



The 2nd Solanaceae Genome Workshop

September 25 - 29, 2005
Island of Ischia, Italy

The deadline for early registration and abstract submission is **June 15**. Please see the meeting website (www.solanaceae2005.org) for details.

Sunday, September 25

- Registration
- Opening Lecture: Dani Zamir, Hebrew University, IL
- Welcome party

Monday, September 26

- Session 1:** Asterid comparative genomics
Keynote Lecture: Steven D. Tanksley, Cornell University, US
- Session 2:** Plant/biotic interactions
Keynote Lecture: Greg Martin, Boyce Thompson Institute, US
- Session 3:** Plant/environment interactions
Keynote Lecture: Klaus-Dieter Scharf, Frankfurt University, DE
- Session 4:** Fruit and tuber development
Keynote Lecture: Jim Giovannoni, USDA-ARS, US



Tuesday, September 27

- Session 5:** Vegetative development
Keynote Lecture: Harry Klee, University of Florida, US
- Session 6:** Floral and reproductive biology
Keynote Lecture: Titti Mariani, University of Nijmegen, NL
- Session 7:** Metabolomics
Keynote Lecture: Alisdair Fernie, MPI Golm, DE
- Session 8:** Signal transduction
Keynote Lecture: Chris Bowler, ENS Paris, FR

Wednesday, September 28

- Session 9:** Biodiversity and breeding
Keynote Lecture: Meredith Bonierbale, CIP, PE
- Session 10:** Status of genome sequencing in Solanaceae species
Keynote Lecture: Satoshi Tabata, Kazusa DNA Research Institute, JP
- Closing lecture: To be announced

Satellite meetings

- Tomato: Chair Lukas Mueller (US)
- Potato: Chair Christiane Gebhardt (DE)
- Tobacco: Chair Paolo Donini (CH)
- Petunia: Chair Tom Gerats (NL)
- Pepper: Chair Ilan Paran (IL)

Farewell banquet

Thursday, September 29

- Satellite meetings (cont'd)
- SOL Steering committee
- Departure



Tomato Sequencing Updates

Chromosomes 1, 10, 11 (US)

The EcoRI BAC library is now complete (approximately 7X) and represents the third library that will be end sequenced to facilitate development of the minimal tiling path for sequencing.

New BAC data was posted on SGN, including data from the HindIII and Mbol libraries. See the "What's New on SGN" section of this newsletter for additional details and information on how to access the data.

Please see the supplemental data file that accompanies this newsletter on SGN (www.sgn.cornell.edu) for FISH images related to this part of the update. These images illustrate results of in situ hybridization with eight tomato BACs. Putative locations for the BACs are included in the captions. All of these experiments were performed without CISS hybridization. On the basis of these results, two of the BACs (045N22, 098L02) (Figure 1) appear to contain only single-copy sequences. The other six contain multiple-copy sequences present either predominantly in the pericentromeric heterochromatin of all of the chromosomes (007K09, 098L02, 251G05, 060G11) or at multiple telomeric locations (209L16, 216M19). One of the BACs having multiple-copies sequences in the pericentromeric heterochromatin (177F12) also has a locus of hybridization at the telomere of the long arm of Chromosome 2. We are currently performing additional experiments with these BACs using CISS hybridization with Cot100 tomato genomic DNA to determine whether their single-copy sequences can be specifically located.

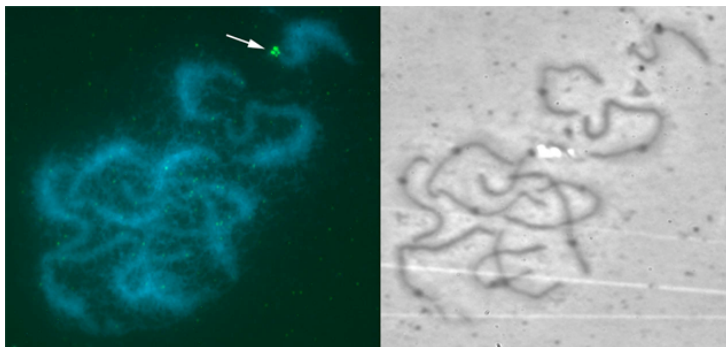


Figure 1: 045N22 Chromosome 12 – Telomere P. Additional images related to this update can be found as a supplemental file posted along with this newsletter on SGN.

