically, it is a huge tomato fight and each year approximately 20,000 people take part in the festival using almost 90,000 pounds (40,823 kg) of tomatoes. The origins of the festival can be traced back to when, for unknown reasons, a number of friends started a tomato fight in Buñol's main town square. People passing by joined in and everyone ended up having a great time. From that time on, La Tomatina has been an annual event, which comes at the end of a week-long celebration that includes various activities such as parades, fireworks, and street parties. Check out the following websites for additional information and images from La Tomatina.

http://www.donquijote.org/culture/spain/fiestas/tomatina.asp
http://www.time.com/time/photogallery/0,29307,1837057_1758241,00.html

The *Solanum lycopersicum* Auxin Response Factor 7 (*Sl*ARF7)

Provided by Wim Vriezen and Maaike de Jong

Fruit set is defined as the transition of a static flower ovary to a rapidly growing young fruit. This initiation of the fruit developmental program depends on the successful completion of pollination and fertilization under suitable environmental conditions. Therefore, the understanding of the regulatory mechanisms involved in fruit set can facilitate the production of agriculturally valuable fruit crops. The influence of the phytohormone auxin on tomato (*Solanum lycopersicum* L.) fruit set has been well established. Gustafson showed already in the 1930s that the exogenous application of this hormone can induce fruit growth, suggesting that normally after pollination, auxin causes the ovary to grow. Possibly, this auxin is produced by the fertilized ovules that develop into the seeds.

Auxin-dependent developmental processes are under the control of a family of transcription factors; the Auxin Response Factors (ARFs). In general, ARFs are believed to act as positive regulators of the auxin signaling pathway by regulating the activity of auxin responsive genes. We identified an ARF gene that is highly expressed in the unpollinated flower. This ARF is mostly similar to the Arabidopsis NPH4/ARF7 and was therefore designated as *Sl*ARF7. *Sl*ARF7 seems to act as an attenuator of the auxin signaling pathway during tomato fruit set and development. The expression of the *SlARF7* gene was found to be up-regulated during flower development to remain at a constant high level in the mature non-growing flowers. Within 48 h after pollination, *SlARF7* expression decreases and at the same time the ovary starts to grow. Transgenic plants with low *SlARF7* transcript levels start fruit growth before pollination has taken place, suggesting that *Sl*ARF7 in wild type inhibits growth until fertilization occurred (Fig. 1). In addition, the seedless transgenic fruits showed phenotypic characteristics typically observed in fruit induced by excessive application of auxin. Hence, both morphological and molecular data indicate that *Sl*ARF7 acts as a negative regulator of auxin signaling during fruit set and fruit development.

Figure 1: Transgenic tomato with decreased *SlARF7* transcript level.

This article was adapted from a publication in Plant Journal 2008 EPub.

Breeders Toolbox

A Breeders Toolbox is currently under construction and can be found on SGN at http://www.sgn.cornell.edu/breeders/. At this time, we are soliciting input from the community on the tools and information to include in this toolbox that would make the results generated by sequencing projects easily accessible and applicable for breeding programs.

Please contact Joyce Van Eck (jv27@cornell.edu) with suggestions for this toolbox.

Early History and Iconography of the Solanaceae: 2. Potato[1]

Marie-Christine Daunay & Jules Janick

[1]This SOL paper is the second in a series on the early history and iconography of the Solanaceae. The first covered mandrake (Janick and Daunay, 2007) and the present paper covers potato, in celebration of the Year of the Potato.

Potato, *Solanum tuberosum* L, a species indigenous to the New World, was cultivated throughout the Andes long before the encounter of Columbus with the Americas. The veneration of pre-Inca populations for the goddess of Earth was closely associated with the worship of various deities associated with plants, in particular *Axomama*, the mother of potato. The first traces of potato are freeze dried remnants known as chuňo found in South American archaeological remains that date as far back to as 7000 years BCE (Spire and Rousselle, 1996). Potato-like potteries (**Fig. 1**) found in tombs of successive Andean cultures such as the Nazca (400 BCE-600 CE), Mochica (1-600), Chimu (900-1450) and Chimu-Inca (1100-1400) are testament to the importance of this species as a food crop. At the time of the conquest of the Inca Empire in Peru (1531-1537) by Francisco Pizarro, potato was cultivated in all temperate regions of western South America, from Chile to Columbia. Its culture by the indigenous population is beautifully illustrated in a calendar of Inca agriculture presented to the King of Spain in 1580 (**Fig. 2**).

