SOL NEWSLETTER

ISSUE NUMBER 10
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COMMUNITY NEWS

Reminder

Early registration deadline (June 15) for *Solanaceae* 2006
Madison, Wisconsin
July 23-27, 2006
Conference website: http://www.horticulture.wisc.edu/PAA-Solanaceae/

The entire international *Solanaceae* community will be meeting together for the first time, which will bring together 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. Estimated participants at this joint conference are 500-700. The tomato genomics group and the International *Solanaceae* Conference will meet together as a group on Monday, Tuesday, and Thursday, as well as the Potato Association of America. Wednesday satellite sessions will provide opportunities for focus groups to meet. Satellite sessions are organized for: Application of FISH in Support of Sequencing Plant Genomes; Bioinformatics, Coffee Genomics; Pepper, Potato Genomics, Secondary Metabolism; *Solanum* Taxonomy, Tobacco; Tomato Sequencing; and Translational Genomics.

Early registration is June 15, after which time costs increase, and the nearby hotels are filling fast, so please consider registering and securing hotels now. The links for both are available on the conference website.

We are publishing a conference volume for submitted papers, similar to the five previous International *Solanaceae* Conferences. The editorial committee consists of Lynn Bohs, Jim Giovannoni, Richard Olmstead, Daisuke Shibata, and David Spooner. We will consider papers from all who are registered and present talks or posters at the conference.

To be considered for publication, all papers must be ***submitted at the Registration desk by noon, Tuesday, July 25.*** Papers will be published in Acta Horticulturae *(changed from our original publisher, the New York Botanical Garden). The editorial committee will be meeting Tuesday evening to discuss these submissions and only papers in-hand at that meeting will be considered for publication.*

All submissions will be subjected to peer review, and we ask all authors to limit the size of their articles regarding number of words and illustrations. Because different papers will require different lengths, we are not establishing word limits here, but long articles may be reduced in size considerably in review. Instructions to authors can be found at: http://www.ishs.org/acta/index.htm.

Authors of invited papers will receive one free copy of the proceedings (entitled *Solanaceae* - Genomics meets Biodiversity). All others will receive a pre-publication discount price of $50.00 per volume, which must be ordered on-line before July 27. Only registered conference attendees are eligible for this pre-publication discount, which is less than half of the estimated sale price of the volume. To purchase the book, go to the main conference website (http://www.horticulture.wisc.edu/PAA-Solanaceae/), click on Registration, login with the email and login address you used (or will use) to register, make sure your mailing address is correct, and add the book to the shopping cart on the merchandise page.

In Memory of Richard Neville Lester
1937-2006

Contributed by Marie-Christine Daunay

The *Solanaceae* community has lost one of its great members, Richard Lester, on April 4, 2006. Botanist and taxonomist of the University of Birmingham, he is well known for his extensive research on the cultivated and wild eggplants, these fruit bearing *Solanum* species that are mostly native from Africa and Asia. Thanks to his stays in Uganda, and IPGRI collecting trips that brought him to the Ivory Coast, Burkina Faso, Ghana, Togo, Benin, Nigeria, and also thanks to his many graduate students, he collected hundreds of accessions that contributed to the exceptional scientific value of the Birmingham *Solanaceae* collection. Together with the many MSc and PhD students he had along the years, he contributed outstandingly to the understanding of the evolution and domestication of the African scarlet (*Solanum aethiopicum*) and Gboma (*S. macrocarpon*) eggplants, together with their Asian counterpart, *S. melongena*, as well as to the biosystematics and the taxonomy of their wild relatives. He was one of those biologists who had acquired a wide knowledge in many fields of science and techniques, and whatever they related to in botany, ecology, taxonomy, chemistry, immunology, information technology, scanning electron microscopy, etc.

