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Editor: Joyce Van Eck

SOL Newsletter

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Community News

2008 - International Year of the Potato

by Joyce Van Eck

Image taken from the website
http://www.potato2008.org

Potatoes are finally receiving the recognition they deserve. The United Nations (UN) has designated 2008 as the International Year of the Potato, which came about as a result of a nomination by the government of Peru. It is part of a move by the UN to persuade developing countries to adopt potato as a staple crop. To further promote potato as a staple crop, The International Potato Center has organized a forum entitled: Potato Science for the Poor – Challenges for the New Millennium in Cuzco, Peru, March 25-28, 2008 (http://www.cipotato.org/pressroom/iyp.asp).

So, why potato? There are many advantages of potatoes as a staple food crop from both agricultural and nutritional standpoints. Some of the agricultural advantages of potatoes are that they produce more on less land and more quickly even under adverse climate conditions than other major staple food crops. From a nutritional standpoint, one medium-sized baked potato provides about one-third of the Recommended Dietary Allowance (RDA) of vitamin C, 25% of the RDA for calcium and 10% of the RDA for iron, whereas, rice in an equivalent serving size provides 1% of the RDA for iron.

In honor of the International Year of the Potato, I'd like to feature articles in future issues of the SOL Newsletter from those of you who work with potatoes. I'm especially interested in any information on what you and/or your organization are doing to highlight potatoes during 2008. You can send your information to me at jv27@cornell.edu. I'll also be sending out reminders for potato articles prior to upcoming newsletters.

Websites used as a resource for this article:
http://www.potato2008.org
http://www.fao.org/ag/magazine/0611sp1.htm
http://www.idahopotato2008.org/
http://www.cipotato.org/pressroom/iyp.asp

ISOL@: an **I**talian **SOLA**naceae Genomics Resource

Contributed by Maria Luisa Chiusano

We are pleased to announce "An **I**talian **SOLA**naceae genomics resource, ISOL@ (http://biosrv.cab.unina.it/isola/)" designed to provide full web access to details of the genome annotation based on experimental evidence derived from EST/full-length cDNA sequences (Chiusano et al., 2008).

The EST database gateway allows the EST/transcript resources, their annotation and their expression patterns to be explored. EST collections were processed using the ParPEST pipeline (D'Agostino et al., 2005). Sixteen EST collections from different *Solanaceae* (14) and *Rubiaceae* (2) species - retrieved from dbEST – are now available.

In case of the tomato EST dataset, the annotation procedure includes the detection of correspondences with the tomato clones from the cDNA arrays TOM1 (http://ted.bti.cornell.edu/) and the probe-sets from the Affymetrix Tomato Genome Array chip currently available. Crosslinks with other platforms can be considered upon request.

The resulting data are organized into relational databases (D'Agostino et al., 2007a) and can be navigated via 'user-friendly' interfaces. A web-based application allows the transcripts to be mapped on-the-fly onto the KEGG metabolic pathways.

The Genome Browser gateway (http://biosrv.cab.unina.it/GBrowse) provides details on the EST-based annotation of the *S. lycopersicum* BAC sequences. The annotation consists of the spliced alignments of the EST/TC collections included in the local EST databases. Furthermore, the tomato gene index, retrieved from SGN (Tomato 200607 build 1) and TIGR (LeGI gene index Release 11.0), are also mapped onto the BACs.

Protein tracks, from the whole UniProt dataset, classified into 3 categories (*Solanaceae*, *Viridiplantae*, all the *other Uniprot* data) are also available as well as the alignments of the TOM1 cDNA clones and the Affymetrix Tomato Genome Array probe-sets.

The genome coordinates of the ESTs and the TCs, which were independently aligned to the BACs, are exploited by the GeneModelEST tool (D'Agostino et al., 2007b) in order to identify TCs appropriate for the definition of gene models and to classify TCs representing putative alternative transcripts. In addition, GeneModelEST checks if the '*expressed*' loci may represent full-length products taking advantage of the TC functional annotations stored in the EST databases, and, as a consequence, supports the definition of complete coding sequences based exclusively on EST evidence.