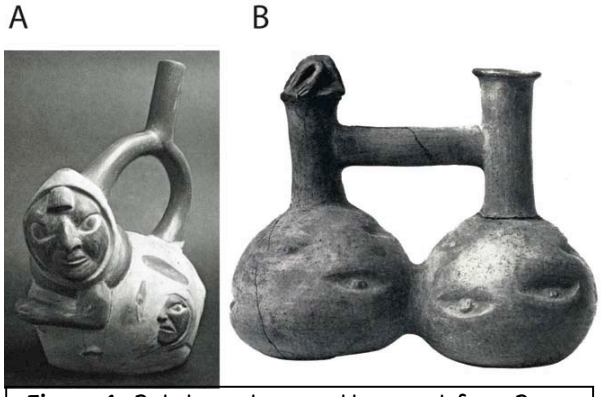

Figure 1: Potato as terra cotta vessel from Peru: (A) proto-Chimu period, ca 300 CE; (B) Chimu period, ca 900 CE. [Leonard, 1973].

It is difficult to trace the first European records of potato. The approximate plant names and descriptions written by the conquistadores or their escorts often do not allow distinguishing potato from several other American tuberous species, in particular *Ipomoea batatas*, *Aracachia xanthorrhiza*, *Oxalis tuberosa*, *Ullucus tuberosus* and *Helianthus tuberosus*. According to Hedrick (1919) the first European record of the Indian *papas* (potato) was made in 1553 by Pedro Cieza de León (1520-1554), Spanish conquistador, chronicler, and historian of Peru.

Figure 2: Potato culture in Peru. Filipe Guaman, Poma de Ayala, 1615. (A) planting, December; (B) harvest, June. [Leonard, 1973].

Potato appears in Renaissance illustrated herbals much later than capsicum peppers, tomato and tobacco (Daunay et al., 2007, 2008), which were described about 20-30 years after Hernando Cortez conquest of the Aztec culture in Mexico in 1519-1521. The Flemish botanist Charles de l'Ecluse (latinized as Clusius) received samples of potato tubers and fruits indirectly from the pope in 1588, and the year after a watercolor labelled *Taratoufli, Papas Peruänum Petri Circae* from the same source (**Fig. 3**), the oldest known European image of potato, now in Plantin-Moretus Museum, Antwerp, Belgium. The first published illustration (**Fig. 4A**) was a woodcut accompanying the description of potato by the Englishman, John Gerard in his famous herbal of 1597. He called it the *Battata virginiana*, *Potatoes of Virginia*, confusing it with the name of the sweet potato *Ipomoea batatas*, a misonomer that persists to the present day.

He described it as follows:

... *"The roote is thicke, fat, and tuberous, not much differing either in shape, colour, or taste from the common potatoes* [=sweetpotato], *saving that the rootes hereof are not so great nor long; some of them round as a ball, some oval or egge fashion; some longer, and others shorter: which knobbie roots are fastened unto the stalkes with an infinite number of threedie strings."* ... *"a food as also a meate for pleasure, equall in goodnesse and wholesomenesse unto the same, being either rosted in the embers, or boyled and eaten with oyle, vinegar, and pepper, or dressed any other way by the hand of some cunning in cookerie."*

Figure 3: Potato watercolor received by Clusius in 1589. [Blunt & Raphael, 1979].

The image in Gerard's Herball was quickly followed by another woodcut in the 1598 herbal of the Italian Pietri Andreae Matthioli (**Fig 4B**). Clusius published his own record only in 1601 (**Fig. 4C**). A stunning botanical illustration of potato was published in 1613 by Besler, in his *Hortus Eystettentis* (**Fig. 5**).

