2nd Annual SolCAP Meeting

The second annual SolCAP meeting was a success! The meeting which was held in San Diego at the Town and Country Resort in conjunction with the Plant and Animal Genomics Conference on January 9th, 2010, had excellent attendance and participation. The SolCAP Executive Committee would like to thank the members of the SolCAP Advisory Board (scientific advisors, stakeholders, education/extension advisors and assessment advisors) for their participation and input. We are all looking forward to another productive year!

Dave D.’s Perspective:

The Solanaceae community has an exciting opportunity before us. The SolCAP team would like to extend an invitation to our fellow Solanaceae scientists to join us in a consortium through Illumina® to develop a potato and a tomato array for the interrogation of SNPs in the respective genomes.

Potato: Approximately 10,000 SNPs are intended for the final content in a high density genotyping chip. Candidate SNPs are being validated for potato in elite germplasm at this moment. The SNPs are identified from Illumina transcriptome sequencing of Atlantic (high solids chip-processor), Snowden (low reducing sugar storage chip processor) and Premier Russet (low reducing sugar frozen processing) lines. We expect >75% of the 10,000 SNP's assayed will be random throughout the genome and <25% of the SNP's assayed will be targeted to candidate genes identified through community input. The DM1-3 516R44 draft genome will be used as a scaffold for transcriptome alignments.

Tomato: The chip contains 7600 SNPs. The SNP content is optimized for cultivated populations as opposed to wild crosses and includes Sanger-based eSNPs from TA496 ESTs (Processing tomato) and the Heinz 1706 (Processing tomato) genome sequence. The majority of SNPs were identified from Illumina transcriptome sequencing of NC84173 (Fresh-Market), FL7600 (Fresh-Market) and OH08-6405 (Fresh-Market), OH9242 (Processing tomato), PI 114490 (Cherry) and PI 128216 (S. pimpinellifolium) lines. We expect >75% of the SNP’s assayed will be random throughout the genome and <25% of the SNP’s assayed will be targeted to candidate genes identified through community input. The DM1-3 516R44 draft genome will be used as a scaffold for transcriptome alignments.

Final SNP content will be selected from SNPs that pass the filtering and design criteria for the Infinium® platform. To help the community assess SNP distribution in cultivated populations we have posted data from a validation of 48 SNPs to the project web site: http://solcap.msu.edu/data.shtml

(Continued on page2)
Dave D’s Perspective: (continued from page 1)

Key benefits are offered to participants:

1. **Early Access:** An opportunity to access a genotyping tool unlike what has been available previously in the tomato and potato communities.
2. **Technology Transfer Opportunity:** Part of the mandate of SolCAP is to facilitate the transfer of technology in the form of genotyping tools into the breeding effort in Solanaceae species. This consortium offers an opportunity to work with experienced SolCAP members to learn the methods associated implementing genotyping methods into characterizing genetic merit in elite potato germplasm.
3. **Reduced Pricing.** The access to consortium members who participate will be at a consortium price that will be below that of available to contributors working alone. Per sample price of chips includes reagents necessary to run chips on an iScan or Bead Array Reader. Regional account specialists can facilitate your access to 3rd party service providers to those participants who do not have immediate access to an Illumina genotyping instrument.

Responsibility of Participants:
Participants are expected to commit to using the chip either by purchasing directly or running samples through a 3rd party testing laboratory. The minimum kit size is suitable to run 48 samples. It is our experience that investment of samples drives stronger and more productive participation in the process.

Current Status and Next Steps:
At this time we are formalizing interest by asking parties to provide a letter or email of intent with potential sample numbers anticipated. This can be achieved by contacting Illumina’s Consortium Manager at: consortia-manager@illumina.com All information regarding sample numbers will remain confidential between individual participants and Illumina.

Journal Highlights:

Schnable, P., et.al., The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, Nov. 2009, 326 (5956), 1112

Achenbach, U., Tang, X., Ballvora, A., de Jong, H., Gebhardt, C. Comparison of the chromosome maps around a resistance hot spot on chromosome 5 of potato and tomato using BAC-FISH painting. Genome, Volume 53, Number 2, 1 February 2010, pp. 103-110(8)


SolCAP Hosts a PBGWORKS Workshop at PAG!

