Sol Newsletter

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Editor: Joyce Van Eck

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Community News

SOL 2012
August 26-30, 2012
Neuchâtel, Switzerland
www.sol2012.ch
from the organizing committee

The 9th Solanaceae Conference ***"From the Bench to Innovative Applications"*** will be held at the University of Neuchâtel from August 26th to 30th, 2012.

This year, the national organizing committee has managed to organize 16 scientific sessions chaired by expert scientists in the field of solanaceae plants. Sessions include biodiversity, Ecology to Genetic of Solanaceae. Parallel sessions are organized on different solanaceae species for more specific scientific discussions; moreover a coffee session is back at the SOL meeting. Details are available on the conference website www.sol2012.ch. Pr. Barrett from the University of Toronto, Canada and Dr. Zamir from the The Hebrew University of Jerusalem, Israel will give keynote lectures. We hope this program will give full satisfaction to the participating delegates. A special rate for student registration fees was arranged to encourage young scientists to attend this meeting. Moreover, a few travel grants will be available to help cover travel costs for PhD students.

Above the scientific program, we also dedicate some time to visit Neuchâtel surroundings with an excursion at the "Creux du Van", a typical mountain site with a tremendous view on the Swiss Alps. If you are more attracted by a typical Swiss industry, a visit to the watch museum will be organized. Neuchâtel is a city that is 1000 years old with very nice spots like the castle and its medieval church. A tour of the city will be organized in order to enjoy the history of Neuchâtel. The registration also includes a welcome apéro and a final banquet as well as the lunches and coffee breaks.

We are looking forward to welcome you in Neuchâtel for the SOL 2012.

Release of a Draft Genome Sequence for *Nicotiana benthamiana*

Contributed by Greg Martin
The Boyce Thompson Institute

Scientists at the Boyce Thompson Institute for Plant Research (BTI) have released a draft sequence of the *Nicotiana benthamiana* genome which is accessible through the SGN BLAST tool and can be downloaded from an ftp site (see: http://solgenomics.net/). The project was funded by BTI and National Science Foundation grants IOS-1025642 and IOS-0343327.

N. benthamiana is a widely used model for plant-microbe biology and other research applications. It is particularly useful because it is related to tomato and potato and is amenable to virus-induced gene silencing (VIGS) which facilitates the efficient functional study of plant genes.

The draft sequence of *N. benthamiana* will allow better design of constructs for virus-induced gene-silencing (VIGS) in order to reduce the possibility of 'off-target' gene silencing. The sequence will also be useful for identifying orthologs of tomato and potato genes, for comparative genomics with other Solanaceae species, and for the retrieval of promoter sequences.

Plant Breeding and Genomics Online Resource Reaches Milestone

by Heather Merk
Ohio State University, OARDC

Growth in the global population is placing an increased demand on the world's resources to sustain our society for food, feed, fuel, fiber, and environment, underscoring a need for safe and efficient crop production systems. To date, traditional plant breeding methods have served well to meet increased demands. Projected increases from 7 billion to 9 billion people in the next 40 years will require continued progress. Improvements in the efficiency and cost of DNA sequencing technologies are providing vital information on the genetics and genomics of crop plants. This information is paving the way for new plant breeding strategies to meet global food demands.

Earlier this year, a group of researchers and educators from America's land-grant universities, government agencies, and industry banded together to create the first-ever internet resource aimed at quickly putting basic research on crop genomes into practice. The resource is housed at eXtension (pronounced E-extension) at www.extension.org/plant_breeding_genomics. Less than one year from its launch, the resource reached a milestone of 100,000 views.

Researchers and Extension personnel regularly contribute webinars, videos, informational articles, reviews, blog entries, and tutorials to the resource. The effort is led by the Solanaceae Coordinated Agricultural Project (SolCAP), a USDA National Institute of Food and Agriculture (NIFA)-funded program. SolCAP recruited a community of experts from a wider range of Coordinated Agricultural Projects (CAPs). Members of the Conifer Translational Genomics Network (CTGN) partnered with SolCAP to publish a multi-part series of online learning modules that cover topics from introductory genetics and genomics to the applied use of genomics tools in tree breeding and ecosystem management. Content previously supported by the NIFA funded Barley CAP are now supported by the Institute of Barley and Malting Sciences (IBMS) at North Dakota State University. Other educational materials include modules developed by the Rosaceae CAP (RosBREED), a project funded through NIFA's Specialty Crop Research Initiative.

