3nd Annual SolCAP Meeting

Mark your calendar for the next SolCAP project meeting. Learn about all the exciting research happening with SolCAP! The meeting will take place at the Plant and Animal Genome XVIII Conference, at the Town and Country Resort, in San Diego, CA. It will be held on Saturday January 15, 2011 from 8am to 10am in the Hampton Room. See page 6 for the meeting agenda. This will be an excellent opportunity to review the accomplishments our team has made over the year and refine our plan of work for 2011. The SolCAP project is unique in that one third of our budget is devoted to education and extension components. SolCAP is the lead CAP for an eXtension.org initiative on plant breeding. On the evening of January 15 at 6pm in the Tiki Pavilion in the Town and Country Resort, SolCAP will be hosting a Launch Party to introduce our internet community PBGWorks. Light refreshments will be served and all plant scientists are welcome to attend. Please see page 3 for more details.

Dave D.’s Perspective:
2010 was an exciting year for SolCAP.

I would like to highlight a few activities that occurred over the past year.

We have completed the design for the Infinium potato and tomato SNP platforms. Both the potato and tomato SNP predictions have been validated using the BeadExpress platform. Currently, ~8300 markers (derived from candidate genes, genetic markers and unique scaffolds) are represented on the Illumina potato Infinium array. Potato data has been shared with international collaborators (Scottish Crops Research Institute, SCRI) and the Potato Genome Sequencing Consortium to help anchor the potato genome sequence. The Illumina tomato SNP chip includes 8,784 loci on a 10,000 SNP array. Of these loci, 4,548 were derived from cultivated types, 1,387 were shared with European germplasm, 552 were in candidate genes, and 2,279 represented unique scaffolds of the tomato genome.
The potato and tomato Illumina Infinium arrays are available to assay at UC Davis, MSU, and Cornell facilities. UC Davis and MSU are also providing service for outside parties for the potato and tomato arrays. Thus far SolCAP has genotyping data for 288 of 480 potato samples, as well as 96 samples from the Michigan State breeding program. We expect the remaining 192 samples to be run by January. We are in the process of calling SNPs for analysis. In validation BeadExpress data for potato, all 5 of the possible genotype alleles were called for 52% of SNPs and an additional 25% had 4 of alleles called, displaying the robustness of the Illumina assay for the first time. We have provided Illumina our data to improve their software to call 5 alleles vs. the current 3 possible. Initial analyses of Infinium data indicate that similar results may be obtained. The complexity of calls is population dependent. In tomato, our validation BeadExpress data on 96 SNPs and 96 samples indicated that SNPs were robust and amenable to genotyping, even with wild accessions. For some SNPs, wild accessions indicated additional or null alleles not detected in sequence data of our breeding lines, again indicating the sensitivity of the Illumina assay. Tomato DNA is being extracted and will be run within the first quarter of 2011.

A call for mapping populations was sent to the potato community. SolCAP has identified two mapping populations for SNP genotyping. One cross is between Atlantic and Superior. Traits such as reducing sugar, starch content, internal defects, scab resistance and maturity are segregating in the population. The second cross is between Atlantic x B1829-5. In addition to the traits segregating in the first population, the Atlantic x B1829-5 population is also segregating for internal heat necrosis susceptibility. These populations will be SNP genotyped in early 2011. These tetraploid mapping populations will be used to link SNPs with segregating trait data. A call for tomato mapping populations will be sent in 1st quarter 2011. The SolCAP tomato and potato panels of elite germplasm were field evaluated in 2010. Field studies were conducted in NC, NY, ID, MN, OR, WI, FL, OH and CA. A database of phenotypes for key traits across accessions of each commodity was initiated and is accessible through SolCAP (http://solcap.msu.edu/) and Solanaceae Genome Network (SGN, http://solgenomics.net/). 2009 phenotype data were uploaded to the SolCAP website for public access and the data is being incorporated into the SGN database and website. Phenotypic data will be maintained on the SolCAP and SGN databases for public access by the research community. We are currently collecting centralized sugar and chip color data (core traits for the project) in the 4x potato mapping population and the potato panel from stored tubers of the 2010 trials. PBGworks is the collaborative workspace that is being used for the Community of Practice. Content is authored and reviewed there and then 'fed' to eXtension.org for publication. There are 5 CAP groups in the workspace, as well as a variety of lab groups and PBG eXtension content development and administrative groups. This report was collaboratively authored in the workspace, and all SolCAP eXtension content is authored in the workspace. The PBGworks workspace currently has 195 people registered as members who represent 30 universities and federal agencies, 11 educational institutions outside of the USA, and 5 industry groups.