The Plant Breeding and Genomics (PBG) Community of Practice (CoP) held informational workshops while at PAG this year. Alex Stone and John McQueen, Oregon State University, spoke to the new RosBREED CAP project, introducing eXtension and PBGworks and letting them know how they can get involved. On January 9th David Francis led a workshop (with Alex Stone, John McQueen, Deana Namuth Covert, and Peggy Lemaux also presenting) which introduced the workshop participants to eXtension, PBG CoP, and PBGworks. The presentations were followed by a working session in which the individuals formed four groups and tasked to develop plans for how to move forward with CoP development.

1) Networking group

This group discussed developing a graduate student networking initiative in PBGworks. The discussion involved issues that might be appropriate for virtual sessions, e.g. candidacy exam preparation, short presentations on procedures, developing video content, brown bag discussions, invited speakers, seminar practice sessions, etc.

2) Educator group

The group developed a plan for content that follows four main learning objectives. From these they developed four main topic areas that each have their own subtopics, plus they assigned a point person to each section. The main topic areas are genetic concepts, plant breeding, DNA and genetic engineering, and genomics.

3) Grower group

The group decided to evaluate the topic areas that were chosen and discussed what kind of content would fill those areas. The group agreed that links made within content to other documents must be done carefully so that it is useful.

4) Professional Plant Breeder group

This group discussed what the learning objectives are for the content to be delivered. They also took names for who could act as reviewers and providers of content.

SolCAP has developed an outline for content which is based on a start to finish example of marker-assisted selection, additionally 5 of 6 content topics learning objectives were established to help focus and guide the content development.

PBGworks is the home for the Plant Breeding and Genomics a proposed Community of Practice with eXtension. Here we are writing eXtension publications, managing projects, and networking. Visit our site to learn more about PBGworks and our Community of Practice:

http://pbgworks.hort.oregonstate.edu/
Breeder Profile: Shelley Jansky Ph.D.

Shelley Jansky is a research geneticist who holds a USDA-ARS Vegetable Crops Research position along with an assistant professor position in the Horticulture department of the University of Wisconsin–Madison. Shelley’s focus is on potato germplasm enhancement using wild Solanum species, identification of valuable traits in wild relatives and the determination of their genetic basis, introgression of wild species germplasm into the cultivated potato, reproductive biology focusing on crossing barriers and mechanisms to overcome these barriers, and ploidy manipulations using haploids and 2n gametes. Shelley is a SolCAP project participant involved in field trials and phenotyping.

While genetic diversity in potato cultivars is low, tremendous variation exists in wild relatives. Many of these relatives contain valuable genes for disease resistance, tuber quality, storability, and stress tolerance. Some are more easily crossable with the cultivated potato than others. In addition, when hybridized with the cultivated potato, variation exists among wild species in the ability to produce desirable tubers, adapted plants, and fertile offspring. The article below summarizes challenges associated with the use of wild potato relatives in breeding and discusses their potential for cultivar improvement.

Potato Improvement Using Exotic Germplasm: Prospects and Challenges

By Shelley Jansky Ph.D., USDA-ARS and UW-Madison

Modified version of the previously published article


With over 100 wild related species at their disposal, potato breeders have access to a tremendous amount of genetic diversity for cultivar improvement. Wild species are found in a diverse array of environments, including the cold high grasslands of the Andes, hot semi-desert habitats, humid subtropical mountain rain forests, cultivated fields, and even as epiphytes in trees. These wild species contain genes encoding traits not found in cultivars and represent an especially rich source of disease resistance and tuber quality genes.

The major cultivars planted in the US today contain only a small amount of exotic germplasm introduced by potato breeders for genetic improvement. Nearly half of the US acreage is planted to Russet Burbank, a clone that was developed well before modern breeding programs were in place. A quick scan of the pedigrees of current major cultivars reveals common parents that were used in potato breeding programs in the mid-twentieth century because they consistently produced adapted offspring with acceptable yields. However, in recent years, potato breeders have become interested in wild relatives of potato as sources of traits not found in traditional breeding program parents. Historically, they have been used as sources of disease resistance, but they are also becoming increasingly important for their contributions to processing and culinary quality.