A student of Jack Hawkes (Birmingham University, UK), he got his PhD on "Immunochemical studies on the genus *Solanum* L." in 1962. He started his career at the Universities of Texas, then Kansas (USA). In 1968, he spent one year in Makerere University College in Uganda as Lecturer in Botany before coming back for over 30 years to Birmingham University, as Lecturer in the Department of Botany (later on successively renamed Plant Biology, Biological Sciences, and eventually Biosciences). He was one of the staff of the famous international MSc course "Conservation and Utilization of Plant Genetic Resources", teaching, crop plant diversity and evolution, biochemical systematics, *in-situ* conservation, agro-ecology, medicinals and spices, etc. He led many field courses in marine and terrestrial ecology, plant ecology, genetic conservation, and was excellent at collecting and identifying plants wherever they grew in Mexico, Uganda, Indonesia, near the Pyrenees summits or in Scotland.

Since his retirement in 2000, he continued to be very active. In particular, he co-coordinated the five-year European contract on the conservation and characterization of eggplant genetic resources (EGGNET), thanks to which the Birmingham *Solanaceae* collection was saved and transferred to Nijmegen Botanical Garden (Netherlands), INRA Montfavet (France) and Valencia Polytechnic University (Spain). He studied and identified hundreds of herbarium specimens when visiting herbaria all over Europe trying to finalize the huge task that he had started in the 1980s to revise the taxonomic treatment of all African *Solanum* species. Unfortunately, destiny did not allow him to live long enough for achieving this project and others. Scientists of the international Solanaceae taxonomic and botanic community are taking on the manuscripts and data he left unfinished, in order to bring them to publication. This concern of his peers is probably one of the best acknowledgements of the high value of the work of this discreet but brilliant scientist.

An Italian Bioinformatics Platform Providing BAC Annotations Based on EST/cDNA Sequences

Contributed by Maria Luisa Chiusano, Nunzio D'Agostino, Alessandra Traini

We set up a bioinformatics platform as an added reference within the *Solanaceae* community for structure and functional analyses of genomic data from *S. lycopersicum* sequencing. Currently, we provide a collection of ESTs from tomato and potato species, downloaded from dbEST (updated November 2005), organized into non-redundant clusters, and annotated using an automated pipeline (D'Agostino et al., 2005). The UNIPROT database (updated March 2006) has been used for a preliminary functional annotation.

The processed ESTs are collected into two repositories: TomatEST and PotatEST. The expressed sequences are mapped onto the upcoming BACs of *S. lycopersicum* retrieved from the SGN ftp server. The experimentally annotated BACs can be accessed through the Generic Genome Browser interface. The Gbrowse interface reports the spliced-alignments of ESTs/contigs tracks from six different *Solanaceae* species as collected in the EST repositories. ESTs from Kazusa Micro-Tom full-length cDNA clones are considered as separated tracks. Coding sequences from *Arabidopsis thaliana* downloaded from the NCBI through a GenBank ENTREZ query are also available. The EST repositories and the Gbrowse system are cross-referenced and are available via a free registration form at http://biosrv.cab.unina.it/.

Contact: Maria Luisa Chiusano at chiusano@unina.it

Letter to the SOL Steering Committee

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

April 10, 2006

Dear SOL-Steering Committee Members,

Our next meeting will be held in Madison, Wisconsin, USA and will be conducted along the theme of "Genomics meets Biodiversity" http://www.horticulture.wisc.edu/PAA-Solanaceae/. This meeting will increase our knowledge about the space of Solanaceae and beyond -- to the Asterids.

The wider scope of the Madison meeting should not come at the expense of the specifics of the job we have at hand – to construct a BAC by BAC sequence of the tomato genome. To facilitate the needed interactions towards our target we reserved a whole day for Satellite Meetings <http://www.horticulture.wisc.edu/PAA-Solanaceae/Satellite.htm>; we encourage you to set up your meeting schedules early since we are short of time with respect to the genomic task. In Madison there will also be ample opportunities for more informal interactions – we hope the meeting will provide time and space for us to discuss how we can best reach our most important current goal, the tomato genome sequence. This "endpoint" is actually a beginning, but we mustn't let our excitement about what we can do in the future distract us too much from the task at hand!!

Presently 7% of the euchromatic genome has been sequenced and we aim for 10% by the Madison meeting. We hope that more of these sequences will be deposited to the hungry community in order to increase our shared discovery base.