Early European iconography of potato is scarce and does not permit a clear representation of tuber size, shape and color of the first introduced forms, though it is acknowledged among potato specialists that the first forms cultivated in Europe belonged to the subspecies *andigena* (Spire and Rousselle, 1996).

The botanical names allocated to potato, as for most plants, were numerous and unreliable prior to the establishment of the nomenclature system established by Linnaeus in the mid 18th century. Gaspard Bauhin provided the name *Solanum tuberosum* with the plant description in his *Phytopinax* of 1596.

Only a few hints of suspicion towards potato as a proper and healthy food are found in the late 16th century and 17th century herbals, even though the herbalists recognized some similarities with its European solanaceous cousins such as mandrake, henbane, and black nightshade with their unwholesome and unsavoury reputations. The subsequent development of potato cultivation in Europe was slowed somewhat, because of remnants of medieval prejudice, contempt, and fear towards everything growing directly in the soil. Thus, the potato which was to become one of the ten most important food crops in present day agriculture had a slow and precarious beginning in the West.

Figure 4: First potato illustrations in European herbals. (A) Gerard, 1597; (B) Matthioli (1598); (C) Clusius, 1601. [(B) and (C), Courtesy of Musée Requien, Avignon, France].

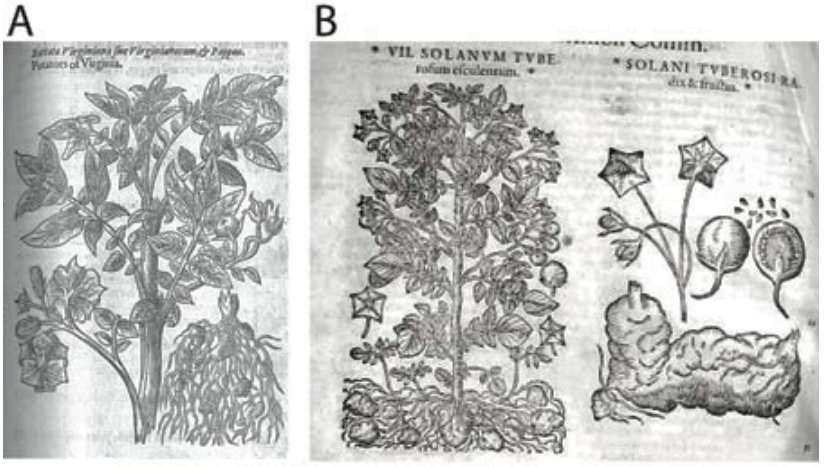

Figure 5: Potato in the *Hortus Eystettentis* of B. Besler, 1613. [Der Garten von Eichstatt, Taschen Köln, Germany, 1999].

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Tomato Sequencing Updates

Chromosomes 1, 10 (US)

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

Since our last report, the Stack lab at Colorado State University has localized an additional seventeen BAC clones using fluorescence in situ hybridization (FISH) on tomato pachytene synaptonemal complex spreads. We have now positioned a total of 164 BACs, distributed among the chromosomes: 1 - 31; 2 - 12; 3 - 13; 4 - 16; 5 - 10; 6 - 9; 7 - 13; 8 - 4; 9 - 18; 10 - 20; 11 - 13; 12 - 5. BAC clones recently FISHed on 2Q (included in a contig sequenced by Korea) are being used in an ongoing study to determine the resolution of our BAC FISH method. The newly localized clones are listed in the table to the right.