In the 1930’s, the wild species *Solanum demissum* was found to have resistance to late blight. Late blight resistant *S. demissum*-derived germplasm was developed by the USDA in the 1930’s and is found in the pedigrees of many cultivars developed in subsequent decades. The major resistance genes in *S. demissum* provided good protection against late blight until the 1960’s, when the pathogen overcame host plant resistance. Current breeding efforts are focusing on more durable forms of late blight resistance. For example, the pedigrees of the new cultivars Jacqueline Lee, Missaukee, and Defender contain diverse wild species as sources of late blight resistance. In another disease resistance example, resistance to PVY, PVX and golden nematode has been introduced from Andigena, a cultivated relative, into the cultivar Eva. The wild species *S. chacoense* has made important contributions to processing quality in potato cultivars. *Solanum chacoense* is a grandparent of the cultivar Lenape, which, in turn is in the pedigrees of several processing cultivars. Lenape has exceptionally high specific
gravity, which presumably contributes to its superiority as a parent for the production of processing clones. Another wild relative, *S. tarijense* (=*S. berthaultii*) is a good source of chip quality, especially at cold storage temperatures.

With increasing interest in culinary quality, breeders will likely be turning to exotic germplasm for traits not found in standard cultivars. South American land races, derived from many sources, contribute red, yellow, and purple flesh as well as unusual patterns of flesh and skin colors. These colors provide unique offerings on dinner plates, but they also add to nutritional quality by contributing to antioxidant activity. The Scottish Crop Research Institute has found that Phureja-derived germplasm has exceptional flavor and shortened cooking times compared to standard cultivars.

Late blight and PVY resistance genes have been reported in 14 and 6 wild *Solanum* species, respectively. Similarly, resistance to other major diseases and improved processing quality traits have been reported in dozens of wild *Solanum* species. Why have only a handful of these species found their way into the pedigrees of potato cultivars? First of all, except for the post-Irish potato famine era, there has not been a strong perceived need for the introgression of exotic germplasm to reduce losses to disease. For the first half of the twentieth century, yield was the principal goal of breeding programs. However, a dramatic increase in processed potato consumption in the last half of the century required breeders to find superior germplasm for specific gravity and processing color. In addition, an increasing interest in alternatives to chemical disease and pest control has led to a search for sources of host plant resistance.

With the realization of the need to increase genetic diversity, it has become necessary to develop strategies to introgress wild germplasm into breeding programs. The US Potato Genebank (NRSP-6) holds 5681 populations of 131 *Solanum* species. Agronomically important traits have been identified in many of these species. Using straightforward methods to overcome crossing barriers, over half of these species can be crossed to the cultivated potato. In addition to contributing specific genes for economically important traits, wild relatives provide the genetic diversity necessary for hybrid vigor. It is interesting to note that hybrids between the cultivated potato and many wild species produce tubers that look “normal” even though they are 50% wild.

Because potato breeding is a time- and cost-intensive endeavor, varietal breeders can not devote substantial resources to the search for useful genetic diversity and its incorporation into their parental lines. Instead, two USDA breeding programs (C. Brown, Prosser, WA and S. Jansky, Madison, WI) are charged with germplasm enhancement. These programs serve as the interface between NRSP-6 and US potato breeders. Our mission is to develop parents to be used by breeders for cultivar development. Ideally, these parents contribute new economically important traits, while simultaneously adding genetic diversity and consequently hybrid vigor to potato breeding programs.

**Fun Facts:**

In 1995, potato plants were taken into space with the space shuttle Columbia. This marked the first time any food was ever grown in space.

At right: Astronaut Catherine G. Coleman, mission specialist, checks out an Astroculture sample on the mid-deck of the Earth-orbiting Space Shuttle Columbia during STS-73 in October 1995. Five small potatoes were grown in orbit from tubers in the Astroculture plant growth facility. Credit: NASA.
Accessing the Potato and Tomato Genome Sequences

By C. Robin Buell Ph.D., Michigan State University

Two consortia, the Tomato Genome Initiative (TGI) and the Potato Genome Sequencing Consortium (PGSC), have been working on obtaining the genome sequence of the tomato and potato genomes, respectively, using whole genome shotgun sequencing approaches. Both consortia have made available to the public, assemblies of the potato and tomato genome. Please note that while the consortia have released the genome sequence, efforts are still underway to improve the quality of the genome sequence and to provide annotation such as genes within the genome. We have provided below a brief description of the potato and tomato genome sequence, how to access the sequence, and how to use the sequence.

Potato Genome Sequence: The PGSC sequenced the *Solanum tuberosum* Group Phureja doubled monohaploid clone DM1-3 516R44 (hereafter referred to as DM1-3). See here for more information on the PGSC: http://potatogenome.net/index.php/Main_Page

Access: The potato genome sequence can be accessed through a BLAST search or by downloading the entire genome sequence.