We are looking forward to seeing everyone in Madison - Happy SOL.

Sandy Knapp and Dani Zamir

DNA LandMarks Announces the Launch of a Tomato SNP Marker Development Consortium

Provided by Charles Pick

DNA LandMarks Inc, a world leader in DNA marker technology and a BASF Plant Science unit, announced today the launch of a major SNP marker development project for tomato. The project represents a collaboration by a number of private companies including Nunhems Netherlands BV, Redi Plants Corp. and Western Seed International BV.

Single nucleotide polymorphisms (SNPs) are rapidly becoming the marker system of choice based on the fact that they are highly efficient to use. SNPs hold tremendous promise in expanding the utility of marker-assisted plant breeding. Potential applications include marker-assisted trait screening, accelerated marker-assisted backcrossing, quantitative trait loci (QTL) mapping and genetic fingerprinting.

The development of new genetic markers in commercial tomato (*L. esculentum*) is of particular interest since the low level of polymorphism in this crop has limited what breeders could do with markers in the past. With the addition of a large SNP library to their marker toolbox, breeders will be able to accelerate their programs and manage complex, multigenic traits.

"We believe that developing a library of SNP markers in tomato will deliver tremendous value to breeders. We have already seen this in the main field crops such as corn and soybean. Tomato now stands to benefit in the same way." said DNA LandMarks CEO Dr. Joachim Richert.

The tomato SNP marker consortium is one of a number of initiatives that DNA LandMarks is spearheading in its drive to deliver improved marker services to the entire agricultural value chain.

About DNA LandMarks

Since its foundation in 1995, DNA LandMarks Inc. has been a world leader in DNA marker development and applications. Today the company offers a full array of marker technologies to the agricultural sector from development to mapping to high-throughput application. DNA LandMarks is a unit of BASF Plant Science and its Centre of Excellence for DNA sequencing and genotyping. For more information regarding this news release, please contact: Charles Pick, Business Development Manager – pickc@dnalandmarks.ca.

Potato Plastid Genome Sequenced

Information provided by Teodoro Cardi

In the framework of the EU-funded "Plastomics" Consortium (https://genesilico.pl/Plastomics/) we have recently sequenced the plastidial genome of *Solanum tuberosum* cv Desiree (GenBank DQ386163).

TOMATO SEQUENCING UPDATES

If you are interested in tracking the progress of the sequencing, there is a link for the International Tomato Project on the SGN homepage (sgn.cornell.edu). As of May 31, the project is 9% complete.

Chromosomes 1, 10, 11 (US)

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

We have sequenced twelve BACS, and five additional BACs are in the sequencing pipeline. We continue to provide BAC libraries, BAC filters, other resources and support to the community.

The Stack lab has localized an additional nine BACs since the last report, bringing the total number of BACs that have been positioned by FISH to forty-three. The new BACs include:

Chromosome Arm	BAC ID
1Q	305F14
	051C14
	208M24
3Q	014A17
4P	036C23
4Q	078E04
	006E18
	053M02
	132O11

FISH experiments have now identified the locations of twelve BACs on chr 1, two on chr 2, one on chr 3, seven on chr 4, three on chr 6, two on chr 7, one on chr 8, nine on chr 9, four on chr 11, and two on chr 12. Figure 1 shows labeling of two BACs, 006E18 (green) and 020F17 (red), on chr 4 in three SC spreads. Figure 2 illustrates labeling of two BACs, 155M04 (green) and 208M24 (red), on chr 1. In both micrographs, pink arrows indicate the positions of the centromeres on the labeled chromosomes.