The launch for the eXtension site will be at the PAG in January. There are currently 79 content pages being actively developed for publication. Content includes profiles of public plant breeding programs, mini-reviews of significant agricultural traits, tutorials of public web-based databases, and tutorials of public plant breeding related software. In addition, SolCAP is actively developing the capacity to 'clone' content published online elsewhere; SolCAP anticipates making available two learning lessons published originally to the plant and soil sciences eLibrary and now available through 'cloning' at eXtension.org.

Continued on page 3.
The Plant Breeding and Genomics Community of Practice (PBG CoP) with eXtension is holding their public release party Saturday, January 15 from 6:00 to 8:00 pm in the Tiki Pavilion at the Town and Country Resort, San Diego, CA. Two years in the making, the PBG CoP is excited to have you join them as they give a demonstration of their free, public educational materials which will be available soon at the Plant Breeding and Genomics Resource area at http://www.extension.org. Leaders of the CoP will be on hand to discuss how you can use their information in your teaching and training efforts and how you can get involved with the CoP. The party will consist of light refreshments, approximately 60 minutes of presentations on eXtension publications and use of the community’s hub, PBGworks.org, followed by an open discussion session. Computers will be available for you to interact with the websites. For more information contact Heather Merk at merk.9@osu.edu.

Two workshops were delivered by SolCAP in person with online webinar components. The PAA 2010 meetings resulted in three separate webinars and their recordings. The 2010 Tomato Disease Workshop (TDW) webinars are still in post-production, but should result in five separate webinar recordings. The TDW webinar had 35 participants with participants from Asia and Europe. The PBGworks.org website was used during the lead up for the TDW webinar for people to sign up and download copies of the handouts. The recordings from both workshops will be available from the SolCAP website and eXtension.org after the launch of public content in January 2011, with some recordings also making it on YouTube.

We have a project web site (www.solcap.msu) which is a centralized resource for SolCAP participants and the Solanaceae breeding community. The site includes project news and personnel, databases, tools, resources, project objectives, and downloads. SGN has been working on a framework for storing the SolCAP phenotyping and genotyping experimental data, providing a user-friendly web-interface for editing the data, and tools for statistical analysis of the results, including association mapping, QTL finder, SNP analysis, and functional annotation of genotypes. Currently we have designed a pipeline for uploading SolCAP accessions and results of genotyping and phenotyping experiments. The information from two phenotyping experimental sets has been uploaded to the SGN database and web site. We've been working with SolCAP researchers on a standard template for future data, which will make uploading of more experiments fast and seamless. The database is loaded with 479 tomato SolCAP accessions, 226 plots with more than 160,000 phenotyping results, and more than 1,000 images taken mostly by the Tomato Analyzer phenotyping software.
Use of Illumina Infinium SNP genotyping facility for Tomato and Potato Communities

A high throughput Single Nucleotide Polymorphism (SNP) genotyping lab has been set up in the Plant and Soil Sciences Building at Michigan State University. The lab is equipped with an Illumina iScan system and the associated facilities to run Illumina high throughput assays. We have been successfully running the Infinium Assay using the system. In an Infinium assay, a sample can be genotyped with 3,000-1,200,000 SNP markers, depending on the format of the BeadChips. We are making the MSU high throughput SNP genotyping system available to Tomato and Potato Communities for their population genotyping. The following table shows the estimated cost for processing Illumina 24-sample BeadChips. The costs include labor, equipment maintenance and consumables for the lab procedures.