ISOL@ provides information from both the genome and the transcriptome levels, which are cross-linked to support web-based navigation. This platform permits an immediate analysis of genes and gene families according to their functional annotation and investigations on gene specific expression patterns, linking the data to reference expression arrays within the *Solanaceae* community.

Chiusano M.L., D'Agostino N., Traini A., Licciardello C., Raimondo E., Aversano M., Frusciante L, Monti L. (2008) ISOL@: an Italian SOLAnaceae genomics resource. *BMC Bioinformatics*, 9 (Suppl 2):S7.

D'Agostino N., Aversano M., Frusciante L., Chiusano M.L. (2007a) TomatEST database: in silico exploitation of EST data to explore expression patterns in tomato species. *Nucleic Acids Research*, 35 (Database issue):D901-905.

D'Agostino N., Traini A., Frusciante L., Chiusano M.L. (2007b) Gene models from ESTs (GeneModelEST): an application on the *Solanum lycopersicum* genome. *BMC Bioinformatics*, 8 (Suppl 1):S9.

D'Agostino N., Aversano M., Chiusano M.L. (2005) ParPEST: A pipeline for EST data analysis based on parallel computing. *BMC Bioinformatics*, 6 (Suppl 4):S9.

Tomato Sequencing Updates

Chromosomes 1, 10 (US)

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

To date, we have sequenced twenty-five BACs. In January, we submitted a proposal to the NSF Plant Genome Research Program for continued funding of our sequencing efforts. Sequences for 100,000 fosmid ends are now available in the SGN database.

Since the publication of the last newsletter (November 2007), the Stack lab at Colorado State University has used fluorescence *in situ* hybridization (FISH) to localize an additional nineteen BAC clones on tomato pachytene synaptonemal complex spreads. This brings the total number of clones positioned by this lab to 135, distributed among the chromosomes as follows: 1 – 19; 2 – 6; 3 – 13; 4 – 16; 5 – 10; 6 – 9; 7 – 12; 8 – 4; 9 – 18; 10 – 10; 11 – 13; 12 – 5. The newly localized clones are listed below.

Chromosome Arm	**BAC ID**
3Q	LE_HBa0254B14
5P	LE_HBa0107A04
6Q	LE_HBa0055B14
6Q	LE_HBa0068M14
7P	LE_HBa0173A21
9P	LE_HBa0308C20
9P	LE_HBa0197E10
10P	LE_HBa0237A02
10P	LE_HBa0222H10
10Q	LE_HBa0043B12
10Q	LE_HBa0037N23
10Q	LE_HBa0053L19
10Q	LE_HBa0156C03
10Q	LE_HBa0011E16
10Q	LE_HBa0256L16
11P	SL_MboI0052K14
11P	LE_HBa0128G07
11Q	LE_HBa0245M17
12Q	LE_HBa0055G18

Chromosome 2 (Korea)

Contact: Sanghyeob Lee (sol6793@kribb.re.kr)

Update pending.

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)

11,433,963 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr4 as of February 20th, 2008. Of this figure, 10,822,500 bp are unique. The sequence has been produced from 106 BACS originating from the LE_HBa and SL_MboI libraries. We intend to finish all BACS that will contribute to chr4 to HTGS phase 3 and currently eighty-five BACs that correspond to 8,892,163 bp of sequence have been deposited in the public databases at EMBL/GenBank/DDBJ as phase 3. All other chr4 BACs with EMBL/GenBank/DDBJ accessions are currently active in our sequencing pipeline at HTGS phases 0 to 2.