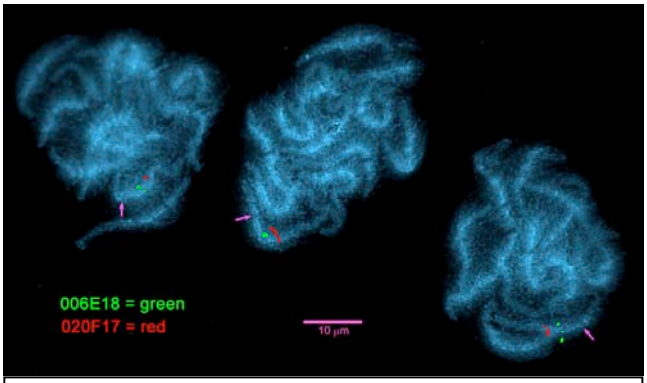

Figure 1: FISH labeling of two BACs on chr 4 in three SC spreads.

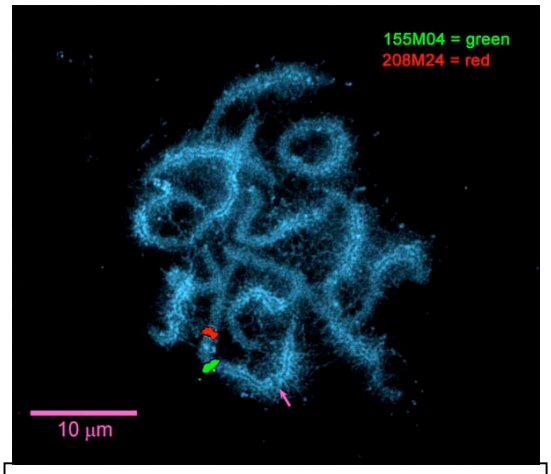

Figure 2: FISH labeling of two BACs on chr 1.

Chromosome 2 (Korea)

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

To date, we have completed the sequence for seventy-four BACs (twenty additional BACs from last month). Fifteen BACs are in the pipeline. Currently, we have faced problems with BAC extension because it is very risky to select the next BAC based on the BAC end sequences. Therefore, we need extensive labor for confirmation of BAC extension. I am waiting for the upgraded version of FPC contig data.

Chromosome 3 (China)

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

Update pending.

Chromosome 4 (UK)

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

Our aim is to build a map of as few contigs as possible to enable us to generate an efficient tiling path across the gene-rich euchromatic regions of our chromosome. The BAC selections are being made from the chr 4 contigs using fingerprint data and BES information where applicable. The selected tiling paths will undergo colony PCR verification prior to sequencing.

Three LE_HBa BACs have been sequenced and fully finished to HTGS phase 3 at the Wellcome Trust Sanger Institute. At present, eight clones are undergoing shotgun sequencing and an additional ten clones are in the subcloning phase prior to shotgun sequencing where they are being transformed into our current sequencing vector. The clones in the pipeline are in some cases initial sequencing points within chr 4 contigs, whilst others extend already selected BACs. Single colony isolates of all BACs selected for sequencing have undergone verification by fingerprint and colony PCR confirmation.

Seven LE_HBa BACs have been positioned by FISH independently of marker information on chr 4 at Colorado State University and a further three BACs that we have sent are undergoing investigation. The same seven single colony isolates that have been confirmed on chr 4 by FISH are now in our sequencing pipeline. The FISH data provide extremely valuable information regarding the placement of heterochromatin and euchromatin across the chromosome. It further enables verification of the marker order along the chromosome and we have seen some variations with this, in particular around the centromeric region.

Using the method that AGI employed for the fingerprinting of the LE_HBa library for the initial construction of the tomato FPC map, we have been fingerprinting the SL_MboI library. This process makes the SL_MboI clones "visible" in an FPC database. The fingerprints generated have been processed using Image and we are beginning to analyze the data. We expect to make the database and all fingerprint data available next month.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

