



Contents of this Issue

| <u>Item</u> | <u>Pages</u> |
|--|--------------|
| <i>Community News</i> | 1 - 2 |
| <i>Tomato Sequencing Updates</i> | 2 - 3 |
| <i>Global Strategy on Plant Conservation</i> | 4 |
| <i>What's New on SGN?</i> | 5 |
| <i>Conferences and Workshops</i> | |
| <i>-Plant and Animal Genome</i> | 5 |
| <i>-Solanaceae 2006</i> | 6 |
| <i>Solanaceae Recipes</i> | 7 |

Community News



The following is a letter that was sent recently to the SOL Steering Committee.

Dear SOL-Steering Committee Members,

The SOL2005 meeting, which was attended by 350 scientists, demonstrated the momentum and incredible synergy generated by our initiative. Ischia was a wonderful setting for SOL2005 with many opportunities for people to interact, strike new collaborations and enjoy the wonders of this beautiful island. It was clear that SOL science is entering a new era with greater funding and an ever-increasing number of new research groups and ideas for working together. We were very glad to have with us representatives from the coffee research community and hope that in the future we will be able to enrich our genetic diversity with additional Asterids – there are a lot to choose from!

Our next meeting, to be held in Madison, Wisconsin, USA (Solanaceae2006 – organized by David Spooner), will be conducted along a theme of “Genomics meets Biodiversity”. We agreed in Ischia that for future SOL meetings we will give an opportunity for additional groups to present their work by not having the same speakers in two consecutive years. Furthermore, we will try to conduct each meeting under a somewhat different theme to increase our knowledge about the different dimensions of SOL and to enable the connections between different plant science disciplines to be made under the SOL umbrella.

This larger vision for the future should not distract us from our current PRIMARY OBJECTIVE, which is to obtain high quality sequence of the tomato genome. In the coming two years we will have to focus our efforts and resources to shift sequencing and bioinformatics into a higher gear in order to achieve this goal.

Finally we take this opportunity to thank Prof. Luigi Frusciante and the Italian organizing Committee for making the Ischia meeting such an amazing and enjoyable celebration of science and pleasure.

Happy SOL
Sandy Knapp and Dani Zamir



Coffee and the Solanaceae

Researchers at Cornell and the Nestlé Research Center have published the results of their joint effort to generate an EST database for coffee, which corresponds to approximately 13,000 unigenes. The paper, "Coffee and tomato share common gene repertoires as revealed by deep sequencing of seed and cherry transcripts" was published in Theoretical and Applied Genetics (TAG) and can be found at this time on the Springer-Verlag link for TAG under the "Online First" option. It is also available as "open proof" on several web sites to make it freely available worldwide. A comparison of the coffee data was made with that of Arabidopsis and members of the Solanaceae (e.g. tomato) and it was found that coffee and tomato have an almost perfect gene-for-gene match. Additional information can be found in the "What's New on SGN?" section of this newsletter on page 5 and on the following web sites:

<http://www.news.cornell.edu/pressoffice1/Oct05/coffee.html>

<http://www.cornelldailysun.com/vnews/display.v/ART/2005/11/01/43670c686adc5>

Tomato Sequencing Updates

I was asked to provide e-mail addresses for contacts on each tomato sequencing project. Therefore, I have provided this information at the beginning of each update.

Chromosomes 1, 10, 11 (US)

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

We submitted a proposal to the NSF Plant Genome Research Program for continued support of our sequencing efforts. Thank you to everyone who provided letters of support.

Currently, we have 11 BACs sequenced, with 3 in the pipeline. There are 401,652 BAC end reads now, with 341,412 high quality inserts (though the latest batch was not yet screened for empty vectors and contamination).

In support of the French sequencing effort for tomato chromosome 7, Corinne Delalande, from the Institut National de la Recherche Agronomique (INRA) in the laboratory of Genomique et Biotechnologie des Fruits in Toulouse, France visited the Stack lab from October 12 through Oct. 25 to learn techniques for fluorescence in situ hybridization (FISH).

Chromosome 2 (Korea)

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

Since our last update, sequencing was completed on two additional BAC clones and five BAC clones are in progress. To date, sequencing has been completed on a total of 33 seed BACs. Currently, BAC extension is being applied.

Chromosome 3 (China)

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

An update will be provided in the next newsletter.

