



# Solanaceae Coordinated Agricultural Project

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## 4th Annual SolCAP Meeting



San Diego, CA

**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 Conference, at the Town and Country Resort, in San Diego, CA. It will be held on Sunday January 15, 2012 from 8am to 10am in the Garden Salon #2 room. (See page 7 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 2012, our final year. 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 called Plant Breeding and Genomics community of practice. On January 17 at 2pm in the Towne Room at the Town and Country Resort, SolCAP will be hosting a PBG Workshop. All plant scientists are welcome to attend. Please see page 7 for more details.

### SolCAP

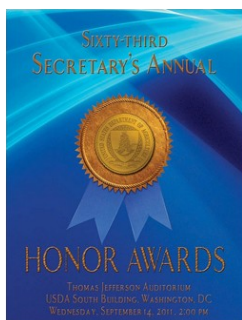
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## Dave D.'s Perspective:

### SNP-based genotyping of populations are a community resource

As part of the core objectives, the potato and tomato communities have developed numerous populations that have been or will be SNP genotyped through SolCAP funding. For potato, the community has developed a potato diversity panel of 320 lines, two diploid populations and a tetraploid population that have been SNP genotyped using the Infinium 8300 potato SNP array ([http://solcap.msu.edu/potato\\_infinium.shtml](http://solcap.msu.edu/potato_infinium.shtml)). Additional bi-parental crosses from the potato community were also SNP-genotyped. (continued on p.2)



## Dave D.'s Perspective: (continued from page 1)

The SNP-genotyped lines are listed below:

Potato diversity panel (1x, 2x, and 4x; yield, specific gravity, maturity, tuber shape, reducing sugars, etc.)

DM x 84SD22 (2x; SNP mapping)

DM x RH (2x; SNP mapping)

Premier Russet x Rio Grande Russet (4x; reducing sugars, FF, chips color, yield, tuber shape, etc.)

Atlantic x Superior (4x; tuber calcium, reducing sugars, internal defects, specific gravity)

B1829-5 x Atlantic (4x; chip color, internal heat necrosis, specific gravity, maturity)

W4 x 524-8 (2x; specific gravity, chip color, disease resistance)

CIP core population (4x)

Waneta x Pike (4x; chip color, specific gravity, scab resistance, pink rot)

Genetic maps from these populations will be used for evaluating concordance with physical positions based on the draft potato genome. QTL and association mapping will also be conducted with these populations to validate known QTL and identify new loci influencing vitamin, sugar and starch content.

Two diploid populations (DM x 84SD22, developed at Michigan State University, and DM x RH, developed at Virginia Tech) are being used to check concordance between the genetic map and the draft genome sequence for potato. Each population has over 1900 SNPs segregating in the progeny. These populations provide complementary resources in that there are few (less than 20%) SNPs that are polymorphic in both populations. The parent, 84SD22, is a hybrid between haploid *S. tuberosum* and *S. chacoense*. The successful number of SNP calls suggests that the Infinium 8300 potato SNP array is robust in genotyping an array of diverse potato germplasm. The potato diversity panel analysis is under way with the SolCAP generated phenotype data. We are also ready to initiate the QTL analysis with the Russet cross (Premier Russet x Rio Grande Russet), having collected both the genotype and phenotype data.

The SolCAP-supported genotyping of bi-parental mapping populations provided by the community should complement the diversity panel and russet mapping population and provide an opportunity for QTL validation. One cross developed at the University of Wisconsin, Madison between Atlantic and Superior is segregating for traits such as reducing sugar, starch content, internal defects, scab resistance and maturity. A second cross, Atlantic x B1829-5, developed at North Carolina State University, is segregating for similar traits, but also internal heat necrosis susceptibility. Recently, a diploid population from USDA/ARS was added that is segregating for tuber quality traits and disease resistance, as well as a tetraploid population from Cornell University that is segregating for chip-processing quality along with common scab resistance. Lastly, CIP was able to send 48 clones from their collection for SNP genotyping. This sub-population will be used to compare the North American and South American germplasm diversity.