1. BLAST sequence search tool to identify sequences via sequence similarity:
   

Step 2: Select the type of search that you wish to use. Note that only BLASTN, TBLASTN, and TBLASTX is supported.

Step 3: Paste your favorite sequence into the search box in the FASTA format.

Step 4: Select the database you wish to search. The potato genome sequence is “Solanum phureja scaffolds v3”. Also provided are databases of BAC and BAC end sequences from *S. phureja* and *S. tuberosum* as well as transcript (PUTs) assemblies of potato from the ISU PlantGDB project (plantgdb.org).

Step 5: Submit your sequence for a BLAST search. An intermediate page will appear telling you that your search is in progress and that the results will be held for 15 minutes via a specific URL.

In your BLAST results, the DM1-3 sequence is represented as scaffolds. A sample scaffold is listed below:

PGSC0003DMS000000150

PGSC0003DM: denotes the PGSC version 3 assembly

S: Scaffold

000000150: Unique identifier

Step 6: A link is available that allows you to download your scaffold sequence(s) of interest directly from the BLAST report. In the table of hits, simply click on the scaffold accession you wish to download and you will be presented with the PGSC data access agreement. After you accept the terms of the agreement, the scaffold file will be retrieved and packaged, and you should be prompted by your browser to save the file.

Note that the DM 1-3 scaffold sequences are being made available under the terms of the PGSC data access agreement, so you must read and agree to these terms before downloading the full scaffold database.

2. Download of the potato genome sequence

While the BLAST site will assist in identifying your sequence within the PGSC DM genome assembly, you will need to download the sequence from the PGSC web site to access the scaffold and genome sequence.

Step 1: Go to http://potatogenomics.plantbiology.msu.edu/index.php?p=download

Step 2: To download the PGSC DM scaffolds, select “Solanum_phureja_DM.scaffolds-v3.tar.bz2”

Step 3: Read and if you agree to the data access agreement, click on Yes, I agree to these terms

(continued on page 7)
Accessing Sequences cont. from page 7.

Step 4: The sequence databases are packaged using the Tar archiver, and then compressed using the bzip2 compression software. These programs are generally available on a linux machine; on a Windows machine, a number of applications are available that should be capable of extracting a bzip2-compressed tar file, including WinZip, WinRAR, and WinAce.

Note: This file will be **LARGE (185 Mb)** and will take some time to download.

Step 5: In the uncompressed file will be:

- README: A description of the DM Scaffolds
- Data_access: Statement of data access agreement
- PGSC0003DMS.fa: Multi-fasta file of the scaffolds

Step 6: How to retrieve a specific sequences from the multi-fasta file.

You can use any text editor that is capable of opening large files and doing a text search, for example 'vim' in Linux (or 'vim' in Windows), 'textedit' on a Mac, or 'wordpad' on Windows.

Better still, there are a number of utilities available for retrieving individual records from a fasta sequence database. The NCBI BLAST package has a utility called 'fastacmd' that serves this purpose, the equivalent utility in the WUBLAST package is called 'xget'. Other tools are available with packages such as EMBOSS or exonerate that will also allow you to index and fetch sequences from a fasta database.

**Tomato Genome Sequence:** The Tomato Genome Initiative has sequenced Heinz 1706, a processing variety. For more information on the project, see [http://solgenomics.net/tomato/](http://solgenomics.net/tomato/).

**Access:** The tomato genome sequence can be accessed through a BLAST search, by downloading the entire genome sequence, or through a Genome Browser.

1. **BLAST sequence search tool to identify sequences via sequence similarity:**

Step 1: Go to the SGN BLAST site at [http://solgenomics.net/tools/blast/index.pl?db_id=93](http://solgenomics.net/tools/blast/index.pl?db_id=93)

Step 2: Select the type of search that you wish to use. Note that only BLASTN, TBLASTN, and TBLASTX are supported.

Step 3: Paste your favorite sequence into the search box in the FASTA format

Step 4: Select the database you wish to search. “Tomato WGS Scaffolds Pre-release” is the whole genome shotgun assembly of the genome.

Step 5: Submit your sequence for a BLAST search. An intermediate page will appear telling you that your search is in progress.