Plant breeding professionals, researchers, educators, students, and the general public are encouraged to follow development of this resource by subscribing to PBG's newsletter (PBG News) at http://pbgworks.org.

Update on the SOL 100

by Joyce Van Eck
The Boyce Thompson Institute

The SOL 100 initiative was originally described in an article published in the March 2010 issue of the Sol Newsletter (http://solgenomics.net/solanaceae-project/index.pl) and includes the SOL 100 Position Paper. In brief, the overarching goal of this initiative is to generate sequences of 100 different *Solanaceae* genomes, which can then be linked to the reference tomato sequence in order to provide additional resources for studies that involve plant biodiversity, genome conservation and phenotypic diversification.

There is a page on the SOL Genomics Network (SGN) with additional information about the SOL 100 (http://solgenomics.net/organism/sol100/view). In addition, there is also a link with accompanying information on how to submit a SOL 100 genome. Progress on various genomes is also available on this page.

A separate initiative is also underway to coordinate and centralize information related to the sequencing of tomato genotypes beyond Heinz 1706. In January, a meeting was held at the Plant and Animal Genome Conference to discuss the current efforts on Heinz 1706 and additional genotypes. Meeting attendees included plant breeders, members of the International Tomato Sequencing Project, bioinformaticians, and several industry representatives. It was evident from the discussion there is a need for a mechanism for communication related to sequencing other genotypes to reduce redundancy and to make the community aware of resources that exist and can be shared. Once such a mechanism is in place, information will be sent out to the *Solanaceae* community.

Resources

Notice from SolRgene Database

Vivianne G.A.A. Vleeshouwers and Richard Finkers
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SolRgene, an online database to explore disease resistance genes in tuber-bearing Solanum species was made publicly available. The SolRgene database contains data on resistance to *Phytophthora infestans* and presence of R genes and R gene homologues in Solanum section Petota. We have explored Solanum section Petota for resistance to late blight in high throughput disease tests under various laboratory conditions and in field trials. From resistant wild germplasm, segregating populations were generated and assessed for the presence of resistance genes. All these data have been entered into the SolRgene database. To facilitate genetic and resistance gene evolution studies, phylogenetic data of the entire SolRgene collection are included, as well as a tool for generating phylogenetic trees of selected groups of germplasm. Data from resistance gene allele-mining studies are

incorporated, which enables detection of R gene homologs in related germplasm. Using these resources, various resistance genes have been detected and some of these have been cloned, whereas others are in the cloning pipeline. All this information is stored in the online SolRgene database, which allows users to query resistance data, sequences, passport data of the accessions, and phylogenic classifications.

The SolRgene database is freely available at http://www.plantbreeding.wur.nl/SolRgenes.

This work has recently been published as Vleeshouwers, V.G.A.A., Finkers, R., Budding, D.J., Visser, M., Jacobs, M.M.J., van Berloo, R., Pel, M., Champouret, N., Bakker, E., Krenek, P., Rietman, H., Huigen, D.J., Hoekstra, R., Goverse, A., Vosman, B., Jacobsen, E., and Visser, R.G.F. (2011) SolRgene: an online database to explore disease resistance genes in tuber-bearing Solanum species. BMC Plant Biology 2011 11:116. doi:10.1186/1471-2229-11-116

Highlight Article

A RNAi-based genome-wide screen to discover genes involved in resistance to *Tomato yellow leaf curl virus* (TYLCV) in tomato

Henryk Czosnek, Dagan Sade, Rena Gorovits, Favi Vidavski, Hila Beeri, Iris Sobol and Assaf Eybishtz

Institute of Plant Science and Genetics in Agriculture, Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, Rehovot 76100, Israel