Chromosome 4 (UK)

Contact: Christine Nicholson (ckb@sanger.ac.uk)

As we presented at the Tomato Satellite Meeting at the 2nd Solanaceae Genome Workshop in Ischia, Italy in September, our current mapping strategy for chromosome 4 is to develop as much as possible the physical map prior to the selection of the majority of the sequence clones. This is to reduce contig number so that we may select more economic minimal tiling paths across larger contigs. We have conducted *in silico* analysis of the FPC database, specifically the contigs containing recognised chromosome 4 markers. We will also augment the



fingerprint database with data from the SL_Mbol library. Final tests are underway at Sanger before commencing fingerprinting of the entire library.

Although we are focusing on map development, we have sequenced two clones from the LE_HBa library; 31H05 and 198L24, which are currently in finishing. An additional four BACs from this library have been selected and are undergoing PCR verification prior to their entering Shotgun sequencing. We are sequencing selected BACs across a number of regions of specific interest to the tomato community, these data will assist ongoing research as well as acting as a starting point to walk from at a later stage. We are happy to hear of regions of chromosome 4 that are of particular interest to the community to use for early BAC selection. Please send details of such regions to ckb@sanger.ac.uk.

Further to the BAC selection across some specific regions, we also intend to FISH approximately 15 BACs from contigs across the chromosome. The BACs will be selected from FPC chromosome 4 contigs. We hope that the FISH data will confirm chromosomal identity of the clones, verify marker order and provide useful information relating to the organisation of the contigs along the chromosome.



Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

The Indian Initiative on Tomato Genome Sequencing has confirmed 17 BAC clones from chromosome 5 with the help of markers (CT101, T1252, C2-At1g60200, cLET-8-B23, T0876, cLED-8-G3, BS4, T1592, T1360, T1777, T1541, T1584, TG69, CT130, TG185, TG597) by sequencing with marker-specific custom primers, end sequencing, and fingerprinting. Shotgun libraries have been made and high throughput sequencing has started. Sequencing of the BACs designated C05HBa0042B19, C05HBa0179K09 and C05HBa0179E24 has been completed to Phase I/Phase II level.

Chromosome 6 (The Netherlands)

Contact: René Klein-Lankhorst (rene.kleinlankhorst@wur.nl)

Basically, we have carried out a high-throughput screening for "seeds" against 350,000 BAC ends for walking. The S(equence)T(agged)C(onnector) strategy we follow was presented at the Ischia meeting and for this screening a significant amount of 21 seeds have been screened. Currently, the candidate BACs for walking are being fingerprinted by Taco Jesse at Keygene and the fingerprint results, binning and physical mapping results will be available in the next couple of weeks. This will provide detailed information to select BACs for the next round of sequencing. The following are highlights of the STC search results:

1. We found 387 significant BLAST hits originating from the three BAC libraries to 21 "seeds".
2. The BAC end sequences were successfully assembled onto the seed consensus without base inconsistencies.
3. 186 candidate BACs are from the HindIII library, 126 are from the EcoRI library, and 75 candidates are from the MboI library.
4. With respect to minimal overlap, we already observed some very good candidates. An overview of the sequence tagged connector search results can be found in Figure 1.

Figure 1: An overview of the sequence tagged connector (STC) search results.

STC search results

- ▶ 21 Seed BACs screened against 350.000 BAC ends
- ▶ 18 overlapping per seed BAC
 - | 186 HindIII, 126 EcoRI, 75 MboI
- ▶ All 'seeds' have candidates from at least 2 libraries
 - | M008H07 maps@3.6kb to P125P18
 - | M027B07 maps@880bp to P153O03
 - | M015K08 maps@5.0kb to P057J04
 - | P103N18 maps@2.1kb to P046G10
 - | P073H07 maps@3.9kb to P250I21
 - | E113K10 maps@4.2kb to P106K23
 - | M067G01 maps@11.9kb & P058H11 maps@25.6 kb to 308F14
- ▶ P103N18 and P073H07 closed and overlap 100%

 BioSystems GENOMICS
The Netherlands Plant Genomics Network

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Update pending

Chromosome 8 (Japan)

Contact: Satoshi Tabata (tabata@kazusa.or.jp)

To date, we have received a total of 246 BAC clones (LE Chr8 FL ARIL Clones) corresponding to 33 DNA markers on chromosome 8. Sequencing of nine BAC clones associated with nine markers (CT64, CT68, CT148, T1123, TG176 cLET-3-M1, cLET-3-O9, T1581, and T1434) has been finished. An additional eleven clones are in the finishing phase. Processing of the clones for the remaining 13 markers is on hold for the reasons previously mentioned. The nucleotide sequences of the finished BAC clones will be publicly released soon.