FISH analysis for additional chr4 contig confirmation performed by the Hans de Jong Laboratory in Wageningen has identified a number of heterochromatic BACs that do not localize to chr4. This affected a total of seven chr4 contigs and eight BACs, which were finished to HTGS phase 3. These BACs have been removed from the chr4 minimal tilepath and will be given a chromosome designation of "unknown" on SGN in the near future. We will continue to use the FISH analysis as a resource for mapping confirmation. Additional chr4 BACs are being verified as potential sequencing candidates following a round of hybridizations for missing markers.

In addition to further chr4 BAC selection, 10,7861 fosmid end sequences were generated at WTSI at the beginning of December 2007 and deposited in the ensembl trace archive in mid-January 2008. These fosmid end sequences are currently in the process of being uploaded to SGN.

The progress of chr4 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.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have been able to confirm sixty BACs on chr5. Sequencing is in progress on all these BACs, out of which nineteen BACs are in phase III, twenty-four BACs are in phase II and eleven BACs are in phase I. The remaining six BACs are in the early phase of sequencing or library preparation. We have been able to successfully pick more BACs using the SSR markers generated by Japan by performing overgo hybridizations on the filters available for the three tomato libraries. In addition, new nucleation points could also be identified from the CAPS markers developed using the 200 BACs assigned to India for mapping purpose.

Chromosome 6 (The Netherlands)

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

We have closed the BACs E097J14, E099J22, E120K02, E129O21, H010E05, H057D21, H084A18, M060E11, M065P01, and M099A03, which map in the long arm of chr6. In total, forty BACs have now been closed. 115 BACs are in the finishing pipeline. For chr6 we have 17.1 Mb of sequence, of which 12.6 Mb is non-redundant.

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Update pending.

Chromosome 8 (Japan)

Contact: Erika Asamizu: (asamizu@kazusa.or.jp)

We finished 107 BACs to Phase 3 that produced a non-redundant length of 11,050,648 bp. We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached 1.4 million files generating 1 Gb of total length. This is half the number of our initially targeted goal. Gene coverage survey using the tomato Gene Index data showed that 60% of the tomato genes were covered by the current SBM data.

Chromosome 9 (Spain)

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

During the last two months, progress on chr9 has focused on the finishing stages. Currently, we have completed fifty-eight BACs and fifteen additional BACs are close to completion. Eight new extension BACs have been identified by different strategies (in silico and 3D BAC pools screen) and after confirmation are in the sequencing pipeline.

We have done FISH (Hans de Jong's lab) for a number of initially selected BACs because they contained markers for chr9, but failed to give a sequence polymorphism in the ILs corresponding to chr9. Four out of nine BACs selected according to the Syngenta FPC landed finally by FISH on a different chromosome. In this case, we started with nine BACs that according to the FPC were in the same contig but did not overlap to BACs previously sequenced on chr9. Sequencing of the DNA region of the ILs corresponding to both BES from several of those BACs, failed to give a polymorphism. The same situation also occurred in two BACs selected with Syngenta and Expen2000 markers for chr9.

The success rate in identifying BACs useful for the sequencing project using chr9 markers provided by Syngenta has been higher than those selected according to the Syngenta FPC information. In some cases the map position provided by Syngenta in cM failed to predict the final heterochromatic physical localization as indicated later by FISH to be in the pericentromeric region. We are currently assaying these two BACs for hybridization against different repetitive sequence fractions and also for gene content to help us in deciding whether or not to sequence them because they show typical heterochromatic features.

Chromosome 11 (China)

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

Currently, thirteen BACs have been finished as Phase 3, and four are at Phase 2. Eight new seed and nine extension BACs are being confirmed for sequencing. Three BACs were selected through comparative genome sequencing based on the potato genome and have been confirmed by FISH on chr11 by the Stack Lab at Colorado State University. Among them, LE_Hba0245M17 is close to the euchromatin/heterochromatin border, and 0.9M is estimated between this BAC and the border. In order to speed up chr11 sequencing, we are developing new markers to screen additional seed BACs.