Chromosome Arm	BAC ID
1P	LE_HBa0291L11
	LE_HBa0305J13
	LE_HBa0263P17
1Q	LE_HBa0033C15
	LE_HBa0128J14
	LE_HBa0057A01
	LE_HBa0034P21
2Q	SL_EcoRI0034H10
	SL_EcoRI0042D07
	LE_HBa0098J01
	SL_EcoRI0061K08
	LE_HBa0032J10
10Q	LE_HBa0206B16
	LE_HBa0071D20
	LE_HBa0204I05
	LE_HBa0189B10
	LE_HBa0248A13

Chromosome 2 (Korea)

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

To date, 166 BAC clones (18,681,922 bp) confirmed on chr2 have been completed as HTGS phase 3. Due to the limitation of extension BAC selection, we decided to sequence twelve BACs (1,224,206 bp), which are overlapping more than 60 kb with already sequenced BAC clones using GS FLX. As a result of shotgun sequencing, two clones were able to fill gaps, three clones were used as bridge BACs to find extending BAC clones and the remaining ones failed to find any extending BAC clones. We are going through recently updated FES (fosmid end sequence) and SBM (selected BAC mixture) to apply for walking forward. Thirty-five contig ends (out of seventy-two contig ends) were examined. We did not find any candidates from FES data, although a couple of clones overlap around 30 kb. No extending clone was found from FES where there was no extending BAC from BES. Eight SBM contigs matched with our contig end. We will try to find extending BACs from SBM contig sequence by conducting a BLAST against BES data. We are also considering gap closing based on synteny of other reference genomes.

Chromosome 3 (China)

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

Update pending.

Chromosome 4 (UK)

Contact: Gerard Bishop (g.bishop@imperial.ac.uk)

The Wellcome Trust Sanger Institute (WTSI) has left the Tomato Genome Sequencing Project and clone selection plus QC-checking activities have been moved to the Imperial College London. The final statistics of WTSI contribution includes the generation of 18,778,752 bp of unique sequence, (18,056,067 bp finished to phase 3) with 19,018,752 bp total sequence being generated. This sequence comes from 182 BACs/Fosmids of which 174 were finished to phase 3 sequence. The rest of the UK team are very grateful for the WTSI contribution to the Tomato Genome Sequencing Project.

The current focus of the UK's efforts is to confirm that all the sequenced BACs are on chr4 using IL mapping. This is because certain BACs/Fosmids that were selected based on overgo-experiments, FPC data, or contig extension lack the appropriate marker sequence etc. It is likely that we have sequenced BACs that will become available to other sequencing projects. These BACs will be placed on chr0 as soon as we have confirmed that they are not on chr4.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have been able to confirm the position of eighty-three BACs on chr5. Sequencing is in progress on all these BACs, out of which forty-two BACs are in phase III, nineteen BACs are in phase II and fourteen BACs are in phase I. The remaining eight BACs are in the early phase of sequencing or library preparation. All the phase II and phase III sequences have been submitted to GenBank and their assembly data uploaded to SGN. A search is on to find new extension BACs by performing overgo hybridization 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 developing CAPS markers for the 200 BACs assigned to India for mapping.

Chromosome 6 (The Netherlands)

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

Update pending.

Chromosome 7 (France)

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

To date, 167 BACs have been selected and validated on chr7. Among these are ninety seed BACs and seventy-seven overlapping BACs. Ninety-two BACs have been sequenced to phase 2 or 3 and seventy-five are in phase 0 or 1. In the last period, we submitted eleven BAC sequences to Genbank and SGN obtained using the NextGen 454 sequencing method (GS-FLX using Long Paired End Tag reads and Multiplex

Identifiers /MIDs). For each BAC, one unique scaffold has been directly released, which considerably reduces the effort for finishing and allows us to extend from the newly sequenced BACs with no need for further work.

Overall, 16.5 Mb of sequences were generated of which 13.9 Mb are non-redundant (51% of the total estimated euchromatin of chr7). The BACs are organized in thirty-eight contigs on chr7. Our largest contig contains nineteen BAC members and covers 1.75 Mb. It is situated in the distal portion of the chr7 long arm and is covering a genetic distance of 22.5 cM. Our second and third largest contigs are respectively 1.13 Mb (thirteen BACs) and 0.9 Mb (nine BACs) long.

The 3D DNA pools from the HindIII and MboI libraries built in collaboration with the CNRGV, have been completed by the creation of macroarray filters for the entire EcoRI library and the first 150,000 clones of the fosmid library. These new resources are available for all the consortium members.