Chromosome 9 (Spain)

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

Update pending

Chromosome 12 (Italy)

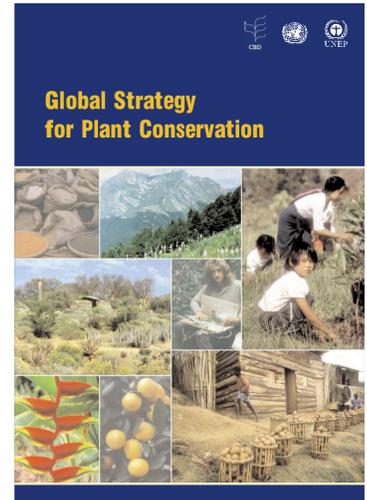
Contact: Mara Ercolano (ercolano@unina.it)

Currently, ten new candidate seed BACs are under selection on both arms of chromosome 12. Processing of nine clones has been suspended for several reasons: no PCR amplification with the marker-primers, disagreement of sequences with the original markers or BAC ends, and contradictory IL mapping data. Evaluation of alternative verification procedures based on customized primer sequencing and BAC-end mapping to recheck the identity of these BACs is in progress. Five confirmed BACs have been sent to CRIBI sequencing center and an additional four seed BACs associated with markers t1211, cLPT-E9, 1045 and t1667 are in advanced sequencing status. Moreover, annotation procedures are being tested on two fully sequenced BACs.



The Global Strategy for Plant Conservation (GSPC) - Linking Genomics with Biodiversity

Contributed by Sandy Knapp



The continuing erosion of the Earth's biodiversity is of concern not only to scientists, but also to governments and societies. The Convention on Biological Diversity (CBD) provides the framework for conservation of biological diversity and for the equitable sharing of benefits arising from its use. The CBD has been signed by more than 180 countries (see www.biodiv.org) and at the World Summit on Sustainable Development endorsed the target "to achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level as a contribution to poverty alleviation and to the benefit of all life on earth" – a huge task. In April 2002, more than 180 countries came together at the Conference of the Parties to the CBD

to back an additional, positive, target-oriented initiative – the Global Strategy for Plant Conservation, or GSPC. The broad support for the GSPC is a reflection of the significance of plants to not only ecosystems and their functioning, but to other elements of sustainability such as agriculture or health. The ultimate and long-term objective of the GSPC is to halt the current and continuing loss of plant diversity, with the target date of 2010, to match that for the CBD itself. The GSPC has five broad areas of work;

- a) Understanding and documenting plant diversity
- b) Conserving plant diversity
- c) Using plant diversity sustainably
- d) Promoting education and awareness about plant diversity
- e) Building capacity for the conservation of plant diversity

Within each of these areas, further, more specific targets are set, for example, that no wild flora endangered by international trade (Target 11), or the construction of a widely accessible list of all known plant species (Target 1). Further information on the targets can be found at <http://www.plants2010.org/targets/index.html>.

But what might this conservation-oriented strategy have to do with the genomics of Solanaceae, or of Asterids? Quite a lot - in my opinion - here are a couple of examples. Target 9, falling under conserving plant diversity, is that "70 per cent of the genetic diversity of crops and other major socioeconomically valuable plant species conserved, and associated indigenous and local knowledge maintained" – a direct link to SOL activities such as the core collection being assembled as part of Work Package 4 of EU-SOL. Target 13 directly relates to food security, with the aim of halting "The decline of plant resources, and associated indigenous and local knowledge, innovations and practices that support sustainable livelihoods, local food security and health care". These two targets directly relate to SOL research, but creative thinking can link many more of the targets to our collective efforts.

The GSPC was conceived and pushed through by the botanical garden community, but it is clear that to achieve its goals, many new plant science communities will need to come together to see how we can each contribute to what is essential not only to us as scientists working with plants, but to us as human beings living on what is an increasingly endangered Earth. This reaching out and collaboration is in the spirit of SOL, and I would encourage everyone to take a look at the GSPC and think of new innovative ways to help achieve its ambitious targets. The theme of our next meeting is genomics meets biodiversity – what better way to start to think about those connections than through the GSPC, whose aim is to conserve the diversity of the organisms we work on and upon whom all life depends.