Tomato crops are under the threat of diseases caused by the Tomato yellow leaf curl virus (TYLCV) complex (Czosnek, 2007). Breeding for resistance consisted in introgressing resistance found in some wild tomato species into the domesticated tomato (Vidavski et al., 2008). As a result, the resistant tomato contains chromosomal fragments from the wild species on a background of the domesticated tomato, identifiable with polymorphic DNA markers. The discovery of multiple loci associated with TYLCV resistance suggests that resistance is sustained by a multigene interacting network of interconnecting genes and signaling pathways leading to inhibition of virus replication and/or movement and prevention of disease symptoms. Part of this network is likely to originate from the wild tomato genitor.

We are performing a genome-wide TRV-VIGS screen to decipher–the gene network underlying resistance to TYLCV. We are using two inbred tomato lines issued from the same breeding program where *S. habrochaites* provided TYLCV resistance: one was resistant (R), the other was susceptible (S) to the virus. To identify genes involved in resistance to TYLCV ("resistance genes"), we hypothesized that these genes are expressed at higher levels in resistance than in susceptible lines. Further we assumed that if these genes were located at important nodes of the resistance network, silencing them would lead to the collapse of resistance. Sixty nine genes preferentially expressed in R tomatoes were identified by differential screening of cDNA libraries from infected and uninfected R and S tomato plants (Eybishtz et al., 2009). From the twenty genes silenced so far, eight answered to this criterion; they encoded membrane proteins such as permease, transporters, and lipocalin as well as antioxidant enzymes such as thioredoxin peroxidase (Eybishtz et al., 2009, 2010).

To extend the scope of the R-associated genes, an oligonucleotide microarray has been designed (Nimblgen) representing 25,591 known genes and 7,335 uncertain or unknown genes retrieved from TIGR and SGN. The transcriptome of R and S tomato plants, before and after TYLCV infection has been compared. Moreover, the transcriptome of R plants before and after gene silencing allowed us to extend the scope of the signaling pathway and to appraise the hierarchy of the various genes in the resistance network. Sequencing of these genes will allow us to determine whether they have been introgressed from *S. habrochaites*.

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Job Announcements

Multiple Positions with the International Potato Center Headquarters in Lima, Peru

Details may be found at the International Potato Center's website: http://cipotato.org/about-cip/jobs/open-positions

Position Title: Head of the CIP Genebank
Location: Lima, Peru
Start Screening Date: 21 March 2012
Closing Date: open until filled

Position Title: Senior Economist
Location: Lima, Peru
Start Screening Date: 20 March 2012
Closing Date: open until filled

Position Title: Geneticist Abiotic Stress Tolerance
Location: Lima, Peru
Start Screening Date: 19 March 2012
Closing Date: open until filled

Publications

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Conferences and Workshops

Biotechnology & Other Omics in Vegetable Science
April 29 – May 2, 2012
Antalya, Turkey
http://www.biotech-omics.org/web/index.html

10th World Processing Tomato Congress & 12th ISHS Symposium on the Processing Tomato
June 9 - 11, 2012
Beijing, China
http://www.worldtomatocongress.com/

The Potato Association of America
August 12 - 16, 2012
Denver, Colorado
http://www.paa2012.colostate.edu/

SOL 2012 The 9th Solanaceae Conference
August 26 - 30, 2012
Neuchatel, Switzerland
http://www2.unine.ch/sol2012/page-3091.html

21st International Pepper Conference
November 4 – 6, 2012
Naples, Florida
http://www.conference.ifas.ufl.edu/pepper2012/

ASIC 2012
24th International Conference on Coffee Science
November 11 – 16, 2012
San José, Costa Rica
http://www.asic2012costarica.org/

Tomato Breeders Roundtable
February 6 - 8, 2013
Chiang Mai, Thailand
http://www.tbrt2013.com/

Plant Breeding Academies

Plant Breeding Academy at University of California, Davis
September 10 - 15, 2012
February 4 - 9, 2013
June 3 - 8, 2013
http://pba.ucdavis.edu/Programs/PBA_in_Davis_Class_IV/