After the mapping studies are completed, we foresee these results being used by the breeding community. In many cases, the donor source of the QTL can be crossed with elite parents to create breeding populations with the expectation that advanced breeding lines or varieties may be selected from the populations. We foresee breeders being able to use the information from these populations to make targeted crosses aimed at integrating desired alleles across the genome into existing germplasm. Additionally, these QTL will provide a framework for future studies to interrogate gene interactions within the carbohydrate/sugar pathways, providing valuable information to breeders about desirable allele combinations. Besides carbohydrates/sugars, in potato there will be a focus on resistance traits. We expect that validation will be carried out by programs that are interested in that specific resistance trait. These studies may be regional in nature due to the environmental conditions necessary to promote disease development or insect pressure. Simply-inherited major genes for resistances should require little validation compared to more complex traits like yield and stability in potato. The ability to have simply-inherited markers linked (continued on p.3)

## Dave D.'s Perspective: (continued from page 2)

to major resistances will reduce the cost of breeding by reducing the amount of germplasm that will be screened through costly and time-consuming in vivo assays.

For tomato, in addition to the 480 tomato diversity panel, six of 12 community bi-parental populations were selected for SNP genotyping. These populations represent six public breeding programs and will assay yield, antioxidants, carbohydrates, late and early blight, virus, bacterial and fungal resistance, and flowering and reproduction traits. One population is being genotyped with support from seed industry/genetic service providers, thus further leveraging SolCAP resources. Based on polymorphism of parents on the Infinium 7600 tomato SNP array, a 384 SNP panel was selected for both processing and fresh market populations. SNPs in each panel were chosen based on genetic and physical locations in the genome. In addition to genotyping using the Infinium SNP platforms described thus far, two populations (one potato and one tomato) will be genotyped by sequencing (GBS).

We feel that the SolCAP SNP genotyping effort is providing a resource for the community. We are able to direct translational research towards promising approaches such as bi-parental mapping, introgression, marker assisted selection, and association mapping approaches.

## SolCAP Awarded USDA HONOR



Photo: Agriculture Secretary Tom Vilsack (l) and Deputy Secretary Kathleen Merrigan (r), (David Douches accepting award) September 14, 2011 in the Jefferson Auditorium at the US Department of Agriculture in Washington, DC. USDA Photo by Lance Cheung.

**SolCAP** was honored in September as a recipient of the U.S. Department of Agriculture (USDA) Secretary's Honor Award. The award was received in the "Helping America promote sustainable agricultural production and biotechnology exports as America works to increase food security" category. Our director, David Douches, accepted the award on behalf of the group of CAPs "Barley, Wheat, Potato and Tomato Coordinated Agricultural Projects (CAP)". The CAP's were recognized for their scientific discoveries and their translation into beneficial agricultural products. The USDA Secretary's Honor Awards are designed to recognize exceptional leadership, contributions, or public service by individuals or groups who support the goals of the USDA. According to the USDA, the awards are the most prestigious presented by the Secretary of Agriculture.

## Potato and Tomato Beadchips are Available Again!!!!

Due to popular demand and beadpool availability, Illumina has extended the deadline for orders on the SolCAP Potato and Tomato genotyping Beadchips through December 2012.

Illumina will accept orders for the base SolCAP Tomato and potato as well as orders for "Add-on" content for these tools Through December of 2012.

Please contact Illumina at [consortiamanager@illumina.com](mailto:consortiamanager@illumina.com) <mailto:[consortiamanager@illumina.com](mailto:consortiamanager@illumina.com)> for details. Cindy Taylor Lawley, PhD Scientist Agriculture Consortia Program Manager Illumina, Inc. 25861 Industrial Blvd. Hayward, CA 94545 Tel: [510 670 9478](tel:5106709478) Mobile: [619 379 9360](tel:6193799360) Fax: [510 670 9302](tel:5106709302) Email: [clawley@illumina.com](mailto:clawley@illumina.com) Web: [www.illumina.com](http://www.illumina.com) Facebook: [www.facebook.com/agconsortia](http://www.facebook.com/agconsortia)

## Affordable SNP genotyping facility at Michigan State University



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.