<table>
<thead>
<tr>
<th>No. of BeadChips</th>
<th>2</th>
<th>4</th>
<th>6</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total No. of samples for 24-sample chips</td>
<td>48</td>
<td>96</td>
<td>144</td>
<td>192</td>
</tr>
<tr>
<td>Per sample cost</td>
<td>$27</td>
<td>$13.50</td>
<td>$10</td>
<td>$8</td>
</tr>
</tbody>
</table>

This cost is for processing of the Infinium chips only. Infinium BeadChips must be purchased separately from Illumina and shipped to Illumina SNP genotyping lab c/o Dr. Dave Douches, A499 Plant and Soil Sciences Building, Department of Crop and Soil Sciences, East Lansing, MI 48824-1325.

When submitting samples, make sure the DNA concentrations is determined with picogreen (specific for double stranded DNA) and the DNA concentration is in the range of 50-100 ng/ul. We find that samples that have been treated with RNAse can perform better. We will also check the DNA concentration with picogreen. If the DNA concentration is less than 50 ng/ul, we will request you to resubmit the DNA samples. An additional cost will be charged for checking the resubmitted samples.

The data need to be processed with Genome Studio software. The software is installed on a computer in the SNP Genotyping lab. If you need a license of the Genome Studio software, you need to purchase the license from Illumina directly (www.illumina.com). A new module of Genome Studio is now available to call up to 5 genotypes.

Journal Highlights:


Repositories: Preserving and Protecting Precious Germplasm

Diane Nelson
UC Davis Department of Plant Sciences

We live in a world of accelerating change affecting climate and crop pests and pathogens, while demands for safe, healthy, plentiful food continue to rise. Adapting crops to shifting conditions requires many things, including genetically diverse germplasm.

Germplasm is living tissue from which new plants can be grown – a seed, a leaf, a stem, pollen or even just a few cells. Germplasm contains the information for a species’ genetic makeup. Researchers travel far and wide to collect wild forms of our cultivated species, which provide a wealth of genetic diversity, but that valuable resource could be lost without repositories where germplasm can be properly stored, multiplied and distributed.

The Department of Plant Sciences houses several such seed and gene collections for a wide variety crops – wheat, lettuce, strawberries, beans, cereal, stone fruits, grapes, nuts, the list goes on. To understand the importance of these collections, let’s take a closer at one such repository: the C.M. Rick Tomato Resource Center.

The tomato, like other cultivated crops, lost much of its genetic diversity during domestication and migration. As a result, tomato breeding progressed slowly in the early part of the 20th century. But all that began to change in the 1940s when (not coincidentally) plant geneticist and botanist Charles Rick joined the faculty at UC Davis in what was then the Division of Truck Crops (now part of our Plant Sciences Dept.). For the next half century, Rick criss-crossed the Andes, the Galapagos and elsewhere, gathering more than 1,000 wild tomato specimens, many of which are now extinct in their native habitat. With his growing collection, Rick made landmark contributions in plant genetics, evolution and genome mapping. As a byproduct of his collecting and research, Rick founded the Tomato Genetics Resource Center TGRC), a seed repository of mutants, genetic stocks and related wild species of tomato.

The repository now holds over 3,600 lines developed at UC Davis and beyond. Its wild species are the source of resistance of 44 major tomato diseases, at least 20 insect pests, improved fruit traits, tolerances to stresses such as drought and salinity and other useful traits.

Thanks in part to Rick and the TGRC, average yields of processing tomatoes in California have increased nearly 10-fold since the 1940s!

Rick passed away in May 2002 at the age of 87.

“And he was active in plant genetics right up to the end,” says Roger Chetelat, a former student and colleague of Rick who has since become director and curator of the TGRC.

Chetelat and his team continue to broaden the genetic diversity accessible for tomato improvement and to study biological processes relevant to biodiversity conservation, domestication and plant breeding.

You can learn more about the TGRC and Chetelat’s research at http://tgrc.ucdavis.edu

The USDA operates a National Clonal Germplasm Repository west of campus. Residents of the repository (continued on pg.7.)