In your BLAST results, the Heinz1706 sequence is represented as scaffolds. A sample scaffold is listed below:

Scaffold01322

Step 6: A link is available that allows you to download your scaffold sequence(s) of interest directly from the BLAST report. In the table of hits, simply click on the scaffold accession to get the scaffold sequence.

2. **Download the tomato genome sequence.**

Step 1: The tomato genome whole genome shotgun assembly can be downloaded at: [ftp://ftp.sgn.cornell.edu/tomato_genome/wgs/assembly/](ftp://ftp.sgn.cornell.edu/tomato_genome/wgs/assembly/)

Step 2: You must first agree to the data access terms which can be read in File:READMEFIRSTACCESSAGREEMENT.txt.

Step 3: Then download the most current version, which as of March 4, 2010 is build_1.03. In this folder are: (continued on page 8)
Accessing Sequences cont. from page 7.

Scaffold data:
S_lycopersicum_scaffolds.1.03.fa.gz - scaffold sequences  S_lycopersicum_scaffolds.1.03.qual.gz - scaffold quality values  S_lycopersicum_scaffolds.1.03.tab.gz - scaffold assembly information

Contig data:
S_lycopersicum_contigs.1.03.fa.gz - contig sequences  S_lycopersicum_contigs.1.03.ace.gz - contig assembly information

The scaffolds are sets of contigs that are ordered and oriented and thus represent a higher order of the genome assembly. In the majority of cases, you will want to use the Scaffolds (S_lycopersicum_scaffolds.1.03.fa.gz).

Step 4: Opening the .gz files.
The sequence databases are packaged using the Tar archiver, and then compressed using the bzip2 compression software. These programs are generally available on a linux machine; on a Windows machine, a number of applications are available that should be capable of extracting a bzip2-compressed tar file, including WinZip, WinRAR, and WinAce.

Note: This file will be LARGE (215 Mb) and will take sometime to download. Here is a sample scaffold sequence name:
>SL1.03sc00001 length=2953

The Scaffold name is SL1.03sc00001 in which
SL: is for Solanum lycopersicon
1.03 is the build number
sc00001 is the unique scaffold number (identifier)

Step 5: How to retrieve a specific sequences from the multi-fasta file.
You can use any text editor that is capable of opening large files and doing a text search, for example 'vim' in Linux (or 'vim' in Windows), 'textedit' on a Mac, or 'wordpad' on Windows.

Better still, there are a number of utilities available for retrieving individual records from a fasta sequence database. The NCBI BLAST package has a utility called 'fastacmd' that serves this purpose, the equivalent utility in the WUBLAST package is called 'xgget'. Other tools are available with packages such as EMBOSS or exonerate that will also allow you to index and fetch sequences from a fasta database.

Announcement - 4th Annual Plant Breeding Meeting

The annual meeting of the National Association of Plant Breeders (NAPB), an initiative of the Plant Breeding Coordinating Committee (PBCC) will be held August 15-17, 2010, at Pioneer Hi-Bred's headquarters in Johnston, Iowa. The PBCC serves as a forum for issues and opportunities of national and global importance to the public and private sectors of the U.S. national plant breeding effort. The meeting will begin at noon on Sunday, August 15, and conclude after lunch on Tuesday, August 17.
The meeting has three goals: 1) to discuss strategies to shape the future of plant breeding, 2) to expose participants to state-of-the-art plant breeding research through invited speakers, and 3) to exchange knowledge through poster presentations by participants.

During the afternoon of Aug 17th, there will be a career session available for graduate students at the Pioneer facilities. More information about other post-conference activities will be provided in future meeting announcements. Central Iowa, where Johnston is located, is home to a number of other public and private plant breeding programs. Participants may wish to make independent arrangements to visit these while they are in the area.

All plant breeders – student and professional, public sector and industry, U.S. and abroad – are encouraged to attend. Please save-the-date on your calendar now. The online registration site is available soon. Contact: Rita Mumm, ritamumm@illinois.edu
The Seed Biotechnology Center (SBC) was established in 1999 as a partnership between the College of Agricultural and Environmental Sciences at the University of California, Davis, and the Californian, national and international seed and plant biotechnology industries. The SBC connects the University with those stakeholders and conducts research, education, outreach and public service activities supporting the fundamental role of seeds as a delivery system for improved agricultural products.