The Indian Initiative on Tomato Genome Sequencing is currently involved in sequencing twenty-two BAC clones from chr 5, anchored to chromosome specific markers (CT101, T1252, C2-At1g60200, cLET-8-B23, T0876, cLED-8-G3, Bs4, T1592, T1360, T1777, T1541, T1584, TG69, CT130, TG185, TG597, cLEX-13-G5 and T1746). Sequencing of BACs has progressed to various stages. The following are at phase I level: C05HBa0169M21, C05HBa0334K22, C05HBa0166A02, C05HBa0040C21, C05HBa0108A18, C05MBa0005B15, C05MBa0050C14. Whereas, these BACS have progressed to phase II: C05HBa0042B19, C05HBa0051A13, C05HBa0179E24, C05HBa0006N20, C05HBa0239D11, C05HBa0027B05, C05HBa0168B11, C05HBa0131D04, C05HBa0245E05, C05HBa0251J13. BACs at phase III are C05HBa0191B01, C05HBa0179K09, C05MBa0077G20, C05HBa0261K11 and C05HBa0058L13. Shotgun library preparation is in progress for C05HBa0053P22, C05HBa0051A18, C05HBa0195M17 and C05HBa0227B07. New seed BACs at C2-At1g60440 and T1632 marker positions have been picked by overgo hybridization and confirmed by marker-specific PCR. Confirmation of all the seed BACs as well as extending BAC clones using chr 5 specific IL lines is in progress.

Chromosome 6 (The Netherlands)

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

The Dutch Initiative, supported by the Centre of Biosystems Genomics, is currently processing twenty-one BACs. These extension BACs have been selected based on a STC strategy as reported in the SOL Newsletter, 9, 2006. From thirteen HindIII BACs, Hba055E14, Hba066I09, Hba021K07, and Hba182D16 have been sequenced and assembled to phase II. Currently, we have seventeen BACs in the sequencing pipeline of which nine are from the HindIII library, four are MboI BACs, and four are EcoRI BACs. Insert sizes for EcoRI and MboI BACs have been verified by Keygene using FIGE and comprise approximately 1020Mb. Based on an average insert size of ~118kb for BACs from the HindIII library, the total insert length currently involved in sequencing comprises 2.1Mb.

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

To date, seventeen BACs have been completed to Phase 1, and one BAC has been fully closed. An additional four BACs are currently in the sequencing pipeline and thirty-three BACs are in the FISH pipeline. Of the completed or the most advanced BACs, four have been uploaded to SGN for public release.

Chromosome 8 (Japan)

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

To date, twenty BACs have been sequenced and five are in the sequencing pipeline. We selected sixteen BACs from the first-round extension of eighteen finished BACs. Selected BACs were verified by sequencing the PCR product amplified from the BAC DNA. Among the clones, LE_HBa0059L14 is currently anchored to a marker on chromosome 3. We plan to physically map this clone as well as its seed HBa0076J13, and we are eager to see the FPC map with additional data from the UK group.

Chromosome 9 (Spain)

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

Le_HBa0278J12 and Le_HBa0203J14 have been finished and submitted to SGN. To date, a total of four BACS have been finished and two other finished BACs will be sent soon. The need for additional BES and contig information is evident. Thus, for the extension BACs corresponding to Le_Hba109D11 there were only two possible (Le_Hba059I05 and Le_Hba033H16) with one over approximately 17 kb and the other at 7 kb. For Le_HBa278J12, we did not find overlapping BACs for one end, and for the other end a BLASTn gave only 93% similarity with a BAC that was received contaminated and was not possible to confirm. For Le_HBa203J14, three extension BACs are in the process of confirmation. Le_Hba165P17 is pending a couple of runs, but the extension BACs have been ordered, unfortunately one overlaps 18

kb and the other end only 500 bp, and there are no other choices. For Le_Hba168F14, there is only one PCR pending for linking two contigs in one, unfortunately the search for extension BACs gave no positives.

There are other BACs in the process of finishing, and extension BACs for those were found in the EcoRI library (no size info). We found in the Arizona FPC, BACs that belong to the same contig, but contain markers of different chromosomes. In summary, we definitively need additional BES and BAC contigs to extend more efficiently in the BAC-by-BAC strategy and this may be specifically true for chr9, which is rather empty of anchored BACs. In the meantime, our strategy is to increase the number of seed BACs to compensate for the dropouts when trying to walk out from the sequence. Thus, we are conducting the mapping of T0486 and T1514 in Dani's lines to confirm location on chr9 and proceeding from two other seed BACs (LeHBa226D21 and LeHBa205P24) previously confirmed by mapping in Dani's lines.