Chromosome 2 (Korea)

We recently finished 17 BACs and are currently doing annotation of these BACs. In addition, 10 BACs are waiting for finishing. We now have one problem in the BAC extension of the 17 finished BACs. Currently, we are using BAC end sequences, and FPC contig information. We could not find any extended BACs with minimum overlapping with previous ones. We usually found overlapping with the new BACs to be 30~50 kb. In addition, the small size of the FPC contig also made it difficult to pick up the next BAC. Therefore, the US group was contacted with these questions: 1) When will we get the full BAC end sequences and more upgraded FPC data? 2) Should we wait for a while or do we need to screen the BAC libraries with BAC end probes (generated from already finished BACs) for BAC extension?



Chromosome 3 (China)

We received the HindIII BAC library in April. DNA sequences of 20 FISH-confirmed BACs were determined and we are currently focusing on data analysis and gene annotation.

Chromosome 4 (UK)

Although the project is in the early stages, we have already obtained copies of the available BAC libraries. Both the HindIII library (129,000 clones) that was used to generate the physical map and the Mbol library (55,000 clones) are at Sanger with the EcoRI due for delivery once construction is complete. The libraries will be used to isolate BAC clones selected for sequencing as well as represent a resource for further targeted mapping experiments to increase map continuity across chromosome 4.

We have downloaded the Tomato FPC (FingerPrintContig) database from the Arizona Genomics Institute. There are currently 88,584 fingerprinted clones and 7155 contigs within the database. In silico assessment and verification of contigs currently assigned to chromosome 4 is underway. In addition, potential contig merges will be identified and examined prior to sequence clone identification.

Chromosome 5 (India)

All logistics and researchers for sequencing are in place and in silico analysis is being done to help start the work when the shipment of libraries and anchored clones arrives.

Chromosome 6 (The Netherlands)

Till now, a total of 52 BACs has been mapped on chromosome 6 using AFLP markers and also some available RFLP markers. After FISH analyses, a total of 30 BACs was found suitable for sequencing. The remaining BACs were either derived from heterochromatic regions on chromosome 6, or were derived from different chromosomes. Of the 30 selected BACs, 16 BACs have been completed to Phase 1 and a further 11 BACs are currently in the sequencing pipeline.

First results have been obtained in using the BAC-end library, which at present holds 40,000 BAC-ends from the HindIII library. When 6 finished tomato-BACs were used for screening the BAC-end library by BLASTN, 5 out of the 6 BACs gave multiple hits with various BAC ends. Two BACs were studied in more detail to assess the relevance of the obtained BLASTN-hits. It appeared that overlapping BAC clones could be obtained that shares only a very small part of overlapping DNA (in the order of a few kb). However, a large percentage of the BAC-end hits appeared to be false positive due to the presence of repetitive DNA in the BAC-ends themselves. Therefore, it was concluded that a thorough verification of potential overlapping BACs is an absolute requirement when using the BAC-end sequence data. Currently, the first two BACs selected using the BAC-end data are sequenced.

Chromosome 7 (France)

Funding has been secured for sequencing chromosome 7. The active phase of the project will begin in June 2005. Anchored seed BACs and two BAC libraries (HindIII and Mbol) have been requested.

Chromosome 8 (Japan)

We received 42 BAC clones corresponding to 8 DNA markers on chromosome 8. Sequencing of three BAC clones associated with the markers, CT64, CT68 and CT148, has been completed, and gene modeling and annotation have been carried out. We performed fingerprinting analysis of the BAC clones for the remaining five markers in parallel with sequencing of the PCR products from primers based on the marker sequences. We were able to select two BAC clones associated with T1123 and TG176. Sequencing of these clones is in progress.

Chromosome 9 (Spain)

The Spanish SOL project has been funded. The project title is "Identification of genes and molecules associated to tomato fruit quality and participation in the sequencing of euchromatic regions of Chr 9. A genomics approach." Funding will be for three years and we have put together a consortium of scientists from universities, research institutes, and two companies.

The total budget is 3 MEuros, which includes 1 MEuro for our participation in the sequencing of Chr 9.

Chromosome 12 (Italy)

A mapping effort based on FISH and *L. pennellii* introgression lines analysis was initiated to integrate information based on overgo hybridization, FPC physical map, and BAC-end sequencing. The positions of three BACs previously identified through PCR-marker association were confirmed by means of SNP polymorphisms. Moreover, FISH mapping of five clones is in progress at Steve Stack's laboratory. Out of three BAC clones sent to the sequencing service, two are in the finishing phase. An overlapping approach has begun for the identification of additional clones to extend the sequencing area in FPC contigs 26 and 1022 using BAC-ends. To increase starting points for sequencing, new candidate seed BACs are under selection on both arms of chromosome 12.