Overall, we have submitted 125 BAC sequences anchored to chr7 to Genbank and SGN and three BACs were allocated to chr0.

Chromosome 8 (Japan)

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

As of November 20, 2008, 160 BAC clones (91% of initial target) have been completed as Phase 3 that produced a non-redundant length of 15,738,637 bp. An additional twenty-four BAC clones are in the sequencing pipeline.

We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached to 3.4 million files generating 1.9 Gb of total length. These shotgun sequences have been assembled into 205,091 contigs covering approximately 580 Mb regions of the genome.

Chromosome 9 (Spain)

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

Sequencing efforts of chr9 have been stalled due to the lack of suitable resources (BACS, fosmids, etc.) for BAC extension on this chromosome. For seed BACs, all resources have basically been exhausted. All possible useful markers for euchromatic regions or nearby have already been screened by in Silico and by PCR on BAC pools. Currently, there are only eighteen possible extension points (ten from BACs, eight from fosmids). Other groups within the tomato sequencing consortium are having similar difficulties. Members of the consortium are working together to identify strategies that will allow for successful extension and gap filling.

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 (ercolano@unina.it)

To date, sixty-five BAC clones belonging to chr12 have been sequenced using Sanger sequencing technology and twenty-one using pyrosequencing technology. Of these, twenty-three are in HTGS3, twelve are in HTGS2, and twenty-one are in HTGS1, and have been submitted to GenBank/SGN. All of these BACs underwent genetic mapping (IL mapping) to confirm their positions on chr12.

Forty-three BACs have been sent for FISH to the De Jong lab in Wageningen to build a genetic-cytogenetic comparison map. Six of these BACs mapped elsewhere, one was shown to be chimeric, and one had multiple foci.

Sixty-one unannotated BACs and fourteen orphan sequenced BACs were mapped using the IL strategy on various chromosomes to find new seed points for the community and to fill sequence gaps. The data have been uploaded on SGN and the mapping protocol has been distributed to the SOL consortium. Using this strategy, it was also possible to verify that sixteen BACs out of seventy-two previously mapped on chr 12 by Syngenta were shown to map on other chromosomes.

Currently, we are using SSR markers in combination with the BAC pools library for the identification of new sequencing starting points. Moreover, 100,000 fosmid sequences have been uploaded to SGN.

The following is a document that was written following the SOL 2008, The 5th Solanaceae Genome Workshop that was held in Cologne, Germany from October 12 – 16.

The International Solanaceae Genome Project (SOL)

Oct 24, 2008

Dear Friends,
We are pleased to write 'our take' on the SOL2008 meeting, where Christiane Gebhardt and her team facilitated a wonderful set up that resulted in a stimulating and exciting workshop.

Most important were the young new faces that joined our community and presented some truly outstanding science.

Relative to creation of the genome sequence resources that will further enable SOL systems biology: Groups from the Netherlands, Italy and Japan proposed plans for using next generation sequencing tools to provide additional sequence that will facilitate completion of a gold-standard BAC-by-BAC sequence and provide important information on sequences and genes residing in the heterochromatin. This activity will be open to others who are willing and able to participate. The leaders of this exciting effort will prepare a draft outlining their specific plans and circulate it to all sequencing centers. After some frank discussion among all the sequencing partners at SOL it was concluded, "we started the journey walking together and now that new bicycles are invented, we will not leave anybody behind". In short, the objective must remain the generation of a high quality sequence that will enable the broad objectives of SOL systems biology. These new shotgun resources will be a great contribution toward this end.

As far as the ongoing BAC-by-BAC sequencing there are new tools that were not tested yet by the community: the shotgun sequences from Japan and the fosmid end sequences from the UK and Italy – how much do they help in closing gaps are important questions we need to begin to address so that new tools can be developed if needed. Also – synteny based gap closing is a possibility. In this regard, establishing collaborations between groups that sequence the homologous chromosomes in tomato and potato is a key tool for getting the job done more comprehensively and was something that both the tomato and potato consortium members agreed should be pursued.