Roger Chetelat collecting seeds of wild tomatoes in the Atacama Desert of Chile.
SolCAP Meeting
Hampton Room, Town & Country Convention Center, San Diego, California
January 15, 2011: 8AM – Noon

8:00-8:05 am  Welcome and Introduction
8:05-8:10am  SolCAP overview
    David Douches, Michigan State University
8:10-8:20am  Objective 1: Create an education program to train graduate students in genome-based breeding and workshop training for the tomato and potato communities.
    Walter De Jong, Cornell University
8:20-8:25am  Objective 2: Amplify outreach efforts by developing an eXtension Plant Breeding and Genomics Community of Practice (PBGCoP).
    David Francis, Ohio State University
8:25-8:35am  Objective 3: Collect standardized phenotypic data for tomato and potato.
    David Douches, Michigan State University
8:35-8:45am  Objective 4: Develop extensive sequence data.
    Robin Buell, Michigan State University
8:45-8:55am  Objective 5: Establish centralized facilities for genotyping a core set of SNPs in standard germplasm panels in tomato and potato.
    Allen Van Deynze, University of California-Davis
8:55-9:00am  Objective 6: Address regional, individual program and emerging needs within the Solanaceae community through a small grants program.
    David Francis, Ohio State University
9:00-9:05am  Objective 7: Create integrated, breeder-focused resources for genotypic and phenotypic analysis.
    Lukas Mueller, Cornell University
9:05-9:15am  Evaluation of extension activities:
    Michael Coe, Cedar Lake Research Group
9:15-10:00am  SolCAP – Future Outlooks/Issues/Open discussion
    David Douches, Michigan State University
10:00-10:10am  Break
10:10-11:00am  Advisory Board meeting: closed session
11:00-11:50am  Discussion: closed session
    Comments and Suggestions from Advisory Board with Executive Committee
11:50am –Noon  Closing Comments
    David Douches, Michigan State University

Repositories: (cont’d from page 5)

are many and diverse – grapes, walnuts, pistachios, pomegranates, plums, olives, fig, almonds, peaches, mulberries, you name it. If it’s a nut or a fruit, you can probably find it there in a vast array or varieties as a ready source of genetic material.

You can learn more about the National Clonal Germplasm Repository at http://www.ars.usda.gov/main/site_main.htm?modecode=53-06-20-00

In addition, many plant geneticists and breeders on campus maintain their own biological collections in connection with their research. For more information, go to www.plantsciences.ucdavis.edu

Article reprinted from The Leaflet, a semiannual newsletter from the Department of Plant Sciences, UCD. Fall 2009 edition.
SolCAP Workshop 2010 at the Potato Association of America Meeting

Michael Coe Ph.D., SolCAP Evaluations
President, Cedar Lake Research Group

On August 15, 2010, SolCAP sponsored an afternoon workshop at the Potato Association of America meeting at Oregon State University in Corvallis, Oregon. Three hands-on sessions focused on Working with the Potato Genome (C. Robin Buell), Working with Infinium Genotype Data (Allen Van Deynze) and Linkage Analysis and QTL Mapping in Tetraploids (Christine Hackett).

The first session, presented by Robin Buell, covered the characterization of the potato genome sequence and annotation, use of the potato genome browser, searching for specific loci, and extracting sequences for marker development. The second session by Allen Van Deynze focused on the use of Infinium data, quality control, exporting genotyping data and working with tetraploid data. Finally, Christine Hackett discussed segregation analysis in tetraploids, linkage and QTL analysis, and the TetraploidMap software.

The hands-on session was conducted in a campus computer lab, where 40 participants had access to the software and example data and could try many of the demonstrated techniques for themselves. In addition, the workshop was broadcast live as a webinar, and 20 people participated online.

Surveys completed at the end of the workshop indicated that participants found the topics relevant and the presentations effective, with clear learning objectives and a good balance between theory and application. Participants reported that they gained new knowledge that they plan to apply in their work, and over 90 percent would recommend the course to others. Some participants wanted more time on particular topics, and many offered suggestions for the next SolCAP workshops.

Recordings of each of the three webinar sessions are available online at http://solcap.msu.edu/extension.shtml

**Calendar of Events:**


**June 4-8, 2011**, In Vitro Biology Meeting, The Raleigh Marriott City Center, Raleigh, NC

**August 6-11, 2011**, Plant Biology 2011- Minneapolis, MN

**August 2011**, 5th Annual Plant Breeding Meeting, Texas A&M University, College Station, TX.