Community News

Potato Genome Sequencing Consortium (PGSC)

Provided by: Richard G.F. Visser & Christian C.W. Bachem

Potato is one of the world's most important food crops with a large associated industry both in the production of the crop and in the processing to food, feed and other industrial uses. The conventional breeding of this crop plant is, however, hampered by its highly heterozygous tetraploid genome and the fact that it is vegetatively propagated. The application of modern molecular methods developed in model species, such as *Arabidopsis thaliana*, is increasingly implemented in potato. The availability of genomic sequence data will make HTP methods available for this key food crop.

A worldwide consortium of research teams from academia has recently been set up with the express aim of determining the complete sequence of the potato genome (Potato Genome Sequencing Consortium). This ambitious project is being coordinated by Wageningen University and Research Center in the Netherlands and is supported by the Dutch National Genomics Initiative. The sequence strategy is centered on the availability of a detailed high-density molecular marker map of more than 10,000 markers, combined with an anchored high-quality physical map of BACs from a diploid *Solanum tuberosum* genotype that also has a very large linked phenotypic data set.



Participating countries have elected to take a chromosome-by-chromosome sequencing strategy and the consortium is rapidly covering the complement of 12 available linkage groups. In the vanguard of countries ready to start sequencing in the framework of financed projects are New Zealand, China, India and the Netherlands with countries including Canada, the United Kingdom and Poland expecting to have grants accepted shortly. A large number of additional countries have either made a direct commitment to sequence parts of the potato genome (Brazil, Finland) and/or are currently looking into the possibilities of securing funding for national projects (France, Japan, USA).

For further information please contact:

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The New Kid in the SOL Neighborhood - Coffee

Update provided by: André Charrier

A meeting to launch the International Coffee Genome Network (ICGN) took place 4-5 April 2005 in Paris. Twenty-nine scientists from 12 countries were in attendance. It was a critical step for ensuring future collaboration in coffee genomics allowing initial steps to be taken for the development of six thematic working groups. Objectives for each of the scientific working groups were established as well as the designation of their respective coordinators. A summary of the meeting will provide further background information about the establishment of ICGN, its mission, goals, and organization (membership, steering committee) as well as giving a brief description of the different thematic groups. Additional information can be found at <http://www.coffeegenomics.org> or you can contact André by e-mail at andre.charrier@ensam.inra.fr (andre.charrier@ensam.inra.fr).

The Solanaceae Collection of the Botanical and Experimental Garden, Radboud University Nijmegen, the Netherlands.

Contributed by:
Gerard M. van der Weerden

The Botanical and Experimental Garden pays special attention to the Solanaceae. The major goal is the conservation and exploitation of Solanaceae germplasm of wild species preferably from known origin. More than forty years ago the Botanical and Experimental Garden initiated its collection. This has over the years resulted in the most extensive *ex situ* Solanaceae germplasm collection of non-tuber bearing Solanaceae in the world. Accessions were gathered via the international seed exchange between botanical gardens, from research institutes as well as by sharing samples from collecting trips. A worldwide collaboration and/or exchange have been established. During the last decade, strong collaboration was established with the Birmingham University Solanaceae collection. During that time, many Birmingham accessions were imported and included in the Solanaceae collection of the Botanical and Experimental Garden of the Radboud University. After the discontinuation of the Birmingham University Solanaceae collection, a large part of the collection was taken over by the Botanical and Experimental Garden of the Radboud University. First priority was given to the regeneration of rare and threatened species. The Solanaceae collection is a part of the Dutch Decentralized National Plant Collection.

Excellent greenhouse facilities allow us to grow Solanaceae accessions year-round. Due to the outside climate conditions, there is no risk that species cultivated in the greenhouses will become invasive weeds, as they will not survive our winters. Harvested seeds are cleaned and carefully dried, put in labeled bags and stored together with silica gel in deepfreeze boxes at about 2°C in a cold room. Since the implementation of the Convention on Biological Diversity, seeds are available on request for scientific research, conservation of species, and the development of recognized plant collections.

The Solanaceae collection maintained at the Botanical and Experimental Garden is well documented by passport data, pictures, herbarium specimens and bibliographic information. To make all this information on Solanaceae readily available to interested parties, all this information is stored in databases, which can be searched online.

The databases are accessible via our website: <http://www.bgard.science.ru.nl>. The Solanaceae database has been developed according to the EURISCO field descriptions for passport data. The search facilities as well as the result pages developed at our department are similar to the ECP/GR Central Crop Databases.