We also talked about the paper/s:
1) Seeing how long it took us to finish the genome snapshot paper there is a need for increased efficiency. We should set up the framework for the needed + Tables and Figures in a manner that could be continuously updated. Also raised was the concept of a WIKI paper that lets everybody take an active role in the writing process.
2) The community should be aware of the plan for a series of papers that could appear after a Genome paper and build on the sequence for Biology.

We are a driven community committed to finish the sequencing of the tomato genome in a manner that will facilitate future explorations. SOL2009 in India will be important for planning the end game.

Happy SOL

Co-Chairs of the SOL Steering Committee:
Akhilesh Tyagi, Sandy Knapp, Jim Giovannoni, Dani Zamir, Giovanni Giuliano

Announcements

Jobs

Plant Metabolomics/Metabolic Engineering
Assistant Professor
Department of Plant Pathology, Physiology & Weed Science College of Agriculture & Life Sciences
Virginia Polytechnic Institute and State University (Virginia Tech)

The Department of Plant Pathology, Physiology & Weed Science at Virginia Tech seeks applicants for a tenure track position in Plant Metabolomics/Metabolic Engineering at the Assistant Professor level. Research focus should be on plant metabolism and metabolic engineering problems, for example in bio-design, bio-processing, bio-fuels, production of novel compounds, improved quality or yield of existing plant natural products, or other value-added traits. The successful applicants are expected to: 1) develop an extramurally funded, internationally recognized research program, 2) mentor students, and 3) team teach graduate-level courses in plant metabolism. The candidate will participate in a strong interdepartmental Molecular Plant Science graduate program. Additional information about the department can be found at http://www.ppws.vt.edu.

Applicants must complete the application for position #081134 on-line at https://www.jobs.vt.edu. A complete application must include a cover letter, curriculum vitae, a research & teaching statement, and contact information for three references submitted on-line by December 15th. Review of applications will begin on that date and will continue until the position is filled.

Virginia Tech has a strong commitment to the principles of diversity, inclusion, and to maintaining a work and learning environment that is free of all forms of discrimination. As a result this institution does not tolerate discrimination or harassment on the basis of age, color, disability, gender, national origin, political affiliation, race, religion, sexual orientation, or veteran status. Anyone having questions concerning discrimination should contact the Office of Equal Opportunity.

Note: Applications received after the December 15th deadline will still be accepted.

Conferences

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

The 7th World Potato Congress
March 22 - 29, 2009
Christchurch, New Zealand
http://www.wpcnz.org.nz

Solanaceae Recipes

For our final recipe of the Year of the Potato, I thought a hearty potato soup would be a good choice considering many of us are experiencing chilly winter weather. As a matter of fact, this recipe is from a website that is devoted entirely to potato soup recipes. Enjoy!

Creamy Garlic Potato Soup

http://www.potatosouprecipe.com

Ingredients

4 (12 ounces) 99% fat-free chicken broth
2 (12 ounces) evaporated skim milk
5 pounds Russet potatoes, peeled and cubed
5 1/2 cups chopped yellow or white onion
8 slices cooked, crumbled bacon
1 slice ham steak, chopped into 1/2" pieces
2 teaspoons diced garlic
3 bay leaves
1 teaspoon celery seed
1 pint whipping cream
1/3 cup chopped fresh parsley
For garnish:
shredded sharp cheddar cheese
chopped green onion

Preparation

Sauté the onions and garlic in butter or margarine over medium heat until translucent. Scrape them into the soup kettle, and turn on the heat to medium. Pour in the chicken broth and evaporated milk. Put in the potato pieces, bacon, ham pieces, bay leaves, celery seed and whipping cream. Bring to boil, and simmer until the potato is tender. Mash a dozen or so potato chunks against the side of the kettle and stir the pot to thicken the soup (you can mash more to make it thicker). Throw in the parsley and stir, and return pot to simmer. Cut up some good rich bread, ladle the soup into your bowl. Sprinkle cheese and green onion on top to taste.