The mission of the Seed Biotechnology Center is to mobilize the research, educational and outreach resources of UC Davis in partnership with the seed and biotechnology industries to facilitate discovery and commercialization of new seed technologies for agricultural and consumer benefit. The SBC conducts collaborative research with private companies and other academic institutions to develop new tools for plant breeding, identify novel traits, improve seed quality, promote commercialization of new products and facilitate co-existence of diverse production systems. The SBC develops and offers continuing education courses and programs for seed industry professionals and the public. These include intensive short courses as well as workshops and symposia to enable personnel to develop new skills and remain current in new technologies. The SBC sponsors meetings and publishes bulletins and popular articles to distribute scientific information about crop improvement to a broad audience. The SBC website contains these and other publications and links to a wide array of related information. The SBC engages in public service activities to support the seed and agricultural industries. The mission is to be a publicly available source of scientifically based information on seeds, crop improvement and agricultural biotechnology.

Allen Van Deynze, a co-Director of the SolCAP project, is the Director of Research for the Seed Biotechnology Center. Allen directs research involving molecular markers and transgenics in vegetable and field crops related to biotechnology. He designs and teaches courses for professionals on biotechnology including “Breeding with molecular markers” and routinely makes presentations on biotechnology and seed industry to professional and public audiences. In regards to SolCAP he oversees normalized library construction, sequencing and initial SNP genotyping through the UCD Genome Center DNA Technologies Core. Allen coordinates SNP genotyping and integration of genotype data into SGN, evaluates tomato trials in CA, coordinates the SolCAP education workshops and extension at UCD through the Seed Biotechnology Center.

For further information visit the Seed Biotechnology Center website at http://sbc.ucdavis.edu/
Plant Breeding Academy Class III

The Seed Biotechnology Center at the University of California, Davis has organized a professional development course to teach the principles of plant breeding to seed industry personnel. This two-year course addresses the reduced numbers of plant breeders being trained in academic programs. Participants meet at UC Davis for six sessions over two years. Readings and exercises continue between sessions via internet to allow participants to maintain their current positions while being involved in the course.

Course goal: This course develops the skills and abilities of current industry personnel to enable them to become independent breeders or more valuable contributors to larger breeding programs.

Who should attend? The course is targeted toward personnel currently involved in plant breeding programs who lack the academic background in genetics theory and practice to advance as independent breeders. Current breeders who desire a refresher course or would like to broaden their expertise would also be potential participants.

When will the in-residence sessions be held? Instruction for the 2010-2012 Academy cohort begins Fall 2010 and runs through Summer 2012. Dates of in-residence sessions in Davis are:

2010-2011
- September 13-18, 2010
- February 7-12, 2011
- June 6-11, 2011
2011-2012
- September 12-17, 2011
- February 6-11, 2012
- June 4-9, 2012

Application and Admission: To provide a personalized learning environment, the program is limited to 20 participants. Applicants should complete the on-line form and separately mail or email a resume in order to be considered for enrollment. Applicants’ background and experience will be reviewed to ensure they meet the minimal requirements before acceptance. Applicants must have a Bachelor of Science degree (or demonstrate equivalent professional experience) and have taken introductory courses in statistics and genetics. Practical experience, academic standing (GPA or equivalent) and rationale for participation in the Academy will be evaluated. Among applicants meeting the program requirements, acceptance will be on a first-come, first-served basis. Acceptance is not secured until the first year's tuition is received.

Tuition: Tuition is US$23,000 per participant for the two-year program. Tuition includes all course materials and fees. Lunches and breaks during residence in Davis are provided. Travel, accommodations and other meals during in-residence sessions are not included. A non-refundable deposit of US$1,000 will be due within 30 days of acceptance into the Academy, and will be applied toward tuition. The balance of the first-year tuition (US$11,000) must be received by June 1, 2010, and the second-year tuition (US$11,000) by June 1, 2011. No refunds will be issued for an annual payment. Payment procedures will be provided to applicants following acceptance into the Academy.

Applications: http://ucce.ucdavis.edu/survey/survey.cfm?surveynumber=3888
For more information contact: Joy Patterson jipatterson@ucdavis.edu 530-752-4414
Calendar of Events:

**June 20-23, 2010**, 9th World Tomato Processing Congress will take place at the Estoril Congress Centre, Portugal


Yes there will be another SolCAP workshop!

**August 15-17, 2010** National Association of Plant Breeders (NAPB), an initiative of the Plant Breeding Coordinating Committee (PBCC) at Pioneer Hi-Bred’s headquarters in Johnston, Iowa.