Plant Breeding Academy in Europe
The schedule for March 2012 to June 2013 is available at
http://pba.ucdavis.edu/PBA_in_Europe/PBA_in_Europe_Class_II/

The Asian Plant Breeding Academy
November 26 – December 1, 2012
Chiang Mai, Thailand
http://pba.ucdavis.edu/PBA_in_Asia/Asian_Plant_Breeding_Academy_Class_I/

Solanaceae Recipes

Eggplant Rolls with Zucchini and Bell Peppers

http://www.foodchannel.com/recipes/recipe/eggplant-rolls-with-zucchini-and-bell-peppers/

Ingredients

1 large (1 1/4 pounds), long (10 inches) eggplant, cut lengthwise into twelve 1/4-inch thick slices
2 tablespoons plus additional extra-virgin olive oil
4 large garlic cloves, minced
1 carrot, peeled, cut into matchstick-sized pieces
1 zucchini, cut into matchstick-sized pieces
1 yellow bell pepper, seeded, thinly sliced
1 1/2 teaspoons ground cumin
1 tomato, seeded, thinly sliced
2 tablespoons fresh lemon juice
2 tablespoons minced fresh cilantro
1 tablespoon minced fresh mint
Fresh cilantro and mint sprigs for garnish

Directions

- Line 2 large baking pans with paper towels. Sprinkle both sides of eggplant slices lightly with salt. Place eggplant on paper towels and let stand until salt draws out water, about 1 hour. Rinse off salt and pat slices dry.
- Preheat broiler or grill. Brush eggplant slices with olive oil. Grill or broil until just golden on both sides and tender, turning once, about 8 minutes. Cool.
- Heat 2 tablespoons olive oil in heavy large skillet over medium heat Add garlic and sauté until fragrant, about 1 minute. Add carrot and sauté until almost tender, about 2 minutes. Toss in zucchini, bell pepper, and cumin and cook until vegetables are crisp-tender, about 5 minutes.
- Remove from heat and stir in tomato, cilantro, and mint. Season to taste with salt and pepper. Cool.
- Place eggplant slices on work surface. Divide vegetable mixture among slices, placing vegetables at narrow end of eggplant slices. Roll up eggplant with colorful vegetables peaking out on each end.
- Transfer to platter, seam side down. Cover with plastic wrap and chill. (Can be prepared 1 day ahead.) Garnish platter with cilantro and mint and serve.

Potato, Greens, and Goat Cheese Quesadillas

http://www.bonappetit.com/recipes

Ingredients

1 1/3 cups 1/2-inch cubes peeled Yukon Gold potatoes (about 2 medium)
2 teaspoons chili powder
1 1/3 cups (packed) coarsely grated hot pepper Monterey Jack cheese (5 to 6 ounces)
1 1/3 cups jarred salsa verde (tomatillo salsa)
4 2/3 cups coarsely chopped stemmed mustard greens (from 1 bunch), divided
4 8-inch-diameter flour tortillas
3 ounces chilled fresh goat cheese, coarsely crumbled
Olive oil

Preparation

- Place baking sheet in oven and preheat to 275°F. Steam potatoes until tender, about 8 minutes. Place in large bowl; sprinkle with salt, pepper, and chili powder. Toss to coat. Cool potatoes 15 minutes. Mix in Jack cheese. Meanwhile, blend salsa and 2/3 cup (packed) greens in mini processor until greens are finely chopped.
- Arrange tortillas on work surface. Divide remaining greens between bottom half of each. Top greens with potato mixture, then goat cheese and 2 tablespoons salsa mixture for each. Fold plain tortilla halves over filling, pressing to compact. Brush with oil.
- Heat large nonstick skillet over medium heat. Place 2 quesadillas, oiled side down, in skillet. Brush tops with oil. Cook until quesadillas are brown, about 3 minutes per side. Transfer to sheet in oven to keep warm. Repeat with remaining 2 quesadillas.
- Cut each quesadilla into 3 or 4 wedges. Serve with remaining salsa.