In addition, LE_Hba0107A04, which has been finished to Phase 3 and has been localized on the short arm of chr5 by the Stack lab.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

Currently, seventy BACs are in various stages of the sequencing process. Of these, eighteen are in HTGS3, nine are in HTGS2, and twenty-one are in HTGS1. They have been submitted to GenBank/SGN. The map positions of sixteen BACs previously mapped on chr12 by Syngenta have been verified using IL mapping procedure. Of these, nine were confirmed on chr12, while seven map on other chromosomes. Moreover, thirty-two BACs have been de novo mapped on various chromosomes, of which three are on chr12. The data obtained will be uploaded on SGN. Twelve seed BAC clones have been sent to the de Jong lab in Wageningen for FISH for further verification.

Tomato Genome Sequencing Meeting

An all-day meeting was held for participants of the tomato genome sequencing project during the Plant and Animal Genome Conference in January. Updates on sequencing progress were presented by representatives from the various groups. In addition, presentations were given on FISH analyses and progress on the physical map. Presentation files, meeting notes, and the agenda are available on SGN (www.sgn.cornell.edu) by following the link on the home page for Bioinformatics Resources.

Participants of the Tomato Genome Sequencing Meeting held during the Plant and Animal Genome Conference in January. Photo provided by Nagendra Singh.

What's New on SGN?

SGN has recently integrated seven QTL populations consisting of over 800 individuals with 900 images and over 300 fruit shape lines, including 864 images. In addition to the images, the dataset contains trait measurements for over thirty different traits, mapping information, and polymorphism information. The populations and images are already available and the other data will be loaded over the next few days.

The information can be accessed through the SGN phenotype search at http://sgn.cornell.edu/search/direct_search.pl?search=phenotypes. Many thanks to Esther van der Knaap for her efforts to provide the complete data set.

Locus Editors

SGN now has over forty-two locus editors for 125 distinct loci. Please consider becoming a locus editor for your favorite *Solanaceae* locus. Locus editors can edit the information about a locus through the web with easy to use interfaces. You can upload descriptions, ontology terms, images, literature associations, and comments. All edits are live immediately. Requests for locus editorship can be sent to sgn-feedback@sgn.cornell.edu or by using the link on any locus page.

Announcements

Publications

Cillo F, Pasciuto MM, De Giovanni C, Finetti-Sialer MM, Ricciardi L, Gallitelli D (2007) Response of tomato and its wild relatives in the genus *Solanum* to cucumber mosaic virus and satellite RNA combinations. J Gen Virol. Nov; 88(Pt 11):3166-3176.

Mattoo AK, Chung S-H, Goyal RK, Fatima T, Solomos T, Srivastava A, Handa AK (2007) Overaccumulation of higher polyamines in ripening transgenic tomato fruit revives metabolic memory, upregulates anabolism-related genes, and positively impacts nutritional quality. J AOAC International 90:1456–1464.

Mattoo AK, Handa AK (2008) Higher polyamines restore and enhance metabolic memory in ripening fruit. Plant Sci doi:10.1016/j.plantsci.2008.01.011.

Toppino L, Mennella G, Rizza F, D'Alessandro A, Sihachakr D, Rotino GL (2008) ISSR and isozyme characterization of androgenetic dihaploids reveals tetrasomic inheritance in tetraploid somatic hybrids between *Solanum melongena* and *Solanum aethiopicum* group Gilo. J Hered, February 2, 2008, 10.1093/jhered/esm122.

Virus des Solanacées : du génome viral à la protection des cultures. Marchoux G, Gognalons P, Gébré Selassié K, coord. Ed. Quae, Collection Synthèses 2008, 843 pages. ISBN 978-2-7592-0076-4 ISSN 1777-4624.
You can get a look at the book by connecting to:
http://www.quae.com/livre/?GCOI=27380100992530
The catalogue of Quae Editions and on line purchase at: www.quae.com
The book costs 85 Euros + transportation fees.