Solanum lidii



Solanum mammosum



Jaborosa sativa

The taxonomic as well as research literature on Solanaceae is very dispersed and not completely covered by digital reference systems and are therefore difficult to find and barely accessible. Therefore, an extensive computer based reference on Solanaceae system has been built. The Solanaceae literature database is online searchable via our web site as well as via our online Solanaceae database and also via the ECP/GR Central Crop Databases developed at our department, since all plant names in these databases are linked to their associated literature references in our Solanaceae literature database.

The Solanaceae collection is also used for research purposes. Within the Institute for Wetland and Water Research, to which the Botanical and Experimental Garden belongs, two other groups are strongly involved in Solanaceae research.

- Department of Genetics, head Prof. Dr. A.G.M. Gerats.
- Department of Plant Cell Biology, head Prof. Dr. C. Mariani

In collaboration with the Department of Cell Biology we participate in the following projects:

- 'Identification of new sources of resistance in wild accessions of *Solanum* section *Solanum*.' This project is a part of the Centre for Biosystems Genomics Programma Potato Genomics. The PhD student involved in this project is Tomasz Golas.
- 'African *Solanum* section *Solanum*: Molecular Systematics'. This is a PhD project carried out by L.M. Manoko, a PhD student from the University of Dar es Salaam, Tanzania.
- 'Diversity, nutritional value, alkaloid content and organoleptic quality of vegetable nightshade (*Solanum* section *Solanum*).' For one year, Gideon Njau Mwai, a tutorial fellow at Maseno University in Kenya and one of the winners of the 2005 Vavilov Frankel Fellowship awards, will stay at our department to carry out his research project.

From 01-01-2000 till 31-03-2005, we participated in EGGNET. This project was funded by the European Community and entitled: Management, Conservation and Valorization of Genetic Resources of Eggplants (*Solanum* species). The main objective of this project was to coordinate the work in the European Union on the conservation of eggplants and related species so as to enhance and ensure their long-term utilization. This project has also lead to the ECP/GR Eggplant database for which an online search website was developed by our Botanical and Experimental Garden.
<http://www.bgard.science.ru.nl/WWW-IPGRI/eggplant.htm>

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What's New on SGN?

SGN sports a new design and a more intuitive home page. We hope that you like it -- please let us know if you have any issues (sgn-feedback@sgn.cornell.edu). Additional information about recent improvements on SGN will be mailed to the SGN announce mailing list. Please subscribe to that list if you haven't already done so. Go to SGN (<http://sgn.cornell.edu/>) and click on the link found on the bottom of every page, "subscribe to sgn-annoucne for updates" to subscribe. Follow the directions. Also, consider making your contact address and interests available on the SGN people database. Go to http://sgn.cornell.edu/cgi-bin/search/direct_search.pl?search=Directory and click on Add/modify information. (Check if you are already in the database first by searching the database with your name).

The first sequences from the Mbol BAC library are available from the SGN ftp server and will also be added to the searchable SGN BAC end database soon. This first batch includes 12,144 sequences from both ends. In addition, 99,328 high quality sequences from a nominal 120,000 reads are now available for the HindIII library. The data can be downloaded from the ftp site at:

ftp://ftp.sgn.cornell.edu/tomato_genome/bac_ends/seq_dir/hindIII/vector_screened/bacends_trimmed_120_2.seq.gz and
ftp://ftp.sgn.cornell.edu/tomato_genome/bac_ends/seq_dir/mbol/vector_screened/bacends_trimmed_14.seq.gz

The BAC database search can be queried at: http://sgn.cornell.edu/cgi-bin/search/direct_search.pl?search=BACs

Job Announcements

Imperial College London
Faculty of Life Sciences, South Kensington Campus

Division of Molecular Biosciences

Genome Annotator, Tomato Genome Sequencing Project

Up to 3 years on Research & Education level B, starting salary guide £ 26,652 (full scale £22,116 - £32,232 including allowances)

The Centre for Bioinformatics seeks a genome annotator to join the UK project to sequence and annotate chromosome 4. The postholder will be expected to provide manual annotation and curation based on automated annotations produced by our collaborators.

The successful candidate will be a postdoctoral scientist with direct experience of hands-on genome annotation and knowledge of *Solanaceae* or other plant genomes. Applicants should have sound understanding of the principles of eukaryotic genome annotation, experience working on a genome annotation project, and a PhD in a relevant discipline or equivalent experience. Familiarity with the genetics of the *Solanaceae*, would be an advantage.

For informal enquiries, please contact Dr Sarah Butcher (s.butcher@imperial.ac.uk). For the full job description, application form and procedure please see www.ic.ac.uk/bioinformatics/bio_jobs.html.