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

A total of twenty-six BAC clones corresponding to eighteen DNA markers on chr 12 have been analyzed to date. The location of three of them was reassigned to other chromosomes. In fact, the analysis performed in Dr. Tanksley's lab on a segregating mapping population revealed that BACs HBa0152M18 and HBa0244J04 are located on chr 11 and 1 respectively, while FISH mapping performed in Dr. Stack's lab revealed that BAC HBa107D15 is located on chr 9.

Till now, ten seed BACs have been sequenced: five of them are in phase I (HBa161H10, HBa163O04, HBa093P12, HBa075C18, HBa147G13), two in phase II (HBa026C13, HBa115G22), and three in phase III (HBa021L02, HBa140M01, HBa032K07). The obtained sequences were subject to gene modeling and annotation using our automatic pipelines. A bioinformatics platform providing BAC annotations based on EST/cDNA sequences has been established by our group. Additional information can be found in the Community News section of this newsletter on page 2.

An additional three seed BACs are in the sequencing pipeline (HBa146I19, HBa180O010 and HbBa260c13) and two are under re-evaluation as during assembling work we found disagreement with sequence of associated markers (HBa244C09 and HBa59A05). Six finished BACS were used for screening the BAC-end library by BLASTN. The verification of potential overlapping BACS based on the construction of PCR based markers allows us to select three extension points. The delivery of ten newly requested overlapping BACs as well as two BAC libraries (HindIII and EcoRI) will speed up the chromosome walking planned for the upcoming months.

WHAT'S NEW ON SGN?

(1) A user updatable gene database. SGN users can now update the recently introduced Gene database with information on genes, alleles, phenotypes, and literature and sequence data. Every locus has an associated editor. To update a gene entry and become its assigned locus editor, locate the gene detail page using the search and click on the link "Request Editor Privileges". Other users can still add new allele and synonym information. The respective submitters own newly created information. User updating of gene and plant ontology annotations will follow soon.

(2) We have migrated to a new and improved marker and map database, and improved the marker search and display. Please take a moment to look at the new interfaces available from the search pages (http://sgn.cornell.edu/search/direct_search.pl?search=markers). The marker search page now features help tooltips and allows download of results as a text file.

(3) We computationally mapped BAC ends to the F2-2000 maps by BLASTing them against the marker sequences, resulting in an additional 290 anchor points for the physical map. The results are displayed on the F2-2000 map (http://sgn.cornell.edu/cview/map.pl=9&physical=1). In the diagram, the computational matches are shown as a red outline, and the experimental matches are shown in green. The raw results can be downloaded from the FTP site at ftp://ftp.sgn.cornell.edu/tomato_genome/physical_mapping/computational/.

(4) A database of *in-situ* images has been added and can be reached through the tools menu or the link http://sgn.cornell.edu/insitu/. The database can also be updated by users, with image add, delete and annotation editing functions. The current images were generated by the floral genome project (FGP). For more information on the FGP, visit http://floralgenome.org/ and http://pgn.cornell.edu/.

(5) A page describing the SOL-ANDINO project has been added. Refer to http://sgn.cornell.edu/about/SOLANDINO/, which is also linked from the SGN homepage.

The following new data is now available on SGN:

(1) 50,000 coffee EST sequences and 13,000 unigene sequences have been added to the database. Previously, they were available only from the FTP site as fasta sequence downloads. BLAST annotations, predicted proteins, interpro domains and gene family information are also available.

(2) A total of 133 BAC sequences have been reported finished in the SGN BAC registry database. Full-length sequences are available for 92 sequences, with many more BACs in the pipeline.

(3) 53,000 new tomato ESTs were added to the SGN database. Daisuke Shibata, Eyal Fridman, Giovanni Giuliano, Bin Cong, and their colleagues provided the sequences. A new tomato unigene will follow soon.

(4) Forty-two BACs have been FISHed by Stephen Stack and his colleagues and are available from the tomato FISH map at http://sgn.cornell.edu/cview/map.pl?map_id=13.