Sandy Knapp, SOL co-chair

Department of Botany, The Natural History Museum, Cromwell Road, London SW7 5BD, UK; s.knapp@nhm.ac.uk

Additional information and links:

www.plants2010.org - the website of the Global Partnership for Plant Conservation, a group dedicated to the implementation of the GSPC.

<http://www.bgci.org.uk/conservation/strategy.html> - a good introduction to why the GSPC is relevant to the SOL community



What's New on SGN?

Coffee ESTs

Nearly 50,000 coffee ESTs have been released on SGN. The data can be downloaded from the SGN ftp site at <ftp://ftp.sgn.cornell.edu/coffee/>. Please refer to the additional information on the coffee data in the Community News of this issue of the SOL Newsletter.

BAC Ends

The last batch of 20,000 BAC ends has been loaded in the SGN database, and the complete set of 400,000 reads is now available of which 340,000 contain sequence above an agreed quality threshold (more than 100 bases at phred 20). The BLAST and ftp sites have been updated. Go to the Search menu on SGN and choose "BACs", or access the BAC search directly at http://sgn.cornell.edu/search/direct_search.pl?search=bacs

Full-length BAC Sequences

The US project has released 5 new complete finished BAC sequences for BACs located on chromosomes 1, 10 and 11. The BAC sequences are available in the BAC search (see above), the BAC BLAST dataset and from the SGN ftp site and through the GBrowse annotation browser at SGN:

<http://sgn.cornell.edu/gbrowse/>

<http://sgn.cornell.edu/tools/blast/simple.pl>

ftp://ftp.sgn.cornell.edu/tomato_genome/bacs/

CAPS Designer

A new tool, the CAPS Designer, has been released on SGN. It takes two input sequences and analyzes them for differences in known restriction sites, which can then be used for designing flanking CAPS primers. The tool is available under the SGN tools menu under "CAPS Designer", or with the direct link:

http://sgn.cornell.edu/tools/caps_designer/caps_input.pl

SOL Online Forum

An on-line forum has been established that allows researchers around the world to log in, post topics and messages. The SOL Forum can be reached by clicking on the link under SOL Forum on the SGN homepage or directly at

<http://sgn.cornell.edu/solpeople/topics.pl>

Featured Lab

Molly Jahn's lab is the featured lab on SGN (<http://www.sgn.cornell.edu/community/feature/200510.pl>).

Conference and Workshop Announcements



International Plant and Animal Genome XIV Conference (PAG-XIV)

January 14-18, 2006

Town & Country Hotel in San Diego*

*A meeting for all tomato genome sequencing participants will be held on Sunday, January 15 from 1:00-6:00 pm. A room assignment will be announced at a later date. The meeting is not limited to sequencing participants. It is open to everyone who is involved in various aspects of tomato genome work. Send an e-mail to Lukas Mueller (lam87@cornell.edu) if you will attend and what topics you would like to see discussed.

Solanaceae 2006 - "Solanaceae - Genomics meets Biodiversity"

Provided by David Spooner



The entire international Solanaceae community will be meeting together for the first time in Madison, Wisconsin on July 23-27, 2006. This meeting will be a coming together of the International Solanaceae Conference (its Sixth Meeting, with meetings held every five to six years), the Third Solanaceae Genome Workshop, and the Potato Association of America (PAA; its 90th Annual Meeting). The theme of the conference is "Solanaceae - Genomics meets Biodiversity."

Details of this conference can be viewed at:

<http://www.hort.wisc.edu/PAA-Solanaceae/>

The estimated number of participants at this joint conference is 500-800. There will be a single registration for all participants. Hotel contracts have already been made, and we encourage you to reserve your rooms as soon as possible to secure the room you want; it is critical that you identify yourself as a member of this conference to get the best rate.

Registration will be \$300.00 for all participants for the entire conference except for a reduced rate of \$175.00 for accompanying persons (who can attend all social events but not the scientific talks), students and single-day registrants. Those needing registration vouchers now for visa applications should contact the registration company; see the website for these details. If you do not need this voucher now, please wait until after January 9 to register for the conference.

The meeting will begin on Sunday evening with a general reception. Monday morning begins a series of invited talks for an inter-conference plenary session. Thereafter (beginning on Monday afternoon), the joint conference will consist of two parallel meetings: 1) the PAA (which will hold four concurrent sessions), and 2) the joint meeting of the Solanaceae Genome Workshop and the International Solanaceae Conference, which will meet together in a single session. All meetings will be held on the same floor of the Monona Terrace and participants are free to attend any session. On Tuesday evening there will be a wine and snacks social event during poster viewing, on Wednesday evening a barbeque, and on Thursday evening closing session banquets for the PAA and Solanaceae/Genomics groups.