<b>Cost for processing Illumina BeadChips</b>				
<b>No. of BeadChips</b>	<b>2</b>	<b>4</b>	<b>6</b>	<b>8</b>
<b>Total No. of samples for 24-sample chips</b>	<b>48</b>	<b>96</b>	<b>144</b>	<b>192</b>
<b>Per sample cost</b>	<b>\$27</b>	<b>\$13.50</b>	<b>\$10</b>	<b>\$8</b>

This cost is for processing of the Infinium chips only. Infinium BeadChips must be purchased separately from Illumina and shipped to Infinium 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.

There are specific requirements needed when submitting samples. See the lab website: [http://potatobg.css.msu.edu/snp\\_genotyping\\_facility.shtm](http://potatobg.css.msu.edu/snp_genotyping_facility.shtm) for specific instructions before preparing and sending your samples.

The data needs 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](http://www.illumina.com)). A new module of Genome Studio is now available to call up to 5 genotypes.

For more information contact Dr. David Douches, Michigan State University, [douchesd@msu.edu](mailto:douchesd@msu.edu) or 517-355-0271



## Access it Online: SolCAP Potato Genomics Workshop at PAA

The SolCAP project hosted the workshop "Using SolCAP phenotype and Infinium SNP data in Potato Breeding" in conjunction with the 95th Annual Meeting of the Potato Association of America. The workshop took place at the Hilton Wilmington Riverside in Wilmington, North Carolina on Sunday, August 14, 2011.

The workshop/webinar is now available online. The topic and links are:

- [Phenotyping the SolCAP potato germplasm panel](#) - Walter De Jong (Cornell University)
- [Potato Genomics: What's Next?](#) - Robin Buell (Michigan State University)
- [SNP-based genetic maps: Linkage and QTL analysis](#) - Dave Douches (Michigan State University)
- [Breeding in a Genomics Era](#) - Dave Francis (The Ohio State University, Wooster)
- [Developing the Breeder's Toolbox at SGN](#) - Joyce Van Eck (Cornell University)
- **Who should view it?** This workshop was specifically designed for potato breeders, breeding assistants and lab personnel.

## Journal Highlights :

Hamilton, J. P., Hansey, C. N., Whitty, B. R., Stoffel, K., Massa, A. N., Van Deynze, A., De Jong, W.S., Douches, D.S. Buell, C. R. (2011). Single nucleotide polymorphism discovery in elite North American potato germplasm. *BMC Genomics*, 12, 302. doi: 10.1186/1471-2164-12-302

Ballvora, Agim, Flath, Kerstin, Lübeck, Jens, Strahwald, Josef, Tacke, Eckhard, Hofferbert, Hans-Reinhard, & Gebhardt, Christiane. Multiple alleles for resistance and susceptibility modulate the defense response in the interaction of tetraploid potato (*Solanum tuberosum*) with *Synchytrium endobioticum* pathotypes 1, 2, 6 and 18. *TAG Theoretical and Applied Genetics*, 1-12. doi: 10.1007/s00122-011-1666-9

The Potato Genome Sequencing Consortium. Genome sequence and analysis of the tuber crop potato. *Nature*, Vol. 475, No. 7355. (10 July 2011), pp. 189-195. doi:10.1038/nature10158

# Plant Breeding and Genomics Web Resource

Did you miss the SolCAP workshop at PAA? Do you want to learn how to use R software to analyze your data? Are you looking for high quality quantitative genetics learning resources? Or maybe you're wondering how to approach the SNP data you've just received from SolCAP? If you answered yes to any of these questions, visit the plant breeding and genomics (PBG) community of practice website ([www.eXtension.org/plant\\_breeding\\_genomics](http://www.eXtension.org/plant_breeding_genomics)).