OUTREACH

Contributed by Joyce Van Eck

I've added this new section to give everyone the opportunity to share information about the activities they have as part of their outreach initiatives. It is important for us to take on the responsibility of not only sharing what we have learned from our specific research efforts, but to also engage the public in an open conversation about science and research. In addition, we need to share our excitement about our work to attract and educate the next generation of plant scientists. So, I look forward to including articles about your outreach programs in future issues.

I'll start off this new section by outlining two of the activities we developed as part of our NSF-funded tomato sequencing effort. The first is a bioinformatics summer internship for high school students and college undergraduates. Students work at the SOL Genomics Network (SGN) for 8 – 10 weeks during the summer on their own bioinformatics-related projects. A staff member of SGN acts as project mentor for each student to help them learn the various programming skills necessary to develop their projects. As part of this internship, they also attend weekly seminars held at the Boyce Thompson Institute (BTI) that are given by plant scientists from Cornell and BTI for students who participate in the larger summer internship program sponsored by the NSF-Plant Genome Research Program. Information about the 2005 bioinformatics summer interns can be found on SGN at http://www.sgn.cornell.edu/about/Summer_Internship_2005.pl.

Figure 1: Looking at different *Solanaceae* family members.

The second activity, "The *Solanaceae* Family goes to School", is geared for students in kindergarten through 5th grade. The purpose is to teach the students about the concepts of plants being grouped in families, biodiversity, and relatedness. I bring as many different types of potatoes, tomatoes, eggplants, and peppers I can find at the largest supermarket in town, and I cut them open to show what they look like on the inside (Figure 1). They taste the different types of tomatoes and peppers (not the hot ones), and even though they think they won't like them, they are willing to give them a try. I also bring petunias and a tobacco plant. We discuss the different uses of each of the family members, centers of origins, and the fact that the ancestors looked a lot different than what we have today. Then we dress up the Sol Family for a party, and end the activity by doing a word find puzzle that contains all the terms we discussed (Figure 2). We have a lot of fun, and these young minds amaze me with their insightful observations and questions.

Figure 2: The Sol Family dressed up for a party.

ANNOUNCEMENTS

8th World Petunia Days
October 12-14, 2006
Jacksonville, Florida

The Environmental Horticulture Department and College of Agricultural and Life Sciences at The University of Florida welcome you to the Eighth World Petunia Days in Jacksonville Beach, Florida on October 12-14, 2006. This is the first time the World Petunia Days have been held in the United States, so it is our privilege to host WPD8 in sunny Florida! Details regarding registration, abstract submission, etc. can be found at http://hort.ifas.ufl.edu/petunia.

SOLANACEAE RECIPES

Peruvian Potato Salad

This recipe was found on the Recipe Source website at http://www.recipesource.com/.

Serves 6

1 small onion, thinly sliced and separated into rings
3 tablespoons lemon juice
1/2 teaspoon salt
1/8 teaspoon ground red pepper
1 1/2 pounds New potatoes
2 packages (3 oz each) cream cheese, softened and cut into 1/2 inch cubes
1/2 cup Half and Half
2 small Serrano chilies, seeded and finely chopped
1/4 teaspoon salt
1/4 teaspoon ground turmeric
Bibb lettuce leaves
12 Greek olives
3 hard-cooked eggs, peeled and cut into fourths

Mix onion, lemon juice, 1/2 t salt and the red pepper; cover and reserve. Heat 1 inch salt water (1 t salt to 1 cup water) to boiling. Add potatoes. Heat to boiling; reduce heat. Cover and cook until tender, 20-25 minutes; drain and cool. Peel potatoes; cut into fourths. Heat cream cheese, half and half, chilies, 1/4 t salt, and the turmeric over low heat, stirring frequently, until mixture is smooth, 10-12 minutes. Arrange potatoes on lettuce leaves. Spoon cheese mixture over potatoes. Drain onion mixture; arrange on cheese and potatoes. Garnish with olives and eggs.