Conferences

SOL 2008

Rhine River, Cologne, Germany

The 5th Solanaceae Genome Conference (SOL2008) will be held from October 12 - 16 in Cologne, Germany. The conference is being organized by the Max-Planck-Institute for Plant Breeding Research (MPIZ). At this time, the committee is planning for a scientific program of approximately two days of plenary sessions, five to six satellite workshops, and a poster session.

If you have suggestions for session topics or other items, you can contact Christiane Gebhardt at gebhardt@mpiz-koeln.mpg.de.

A website and information on registration, conference site, accommodation, etc. will be available soon.

4th European Plant Science Organization (EPSO) Conference
Near Toulon (Côte d'Azur), France, June 22 - 26, 2008

The fourth EPSO Conference - which will explore the theme 'Plants for life' - will be held on the beautiful French Côte d'Azur, near Toulon, from June 22 - 26, 2008. The conference will address many of the challenges faced by the plant research community in an evolving world: climate change, preservation of the environment and of natural biodiversity, as well as the food and feed demands of a growing world population. Non-food crops for energy, biomaterials, biopharmaceuticals and other new products will also be an important focus of the conference.

The fourth EPSO Conference will bring together international scientists and experts who will provide insights into the most recent breakthroughs in the fields of genome structure and evolution, evolutionary biology, developmental biology, ecophysiology, system biology, economics, plant breeding and the challenges facing developing countries.

The conference is organized by the EPSO Board and coordinated by Karin Metzlaff, EPSO's Executive Director, and Hélène Lucas, Director of the Genetics and Plant Breeding Division at the French National Institute for Agricultural Research (INRA).

EPSO is looking forward to welcoming you in southern France.

Important dates:
Registration deadline: May 11, 2008
Abstract submission: April 25, 2008 (to be considered for speaker selection), May 11, 2008 (poster presentation)

Weblinks:
Conference webpage: http://www.epsoweb.org/catalog/conf2008.htm
Registration: http://www.epsoweb.org/catalog/conf2008/register.htm
Program: http://www.epsoweb.org/catalog/conf2008/4CF_Programme_web.pdf

Solanaceae Recipes

To celebrate the International Year of the Potato, potato recipes will be featured throughout 2008. This recipe for Potatoes Au Gratin is a favorite of my family. If you have any potato recipes you would like to share, send them to Joyce Van Eck (jv27@cornell.edu).

Potatoes Au Gratin

From Food Network (http://www.foodnetwork.com)

1/3 cup unsalted butter, softened
1 1/2 pounds potatoes, peeled and cut into 1/4-inch-thick slices
1/2 cup grated Gruyere
1/2 cup freshly grated Parmesan
1 cup heavy cream
1 teaspoon salt
1/2 teaspoon ground black pepper
1/8 teaspoon paprika

Preheat the oven to 350 degrees F.

-Butter a 1 1/2 quart baking dish with about 1 tablespoon of the softened butter.
-Arrange a layer of potatoes in the baking dish, and sprinkle some of the cheeses over them.
-Continue layering potatoes and cheeses until you've used them all, ending with a layer of potatoes.
-In a small bowl, whisk the cream with the salt and pepper; pour this over the potatoes.
-Dot the remaining butter over the top and sprinkle with the paprika.
-Bake for 1 to 1 1/4 hours, or until the potatoes are tender and golden brown on top.
-Let stand for 5 minutes before serving.

Potato Peanut Butter Candy

When I was looking for potato recipes for this issue of the newsletter, I was curious if there were any recipes for potato desserts, so I did a search on the internet. I found this one at http://www.cooks.com, but can't give any recommendation because I haven't tried it. Although, if I do make it, I think chocolate, one of my favorites would be a good addition!

1 large potato, cooked & peeled
Powdered or confectioner's sugar
Peanut butter

-Mash potato with powdered sugar, may take 1 pound or more.
-Mix until a stiff dough is formed.
-Roll out like dough on a surface dusted with powdered sugar.
-Spread with peanut butter.
-Roll up like a jellyroll.
-Refrigerate for at least 1 hour.
-Cut into slices.