PBG is a major outreach initiative of SolCAP that includes 165 peer-reviewed flat-text pages, animations, blogs, tutorials, videos, and webinars. Contributions to PBG extend beyond SolCAP; the Conifer Translational Genomics Network (CTGN), RosBREED, and Barley CAP are also active contributors to PBG. Efforts initiated by Barley CAP are currently supported by the Institute of Barley and Malt Sciences at North Dakota State University. Since PBG's public launch in January, the website has received more than 84,000 page views from 122 countries.

This fall, PBG launched a "how to" methods in plant breeding webinar series (<http://www.extension.org/pages/60426>). This series has been widely popular with graduate students, post docs, educators, professional plant breeders, and technical staff. In addition to reaching a broader community, the webinars provide opportunity for evaluation and feedback, giving our audience a chance to determine future topics and content. Webinar feedback so far has been very positive, with participants indicating intent to apply the knowledge and skills they gained from the webinar. For example, a participant in the "how to align sequences" webinar reported "The knowledge I gained from the webinar will be useful to develop molecular markers via sequence analysis." A participant in the "how to use R" webinar reported:

*"The benefit for me was to see some of the options available for ANOVA analyses with fixed and mixed models. I would like to understand the advantages and disadvantages of using R compared to other available software, and this webinar was a step in that direction. The online resources are very helpful and I expect to refer to them for data analysis and for preparation of classes that I teach."*

Participants have also actively requested further training in a variety of current techniques and analyses relevant to plant breeding and SolCAP, including genomic selection. The webinars currently being planned for 2012 will address this community need.

The webinar series continues through November. On November 10<sup>th</sup>, Dr. Jennifer Kling of Oregon State University will present an introduction to augmented experimental designs. During the webinar Dr. Kling will perform sample analyses using examples from her breeding program. On November 17<sup>th</sup>, Dr. Bill Berzonsky and Dr. Melanie Caffè will discuss their efforts to improve winter wheat using double haploids. To register for these webinars and learn more about the series, visit <http://www.extension.org/pages/60426>.

To receive announcements about upcoming webinars and PBG-related events, subscribe to pbgnews at <http://pbgworks.org>.

Learn more about the Plant Breeding and Genomics Community of Practice and see how you can get involved by attending the Plant Breeding and Genomics CoP Workshop at PAG in January. The workshop will take place on January 17<sup>th</sup>, 2012 from 2pm to 3pm in the Towne Room of the Town and Country Resort.

## SolCAP Meeting

Garden Salon #2, Town & Country Convention Center, San Diego, California

**January 15, 2012: 8AM –Noon**

- 8:00-8:05am 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*

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<http://solcap.msu.edu>

## Calendar of Events:



**November 28-Dec 1, 2011**, The [SOL & ICuGI 2011](#) joint conference will be held at the Kobe Convention Center, 6-9-1 Minatojima-nakamichi, Chuo-ku, Kobe, Japan.

**December 6-8**, [Great Lakes Fruit, Vegetable and Farm Market EXPO](#) DeVos Place Convention Center, Grand Rapids, MI.

**January 4-6, 2012**, [National Potato Expo](#), Loews Royal Pacific Resort, Orlando, FL.

**January 15, 2012**, Annual SolCAP Meeting and Advisory Board Meeting, 8am– Noon, in Garden Salon #2, Town and Country Resort and Convention Center, San Diego, CA.

**January 17, 2012**, Plant Breeding and Genomics CoP Workshop, 2-3pm, in the Towne Room, Town and Country Resort and Convention Center, San Diego, CA.

**January 14-18, 2012**, [Plant and Animal Genome \(PAG\) Conference](#), Town and Country Resort and Convention Center, San Diego, CA.

**June 3 – 7, 2012**, [The 2012 World Congress on InVitro Biology](#), Bellevue, WA.

**July 20 - 24**, [Plant Biolgy 2012](#), Austin Convention Center, Austin, TX



United States  
Department of  
Agriculture

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