Wednesday Satellite Sessions will provide opportunities for focus groups to meet. To date, satellite sessions are being organized for:

- Application of FISH in Support of Sequencing Plant Genomes: (Stephen M. Stack, Colorado State University)
- Tobacco: (Paolo Donini, Philip Morris International, Switzerland)
- Translational Genomics: (Allen Van Deynze, Seed Biotechnology Center, California)
- Coffee Genomics (Steven Tanksley, Cornell University, USA)
- Pepper (Byoung-Cheorl Kang, Plant Breeding and Genetics, Cornell University, USA)
- Potato Genomics (Christian Bachem, Wageningen University and Research Centre, the Netherlands)

- Secondary Metabolism (Giovanni Giuliano, Italian National Agency for New Technologies, Energy and the Environment, Casaccia Research Center, Rome, Italy)
- Tomato sequencing (Lucas Mueller, Cornell University, USA)

Note: Chairs must volunteer by December 9th. Those interested in organizing these sessions, or any other session, should contact David Spooner at 1-608-890-0309; email: dspooner@wisc.edu.

In addition to the satellite sessions there will be agricultural and social tours on Wednesday.

Because of the unifying theme of the meeting and the numbers of people anticipated to attend, opportunities for oral presentations in the International Solanaceae Conference will be more limited than in previous Solanaceae conferences. Therefore, ample space for posters will be provided and we encourage poster contributions. The PAA will have ample time for oral presentations and a poster session. The scientific meetings will continue Monday, Tuesday, and Thursday, with Wednesday devoted to tours and satellite sessions.

The \$300.00 registration is a deal! This includes all scientific events including the Sunday opening wine and snacks reception, the Tuesday evening wine and snacks social/poster viewing session, the Wednesday satellite sessions, three breakfasts, three lunches, and snacks during breaks on Monday, Tuesday, and Thursday. There will be a separate charge for the Wednesday evening barbeque, Wednesday tours, and Thursday evening banquet.

We are working on obtaining funds to defray partial expenses for students and other participants. These opportunities will be announced on the website when registration and abstract submissions open on January 9 (<http://www.hort.wisc.edu/PAA-Solanaceae/>)

The Monona Terrace is a premier convention facility with state of the art meeting and projection facilities:

<http://www.mononaterrace.com/>

In addition, Madison Wisconsin is a visitor-friendly city with the Wisconsin State Capitol adjacent to the Monona Terrace, and picturesque nearby State Street providing scores of venues for evening socializing:

<http://www.visitmadison.com/>

Madison also offers a variety of housing options, from luxurious (such as the main conference hotel at the Madison Hilton adjacent to the Monona Terrace) to more affordable hotels within walking distance.

We look forward to welcoming everyone to next year's conference.

Solanaceae Recipes

Ratatouille

From Better Homes and Gardens Cookbook



This Mediterranean dish featuring eggplant, peppers, and tomatoes is equally delicious served cold.

1/2 cup finely chopped onion (1 medium)
1 clove garlic, minced
1 tablespoon olive oil
2 cups cubed, peeled eggplant
1 small zucchini or yellow summer squash, halved lengthwise and cut into 1/4-inch thick slices (1 cup)

1 cup peeled, chopped tomatoes or one 7 1/2 oz can of tomatoes, cut up
1/2 cup chopped sweet, green pepper
2 tablespoons dry white wine or water
1 1/2 teaspoons snipped fresh basil or 1/2 teaspoon dried basil, crushed
Salt and pepper (see below)
1/2 cup shredded Swiss cheese (optional)

In a large pan, cook onion and garlic in hot oil until onion is tender. Stir in the wine, vegetables, basil, 1/8 teaspoon salt, and 1/8 teaspoon black pepper (Salt and pepper amounts can be adjusted to your preferences). Bring to boiling. Reduce heat; simmer, covered, 20 minutes or until tender. Uncover; cook 5 to 10 minutes or until thickened, stirring occasionally. If desired, sprinkle with cheese. Makes 4

If you would like to contribute your favorite recipes that have at least one or more Solanaceae family members as part of the ingredients, send them to Joyce Van Eck at jv27@cornell.edu.